```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
df = pd.read_csv(r"C:\Users\chava\Desktop\
heart_disease_prediction.csv")
df
```

```
     Age Sex ChestPainType RestingBP Cholesterol RestingECG  MaxHR  \
0     40   M           ATA       140         289     Normal    172
1     49   F           NAP       160         180     Normal    156
2     37   M           ATA       130         283         ST     98
3     48   F           ASY       138         214     Normal    108
4     54   M           NAP       150         195     Normal    122
..   ...  ..           ...       ...         ...        ...    ...
913   45   M            TA       110         264     Normal    132
914   68   M           ASY       144         193     Normal    141
915   57   M           ASY       130         131     Normal    115
916   57   F           ATA       130         236        LVH    174
917   38   M           NAP       138         175     Normal    173

    ExerciseAngina  Oldpeak ST_Slope HeartDisease
0               No      0.0       Up      Absence
1               No      1.0     Flat     Presence
2               No      0.0       Up      Absence
3              Yes      1.5     Flat     Presence
4               No      0.0       Up      Absence
..             ...      ...      ...          ...
913             No      1.2     Flat     Presence
914             No      3.4     Flat     Presence
915            Yes      1.2     Flat     Presence
916             No      0.0     Flat     Presence
917             No      0.0       Up      Absence

[918 rows x 11 columns]
```

EDA process part in Dataset

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 11 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    object
 4   Cholesterol     918 non-null    object
 5   RestingECG      918 non-null    object
 6   MaxHR           918 non-null    int64
 7   ExerciseAngina  918 non-null    object
 8   Oldpeak         918 non-null    float64
 9   ST_Slope        918 non-null    object
 10  HeartDisease    918 non-null    object
dtypes: float64(1), int64(2), object(8)
memory usage: 79.0+ KB
```

need to count target column values, for our data set good or not

```
df['HeartDisease'].value_counts()

Presence    508
Absence     410
Name: HeartDisease, dtype: int64
```

i found ? in RestingBP and Cholesterol column, so i replace the ? with NAN because pandas and sklearn only handle NaN values

```
df["RestingBP"].replace("?", np.nan, inplace=True)
df["Cholesterol"].replace("?", np.nan, inplace=True)
```

change the datatype because in the latest steps we need to get mean value of RestingBP and Cholesterol column

```
 df["RestingBP"] = df["RestingBP"].astype("float64")
df["Cholesterol"] = df["Cholesterol"].astype("float64")

df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 11 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       910 non-null    float64
 4   Cholesterol     911 non-null    float64
 5   RestingECG      918 non-null    object
 6   MaxHR           918 non-null    int64
 7   ExerciseAngina  918 non-null    object
 8   Oldpeak         918 non-null    float64
 9   ST_Slope        918 non-null    object
```

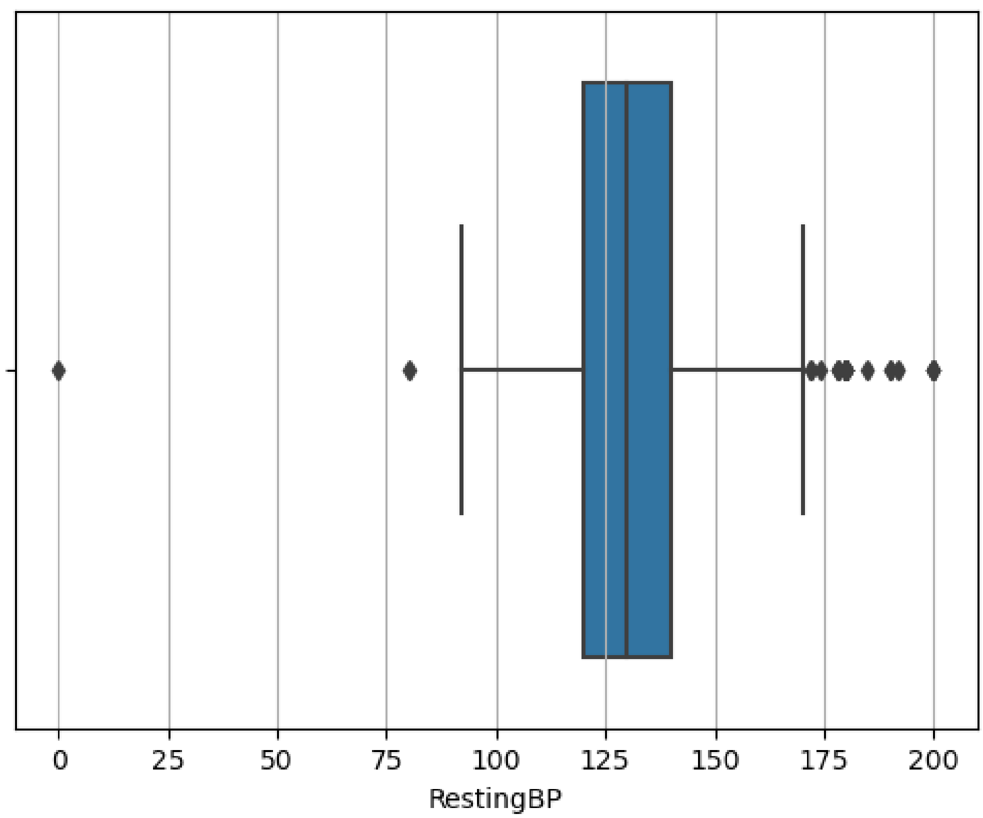
```
 10  HeartDisease    918 non-null    object
dtypes: float64(3), int64(2), object(6)
memory usage: 79.0+ KB
```

