Capstone_project

October 16, 2022

[1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

[2]:
```
theWholeData =pd.read_csv(r'E:\Data_Analysis\PG DS - Capstone\Healthcare -␣
↪Diabetes\diabetes.csv')
```

[3]:
```
theWholeData.describe()
```

[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	\
count	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	
std	3.369578	31.972618	19.355807	15.952218	115.244002	
min	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	

	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000
mean	31.992578	0.471876	33.240885	0.348958
std	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.078000	21.000000	0.000000
25%	27.300000	0.243750	24.000000	0.000000
50%	32.000000	0.372500	29.000000	0.000000
75%	36.600000	0.626250	41.000000	1.000000
max	67.100000	2.420000	81.000000	1.000000

[4]:
```
theWholeData.isnull().values.any()
```

[4]:
```
False
```

[5]:
```
med_val_bloodpressure = theWholeData['BloodPressure'].median()
count = (theWholeData['BloodPressure'] ==0).sum()
count
```

[5]: 35

[6]:
```
theWholeData['BloodPressure'] = theWholeData['BloodPressure'].replace(0,␣
↪med_val_bloodpressure)
#␣
↪=============================================================================================
```

[7]:
```
med_val_glucose = theWholeData['Glucose'].median()
count = (theWholeData['Glucose'] ==0).sum()
count
```

[7]: 5

[8]:
```
theWholeData['Glucose'] = theWholeData['Glucose'].replace(0, med_val_glucose)
# ================================================================================
```

[9]:
```
med_val_SkinThickness = theWholeData['SkinThickness'].median()
count = (theWholeData['SkinThickness'] ==0).sum()
count
```

[9]: 227

[10]:
```
theWholeData['SkinThickness'] = theWholeData['SkinThickness'].replace(0,␣
↪med_val_SkinThickness)
#␣
↪=============================================================================================
```

[11]:
```
med_val_BMI = theWholeData['BMI'].median()
count = (theWholeData['BMI'] ==0).sum()
count
```

[11]: 11

[12]:
```
theWholeData['BMI'] = theWholeData['BMI'].replace(0, med_val_BMI)
# ================================================================
```

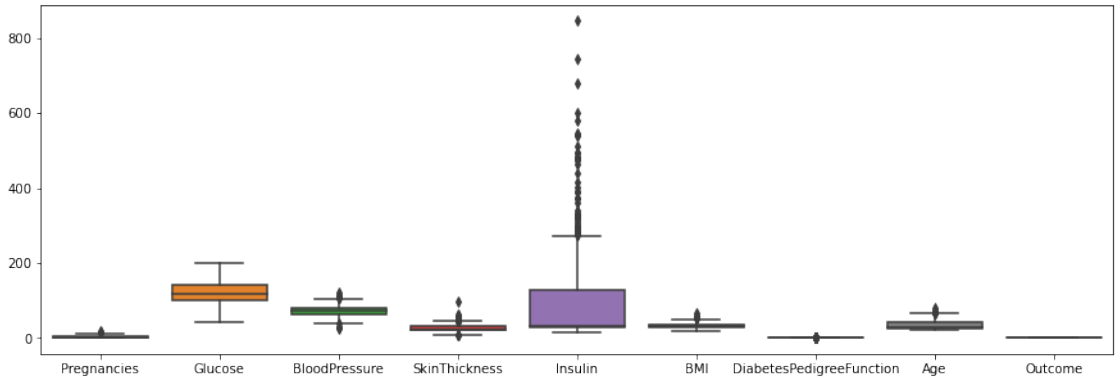
[13]:
```
med_val_Insulin = theWholeData['Insulin'].median()
count = (theWholeData['Insulin'] ==0).sum()
count
```

[13]: 374

[14]:
```
theWholeData['Insulin'] = theWholeData['Insulin'].replace(0, med_val_Insulin)
# ================================================================
```

[15]:
```
fig = plt.figure(figsize = (15,5))
sns.boxplot(data = theWholeData)
```

[15]: <AxesSubplot:>

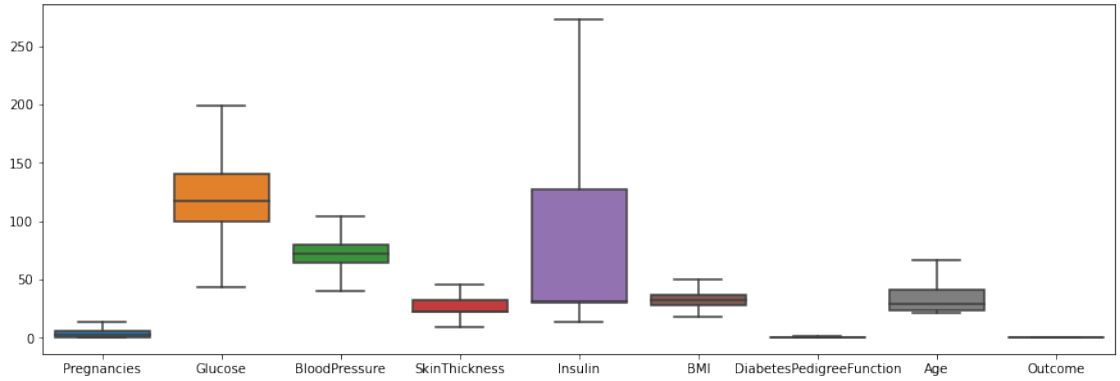


[16]:
```
def Outlier(data, cols):
    for column in data.drop(cols, axis=1).columns:
        if data[column].dtype != object:
            Q1 = np.percentile(data[column],25)
            Q3 = np.percentile(data[column],75)
            IQR =  Q3 - Q1
            lower = Q1 - (1.5 * IQR) # min value allowed
            upper = Q3 + (1.5 * IQR)  # max. value allowed

            data[column] = data[column].apply(lambda x: upper if x>upper else ␣
 ↪lower if x<lower else x)

    return data

df = Outlier(data = theWholeData, cols = ['Outcome'])
df.columns
```

[16]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

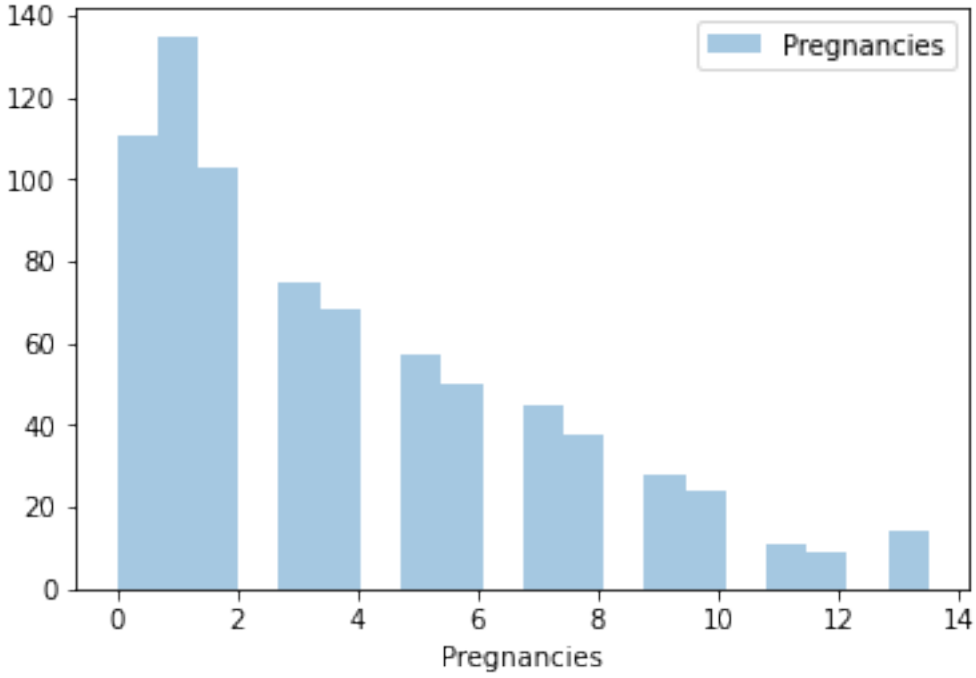
[17]:
```
fig = plt.figure(figsize = (15,5))
sns.boxplot(data = df)
```

