Project: Heart Failure Prediction

This is the notebook corresponding to the Final Project of ECE 523 Engineering Applications of Machine Learning of The University of Arizona by Jeffin George Johnson and Reya Jijy Abraham

```
#Importing the libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn import metrics
from sklearn.model_selection import train_test_split, cross_val_score,
GridSearchCV
from sklearn.linear_model import LogisticRegression
from pandas.plotting import scatter_matrix
from sklearn.metrics import plot_confusion_matrix, r2_score,
mean_absolute_error, mean_squared_error, classification_report,
confusion_matrix, accuracy_score, classification_report
from sklearn.metrics import make_scorer, precision_score,
precision_recall_curve, plot_precision_recall_curve, plot_roc_curve,
roc_auc_score, roc_curve, f1_score, accuracy_score, recall_score
from sklearn.svm import SVC
from sklearn.svm import SVR
from sklearn.model_selection import RepeatedStratifiedKFold, KFold,
cross_val_predict, train_test_split, GridSearchCV, cross_val_score,
cross_validate
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import AdaBoostClassifier
import eli5 #for purmutation importance
from eli5.sklearn import PermutationImportance
import shap #for SHAP values
from pdpbox import pdp, info_plots #for partial plots
from xgboost import XGBRegressor, XGBClassifier
from xgboost import plot_importance
from sklearn.metrics import roc_curve, auc
```

```
#Reading data from file

data = pd.read_csv('heart.csv')
data.head()
```

```
   Age Sex ChestPainType  RestingBP  Cholesterol  FastingBS RestingECG
MaxHR  \
0   40   M           ATA        140          289          0     Normal
```

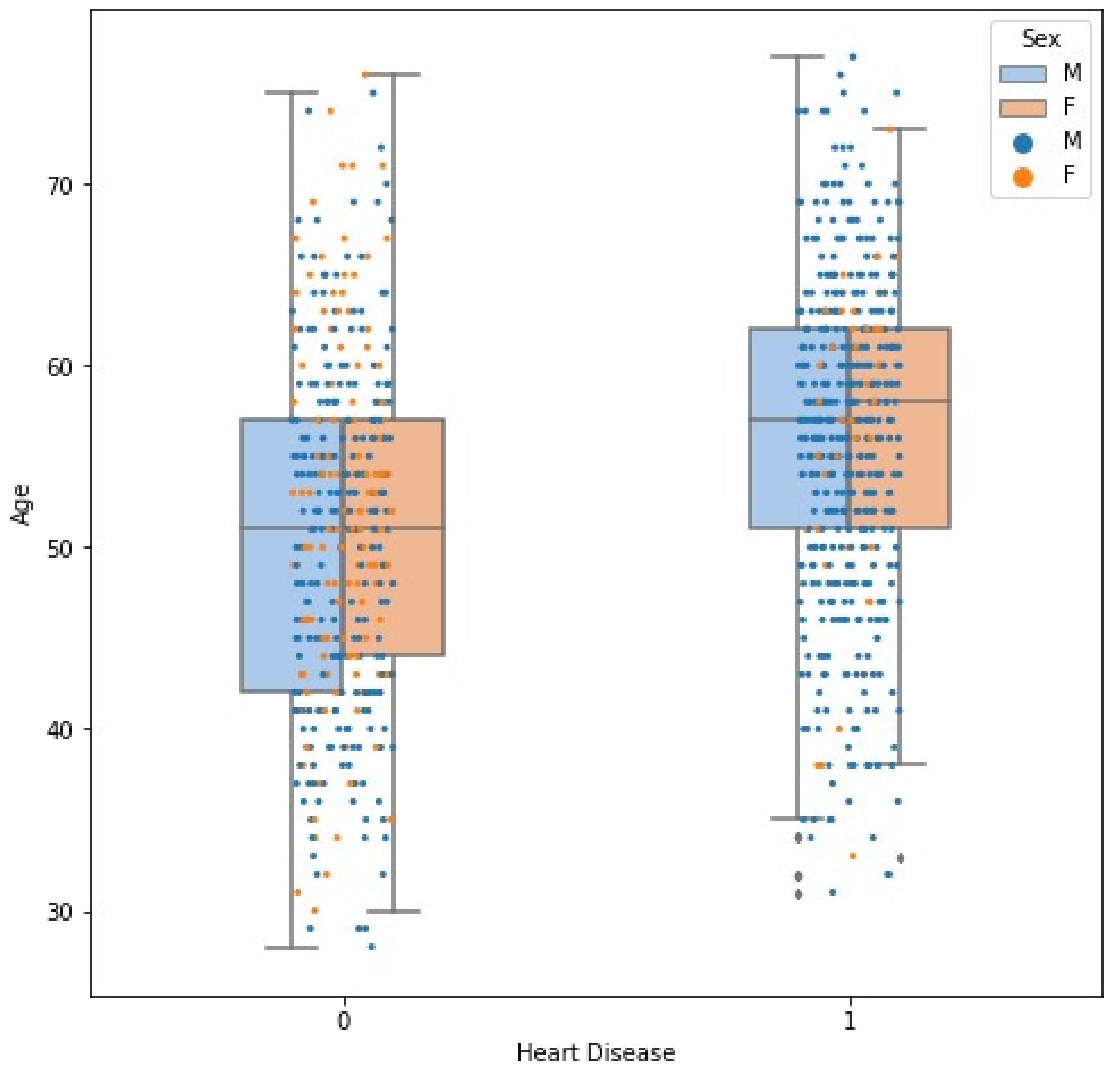
```
172
1   49   F            NAP        160           180           0     Normal
156
2   37   M            ATA        130           283           0         ST
98
3   48   F            ASY        138           214           0     Normal
108
4   54   M            NAP        150           195           0     Normal
122

  ExerciseAngina  Oldpeak ST_Slope  HeartDisease
0              N      0.0       Up             0
1              N      1.0     Flat             1
2              N      0.0       Up             0
3              Y      1.5     Flat             1
4              N      0.0       Up             0
```

1. Data Analysis and Visualisation

The boxplot below illustrates the relationship between age and heart disease. Overall the average age of patients without heart diease is 50 years old. The patients with heart disease have an average age of 55 for men and older for women

```
fig, ax = plt.subplots(figsize = (8, 8))
survive = data.loc[(data.HeartDisease == 0)].Age
death = data.loc[(data.HeartDisease == 1)].Age
print(survive.mean())

sns.boxplot(data = data, x = 'HeartDisease', y = 'Age', hue = 'Sex',
width = 0.4, ax = ax, fliersize = 3,
palette=sns.color_palette("pastel"))
sns.stripplot(data = data, x = 'HeartDisease', y = 'Age', hue = 'Sex',
size = 3, palette=sns.color_palette())
ax.set(xlabel = 'Heart Disease', ylabel="Age")
plt.show()
```

```
50.551219512195125
```

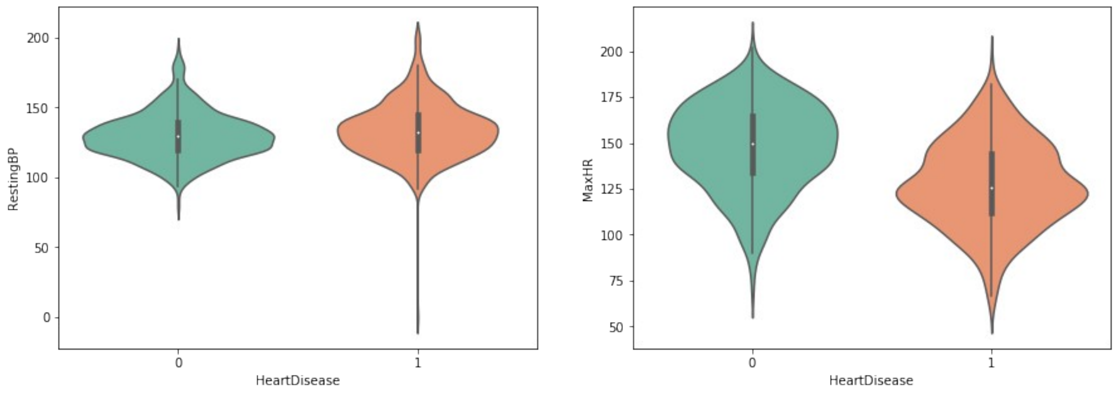


1.2 Resting BP/Maximum Heart rate and Heart Disease

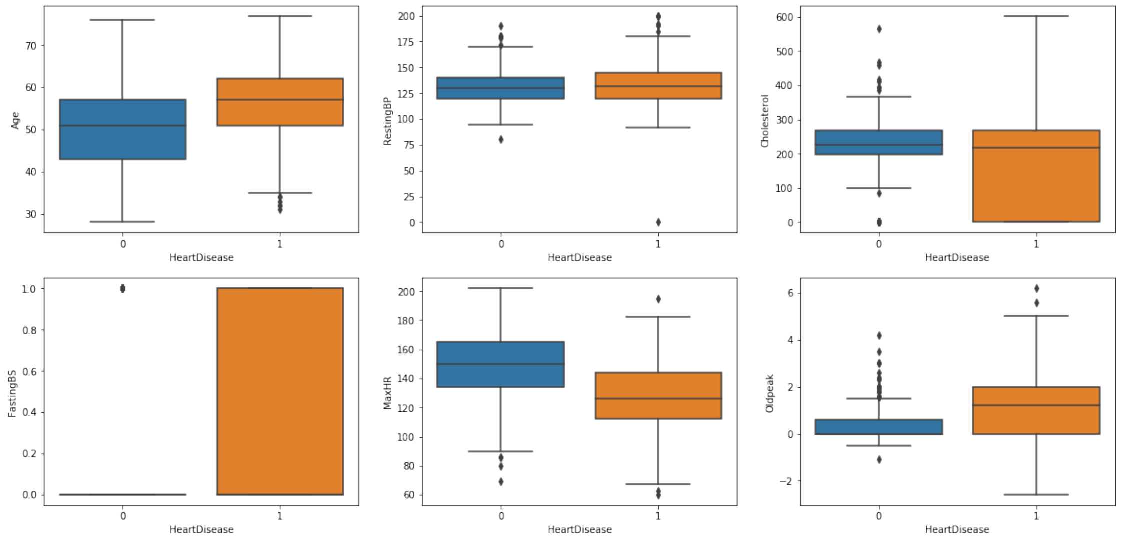
The violin plots display the relationship between `Resting BP`(left)/`Maximum Heart Rate`(right) and Heart Disease. On the right hand side, there is a significant difference in `MaxHR` between patients who have heart disease and patients who don't. On the other hand, in the chart on the left, there is no significant difference in the level of `RestingBP` between two types of patients.

```
fig, ax = plt.subplots(ncols=2, figsize = (15, 5))
sns.violinplot(data=data, x='HeartDisease', y='RestingBP', ax=ax[0],
palette=sns.color_palette('Set2'))
sns.violinplot(data=data, x='HeartDisease', y='MaxHR', ax=ax[1],
palette=sns.color_palette('Set2'))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fb5535d65b0>
```



```
#Dropping the Y-label from the Dataset
numerical= data.drop(['HeartDisease'],
axis=1).select_dtypes('number').columns

categorical = data.select_dtypes('object').columns

#Plotting the range of values of different features that is likely to
cause Heart Disease

index = 0
plt.figure(figsize=(20,20))
for feature in numerical:
    if feature != "HeartDisease":
        index += 1
        plt.subplot(4, 3, index)
        sns.boxplot(x='HeartDisease', y=feature, data=data)
```

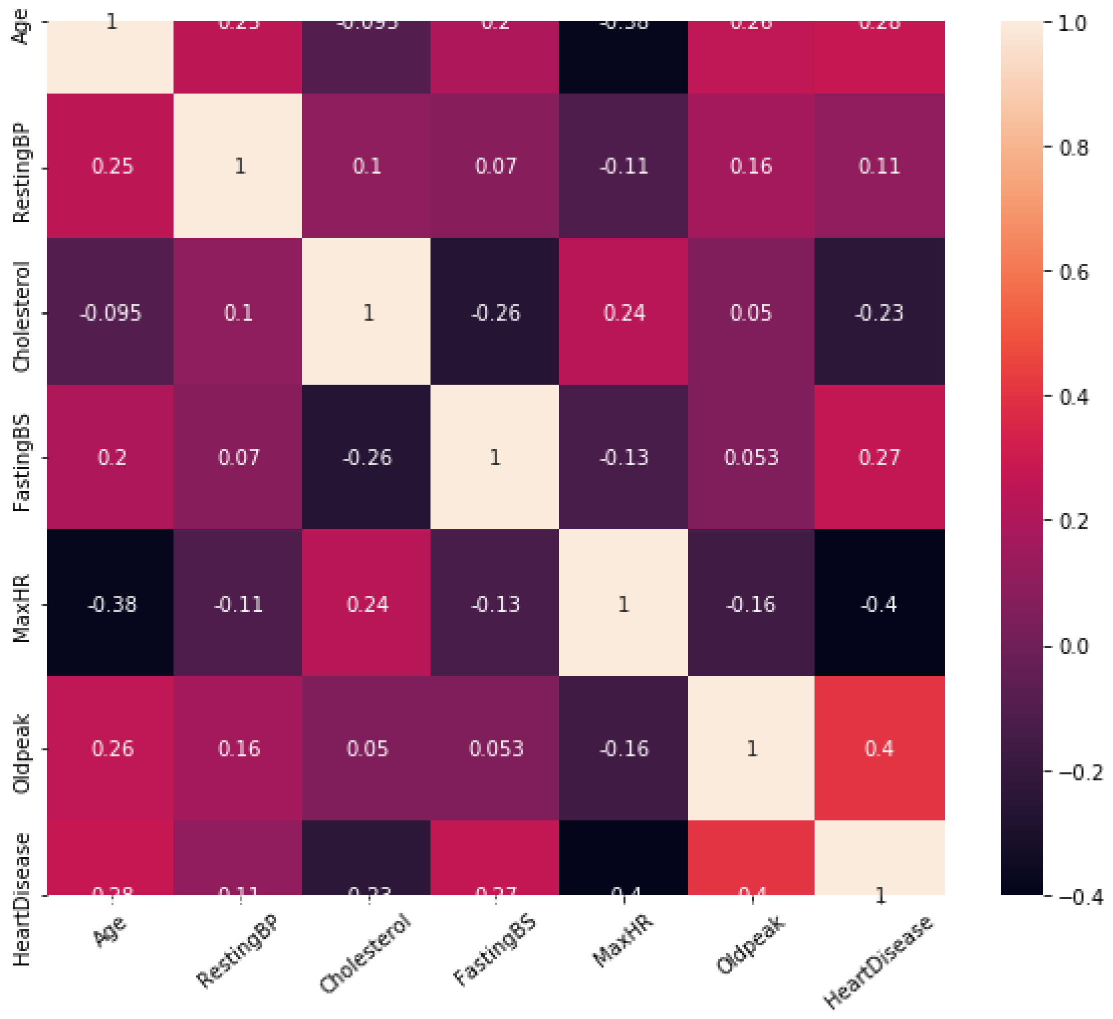


Correlation among variables using Heatmap:

The numbers below are the correlation between features and `Heart Disease`. The correlation close to 1.0 and -1.0 means the variable is positively and negatively correlated, respectively. The correlation close to 0 is less correlated.

```
plt.figure(figsize=(10, 8))
sns.heatmap(data.corr(), annot=True)
plt.xticks(rotation=40)
```

```
(array([0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5]),
 <a list of 7 Text xticklabel objects>)
```



Data Cleaning

Data cleaning is the first step to prepare datasets to ensure that there is no missing values occurs during the application because most machine learning algorithms cannot work with missing features. Two common ways to deal with missing values are as follows:

- Get rid of data with missing values by using `dropna()`.
- Fill in some values to missing values by using `fillna()`.

```
data.info()
data.isnull().sum()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   Age             918 non-null    int64  
 1   Sex             918 non-null    object 
 2   ChestPainType   918 non-null    object 
 3   RestingBP       918 non-null    int64  
 4   Cholesterol     918 non-null    int64  
 5   FastingBS       918 non-null    int64  
 6   RestingECG      918 non-null    object 
 7   MaxHR           918 non-null    int64  
 8   ExerciseAngina  918 non-null    object 
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    object 
 11  HeartDisease    918 non-null    int64  
dtypes: float64(1), int64(6), object(5)
memory usage: 86.2+ KB
```

```
Age               0
Sex               0
ChestPainType     0
RestingBP         0
Cholesterol       0
FastingBS         0
RestingECG        0
MaxHR             0
ExerciseAngina    0
Oldpeak           0
ST_Slope          0
HeartDisease      0
dtype: int64
```

Feature Scaling

Feature Scaling is a preprocessing to scale data to a standard range before building machine learning models. Without feature scaling, one significant number can impact the model because of its large magnitude. This results the model to suffer from poor performance during learning.

Binary and Non-binary Data

Dataset contains both binary and non-binary values. We now call the binary as `discrete_features` and the non-binary as `continuous_features`. The standard deviation of `discrete_features` is already small, ranging between `0` and `1`, so we do not have to scale them. Unlike `continuous_features`, the standard deviation varies from `1.03` to `97,804`. Hence, we have to scale these features. We categorise features before performing feature scaling as follows.

```
data.describe()
```

```
              Age   RestingBP  Cholesterol   FastingBS       MaxHR  \
count  918.000000  918.000000   918.000000  918.000000  918.000000   
mean    53.510893  132.396514   198.799564    0.233115  136.809368   
std      9.432617   18.514154   109.384145    0.423046   25.460334   
min     28.000000    0.000000     0.000000    0.000000   60.000000   
25%     47.000000  120.000000   173.250000    0.000000  120.000000   
50%     54.000000  130.000000   223.000000    0.000000  138.000000   
75%     60.000000  140.000000   267.000000    0.000000  156.000000   
max     77.000000  200.000000   603.000000    1.000000  202.000000   

          Oldpeak  HeartDisease  
count  918.000000    918.000000  
mean     0.887364      0.553377  
std      1.066570      0.497414  
min     -2.600000      0.000000  
25%      0.000000      0.000000  
50%      0.600000      1.000000  
75%      1.500000      1.000000  
max      6.200000      1.000000  
```

We categorise features by calculating the distinct values of each feature. If the feature contains more than 2 values, it is `continuous_features`. Otherwise, it is `discrete_features`.

```
discrete_features, continuous_features = [], []
for feature in data.columns:
    if feature == 'HeartDisease':
        label = feature
    elif len(data[feature].unique()) > 2:
        continuous_features.append(feature)
    else:
        discrete_features.append(feature)

print('Discrete: ', discrete_features, '\n', 'Continuous:', 
continuous_features, '\n', 'Label:', label)
```

```
Discrete:  ['Sex', 'FastingBS', 'ExerciseAngina']
 Continuous: ['Age', 'ChestPainType', 'RestingBP', 'Cholesterol', 
'RestingECG', 'MaxHR', 'Oldpeak', 'ST_Slope']
 Label: HeartDisease
```

```
data[discrete_features].head()
```

```
  Sex  FastingBS ExerciseAngina
0   M          0              N
1   F          0              N
2   M          0              N
3   F          0              Y
4   M          0              N
```

```
data[continuous_features].head()
```

```
   Age ChestPainType  RestingBP  Cholesterol RestingECG  MaxHR
Oldpeak  \
0   40           ATA        140          289     Normal    172
0.0
1   49           NAP        160          180     Normal    156
1.0
2   37           ATA        130          283         ST     98
0.0
3   48           ASY        138          214     Normal    108
1.5
4   54           NAP        150          195     Normal    122
0.0

  ST_Slope
0       Up
1     Flat
2       Up
3     Flat
4       Up
```

```
data.shape
```

```
(918, 12)
```

Dummy Variables Operation

A dummy variable is a variable that takes values of 0 and 1, where the values indicate the presence or absence of something (e.g., a 0 may indicate a placebo and 1 may indicate a drug). Where a categorical variable has more than two categories, it can be represented by a set of dummy variables, with one variable for each category. Numeric variables can also be dummy coded to explore nonlinear effects. Dummy variables are also known as indicator variables, design variables, contrasts, one-hot coding, and binary basis variables.

```
data.head()
```

```
   Age Sex ChestPainType  RestingBP  Cholesterol  FastingBS RestingECG
MaxHR  \
0   40   M           ATA        140          289          0     Normal
172
1   49   F           NAP        160          180          0     Normal
156
2   37   M           ATA        130          283          0         ST
```

```
98
3   48   F           ASY        138          214          0     Normal
108
4   54   M           NAP        150          195          0     Normal
122

  ExerciseAngina  Oldpeak ST_Slope  HeartDisease
0              N      0.0       Up             0
1              N      1.0     Flat             1
2              N      0.0       Up             0
3              Y      1.5     Flat             1
4              N      0.0       Up             0
```

```
data[categorical].value_counts()
```

```
Sex  ChestPainType  RestingECG  ExerciseAngina  ST_Slope
M    ASY            Normal      Y               Flat        109
     ATA            Normal      N               Up           64
     ASY            Normal      N               Flat         55
                    ST          Y               Flat         49
     NAP            Normal      N               Up           46
                                                            ...
F    NAP            ST          Y               Flat          1
     TA             LVH         N               Up            1
                    Normal      N               Down          1
M    ATA            LVH         Y               Flat          1
     TA             ST          Y               Flat          1
Length: 95, dtype: int64
```

```
data=pd.get_dummies(data,drop_first=True)
data.shape
```

```
(918, 16)
```

```
data.head()
```

```
   Age  RestingBP  Cholesterol  FastingBS  MaxHR  Oldpeak
HeartDisease  \
0   40        140          289          0    172      0.0
0
1   49        160          180          0    156      1.0
1
2   37        130          283          0     98      0.0
0
3   48        138          214          0    108      1.5
1
4   54        150          195          0    122      0.0
0

   Sex_M  ChestPainType_ATA  ChestPainType_NAP  ChestPainType_TA  \
0      1                  1                  0                 0
```

```
1      0                  0                  1                0
2      1                  1                  0                0
3      0                  0                  0                0
4      1                  0                  1                0

   RestingECG_Normal  RestingECG_ST  ExerciseAngina_Y  
ST_Slope_Flat  \
0                  1              0                 0              0  

1                  1              0                 0              1  

2                  0              1                 0              0  

3                  1              0                 1              1  

4                  1              0                 0              0  


   ST_Slope_Up  
0            1  
1            0  
2            1  
3            0  
4            1  
```

```
X = data.drop(["HeartDisease"], axis=1)
y = data["HeartDisease"]
```

2. Standardisation by MinMaxScaler

After we obtain `continuous_feature`, we perform the standardisation by using `MinMaxScaler` to scale features. The scaled data lies between 0 and 1 and the standard deviation of every features is in the range of 0 and 1 as well. The dataset is now ready to be used in building models.

```
X_train, X_test, y_train, y_test = train_test_split(X, y, 
test_size=0.15, stratify = y, random_state = 101)
```

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

2.3 Train and Test Set

The scaled dataset is split into a train and a test set in building machine learning models. We set 70% of the dataset as a train set and 30% of the dataset as a test set by using the `train_test_split` function. When we split the data, we `stratify` according to the label to ensure that both train and test data will be balance in terms of the number of `Heart Disease`.

```
num_all = np.unique(data['HeartDisease'], return_counts=True)
print('              The number of HeartDisease')
print('                    0        |      1')
print('------------------------------------------')
print('All dataset      ', num_all[1][0], ' '*5, '|', ' '*4,
num_all[1][1])
num_train = np.unique(y_train, return_counts=True)
print('Train set (70%)  ', num_train[1][0], ' '*5, '|', ' '*4,
num_train[1][1])
num_test = np.unique(y_test, return_counts=True)
print('Test set (30%)    ', num_test[1][0], ' '*5, '|', ' '*4,
num_test[1][1])
```

```
             The number of HeartDisease
                   0        |      1
------------------------------------------
All dataset       410       |      508
Train set (70%)   348       |      432
Test set (30%)     62       |      76
```

Training

1. Decision Tree

First of all, we construct a classifier of Decision Tree using `gini` as a criterion without defining the `max_depth` parameter. The tree performs until all left nodes are pure, meaning there is no ability to split leaf nodes. The maximum depth of the tree is 14.

```
from sklearn.tree import DecisionTreeClassifier, plot_tree

tree_clf = DecisionTreeClassifier(criterion='gini')
tree_clf = tree_clf.fit(X_train, y_train)
print('The maximum depth of the tree is ', tree_clf.get_depth())
y_pred = tree_clf.predict(X_test)
```

```
The maximum depth of the tree is  14
```

We calculate `Train Accuracy`, `Test Accuracy` of depth 1 to 14. `Train Accuracy` and `Test Accuracy` are the accuracy of the train and test set split. We clearly see that the higher depth of tree, the closer of `Train Accuracy` reaches to 1. This happens because the model at the depth of 14 splits until left nodes are pure, resulting the model to be perfect in prediction. However, it causes an `overfitting` issue for a decision tree classifier.

