ECGR_4105_HW3

October 25, 2022

[1]:
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.linear_model import LogisticRegression
from sklearn import datasets
from sklearn.preprocessing import Normalizer
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn import metrics
from sklearn.metrics import confusion_matrix,accuracy_score
from sklearn.metrics import classification_report
from sklearn.datasets import load_breast_cancer
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import precision_recall_curve
```

[2]:
```
cancer = load_breast_cancer()
```

[3]:
```
cancer_data = cancer.data
cancer_data.shape
```

[3]: (569, 30)

[4]:
```
cancer_input = pd.DataFrame(cancer_data)
cancer_input.head()
```

[4]:
```
       0      1       2       3        4        5       6        7       8   \
0  17.99  10.38  122.80  1001.0  0.11840  0.27760  0.3001  0.14710  0.2419
1  20.57  17.77  132.90  1326.0  0.08474  0.07864  0.0869  0.07017  0.1812
2  19.69  21.25  130.00  1203.0  0.10960  0.15990  0.1974  0.12790  0.2069
3  11.42  20.38   77.58   386.1  0.14250  0.28390  0.2414  0.10520  0.2597
4  20.29  14.34  135.10  1297.0  0.10030  0.13280  0.1980  0.10430  0.1809

        9   …     20     21      22      23      24      25      26      27  \
0  0.07871  …  25.38  17.33  184.60  2019.0  0.1622  0.6656  0.7119  0.2654
1  0.05667  …  24.99  23.41  158.80  1956.0  0.1238  0.1866  0.2416  0.1860
```

```
2  0.05999  …  23.57  25.53  152.50  1709.0  0.1444  0.4245  0.4504  0.2430
3  0.09744  …  14.91  26.50   98.87   567.7  0.2098  0.8663  0.6869  0.2575
4  0.05883  …  22.54  16.67  152.20  1575.0  0.1374  0.2050  0.4000  0.1625

       28       29
0  0.4601  0.11890
1  0.2750  0.08902
2  0.3613  0.08758
3  0.6638  0.17300
4  0.2364  0.07678

[5 rows x 30 columns]
```

[5]:
```
cancer_labels = cancer.target
```

[6]:
```
cancer_labels.shape
```

[6]:
```
(569,)
```

[7]:
```
labels = np.reshape(cancer_labels, (569,1))
```

[8]:
```
final_cancer_data = np.concatenate([cancer_data,labels],axis=1)
```

[9]:
```
final_cancer_data.shape
```

[9]:
```
(569, 31)
```

[10]:
```
cancer_dataset = pd.DataFrame(final_cancer_data)
```

[11]:
```
features = cancer.feature_names
features
```

[11]:
```
array(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
       'mean smoothness', 'mean compactness', 'mean concavity',
       'mean concave points', 'mean symmetry', 'mean fractal dimension',
       'radius error', 'texture error', 'perimeter error', 'area error',
       'smoothness error', 'compactness error', 'concavity error',
       'concave points error', 'symmetry error',
       'fractal dimension error', 'worst radius', 'worst texture',
       'worst perimeter', 'worst area', 'worst smoothness',
       'worst compactness', 'worst concavity', 'worst concave points',
       'worst symmetry', 'worst fractal dimension'], dtype='<U23')
```

[12]:
```
features_labels = np.append(features, 'label')
```

[13]:
```
cancer_dataset.columns = features_labels
```

[14]:
```
cancer_dataset.head()
```

[14]:

```
   mean radius  mean texture  mean perimeter  mean area  mean smoothness  \
0        17.99         10.38          122.80     1001.0          0.11840
1        20.57         17.77          132.90     1326.0          0.08474
2        19.69         21.25          130.00     1203.0          0.10960
3        11.42         20.38           77.58      386.1          0.14250
4        20.29         14.34          135.10     1297.0          0.10030

   mean compactness  mean concavity  mean concave points  mean symmetry  \
0           0.27760          0.3001              0.14710         0.2419
1           0.07864          0.0869              0.07017         0.1812
2           0.15990          0.1974              0.12790         0.2069
3           0.28390          0.2414              0.10520         0.2597
4           0.13280          0.1980              0.10430         0.1809