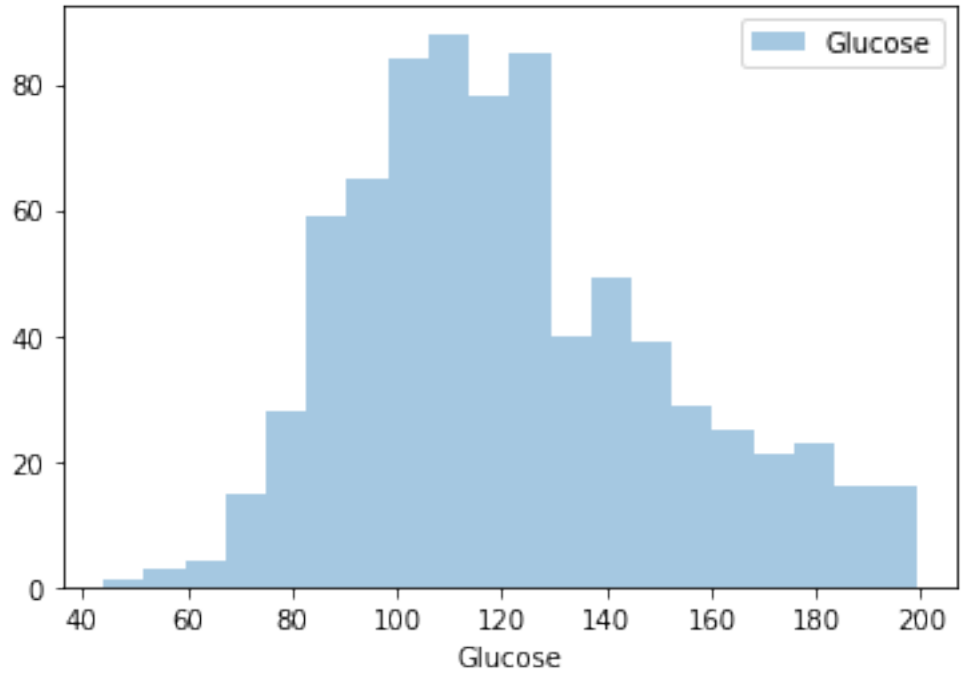
[17]: <AxesSubplot:>

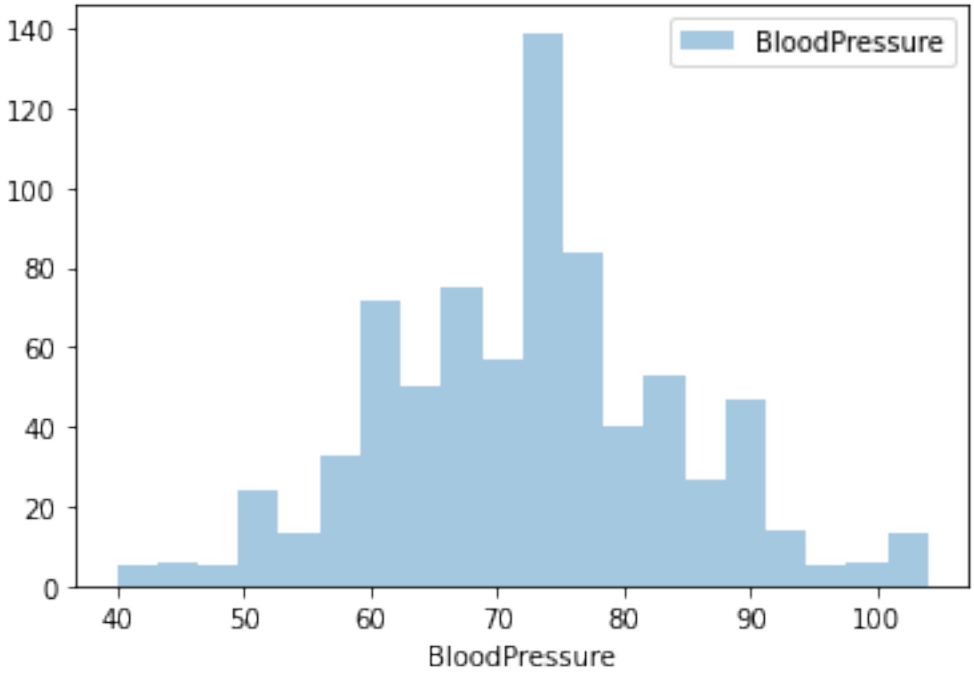


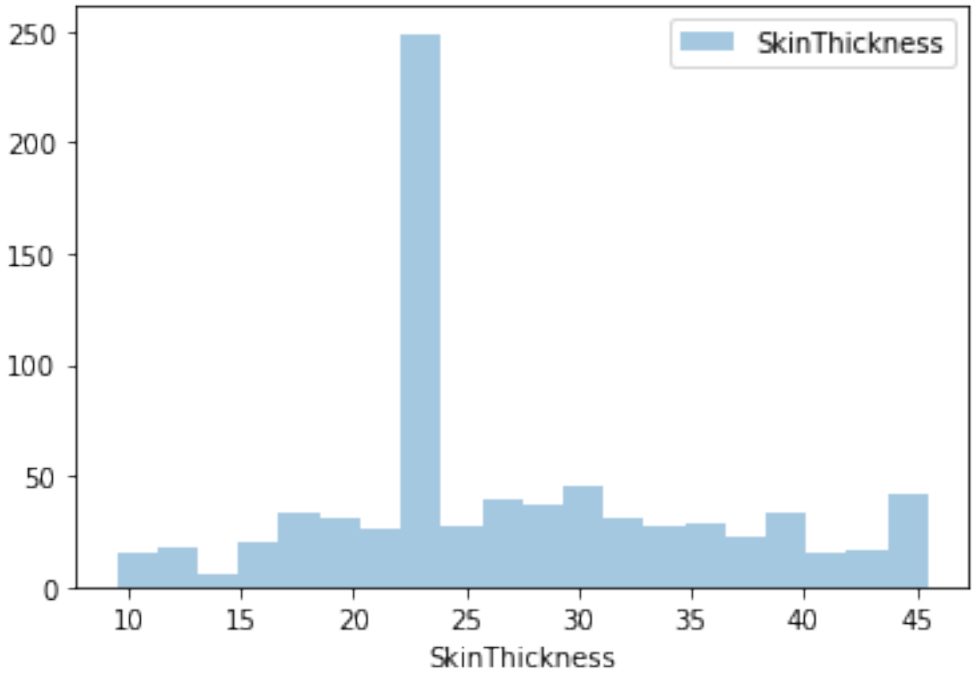
[18]:
```
for val in df.drop(['Outcome'], axis = 1):
    sns.distplot(df[val], kde = False,bins=20,label=val)
    plt.legend()
    plt.show()
```