To avoid the overfitting, the `k-Fold Cross-Validation` procedure is applied to mitigate this issue. The model is trained using k-1 of the folds as training data. The remaining part is used as testing data to measure the accuracy of each fold. Then, the average of accuracy is calculated as a result. After applying the cross-validation, the model does not suffer from overfitting anymore.

```
accuracies = []
print('Depth', ' Train Accuracy', ' Test Accuracy', ' CV Accuracy')

for d in range(1,15):
    tree_clf = DecisionTreeClassifier(criterion='gini', max_depth = d)
    tree_clf = tree_clf.fit(X_train, y_train)

    train_accuracy = tree_clf.score(X_train, y_train)
    test_accuracy = tree_clf.score(X_test, y_test)

    cv_accuracy = np.mean(cross_val_score(tree_clf, X_train, y_train, 
cv=5))
    accuracies.append([d, train_accuracy, test_accuracy, cv_accuracy])

    print(' ', d, ' '*6, '%.4f' % train_accuracy, ' '*8, '%.4f'% 
test_accuracy, ' '*5, '%.4f'% cv_accuracy)
```

```
Depth  Train Accuracy  Test Accuracy  CV Accuracy
  1        0.8064          0.8551       0.8064
  2        0.8321          0.8551       0.8256
  3        0.8449          0.8913       0.8218
  4        0.8641          0.8696       0.8000
  5        0.8846          0.8841       0.7936
  6        0.9115          0.8406       0.8000
  7        0.9308          0.8478       0.8038
  8        0.9462          0.7681       0.7833
  9        0.9615          0.7899       0.7795
  10         0.9744          0.7754       0.7654
  11         0.9910          0.7609       0.7769
  12         0.9962          0.7754       0.7577
  13         0.9974          0.7681       0.7641
  14         1.0000          0.7609       0.7577
```

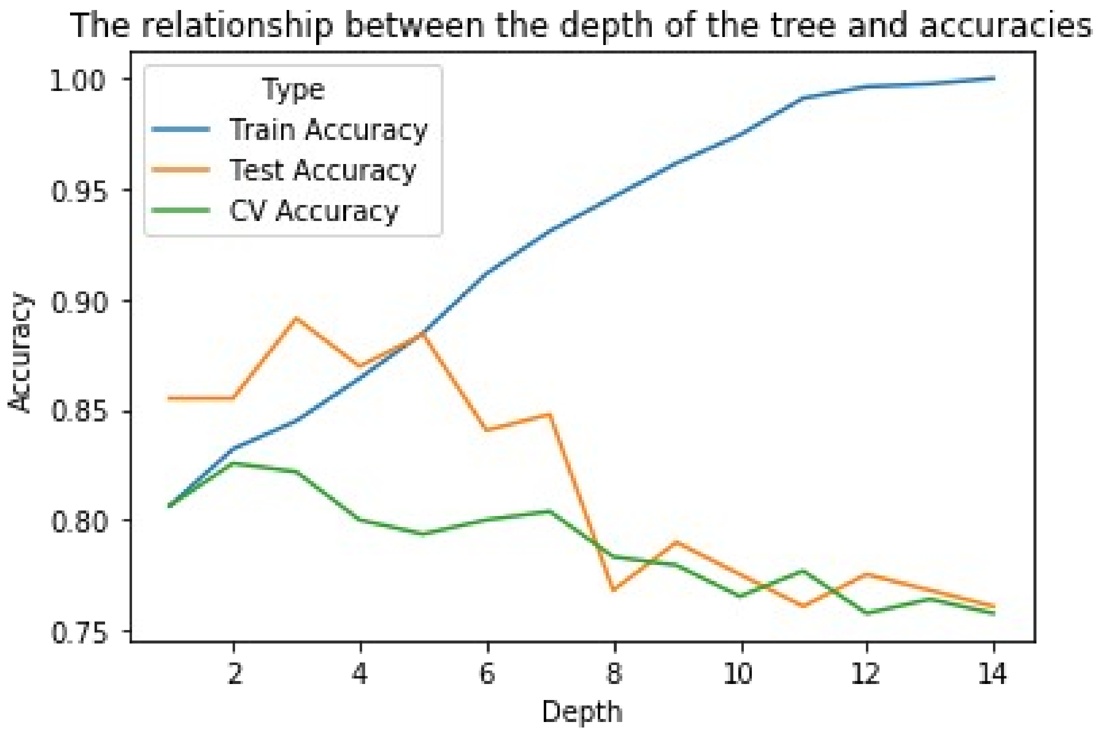
Accuracy by Depth of Tree

The line graph below illustrates `Train Accuracy`, `Test Accuracy` and `CV Accuracy`. We ignore the train accuracy because it causes the overfitting issue. We now focus on `Test accuracy` and `CV Accuracy`. Both accuracy keep decreasing when the depth increases. The test accuracy fluctuates along the way while the CV accuracy drops smoothly. To choose the most accurate model, we consider a model with the highest accuracy. The highest accuracy is the tree with cross-validation at the depth of 1.

The decision tree with the highest performance is the model with `max_depth`=1. The train and test accuracy are 0.8551 and 0.8064, respectively.

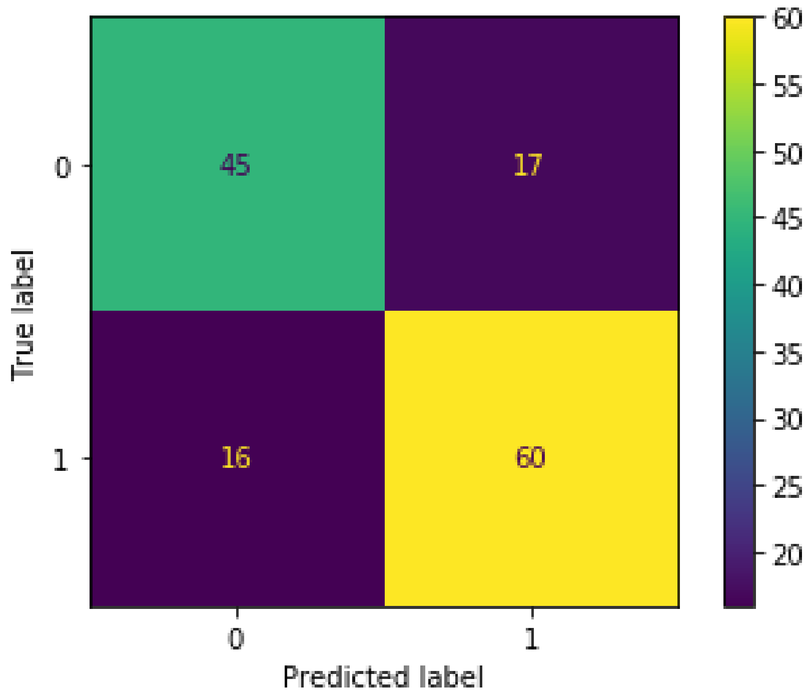
```
accuracies = pd.DataFrame(
    data = accuracies,
    columns = ['Depth', 'Train Accuracy','Test Accuracy', 'CV
Accuracy']
)

accuracies = pd.melt(
    accuracies,
    id_vars = ['Depth'],
    var_name = 'Type',
    value_name = 'Accuracy'
)
sns.lineplot(
    x = 'Depth',
    y = 'Accuracy',
    hue = 'Type',
    data = accuracies,

).set_title('The relationship between the depth of the tree and
accuracies')
```

```
Text(0.5, 1.0, 'The relationship between the depth of the tree and
accuracies')
```



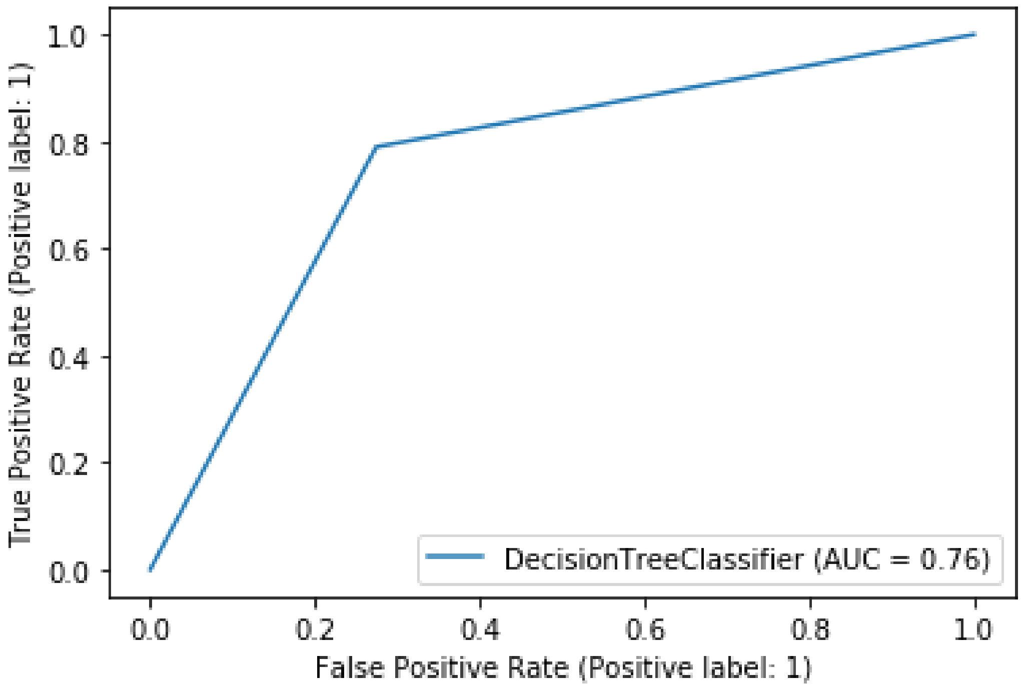
```
plot_confusion_matrix(tree_clf, X_test, y_test)
print(classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.74      0.73      0.73        62
           1       0.78      0.79      0.78        76

    accuracy                           0.76       138
   macro avg       0.76      0.76      0.76       138
weighted avg       0.76      0.76      0.76       138
```



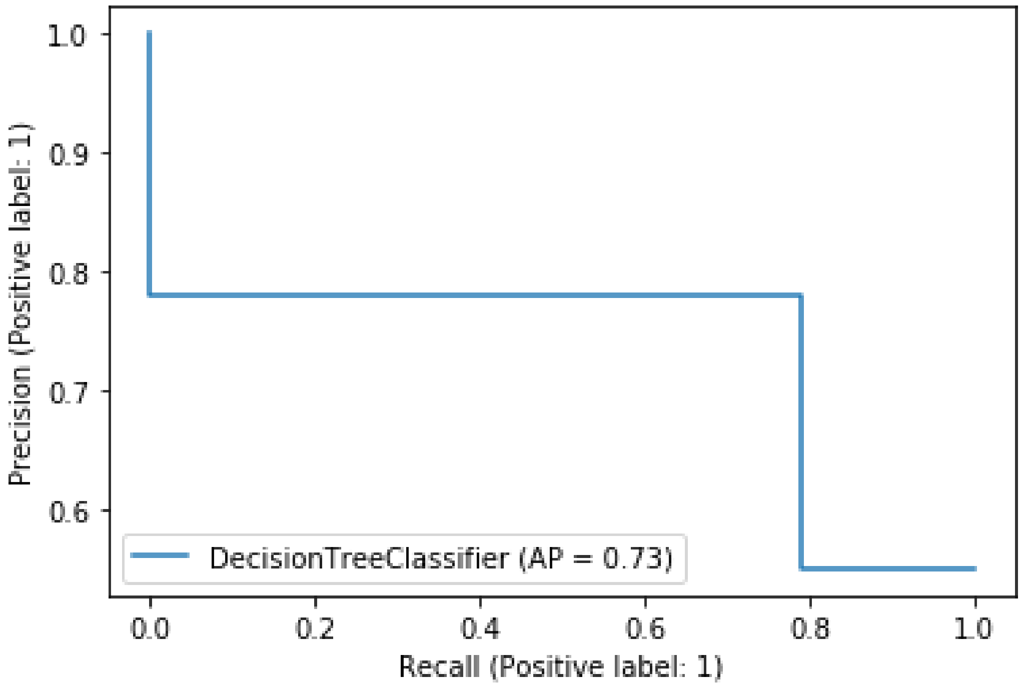
```
plot_roc_curve(tree_clf, X_test, y_test, response_method='auto')
```

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x7fb55386ae20>
```



```
plot_precision_recall_curve(tree_clf, X_test, y_test)
```

```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay
at 0x7fb530aa2610>
```



```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
auc(fpr, tpr)
```

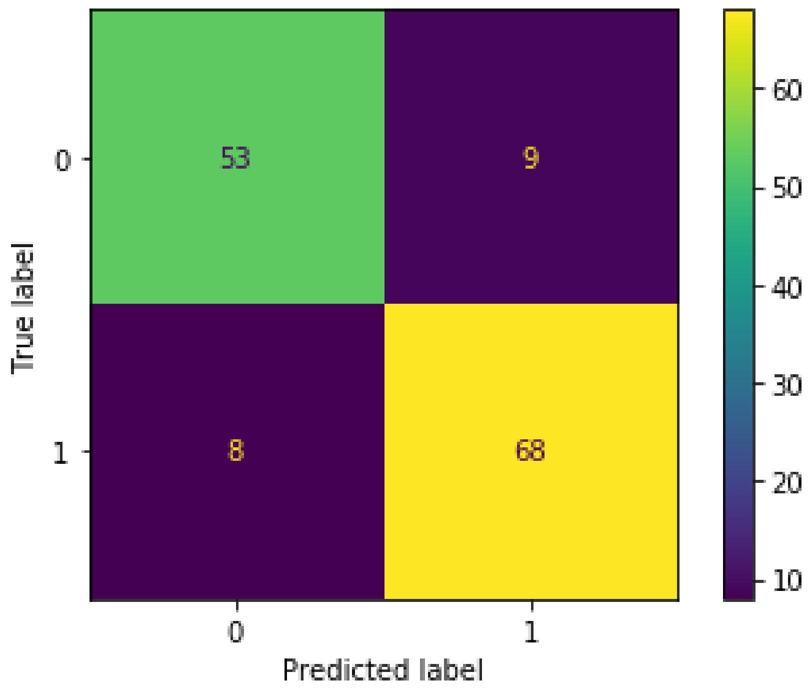
```
0.7576400679117148
```

2.Logistic Regression

```
log = LogisticRegression(random_state=101, class_weight=None,
solver='liblinear')
log.fit(X_train, y_train)
y_pred = log.predict(X_test)

print(f"\033[1m1) Logistic Regression Training Accuracy:\033[0m
{log}")

1) Logistic Regression Training Accuracy:
LogisticRegression(random_state=101, solver='liblinear')

log.score(X_train, y_train)

0.8705128205128205


y_train_pred = log.predict(X_train)

print(confusion_matrix(y_test, y_pred))
print(classification_report(y_test, y_pred))

[[53  9]
 [ 8 68]]
              precision    recall  f1-score   support

           0       0.87      0.85      0.86        62
           1       0.88      0.89      0.89        76

    accuracy                           0.88       138
   macro avg       0.88      0.87      0.88       138
weighted avg       0.88      0.88      0.88       138




print(confusion_matrix(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")
print(classification_report(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")

plot_confusion_matrix(log, X_test, y_test)
```

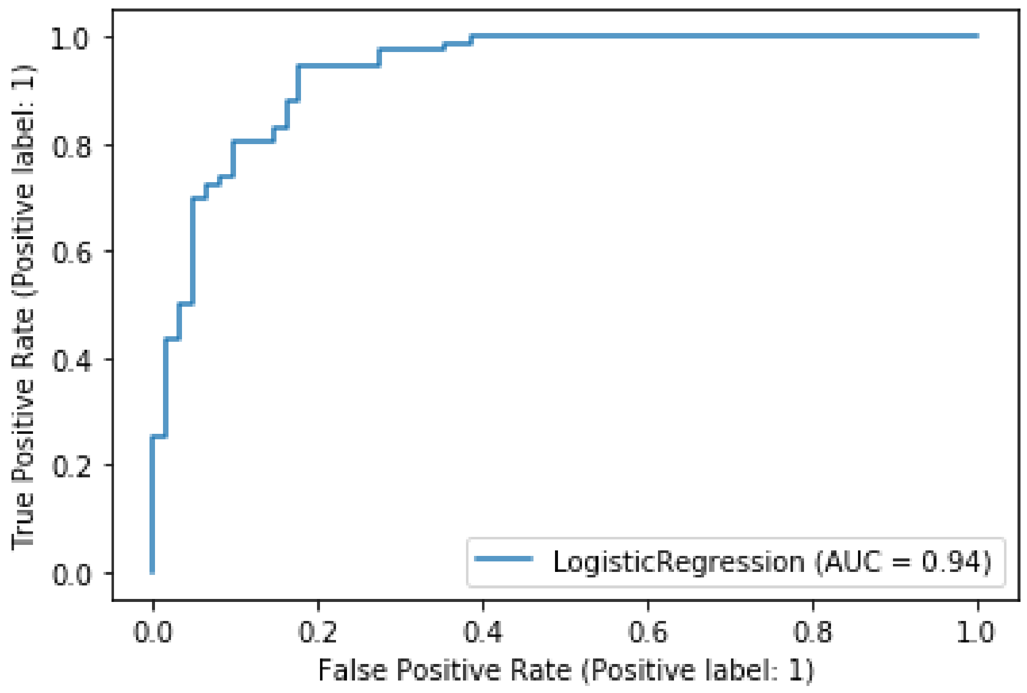
```
[[53  9]
 [ 8 68]]
--------------------------------------------------------
              precision    recall  f1-score   support

           0       0.87      0.85      0.86        62
           1       0.88      0.89      0.89        76

    accuracy                           0.88       138
   macro avg       0.88      0.87      0.88       138
weighted avg       0.88      0.88      0.88       138

--------------------------------------------------------
```

```
<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at
0x7fb5538b4fd0>
```



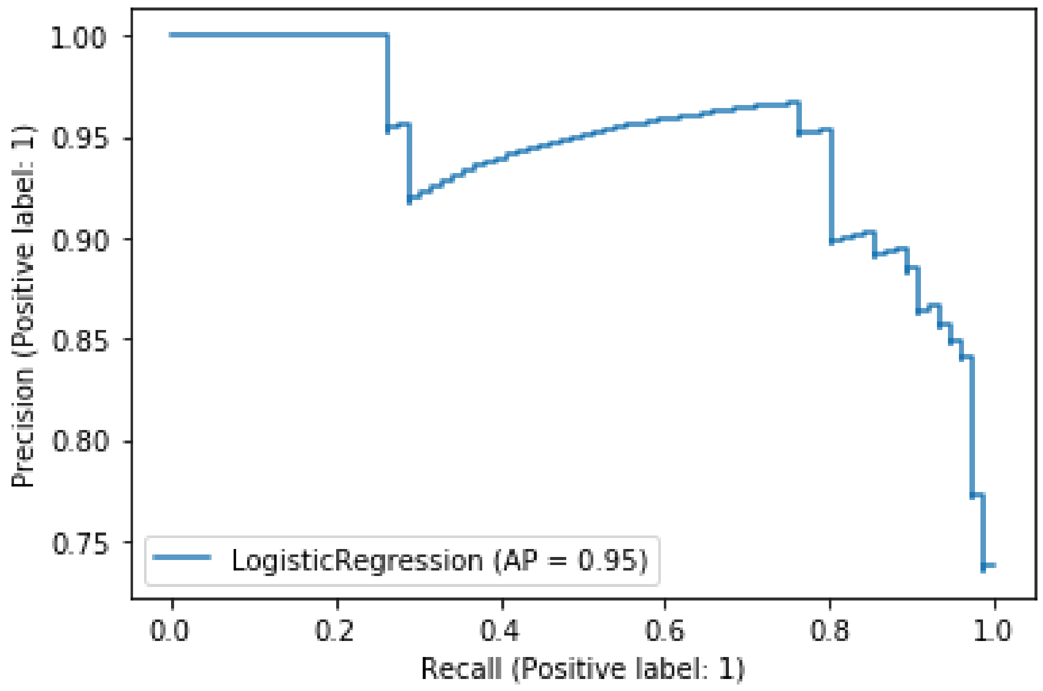
```
plot_roc_curve(log, X_test_scaled, y_test, response_method='auto')
```

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x7fb5538b4e50>
```



```
plot_precision_recall_curve(log, X_test, y_test)
```

```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay
at 0x7fb510926eb0>
```



```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
auc(fpr, tpr)
```