   mean fractal dimension  …  worst texture  worst perimeter  worst area  \
0                 0.07871  …          17.33           184.60      2019.0
1                 0.05667  …          23.41           158.80      1956.0
2                 0.05999  …          25.53           152.50      1709.0
3                 0.09744  …          26.50            98.87       567.7
4                 0.05883  …          16.67           152.20      1575.0

   worst smoothness  worst compactness  worst concavity  worst concave points  \
0            0.1622             0.6656           0.7119                0.2654
1            0.1238             0.1866           0.2416                0.1860
2            0.1444             0.4245           0.4504                0.2430
3            0.2098             0.8663           0.6869                0.2575
4            0.1374             0.2050           0.4000                0.1625

   worst symmetry  worst fractal dimension  label
0          0.4601                  0.11890    0.0
1          0.2750                  0.08902    0.0
2          0.3613                  0.08758    0.0
3          0.6638                  0.17300    0.0
4          0.2364                  0.07678    0.0

[5 rows x 31 columns]
```

[15]:

```
cancer_dataset['label'].replace(0, 'Benign', inplace=True)
cancer_dataset['label'].replace(1, 'Malignant', inplace=True)
```

[16]:

```
cancer_dataset.tail()
```

[16]:

```
     mean radius  mean texture  mean perimeter  mean area  mean smoothness  \
564        21.56         22.39          142.00     1479.0          0.11100
565        20.13         28.25          131.20     1261.0          0.09780
566        16.60         28.08          108.30      858.1          0.08455
567        20.60         29.33          140.10     1265.0          0.11780
```

```
568          7.76          24.54             47.92      181.0            0.05263

     mean compactness  mean concavity  mean concave points  mean symmetry  \
564           0.11590         0.24390              0.13890         0.1726
565           0.10340         0.14400              0.09791         0.1752
566           0.10230         0.09251              0.05302         0.1590
567           0.27700         0.35140              0.15200         0.2397
568           0.04362         0.00000              0.00000         0.1587

     mean fractal dimension  …  worst texture  worst perimeter  worst area  \
564                 0.05623  …          26.40           166.10      2027.0
565                 0.05533  …          38.25           155.00      1731.0
566                 0.05648  …          34.12           126.70      1124.0
567                 0.07016  …          39.42           184.60      1821.0
568                 0.05884  …          30.37            59.16       268.6

     worst smoothness  worst compactness  worst concavity  \
564           0.14100            0.21130           0.4107
565           0.11660            0.19220           0.3215
566           0.11390            0.30940           0.3403
567           0.16500            0.86810           0.9387
568           0.08996            0.06444           0.0000

     worst concave points  worst symmetry  worst fractal dimension      label
564                0.2216          0.2060                  0.07115     Benign
565                0.1628          0.2572                  0.06637     Benign
566                0.1418          0.2218                  0.07820     Benign
567                0.2650          0.4087                  0.12400     Benign
568                0.0000          0.2871                  0.07039  Malignant

[5 rows x 31 columns]
```

[17]:
```
cancer_X = cancer_dataset.iloc[:,0:29].values
cancer_Y = cancer_dataset.iloc[:,30].values
```

[18]:
```
cancer_X_train, cancer_X_test, cancer_Y_train, cancer_Y_test =␣
 ↪train_test_split(cancer_X, cancer_Y, test_size=0.2, random_state=42)
```

[19]:
```
sc_X = StandardScaler()
cancer_X_trainstd = sc_X.fit_transform(cancer_X_train)
cancer_X_teststd = sc_X.transform(cancer_X_test)
```

[20]:
```
BayesClass = GaussianNB()
```

[21]:
```
BayesClass.fit(cancer_X_trainstd, cancer_Y_train)
print(BayesClass)
```