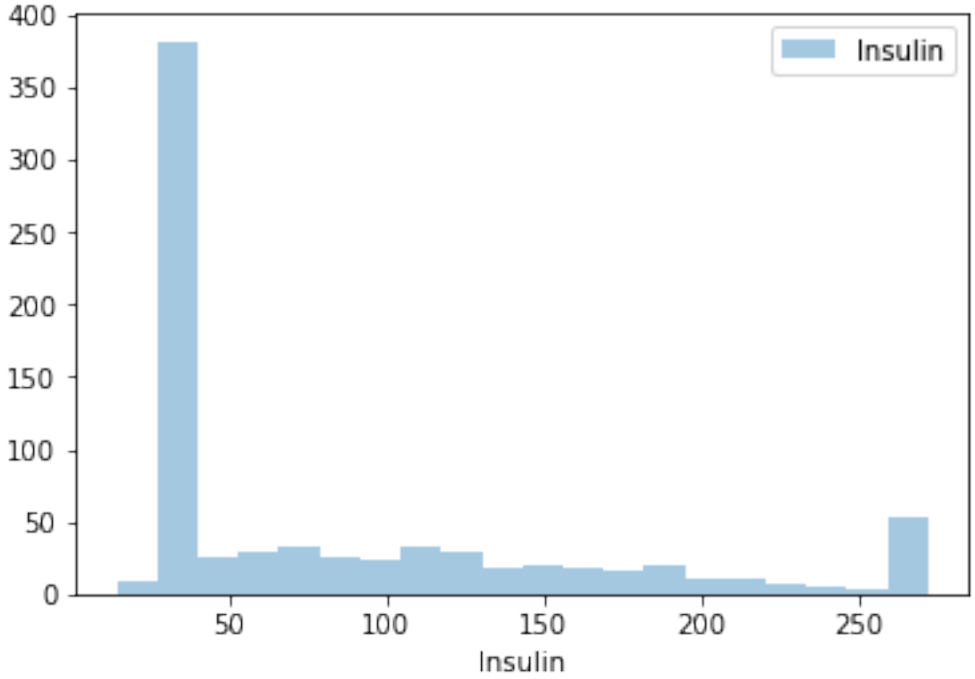
```
C:\Users\Sameriah\anaconda3\lib\site-packages\seaborn\distributions.py:2619:
FutureWarning: `distplot` is a deprecated function and will be removed in a
future version. Please adapt your code to use either `displot` (a figure-level
function with similar flexibility) or `histplot` (an axes-level function for
histograms).
  warnings.warn(msg, FutureWarning)
```

