Predict a possible heart disease ¶

In this notebook, the main objective is to build a predictive model to see whether a patient would be diagnosed with heart disease. This model can help those with cardiovascular disease or who are at high cardiovascular risk (due to the presence of one or more risk factors such as hypertension, diabetes, hyperlipidaemia or already established disease), an early detection and management of heart disease would be very helpful.

Not only that, we are also going to give insights of the data through visualization and graphing so that we can have an overview on the datasets.

Cardiovascular diseases (CVDs) are the number 1 cause of death globally, taking an estimated 17.9 million lives each year, which accounts for 31% of all deaths worldwide. Four out of 5CVD deaths are due to heart attacks and strokes, and one-third of these deaths occur prematurely in people under 70 years of age. Heart failure is a common event caused by CVDs and this dataset contains 11 features that can be used to predict a possible heart disease.

People with cardiovascular disease or who are at high cardiovascular risk (due to the presence of one or more risk factors such as hypertension, diabetes, hyperlipidaemia or already established disease) need early detection and management wherein a machine learning model can be of great help

Import all neccessary libraries

In [1]:

```
import os
import numpy as np
import pandas as pd
import warnings
import seaborn as sns
import matplotlib.pyplot as plt
import plotly.express as px
warnings.filterwarnings("ignore")
pd.set_option("display.max_rows",None)
from sklearn import preprocessing
import matplotlib
matplotlib.style.use('ggplot')
from sklearn.preprocessing import LabelEncoder
```

1.0 Data Understanding

1.1 Reading dataset using Pandas library

In [2]:

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

Out[2]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina
0	40	M	ATA	140	289	0	Normal	172	N
1	49	F	NAP	160	180	0	Normal	156	N
2	37	M	ATA	130	283	0	ST	98	N
3	48	F	ASY	138	214	0	Normal	108	Y
4	54	M	NAP	150	195	0	Normal	122	N
5	39	M	NAP	120	339	0	Normal	170	N
6	45	F	ATA	130	237	0	Normal	170	N
7	54	M	ATA	110	208	0	Normal	142	N
8	37	M	ASY	140	207	0	Normal	130	Y

In [3]:

```
heart.shape
```

Out[3]:

```
(918, 12)
```

From the above dataframe we can tell that,

- Our **target variable** on this dataset is the 'Heart Disease' column
- There are 918 rows and 12 columns

1.2 Data Description

In this section, we will get to know the all data types and its value

1.2.1 Understanding each columns

To know the data types of each columns

In [4]:

```
heart.dtypes
```

Out[4]:

```
Age                 int64
Sex                object
ChestPainType      object
RestingBP           int64
Cholesterol         int64
FastingBS           int64
RestingECG         object
MaxHR               int64
ExerciseAngina     object
Oldpeak           float64
ST_Slope           object
HeartDisease        int64
dtype: object
```

There are some string data are saved as the form of object, so we have to convert it back to work on it

In [5]:

```
objectData = heart.select_dtypes(include="object").columns
heart[objectData]=heart[objectData].astype("string")
```

In [6]:

```
heart.dtypes
```

Out[6]:

```
Age                 int64
Sex                string
ChestPainType      string
RestingBP           int64
Cholesterol         int64
FastingBS           int64
RestingECG         string
MaxHR               int64
ExerciseAngina     string
Oldpeak           float64
ST_Slope           string
HeartDisease        int64
dtype: object
```

Now, all object data are converted into string format

Identifying the categorical and numerical columns

In [7]:

```
#Identifying columns with categorical data
string_col=heart.select_dtypes("string").columns.to_list()
string_col
```

Out[7]:

```
['Sex', 'ChestPainType', 'RestingECG', 'ExerciseAngina', 'ST_Slope']
```

In [8]:

```
categorical_features = heart.columns.tolist()
categorical_features
```

Out[8]:

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

In [9]:

```
#Identifying columns with numerical data excluding the target feature
num_col=heart.columns.to_list()
#remove columns with string data
for col in string_col:
    num_col.remove(col)
num_col.remove("HeartDisease")
print(num_col)
```

```
['Age', 'RestingBP', 'Cholesterol', 'FastingBS', 'MaxHR', 'Oldpeak']
```

Understanding values of categorical columns

In [10]:

```
heart.Sex.unique()
```

Out[10]:

```
<StringArray>
['M', 'F']
Length: 2, dtype: string
```

In [11]:

```
heart.ChestPainType.unique()
```

Out[11]:

```
<StringArray>
['ATA', 'NAP', 'ASY', 'TA']
Length: 4, dtype: string
```

In [12]:

```
heart.RestingECG.unique()
```

Out[12]:

```
<StringArray>
['Normal', 'ST', 'LVH']
Length: 3, dtype: string
```

In [13]:

```
heart.ExerciseAngina.unique()
```

Out[13]:

```
<StringArray>
['N', 'Y']
Length: 2, dtype: string
```

In [14]:

```
heart.ST_Slope.unique()
```

Out[14]:

```
<StringArray>
['Up', 'Flat', 'Down']
Length: 3, dtype: string
```

Understanding values of numerical columns

In [15]:

```
heart.FastingBS.unique()
```

Out[15]:

```
array([0, 1], dtype=int64)
```

From here, we know that FastingBS is a categorical data instead of numerical data even though its data type is int.

In [16]:

```
heart.Age.unique()
```

Out[16]:

```
array([40, 49, 37, 48, 54, 39, 45, 58, 42, 38, 43, 60, 36, 44, 53, 52, 51,
       56, 41, 32, 65, 35, 59, 50, 47, 31, 46, 57, 55, 63, 66, 34, 33, 61,
       29, 62, 28, 30, 74, 68, 72, 64, 69, 67, 73, 70, 77, 75, 76, 71],
      dtype=int64)
```

In [17]:

```
heart.MaxHR.unique()
```

Out[17]:

```
array([172, 156,  98, 108, 122, 170, 142, 130, 120,  99, 145, 140, 137,
       150, 166, 165, 125, 160, 164, 138, 178, 112, 118, 127, 114, 154,
       155,  87, 148, 100, 168, 184, 121, 153, 134,  96, 174, 175, 144,
        82, 135, 115, 128, 116,  94, 110,  92, 180, 152, 124, 106, 185,
       139, 190, 146, 158, 132, 176, 119, 188, 162, 105,  90, 136, 167,
       129, 102, 143, 103,  91, 126,  93, 131, 149, 123, 182, 141,  77,
       109, 133, 179, 113, 104,  95,  72,  97, 117,  86,  63, 157,  83,
        60,  70, 163,  67,  78,  84, 111,  80, 107, 161,  69,  88,  73,
       159, 151, 181, 186, 177, 173, 169, 171, 147,  71, 192, 195, 194,
       187, 202], dtype=int64)
```

In [18]:

```
heart.Oldpeak.unique()
```

Out[18]:

```
array([ 0. ,  1. ,  1.5,  2. ,  3. ,  4. ,  0.5,  2.5,  5. ,  0.8,  0.7,
        1.4,  2.1,  0.4,  0.2,  1.7,  2.2,  0.1,  1.6,  1.3,  0.3,  1.8,
        2.6, -0.9,  2.8, -2.6, -1.5, -0.1,  0.9,  1.1,  2.4, -1. , -1.1,
       -0.7, -0.8,  3.7,  1.2, -0.5, -2. ,  1.9,  3.5,  0.6,  3.1,  2.3,
        3.4,  3.6,  4.2,  3.2,  5.6,  3.8,  2.9,  6.2,  4.4])
```

In [19]:

```
heart.RestingBP.unique()
```

Out[19]:

```
array([140, 160, 130, 138, 150, 120, 110, 136, 115, 100, 124, 113, 125,
       145, 112, 132, 118, 170, 142, 190, 135, 180, 108, 155, 128, 106,
        92, 200, 122,  98, 105, 133,  95,  80, 137, 185, 165, 126, 152,
       116,   0, 144, 154, 134, 104, 139, 131, 141, 178, 146, 158, 123,
       102,  96, 143, 172, 156, 114, 127, 101, 174,  94, 148, 117, 192,
       129, 164], dtype=int64)
```

We found that there are columns with zero values in 'RestingBP' which is impossible, therefore we will work on these columns during data preparation

```
In [20]:
```

```
heart.Cholesterol.unique()
```

```
Out[20]:
```

```
array([289, 180, 283, 214, 195, 339, 237, 208, 207, 284, 211, 164, 204,
       234, 273, 196, 201, 248, 267, 223, 184, 288, 215, 209, 260, 468,
       188, 518, 167, 224, 172, 186, 254, 306, 250, 177, 227, 230, 294,
       264, 259, 175, 318, 216, 340, 233, 205, 245, 194, 270, 213, 365,
       342, 253, 277, 202, 297, 225, 246, 412, 265, 182, 218, 268, 163,
       529, 100, 206, 238, 139, 263, 291, 229, 307, 210, 329, 147,  85,
       269, 275, 179, 392, 466, 129, 241, 255, 276, 282, 338, 160, 156,
       272, 240, 393, 161, 228, 292, 388, 166, 247, 331, 341, 243, 279,
       198, 249, 168, 603, 159, 190, 185, 290, 212, 231, 222, 235, 320,
       187, 266, 287, 404, 312, 251, 328, 285, 280, 192, 193, 308, 219,
       257, 132, 226, 217, 303, 298, 256, 117, 295, 173, 315, 281, 309,
       200, 336, 355, 326, 171, 491, 271, 274, 394, 221, 126, 305, 220,
       242, 347, 344, 358, 169, 181,   0, 236, 203, 153, 316, 311, 252,
       458, 384, 258, 349, 142, 197, 113, 261, 310, 232, 110, 123, 170,
       369, 152, 244, 165, 337, 300, 333, 385, 322, 564, 239, 293, 407,
       149, 199, 417, 178, 319, 354, 330, 302, 313, 141, 327, 304, 286,
       360, 262, 325, 299, 409, 174, 183, 321, 353, 335, 278, 157, 176,
       131], dtype=int64)
```

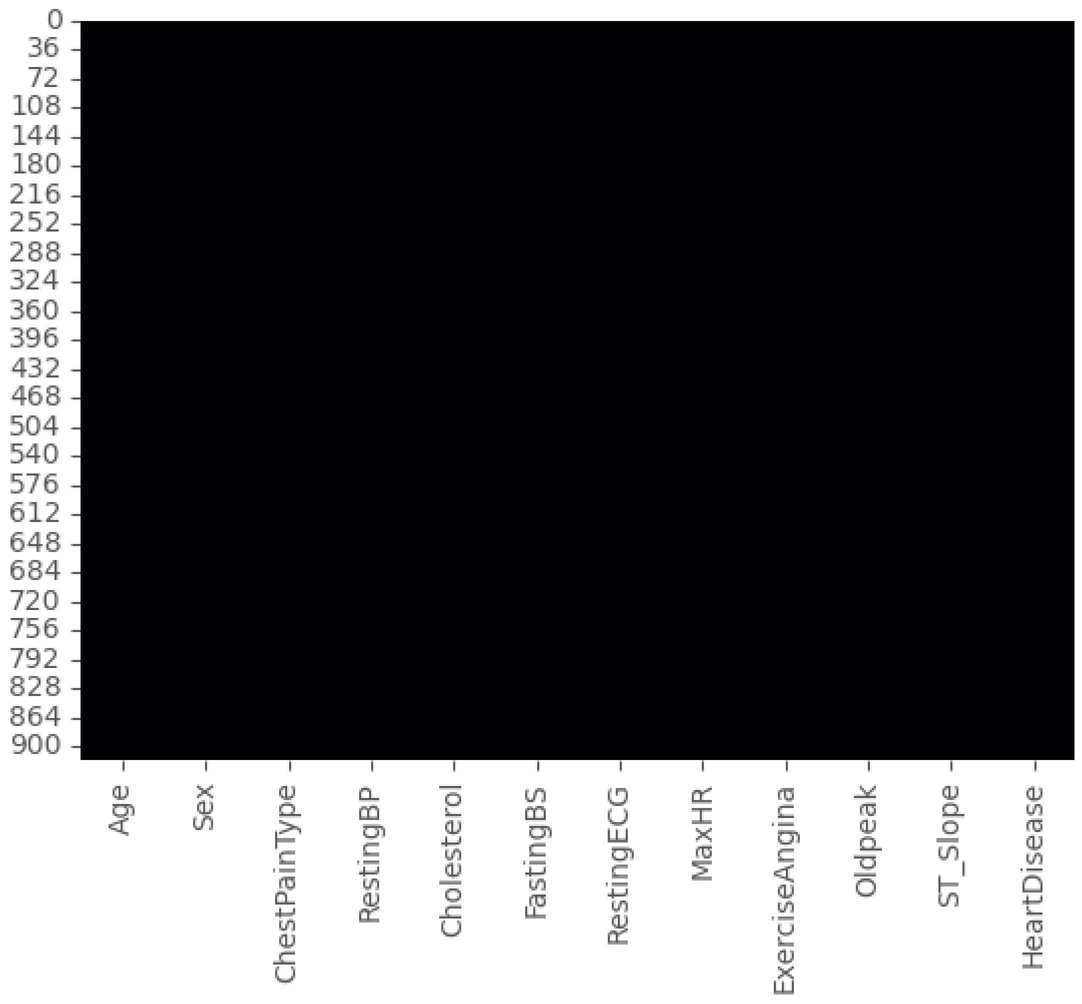
We found that there are columns with zero values in 'Cholesterol' which is impossible, therefore we will work on these columns during data preparation

Numerical columns above are the columns we need to check for outliers in data preparation step

Checking for null value

In [21]:

```
#Null Value
sns.heatmap(heart.isnull(),cmap = 'magma',cbar = False);
```



From here, we know that there is no null values in this dataset. Therefore, there is no need to eliminate null values during data preparation step later.