```
GaussianNB()
```

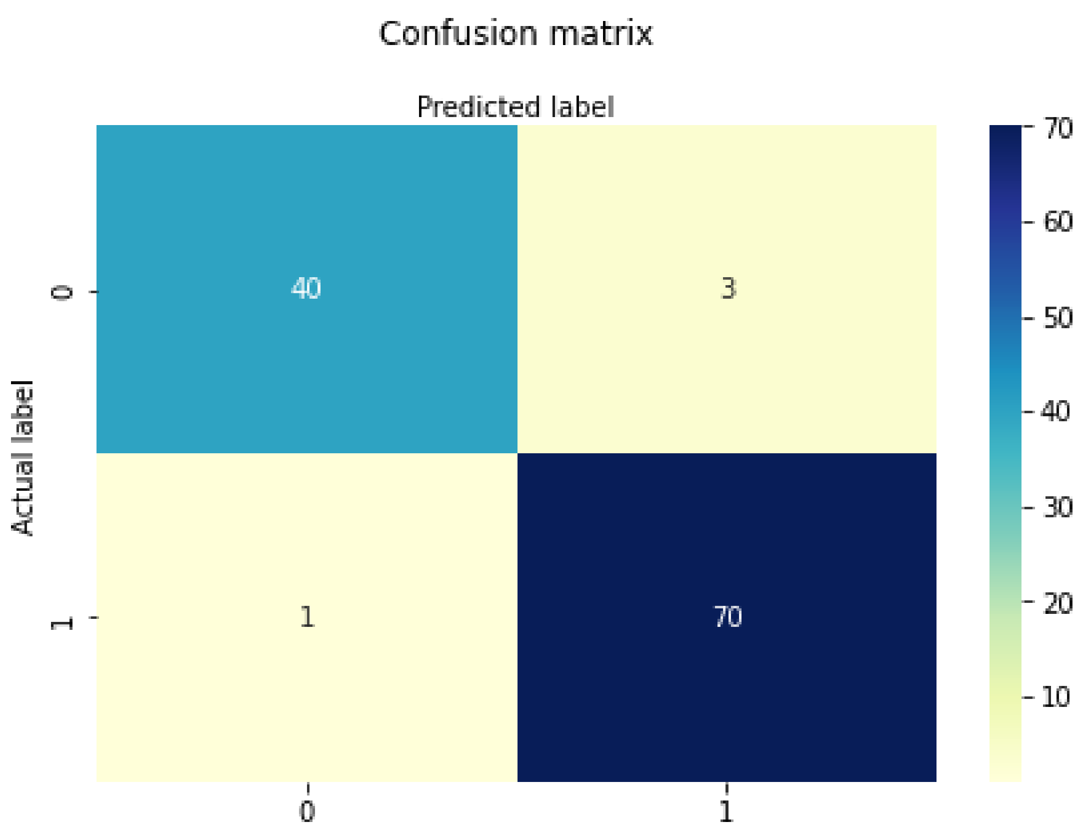
[22]:
```
cancer_Y_pred = BayesClass.predict(cancer_X_teststd)
```

[23]:
```
cancer_Y_pred[0:9]
```

[23]:
```
array(['Malignant', 'Benign', 'Benign', 'Malignant', 'Malignant',
       'Benign', 'Benign', 'Benign', 'Benign'], dtype='<U9')
```

[24]:
```
cancer_cnf_matrix = confusion_matrix(cancer_Y_test, cancer_Y_pred)
cancer_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(cancer_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')
```

[24]:
```
Text(0.5, 257.44, 'Predicted label')
```



[25]:
```
print("Accuracy:",metrics.accuracy_score(cancer_Y_test, cancer_Y_pred))
print("Precision:",metrics.precision_score(cancer_Y_test, cancer_Y_pred,␣
 ↪pos_label="Benign"))
print("Recall:",metrics.recall_score(cancer_Y_test, cancer_Y_pred,␣
 ↪pos_label="Benign"))
```