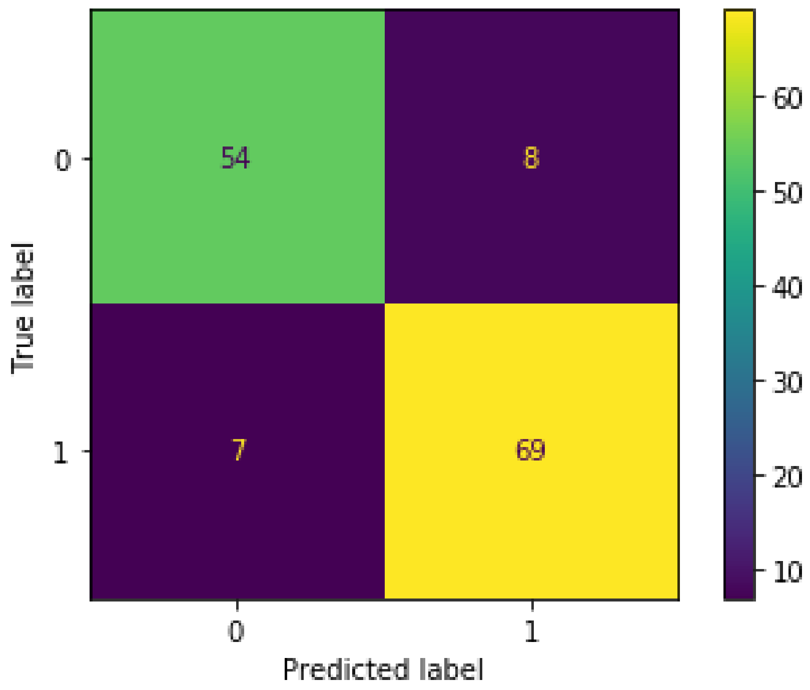
```
0.8747877758913414
```

3. Support Vector Machine (SVM)

SVM provides three kernels: linear, polynomial and rbf. We use `GridSearchCV` to select the best parameters for the support vectore classifier. The result is `kernel='linear'` and `C=10`. We can ignore degree and gamma because they are only used in poly and rbf kernel. The higest accuracy 0.8560 is a model performed with cross-validation.

```
SVM_model = SVC(random_state=42)
SVM_model.fit(X_train_scaled, y_train)
y_pred = SVM_model.predict(X_test_scaled)
y_train_pred = SVM_model.predict(X_train_scaled)

svm_f1 = f1_score(y_test, y_pred)
svm_acc = accuracy_score(y_test, y_pred)
svm_recall = recall_score(y_test, y_pred)
svm_auc = roc_auc_score(y_test, y_pred)

print(confusion_matrix(y_test, y_pred))
print("\
033[1m-------------------------------------------------------\
033[0m")
print(classification_report(y_test, y_pred))
print("\
033[1m-------------------------------------------------------\
033[0m")

plot_confusion_matrix(SVM_model, X_test_scaled, y_test)
```

```
[[54  8]
 [ 7 69]]
-------------------------------------------------------
              precision    recall  f1-score   support

           0       0.89      0.87      0.88        62
           1       0.90      0.91      0.90        76

    accuracy                           0.89       138
   macro avg       0.89      0.89      0.89       138
weighted avg       0.89      0.89      0.89       138

-------------------------------------------------------

<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at
0x7fb5538d25e0>
```



```
svm_xvalid_model = SVC()

svm_xvalid_model_scores = cross_validate(svm_xvalid_model,
X_train_scaled, y_train, scoring = ['accuracy', 'precision','recall',

'f1'], cv = 10)
svm_xvalid_model_scores = pd.DataFrame(svm_xvalid_model_scores, index
= range(1, 11))

svm_xvalid_model_scores
```

```
    fit_time  score_time  test_accuracy  test_precision  test_recall
test_f1
1   0.014406    0.003912       0.833333        0.800000     0.930233
0.860215
2   0.014085    0.003882       0.820513        0.808511     0.883721
0.844444
3   0.014053    0.004012       0.858974        0.880952     0.860465
0.870588
4   0.013385    0.003914       0.820513        0.837209     0.837209
0.837209
5   0.014022    0.003720       0.923077        0.951220     0.906977
0.928571
6   0.012821    0.003568       0.794872        0.800000     0.837209
0.818182
7   0.013615    0.003637       0.884615        0.854167     0.953488
0.901099
8   0.013110    0.003543       0.858974        0.847826     0.906977
0.876404
```

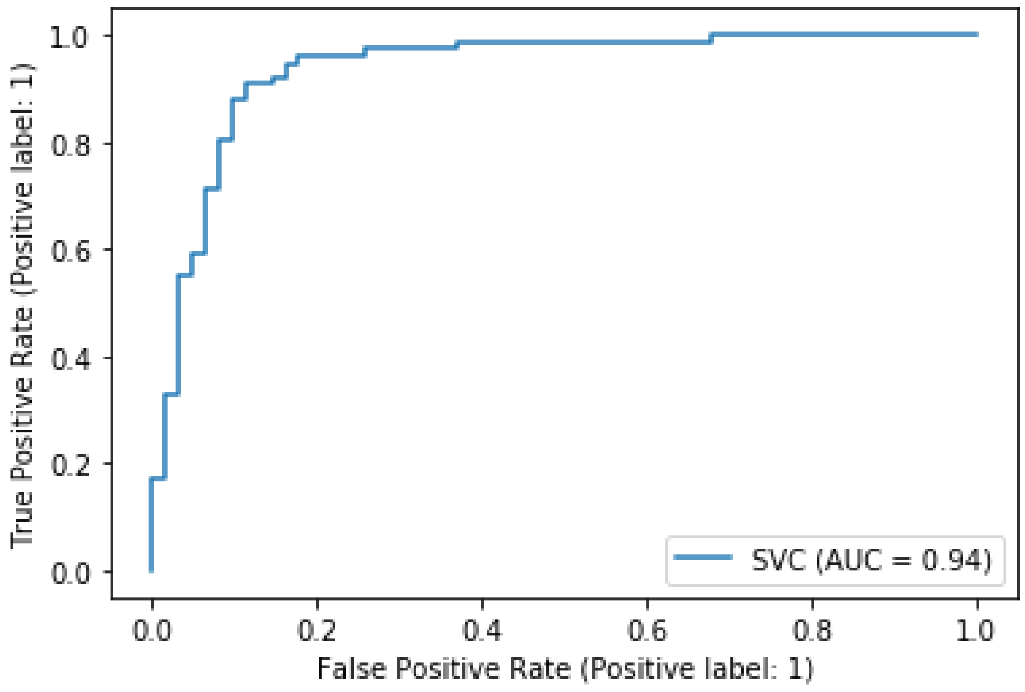
```
9   0.013314    0.003560       0.833333        0.897436     0.795455
0.843373
10  0.013694    0.003720       0.923077        0.913043     0.954545
0.933333
```

```
svm_xvalid_model_scores.mean()[2:]
```

```
test_accuracy     0.855128
test_precision    0.859036
test_recall       0.886628
test_f1           0.871342
dtype: float64
```

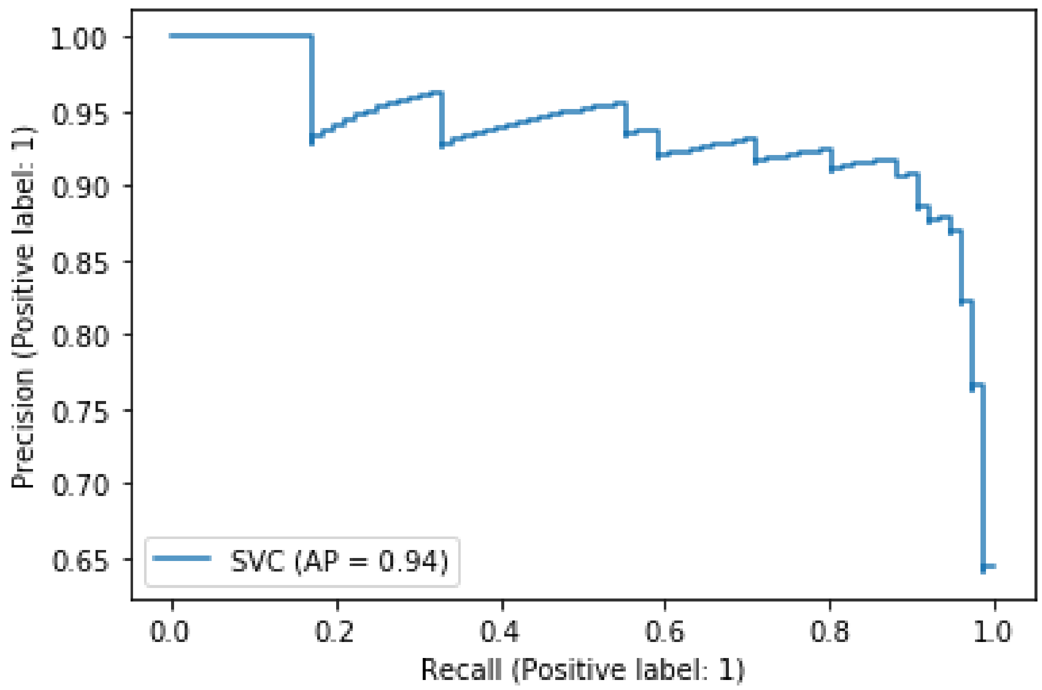
```
plot_roc_curve(SVM_model, X_test_scaled, y_test)
```

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x7fb53093a3d0>
```



```
plot_precision_recall_curve(SVM_model, X_test_scaled, y_test)
```

```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay
at 0x7fb553486d00>
```



```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
auc(fpr, tpr)
```

```
0.8894312393887946
```

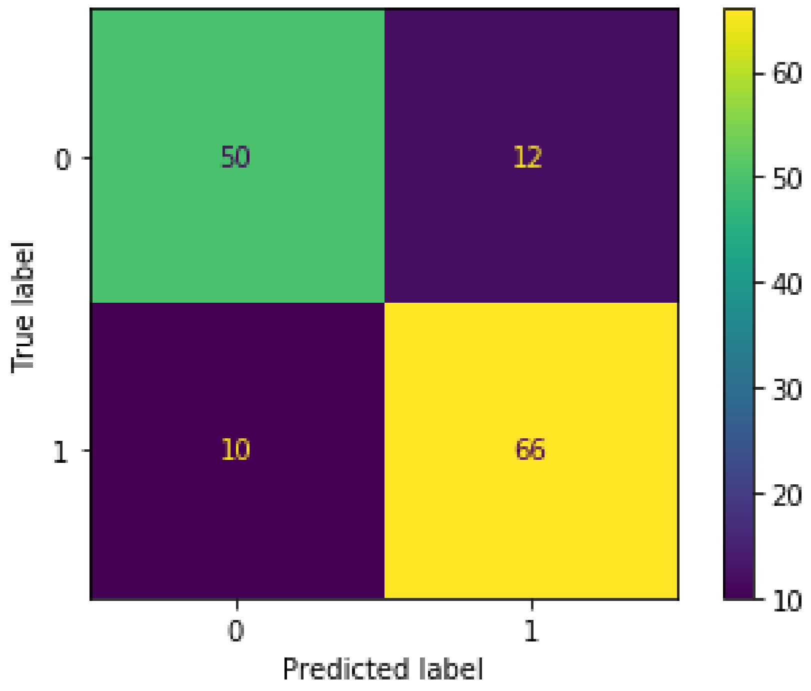
```
SVM2 = SVC(gamma='scale',decision_function_shape='ovo')
SVM2.fit(X_train,y_train)
svm_explainer = shap.KernelExplainer(SVM2.predict,X_test)
svm_shap_values = svm_explainer.shap_values(X_test)
```

```
Using 138 background data samples could cause slower run times.
Consider using shap.sample(data, K) or shap.kmeans(data, K) to
summarize the background as K samples.
100%|██████████| 138/138 [53:23<00:00, 23.21s/it]
```

4. KNN

```
KNN_model = KNeighborsClassifier(n_neighbors=5, algorithm="kd_tree")
KNN_model.fit(X_train_scaled, y_train)
y_pred = KNN_model.predict(X_test_scaled)
y_train_pred = KNN_model.predict(X_train_scaled)

knn_f1 = f1_score(y_test, y_pred)
knn_acc = accuracy_score(y_test, y_pred)
knn_recall = recall_score(y_test, y_pred)
knn_auc = roc_auc_score(y_test, y_pred)

print(confusion_matrix(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")
print(classification_report(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")

plot_confusion_matrix(KNN_model, X_test_scaled, y_test)
```

```
[[50 12]
 [10 66]]
--------------------------------------------------------
              precision    recall  f1-score   support

           0       0.83      0.81      0.82        62
           1       0.85      0.87      0.86        76

    accuracy                           0.84       138
   macro avg       0.84      0.84      0.84       138
weighted avg       0.84      0.84      0.84       138

--------------------------------------------------------

<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at
0x7fb510915a30>
```



```
y_pred_proba = KNN_model.predict_proba(X_test_scaled)
```

```
pd.DataFrame(y_pred_proba)

       0    1
0    0.0  1.0
1    0.2  0.8
2    0.2  0.8
3    0.8  0.2
4    0.4  0.6
..   ...  ...
133  0.8  0.2
134  1.0  0.0
135  0.6  0.4
136  0.0  1.0
137  0.8  0.2

[138 rows x 2 columns]

my_dict = {"Actual": y_test, "Pred": y_pred, "Proba_1":
y_pred_proba[:,1], "Proba_0":y_pred_proba[:,0]}

pd.DataFrame.from_dict(my_dict).sample(10)

     Actual  Pred  Proba_1  Proba_0
615       1     1      1.0      0.0
589       1     1      1.0      0.0
360       1     1      1.0      0.0
338       1     1      0.8      0.2
216       1     1      1.0      0.0
659       1     1      0.8      0.2
595       1     1      1.0      0.0
137       0     0      0.0      1.0
685       1     1      1.0      0.0
550       1     1      1.0      0.0

knn_xvalid_model = KNeighborsClassifier(n_neighbors=5)

knn_xvalid_model_scores = cross_validate(knn_xvalid_model,
X_train_scaled, y_train, scoring = ["accuracy", "precision", "recall",
"f1"], cv = 10)
knn_xvalid_model_scores = pd.DataFrame(knn_xvalid_model_scores, index
= range(1, 11))

knn_xvalid_model_scores

    fit_time  score_time  test_accuracy  test_precision  test_recall
test_f1
1   0.001457    0.004014       0.807692        0.791667     0.883721
0.835165
2   0.000824    0.003676       0.858974        0.833333     0.930233
0.879121
3   0.000668    0.003699       0.923077        0.930233     0.930233
```

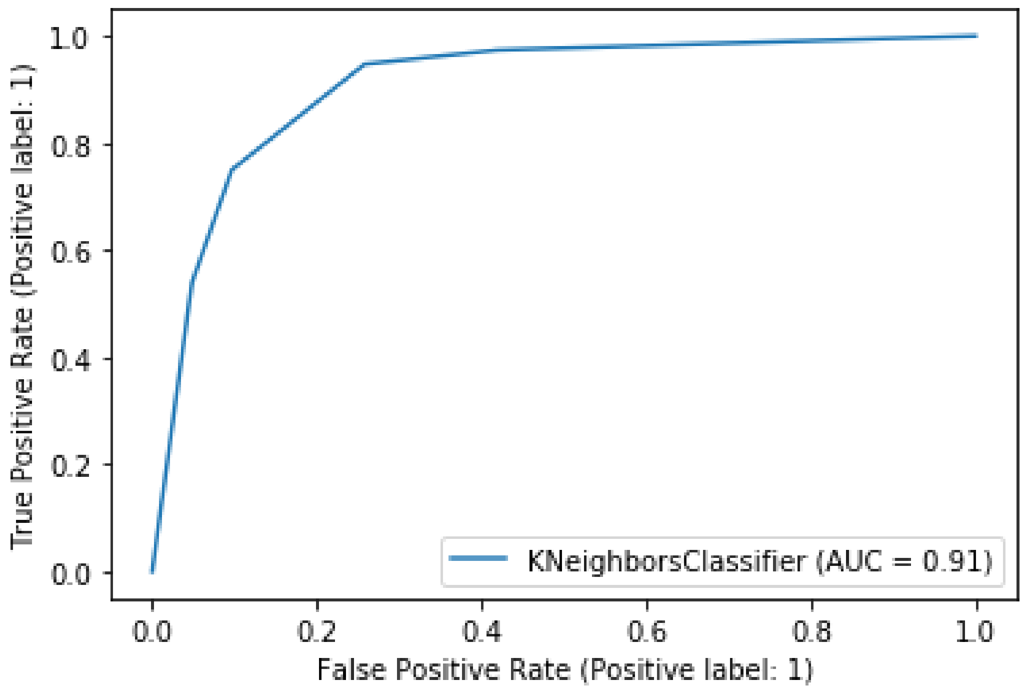
```
0.930233
4   0.000692    0.003547       0.820513        0.837209     0.837209
0.837209
5   0.000654    0.003531       0.923077        0.893617     0.976744
0.933333
6   0.000637    0.003541       0.820513        0.822222     0.860465
0.840909
7   0.000635    0.003517       0.871795        0.836735     0.953488
0.891304
8   0.000626    0.003527       0.858974        0.847826     0.906977
0.876404
9   0.000645    0.003621       0.833333        0.897436     0.795455
0.843373
10  0.000638    0.003487       0.935897        0.914894     0.977273
0.945055
```

```
knn_xvalid_model_scores.mean()[2:]
```

```
test_accuracy     0.865385
test_precision    0.860517
test_recall       0.905180
test_f1           0.881211
dtype: float64
```

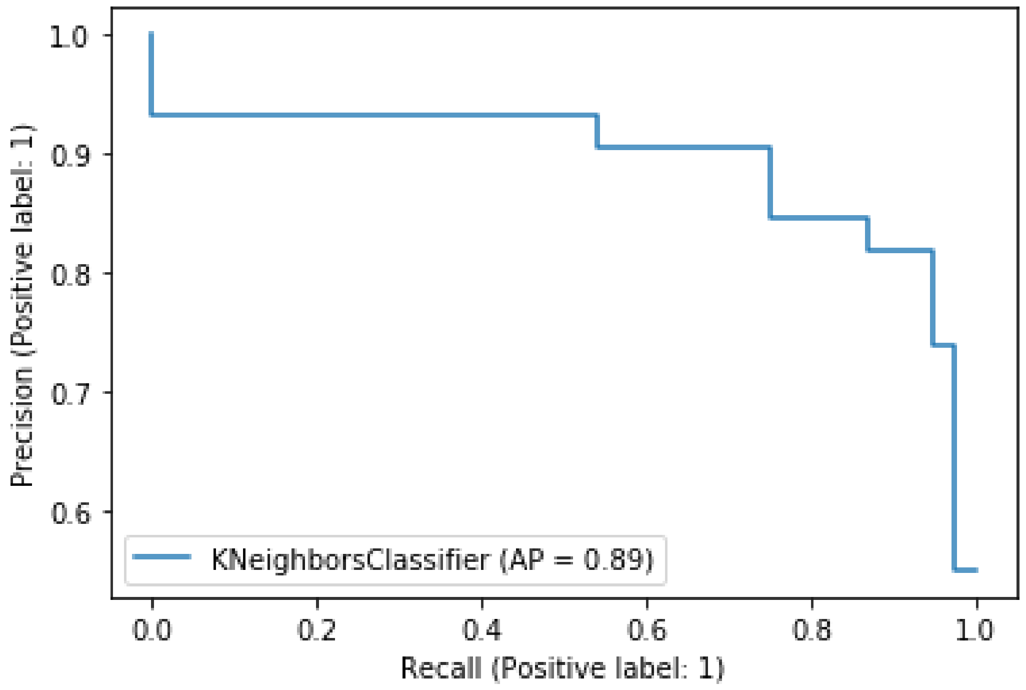
```
plot_roc_curve(KNN_model, X_test_scaled, y_test)
```

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x7fb55353d460>
```



```
plot_precision_recall_curve(KNN_model, X_test_scaled, y_test)
```

```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay
at 0x7fb5108f7940>
```



```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
auc(fpr, tpr)
```