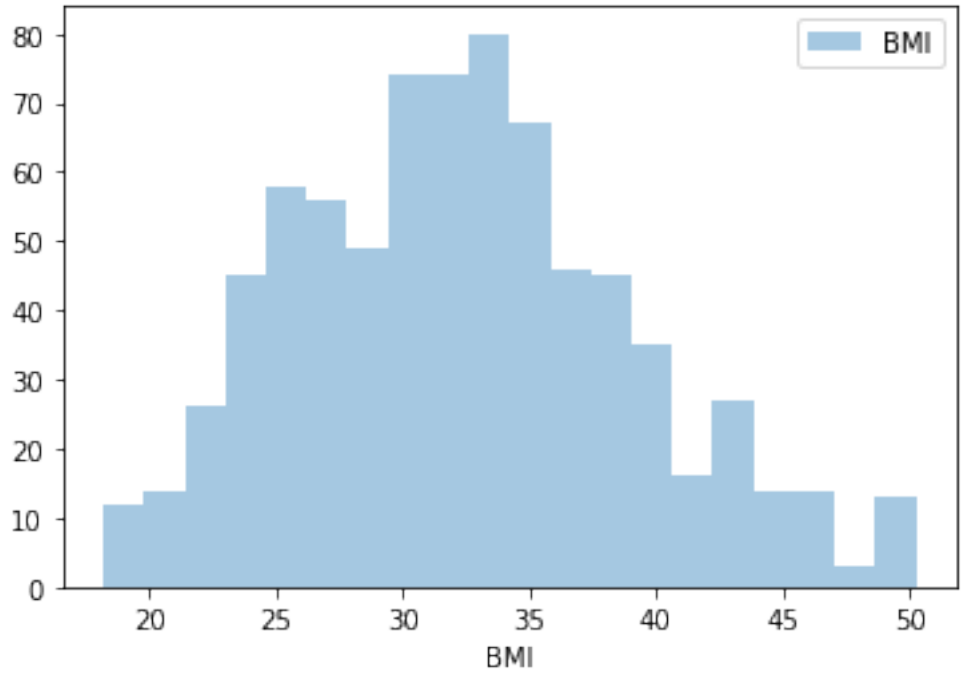


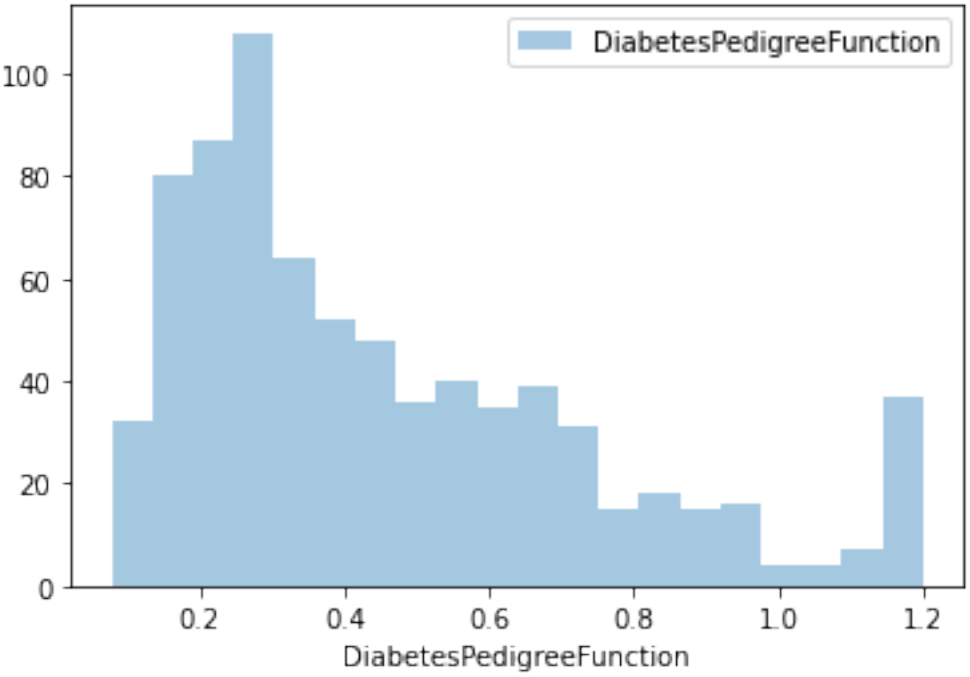

Glucose
80
60
40
20
0
40
60
80
100
120
140
160
180
200
Glucose

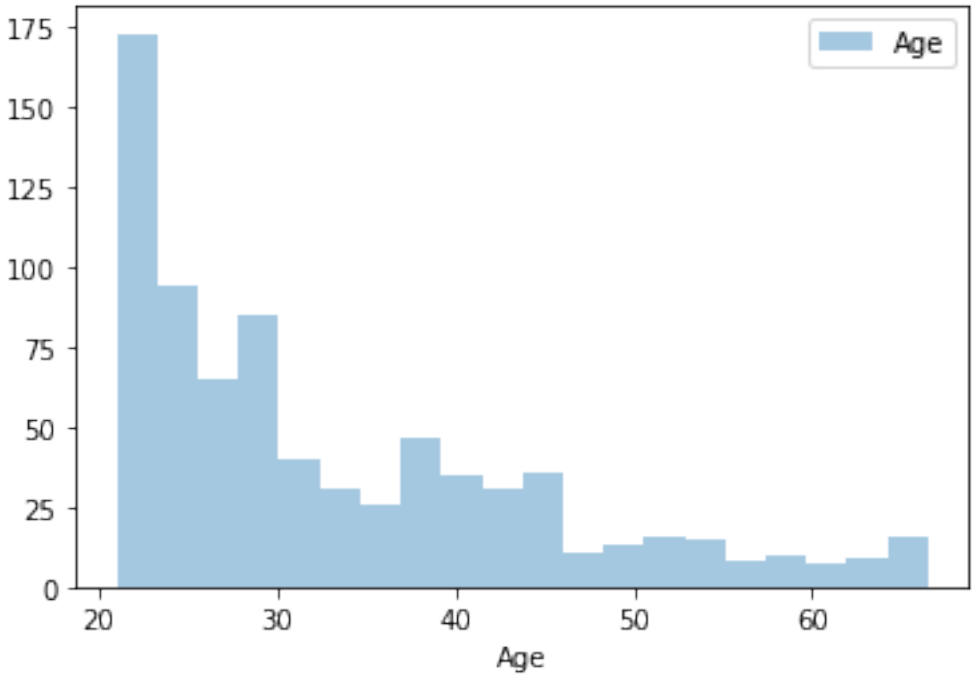

BloodPressure
140
120
100
80
60
40
20
0
40
50
60
70
80
90
100
BloodPressure


SkinThickness
250
200
150
100
50
0
10
15
20
25
30
35
40
45
SkinThickness


Insulin
400
350
300
250
200
150
100
50
0
50
100
150
200
250
Insulin


BMI
80
70
60
50
40
30
20
10
0
20
25
30
35
40
45
50
BMI


DiabetesPedigreeFunction
100
80
60
40
20
0
0.2
0.4
0.6
0.8
1.0
1.2
DiabetesPedigreeFunction



[19]:
```
df.corr()
```

[19]:

	Pregnancies	Glucose	BloodPressure	SkinThickness
Pregnancies	1.000000	0.126856	0.210906	0.047563
Glucose	0.126856	1.000000	0.220199	0.162030
BloodPressure	0.210906	0.220199	1.000000	0.159782
SkinThickness	0.047563	0.162030	0.159782	1.000000
Insulin	-0.061192	0.338429	-0.033847	0.285411
BMI	0.027145	0.233953	0.286410	0.562499
DiabetesPedigreeFunction	-0.017398	0.118457	0.012305	0.118426
Age	0.549695	0.268912	0.332898	0.045434
Outcome	0.220392	0.492782	0.168971	0.191333

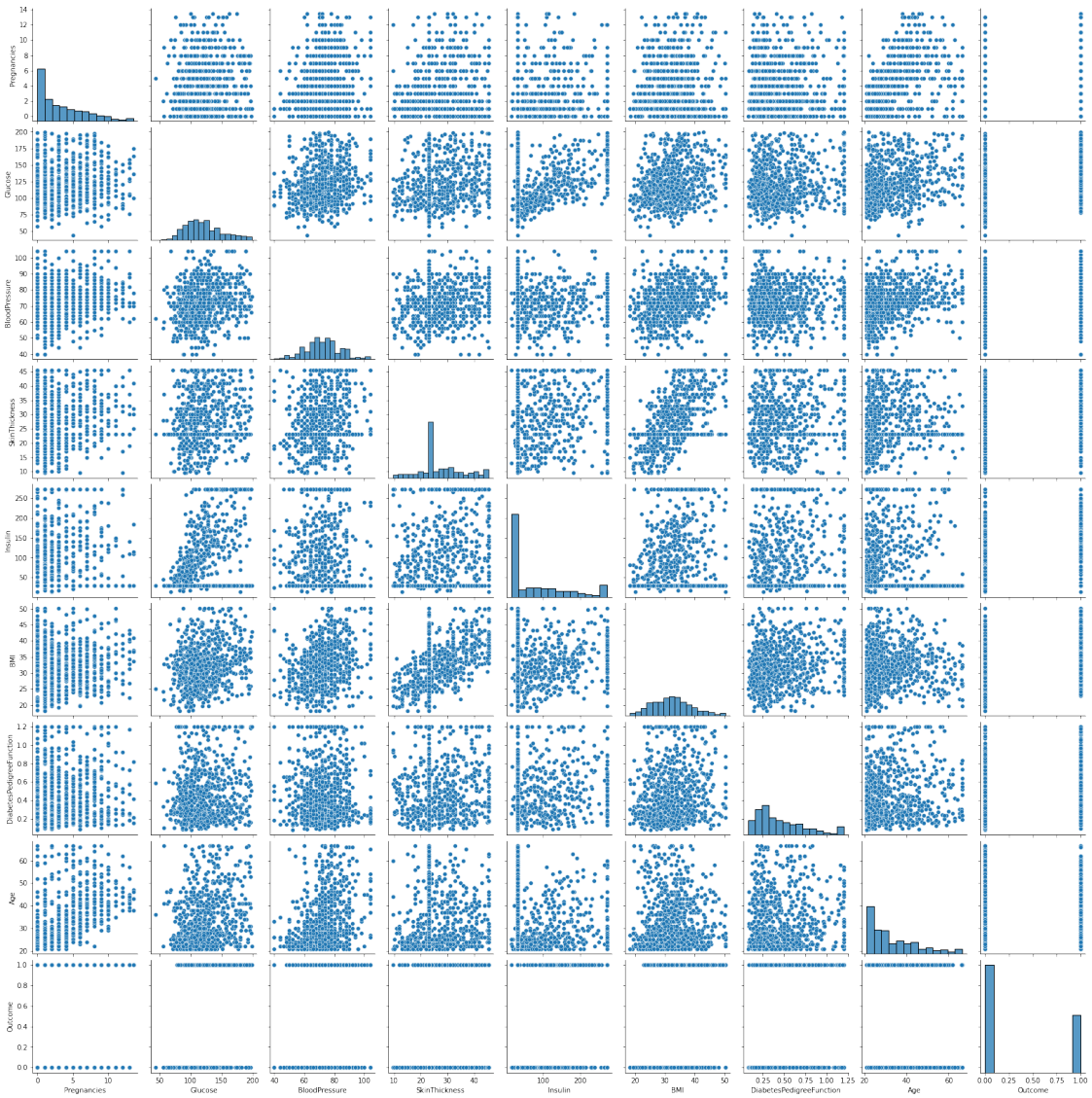
	Insulin	BMI	DiabetesPedigreeFunction
Pregnancies	-0.061192	0.027145	-0.017398
Glucose	0.338429	0.233953	0.118457
BloodPressure	-0.033847	0.286410	0.012305
SkinThickness	0.285411	0.562499	0.118426
Insulin	1.000000	0.207474	0.191870
BMI	0.207474	1.000000	0.138541
DiabetesPedigreeFunction	0.191870	0.138541	1.000000
Age	-0.040448	0.035861	0.047289
Outcome	0.147295	0.313030	0.184969

	Age	Outcome

```
Pregnancies                 0.549695  0.220392
Glucose                     0.268912  0.492782
BloodPressure               0.332898  0.168971
SkinThickness               0.045434  0.191333
Insulin                    -0.040448  0.147295
BMI                         0.035861  0.313030
DiabetesPedigreeFunction    0.047289  0.184969
Age                         1.000000  0.242702
Outcome                     0.242702  1.000000
```

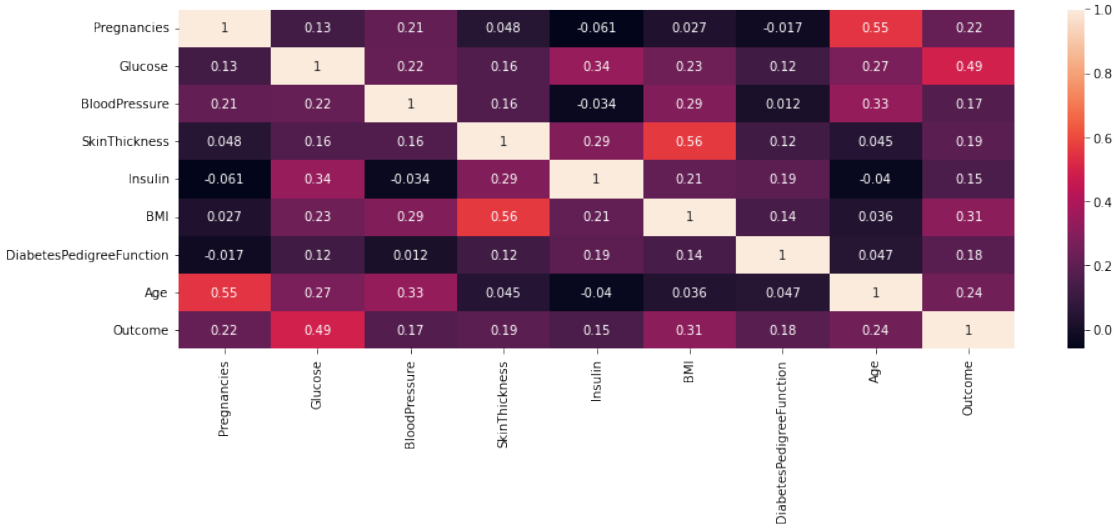
[20]:
```
sns.pairplot(df)
```

[20]:
```
<seaborn.axisgrid.PairGrid at 0x1e7542d06a0>
```



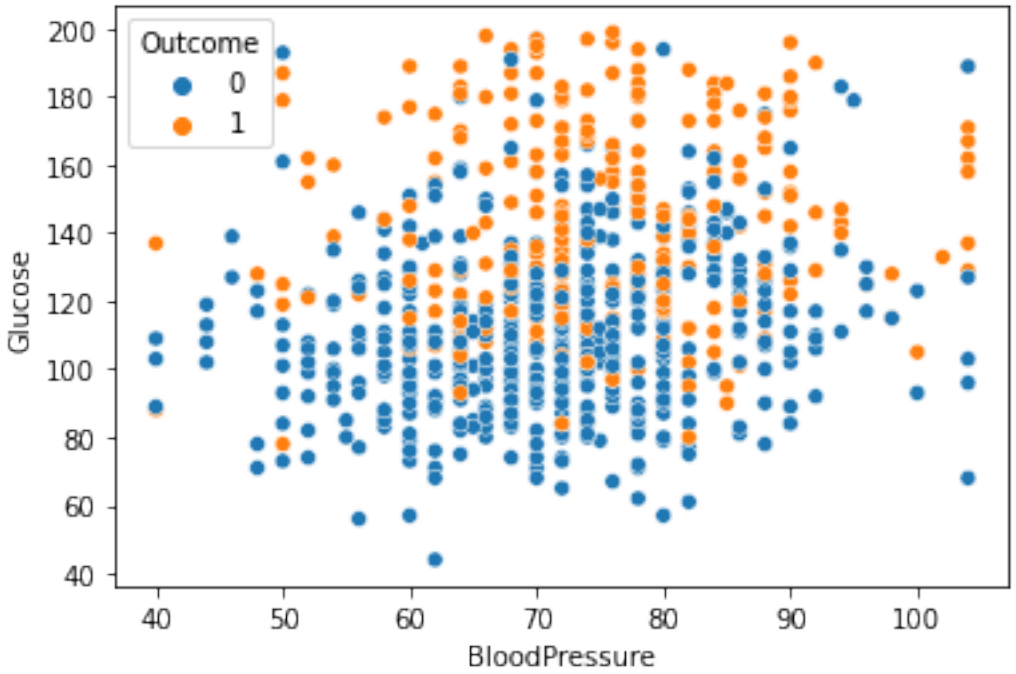
[21]:
```
fig = plt.figure(figsize = (15,5))
sns.heatmap(df.corr(), annot = True)
```

[21]: <AxesSubplot:>



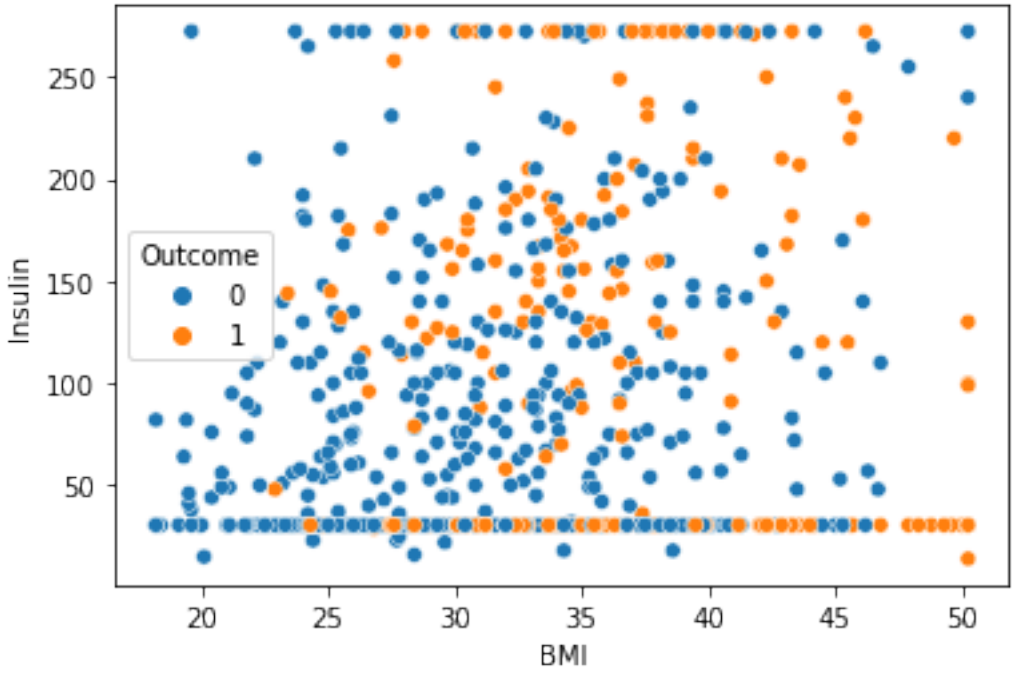
[38]:
```
sns.scatterplot(x ="BloodPressure", y ="Glucose", hue ="Outcome", data= df )
```

[38]: <AxesSubplot:xlabel='BloodPressure', ylabel='Glucose'>



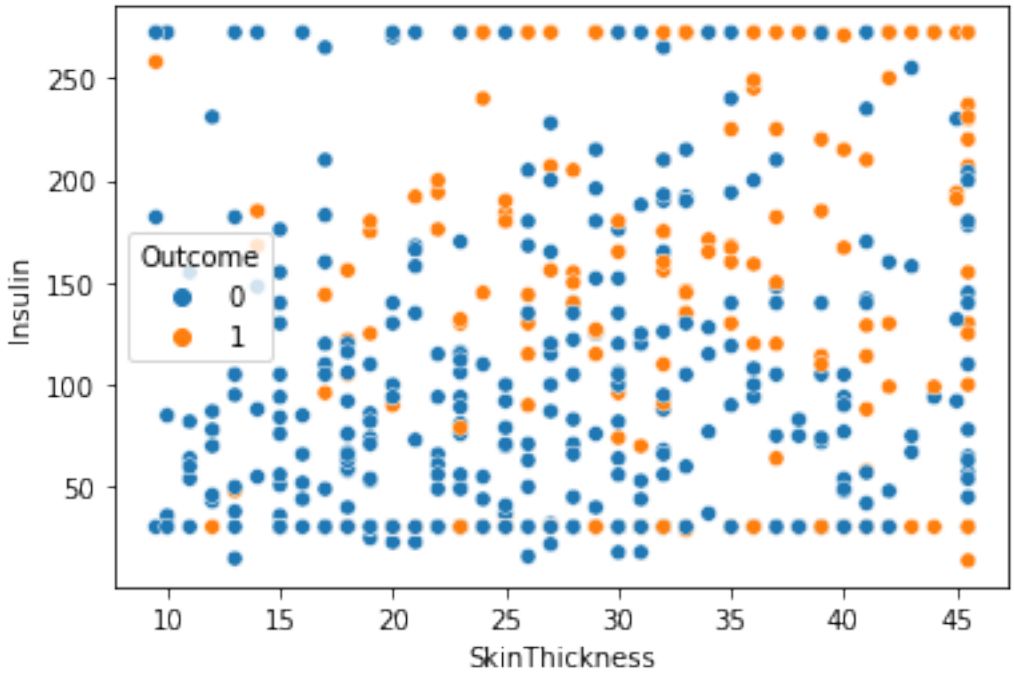
[39]:
```
sns.scatterplot(x ="BMI", y ="Insulin", hue ="Outcome", data= df )
```

[39]: <AxesSubplot:xlabel='BMI', ylabel='Insulin'>



[40]:
```
sns.scatterplot(x ="SkinThickness", y ="Insulin", hue ="Outcome", data= df )
```

[40]: <AxesSubplot:xlabel='SkinThickness', ylabel='Insulin'>



[22]:
```
X = df.drop(['Outcome'], axis = 1) # Independet Feature
y = df['Outcome'] # Target
```

[23]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X,y,test_size = 0.25,␣
 ↪random_state = 1)
```

[24]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn import metrics

decTree = DecisionTreeClassifier(criterion='entropy', max_depth =3,␣
 ↪random_state =1)
decTree = decTree.fit(X_train, y_train)

y_pred = decTree.predict(X_test)
y_train_pred = decTree.predict(X_train)

print("Accuracy of the testing data:",metrics.accuracy_score(y_test, y_pred))
print("Accuracy of the training data:",metrics.accuracy_score(y_train,␣
 ↪y_train_pred))
```

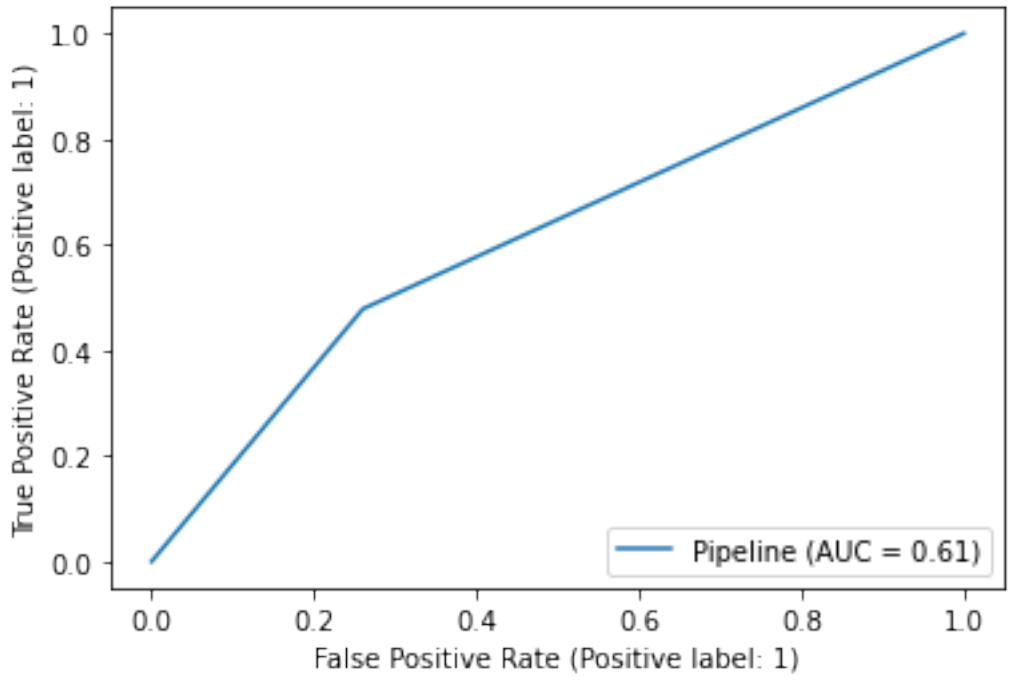
```
Accuracy of the testing data: 0.7708333333333334
Accuracy of the training data: 0.765625
```

[25]:
```
from sklearn.metrics import classification_report, confusion_matrix
print(confusion_matrix(y_test, y_pred))
print(classification_report(y_test, y_pred))
```

```
[[110  13]
 [ 31  38]]
              precision    recall  f1-score   support

           0       0.78      0.89      0.83       123
           1       0.75      0.55      0.63        69

    accuracy                           0.77       192
   macro avg       0.76      0.72      0.73       192
weighted avg       0.77      0.77      0.76       192
```