Summary Statistics

In [22]:

```
heart.describe().T
```

Out[22]:

	count	mean	std	min	25%	50%	75%	max
Age	918.0	53.510893	9.432617	28.0	47.00	54.0	60.0	77.0
RestingBP	918.0	132.396514	18.514154	0.0	120.00	130.0	140.0	200.0
Cholesterol	918.0	198.799564	109.384145	0.0	173.25	223.0	267.0	603.0
FastingBS	918.0	0.233115	0.423046	0.0	0.00	0.0	0.0	1.0
MaxHR	918.0	136.809368	25.460334	60.0	120.00	138.0	156.0	202.0
Oldpeak	918.0	0.887364	1.066570	-2.6	0.00	0.6	1.5	6.2
HeartDisease	918.0	0.553377	0.497414	0.0	0.00	1.0	1.0	1.0

From here, we can list out all the attributes of this dataset

- Age: age of the patient [years]
- Sex: sex of the patient [M: Male, F: Female]
- ChestPainType: chest pain type [TA: Typical Angina, ATA: Atypical Angina, NAP: Non-Anginal Pain, ASY: Asymptomatic]
- RestingBP: resting blood pressure [mm Hg]
- Cholesterol: serum cholesterol [mm/dl]
- FastingBS: fasting blood sugar [1: if FastingBS > 120 mg/dl, 0: otherwise]
- RestingECG: resting electrocardiogram results [Normal: Normal, ST: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV), LVH: showing probable or definite left ventricular hypertrophy by Estes' criteria]
- MaxHR: maximum heart rate achieved [Numeric value between 60 and 202]
- ExerciseAngina: exercise-induced angina [Y: Yes, N: No]
- Oldpeak: oldpeak = ST [Numeric value measured in depression]
- ST_Slope: the slope of the peak exercise ST segment [Up: upsloping, Flat: flat, Down: downsloping]
- HeartDisease: output class [1: heart disease, 0: Normal]

2.3 Exploratory Data Analysis

The purpose of this step :

- Understanding the given dataset and helps clean up the given dataset.
- It gives you a clear picture of the features and the relationships between them.
- Providing guidelines for essential variables and leaving behind/removing non-essential variables.
- Handling Missing values or human error.
- Identifying outliers.
- EDA process would be maximizing insights of a dataset.
- This process is time-consuming but very effective,

2.3.1 Understanding average values of all the attributes for cases of with heart disease and withou heart disease

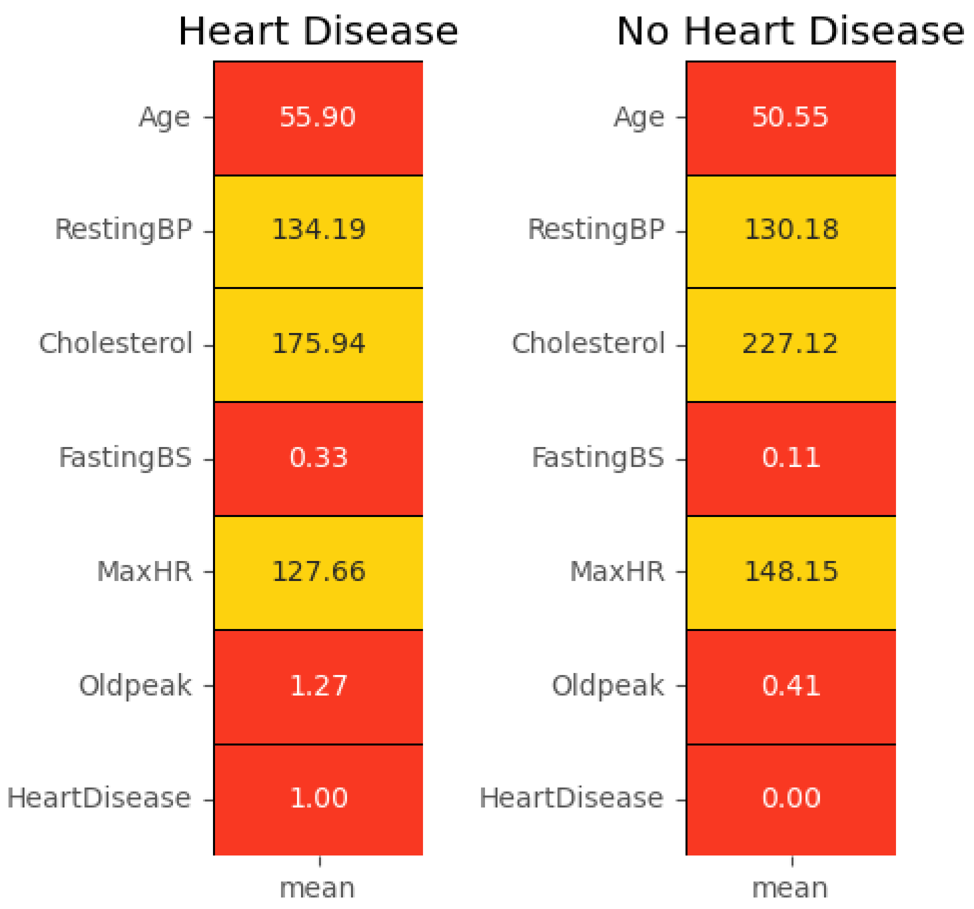
In [23]:

```
yes = heart[heart['HeartDisease'] == 1].describe().T
no = heart[heart['HeartDisease'] == 0].describe().T
colors = ['#F93822','#FDD20E']

fig,ax = plt.subplots(nrows = 1,ncols = 2,figsize = (5,5))
plt.subplot(1,2,1)
sns.heatmap(yes[['mean']],annot = True,cmap = colors,linewidths = 0.4,linecolor = 'black
plt.title('Heart Disease');

plt.subplot(1,2,2)
sns.heatmap(no[['mean']],annot = True,cmap = colors,linewidths = 0.4,linecolor = 'black'
plt.title('No Heart Disease');

fig.tight_layout(pad = 2)
```



2.3 Data Visualization

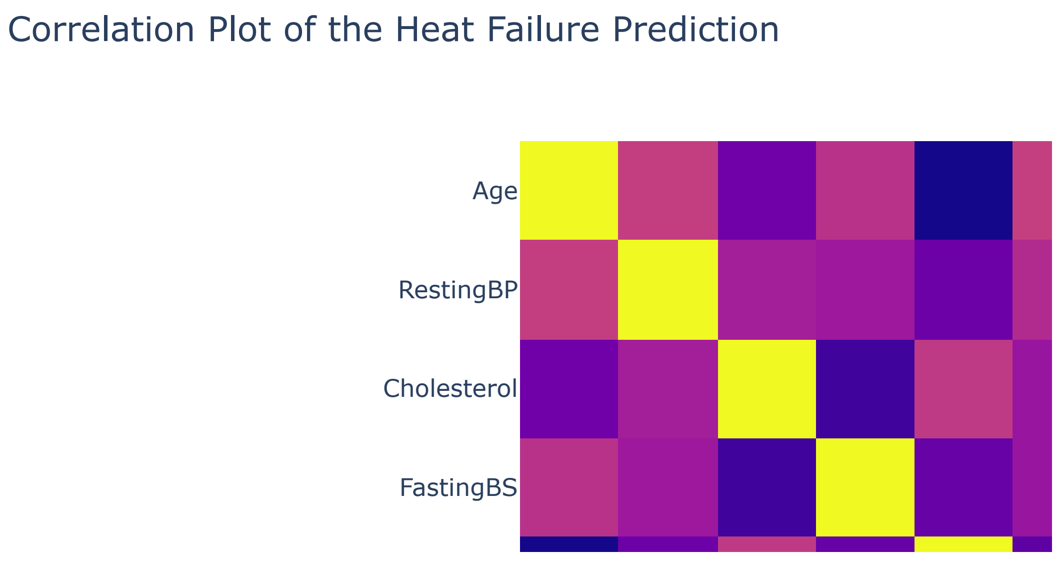
Correlation Matrix wtih Heatmap

It's necessary to remove correlated variables to improve your model.One can find correlations using pandas “.corr()” function and can visualize the correlation matrix using plotly express.

- Lighter shades represents positive correlation
- Darker shades represents negative correlation

In [24]:

```
px.imshow(heart.corr(),title="Correlation Plot of the Heat Failure Prediction")
```



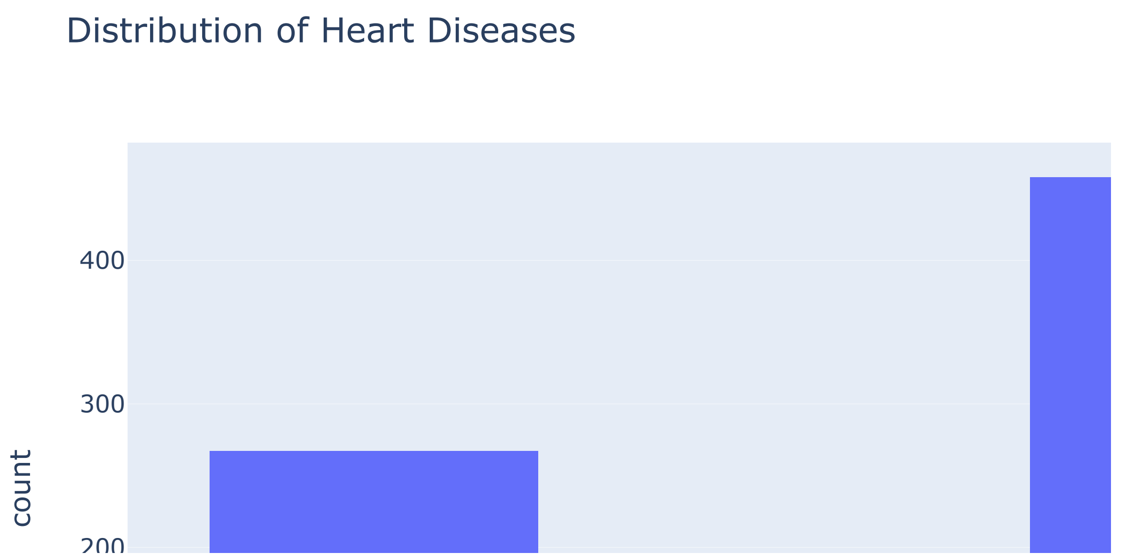
Here we can see Heart Disease has a high negative correlation with "MaxHR" and somewhat negative correlation with "Cholesterol", where as here positive correatlation with "Oldpeak","FastingBS" and "RestingBP

Data Visualization with Histogram

- Visualizing the distribution of heart disease between genders

In [25]:

```
fig=px.histogram(heart,
                 x="HeartDisease",
                 color="Sex",
                 hover_data=heart.columns,
                 title="Distribution of Heart Diseases",
                 barmode="group")
fig.show()
```

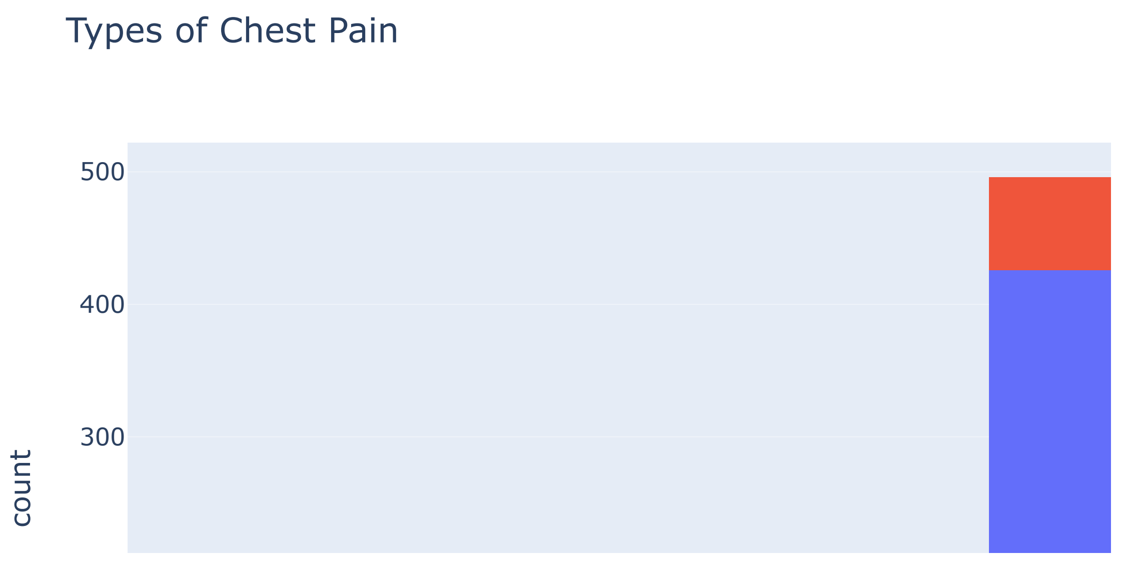


From here, we can know that male have a higher chance of getting heart disease when compared to female

- Visualizing distribution of chest pain type with respect to genders

In [26]:

```
fig=px.histogram(heart,
                 x="ChestPainType",
                 color="Sex",
                 hover_data=heart.columns,
                 title="Types of Chest Pain",
                 barmode = "stack")
fig.show()
```



In [27]:

```
# grouped = heart.groupby(['ChestPainType', 'Sex']).size().unstack(fill_value=0)

# grouped.plot(kind='bar', stacked=False)
# plt.title("Types of Chest Pain")
# plt.show()
```

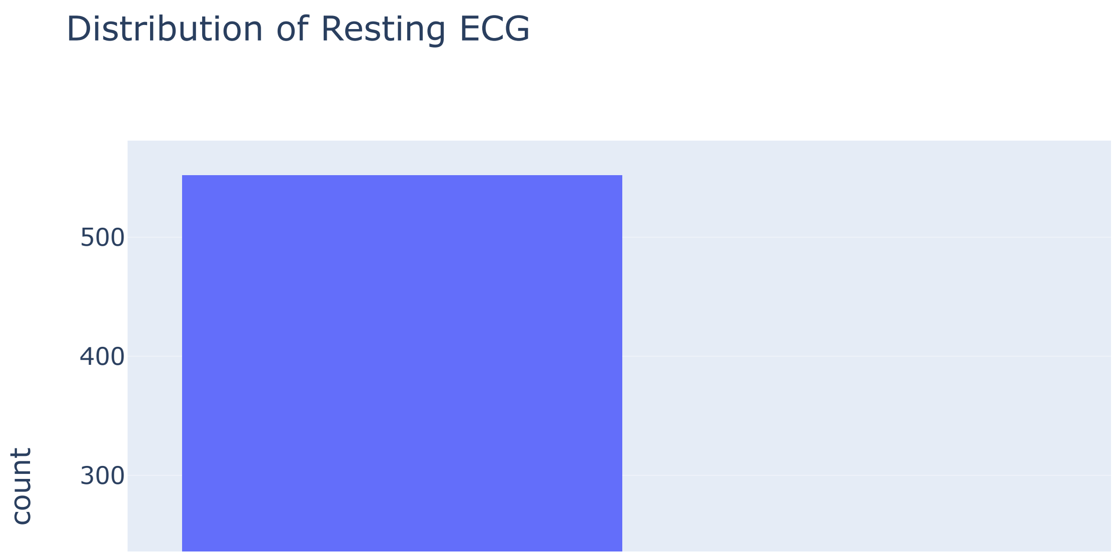
From here, we can see that most of the male is having 'ASY' chest pain and most female is having 'ATA' chest pain

In [28]:

```
# fig=px.histogram(heart,
#                    x="Sex",
#                    hover_data=heart.columns,
#                    title="Sex Ratio in the Data")
# fig.show()
```

In [29]:

```
fig=px.histogram(heart,
                  x="RestingECG",
                  hover_data=heart.columns,
                  title="Distribution of Resting ECG")
fig.show()
```

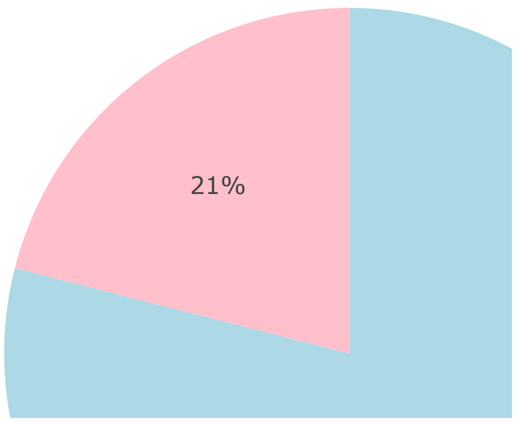


Distribution of gender with pie chart

In [30]:

```
fig=px.pie(heart,
           names='Sex',
           title='Sex Ratio in the Data',
           color='Sex',
           color_discrete_map = {'M':'lightblue', 'F':'pink'})
fig.show()
```

Sex Ratio in the Data

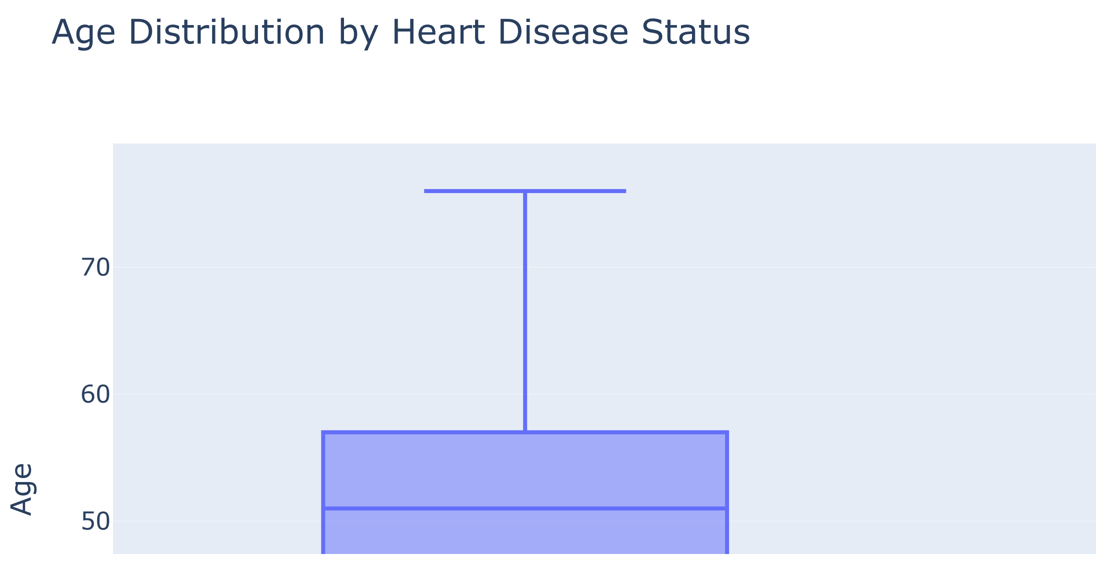


Most of the respondents in this dataset are males

Distribution of Age for patients with and without heart disease

In [31]:

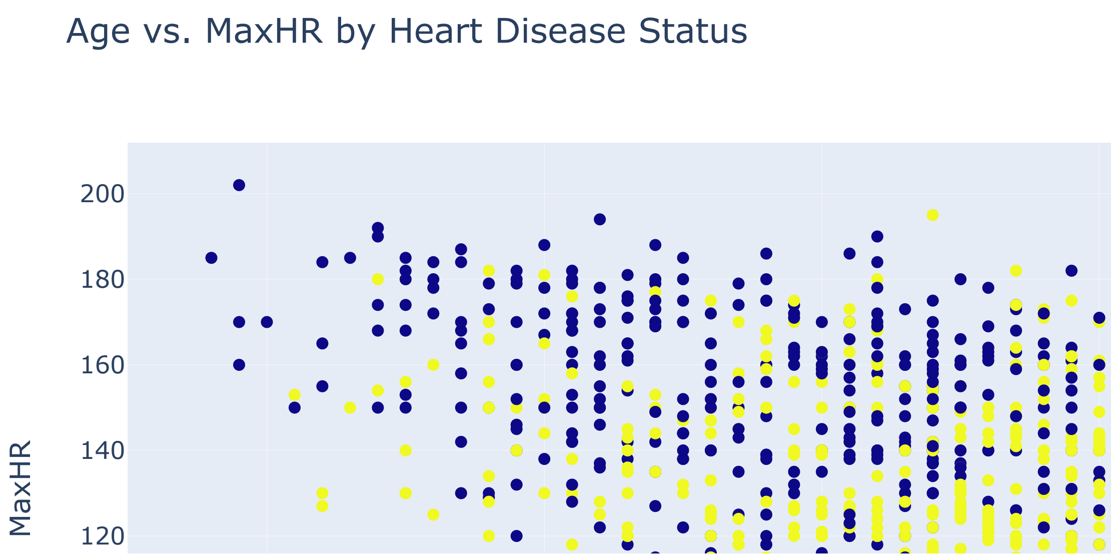
```
fig = px.box(heart, x='HeartDisease', y='Age', title='Age Distribution by Heart Disease
fig.show()
```



Relationship between Age and MaxHR with presence of HeartDisease

In [32]:

```
fig = px.scatter(heart, x='Age',
                 y='MaxHR',
                 color='HeartDisease',
                 title='Age vs. MaxHR by Heart Disease Status')
fig.show()
```



3.0 Data Preparation

3.1 Handling null values

In [33]:

```
heart.isnull().sum()
```

Out[33]:

```
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
```

Since there is no null values in the dataset no data cleaning is needed

In [34]:

```
heartCleaned = heart.copy()
```

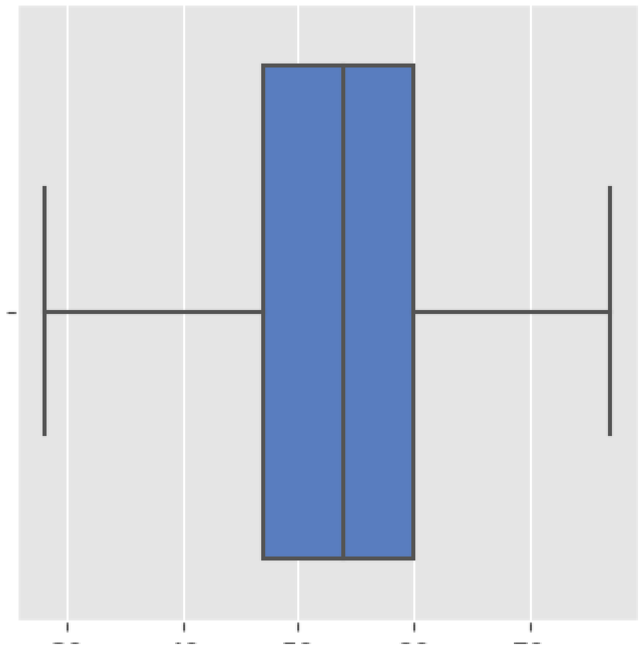
3.2 Handling Outliers

From section 1.2.1, we know that numerical data are 'Age', 'RestingBP', 'Cholesterol', 'MaxHR', 'Oldpeak'

We have to detect outliers for numerical data only by using boxplot

```
In [35]:
```

```python
#check outlier using boxplots
lst = ['Age', 'RestingBP', 'Cholesterol', 'MaxHR', 'Oldpeak']
fig= plt.figure(figsize=(4,4))
for i in lst:
    sns.boxplot(heart[i],palette='muted')
    plt.show()
```



There are lots of outliers in RestingBP and Cholesterol

```
In [36]:
```

```python
heart['RestingBP'].describe()
```

```
Out[36]:

count    918.000000
mean     132.396514
std       18.514154
min        0.000000
25%      120.000000
50%      130.000000
75%      140.000000
max      200.000000
Name: RestingBP, dtype: float64
```

In [37]:

```
heart['Cholesterol'].describe()
```

Out[37]:

```
count    918.000000
mean     198.799564
std      109.384145
min        0.000000
25%      173.250000
50%      223.000000
75%      267.000000
max      603.000000
Name: Cholesterol, dtype: float64
```

It is impossible to have 0 Cholesterol and 0 RestingBP

In [38]:

```
heart['MaxHR'].describe()
```

Out[38]:

```
count    918.000000
mean     136.809368
std       25.460334
min       60.000000
25%      120.000000
50%      138.000000
75%      156.000000
max      202.000000
Name: MaxHR, dtype: float64
```

In [39]:

```
heart['Oldpeak'].describe()
```

Out[39]:

```
count    918.000000
mean       0.887364
std        1.066570
min       -2.600000
25%        0.000000
50%        0.600000
75%        1.500000
max        6.200000
Name: Oldpeak, dtype: float64
```

Based on the box plot and .describe(), we can see that outliers has been detected. It is known that for these features having a maximum values much more larger than 75% quartile.

However, depending on the context of heart failure and our analysis purpose, we will only impute the outliers with zero values with their median, as the other outliers may contain valueble information and should not be removed

In [40]:

```
#RestingBP

## Checking the number of 0 present in the RestingBP
RestingBP = heart[heart['RestingBP'] == 0]
RestingBP.shape
```

Out[40]:

```
(1, 12)
```

Only 1 row is having the RestingBP of 0

In [41]:

```
#RestingBP represents the blood pressure of the patient.
#It is not possible to have values equal to Zero(0).
# remove the value Zero(0)
heart = heart.drop(heart[(heart['RestingBP'] == 0)].index)
heart['RestingBP']
```

Out[41]:

```
0      140
1      160
2      130
3      138
4      150
5      120
6      130
7      110
8      140
9      120
10     130
11     136
12     120
13     140
14     115
15     120
16     110
17     120
```

In [42]:

```
# Checking the number of 0 present in the Cholesterol
Cholesterol = heart[heart['Cholesterol'] == 0]
Cholesterol.shape
```

Out[42]:

```
(171, 12)
```

There are 171 rows having the Cholesterol of 0, we have to replace the zeros with median.

In [43]:

```
from sklearn.impute import SimpleImputer

imputer = SimpleImputer(missing_values=0, strategy='median')
imputer = imputer.fit(heart[['Cholesterol']])
heart['Cholesterol'] = imputer.transform(heart[['Cholesterol']])
```

In [44]:

```
# set Cholesterol data that has zero values to null
# heart.loc[heart['Cholesterol'] == 0,'Cholesterol'] = np.nan
```

In [45]:

```
# filling null value with median value of Cholesterol
# heart['Cholesterol'].fillna(heart['Cholesterol'].median,inplace = True)
```

In [46]:

```
heart['Cholesterol'].max
```

Out[46]:

```
<bound method NDFrame._add_numeric_operations.<locals>.max of 0      28
9.0
1      180.0
2      283.0
3      214.0
4      195.0
5      339.0
6      237.0
7      208.0
8      207.0
9      284.0
10     211.0
11     164.0
12     204.0
13     234.0
14     211.0
15     273.0
16     196.0
```

In [47]:

```
#dataset after outlier is cleared
heartClearOutlier = heart.copy()
```

3.3 Label Encoding

To handle categorical data including ordinal and nominal data

- One - Hot Encoding is suitable for nominal data with a small no of unique values [For working with non-tree based algortihms]

- Label Encoding is suitable for ordinal data with a small no of unique values [For working with non-tree based algortihms]

In this project, we will use both tree-based and non-tree based algorithms. Therefore, we will apply both

3.3.1 One-Hot Encoding for non-tree based algorithms

In [48]:

```
df_nontree=pd.get_dummies(heart,columns=string_col,drop_first=False)
df_nontree.head()
```

Out[48]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease	Sex_F	Sex_M
0	40	140	289.0	0	172	0.0	0	0	1
1	49	160	180.0	0	156	1.0	1	1	0
2	37	130	283.0	0	98	0.0	0	0	1
3	48	138	214.0	0	108	1.5	1	1	0
4	54	150	195.0	0	122	0.0	0	0	1

5 rows × 21 columns

In [49]:

```
# Getting the target column at the end
target="HeartDisease"
y=df_nontree[target].values
df_nontree.drop("HeartDisease",axis=1,inplace=True)
df_nontree=pd.concat([df_nontree,heart[target]],axis=1)
df_nontree.head()
```

Out[49]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	Sex_F	Sex_M	ChestPainType
0	40	140	289.0	0	172	0.0	0	1	
1	49	160	180.0	0	156	1.0	1	0	
2	37	130	283.0	0	98	0.0	0	1	
3	48	138	214.0	0	108	1.5	1	0	
4	54	150	195.0	0	122	0.0	0	1	

5 rows × 21 columns

3.3.2 Label Encoding for tree based algorithms

In [50]:

```
df_tree = heart.copy()
encoder = LabelEncoder()
for col in string_col:
    df_tree[col] = encoder.fit_transform(df_tree[col])
df_tree.head()
```

Out[50]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	Exer
0	40	1	1	140	289.0	0	1	172	
1	49	0	2	160	180.0	0	1	156	
2	37	1	1	130	283.0	0	2	98	
3	48	0	0	138	214.0	0	1	108	
4	54	1	2	150	195.0	0	1	122	

Data Preprocessing

3.4 Data Spliting

Label encoded data (for tree-based algorithms)

In [51]:

```
# feature selection - drop our target feature (Response) - our x input
df_tree_without_target_col = np.array (df_tree.drop('HeartDisease', axis = 1))

# create our targeted feature(Response) array - our y output
tree_trainHeartDiseaseData = np.array (df_tree['HeartDisease'], dtype = 'int64')


tree_trainData = df_tree_without_target_col
```