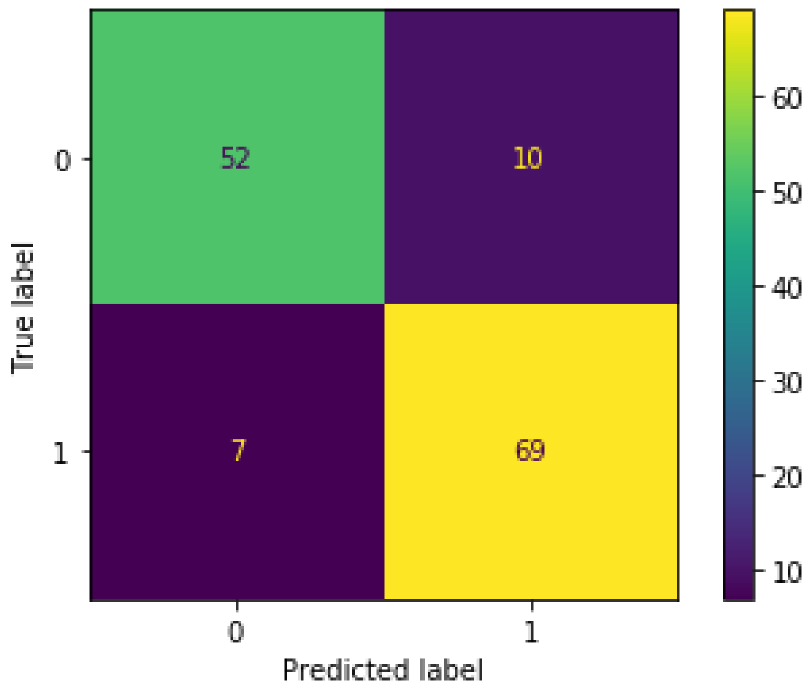
```
0.8374363327674023
```

5. AdaBoost

```
AB_model = AdaBoostClassifier(n_estimators=50, random_state=101)
AB_model.fit(X_train, y_train)
y_pred = AB_model.predict(X_test)
y_train_pred = AB_model.predict(X_train)

ab_f1 = f1_score(y_test, y_pred)
ab_acc = accuracy_score(y_test, y_pred)
ab_recall = recall_score(y_test, y_pred)
ab_auc = roc_auc_score(y_test, y_pred)

print(confusion_matrix(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")
print(classification_report(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")
```

```
plot_confusion_matrix(AB_model, X_test, y_test)
```

```
[[52 10]
 [ 7 69]]
--------------------------------------------------------
              precision    recall  f1-score   support

           0       0.88      0.84      0.86        62
           1       0.87      0.91      0.89        76

    accuracy                           0.88       138
   macro avg       0.88      0.87      0.87       138
weighted avg       0.88      0.88      0.88       138

--------------------------------------------------------

<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at
0x7fb5108dac40>
```



```
ab_xvalid_model = AdaBoostClassifier(n_estimators=50,
random_state=101)

ab_xvalid_model_scores = cross_validate(ab_xvalid_model, X_train,
y_train, scoring = ['accuracy', 'precision','recall', 'f1'], cv = 10)
ab_xvalid_model_scores = pd.DataFrame(ab_xvalid_model_scores, index =
range(1, 11))
```

```
ab_xvalid_model_scores
```

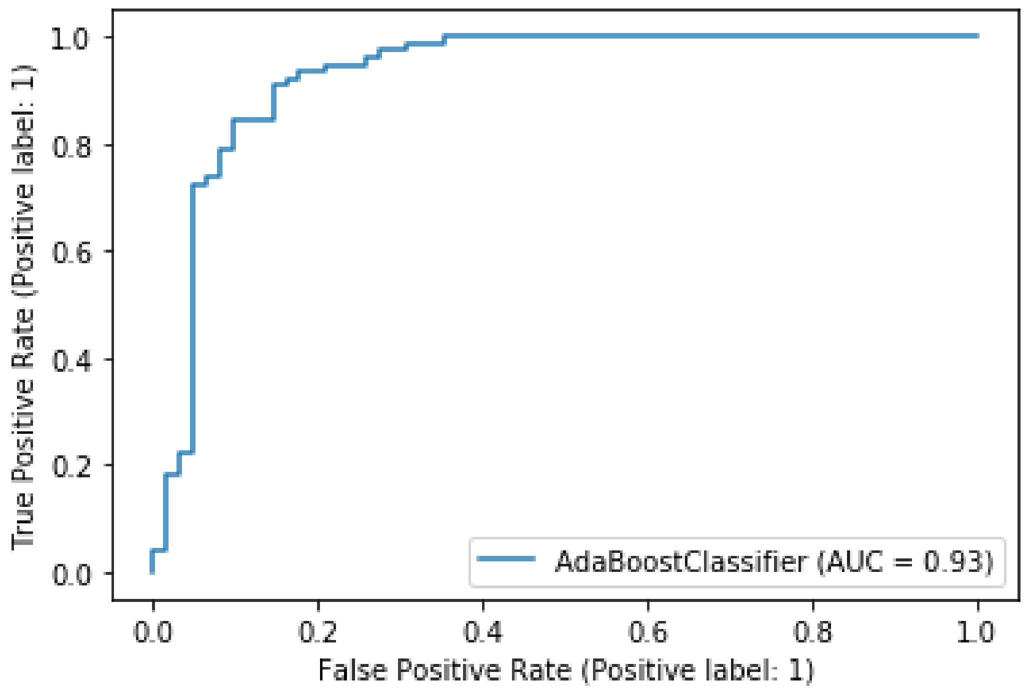
```
    fit_time  score_time  test_accuracy  test_precision  test_recall
test_f1
1   0.047987    0.005356       0.782051        0.795455     0.813953
0.804598
2   0.042579    0.005095       0.807692        0.833333     0.813953
0.823529
3   0.042883    0.005140       0.871795        0.883721     0.883721
0.883721
4   0.042217    0.005093       0.794872        0.813953     0.813953
0.813953
5   0.042189    0.005079       0.833333        0.840909     0.860465
0.850575
6   0.042145    0.005073       0.833333        0.857143     0.837209
0.847059
7   0.042070    0.005088       0.923077        0.893617     0.976744
0.933333
8   0.042315    0.005118       0.833333        0.857143     0.837209
0.847059
9   0.042017    0.005064       0.833333        0.878049     0.818182
0.847059
10  0.042137    0.005109       0.923077        0.931818     0.931818
0.931818
```

```
ab_xvalid_model_scores.mean()
```

```
fit_time          0.042854
score_time        0.005122
test_accuracy     0.843590
test_precision    0.858514
test_recall       0.858721
test_f1           0.858270
dtype: float64
```

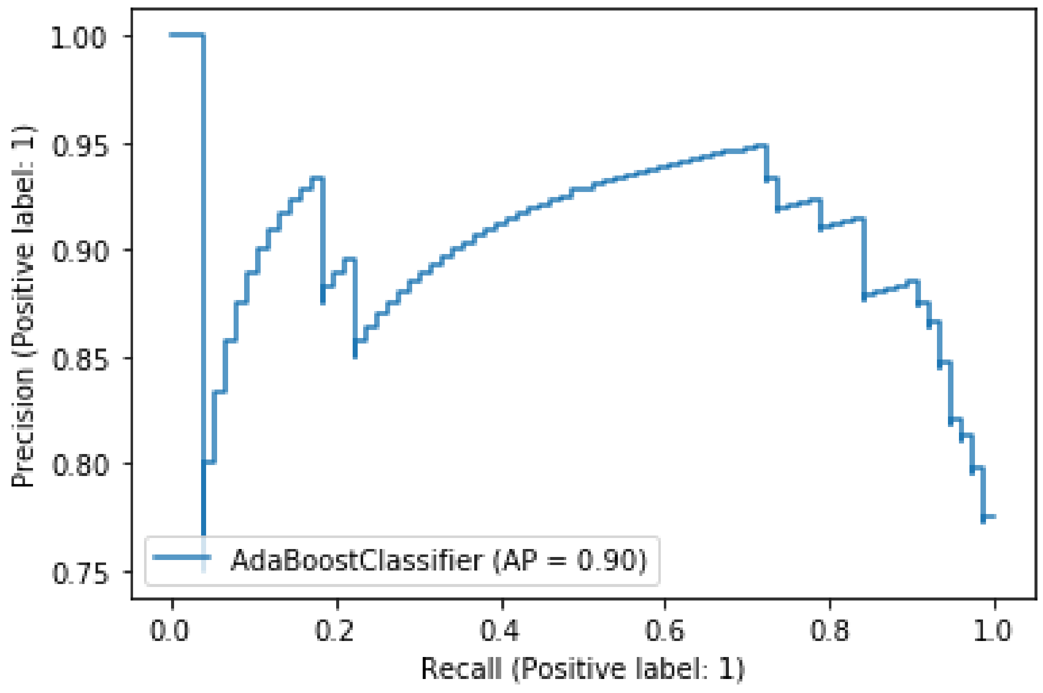
```
plot_roc_curve(AB_model, X_test, y_test)
```

```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x7fb530bc56d0>
```



```
plot_precision_recall_curve(AB_model, X_test, y_test)
```

```
<sklearn.metrics._plot.precision_recall_curve.PrecisionRecallDisplay
at 0x7fb530c78400>
```



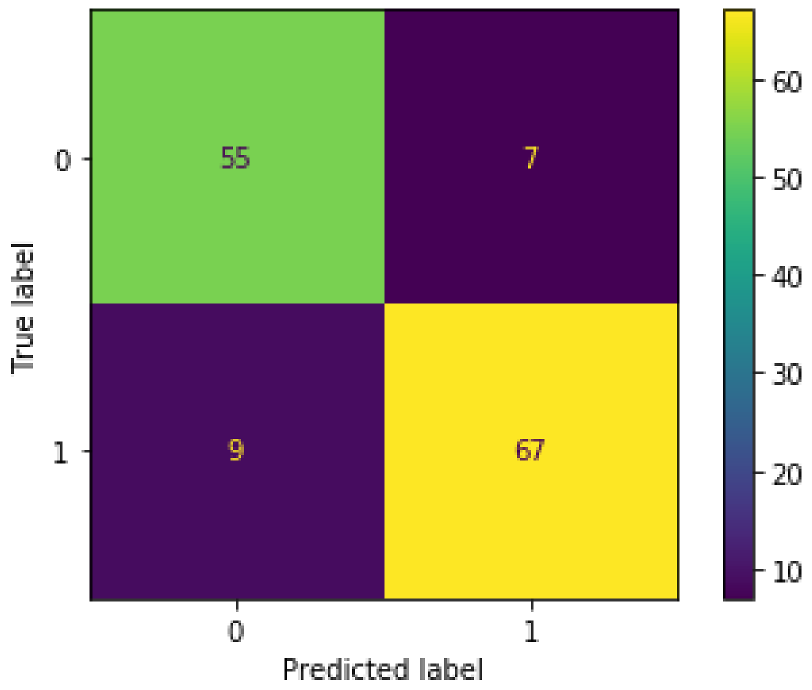
```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
auc(fpr, tpr)
```

```
0.8733022071307301
```

6. XGBoost

```
XGB_model = XGBClassifier(random_state=101)
XGB_model.fit(X_train_scaled, y_train)
y_pred = XGB_model.predict(X_test_scaled)
y_train_pred = XGB_model.predict(X_train_scaled)

xgb_f1 = f1_score(y_test, y_pred)
xgb_acc = accuracy_score(y_test, y_pred)
xgb_recall = recall_score(y_test, y_pred)
xgb_auc = roc_auc_score(y_test, y_pred)

print(confusion_matrix(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")
print(classification_report(y_test, y_pred))
print("\
033[1m--------------------------------------------------------\
033[0m")

plot_confusion_matrix(XGB_model, X_test_scaled, y_test)
```

```
[[55  7]
 [ 9 67]]
--------------------------------------------------------
              precision    recall  f1-score   support

           0       0.86      0.89      0.87        62
           1       0.91      0.88      0.89        76

    accuracy                           0.88       138
   macro avg       0.88      0.88      0.88       138
weighted avg       0.88      0.88      0.88       138

--------------------------------------------------------

<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at
0x7fb530c78550>
```



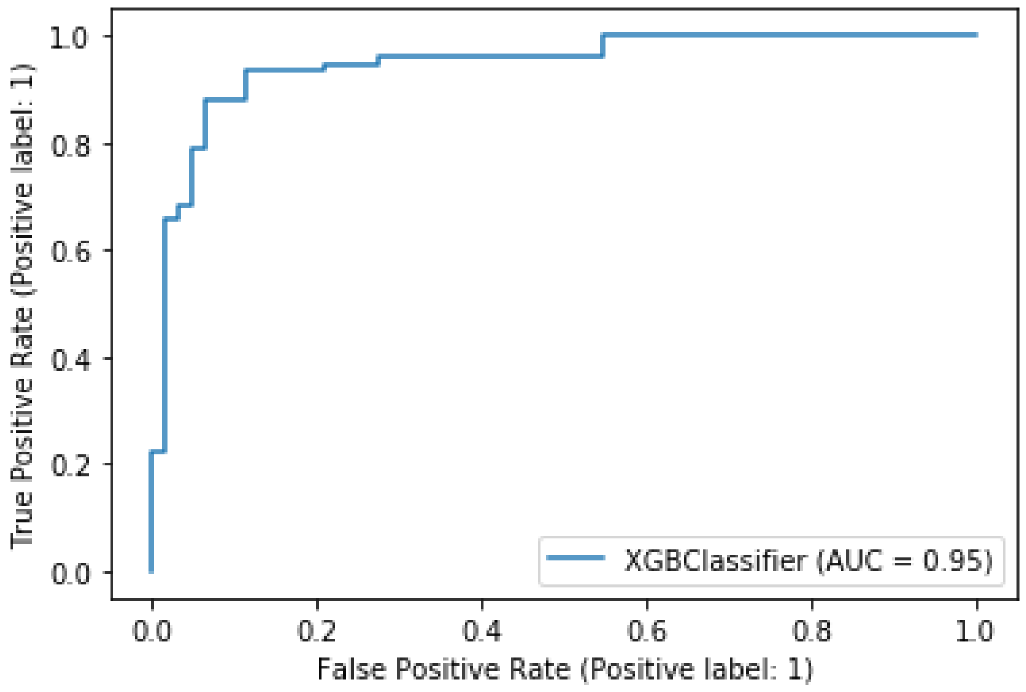
```
xgb_xvalid_model = XGBClassifier(random_state=101)

xgb_xvalid_model_scores = cross_validate(xgb_xvalid_model,
X_train_scaled, y_train, scoring = ["accuracy", "precision", "recall",
"f1"], cv = 10)
xgb_xvalid_model_scores = pd.DataFrame(xgb_xvalid_model_scores, index
= range(1, 11))

xgb_xvalid_model_scores

    fit_time  score_time  test_accuracy  test_precision  test_recall
test_f1
1   0.075475    0.002784       0.820513        0.837209     0.837209
0.837209
2   0.058356    0.002511       0.756410        0.772727     0.790698
0.781609
3   0.061254    0.002537       0.897436        0.888889     0.930233
0.909091
4   0.063938    0.003054       0.846154        0.860465     0.860465
0.860465
5   0.058550    0.002478       0.846154        0.878049     0.837209
0.857143
6   0.058123    0.002985       0.884615        0.854167     0.953488
0.901099
7   0.065888    0.002515       0.846154        0.816327     0.930233
0.869565
8   0.061777    0.002487       0.820513        0.837209     0.837209
0.837209
9   0.086297    0.002788       0.807692        0.871795     0.772727
```

```
0.819277
10  0.062380    0.002563       0.897436        0.891304     0.931818
0.911111
```

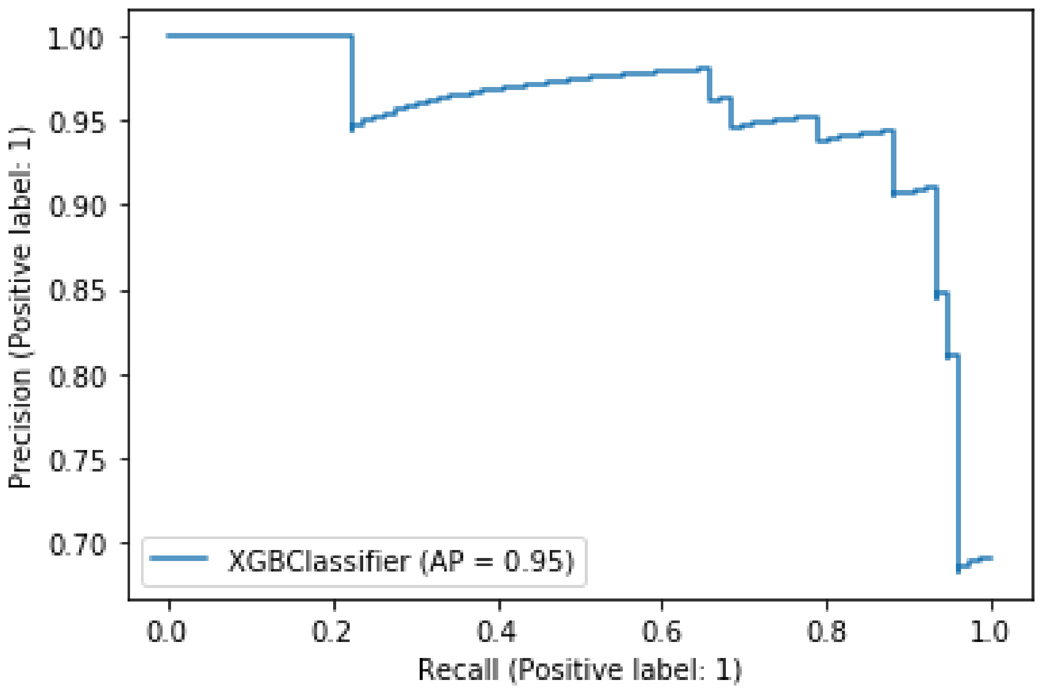
```
xgb_xvalid_model_scores.mean()
```

```
fit_time           0.065204
score_time         0.002670
test_accuracy      0.842308
test_precision     0.850814
test_recall        0.868129
test_f1            0.858378
dtype: float64
```

```
plot_roc_curve(XGB_model, X_test_scaled, y_test);
```



```
plot_precision_recall_curve(XGB_model, X_test_scaled, y_test);
```



```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
auc(fpr, tpr)
```

```
0.8843378607809848
```

Explaining the model

Permutation Tables

```
perm = PermutationImportance(log, random_state=1).fit(X_test, y_test)
eli5.show_weights(perm, feature_names = X_test.columns.tolist())
```

```
<IPython.core.display.HTML object>
```

```
perm = PermutationImportance(tree_clf, random_state=1).fit(X_test,
y_test)
eli5.show_weights(perm, feature_names = X_test.columns.tolist())
```

```
<IPython.core.display.HTML object>
```

```
perm = PermutationImportance(SVM2, random_state=1).fit(X_test, y_test)
eli5.show_weights(perm, feature_names = X_test.columns.tolist())
```

```
<IPython.core.display.HTML object>
```

```
perm = PermutationImportance(KNN_model, random_state=1).fit(X_test,
y_test)
eli5.show_weights(perm, feature_names = X_test.columns.tolist())
```

```
<IPython.core.display.HTML object>
```

```
perm = PermutationImportance(AB_model, random_state=1).fit(X_test,
y_test)
eli5.show_weights(perm, feature_names = X_test.columns.tolist())
```

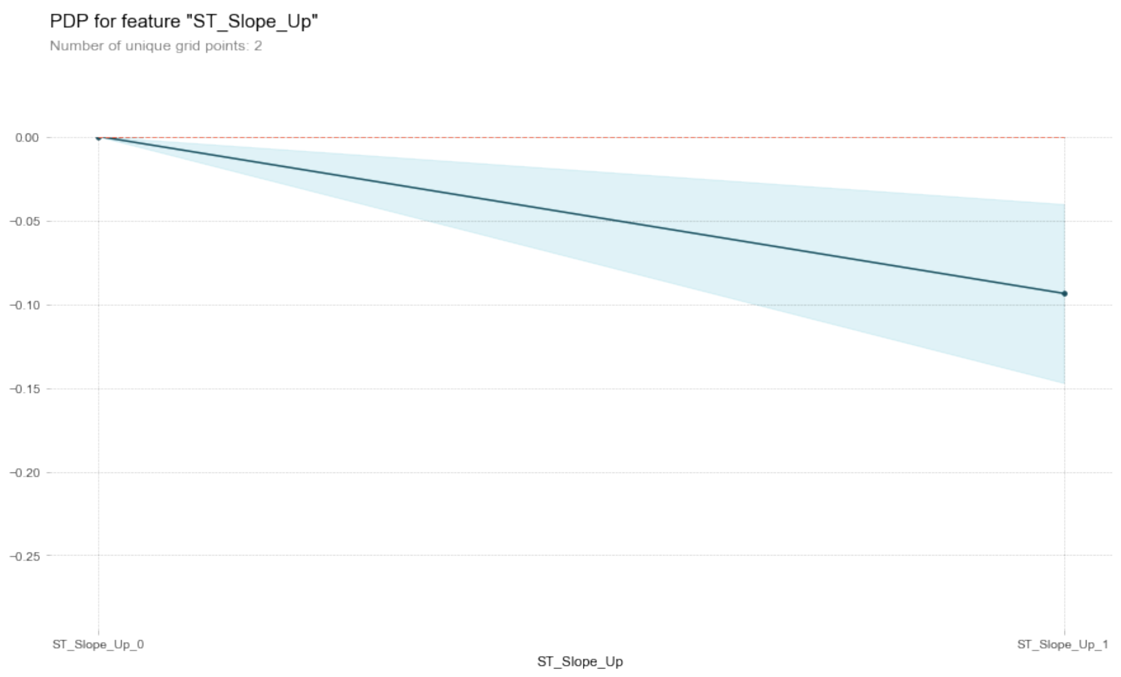
```
<IPython.core.display.HTML object>
```

```
perm = PermutationImportance(XGB_model, random_state=1).fit(X_test,
y_test)
eli5.show_weights(perm, feature_names = X_test.columns.tolist())
```

```
<IPython.core.display.HTML object>
```

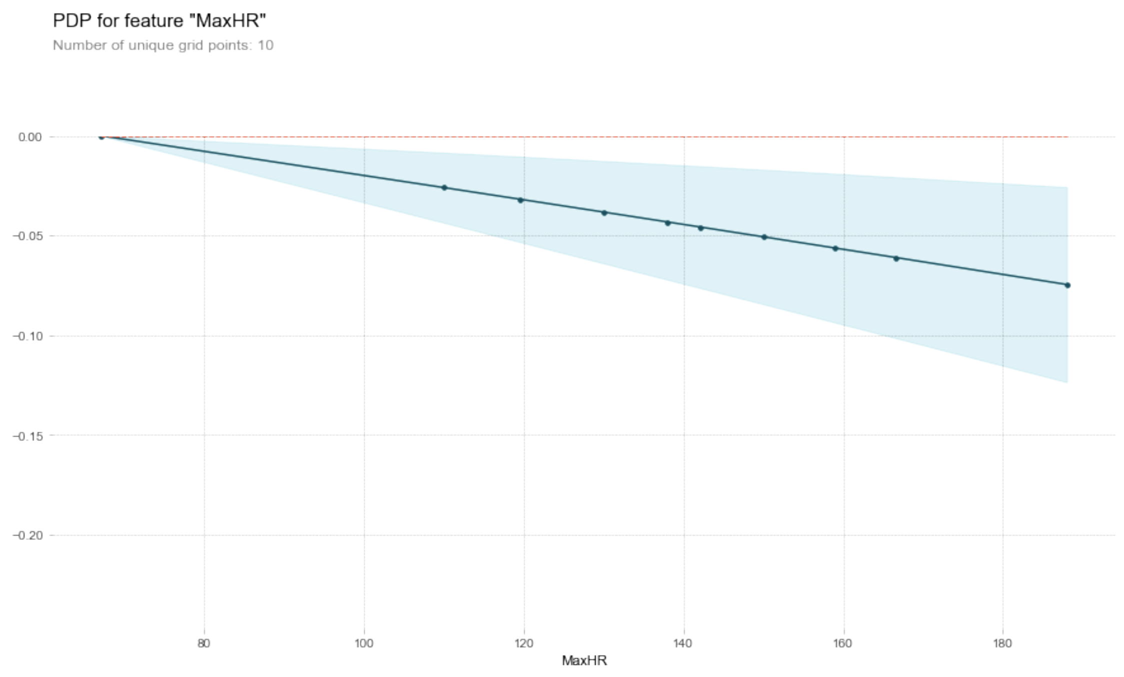
Partial Dependence Plot

```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'ST_Slope_Up'
pdp_dist = pdp.pdp_isolate(model=log, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```

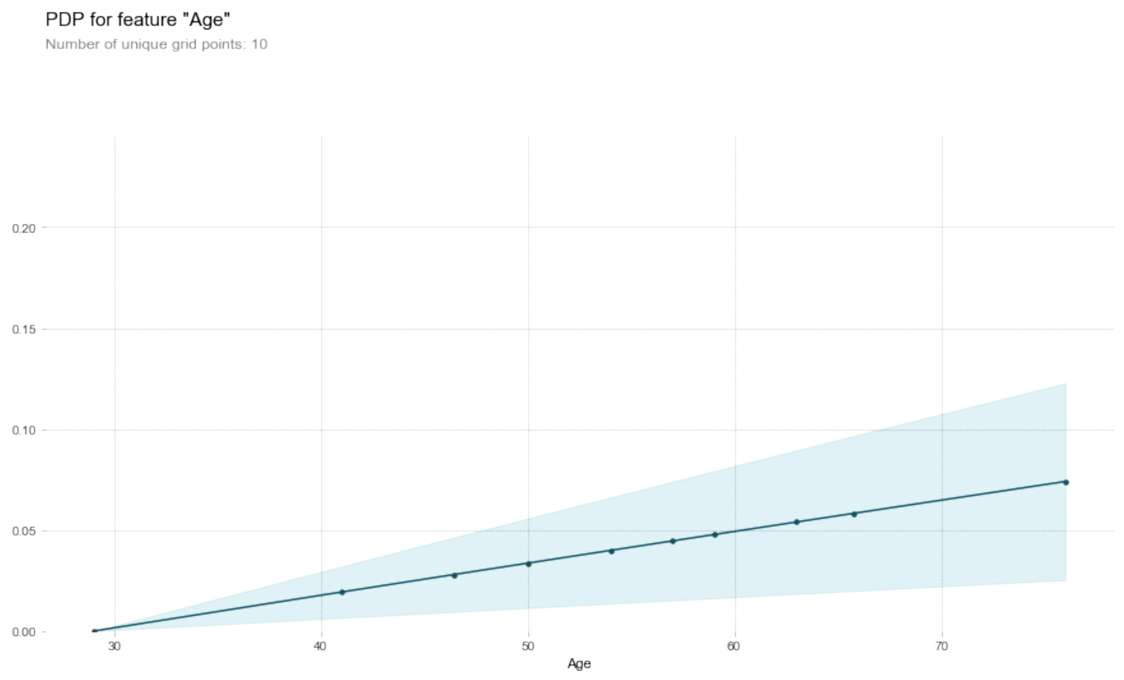


```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')
```

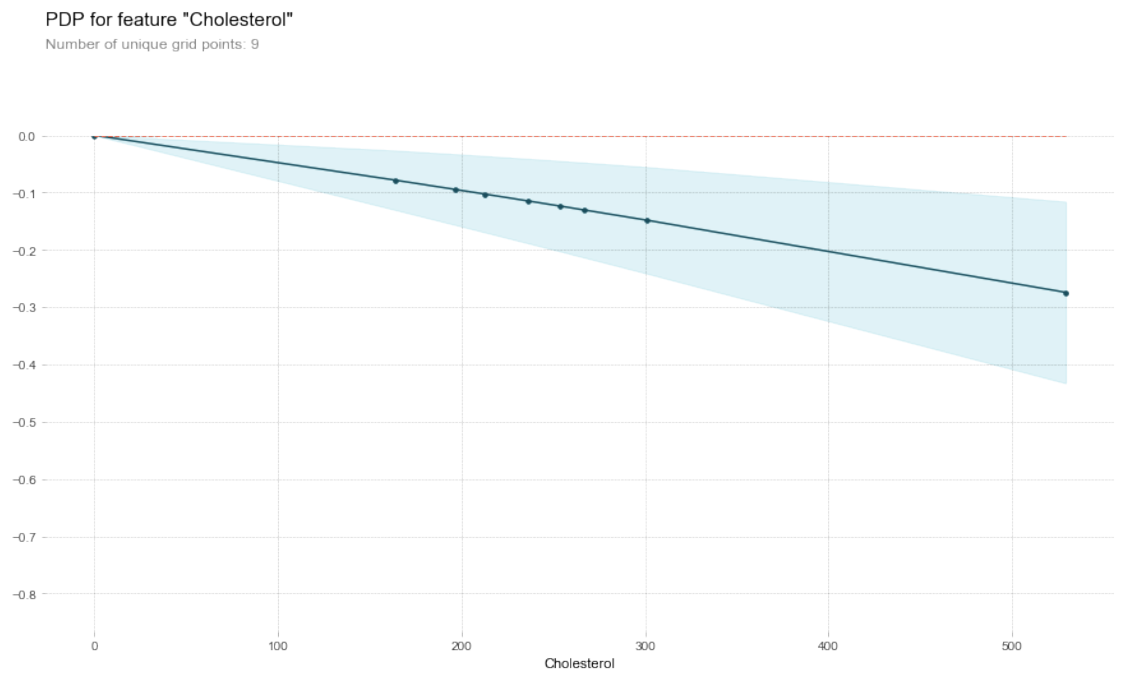
```
feat_name = 'MaxHR'
pdp_dist = pdp.pdp_isolate(model=log, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



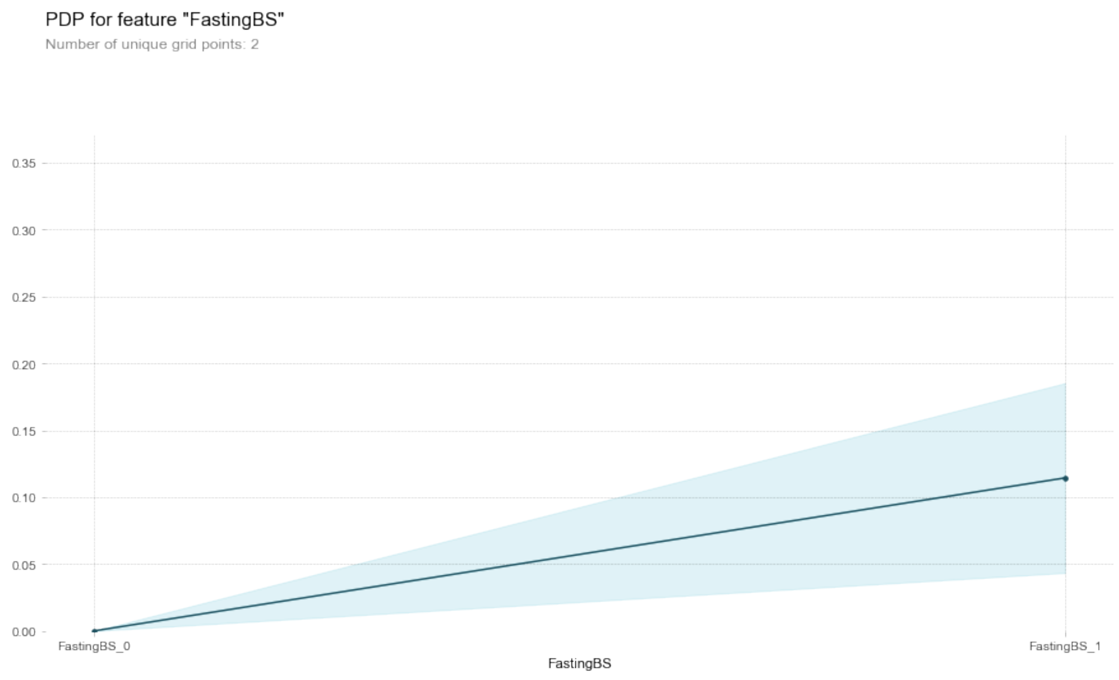
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'Age'
pdp_dist = pdp.pdp_isolate(model=log, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



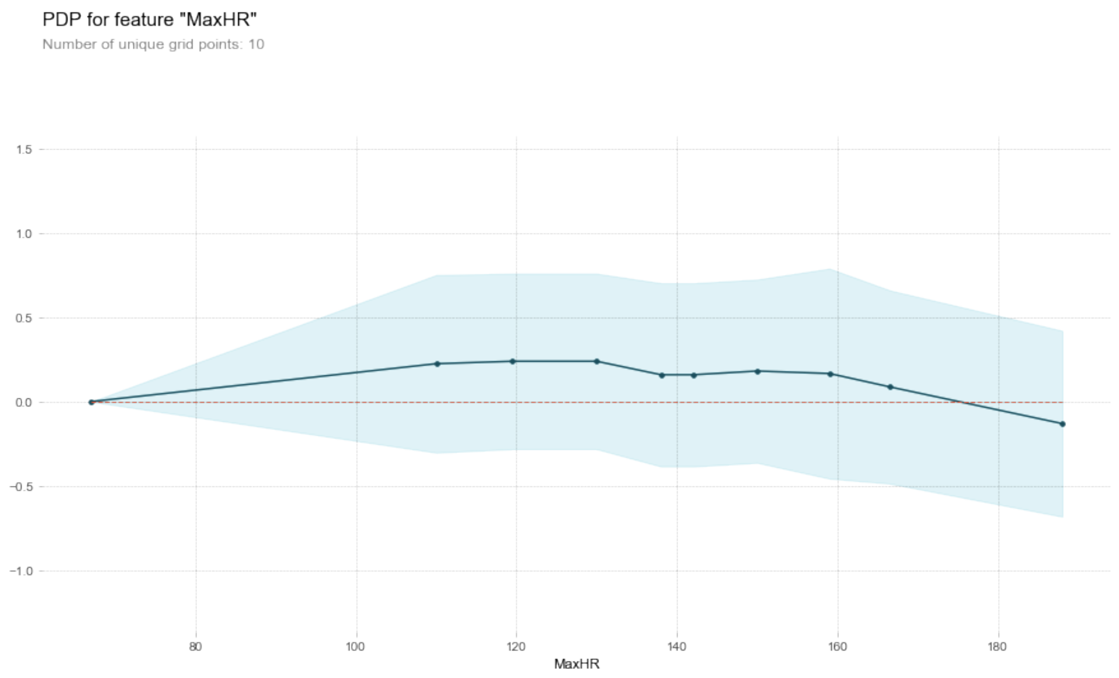
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'Cholesterol'
pdp_dist = pdp.pdp_isolate(model=log, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



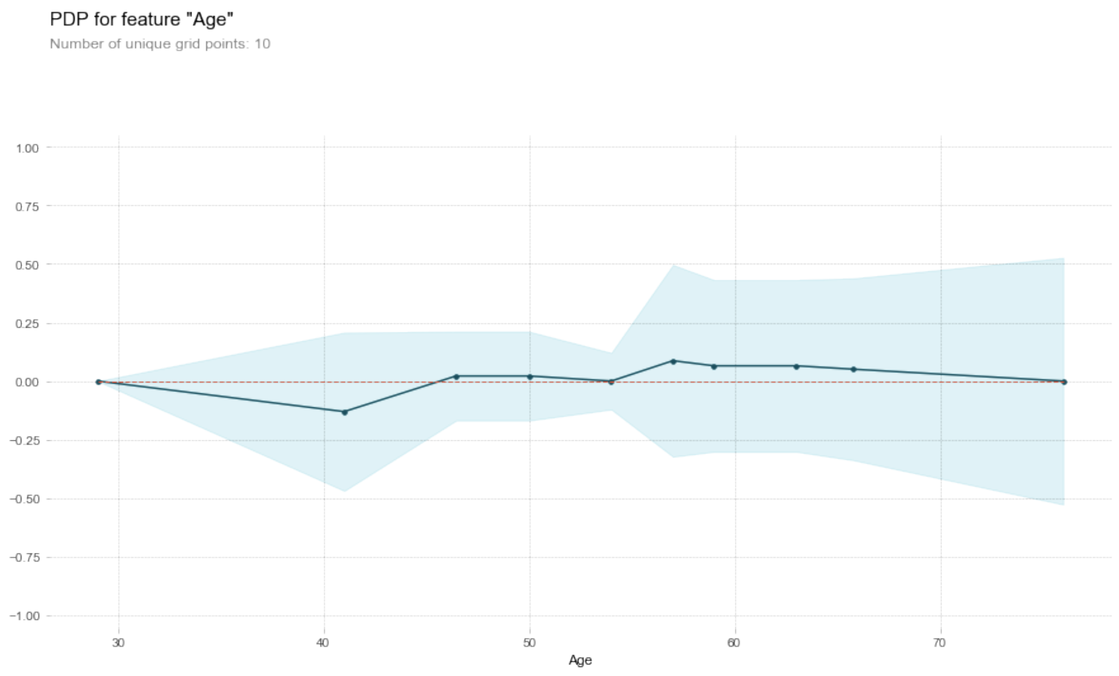
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'FastingBS'
pdp_dist = pdp.pdp_isolate(model=log, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



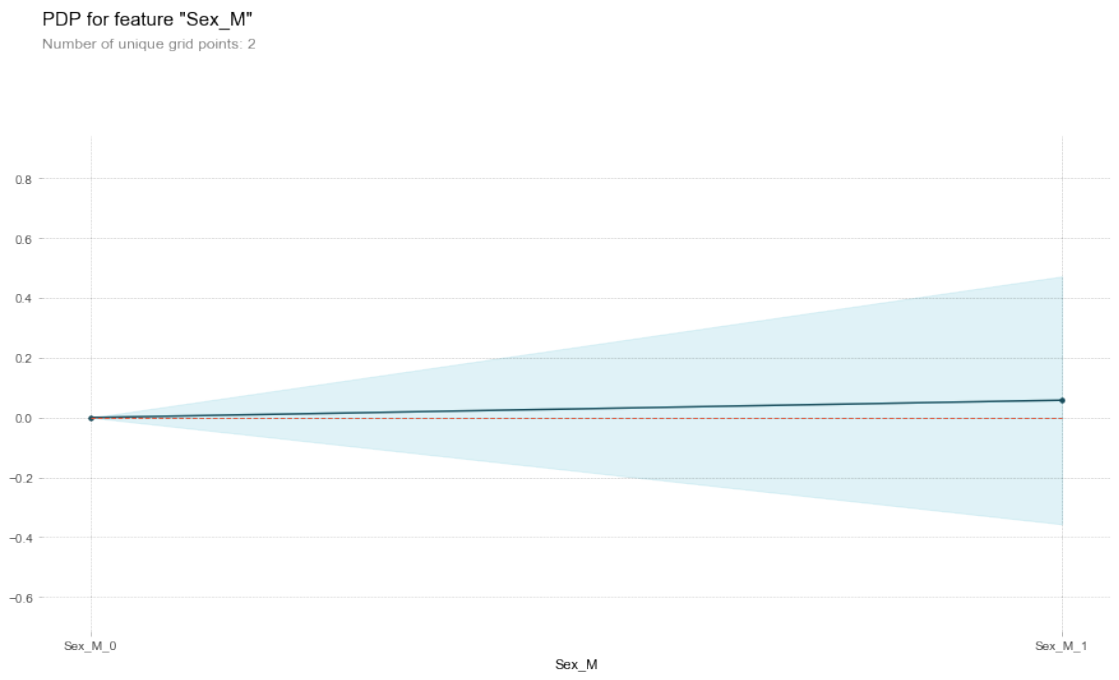
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'MaxHR'
pdp_dist = pdp.pdp_isolate(model=tree_clf, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



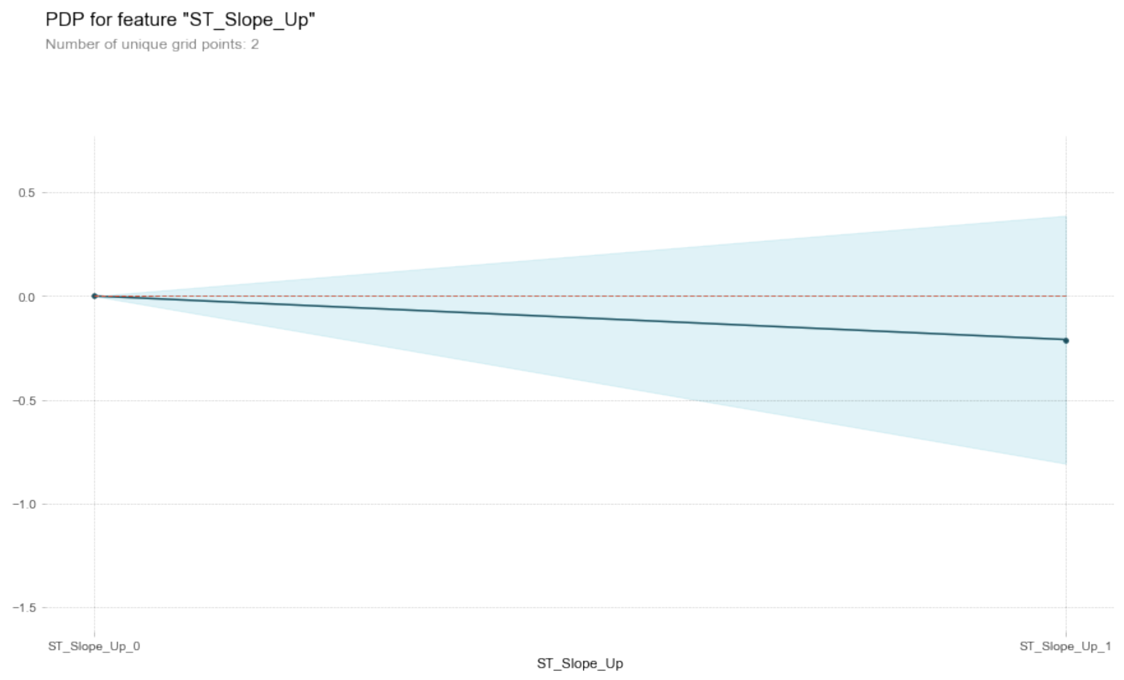
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'Age'
pdp_dist = pdp.pdp_isolate(model=tree_clf, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



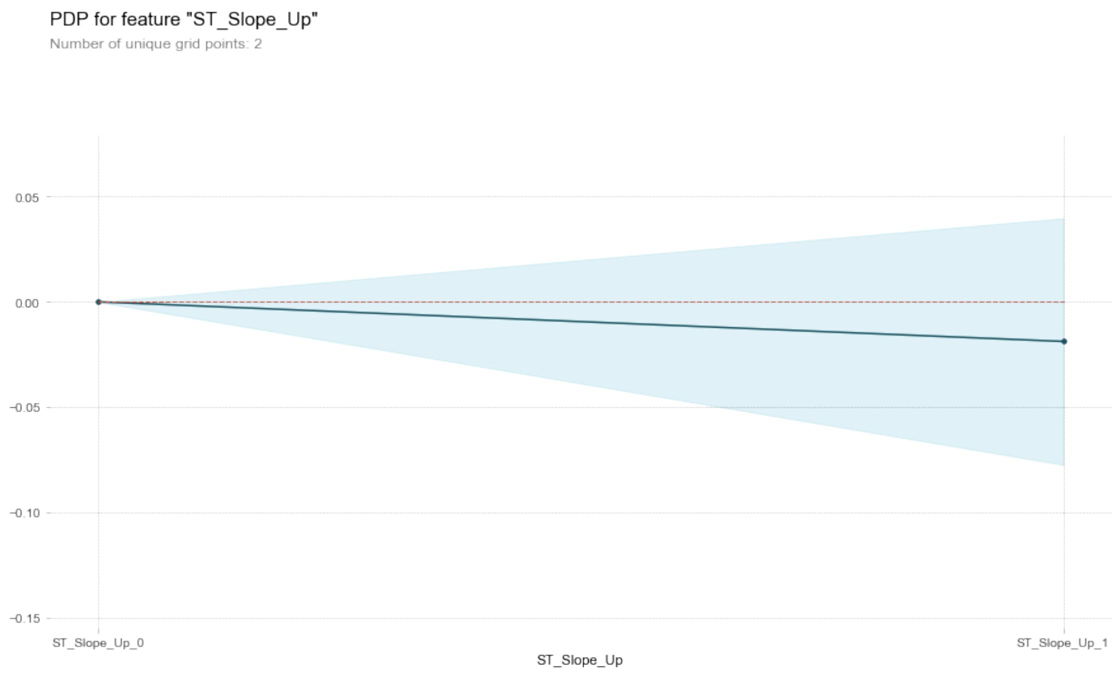
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'Sex_M'
pdp_dist = pdp.pdp_isolate(model=tree_clf, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