```
df.describe()
```

	Age	RestingBP	Cholesterol	MaxHR	Oldpeak
count	918.000000	910.000000	911.000000	918.000000	918.000000
mean	53.510893	132.400000	198.656422	136.809368	0.887364
std	9.432617	18.562723	109.753487	25.460334	1.066570
min	28.000000	0.000000	0.000000	60.000000	-2.600000
25%	47.000000	120.000000	172.500000	120.000000	0.000000
50%	54.000000	130.000000	223.000000	138.000000	0.600000
75%	60.000000	140.000000	267.000000	156.000000	1.500000
max	77.000000	200.000000	603.000000	202.000000	6.200000

```
plt.grid()
sns.boxplot(df["RestingBP"])
```

```
<AxesSubplot:xlabel='RestingBP'>
```



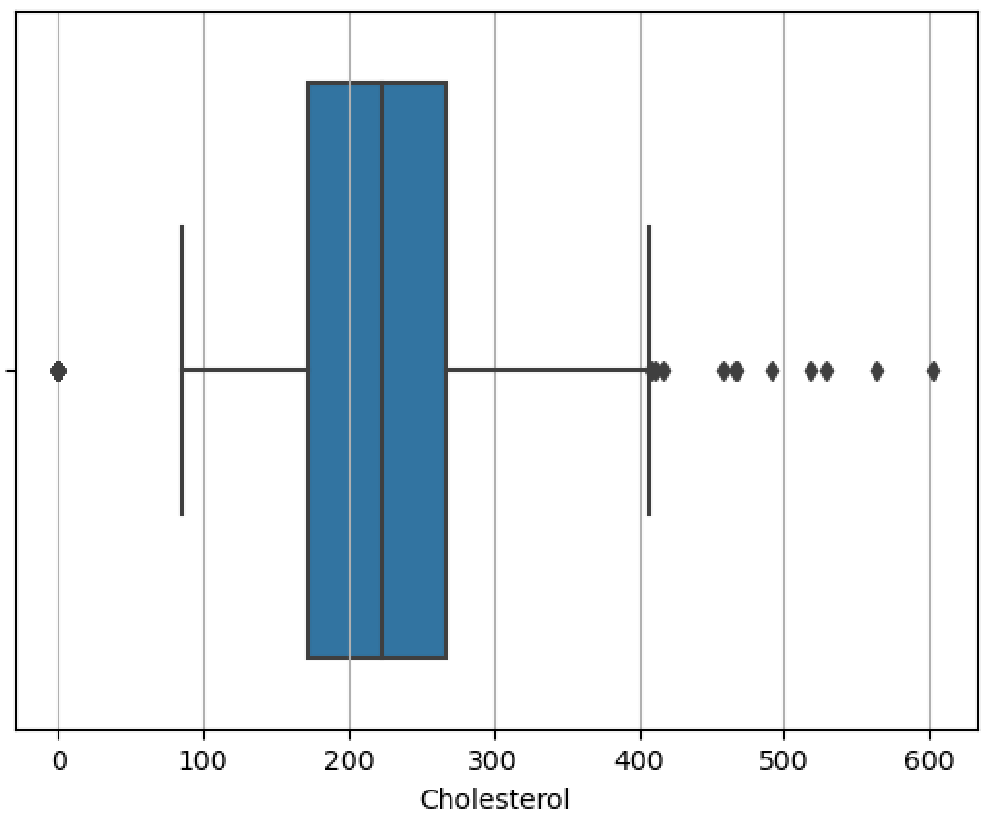
from describe i found that RestingBP has min 0 value, but RestingBP must be greater than zero,so i need to 1st replace 0 value with NAN and then again NAN repalce with mean of RestingBP

```
df["RestingBP"].replace(0, np.nan, inplace=True)

df["RestingBP"].replace(np.nan,df["RestingBP"].mean(),inplace=True)

plt.grid()
sns.boxplot(df["Cholesterol"])
```

```
<AxesSubplot:xlabel='Cholesterol'>
```




```
df[(df['Cholesterol']==0)]
```

```
     Age Sex ChestPainType  RestingBP  Cholesterol RestingECG
MaxHR  \
293   65   M           ASY      115.0          0.0     Normal     93

294   32   M            TA       95.0          0.0     Normal    127

295   61   M           ASY      105.0          0.0     Normal    110

296   50   M           ASY      145.0          0.0     Normal    139
```

```
297   57   M           ASY     110.0          0.0         ST   131
..   ...  ..           ...       ...          ...        ...   ...
514   43   M           ASY     122.0          0.0     Normal   120
515   63   M           NAP     130.0          0.0         ST   160
518   48   M           NAP     102.0          0.0         ST   110
535   56   M           ASY     130.0          0.0        LVH   122
536   62   M           NAP     133.0          0.0         ST   119

    ExerciseAngina  Oldpeak ST_Slope HeartDisease
293            Yes      0.0     Flat     Presence
294             No      0.7       Up     Presence
295            Yes      1.5       Up     Presence
296            Yes      0.7     Flat     Presence
297            Yes      1.4       Up     Presence
..             ...      ...      ...          ...
514             No      0.5       Up     Presence
515             No      3.0     Flat      Absence
518            Yes      1.0     Down     Presence
535            Yes      1.0     Flat     Presence
536            Yes      1.2     Flat     Presence

[172 rows x 11 columns]
```

in Cholesterol i found that 172 rows 0 value,Cholesterol must be greater than zero

so 1st i need to replace this 0 value with NAN and then replace NAN value with Cholesterol mean value

```
df["Cholesterol"].replace(0, np.nan, inplace=True)

df["Cholesterol"].replace(np.nan,df["Cholesterol"].mean(),inplace=True
)

df.describe()

              Age   RestingBP  Cholesterol       MaxHR     Oldpeak
count  918.000000  918.000000   918.000000  918.000000  918.000000
mean    53.510893  132.545655   244.893099  136.809368    0.887364
std      9.432617   17.956368    53.186105   25.460334    1.066570
min     28.000000   80.000000    85.000000   60.000000   -2.600000
25%     47.000000  120.000000   215.000000  120.000000    0.000000
50%     54.000000  130.000000   244.893099  138.000000    0.600000
75%     60.000000  140.000000   267.000000  156.000000    1.500000
max     77.000000  200.000000   603.000000  202.000000    6.200000
```

in oldpeak column positive and negative value between -2.60 to 6.20, so we need to scaling this column

```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
df[['Oldpeak']] = scaler.fit_transform(df[['Oldpeak']])

df.describe()
```

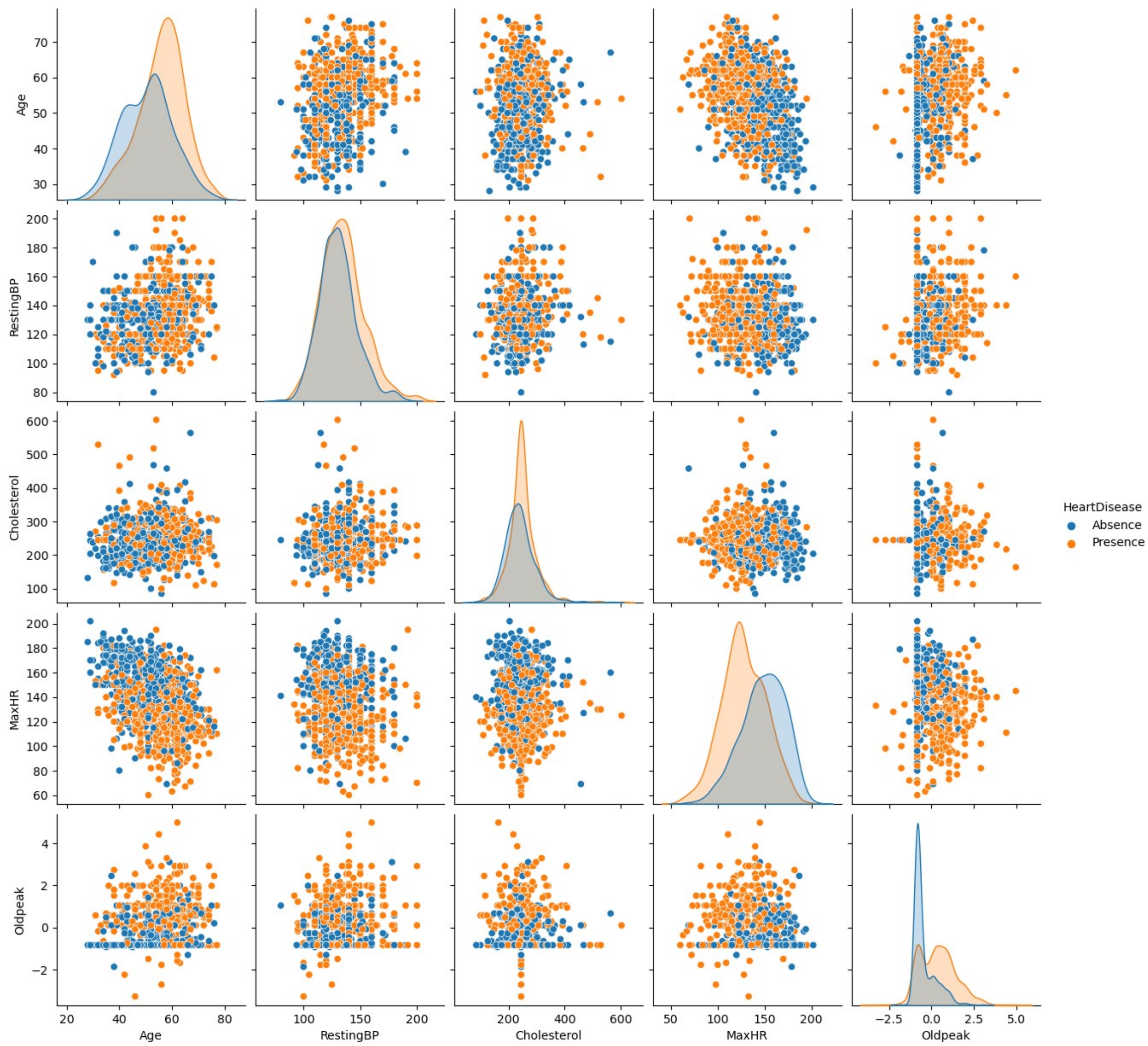
	Age	RestingBP	Cholesterol	MaxHR	Oldpeak
count	918.000000	918.000000	918.000000	918.000000	9.180000e+02
mean	53.510893	132.545655	244.893099	136.809368	-2.024524e-16
std	9.432617	17.956368	53.186105	25.460334	1.000545e+00
min	28.000000	80.000000	85.000000	60.000000	-3.271482e+00
25%	47.000000	120.000000	215.000000	120.000000	-8.324324e-01
50%	54.000000	130.000000	244.893099	138.000000	-2.695748e-01
75%	60.000000	140.000000	267.000000	156.000000	5.747115e-01
max	77.000000	200.000000	603.000000	202.000000	4.983762e+00

now our dataframe EDA part finished, so we can start data visualization

data visualization in dataset

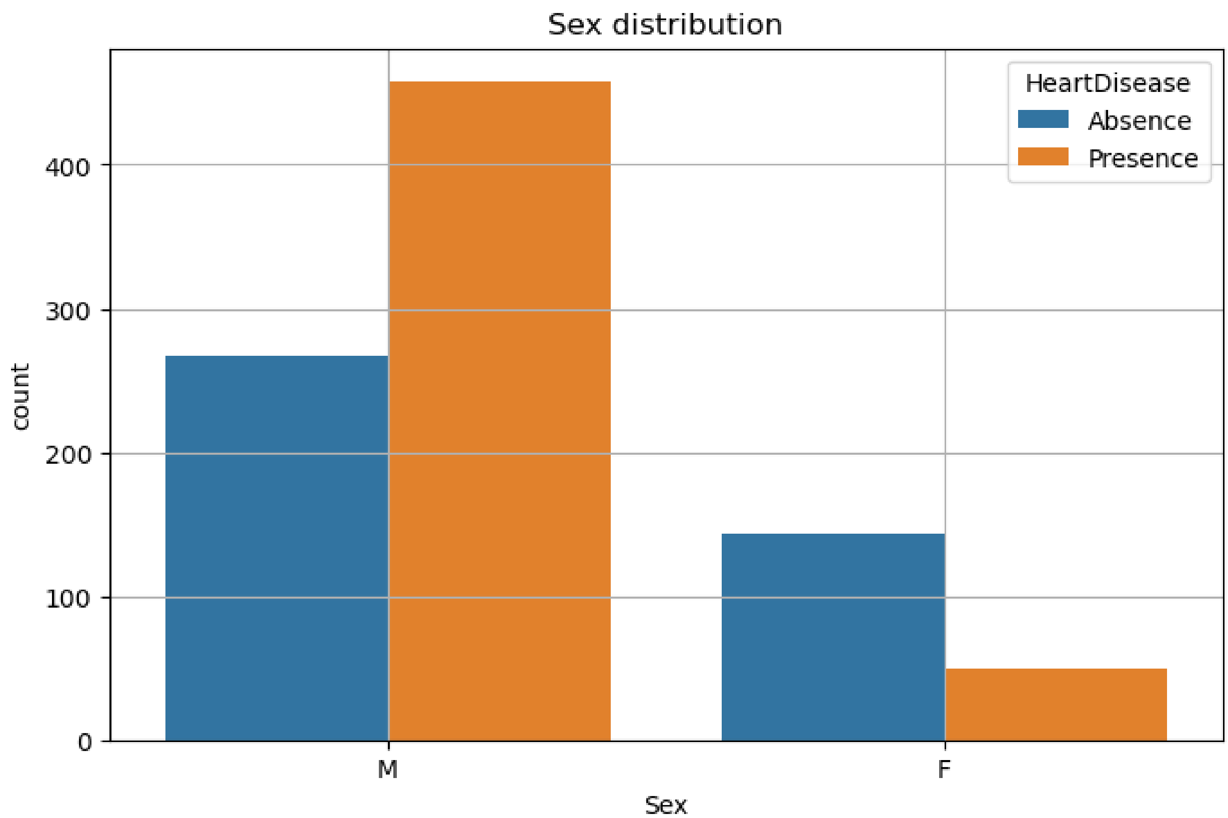
data visualization for numerical dataset

```
sns.pairplot(df[['Age', 'RestingBP', 'Cholesterol', 'MaxHR',
'Oldpeak', 'HeartDisease']], hue='HeartDisease')
plt.show()
```

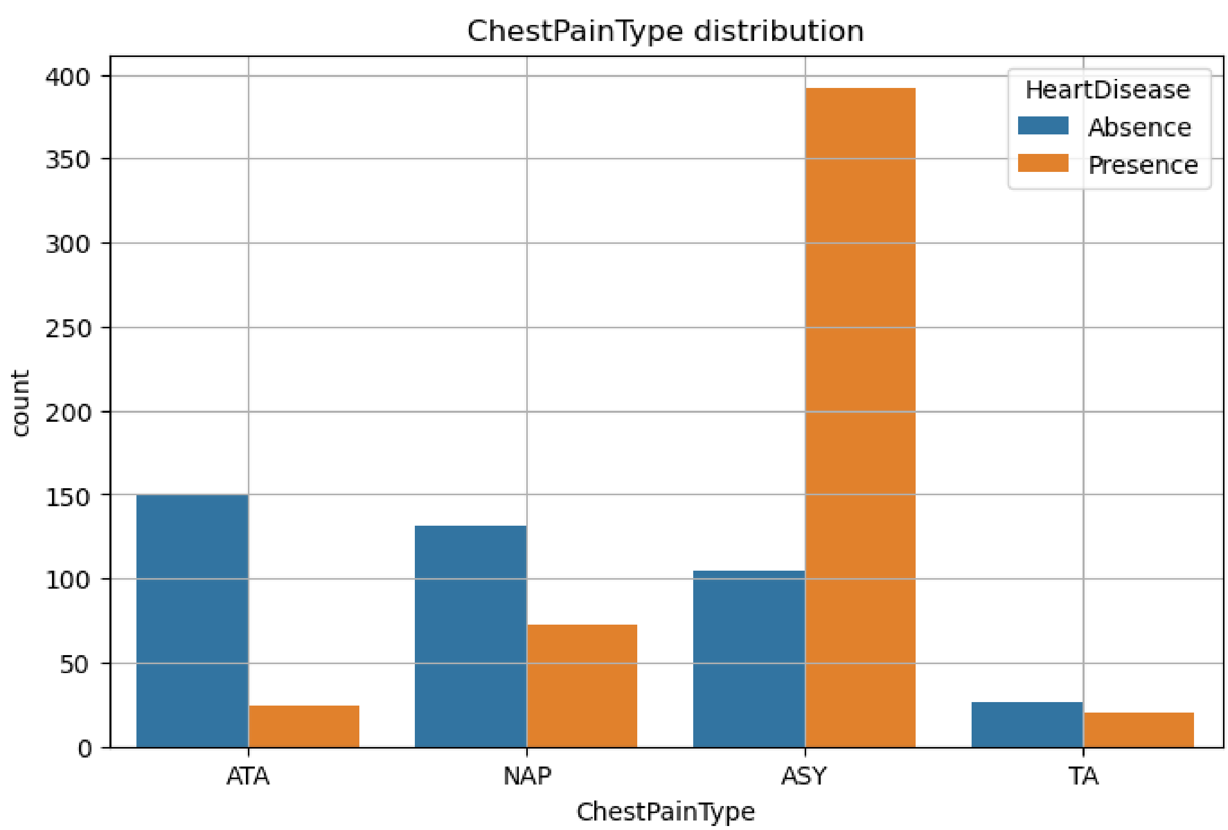


data visualization for categorical dataset

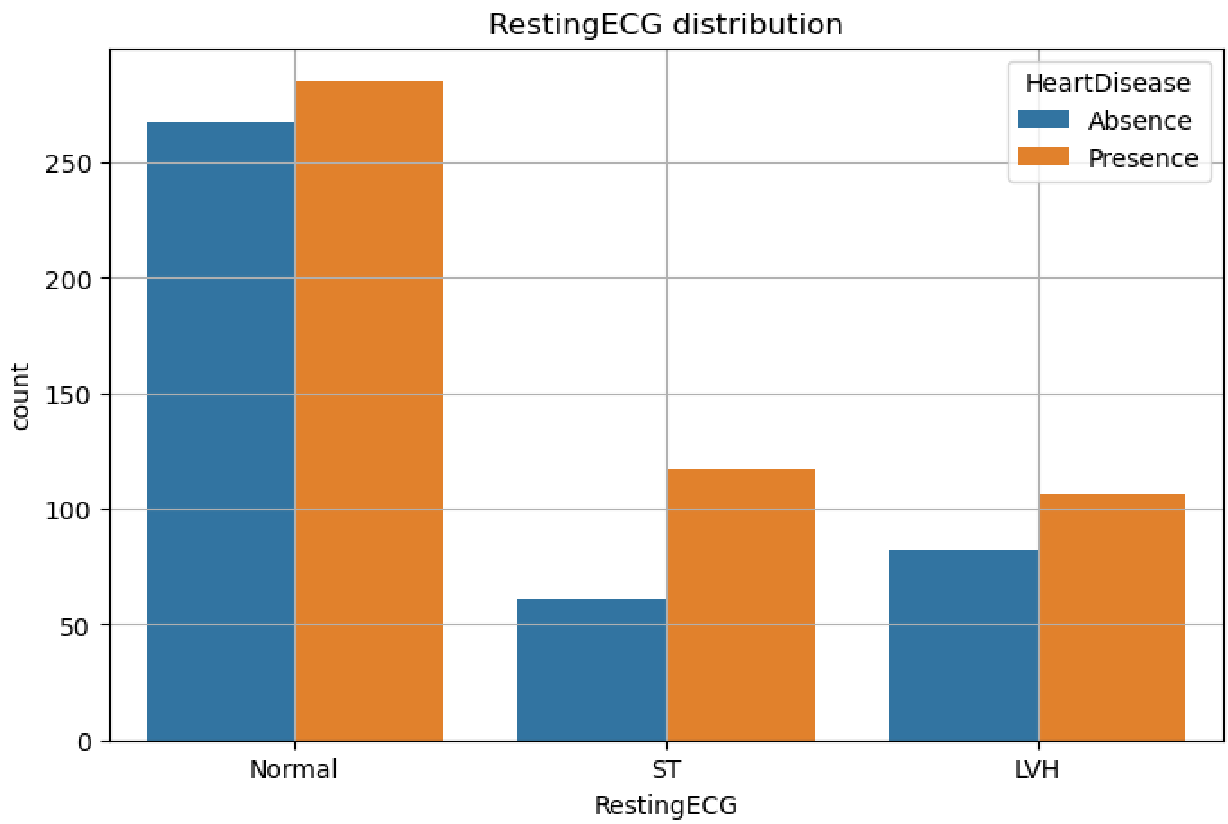
```
categorical_columns = ['Sex', 'ChestPainType', 'RestingECG',
'ExerciseAngina', 'ST_Slope']
for column in categorical_columns:
    plt.figure(figsize=(8, 5))
    sns.countplot(x=column, hue='HeartDisease', data=df)
    plt.title(f'{column} distribution')
    plt.grid()
    plt.show()
```

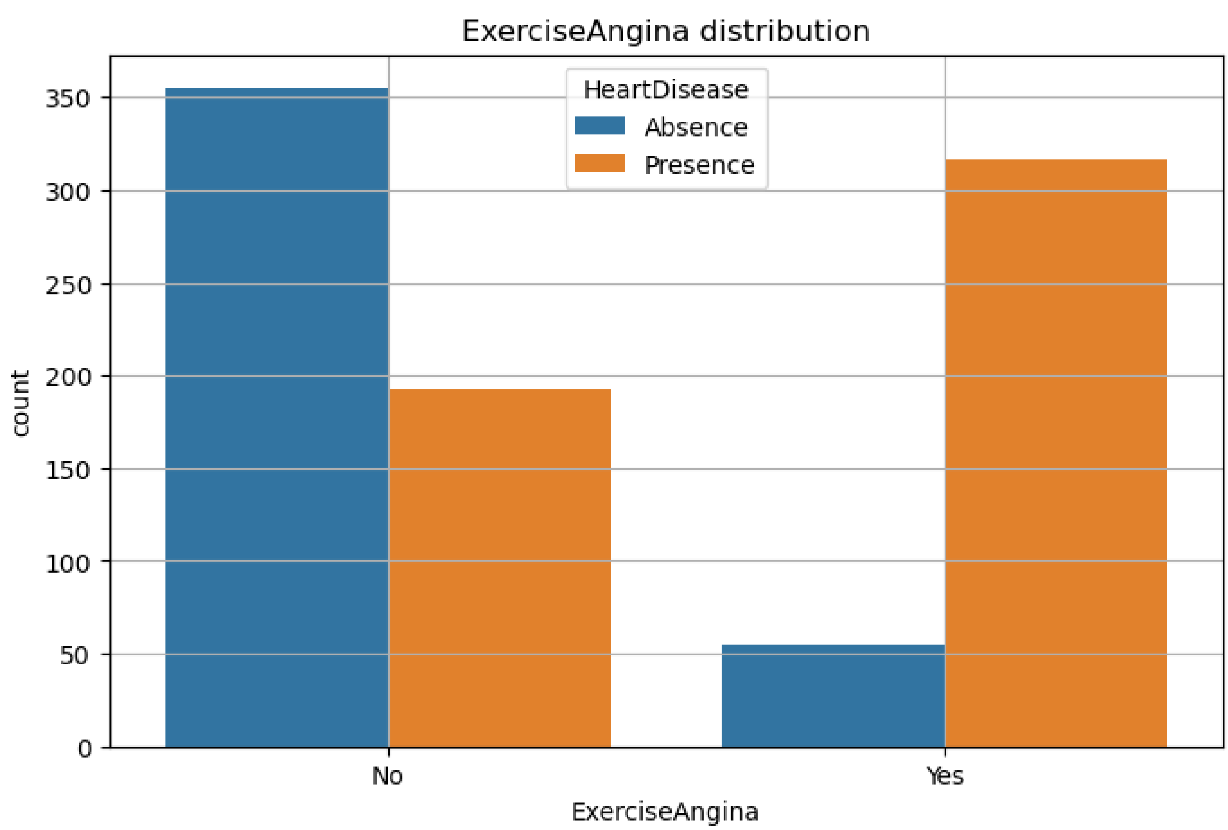


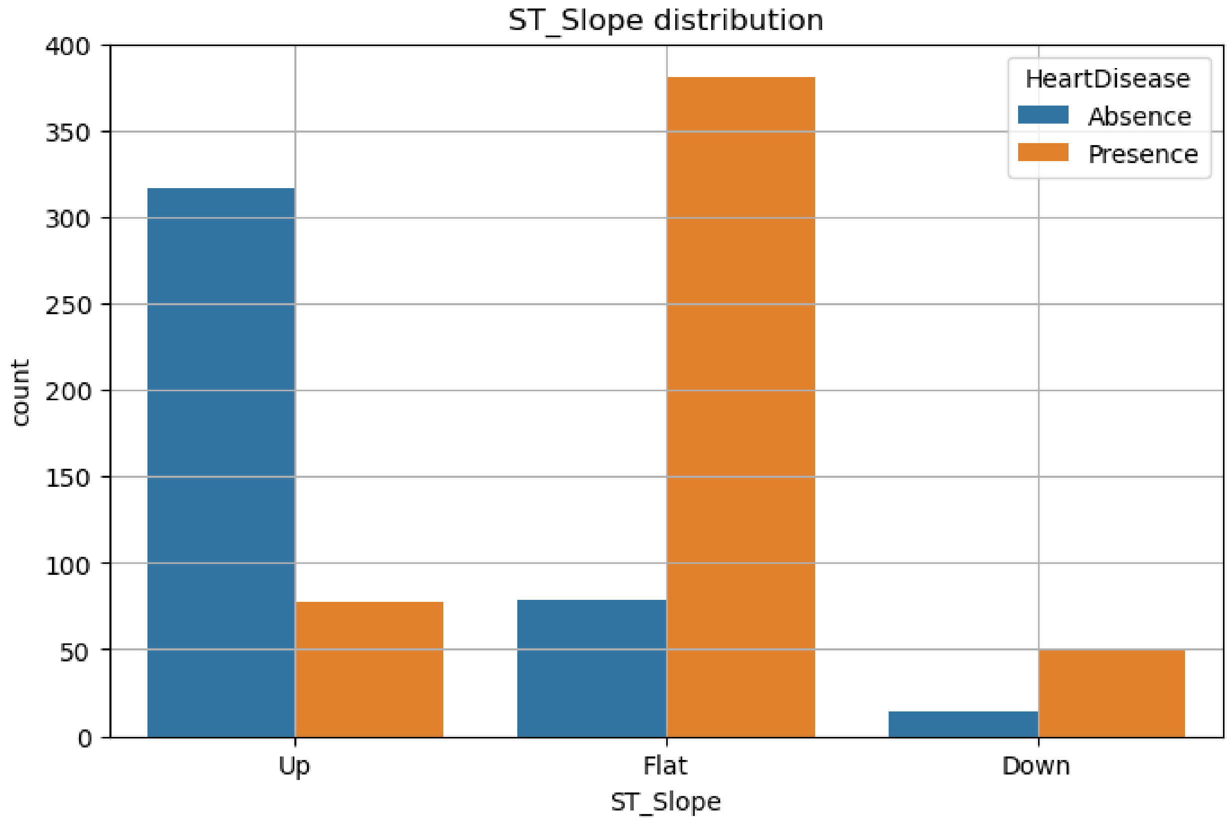
Sex distribution
HeartDisease
Absence
Presence
count
0
100
200
300
400
M
F
Sex



ChestPainType distribution
HeartDisease
Absence
Presence
count
0
50
100
150
200
250
300
350
400
ATA
NAP
ASY
TA
ChestPainType


RestingECG distribution
HeartDisease
Absence
Presence
count
0
50
100
150
200
250
Normal
ST
LVH
RestingECG


ExerciseAngina distribution
HeartDisease
Absence
Presence
count
0
50
100
150
200
250
300
350
No
Yes
ExerciseAngina



ST_Slope distribution
400
350
300
250
200
150
100
50
0
count
HeartDisease
Absence
Presence
Up
Flat
Down
ST_Slope

(1)from above 1st male and female bar chart i can conclusion that male Heart disease presence 63% and female 25% meance heart disease presence percentage in male greater than female

(2) from above 2nd bar chart ChestPainType i can conclusion that Heart disease presence in ASY (asymptomatic) 79%,ATA (atypical angina) 13%,NAP(non-anginal pain) 35%,TA(truncus arteriosus) 43% meance ASY most important role in heart disease presence

(3)above 4th bar graph ExerciseAngina i can conclusion that heart disease presence due to doing exercise 85% and not doing exercise 35% meance due to Exercise heart disease increase

(4) above 4th bar graph ST Slope i can conclusion that Heart disease presence in up 19% ,flat 82% and down 77% meance the ST segment shift relative to exercise-induced increments in heart rate and flat slope increase heart disease presence percentage

Machine Learning with Logistic Regression

import important libraries for logistic regression