In [52]:

```
X_tree = tree_trainData
y_tree = tree_trainHeartDiseaseData

from sklearn.model_selection import train_test_split

X_train_tree, X_test_tree, y_train_tree, y_test_tree = train_test_split(X_tree,
                                                                        y_tree,
                                                                        test_size = 0.2,
                                                                        random_state = 4
#using the random state 40, we split the data into 80:20 for training:test
```

One-Hot Encoded data (for non-tree based algorithms)

In [53]:

```
# feature selection - drop our target feature (Response) - our x input
df_nontree_without_target_col = np.array (df_nontree.drop('HeartDisease', axis = 1))

# create our targeted feature(Response) array - our y output
nontree_trainHeartDiseaseData = np.array (df_nontree['HeartDisease'], dtype = 'int64')


nontree_trainData = df_nontree_without_target_col
```

In [54]:

```
X_nontree = nontree_trainData
y_nontree = nontree_trainHeartDiseaseData

from sklearn.model_selection import train_test_split

X_train_nontree, X_test_nontree, y_train_nontree, y_test_nontree = train_test_split(X_no
                                                                                    y_no
                                                                                    test
                                                                                    rand
#using the random state 40, we split the data into 80:20 for training:test
```

4.0 Modeling

In this modelling stage, we will be testing the dataset with four major models:

1. **KNN (K-Nearest Neighbour Classifier)** *requires feature scaling*
2. **SVM** *requires feature scaling*
3. **Decision Tree**
4. **Random Forest**

In [55]:

```
#import libraries for model evaluation
from sklearn.metrics import plot_confusion_matrix,roc_auc_score, roc_curve, f1_score, ac
from sklearn.metrics import make_scorer, precision_score, precision_recall_curve, plot_p
from sklearn.metrics import recall_score, plot_roc_curve

import warnings
warnings.filterwarnings('ignore')
```

In [56]:

```
plt.rcParams['figure.figsize'] = (14,8)
plt.rcParams['figure.facecolor'] = '#F0F8FF'
plt.rcParams['figure.titlesize'] = 'medium'
plt.rcParams['figure.dpi'] = 100
plt.rcParams['figure.edgecolor'] = 'green'
plt.rcParams['figure.frameon'] = True

plt.rcParams["figure.autolayout"] = True

plt.rcParams['axes.facecolor'] = '#F5F5DC'
plt.rcParams['axes.titlesize'] = 25
plt.rcParams["axes.titleweight"] = 'normal'
plt.rcParams["axes.titlecolor"] = 'Olive'
plt.rcParams['axes.edgecolor'] = 'pink'
plt.rcParams["axes.linewidth"] = 2
plt.rcParams["axes.grid"] = True
plt.rcParams['axes.titlelocation'] = 'center'
plt.rcParams["axes.labelsize"] = 20
plt.rcParams["axes.labelpad"] = 2
plt.rcParams['axes.labelweight'] = 1
plt.rcParams["axes.labelcolor"] = 'Olive'
plt.rcParams["axes.axisbelow"] = False
plt.rcParams['axes.xmargin'] = .2
plt.rcParams["axes.ymargin"] = .2


plt.rcParams["xtick.bottom"] = True
plt.rcParams['xtick.color'] = '#A52A2A'
plt.rcParams["ytick.left"] = True
plt.rcParams['ytick.color'] = '#A52A2A'

plt.rcParams['axes.grid'] = True
plt.rcParams['grid.color'] = 'green'
plt.rcParams['grid.linestyle'] = '--'
plt.rcParams['grid.linewidth'] = .5
plt.rcParams['grid.alpha'] = .3

plt.rcParams['legend.loc'] = 'best'
plt.rcParams['legend.facecolor'] =  'NavajoWhite'
plt.rcParams['legend.edgecolor'] = 'pink'
plt.rcParams['legend.shadow'] = True
plt.rcParams['legend.fontsize'] = 20


plt.rcParams['font.family'] = 'Lucida Calligraphy'
plt.rcParams['font.size'] = 14

plt.rcParams['figure.dpi'] = 200
plt.rcParams['figure.edgecolor'] = 'Blue'
```

Perform feature scaling for KNN and SVM models

In [57]:

```
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
scaled_X_train_nontree = scaler.fit_transform(X_train_nontree)
scaled_X_test_nontree = scaler.fit_transform(X_test_nontree)
```

1. KNN (K-Nearest Neighbour Classifier)

Without feature scaling

In [58]:

```
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors = 3)
knn.fit(X_train_nontree, y_train_nontree)
y_pred_knn = knn.predict(X_test_nontree)

knn_train = round(knn.score(X_train_nontree, y_train_nontree) * 100, 2)
knn_accuracy = round(accuracy_score(y_pred_knn, y_test_nontree) * 100, 2)
knn_f1 = round(f1_score(y_pred_knn, y_test_nontree) * 100, 2)

print("Training Accuracy     :",knn_train,"%")
print("Model Accuracy Score  :",knn_accuracy,"%")
print("\033[1m--------------------------------------------------------\033[0m")
print("Classification_Report: \n",classification_report(y_test_nontree,y_pred_knn))
```

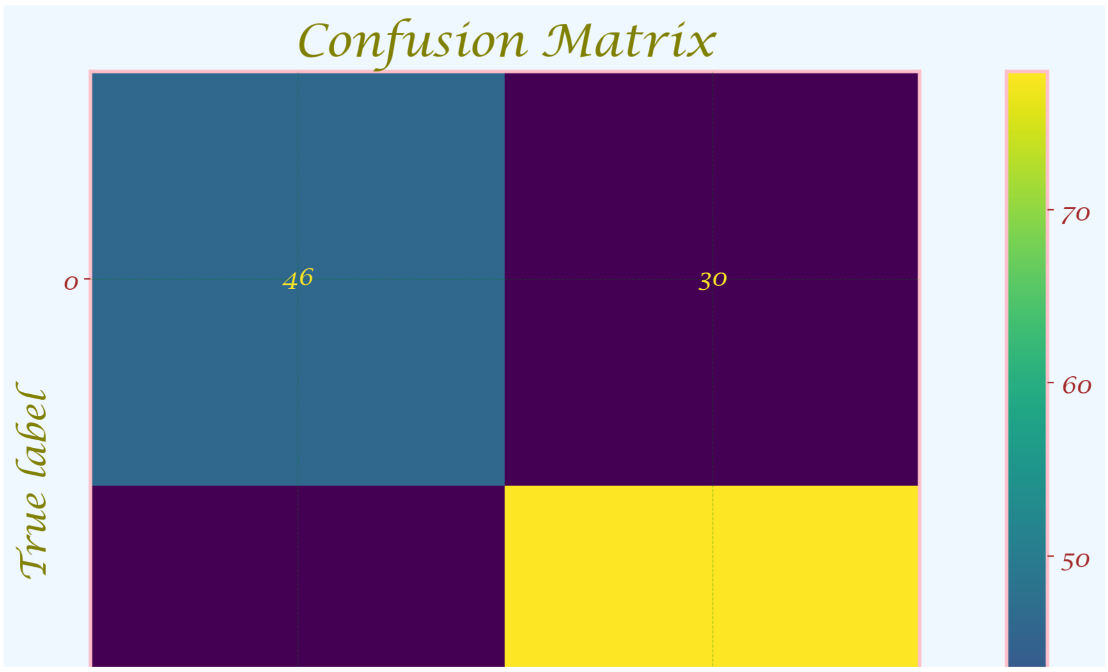
```
Training Accuracy     : 81.17 %
Model Accuracy Score  : 67.39 %
--------------------------------------------------------
Classification_Report: 
               precision    recall  f1-score   support

           0       0.61      0.61      0.61        76
           1       0.72      0.72      0.72       108

    accuracy                           0.67       184
   macro avg       0.66      0.66      0.66       184
weighted avg       0.67      0.67      0.67       184
```

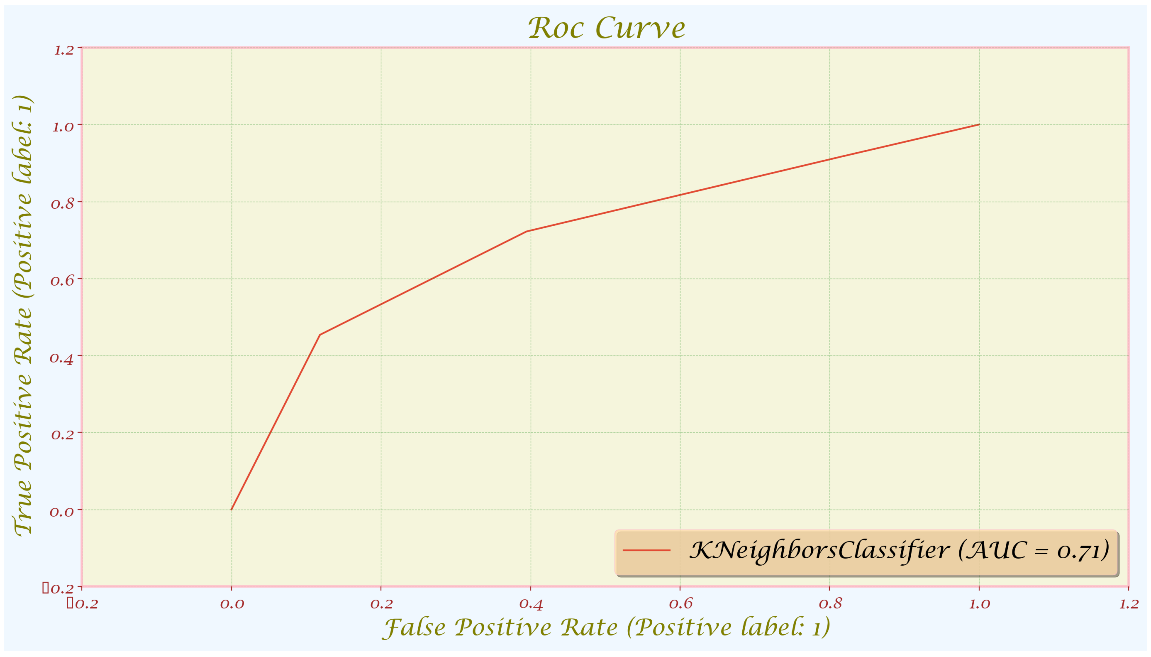
In [59]:

```
plot_confusion_matrix(knn, X_test_nontree, y_test_nontree);
plt.title('Confusion Matrix');
```



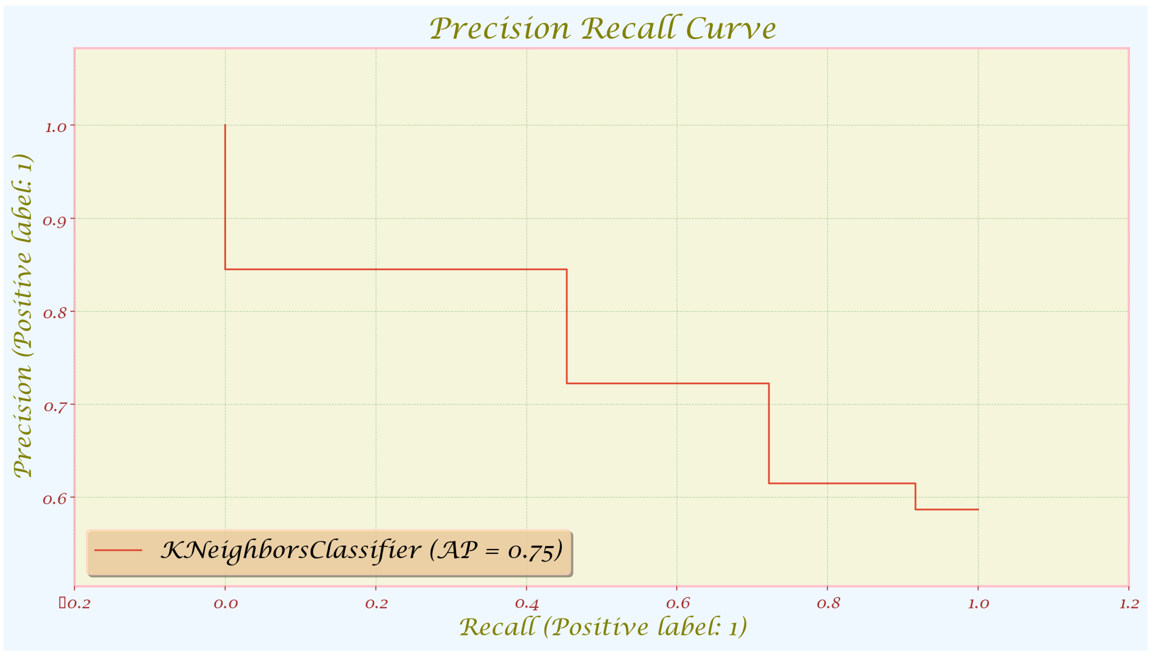
In [60]:

```
plot_roc_curve(knn, X_test_nontree, y_test_nontree);
plt.title('Roc Curve');
```



In [61]:

```
plot_precision_recall_curve(knn, X_test_nontree, y_test_nontree)
plt.title('Precision Recall Curve');
```



In [62]:

```
from sklearn.model_selection import cross_val_score
val_score = cross_val_score(estimator=knn, X = X_train_nontree, y=y_train_nontree, cv=10
print("Model Accuracy Score: {:.2f} %".format(val_score.mean()*100))
print("Std. Dev: {:.2f} %".format(val_score.std()*100))
```

```
Model Accuracy Score: 65.62 %
Std. Dev: 4.03 %
```

With feature scaling

In [63]:

```
# from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors = 3)
knn.fit(scaled_X_train_nontree, y_train_nontree)
y_pred_knn = knn.predict(scaled_X_test_nontree)

knn_train = round(knn.score(scaled_X_train_nontree, y_train_nontree) * 100, 2)
knn_accuracy = round(accuracy_score(y_pred_knn, y_test_nontree) * 100, 2)
knn_f1 = round(f1_score(y_pred_knn, y_test_nontree) * 100, 2)

print("Training Accuracy     :",knn_train,"%")
print("Model Accuracy Score  :",knn_accuracy,"%")
print("\033[1m--------------------------------------------------------\033[0m")
print("Classification_Report: \n",classification_report(y_test_nontree,y_pred_knn))
```

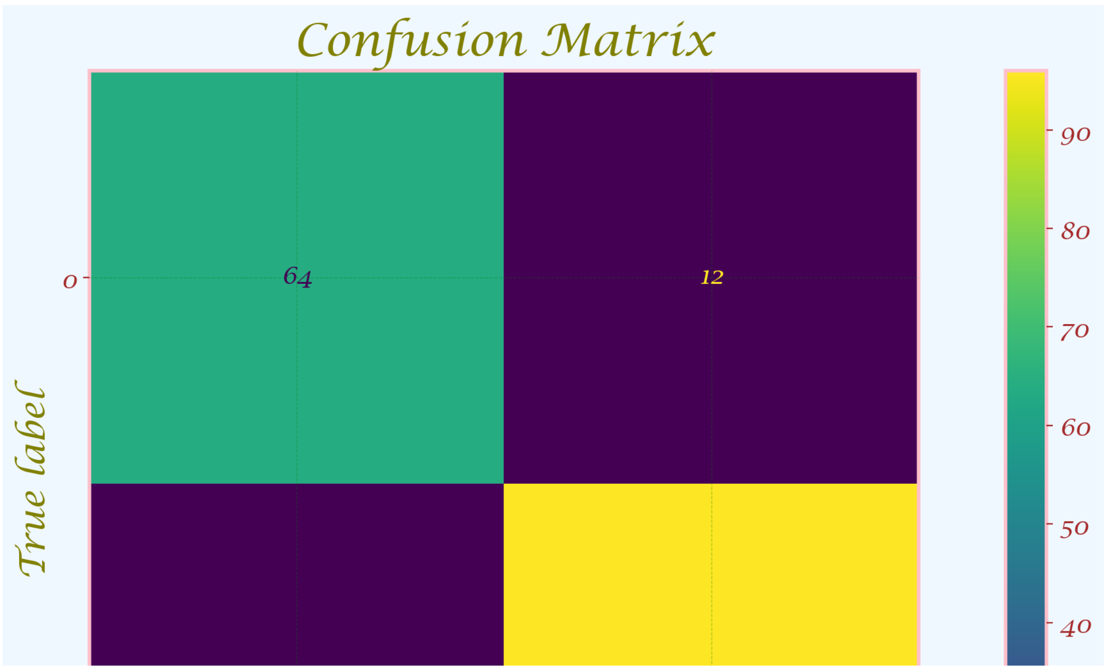
```
Training Accuracy     : 90.59 %
Model Accuracy Score  : 86.96 %
--------------------------------------------------------
Classification_Report: 
               precision    recall  f1-score   support

           0       0.84      0.84      0.84        76
           1       0.89      0.89      0.89       108

    accuracy                           0.87       184
   macro avg       0.87      0.87      0.87       184
weighted avg       0.87      0.87      0.87       184
```

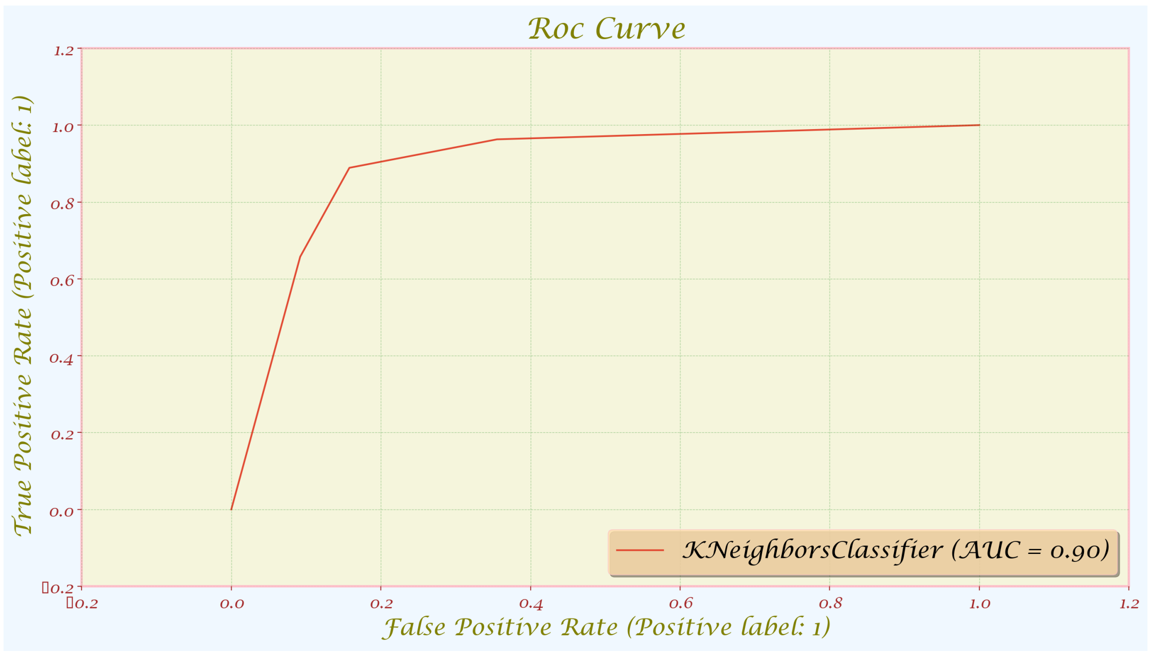
In [64]:

```
plot_confusion_matrix(knn, scaled_X_test_nontree, y_test_nontree);
plt.title('Confusion Matrix');
```



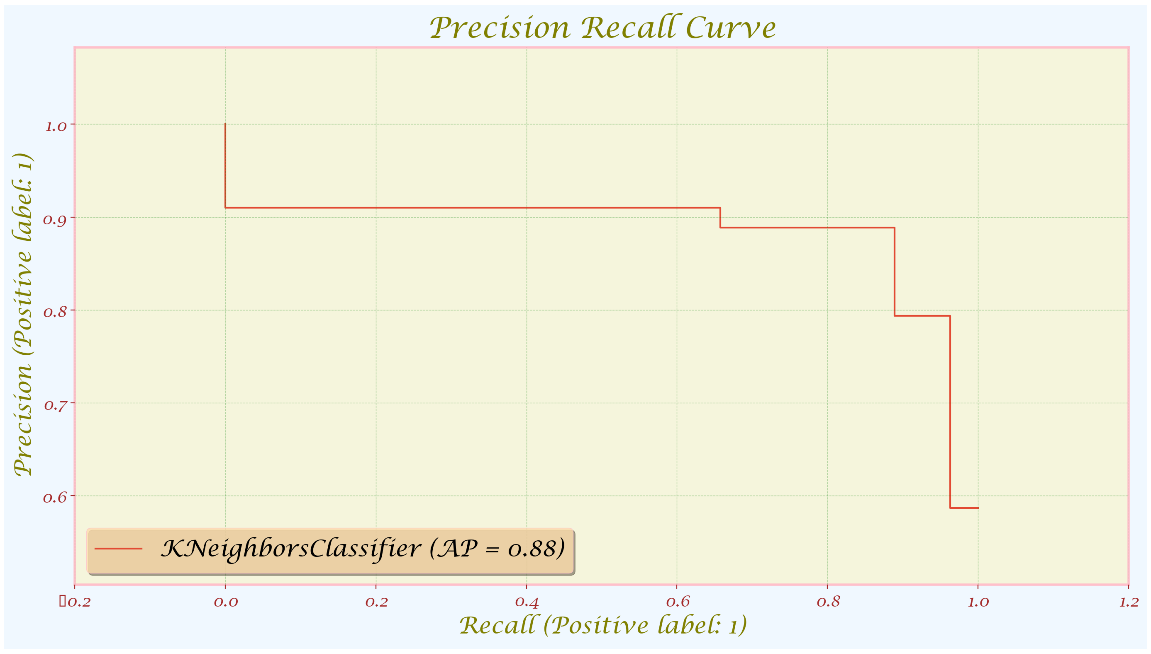
In [65]:

```
plot_roc_curve(knn, scaled_X_test_nontree, y_test_nontree);
plt.title('Roc Curve');
```



In [66]:

```
plot_precision_recall_curve(knn, scaled_X_test_nontree, y_test_nontree)
plt.title('Precision Recall Curve');
```



In [67]:

```
from sklearn.model_selection import cross_val_score
val_score = cross_val_score(estimator=knn, X = scaled_X_train_nontree, y=y_train_nontree
print("Model Accuracy Score: {:.2f} %".format(val_score.mean()*100))
print("Std. Dev: {:.2f} %".format(val_score.std()*100))
```

```
Model Accuracy Score: 83.91 %
Std. Dev: 3.78 %
```

2. SVM

Without feature scaling

In [68]:

```
# Support Vector Machines
from sklearn.svm import SVC
svc = SVC()
svc.fit(X_train_nontree, y_train_nontree)
y_pred_svc = svc.predict(X_test_nontree)

svc_train = round(svc.score(X_train_nontree, y_train_nontree) * 100, 2)
svc_accuracy = round(accuracy_score(y_pred_svc, y_test_nontree) * 100, 2)
svc_f1 = round(f1_score(y_pred_svc, y_test_nontree) * 100, 2)

print("Training Accuracy     :",svc_train,"%")
print("Model Accuracy Score  :",svc_accuracy,"%")
print("\033[1m--------------------------------------------------------\033[0m")
print("Classification_Report: \n",classification_report(y_test_nontree,y_pred_svc))
```

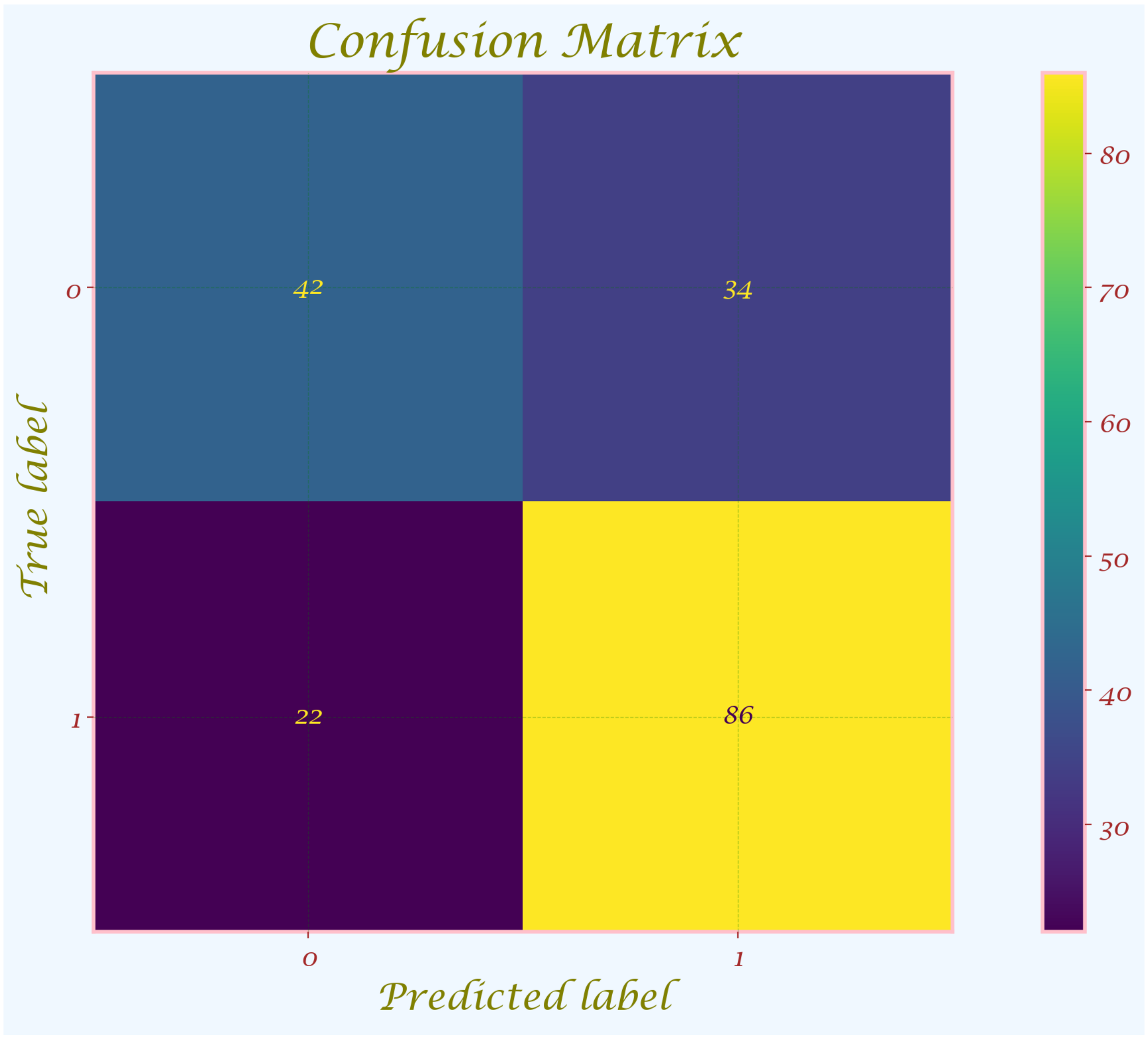
```
Training Accuracy     : 69.03 %
Model Accuracy Score  : 69.57 %
--------------------------------------------------------
Classification_Report: 
               precision    recall  f1-score   support

           0       0.66      0.55      0.60        76
           1       0.72      0.80      0.75       108

    accuracy                           0.70       184
   macro avg       0.69      0.67      0.68       184
weighted avg       0.69      0.70      0.69       184
```