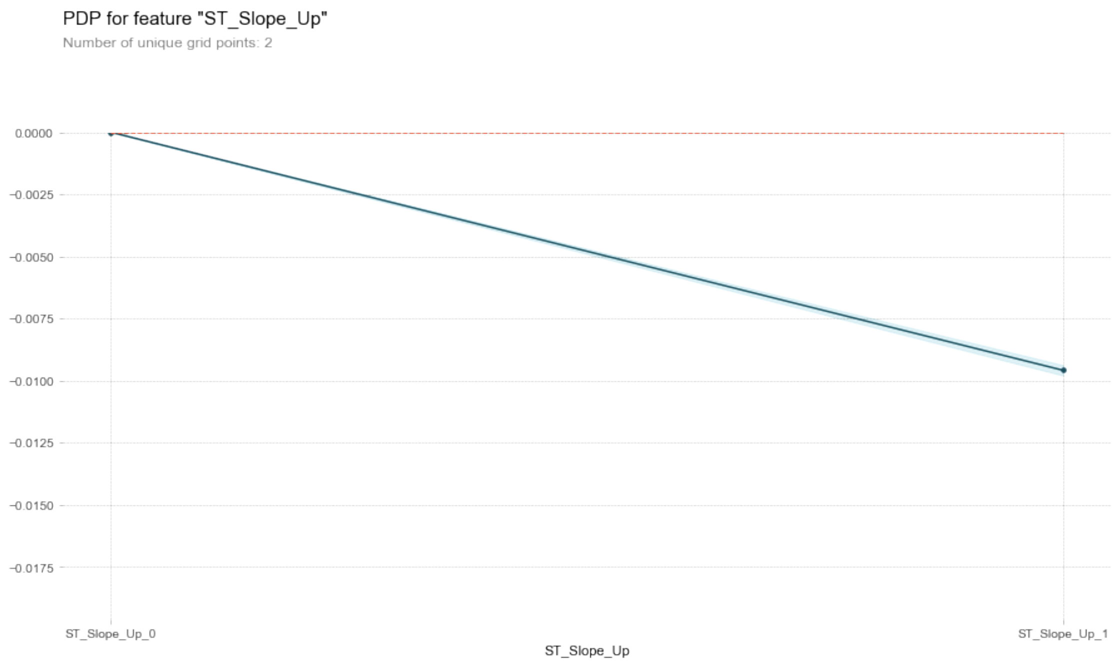
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'ST_Slope_Up'
pdp_dist = pdp.pdp_isolate(model=tree_clf, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



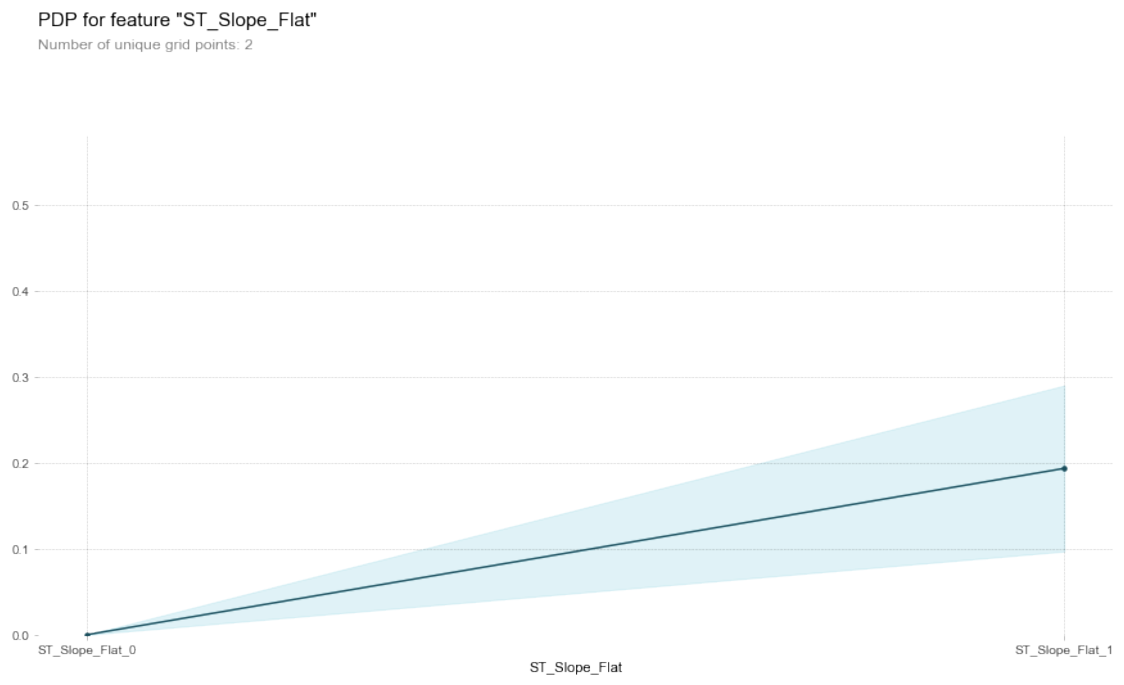
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'ST_Slope_Up'
pdp_dist = pdp.pdp_isolate(model=KNN_model, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



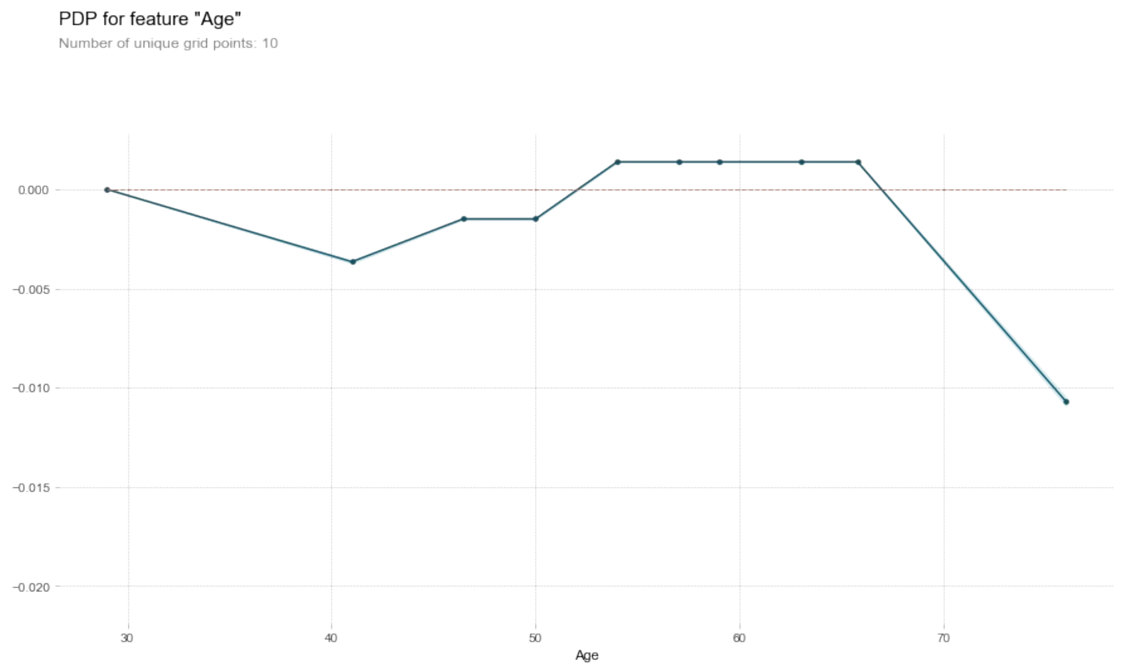
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'ST_Slope_Up'
pdp_dist = pdp.pdp_isolate(model=AB_model, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



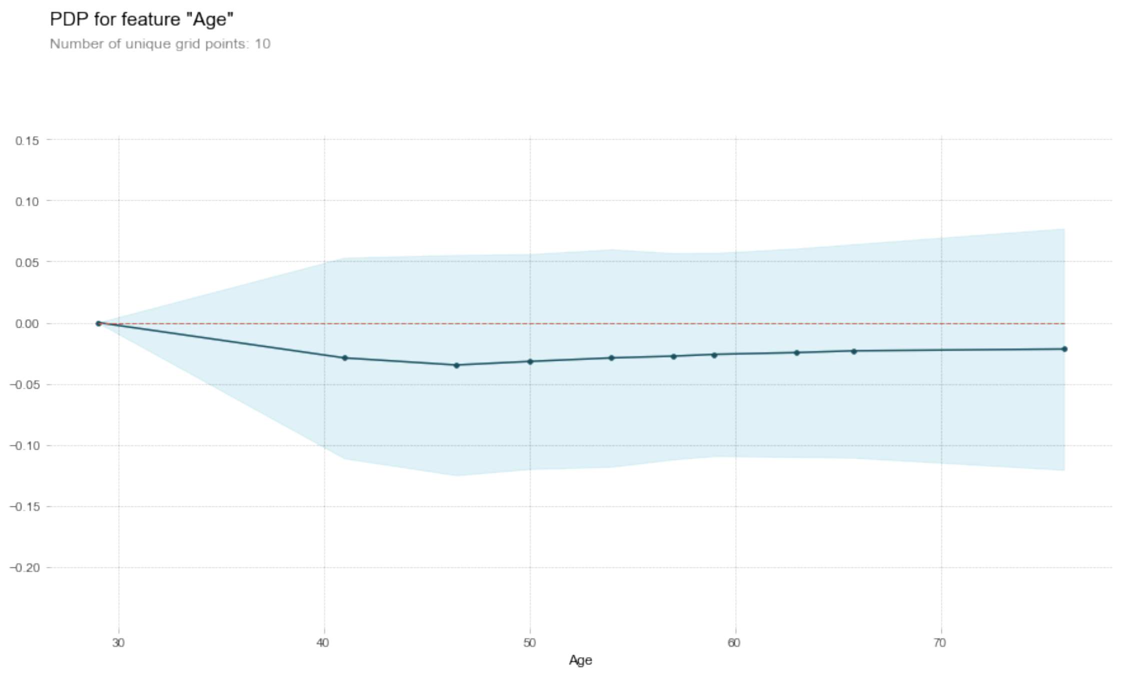
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'ST_Slope_Flat'
pdp_dist = pdp.pdp_isolate(model=log, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



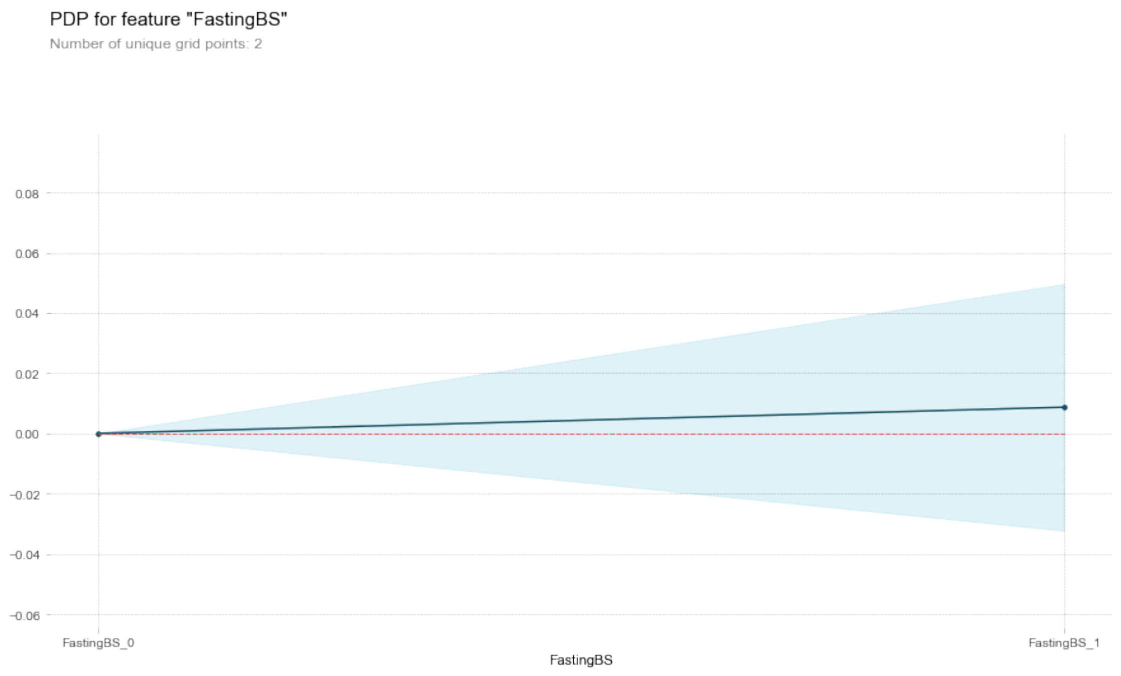
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'Age'
pdp_dist = pdp.pdp_isolate(model=AB_model, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



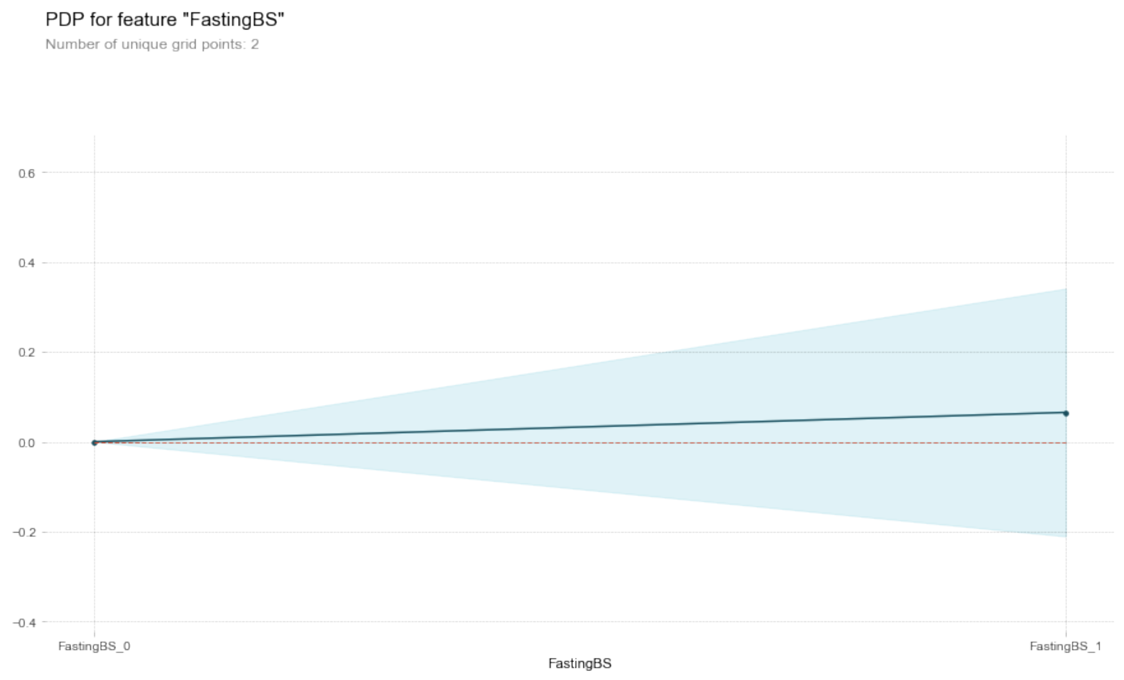
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'Age'
pdp_dist = pdp.pdp_isolate(model=KNN_model, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



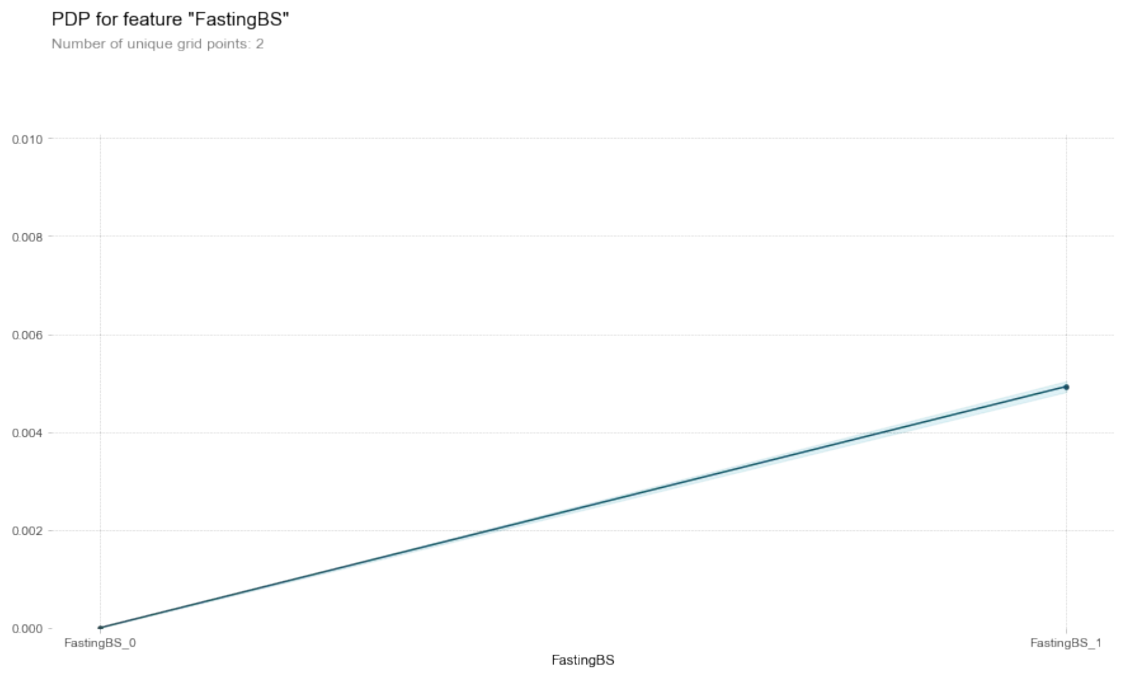
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'FastingBS'
pdp_dist = pdp.pdp_isolate(model=KNN_model, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```