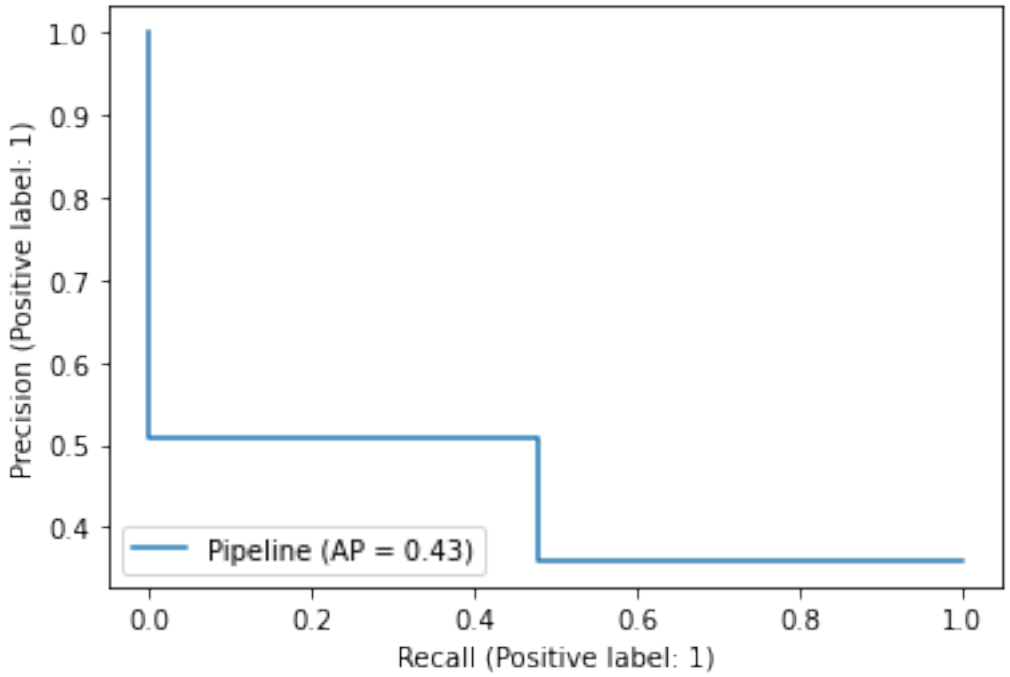
[26]:
```
from sklearn.metrics import plot_roc_curve, plot_precision_recall_curve,␣
 ↪roc_curve
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler


p =Pipeline([('scaler',StandardScaler()),('dt',DecisionTreeClassifier())])
p.fit(X_train, y_train)
plot_roc_curve(p,X_test,y_test)
```

[26]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1e758b99bb0>



[27]:
```
plot_precision_recall_curve(p,X_test,y_test)
```

[27]:
```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay at
0x1e7578042e0>
```



[28]:
```
# ================================================================================
```

[29]:
```
from sklearn.svm import SVC

modelsvc = SVC()
modelsvc.fit(X_train , y_train)

pred_svc = modelsvc.predict(X_test)
pred_train_svc = modelsvc.predict(X_train)

print("Accuracy of the testing data:",metrics.accuracy_score(y_test, pred_svc))
print("Accuracy of the training data:",metrics.accuracy_score(y_train,␣
 ↪pred_train_svc))
```

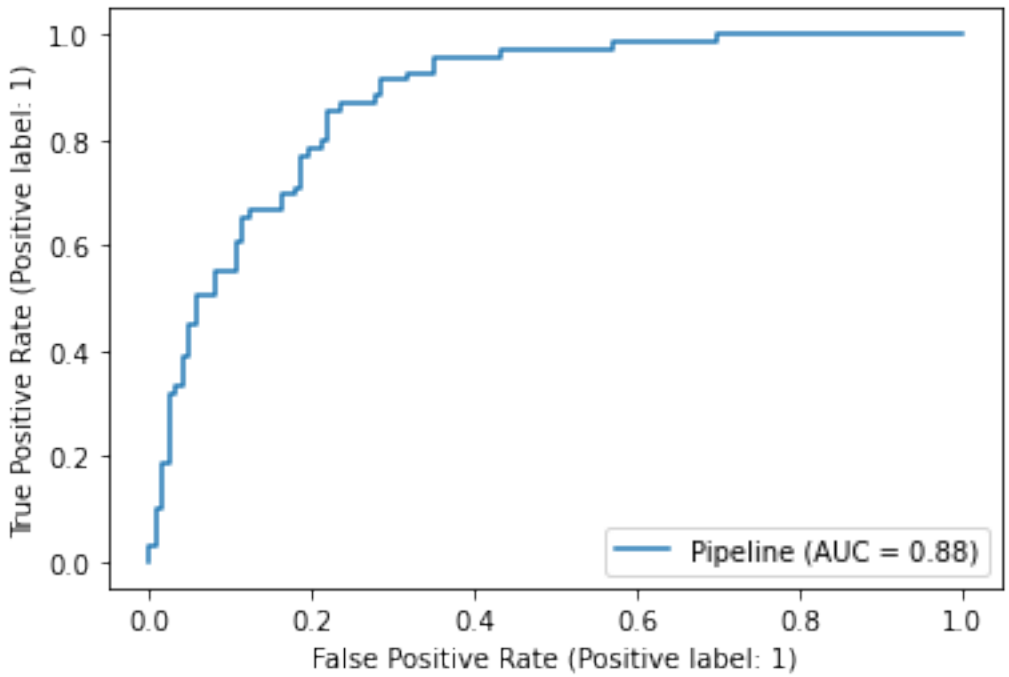
```
Accuracy of the testing data: 0.7864583333333334
Accuracy of the training data: 0.7517361111111112
```

[30]:
```
print(confusion_matrix(y_test, pred_svc))
print(classification_report(y_test, pred_svc))
```

```
[[114   9]
 [ 32  37]]
              precision    recall  f1-score   support

           0       0.78      0.93      0.85       123
           1       0.80      0.54      0.64        69

    accuracy                           0.79       192
   macro avg       0.79      0.73      0.75       192
weighted avg       0.79      0.79      0.77       192
```

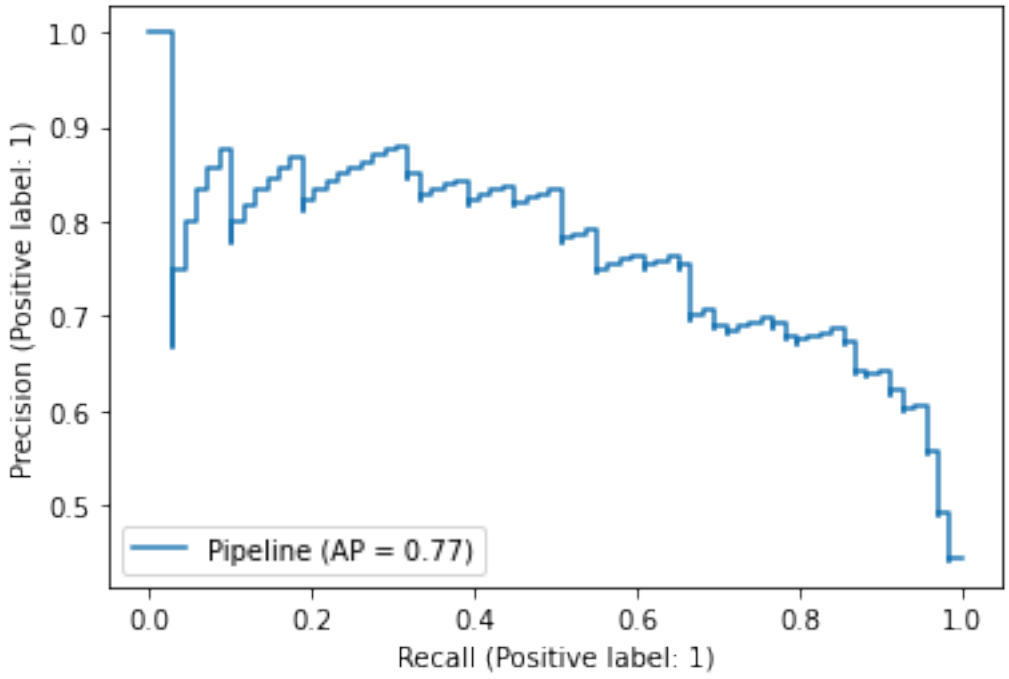
[31]:
```
p =Pipeline([('scaler',StandardScaler()),('svc',SVC())])
p.fit(X_train, y_train)
plot_roc_curve(p,X_test,y_test)
```