```
Accuracy: 0.9649122807017544
Precision: 0.975609756097561
Recall: 0.9302325581395349
```

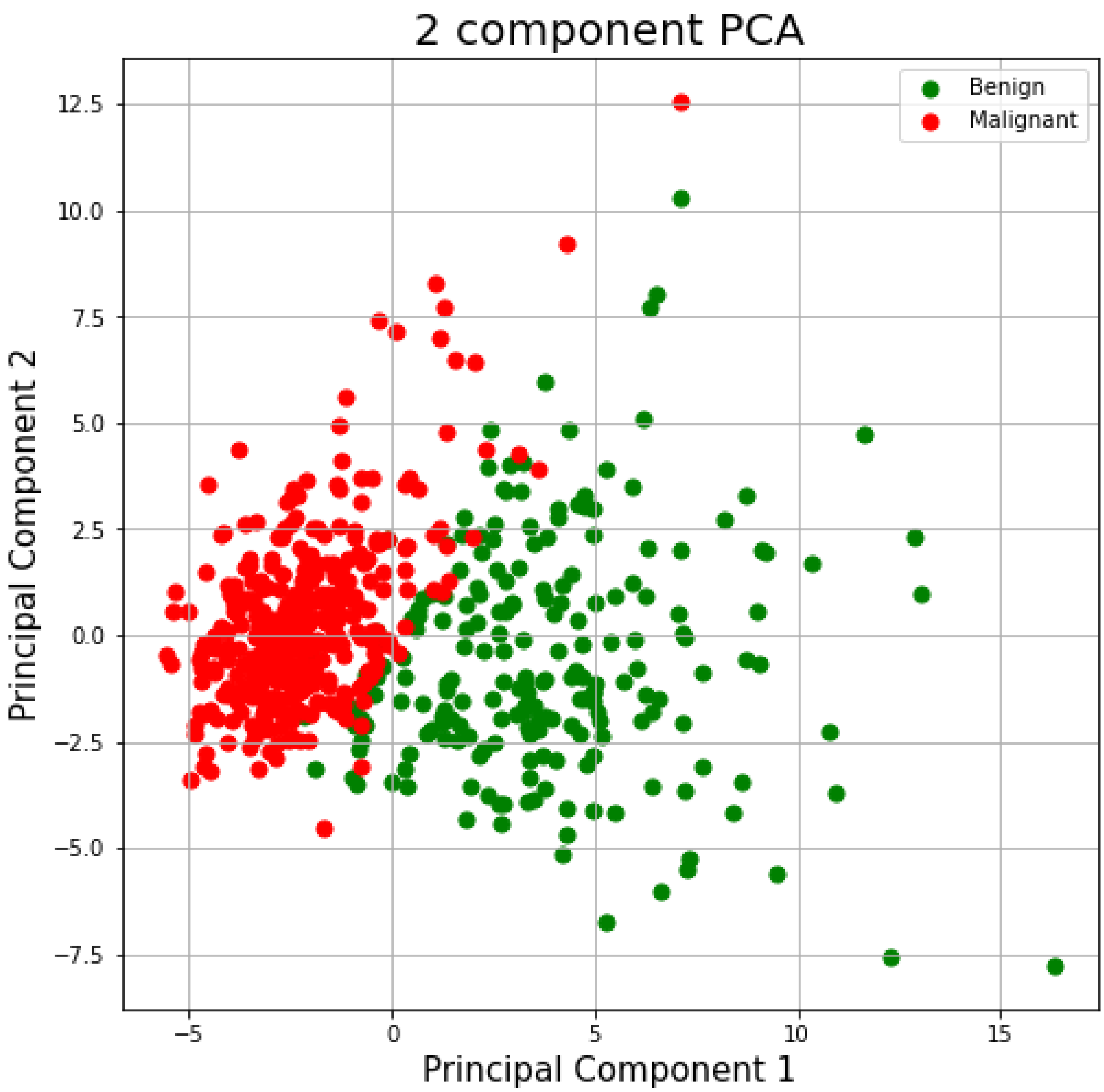
[26]:
```
features = ['mean radius', 'mean texture', 'mean perimeter', 'mean area',
       'mean smoothness', 'mean compactness', 'mean concavity',
       'mean concave points', 'mean symmetry', 'mean fractal dimension',
       'radius error', 'texture error', 'perimeter error', 'area error',
       'smoothness error', 'compactness error', 'concavity error',
       'concave points error', 'symmetry error',
       'fractal dimension error', 'worst radius', 'worst texture',
       'worst perimeter', 'worst area', 'worst smoothness',
       'worst compactness', 'worst concavity', 'worst concave points',
       'worst symmetry', 'worst fractal dimension']

x = cancer_dataset.loc[:, features].values
y = cancer_dataset.loc[:,['label']].values
x = StandardScaler().fit_transform(x)
```

[27]:
```
from sklearn.decomposition import PCA
pca = PCA(n_components=2)
principalComponents = pca.fit_transform(x)
principalDf = pd.DataFrame(data = principalComponents, columns = ['principal␣
 ↪component 1','principal component 2'])
```

[28]:
```
finalDf = pd.concat([principalDf, cancer_dataset[['label']]], axis = 1)
```

[29]:
```
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 = ['Benign', 'Malignant']
colors = ['g', 'r']
for target, color in zip(targets,colors):
    indicesToKeep = finalDf['label'] == target
    ax.scatter(finalDf.loc[indicesToKeep, 'principal component 1']
               , finalDf.loc[indicesToKeep, 'principal component 2']
               , c = color
               , s = 50)
```