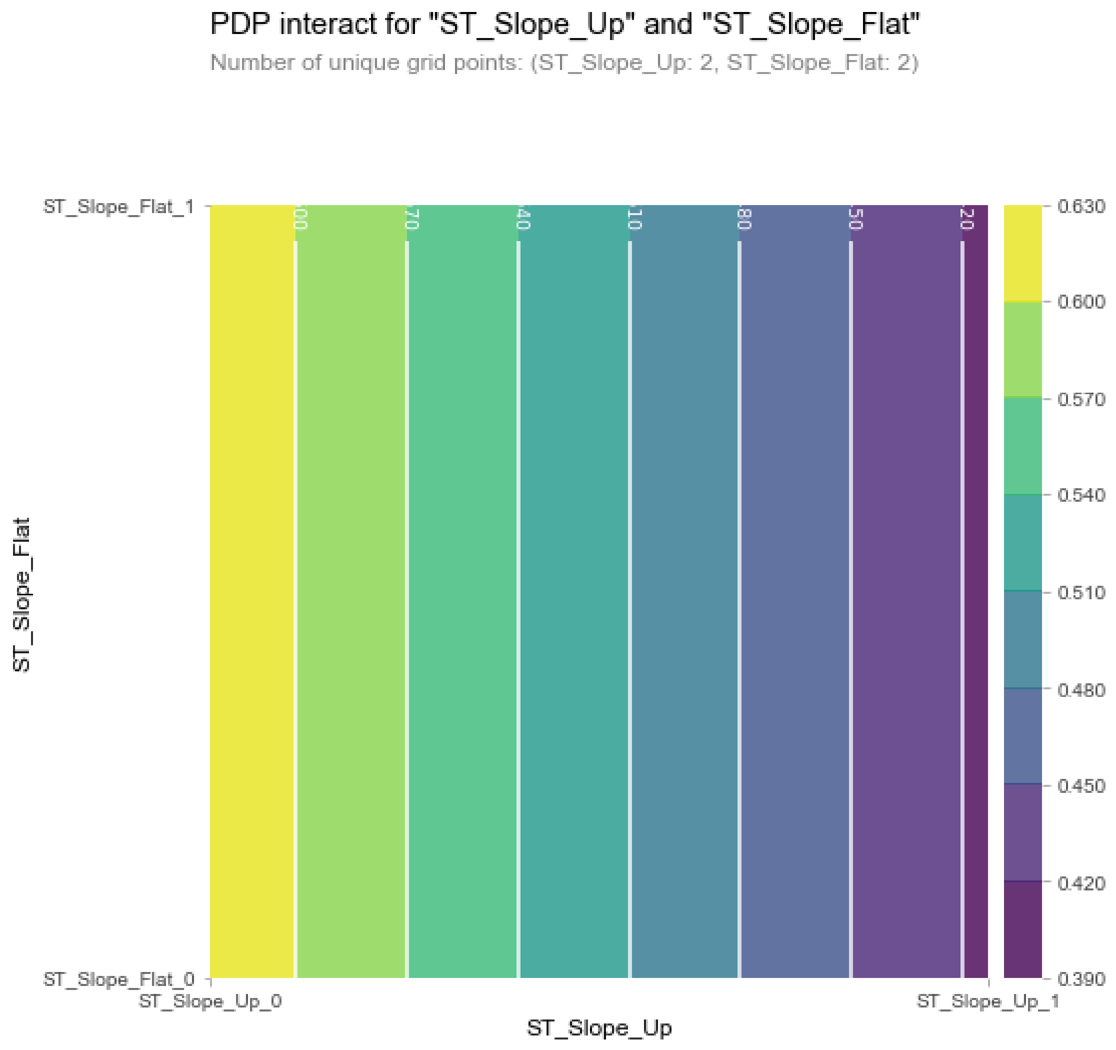
```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'FastingBS'
pdp_dist = pdp.pdp_isolate(model=tree_clf, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```

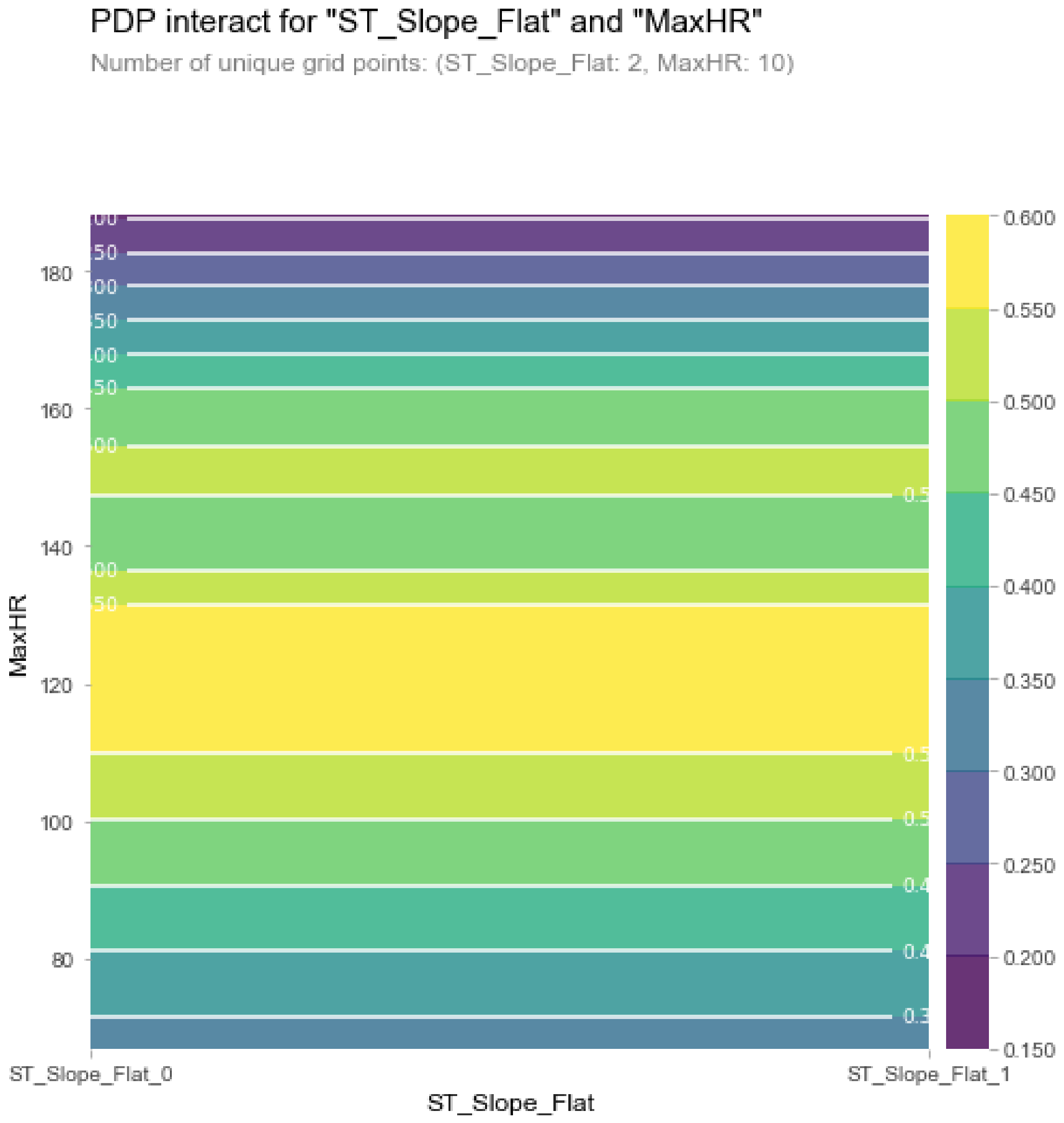


```
base_features = data.columns.values.tolist()
base_features.remove('HeartDisease')

feat_name = 'FastingBS'
pdp_dist = pdp.pdp_isolate(model=AB_model, dataset=X_test,
model_features=base_features, feature=feat_name)

pdp.pdp_plot(pdp_dist, feat_name)
plt.show()
```

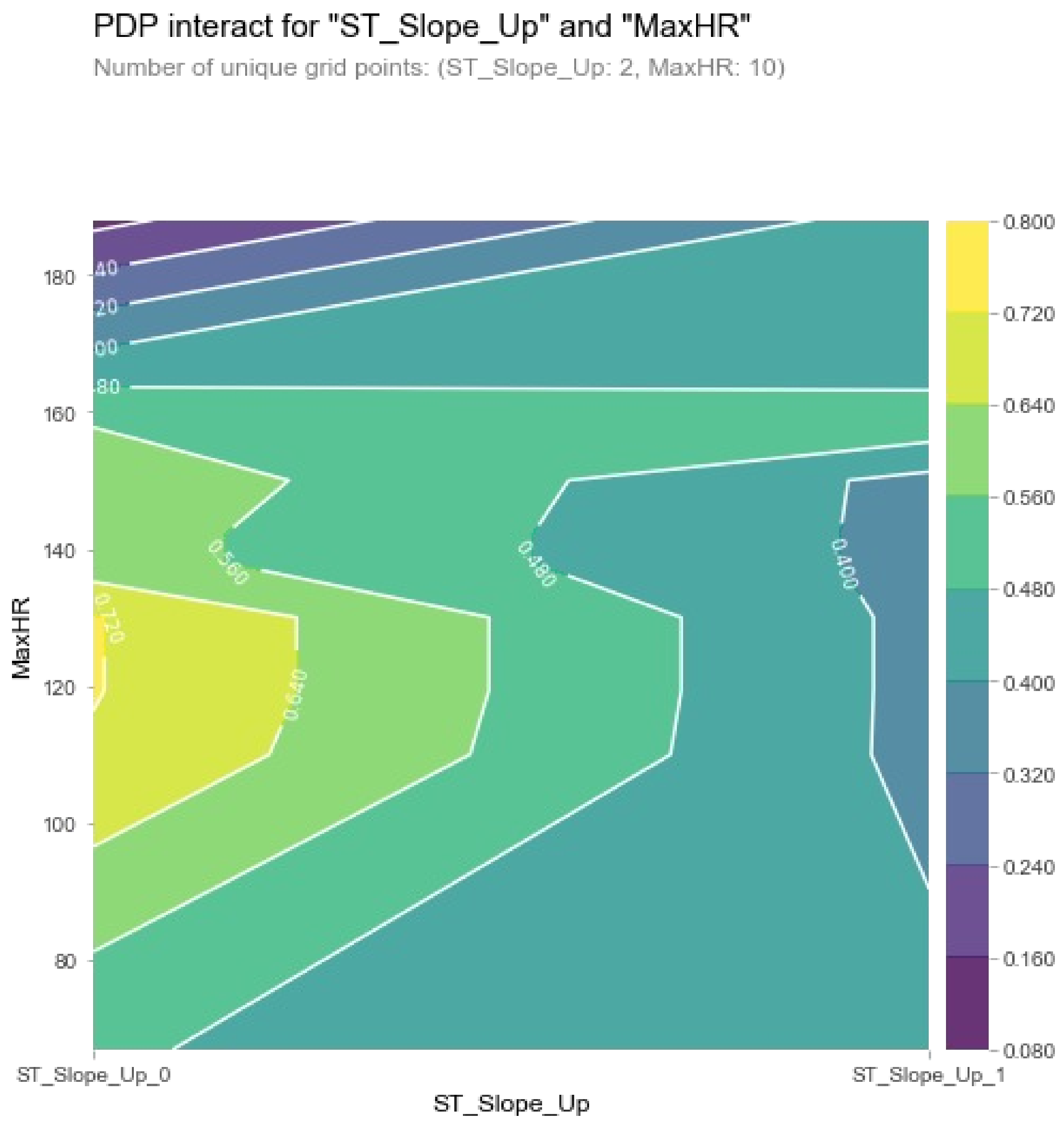


```
inter1  =  pdp.pdp_interact(model=tree_clf, dataset=X_test,
model_features=base_features, features=['ST_Slope_Up',
'ST_Slope_Flat'])

pdp.pdp_interact_plot(pdp_interact_out=inter1,
feature_names=['ST_Slope_Up', 'ST_Slope_Flat'], plot_type='contour')
plt.show()

inter1  =  pdp.pdp_interact(model=tree_clf, dataset=X_test,
model_features=base_features, features=['ST_Slope_Flat', 'MaxHR'])

pdp.pdp_interact_plot(pdp_interact_out=inter1,
feature_names=['ST_Slope_Flat', 'MaxHR'], plot_type='contour')
plt.show()
```

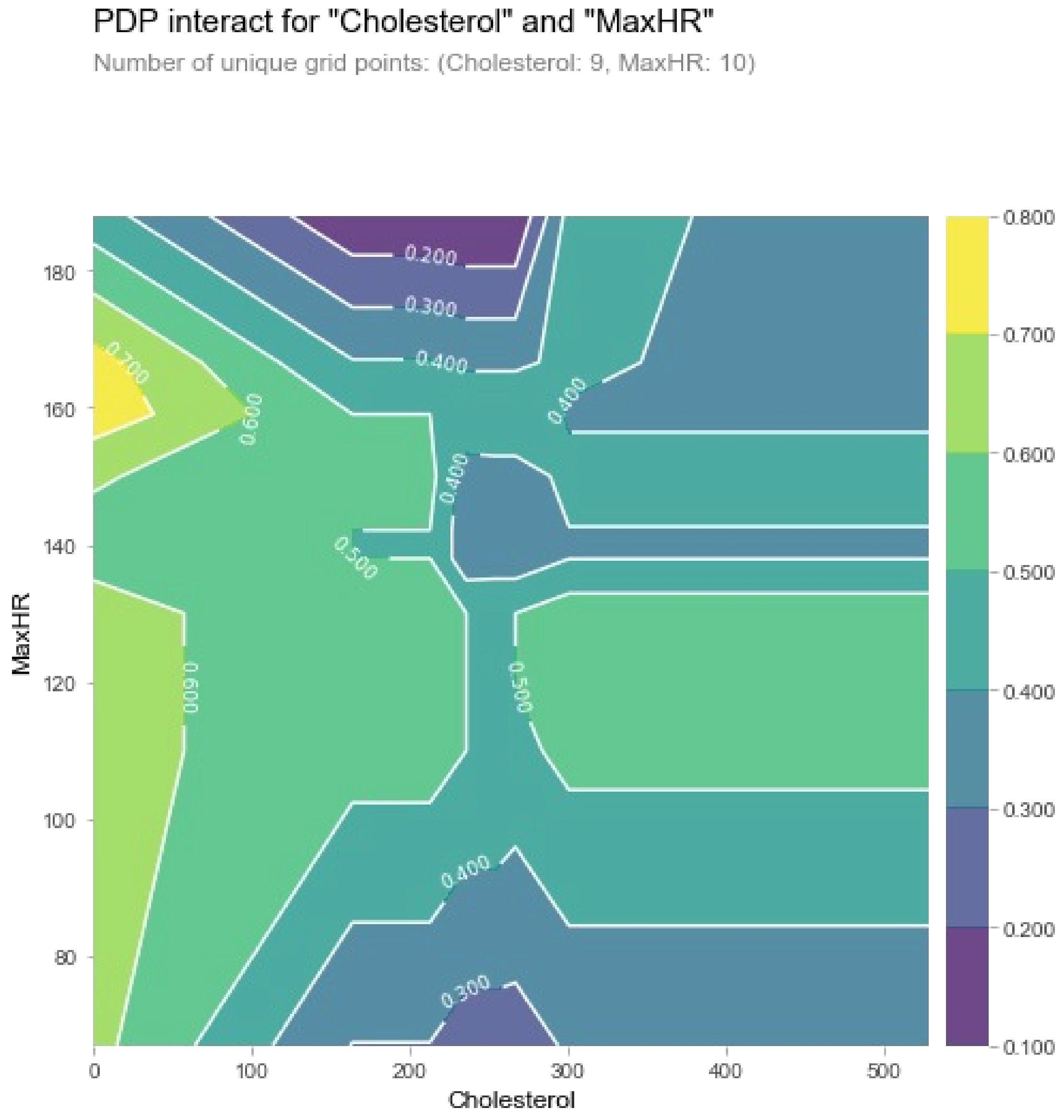

PDP interact for "ST_Slope_Up" and "ST_Slope_Flat"
Number of unique grid points: (ST_Slope_Up: 2, ST_Slope_Flat: 2)
ST_Slope_Flat
ST_Slope_Flat_1
ST_Slope_Flat_0
ST_Slope_Up
ST_Slope_Up_0
ST_Slope_Up_1
0.630
0.600
0.570
0.540
0.510
0.480
0.450
0.420
0.390



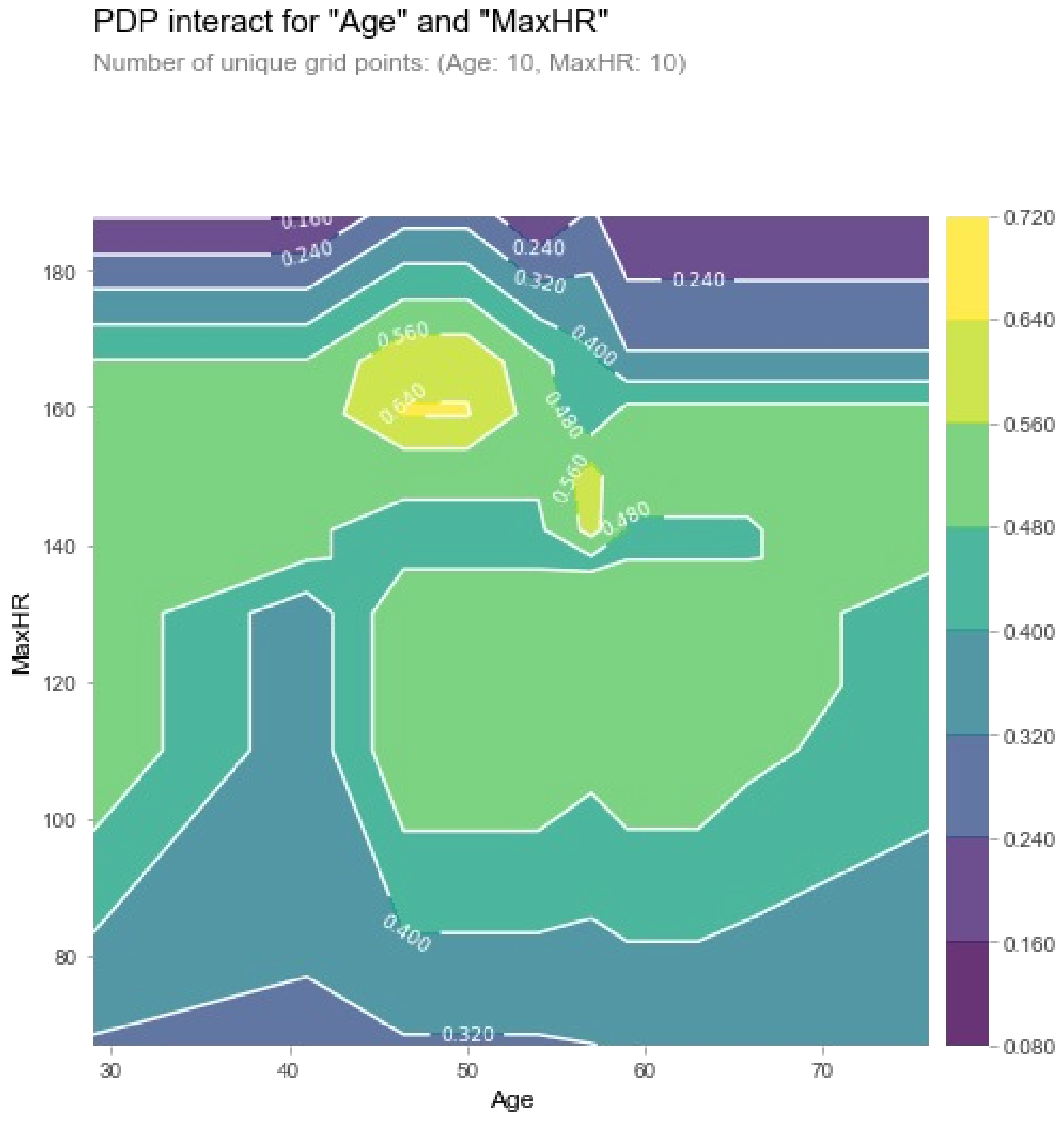
```
inter1  =  pdp.pdp_interact(model=tree_clf, dataset=X_test,
model_features=base_features, features=['ST_Slope_Up', 'MaxHR'])

pdp.pdp_interact_plot(pdp_interact_out=inter1,
feature_names=['ST_Slope_Up', 'MaxHR'], plot_type='contour')
plt.show()
```



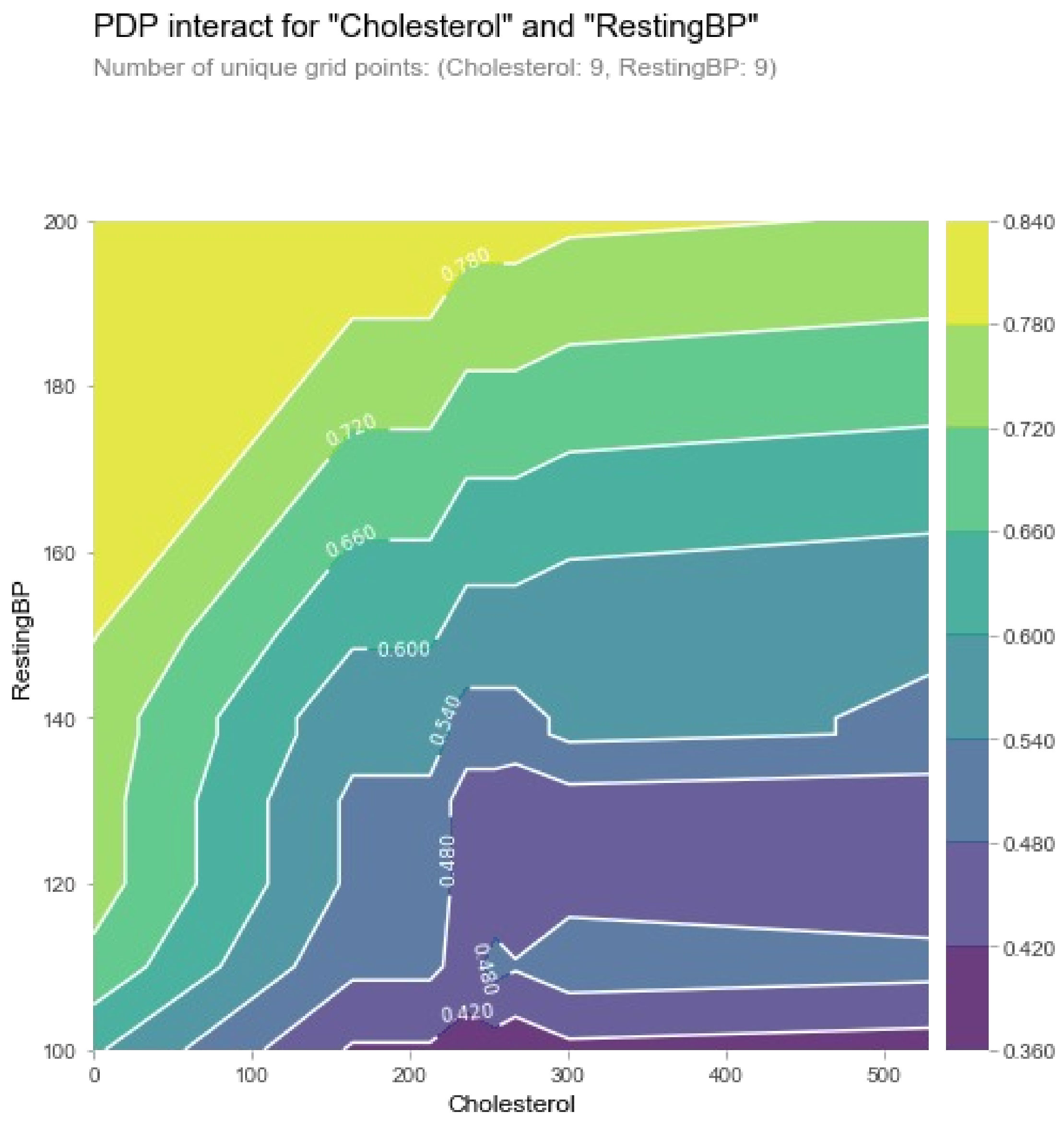
```
inter1  =  pdp.pdp_interact(model=tree_clf, dataset=X_test,
model_features=base_features, features=['Cholesterol', 'MaxHR'])

pdp.pdp_interact_plot(pdp_interact_out=inter1,
feature_names=['Cholesterol', 'MaxHR'], plot_type='contour')
plt.show()
```