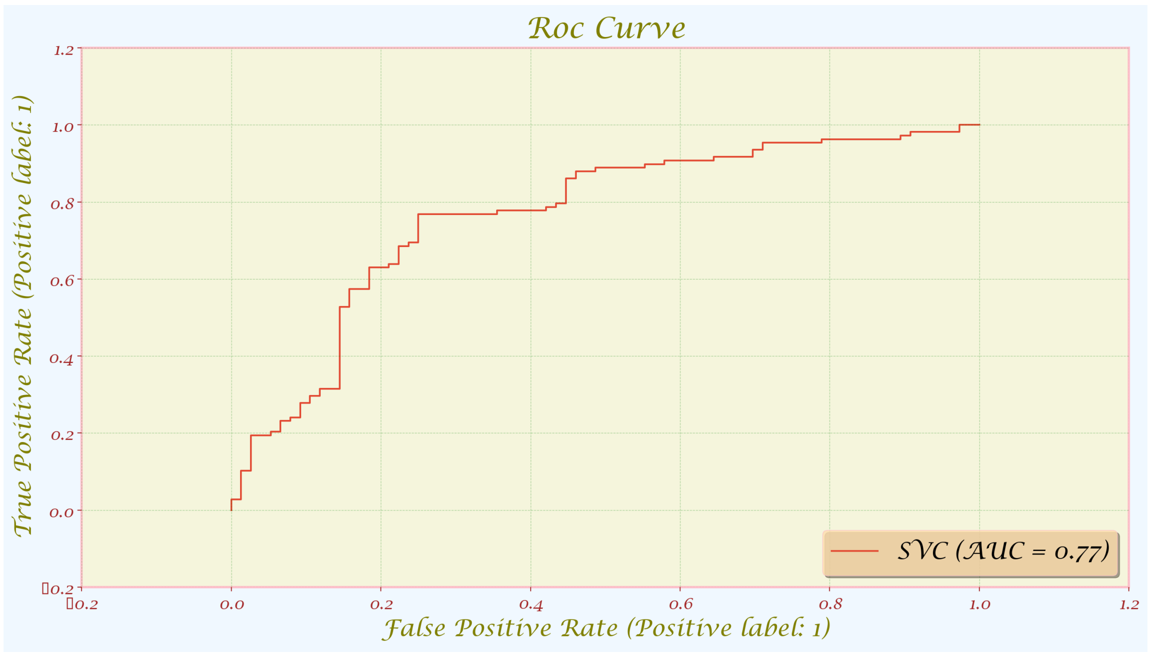
In [69]:

```
plot_confusion_matrix(svc, X_test_nontree, y_test_nontree);
plt.title('Confusion Matrix');
```



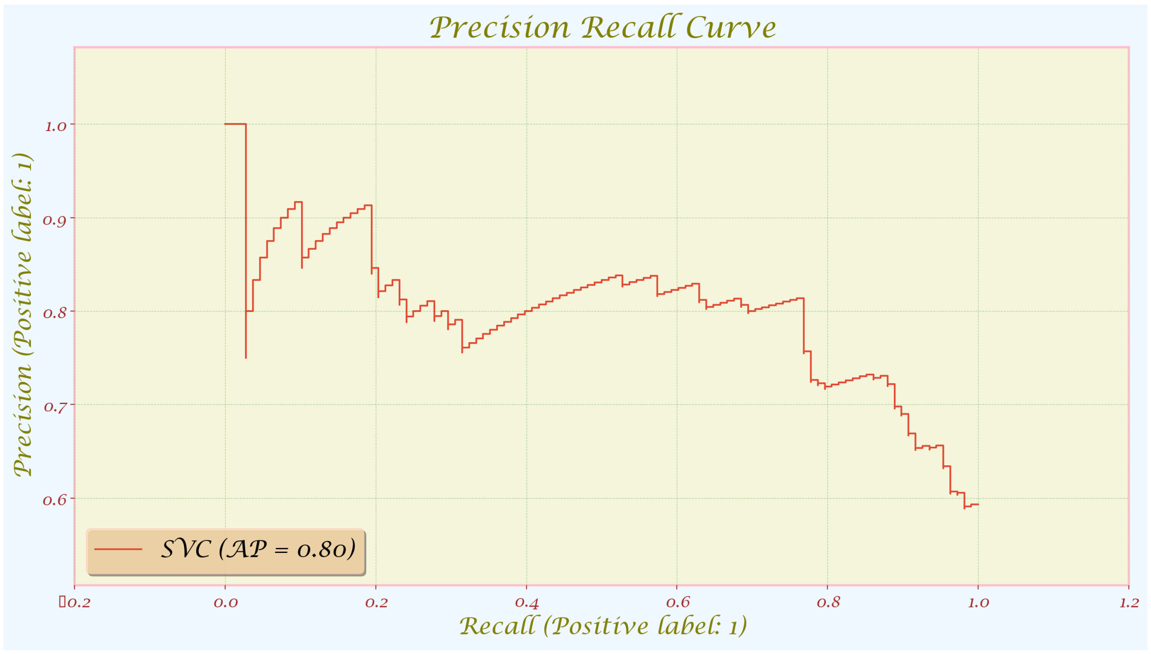
In [70]:

```
plot_roc_curve(svc, X_test_nontree, y_test_nontree);
plt.title('Roc Curve');
```



In [71]:

```
plot_precision_recall_curve(svc,  X_test_nontree, y_test_nontree)
plt.title('Precision Recall Curve');
```



In [72]:

```
from sklearn.model_selection import cross_val_score
val_score = cross_val_score(estimator=svc, X = X_train_nontree, y=y_train_nontree, cv=10
print("Model Accuracy Score: {:.2f} %".format(val_score.mean()*100))
print("Std. Dev: {:.2f} %".format(val_score.std()*100))
```

```
Model Accuracy Score: 68.76 %
Std. Dev: 3.54 %
```

With feature scaling

In [73]:

```
# Support Vector Machines
from sklearn.svm import SVC
svc = SVC()
svc.fit(scaled_X_train_nontree, y_train_nontree)
y_pred_svc = svc.predict(scaled_X_test_nontree)

svc_train = round(svc.score(scaled_X_train_nontree, y_train_nontree) * 100, 2)
svc_accuracy = round(accuracy_score(y_pred_svc, y_test_nontree) * 100, 2)
svc_f1 = round(f1_score(y_pred_svc, y_test_nontree) * 100, 2)

print("Training Accuracy     :",svc_train,"%")
print("Model Accuracy Score  :",svc_accuracy,"%")
print("\033[1m--------------------------------------------------------\033[0m")
print("Classification_Report: \n",classification_report(y_test_nontree,y_pred_svc))
```

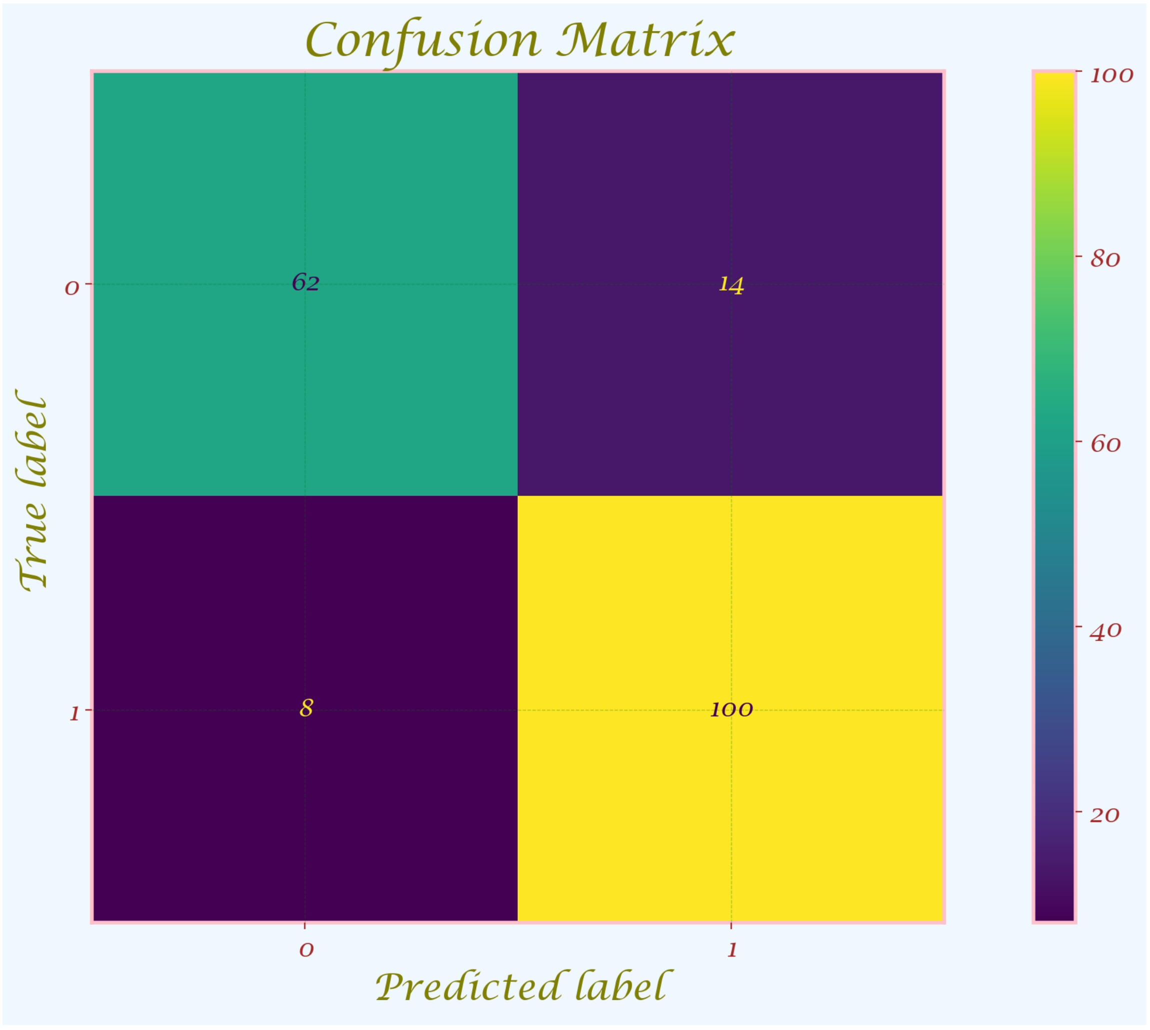
```
Training Accuracy     : 90.31 %
Model Accuracy Score  : 88.04 %
--------------------------------------------------------
Classification_Report:
               precision    recall  f1-score   support

           0       0.89      0.82      0.85        76
           1       0.88      0.93      0.90       108

    accuracy                           0.88       184
   macro avg       0.88      0.87      0.88       184
weighted avg       0.88      0.88      0.88       184
```

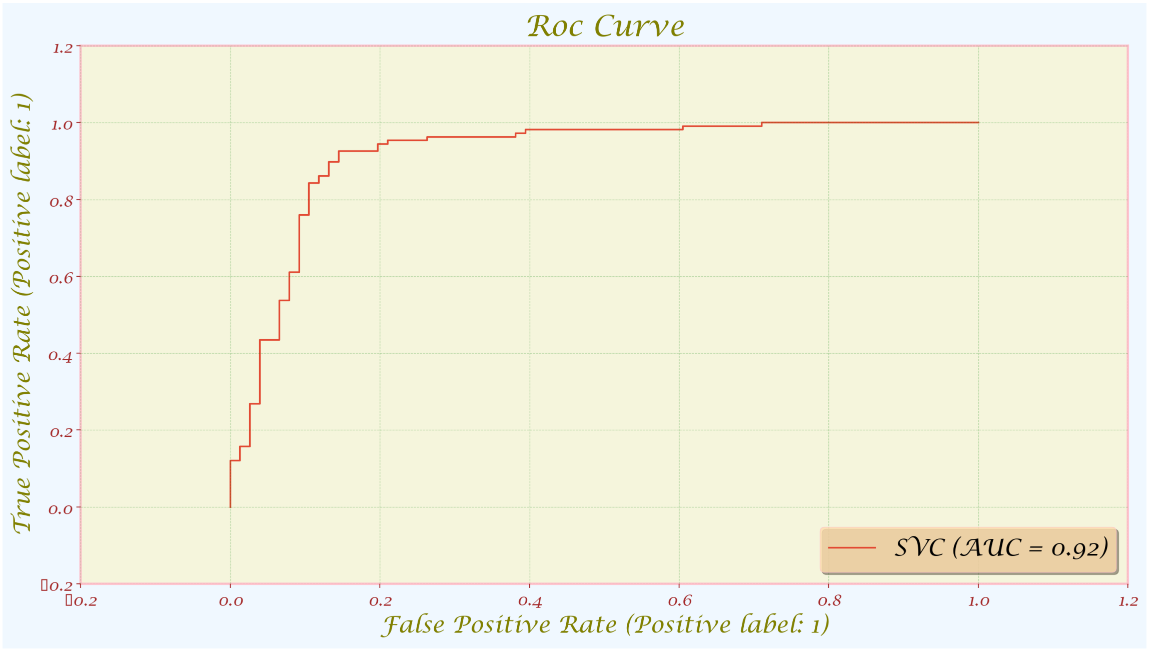
In [74]:

```
plot_confusion_matrix(svc, scaled_X_test_nontree, y_test_nontree);
plt.title('Confusion Matrix');
```



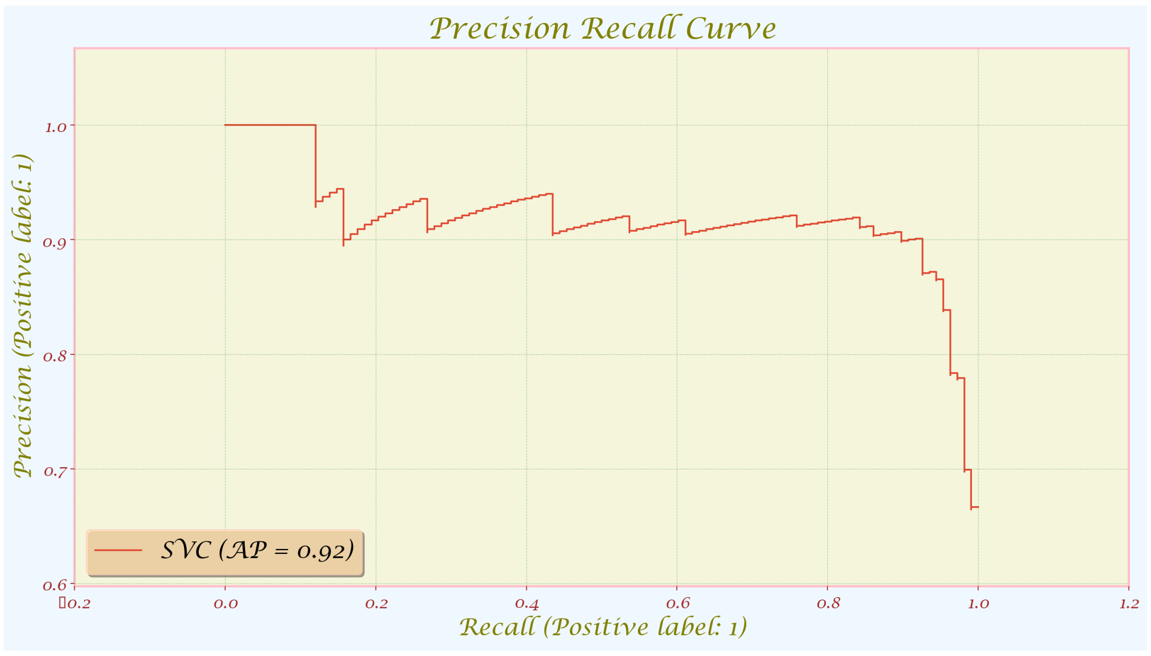
In [75]:

```
plot_roc_curve(svc, scaled_X_test_nontree, y_test_nontree);
plt.title('Roc Curve');
```