```
ax.legend(targets)
ax.grid()
```



[30]:

```
Log_Model = LogisticRegression()
columns = []
LogPCAaccuracy = np.zeros(30)
LogPCAPrecision = np.zeros(30)
LogPCARecall = np.zeros(30)
for i in range(1,30):
    pca = PCA(n_components=i)
    columns = np.append(columns, ['principal component ' + str(i)])
    columns = list(columns)
    principalComponentstrain = pca.fit_transform(cancer_X_trainstd)
```

```python
    principalDftrain = pd.DataFrame(data = principalComponentstrain, columns = columns)

    finalDftrain = pd.concat([principalDftrain, cancer_dataset[['label']]], axis = 1)
    principalComponentstest = pca.fit_transform(cancer_X_teststd)
    principalDftest = pd.DataFrame(data = principalComponentstest, columns = columns)
    finalDftest = pd.concat([principalDftest, cancer_dataset[['label']]], axis = 1)
    Log_Model_train = Log_Model.fit(principalDftrain.values, cancer_Y_train)
    cancer_Y_predPCA = Log_Model_train.predict(principalDftest.values)
    print("Accuracy " + str(i) + ":",metrics.accuracy_score(cancer_Y_test, cancer_Y_predPCA))
    LogPCAaccuracy[i] = metrics.accuracy_score(cancer_Y_test, cancer_Y_predPCA)
    print("Precision " + str(i) + ":", metrics.precision_score(cancer_Y_test, cancer_Y_predPCA, pos_label="Benign"))
    LogPCAPrecision[i] = metrics.precision_score(cancer_Y_test, cancer_Y_predPCA, pos_label="Benign")
    print("Recall " + str(i) + ":",metrics.recall_score(cancer_Y_test, cancer_Y_predPCA, pos_label="Benign"))
    LogPCARecall[i] = metrics.recall_score(cancer_Y_test, cancer_Y_predPCA, pos_label="Benign")
    columns = np.array(columns)
```

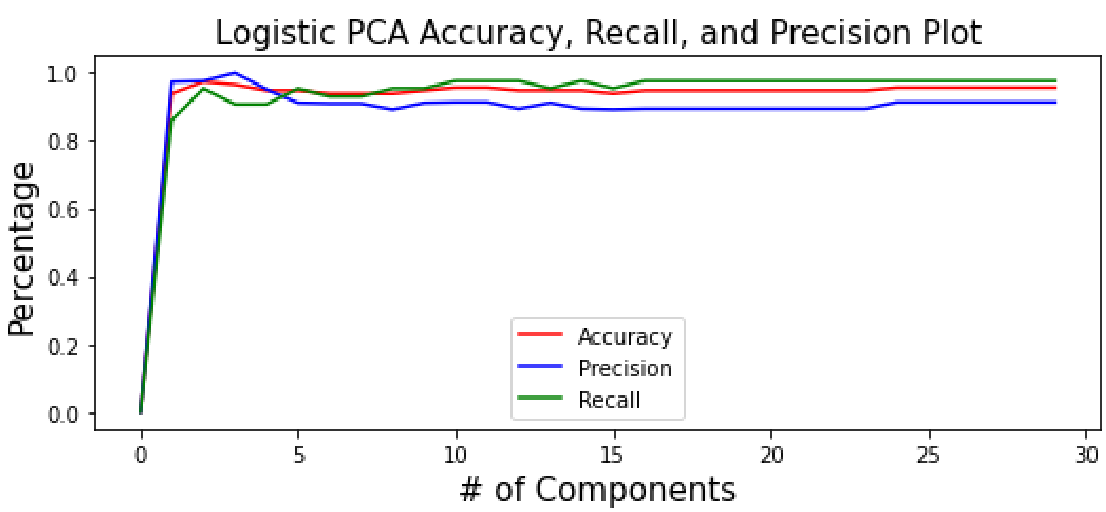
```
Accuracy 1: 0.9385964912280702
Precision 1: 0.9736842105263158
Recall 1: 0.8604651162790697
Accuracy 2: 0.9736842105263158
Precision 2: 0.9761904761904762
Recall 2: 0.9534883720930233
Accuracy 3: 0.9649122807017544
Precision 3: 1.0
Recall 3: 0.9069767441860465
Accuracy 4: 0.9473684210526315
Precision 4: 0.9512195121951219
Recall 4: 0.9069767441860465
Accuracy 5: 0.9473684210526315
Precision 5: 0.9111111111111111
Recall 5: 0.9534883720930233
Accuracy 6: 0.9385964912280702
Precision 6: 0.9090909090909091
Recall 6: 0.9302325581395349
Accuracy 7: 0.9385964912280702
Precision 7: 0.9090909090909091
Recall 7: 0.9302325581395349
Accuracy 8: 0.9385964912280702
```