```
inter1  =  pdp.pdp_interact(model=tree_clf, dataset=X_test,
model_features=base_features, features=['Age', 'MaxHR'])

pdp.pdp_interact_plot(pdp_interact_out=inter1, feature_names=['Age',
'MaxHR'], plot_type='contour')
plt.show()
```

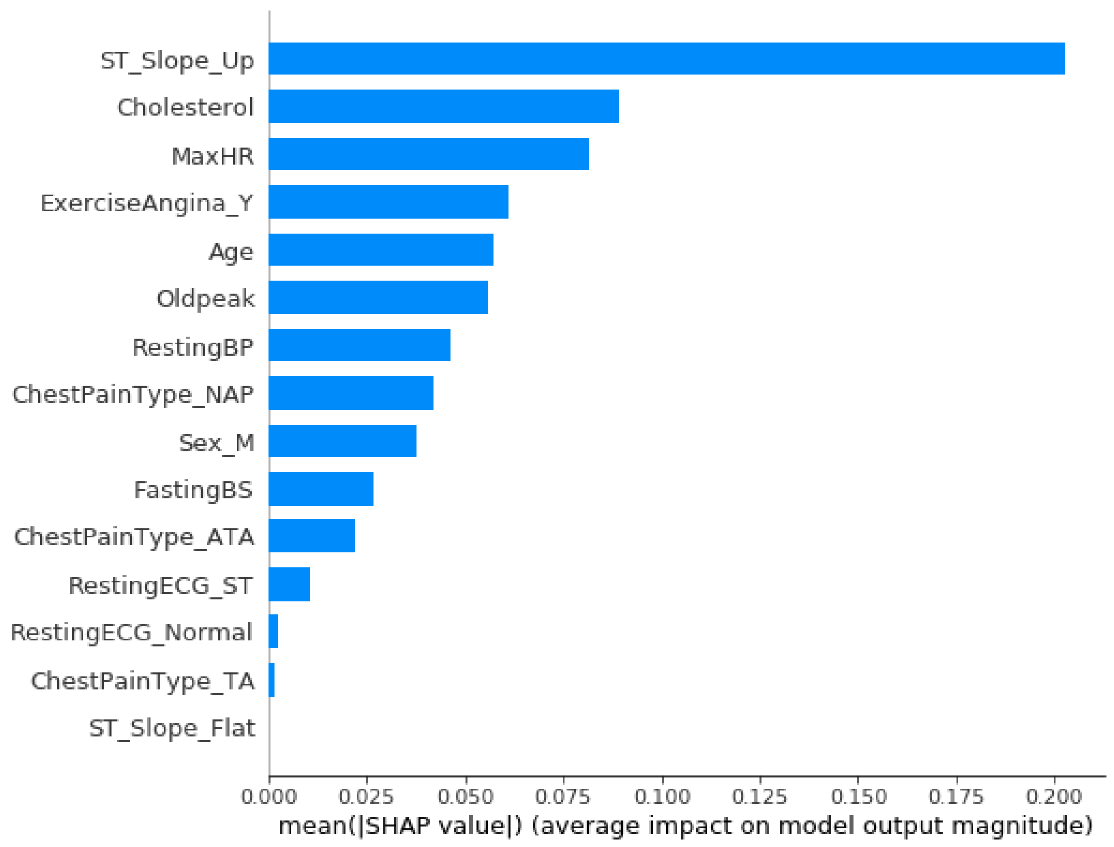


```
inter1  =  pdp.pdp_interact(model=tree_clf, dataset=X_test,
model_features=base_features, features=['Cholesterol', 'RestingBP'])

pdp.pdp_interact_plot(pdp_interact_out=inter1,
feature_names=['Cholesterol', 'RestingBP'], plot_type='contour')
plt.show()
```

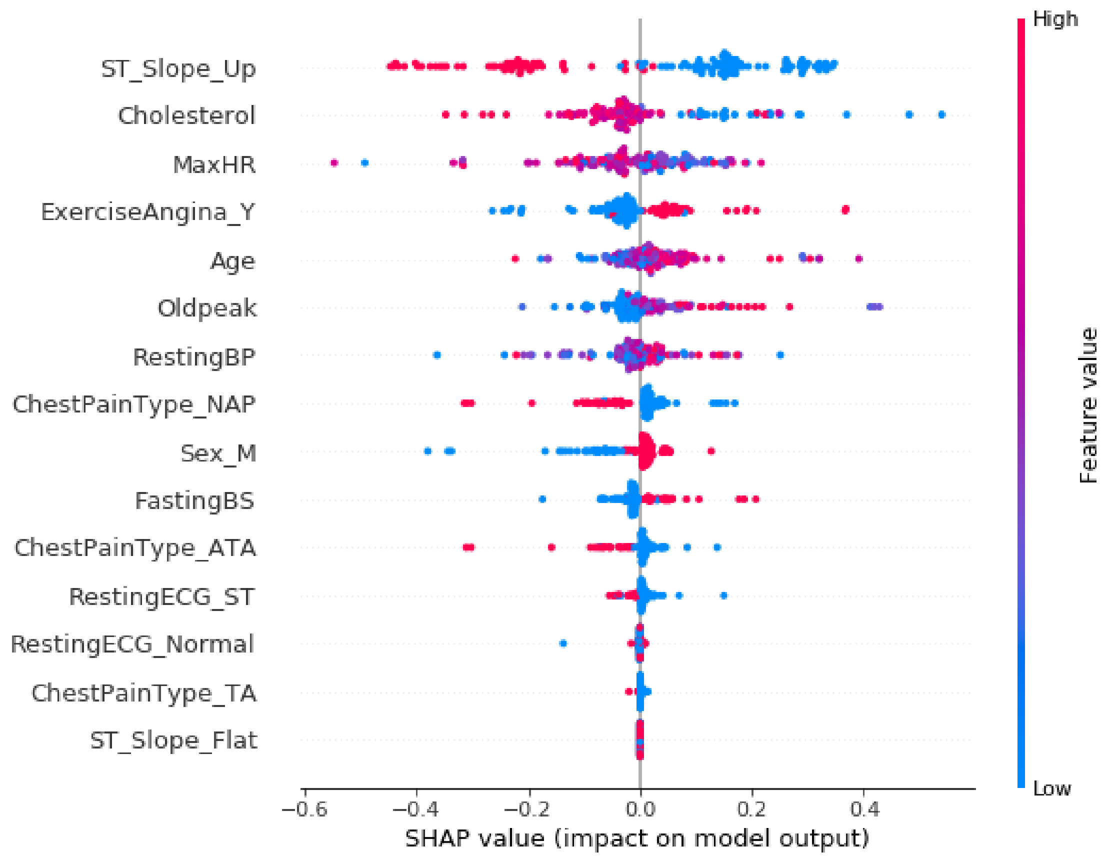


Summary Plots

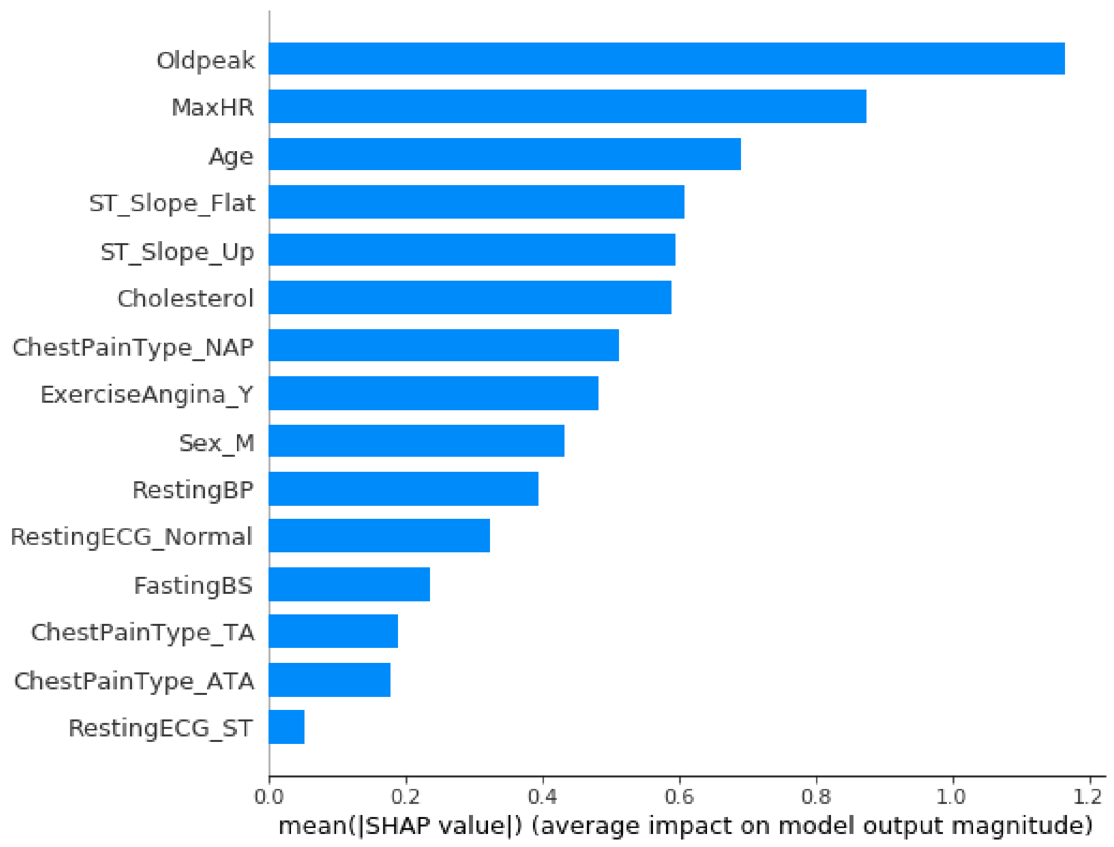
```
tree_explainer = shap.TreeExplainer(tree_clf)
tree_shap_values = tree_explainer.shap_values(X_test)

shap.summary_plot(tree_shap_values[1], X_test, plot_type="bar")
```



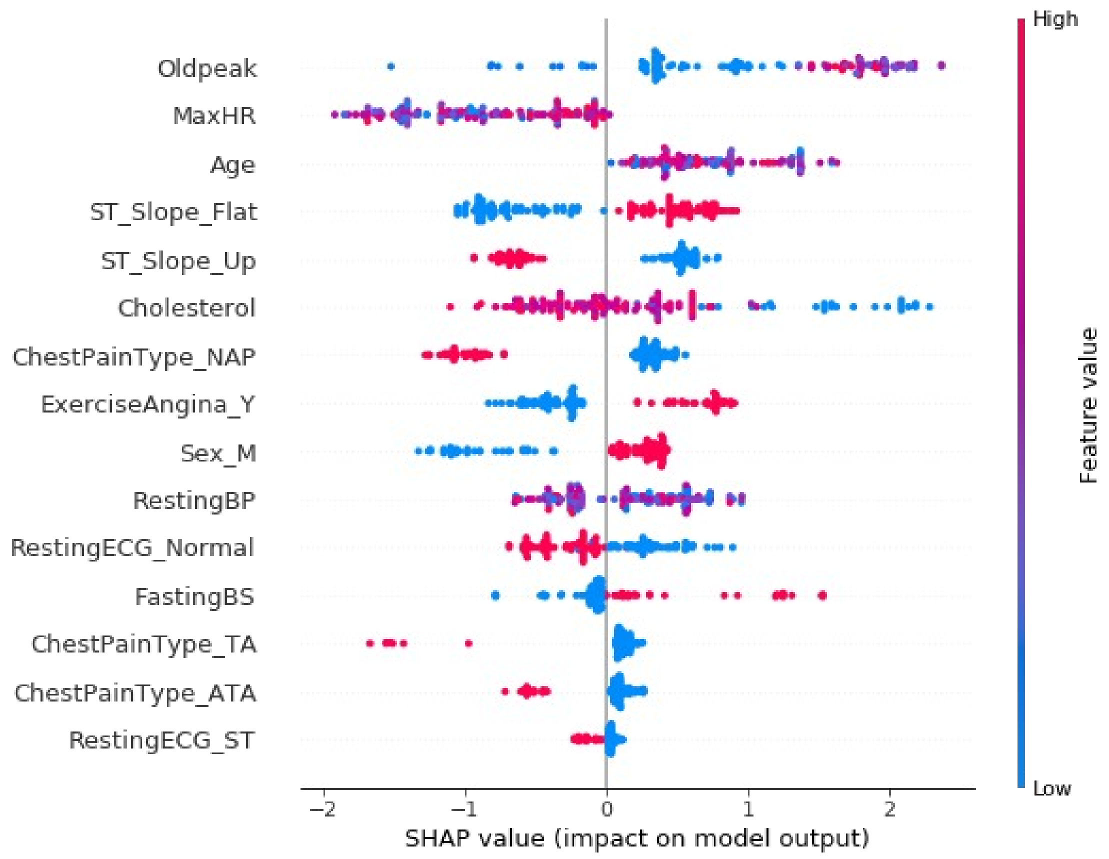
```
shap.summary_plot(tree_shap_values[1], X_test)
```



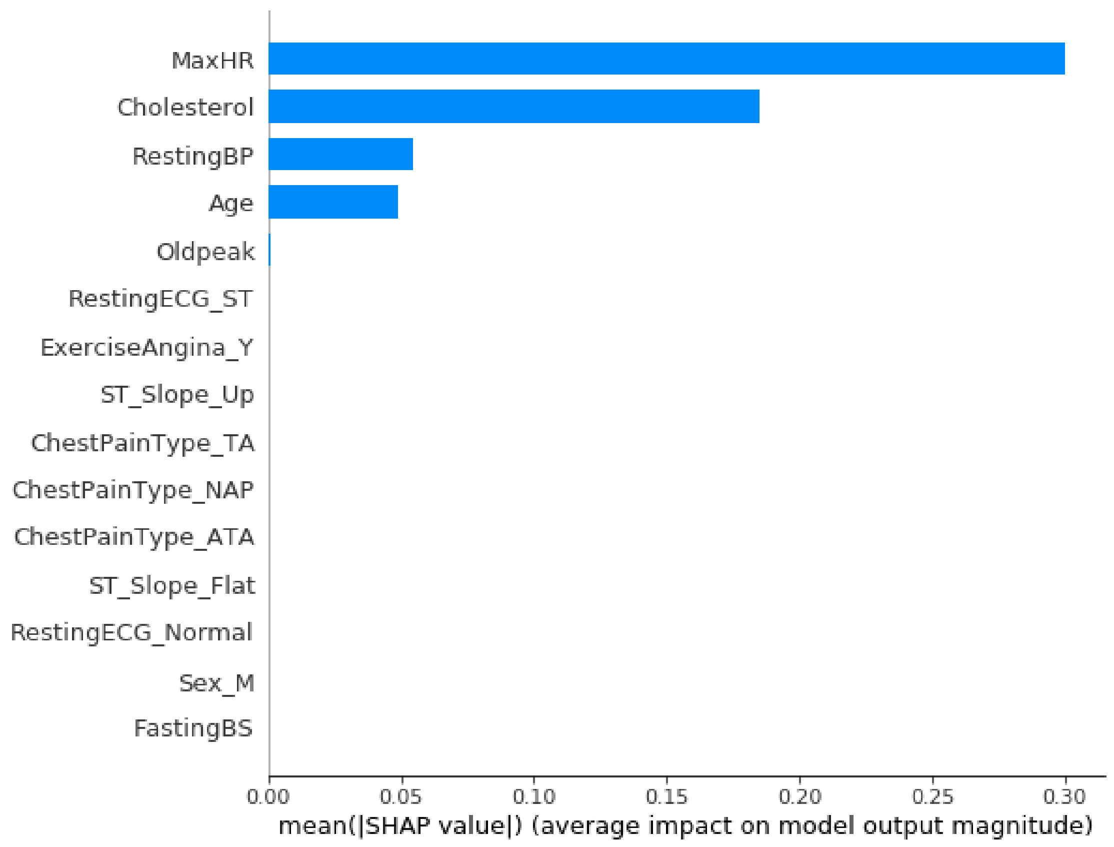
```
xgb_explainer = shap.Explainer(XGB_model)
xgb_shap_values = xgb_explainer.shap_values(X_test)


shap.summary_plot(xgb_shap_values, X_test, plot_type="bar")
```



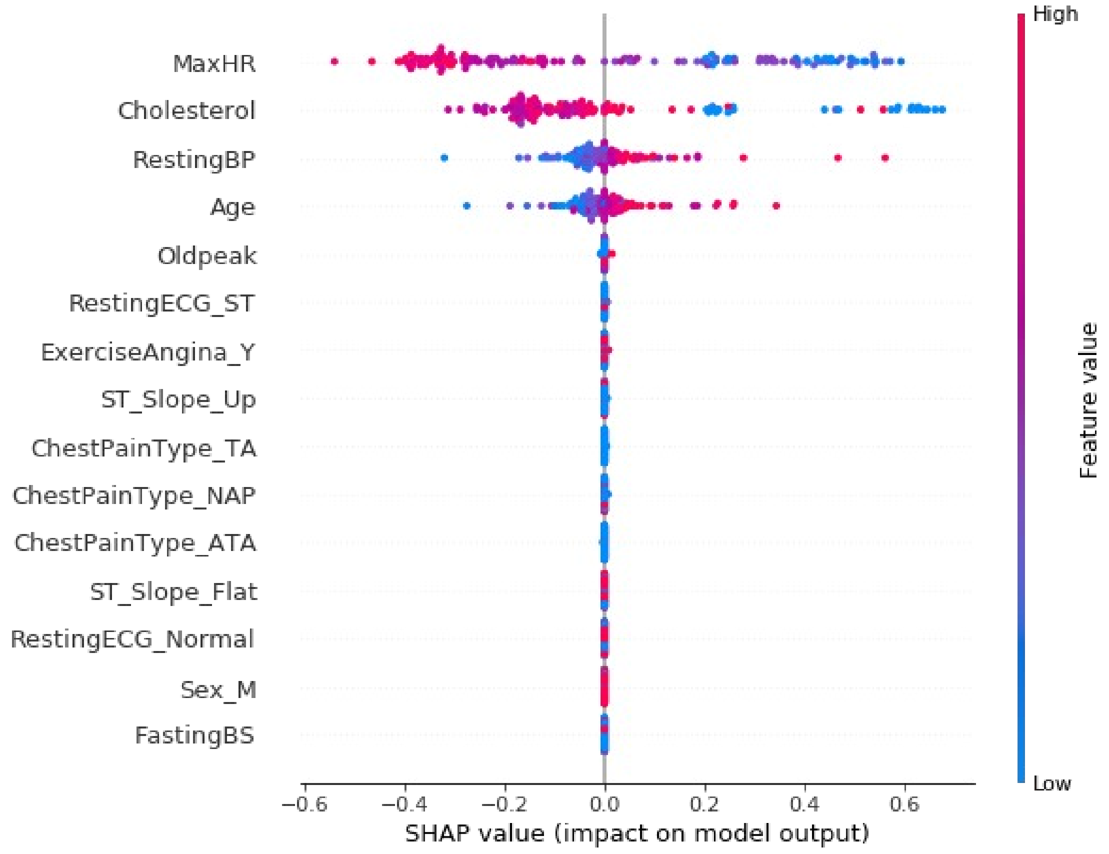
```
shap.summary_plot(xgb_shap_values, X_test)
```



```
shap.summary_plot(svm_shap_values, X_test, plot_type="bar")
```



```
shap.summary_plot(svm_shap_values, X_test)
```



```
#KNN_model = KNeighborsClassifier(n_neighbors=5)
#KNN_model.fit(X_train_scaled, y_train)
#knn_explainer =
shap.KernelExplainer(KNN_model.predict,X_train_scaled)
#knn_shap_values = knn_explainer.shap_values(X_test)
#shap.summary_plot(knn_shap_values, X_test)#

shap.sample(data, 5)
```

```
     Age  RestingBP  Cholesterol  FastingBS  MaxHR  Oldpeak  
HeartDisease  \
684   47        108          243          0    152      0.0  
1  
559   64        134          273          0    102      4.0  
1  
629   57        128          303          0    159      0.0  
0  
192   48        130          245          0    160      0.0  
0  
835   54        110          239          0    126      2.8  
1  

     Sex_M  ChestPainType_ATA  ChestPainType_NAP  ChestPainType_TA  \
684      1                  0                  1                 0  
```

```
559      1                  0                  0                0
629      0                  0                  0                0
192      1                  1                  0                0
835      1                  0                  0                0

     RestingECG_Normal  RestingECG_ST  ExerciseAngina_Y  ST_Slope_Flat  
\
684                  1              0                 0              0   

559                  1              0                 1              0   

629                  0              0                 0              0   

192                  1              0                 0              0   

835                  1              0                 1              1   


     ST_Slope_Up  
684            1  
559            0  
629            1  
192            1  
835            0  
```

Individual Force Plots

```
def heart_disease_risk_factors(model, patient):

    explainer = shap.TreeExplainer(model)
    shap_values = explainer.shap_values(patient)
    shap.initjs()
    return shap.force_plot(explainer.expected_value[1], 
shap_values[1], patient)

#Decision_Tree
data_for_prediction = X_test.iloc[1,:].astype(float)
heart_disease_risk_factors(tree_clf, data_for_prediction)

<IPython.core.display.HTML object>

<shap.plots._force.AdditiveForceVisualizer at 0x7fb50114c610>

data_for_prediction = X_test.iloc[20,:].astype(float)
heart_disease_risk_factors(tree_clf, data_for_prediction)

<IPython.core.display.HTML object>

<shap.plots._force.AdditiveForceVisualizer at 0x7fb500e92310>
```

```
shap.force_plot(xgb_explainer.expected_value,xgb_shap_values[10,:],
X_test.iloc[10,:])
```

```
<shap.plots._force.AdditiveForceVisualizer at 0x7fb500ea2790>
```

```
shap.force_plot(xgb_explainer.expected_value,xgb_shap_values[35,:],
X_test.iloc[35,:])
```

```
<shap.plots._force.AdditiveForceVisualizer at 0x7fb500ea28e0>
```

```
shap.force_plot(svm_explainer.expected_value,svm_shap_values[10,:],
X_test.iloc[10,:])
```

```
<shap.plots._force.AdditiveForceVisualizer at 0x7fb522082f10>
```

```
shap.force_plot(svm_explainer.expected_value,svm_shap_values[6,:],
X_test.iloc[6,:])
```

```
<shap.plots._force.AdditiveForceVisualizer at 0x7fb522082970>
```

Collective Force Plots

```
shap_values = xgb_explainer.shap_values(X_train.iloc[:50])
shap.force_plot(xgb_explainer.expected_value, shap_values,
X_test.iloc[:50])
```

```
<shap.plots._force.AdditiveForceArrayVisualizer at 0x7fb540787d30>
```

```
shap.force_plot(svm_explainer.expected_value, svm_shap_values, X_test)
```

```
<shap.plots._force.AdditiveForceArrayVisualizer at 0x7fb500e92820>
```