In [76]:

```
plot_precision_recall_curve(svc,  scaled_X_test_nontree, y_test_nontree)
plt.title('Precision Recall Curve');
```



In [77]:

```
from sklearn.model_selection import cross_val_score
val_score = cross_val_score(estimator=svc, X = scaled_X_train_nontree, y=y_train_nontree
print("Model Accuracy Score: {:.2f} %".format(val_score.mean()*100))
print("Std. Dev: {:.2f} %".format(val_score.std()*100))
```

```
Model Accuracy Score: 84.73 %
Std. Dev: 2.59 %
```

It is very obvious that feature scaling is necessary for Support Vector Machines as the model accuracy score of modeling with feature scaling(84.73 %) is much higher than modeling without feature scaling(68.76 %)

3. Decision Tree

In [78]:

```
# Decision Tree
from sklearn.tree import DecisionTreeClassifier
decision = DecisionTreeClassifier()
decision.fit(X_train_tree, y_train_tree)
y_pred_Decision = decision.predict(X_test_tree)

decision_train = round(decision.score(X_train_tree, y_train_tree) * 100, 2)
decision_accuracy = round(accuracy_score(y_pred_Decision, y_test_tree) * 100, 2)
decision_f1 = round(f1_score(y_pred_Decision, y_test_tree) * 100, 2)

print("Training Accuracy     :",decision_train,"%")
print("Model Accuracy Score  :",decision_accuracy,"%")
print("\033[1m--------------------------------------------------------\033[0m")
print("Classification_Report: \n",classification_report(y_test_tree,y_pred_Decision))
```

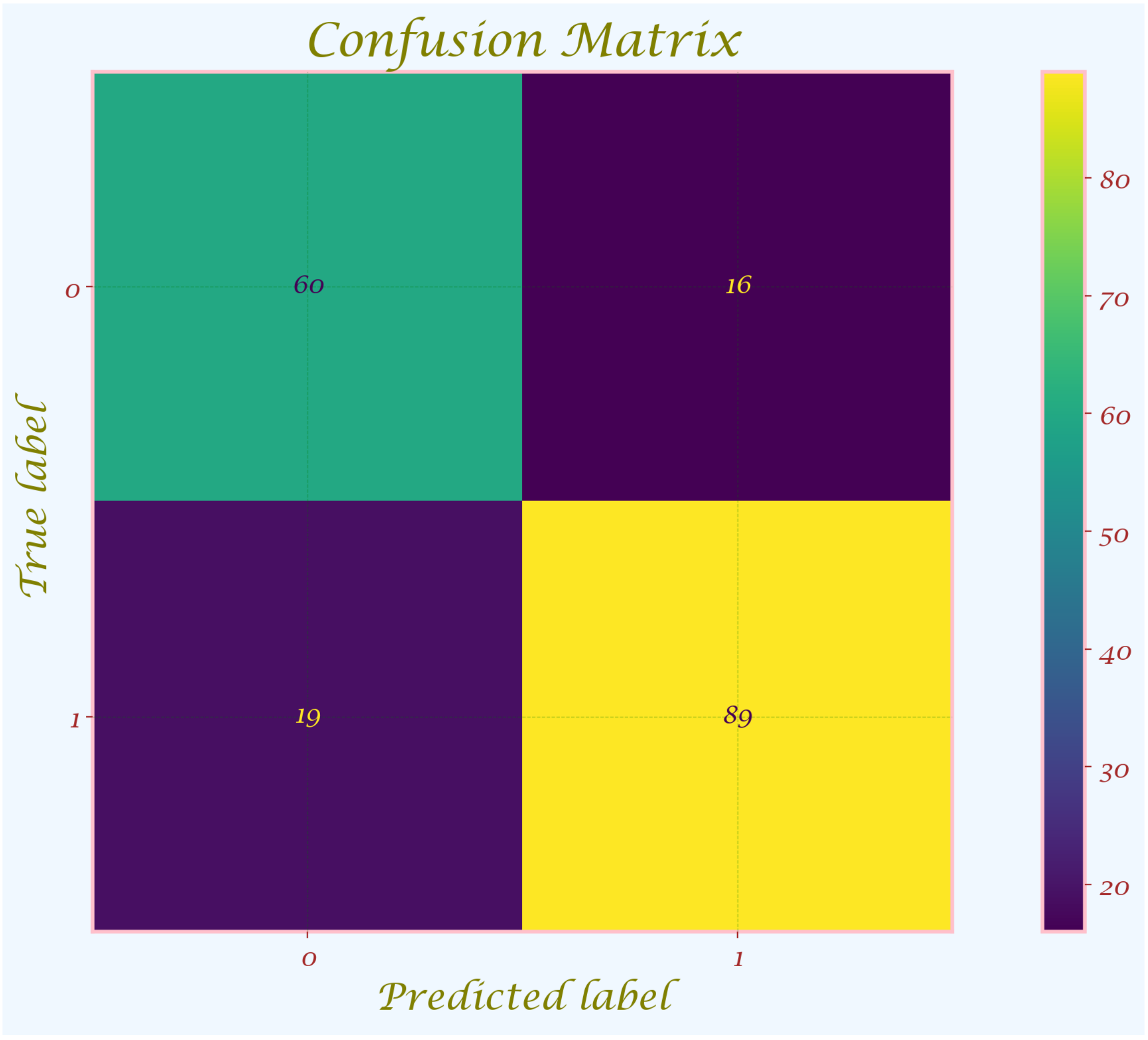
```
Training Accuracy     : 100.0 %
Model Accuracy Score  : 80.98 %
--------------------------------------------------------
Classification_Report:
               precision    recall  f1-score   support

           0       0.76      0.79      0.77        76
           1       0.85      0.82      0.84       108

    accuracy                           0.81       184
   macro avg       0.80      0.81      0.80       184
weighted avg       0.81      0.81      0.81       184
```

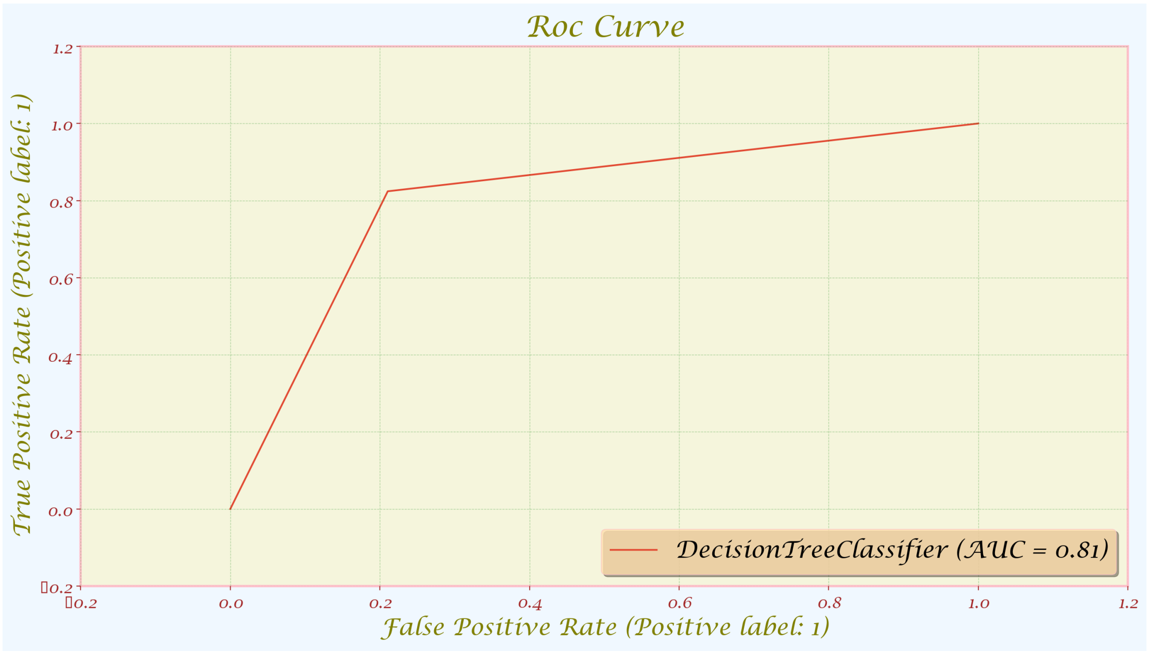
In [79]:

```
plot_confusion_matrix(decision, X_test_tree, y_test_tree);
plt.title('Confusion Matrix');
```



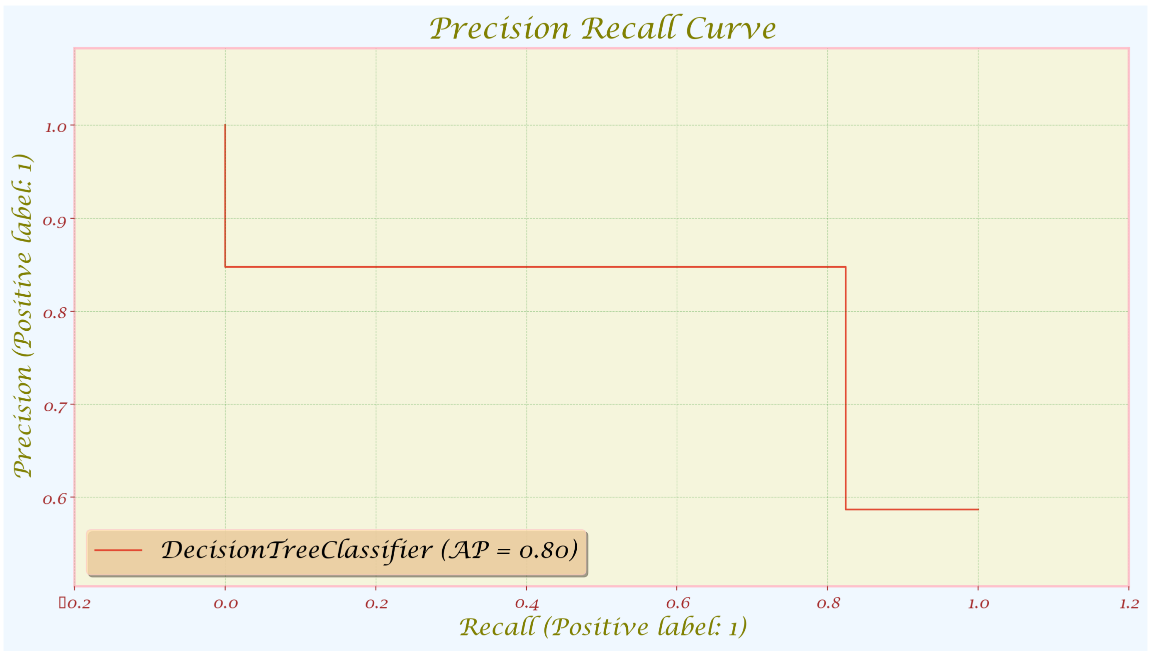
In [80]:

```
plot_roc_curve(decision, X_test_tree, y_test_tree);
plt.title('Roc Curve');
```



In [81]:

```
plot_precision_recall_curve(decision, X_test_tree, y_test_tree)
plt.title('Precision Recall Curve');
```



In [82]:

```
from sklearn.model_selection import cross_val_score
val_score = cross_val_score(estimator=decision, X = X_train_tree, y=y_train_tree, cv=10)
print("Model Accuracy Score: {:.2f} %".format(val_score.mean()*100))
print("Std. Dev: {:.2f} %".format(val_score.std()*100))
```

```
Model Accuracy Score: 77.89 %
Std. Dev: 3.71 %
```

4. Random Forest

In [83]:

```
# Random Forest
from sklearn.ensemble import RandomForestClassifier
random_forest = RandomForestClassifier(n_estimators=100)
random_forest.fit(X_train_tree, y_train_tree)
y_pred_random = random_forest.predict(X_test_tree)
random_forest.score(X_train_tree, y_train_tree)

random_forest_train = round(random_forest.score(X_train_tree, y_train_tree) * 100, 2)
random_forest_accuracy = round(accuracy_score(y_pred_random, y_test_tree) * 100, 2)
random_forest_f1 = round(f1_score(y_pred_random, y_test_tree) * 100, 2)

print("Training Accuracy     :",random_forest_train,"%")
print("Model Accuracy Score  :",random_forest_accuracy,"%")
print("\033[1m--------------------------------------------------------\033[0m")
print("Classification_Report: \n",classification_report(y_test_tree,y_pred_random))
```