```
Precision 8: 0.8913043478260869
Recall 8: 0.9534883720930233
Accuracy 9: 0.9473684210526315
Precision 9: 0.9111111111111111
Recall 9: 0.9534883720930233
Accuracy 10: 0.956140350877193
Precision 10: 0.9130434782608695
Recall 10: 0.9767441860465116
Accuracy 11: 0.956140350877193
Precision 11: 0.9130434782608695
Recall 11: 0.9767441860465116
Accuracy 12: 0.9473684210526315
Precision 12: 0.8936170212765957
Recall 12: 0.9767441860465116
Accuracy 13: 0.9473684210526315
Precision 13: 0.9111111111111111
Recall 13: 0.9534883720930233
Accuracy 14: 0.9473684210526315
Precision 14: 0.8936170212765957
Recall 14: 0.9767441860465116
Accuracy 15: 0.9385964912280702
Precision 15: 0.8913043478260869
Recall 15: 0.9534883720930233
Accuracy 16: 0.9473684210526315
Precision 16: 0.8936170212765957
Recall 16: 0.9767441860465116
Accuracy 17: 0.9473684210526315
Precision 17: 0.8936170212765957
Recall 17: 0.9767441860465116
Accuracy 18: 0.9473684210526315
Precision 18: 0.8936170212765957
Recall 18: 0.9767441860465116
Accuracy 19: 0.9473684210526315
Precision 19: 0.8936170212765957
Recall 19: 0.9767441860465116
Accuracy 20: 0.9473684210526315
Precision 20: 0.8936170212765957
Recall 20: 0.9767441860465116
Accuracy 21: 0.9473684210526315
Precision 21: 0.8936170212765957
Recall 21: 0.9767441860465116
Accuracy 22: 0.9473684210526315
Precision 22: 0.8936170212765957
Recall 22: 0.9767441860465116
Accuracy 23: 0.9473684210526315
Precision 23: 0.8936170212765957
Recall 23: 0.9767441860465116
Accuracy 24: 0.956140350877193
```

```
Precision 24: 0.9130434782608695
Recall 24: 0.9767441860465116
Accuracy 25: 0.956140350877193
Precision 25: 0.9130434782608695
Recall 25: 0.9767441860465116
Accuracy 26: 0.956140350877193
Precision 26: 0.9130434782608695
Recall 26: 0.9767441860465116
Accuracy 27: 0.956140350877193
Precision 27: 0.9130434782608695
Recall 27: 0.9767441860465116
Accuracy 28: 0.956140350877193
Precision 28: 0.9130434782608695
Recall 28: 0.9767441860465116
Accuracy 29: 0.956140350877193
Precision 29: 0.9130434782608695
Recall 29: 0.9767441860465116
```

[31]:

```
plt.rcParams["figure.figsize"] = [7.50, 3.50]
plt.rcParams["figure.autolayout"] = True
x = np.array(range(0,30))
y = LogPCAaccuracy
z = LogPCAPrecision
v = LogPCARecall
plt.title("Logistic PCA Accuracy, Recall, and Precision Plot", fontsize = 15)
plt.plot(x, y, color="red", label="Accuracy")
plt.plot(x, z, color="blue", label="Precision")
plt.plot(x, v, color="green", label="Recall")
plt.xlabel('# of Components', fontsize = 15)
plt.ylabel('Percentage', fontsize = 15)
leg = plt.legend(loc = 'lower center')
plt.show()
```



[32]:
```
columns = []
BayesPCAaccuracy = np.zeros(30)
BayesPCAPrecision = np.zeros(30)
BayesPCARecall = np.zeros(30)
for i in range(1,30):
    pca = PCA(n_components=i)
    columns = np.append(columns, ['principal component ' + str(i)])
    columns = list(columns)
    principalComponentstrain = pca.fit_transform(cancer_X_trainstd)
    principalDftrain = pd.DataFrame(data = principalComponentstrain, columns =␣
 ↪columns)

    finalDftrain = pd.concat([principalDftrain, cancer_dataset[['label']]],␣
 ↪axis = 1)
    principalComponentstest = pca.fit_transform(cancer_X_teststd)
    principalDftest = pd.DataFrame(data = principalComponentstest, columns =␣
 ↪columns)
    finalDftest = pd.concat([principalDftest, cancer_dataset[['label']]], axis␣
 ↪= 1)
    Bayes_Model_train = BayesClass.fit(principalDftrain.values, cancer_Y_train)
    cancer_Y_predPCA = Bayes_Model_train.predict(principalDftest.values)
    print("Accuracy " + str(i) + ":",metrics.accuracy_score(cancer_Y_test,␣
 ↪cancer_Y_predPCA))
    BayesPCAaccuracy[i] = metrics.accuracy_score(cancer_Y_test,␣
 ↪cancer_Y_predPCA)
    print("Precision " + str(i) + ":", metrics.precision_score(cancer_Y_test,␣
 ↪cancer_Y_predPCA, pos_label="Benign"))
    BayesPCAPrecision[i] = metrics.precision_score(cancer_Y_test,␣
 ↪cancer_Y_predPCA, pos_label="Benign")
    print("Recall " + str(i) + ":",metrics.recall_score(cancer_Y_test,␣
 ↪cancer_Y_predPCA, pos_label="Benign"))
    BayesPCARecall[i] = metrics.recall_score(cancer_Y_test, cancer_Y_predPCA,␣
 ↪pos_label="Benign")
    columns = np.array(columns)
```

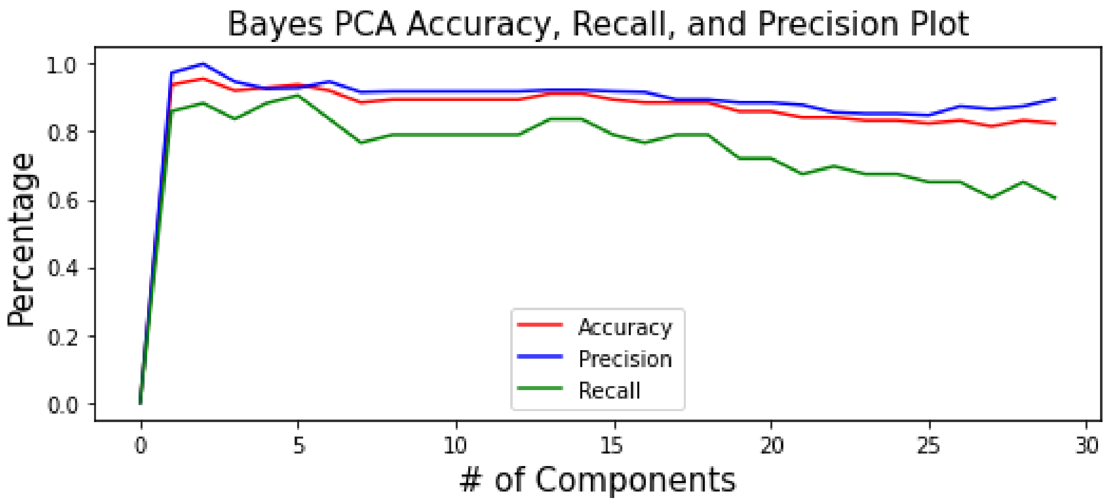
```
Accuracy 1: 0.9385964912280702
Precision 1: 0.9736842105263158
Recall 1: 0.8604651162790697
Accuracy 2: 0.956140350877193
Precision 2: 1.0
Recall 2: 0.8837209302325582
Accuracy 3: 0.9210526315789473
Precision 3: 0.9473684210526315
Recall 3: 0.8372093023255814
```