[31]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1e758b999a0>



[32]:
```
plot_precision_recall_curve(p,X_test,y_test)
```

[32]: <sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay at 0x1e74e159df0>



[33]:
```
#␣
↪==========================================================================
```

[34]:
```
from sklearn.neighbors import KNeighborsClassifier

classifier = KNeighborsClassifier(n_neighbors=5)
classifier.fit(X_train, y_train)

y_pred_knn = classifier.predict(X_test)
y_pred_train_knn = classifier.predict(X_train)

print("Accuracy of the testing data:",metrics.accuracy_score(y_test, y_pred_knn␣
↪))
print("Accuracy of the training data:",metrics.accuracy_score(y_train,␣
↪y_pred_train_knn ))
```

```
Accuracy of the testing data: 0.75
Accuracy of the training data: 0.7986111111111112
```

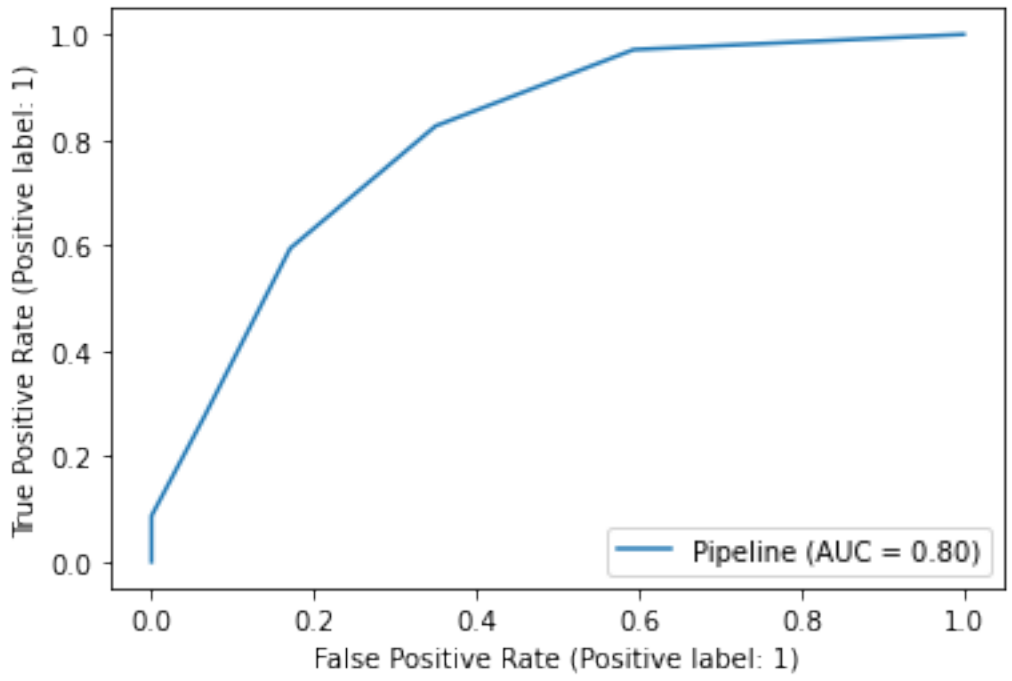
[35]:
```
print(confusion_matrix(y_test, y_pred_knn))
print(classification_report(y_test, y_pred_knn))
```

```
[[101  22]
 [ 26  43]]
              precision    recall  f1-score   support
```

```
              0       0.80      0.82      0.81       123
              1       0.66      0.62      0.64        69

    accuracy                            0.75       192
   macro avg       0.73      0.72      0.72       192
weighted avg       0.75      0.75      0.75       192
```

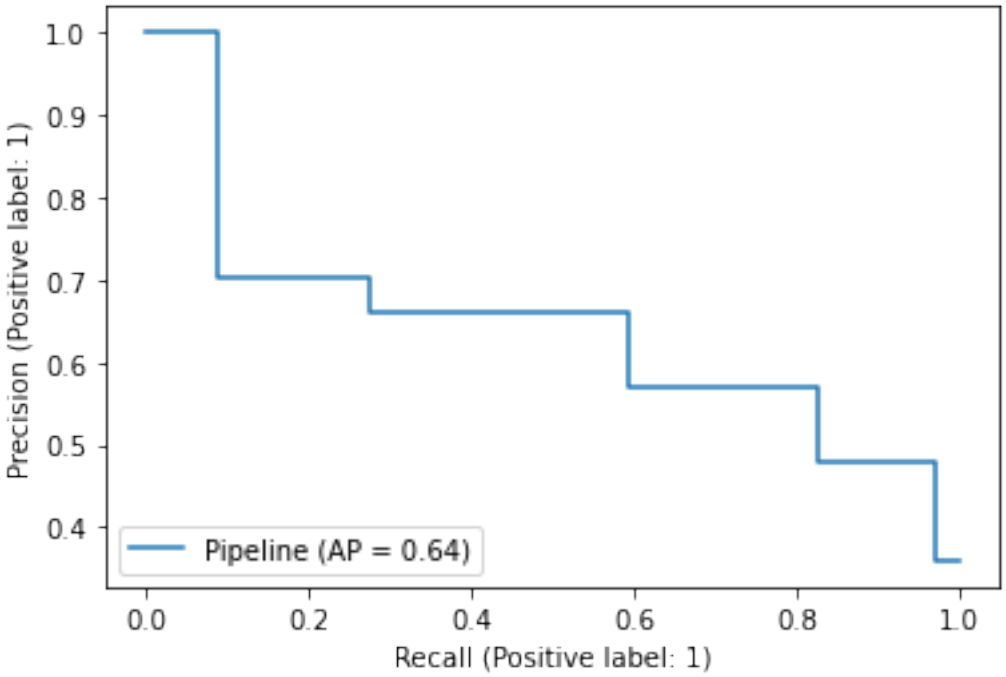
[36]:
```
p =Pipeline([('scaler',StandardScaler()),('knn',KNeighborsClassifier())])
p.fit(X_train, y_train)
plot_roc_curve(p,X_test,y_test)
```

[36]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1e759cd72b0>
```



[37]:
```
plot_precision_recall_curve(p,X_test,y_test)
```

[37]:
```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay at
0x1e759d0bf10>
```


1.0
0.9
0.8
0.7
0.6
0.5
0.4
Precision (Positive label: 1)
Pipeline (AP = 0.64)
0.0
0.2
0.4
0.6
0.8
1.0
Recall (Positive label: 1)