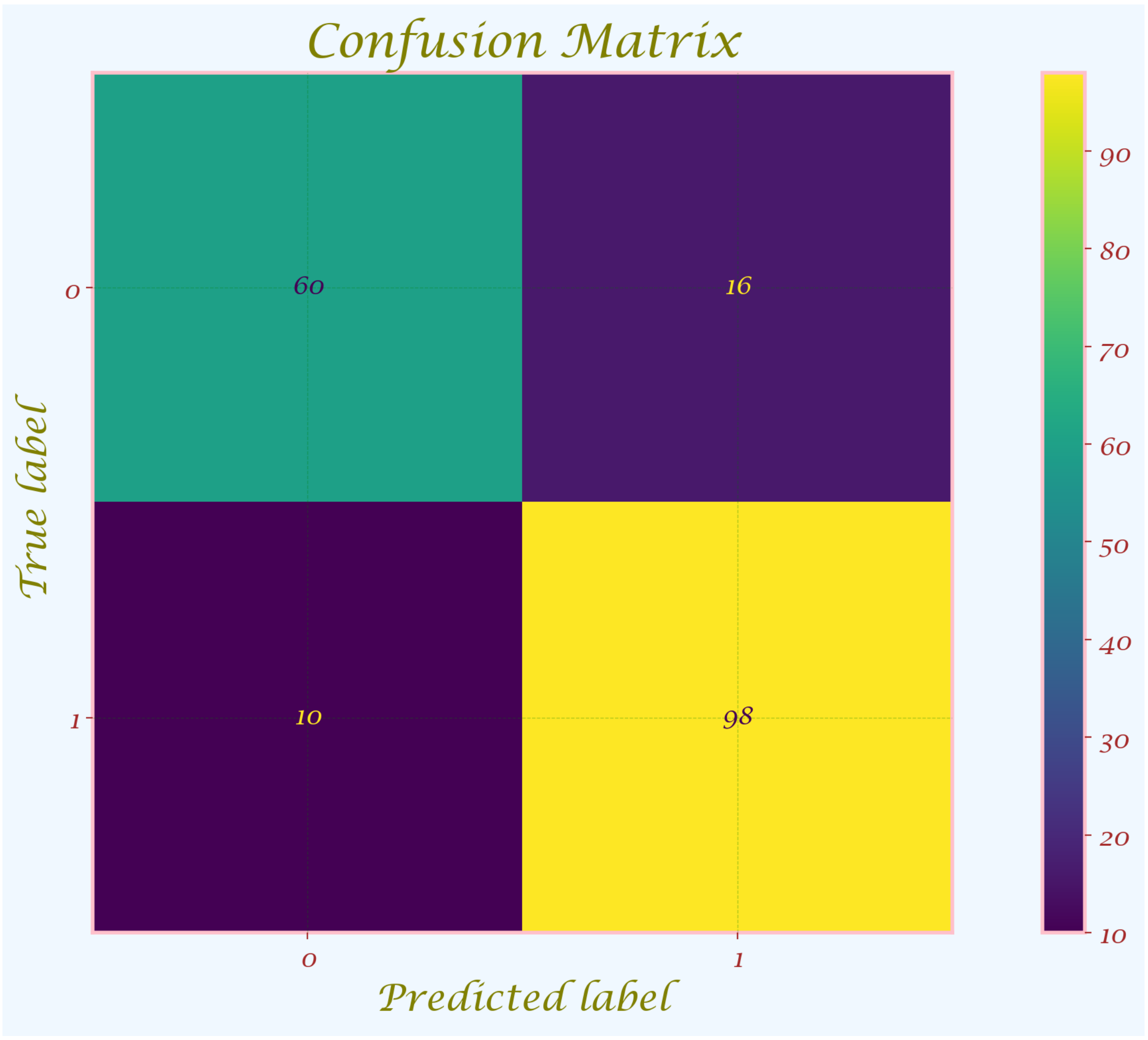
```
Training Accuracy     : 100.0 %
Model Accuracy Score  : 85.87 %
--------------------------------------------------------
Classification_Report:
               precision    recall  f1-score   support

           0       0.86      0.79      0.82        76
           1       0.86      0.91      0.88       108

    accuracy                           0.86       184
   macro avg       0.86      0.85      0.85       184
weighted avg       0.86      0.86      0.86       184
```

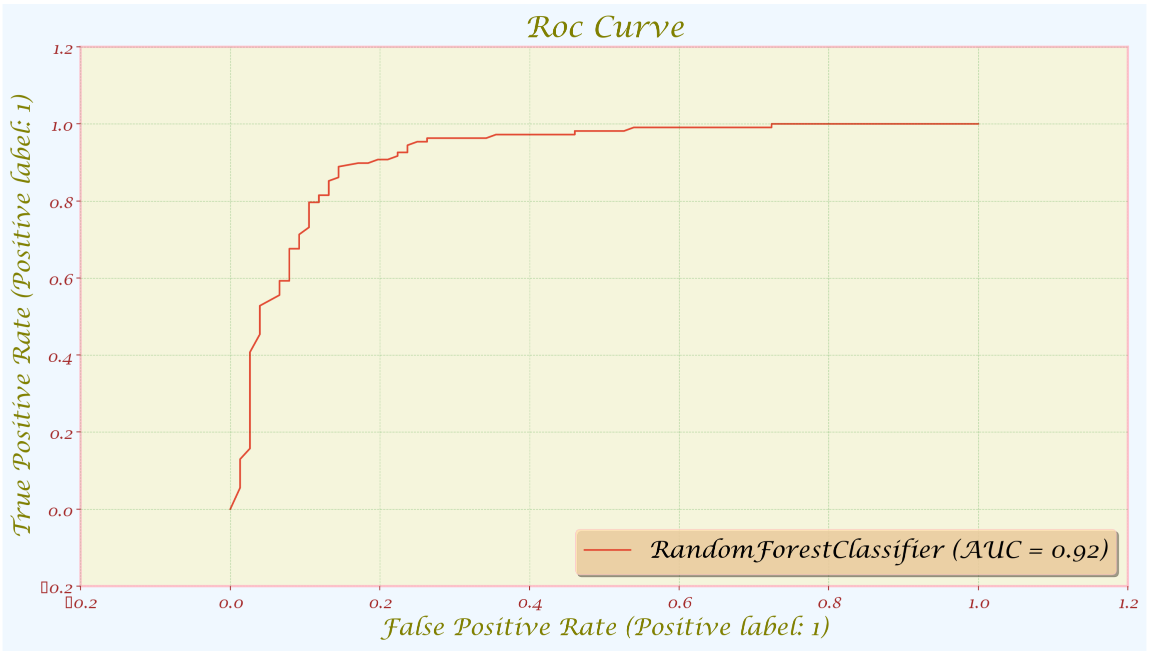
In [84]:

```
plot_confusion_matrix(random_forest, X_test_tree, y_test_tree);
plt.title('Confusion Matrix');
```



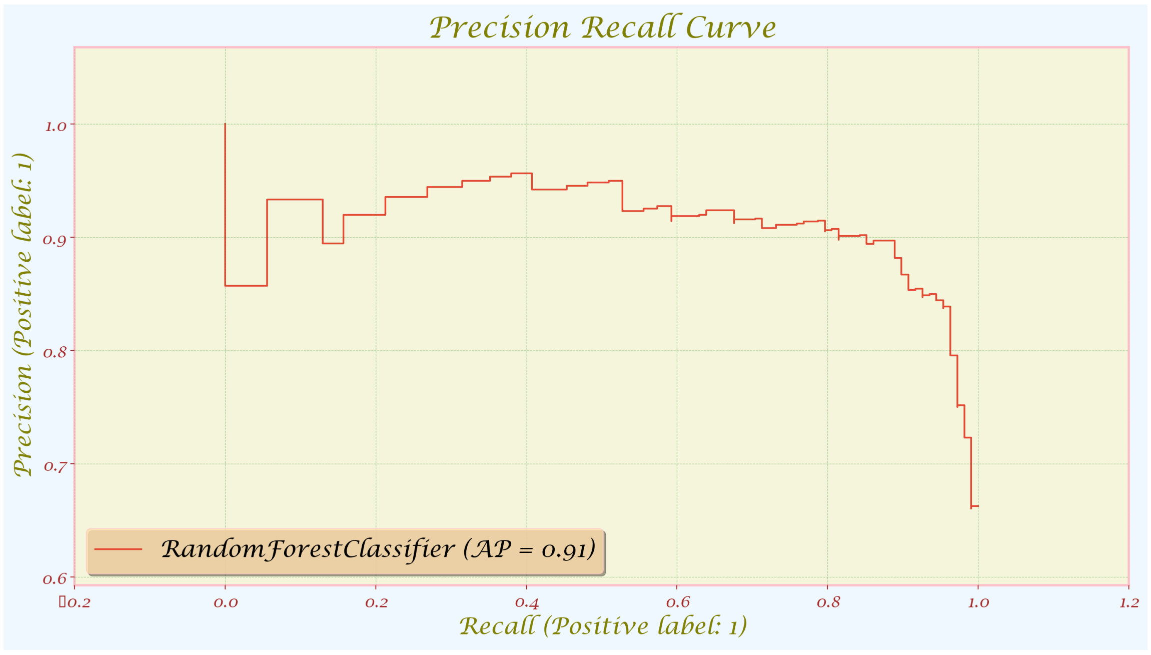
In [85]:

```
plot_roc_curve(random_forest, X_test_tree, y_test_tree);
plt.title('Roc Curve');
```



In [86]:

```
plot_precision_recall_curve(random_forest, X_test_tree, y_test_tree)
plt.title('Precision Recall Curve');
```



In [87]:

```
from sklearn.model_selection import cross_val_score
val_score = cross_val_score(estimator=random_forest, X = X_train_tree, y=y_train_tree, c
print("Model Accuracy Score: {:.2f} %".format(val_score.mean()*100))
print("Std. Dev: {:.2f} %".format(val_score.std()*100))
```

```
Model Accuracy Score: 86.23 %
Std. Dev: 3.83 %
```

5.0 Model Evaluation

In [88]:

```
models = pd.DataFrame({
    'Model': [
        'KNeighborsClassifier','Support Vector Machines',
        'Decision Tree','Random Forest'],
    'Training Accuracy': [
         knn_train,svc_train,
        decision_train, random_forest_train],
    'Model f1 Score': [
        knn_f1,svc_f1,
        decision_f1, random_forest_f1],
    'Model Accuracy Score': [
        knn_accuracy,svc_accuracy,
       decision_accuracy, random_forest_accuracy]

})
```

In [89]:

```
# Accuracy Comparison Table
models.sort_values(
    by='Model Accuracy Score', ascending=False).style.background_gradient(
        cmap='cool').hide_index().set_properties(**{
            'font-family': 'Lucida Calligraphy',
            'color': 'LigntGreen',
            'font-size': '15px'
        })
```

Out[89]:

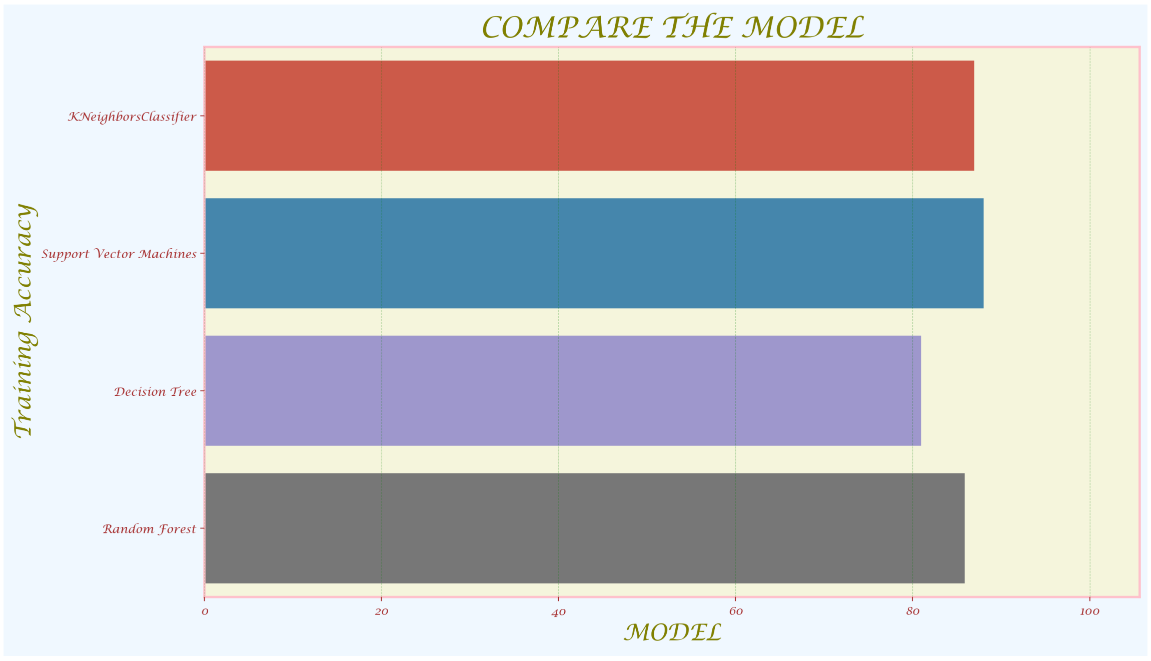
Model	Training Accuracy	Model f1 Score	Model Accuracy Score
Support Vector Machines	90.310000	90.090000	88.040000
KNeighborsClassifier	90.590000	88.890000	86.960000
Random Forest	100.000000	88.290000	85.870000
Decision Tree	100.000000	83.570000	80.980000

In [90]:

```
plt.rcParams['figure.figsize'] = (14,8)
plt.rcParams['font.size'] = 10
plt.rcParams['axes.xmargin'] = .2
plt.rcParams["axes.ymargin"] = .2


import seaborn as sns

sns.barplot(y= 'Model', x= 'Model Accuracy Score', data= models)
plt.title('COMPARE THE MODEL')
plt.xlabel('MODEL')
plt.ylabel('Training Accuracy');
```



We can see that Support Vector Machines have the highest training accuracy

In [91]:

```
prediction1 = random_forest.predict(X_test_tree)
print(prediction1)
```

```
[1 0 1 1 1 1 1 0 1 1 0 0 1 1 1 1 0 0 0 1 1 1 0 1 1 1 1 0 0 1 0 0 0 0 1 1 0
 0 1 1 0 1 1 1 1 1 1 1 1 0 1 1 0 0 1 1 0 1 0 0 1 1 0 1 1 0 0 1 1 1 1 0 1 1
 0 1 1 0 1 1 1 1 1 1 1 0 1 1 1 1 0 1 0 1 0 1 1 1 1 1 1 1 1 0 1 0 1 1 0 1 0
 0 1 1 0 0 0 1 0 1 1 0 0 1 1 1 0 1 1 0 0 1 1 0 0 0 1 0 0 1 0 1 1 0 0 1 0 0
 1 1 0 1 0 1 1 0 0 0 1 0 1 1 0 1 1 1 0 1 1 1 1 1 0 0 1 0 1 1 1 1 0 0 1 1]
```

In [92]:

```
cross_checking = pd.DataFrame({'Actual' : y_test_tree , 'Predicted' : prediction1})
cross_checking.sample(15).style.background_gradient(
        cmap='coolwarm').set_properties(**{
            'font-family': 'Lucida Calligraphy',
            'color': 'LigntGreen',
            'font-size': '15px'
        })
```

Out[92]:

	Actual	Predicted
135	0	0
169	1	1
177	0	1
139	1	1
123	1	1
24	1	1
134	0	0
183	1	1
144	0	0
105	1	0
37	0	0
50	1	1
52	0	0
91	1	1
182	1	1