```
Accuracy 4: 0.9298245614035088
Precision 4: 0.926829268292683
Recall 4: 0.8837209302325582
Accuracy 5: 0.9385964912280702
Precision 5: 0.9285714285714286
Recall 5: 0.9069767441860465
Accuracy 6: 0.9210526315789473
Precision 6: 0.9473684210526315
Recall 6: 0.8372093023255814
Accuracy 7: 0.8859649122807017
Precision 7: 0.9166666666666666
Recall 7: 0.7674418604651163
Accuracy 8: 0.8947368421052632
Precision 8: 0.918918918918919
Recall 8: 0.7906976744186046
Accuracy 9: 0.8947368421052632
Precision 9: 0.918918918918919
Recall 9: 0.7906976744186046
Accuracy 10: 0.8947368421052632
Precision 10: 0.918918918918919
Recall 10: 0.7906976744186046
Accuracy 11: 0.8947368421052632
Precision 11: 0.918918918918919
Recall 11: 0.7906976744186046
Accuracy 12: 0.8947368421052632
Precision 12: 0.918918918918919
Recall 12: 0.7906976744186046
Accuracy 13: 0.9122807017543859
Precision 13: 0.9230769230769231
Recall 13: 0.8372093023255814
Accuracy 14: 0.9122807017543859
Precision 14: 0.9230769230769231
Recall 14: 0.8372093023255814
Accuracy 15: 0.8947368421052632
Precision 15: 0.918918918918919
Recall 15: 0.7906976744186046
Accuracy 16: 0.8859649122807017
Precision 16: 0.9166666666666666
Recall 16: 0.7674418604651163
Accuracy 17: 0.8859649122807017
Precision 17: 0.8947368421052632
Recall 17: 0.7906976744186046
Accuracy 18: 0.8859649122807017
Precision 18: 0.8947368421052632
Recall 18: 0.7906976744186046
Accuracy 19: 0.8596491228070176
Precision 19: 0.8857142857142857
Recall 19: 0.7209302325581395
```

```
Accuracy 20: 0.8596491228070176
Precision 20: 0.8857142857142857
Recall 20: 0.7209302325581395
Accuracy 21: 0.8421052631578947
Precision 21: 0.8787878787878788
Recall 21: 0.6744186046511628
Accuracy 22: 0.8421052631578947
Precision 22: 0.8571428571428571
Recall 22: 0.6976744186046512
Accuracy 23: 0.8333333333333334
Precision 23: 0.8529411764705882
Recall 23: 0.6744186046511628
Accuracy 24: 0.8333333333333334
Precision 24: 0.8529411764705882
Recall 24: 0.6744186046511628
Accuracy 25: 0.8245614035087719
Precision 25: 0.8484848484848485
Recall 25: 0.6511627906976745
Accuracy 26: 0.8333333333333334
Precision 26: 0.875
Recall 26: 0.6511627906976745
Accuracy 27: 0.8157894736842105
Precision 27: 0.8666666666666667
Recall 27: 0.6046511627906976
Accuracy 28: 0.8333333333333334
Precision 28: 0.875
Recall 28: 0.6511627906976745
Accuracy 29: 0.8245614035087719
Precision 29: 0.896551724137931
Recall 29: 0.6046511627906976
```

[33]:

```
plt.rcParams["figure.figsize"] = [7.50, 3.50]
plt.rcParams["figure.autolayout"] = True
x = np.array(range(0,30))
y = BayesPCAaccuracy
z = BayesPCAPrecision
v = BayesPCARecall
plt.title("Bayes PCA Accuracy, Recall, and Precision Plot", fontsize = 15)
plt.plot(x, y, color="red", label="Accuracy")
plt.plot(x, z, color="blue", label="Precision")
plt.plot(x, v, color="green", label="Recall")
plt.xlabel('# of Components', fontsize = 15)
plt.ylabel('Percentage', fontsize = 15)
leg = plt.legend(loc = 'lower center')
plt.show()
```



Bayes PCA Accuracy, Recall, and Precision Plot
Percentage
# of Components
Accuracy
Precision
Recall
1.0
0.8
0.6
0.4
0.2
0.0
0
5
10
15
20
25
30


```
[ ]:
```