```
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix
from sklearn.preprocessing import StandardScaler, LabelEncoder
```

Preprocessing: Convert categorical variables to numerical

```
le = LabelEncoder()
df['Sex'] = le.fit_transform(df['Sex'])
df['ChestPainType'] = le.fit_transform(df['ChestPainType'])
df['RestingECG'] = le.fit_transform(df['RestingECG'])
df['ExerciseAngina'] = le.fit_transform(df['ExerciseAngina'])
df['ST_Slope'] = le.fit_transform(df['ST_Slope'])
```

Separate features (X) and target variable (y)

```
X = df.drop('HeartDisease', axis=1)
y = df['HeartDisease']
```

Split the data into training and testing sets

```
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)
```

Initialize and train the logistic regression model

```
model = LogisticRegression()
model.fit(X_train, y_train)

LogisticRegression()
```

Make predictions on the test set

```
y_pred = model.predict(X_test)
```

Evaluate the model

```
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
classification_rep = classification_report(y_test, y_pred)

print(f'Accuracy: {accuracy}')
print(f'Confusion Matrix:\n{conf_matrix}')
print(f'Classification Report:\n{classification_rep}')

Accuracy: 0.8260869565217391
Confusion Matrix:
[[68  9]
 [23 84]]
Classification Report:
              precision    recall  f1-score   support

     Absence       0.75      0.88      0.81        77
    Presence       0.90      0.79      0.84       107

    accuracy                           0.83       184
   macro avg       0.83      0.83      0.82       184
weighted avg       0.84      0.83      0.83       184
```

Machine Learning with DecisionTreeClassifier

import important libraries for DecisionTreeClassifier

```
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix
from sklearn.preprocessing import StandardScaler, LabelEncoder
```

Preprocessing: Convert categorical variables to numerical

```
le = LabelEncoder()
df['Sex'] = le.fit_transform(df['Sex'])
df['ChestPainType'] = le.fit_transform(df['ChestPainType'])
df['RestingECG'] = le.fit_transform(df['RestingECG'])
df['ExerciseAngina'] = le.fit_transform(df['ExerciseAngina'])
df['ST_Slope'] = le.fit_transform(df['ST_Slope'])
```

Separate features (X) and target variable (y)

```
X = df.drop('HeartDisease', axis=1)
y = df['HeartDisease']
```

Split the data into training and testing sets

```
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)
```

Initialize and train the decision tree model

```
model = DecisionTreeClassifier(random_state=42)
model.fit(X_train, y_train)
model = DecisionTreeClassifier(max_depth=5, min_samples_leaf=5,
random_state=42)
model.fit(X_train, y_train)

DecisionTreeClassifier(max_depth=5, min_samples_leaf=5,
random_state=42)
```

Make predictions on the test set

```
y_pred = model.predict(X_test)
```

Evaluate the model

```
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
classification_rep = classification_report(y_test, y_pred)

print(f'Accuracy: {accuracy}')
print(f'Confusion Matrix:\n{conf_matrix}')
print(f'Classification Report:\n{classification_rep}')

Accuracy: 0.8478260869565217
Confusion Matrix:
[[69  8]
 [20 87]]
Classification Report:
              precision    recall  f1-score   support

     Absence       0.78      0.90      0.83        77
```

```
    Presence       0.92      0.81      0.86       107

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

Machine Learning with SVC

import important libraries for SVC

```
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix
from sklearn.preprocessing import StandardScaler, LabelEncoder
```

Preprocessing: Convert categorical variables to numerical

```
le = LabelEncoder()
df['Sex'] = le.fit_transform(df['Sex'])
df['ChestPainType'] = le.fit_transform(df['ChestPainType'])
df['RestingECG'] = le.fit_transform(df['RestingECG'])
df['ExerciseAngina'] = le.fit_transform(df['ExerciseAngina'])
df['ST_Slope'] = le.fit_transform(df['ST_Slope'])
```

Separate features (X) and target variable (y)

```
X = df.drop('HeartDisease', axis=1)
y = df['HeartDisease']
```

Split the data into training and testing sets

```
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)
```

Standardize the features (SVMs are sensitive to feature scaling)

```
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

Initialize and train the SVM model

```
model = SVC(C=1.0, gamma='scale', random_state=42)
model.fit(X_train, y_train)

SVC(random_state=42)
```

Make predictions on the test set

```
y_pred = model.predict(X_test)
```

Evaluate the model

```
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
classification_rep = classification_report(y_test, y_pred)

print(f'Accuracy: {accuracy}')
print(f'Confusion Matrix:\n{conf_matrix}')
print(f'Classification Report:\n{classification_rep}')
```

```
Accuracy: 0.8369565217391305
Confusion Matrix:
[[64 13]
 [17 90]]
Classification Report:
              precision    recall  f1-score   support

     Absence       0.79      0.83      0.81        77
    Presence       0.87      0.84      0.86       107

    accuracy                           0.84       184
   macro avg       0.83      0.84      0.83       184
weighted avg       0.84      0.84      0.84       184
```