In [1]:
```
#Gabriel Maldonado ID: 801071135
#Homework #3

#https://github.com/Gmaldonad17/4105-Machine-Learning/tree/main/HW3
```

In [2]:
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
from sklearn.datasets import load_breast_cancer
```

In [3]:
```
#Functions

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

#Scales X variables
def scale_x(raw_x):

    sc_x = StandardScaler()
    scled_x = sc_x.fit_transform(raw_x)
    return scled_x

from sklearn import metrics

def metrics_print(y_pred, y_test):

    print("Accuracy:", metrics.accuracy_score(y_test, y_pred))
    print("Precision:", metrics.precision_score(y_test, y_pred))
    print("Recall:", metrics.recall_score(y_test, y_pred))

from sklearn.metrics import confusion_matrix
import seaborn as sns

#Prints the matrix
def matrix_print(cnf_matrix):

    class_names = [0,1]
    fig, ax = plt.subplots()
    tick_marks = np.arange(len(class_names))
    plt.xticks(tick_marks, class_names)
    plt.yticks(tick_marks, class_names)

    sns.heatmap(pd.DataFrame(cnf_matrix), annot = True, cmap = "YlGnBu", fmt = 'g')
    ax.xaxis.set_label_position("top")
    plt.tight_layout()
    plt.title('Confusion matrix', y=1.1)
    plt.ylabel('Actual label')
    plt.xlabel('Predicted label')

from sklearn.linear_model import LogisticRegression

#Creates and trains log classifer and returns the classifier and matrix evaulation
def log_reg(raw_x, raw_y):

    #Splits the data
    x_train, x_test, y_train, y_test = train_test_split(raw_x, breast.target, test_size
```

```
    #Creates model for Logistic Regression in terms of the data
    classifier = LogisticRegression()
    classifier.fit(x_train, y_train)

    #Scoring for model
    y_pred = classifier.predict(x_test)
    metrics_print(y_pred, y_test)
    #print("Score: ", classifier.score(x_test, y_test))

    #Creates Logistic Regression Confusion Matrix
    matrix = confusion_matrix(y_test, y_pred)
    print("Matrix: \n\n", matrix)

    return classifier, matrix

from sklearn.decomposition import PCA

#Creates PCA based on parameters and returns final data set
def create_pca(scled_x, raw_y, columns, n):

    pca = PCA(n_components = n)
    principalComponents = pca.fit_transform(scled_x)
    principalDf = pd.DataFrame(data = principalComponents, columns = columns)

    finalDf = pd.concat([principalDf, raw_y], axis = 1)
    return finalDf

#Graphcs the first 2 Principal Components
def graph_pca(data):

    fig = plt.figure(figsize = (8,8))
    ax = fig.add_subplot(1,1,1)
    ax.set_xlabel('Principal Component 1', fontsize = 15)
    ax.set_ylabel('Principal Component 2', fontsize = 15)
    ax.set_title('2 component PCA', fontsize = 20)
    targets = ['Malignant','Benign']
    colors = ['r', 'g', 'b']
    for target, color in zip(targets,colors):
        indicesToKeep = pca_y == target
        ax.scatter(data.loc[indicesToKeep, 'principal component 1'], data.loc[indicesTo
    ax.legend(targets)
    ax.grid()
```

In [4]:

```
#Creating useable dataset

#Raw data from the function
breast = load_breast_cancer()
breast_data = breast.data

#Takes the inputs as well as the labels/ Target grabs labels
breast_input = pd.DataFrame(breast_data)
labels = breast.target

#Reshapes the labels in order to place in y-axis
labels = np.reshape(labels,(labels.size,1))
final_breast_data = np.concatenate([breast_data,labels],axis=1)

#DataFrame takes list and set into proper table
```

```
breast_dataset = pd.DataFrame(final_breast_data)

#Creates y-axis labels, adds last label
features_x = breast.feature_names
features_labels = np.append(features_x,'cancer type')
#Benign = 0 | Malignant = 1

#Sets y-axis to colums of the data set
breast_dataset.columns = features_labels

breast_dataset['cancer type'].replace(0, 'Benign',inplace=True)
breast_dataset['cancer type'].replace(1, 'Malignant',inplace=True)
breast_dataset.head()
```

Out[4]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	m fra dimen
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05

5 rows × 31 columns

In [5]:

```
#Seperation of data as well as spliting

raw_x = breast_dataset[features_x]
raw_y = breast_dataset['cancer type']
```

In [6]:

```
#Problem 1: Logistic Regression Model
```

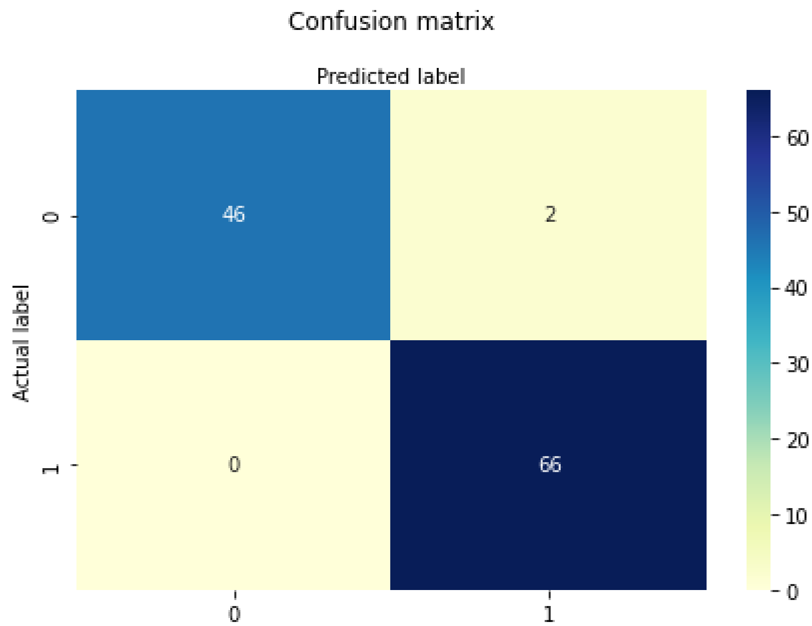
In [7]:

```
scled_x = scale_x(raw_x)

nonPCA_classifier, nonPCA_matrix = log_reg(scled_x, raw_y)
```

```
Accuracy: 0.9824561403508771
Precision: 0.9705882352941176
Recall: 1.0
Matrix:

 [[46  2]
 [ 0 66]]
```

In [8]:

```
matrix_print(nonPCA_matrix)
```



In [9]:

```
#Problem 2
```

In [10]:

```
columns = ['principal component 1', 'principal component 2']
pca_data = create_pca(scled_x, raw_y, columns, 2)
pca_data
```

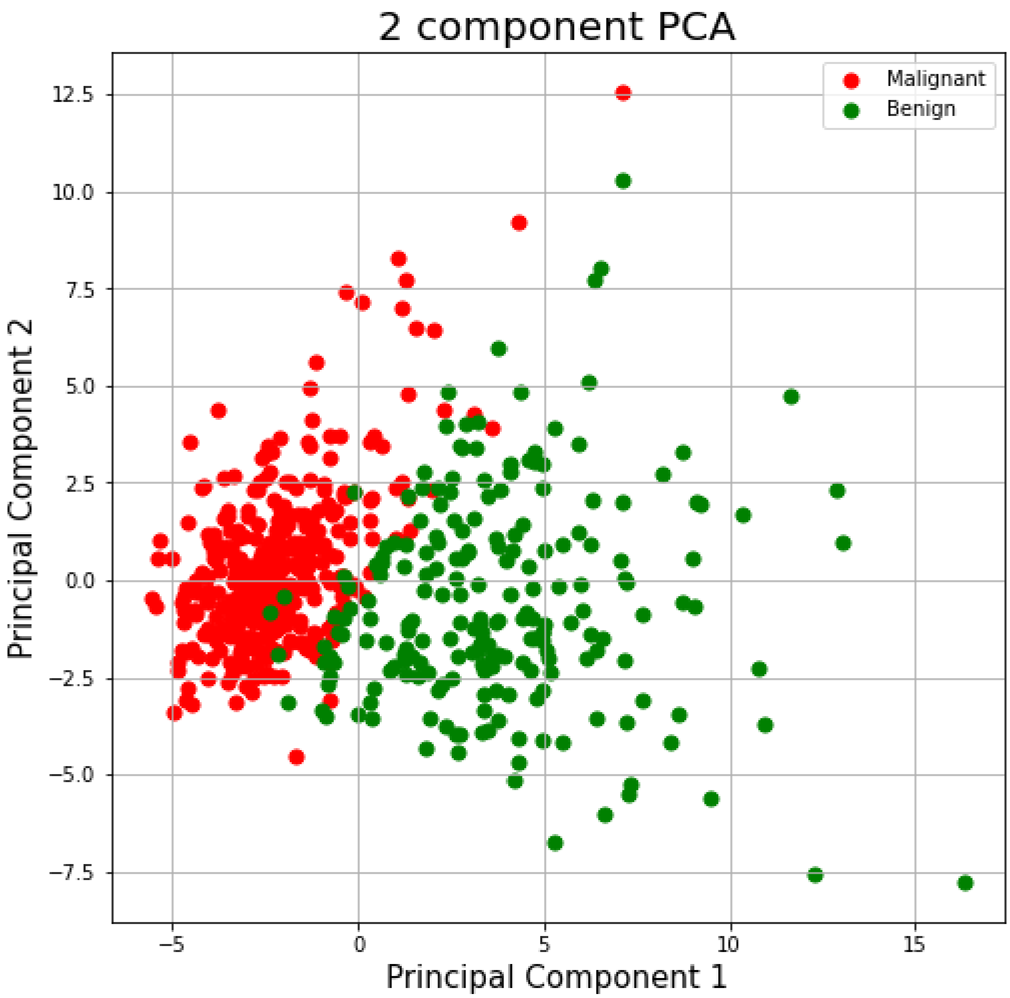
Out[10]:

	principal component 1	principal component 2	cancer type
0	9.192837	1.948583	Benign
1	2.387802	-3.768172	Benign
2	5.733896	-1.075174	Benign
3	7.122953	10.275589	Benign
4	3.935302	-1.948072	Benign
...	...	...	...
564	6.439315	-3.576817	Benign
565	3.793382	-3.584048	Benign
566	1.256179	-1.902297	Benign
567	10.374794	1.672010	Benign
568	-5.475243	-0.670637	Malignant

569 rows × 3 columns

In [11]:

```
pca_x = pca_data[columns]
pca_y = pca_data['cancer type']

graph_pca(pca_data)
```



In [12]:

```
#Two principal components
pca_classifier, pca_matrix = log_reg(pca_x, pca_y)
```

```
Accuracy: 0.9473684210526315
Precision: 0.9166666666666666
Recall: 1.0
Matrix:

 [[42  6]
 [ 0 66]]
```

In [13]:

```
#Three principal components
columns = ['1', '2', '3']
pca_data = create_pca(scled_x, raw_y, columns, 3)

pca_x = pca_data[columns]
pca_y = pca_data['cancer type']

pca_classifier, pca_matrix = log_reg(pca_x, pca_y)
```

```
Accuracy: 0.9385964912280702
Precision: 0.9402985074626866
Recall: 0.9545454545454546
Matrix:

 [[44  4]
 [ 3 63]]
```

In [14]:
```
#Six principal components
columns = ['1', '2', '3', '4', '5','6']
pca_data = create_pca(scled_x, raw_y, columns, 6)

pca_x = pca_data[columns]
pca_y = pca_data['cancer type']

pca_classifier, pca_matrix = log_reg(pca_x, pca_y)
```

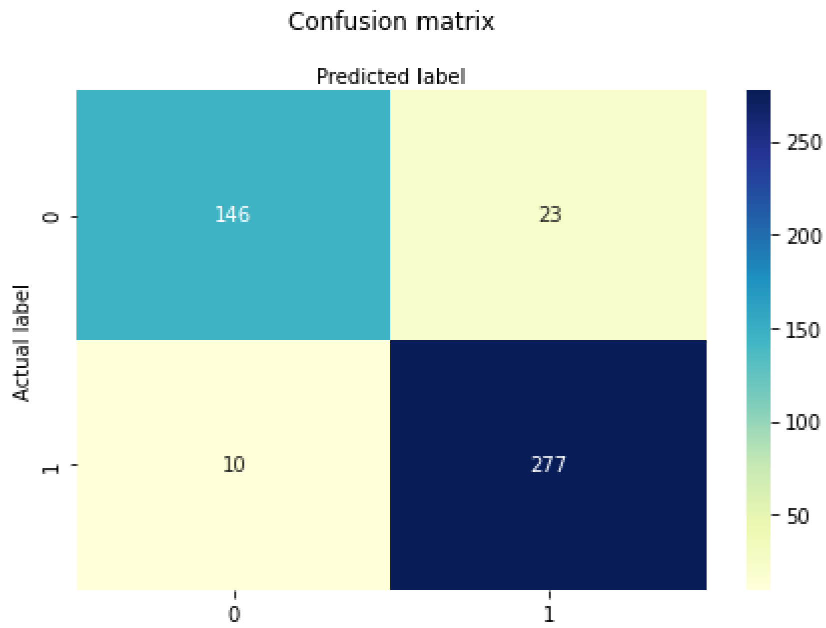
```
Accuracy: 0.9824561403508771
Precision: 0.9705882352941176
Recall: 1.0
Matrix:

 [[46  2]
 [ 0 66]]
```

In [15]:
```
#I will be graphing the increase and then eventual decrease as you increase the pricpal
#I do not have enough time. I tend to like my code to look very neat and that takes a l
#Although this does show how six prinicple compoments can have the same accuracy as 30
```

In [16]:
```
#Problem 3
```

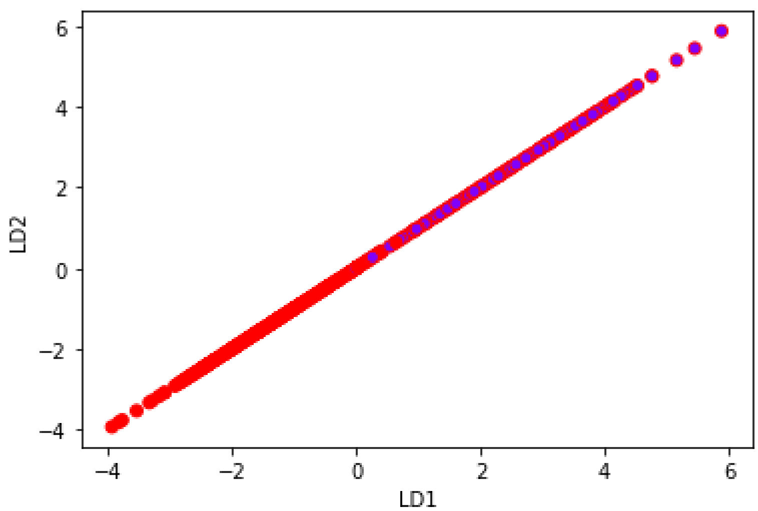
In [26]:
```
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis

LDA = LinearDiscriminantAnalysis(n_components=1)
LDA_t = LDA.fit_transform(breast.data, breast.target)

x_train, x_test, y_train, y_test = train_test_split(breast.data, breast.target, test_si
LDA.fit(x_train, y_train)
y_pred = LDA.predict(x_test)

metrics_print(y_pred, y_test)

lda_matrix = confusion_matrix(y_test, y_pred)

matrix_print(lda_matrix)
```

```
Accuracy: 0.9276315789473685
Precision: 0.9233333333333333
Recall: 0.9651567944250871
```



In [27]:

```
def graph_lda(LDA_t):
    plt.xlabel('LD1')
    plt.ylabel('LD2')
    plt.scatter(LDA_t[:,0],LDA_t[:,0],c=breast.target,cmap='rainbow',edgecolors='r')

graph_lda(LDA_t)
```



In [18]:

```
x_train, x_test, y_train, y_test = train_test_split(breast.data, breast.target, test_si
LDA.fit(x_train, y_train)
y_pred = LDA.predict(x_test)

metrics_print(y_pred, y_test)
```

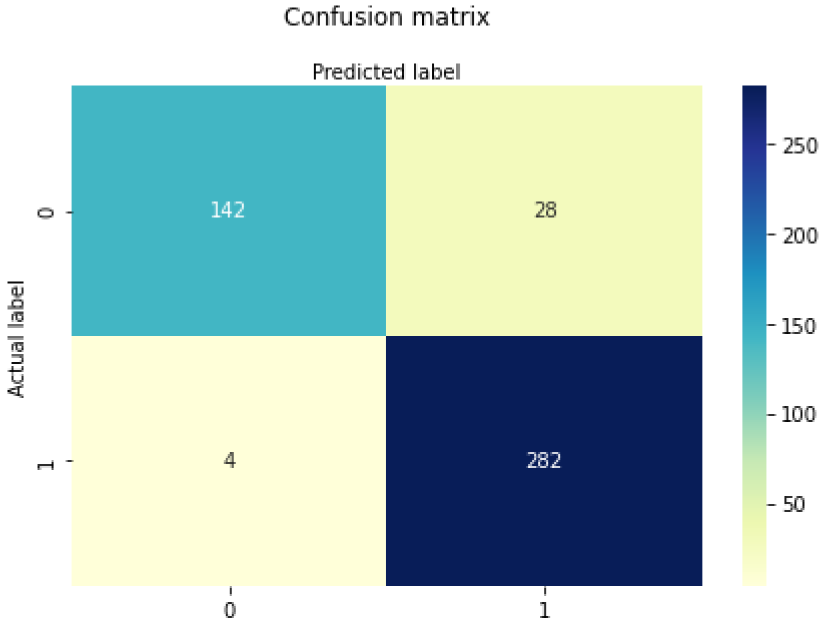
```
Accuracy: 0.9298245614035088
Precision: 0.9096774193548387
Recall: 0.986013986013986
```

In [19]:

```
lda_matrix = confusion_matrix(y_test, y_pred)
lda_matrix
```

Out[19]:
```
array([[142,  28],
       [  4, 282]], dtype=int64)
```

In [20]:
```
matrix_print(lda_matrix)
```



In [ ]: