

EXPLORATORY DATA ANALYSIS

AIM: To do exploratory data analysis on heart disease UCI dataset.

DESCRIPTION:

Exploratory Data Analysis (EDA) is a pre-processing step to understand the data. There are numerous methods and steps in performing EDA, however, most of them are specific, focusing on either visualization or distribution, and are incomplete. Therefore, we have to understand, explore, and extract the information from the data to answer the questions or assumptions.

Data Set Explanations:

Here we will be using the dataset consisting of 303 patients with 14 features set.

Features explanation:

1. age (Age in years)
2. sex : (1 = male, 0 = female)
3. cp (Chest Pain Type): [0: asymptomatic, 1: atypical angina, 2: non-anginal pain, 3: typical angina]
4. trestbps (Resting Blood Pressure in mm/hg)
5. chol (Serum Cholesterol in mg/dl)
6. fbs (Fasting Blood Sugar > 120 mg/dl): [0 = no, 1 = yes]
7. restecg (Resting ECG): [0: showing probable or definite left ventricular hypertrophy by Estes' criteria, 1: normal, 2: having ST-T wave abnormality]
8. thalach (maximum heart rate achieved)
9. exang (Exercise Induced Angina): [1 = yes, 0 = no]
- 10.oldpeak (ST depression induced by exercise relative to rest)
- 11.slope (the slope of the peak exercise ST segment): [0: downsloping; 1: flat; 2: upsloping]

12.ca [number of major vessels (0–3)]

13.thal : [1 = normal, 2 = fixed defect, 3 = reversible defect]

14.target: [0 = disease, 1 = no disease]

CODE AND ANALYSIS:

1. Import and get to know the data

```
In [2]: # Libraries for Exploratory Data Analysis
import os
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

```
In [3]: df = pd.read_csv('/content/drive/My Drive/csv/github/heart.csv')
df.head(3)
```

```
Out[3]:   age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  slope  ca  thal  target
0    63     1    3      145    233    1      0     150      0     2.3      0    0    1     1
1    37     1    2      130    250    0      1     187      0     3.5      0    0    2     1
2    41     0    1      130    204    0      0     172      0     1.4      2    0    2     1
```

```
In [4]: df.shape
```

```
Out[4]: (303, 14)
```

```
In [5]: df.columns
```

```
Out[5]: Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
       dtype='object')
```

```
In [6]: df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
--- 
 0   age        303 non-null    int64  
 1   sex         303 non-null    int64  
 2   cp          303 non-null    int64  
 3   trestbps   303 non-null    int64  
 4   chol        303 non-null    int64  
 5   fbs         303 non-null    int64  
 6   restecg    303 non-null    int64  
 7   thalach    303 non-null    int64  
 8   exang       303 non-null    int64  
 9   oldpeak    303 non-null    float64 
 10  slope       303 non-null    int64  
 11  ca          303 non-null    int64  
 12  thal        303 non-null    int64  
 13  target      303 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 33.3 KB

there are no nulls
```

Here we have 303 rows with 14 variables.

2.Data Cleaning

a) Check the data type.

The variables types are

- Binary: sex, fbs, exang, target
- Categorical: cp, restecg, slope, ca, thal
- Continuous: age, trestbps, chol, thalac, oldpeak

```
In [7]: # to know the type of variable  
df.unique()
```

```
Out[7]: age      41  
sex      2  
cp      4  
trestbps 49  
chol    152  
fbs      2  
restecg  3  
thalach  91  
exang   2  
oldpeak  40  
slope    3  
ca      5  
thal    4  
target   2  
dtype: int64
```

```
In [8]: df.dtypes
```

```
Out[8]: age      int64  
sex      int64  
cp      int64  
trestbps int64  
chol    int64  
fbs      int64  
restecg  int64  
thalach  int64  
exang   int64  
oldpeak float64  
slope    int64  
ca      int64  
thal    int64  
target   int64  
dtype: object
```

Note here that the binary and categorical variable are classified as different integer type by python. We will need to change them to 'object' type.

```
In [9]: # change the categorical type to categorical variables  
df['sex'] = df['sex'].astype('object')  
df['cp'] = df['cp'].astype('object')  
df['fbs'] = df['fbs'].astype('object')  
df['restecg'] = df['restecg'].astype('object')  
df['exang'] = df['exang'].astype('object')  
df['slope'] = df['slope'].astype('object')  
df['ca'] = df['ca'].astype('object')  
df['thal'] = df['thal'].astype('object')  
df.dtypes
```

```
Out[9]: age      int64  
sex      object  
cp      object  
trestbps int64  
chol    int64  
fbs      object  
restecg  object  
thalach  int64  
exang   object  
oldpeak float64  
slope    object  
ca      object  
thal    object  
target   int64  
dtype: object
```

b. Check for the data characters mistakes

1. Feature 'ca' ranges from 0–3, however, df.unique() listed 0–4. So lets find the '4' and change them to NaN.

```
In [10]: df['ca'].unique()
```

```
Out[10]: array([0, 2, 1, 3, 4], dtype=object)
```

```
In [11]: # to count the number in of each category decending order  
df.ca.value_counts()
```

```
Out[11]: 0    175  
1     65  
2     38  
3     20  
4      5  
Name: ca, dtype: int64
```

```
In [12]: # to check missing values  
df.isnull().sum()
```

```
Out[12]: age      0  
sex      0  
cp       0  
trestbps 0  
chol     0  
fbs      0  
restecg   0  
thalach   0  
exang    0  
oldpeak   0  
slope     0  
ca       0  
thal     0  
target    0  
dtype: int64
```

c) Check for missing values and replace them

```
In [12]: # to check missing values  
df.isnull().sum()
```

```
Out[12]: age      0  
sex      0  
cp       0  
trestbps 0  
chol     0  
fbs      0  
restecg   0  
thalach   0  
exang    0  
oldpeak   0  
slope    0  
ca       0  
thal     0  
target    0  
dtype: int64
```

d) Statistics summary

```
In [13]: # change the labelling for better interpretation/ visualization understanding  
df['target'] = df.target.replace({1: "Disease", 0: "No_disease"})  
df['sex'] = df.sex.replace({1: "Male", 0: "Female"})  
df['cp'] = df.cp.replace({1: "typical_angina",  
                         2: "atypical_angina",  
                         3: "non-anginal pain",  
                         4: "asymtomatic"})  
df['exang'] = df.exang.replace({1: "Yes", 0: "No"})  
df['slope'] = df.cp.replace({1: "upsloping",  
                           2: "flat",  
                           3: "downsloping"})  
df['thal'] = df.thal.replace({1: "fixed_defect", 2: "reversible_defect", 3: "normal"})
```

```
In [14]: # to know the basic stats  
df.describe()
```

```
Out[14]:
```

	age	trestbps	chol	thalach	oldpeak
count	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	131.623762	246.264026	149.646865	1.039604
std	9.082101	17.538143	51.830751	22.905161	1.161075
min	29.000000	94.000000	126.000000	71.000000	0.000000
25%	47.500000	120.000000	211.000000	133.500000	0.000000
50%	55.000000	130.000000	240.000000	153.000000	0.800000
75%	61.000000	140.000000	274.500000	166.000000	1.600000
max	77.000000	200.000000	564.000000	202.000000	6.200000

BARPLOTS: target variable distribution

```
In [17]: df.columns
```

```
Out[17]: Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
   'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
   dtype='object')
```

```
In [35]: print(df.target.value_counts())
df['target'].value_counts().plot(kind='bar').set_title('Heart Disease Classes')
```

```
Disease      165
No_disease  138
Name: target, dtype: int64
```

```
Out[35]: Text(0.5, 1.0, 'Heart Disease Classes')
```

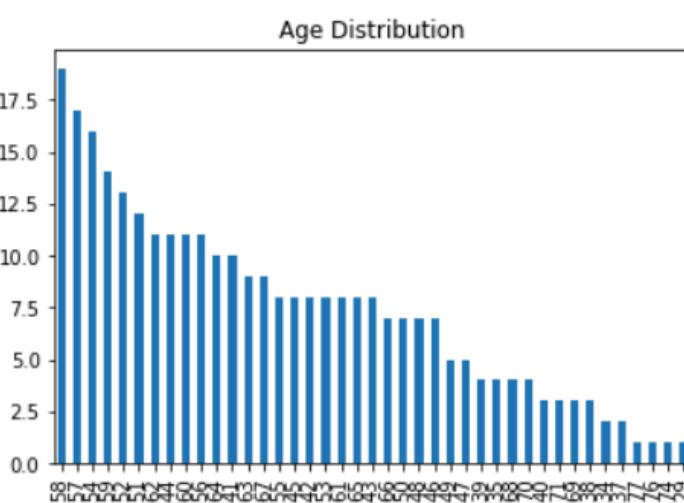
The bar chart, titled "Heart Disease Classes", displays two categories: "Disease" and "No_disease". The y-axis represents the count of patients, ranging from 0 to 160 in increments of 20. The "Disease" category has a count of 165, and the "No_disease" category has a count of 138.

There are more diseased than healthy patients.

Age variable distribution

```
In [23]: # print(df.age.value_counts())
df['age'].value_counts().plot(kind='bar').set_title('Age Distribution')
```

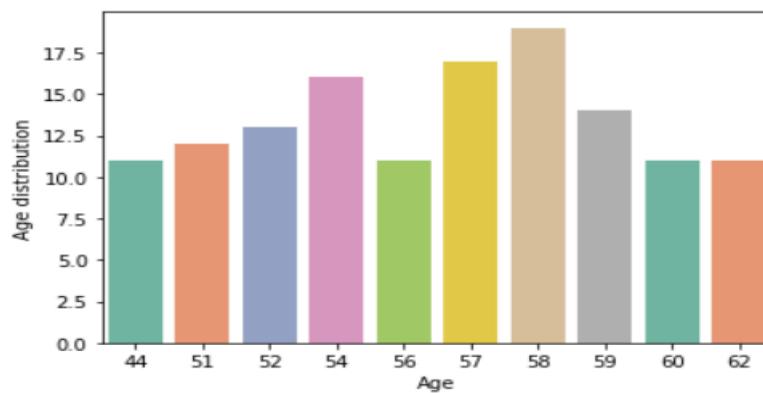
```
Out[23]: Text(0.5, 1.0, 'Age Distribution')
```



```
In [24]: # Analyze distribution in age in range 10
print(df.age.value_counts()[:10])
sns.barplot(x=df.age.value_counts()[:10].index,
            y=df.age.value_counts()[:10].values,
            palette='Set2')
plt.xlabel('Age')
plt.ylabel('Age distribution')

58      19
57      17
54      16
59      14
52      13
51      12
62      11
44      11
60      11
56      11
Name: age, dtype: int64
Text(0, 0.5, 'Age distribution')

Out[24]:
```



The age are normally distributed. Most of the patients are in the age between 50s to 60s. Let's take a quick look basic stats. The mean age is about 54 years with ± 9.08 std, the youngest is at 29 and the oldest is at 77.

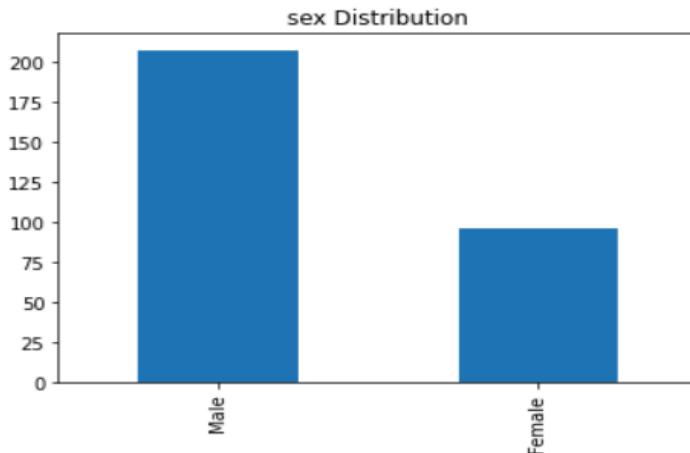
```
In [ ]: # to know the youngest or oldest in age  
print(min(df.age))  
print(max(df.age))  
print(df.age.mean())
```

```
29  
77  
54.366336633663366
```

```
In [25]: print(df.sex.value_counts())  
df['sex'].value_counts().plot(kind='bar').set_title('sex Distribution')
```

```
Male      207  
Female     96  
Name: sex, dtype: int64  
Text(0.5, 1.0, 'sex Distribution')
```

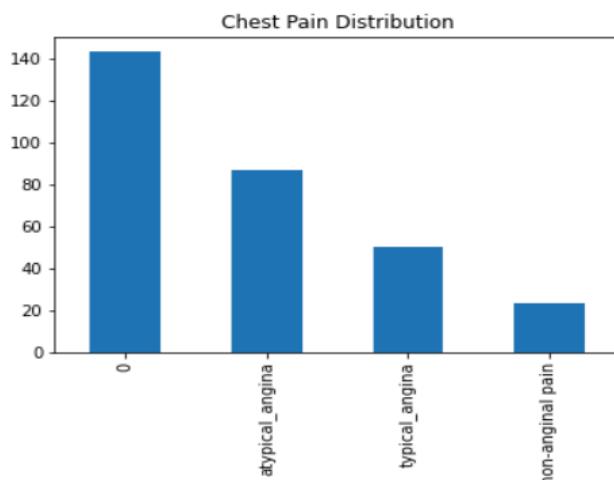
```
Out[25]:
```



```
In [26]: print(df.cp.value_counts())  
df['cp'].value_counts().plot(kind='bar').set_title('Chest Pain Distribution')
```

```
0           143  
atypical_angina    87  
typical_angina     50  
non-anginal pain    23  
Name: cp, dtype: int64  
Text(0.5, 1.0, 'Chest Pain Distribution')
```

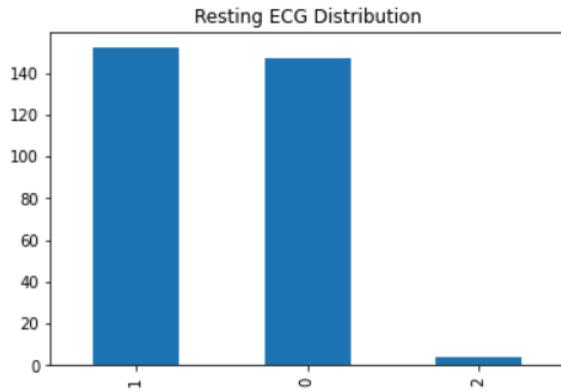
```
Out[26]:
```



```
In [43]: print(df.restecg.value_counts())
df['restecg'].value_counts().plot(kind='bar').set_title('Resting ECG Distribution')

1    152
0    147
2     4
Name: restecg, dtype: int64
Text(0.5, 1.0, 'Resting ECG Distribution')

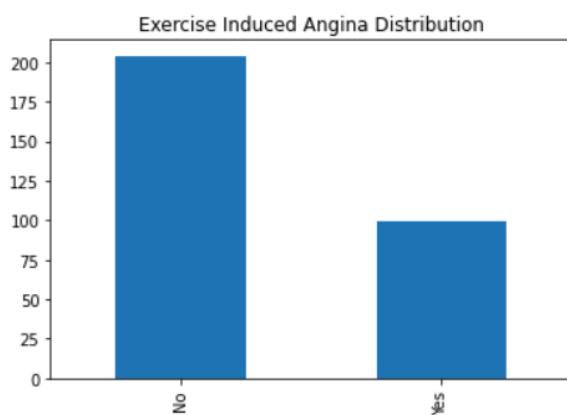
Out[43]:
```



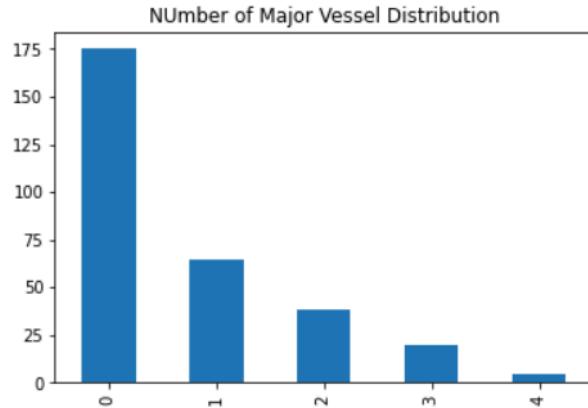
```
In [32]: print(df.exang.value_counts())
df['exang'].value_counts().plot(kind='bar').set_title('Exercise Induced Angina Distribution')

No      204
Yes     99
Name: exang, dtype: int64
Text(0.5, 1.0, 'Exercise Induced Angina Distribution')

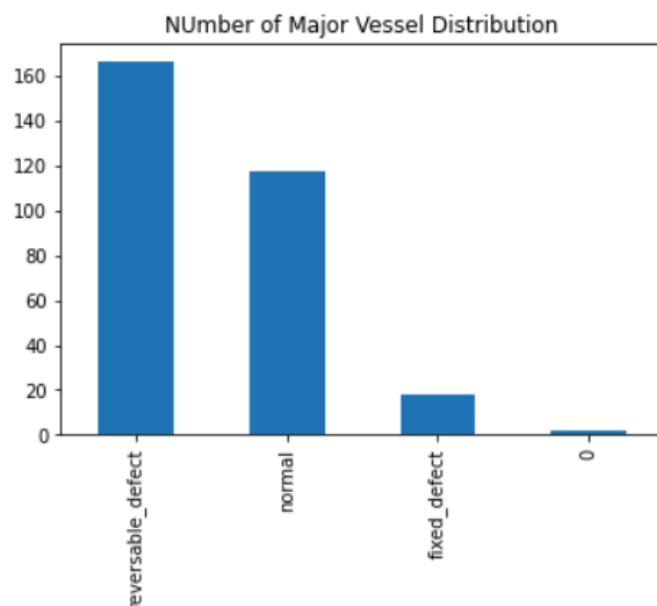
Out[32]:
```



```
In [33]:  
print(df.ca.value_counts())  
df['ca'].value_counts().plot(kind='bar').set_title('NUmber of Major Vessel Distribution')  
  
0    175  
1     65  
2     38  
3     20  
4      5  
Name: ca, dtype: int64  
Text(0.5, 1.0, 'NUmber of Major Vessel Distribution')  
Out[33]:
```



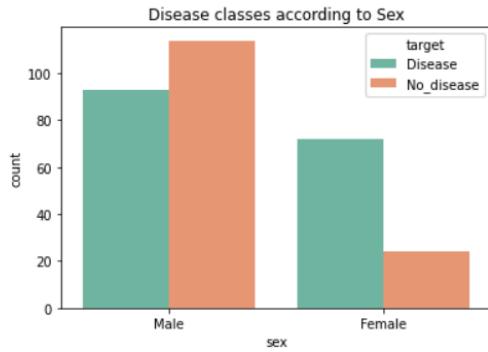
```
In [34]:  
print(df.thal.value_counts())  
df['thal'].value_counts().plot(kind='bar').set_title('thal Distribution')  
  
reversible_defect    166  
normal                117  
fixed_defect          18  
0                      2  
Name: thal, dtype: int64  
Text(0.5, 1.0, 'NUmber of Major Vessel Distribution')  
Out[34]:
```



Visualize categorical data distribution -COUNTPLOTS

Gender distribution according to target variable

```
In [38]: sns.countplot(x='sex', hue='target', data=df, palette='Set2').set_title('Disease classes according to Sex')  
Out[38]: Text(0.5, 1.0, 'Disease classes according to Sex')
```

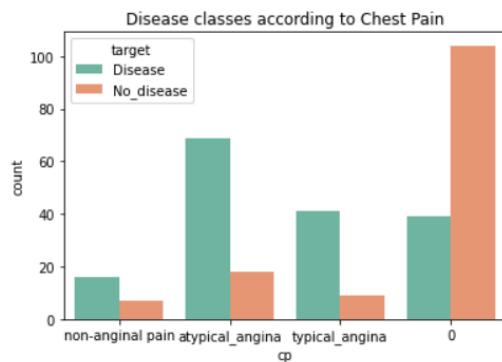


From the bar graph, we can observe that among disease patients, male are higher than female.

Chest pain distribution according to target variable

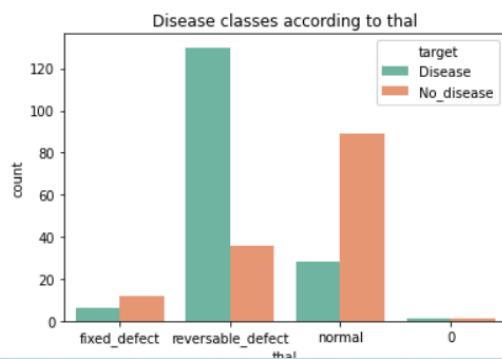
```
In [40]: sns.countplot(x='cp', hue='target', data=df, palette='Set2').set_title('Disease classes according to Chest Pain')
```

```
Out[40]: Text(0.5, 1.0, 'Disease classes according to Chest Pain')
```



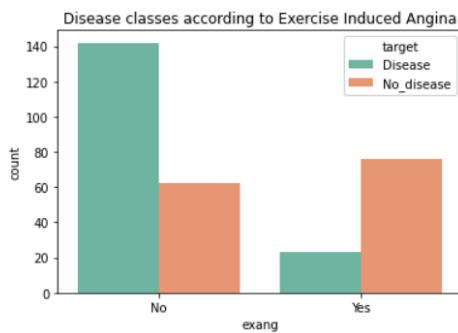
```
In [41]: sns.countplot(x='thal', hue='target', data=df, palette='Set2').set_title('Disease classes according to thal')
```

```
Out[41]: Text(0.5, 1.0, 'Disease classes according to thal')
```



```
In [44]: sns.countplot(x='exang', hue='target', data=df, palette='Set2').set_title('Disease classes according to Exercise Induced Angina')
```

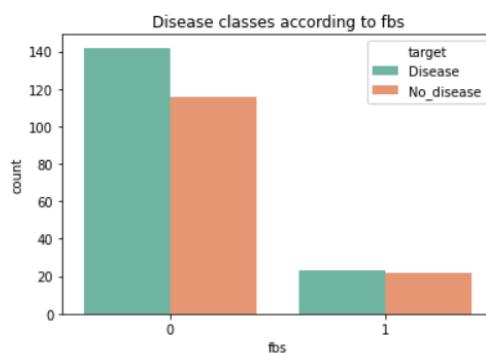
```
Out[44]: Text(0.5, 1.0, 'Disease classes according to Exercise Induced Angina')
```



Fasting blood sugar distribution according to target variable

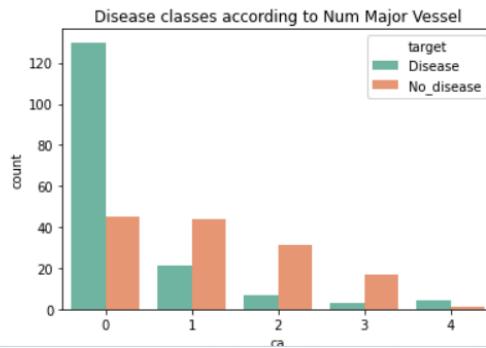
```
In [45]: sns.countplot(x='fbs', hue='target', data=df, palette='Set2').set_title('Disease classes according to fbs')
```

```
Out[45]: Text(0.5, 1.0, 'Disease classes according to fbs')
```



```
In [46]: sns.countplot(x='ca', hue='target', data=df, palette='Set2').set_title('Disease classes according to Num Major Vessel')
```

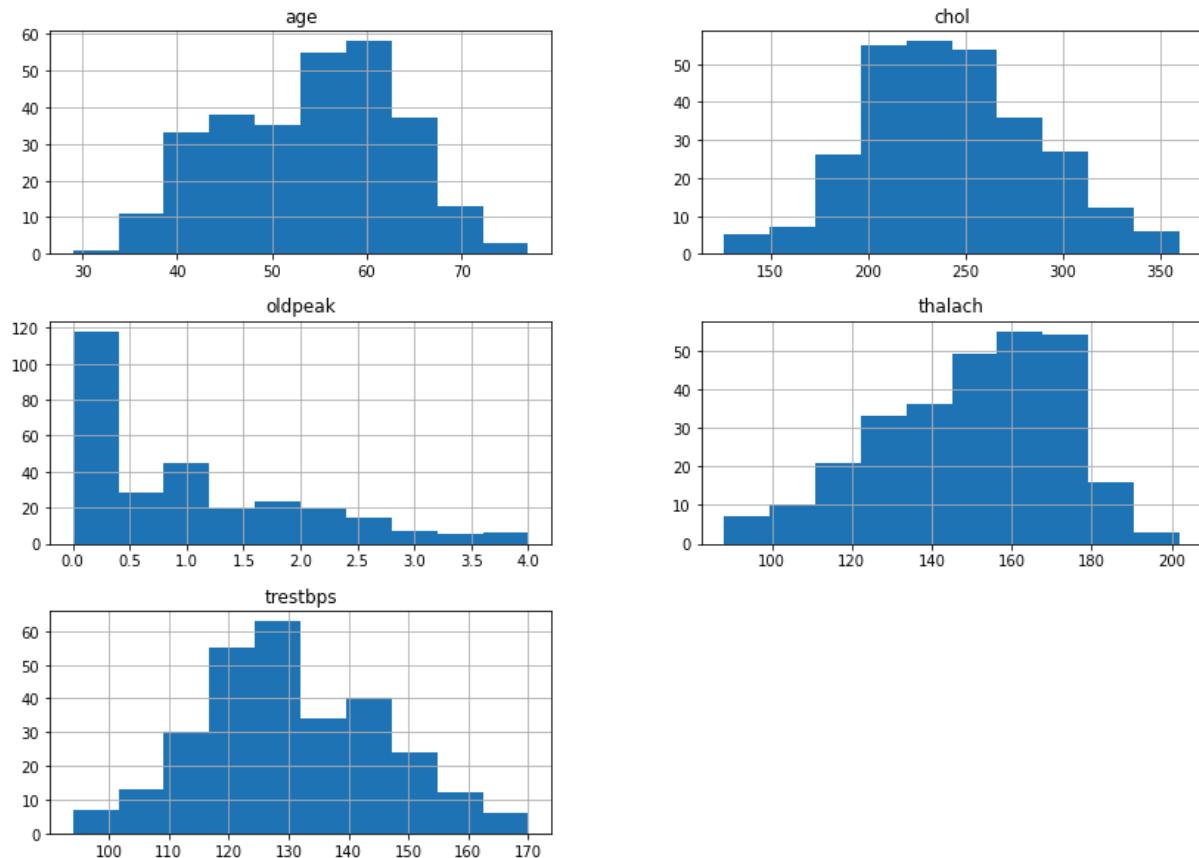
```
Out[46]: Text(0.5, 1.0, 'Disease classes according to Num Major Vessel')
```



Looking at the bar graph above, it's raised a question of higher number of healthy subject having typical_angina. Or in other word, most of the healthy subject having chest pain.

Fasting blood sugar or fbs is a diabetes indicator with fbs >120 mg/d is considered diabetic (True class). Here, we observe that the number for class true, is lower compared to class false. However, if we look closely, there are higher number of heart disease patient without diabetes. This provide an indication that fbs might not be a strong feature differentiating between heart disease an non-disease patient.

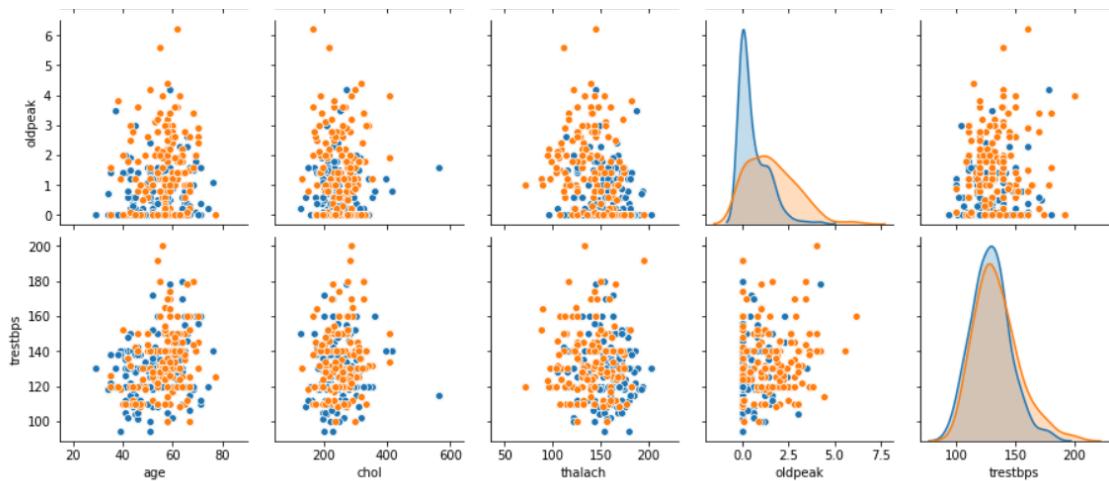
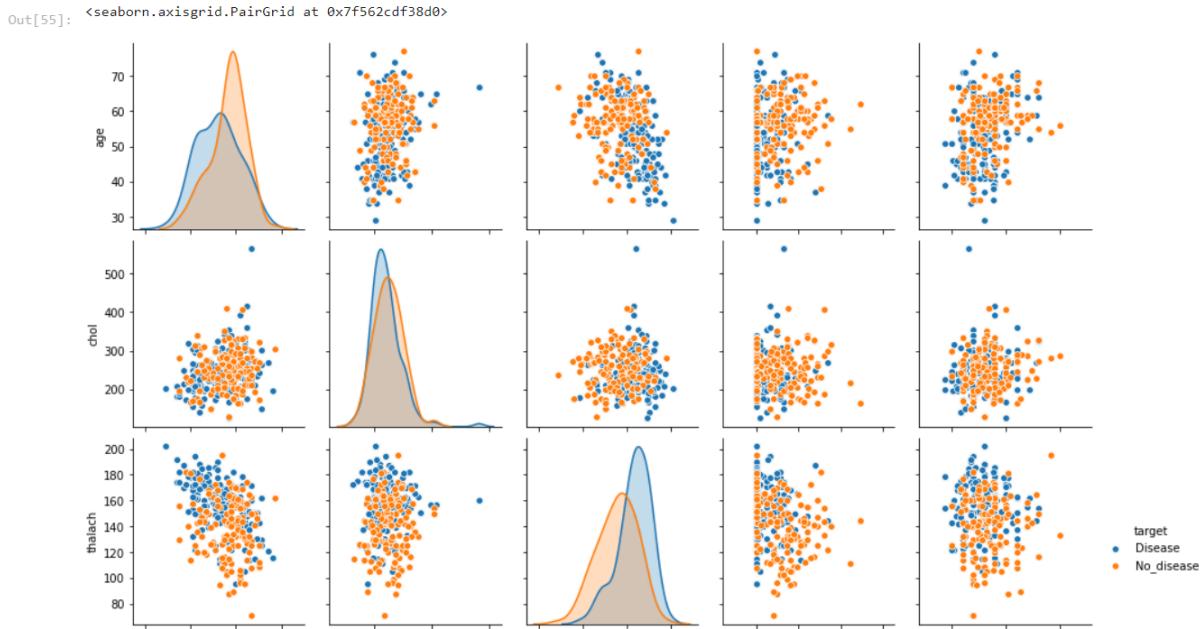
Distribution plot on continuous variables.



- normal distribution for: age, trestbps and almost for chol
- oldpeak is left-skewed
- thalac is right-skewed

Visualize the distribution of continuous variable across target variable-PAIRPLOTS

```
In [55]: # define continuous variable & plot
continuous_features = ['age', 'chol', 'thalach', 'oldpeak','trestbps']
sns.pairplot(df[continuous_features + ['target']], hue='target')
```



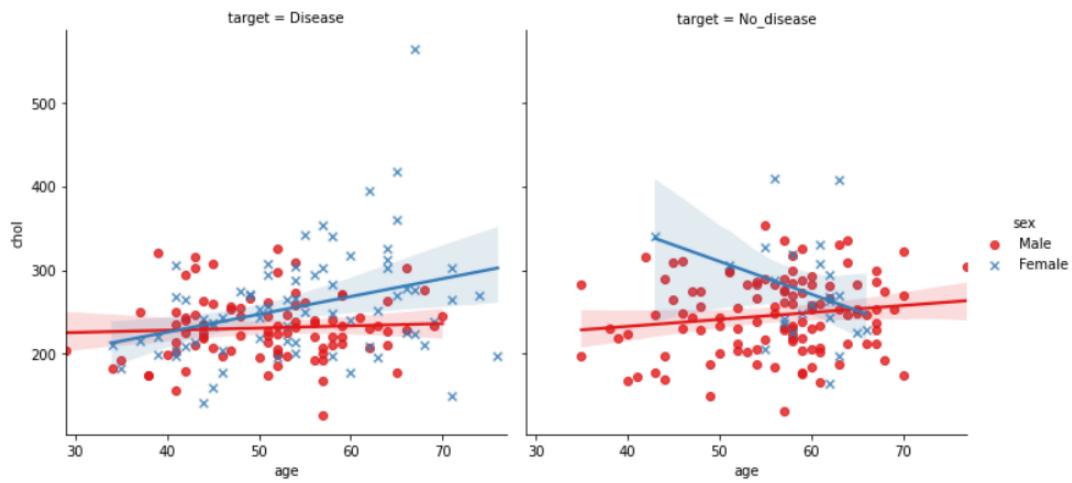
- oldpeak having a linear separation relation between disease and non-disease.
- thalach having a mild separation relation between disease and non-disease.

- Other features don't form any clear separation

Lineplots:

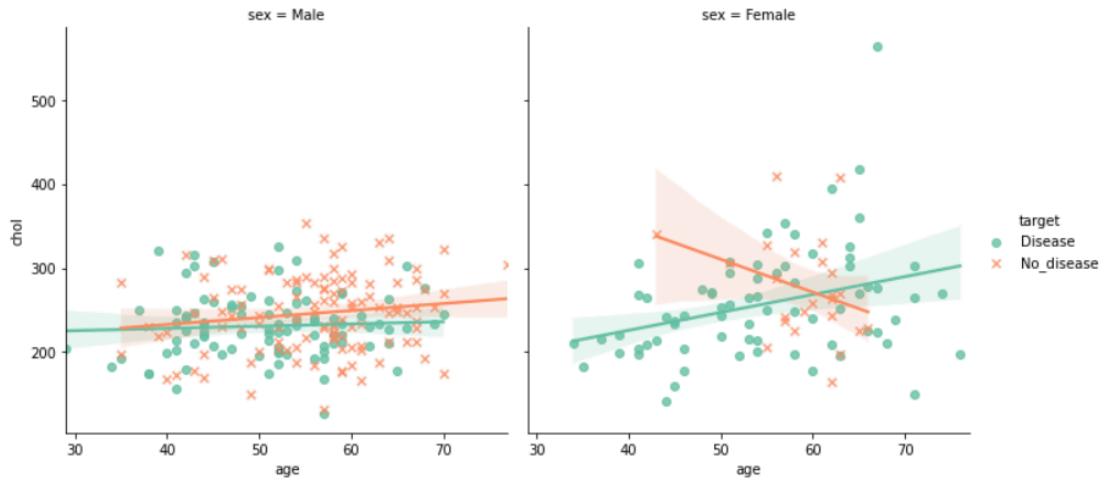
In [56]:

```
# to understand the relationship between age and chol in each of the target based on sex.
sns.lmplot(x="age", y="chol", hue="sex", col="target",
            markers=["o", "x"],
            palette="Set1",
            data=df)
plt.show()
```



In []:

```
# to understand the relationship between age and chol in each of the sex, based on target.
sns.lmplot(x="age",
            y="chol",
            hue="target",
            col="sex",
            # row="target",
            # order=2,
            markers=["o", "x"],
            palette="Set2",
            data=df)
plt.show()
```



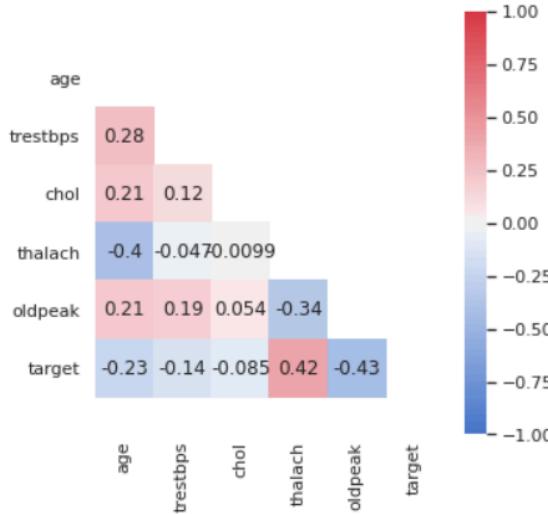
correlation

```
In [ ]: # Correlation with Heatmap Visualization
sns.set(style="white")
mask = np.zeros_like(df.corr(), dtype=np.bool)
mask[np.triu_indices_from(mask)] = True

fig, ax = plt.subplots(figsize=(5,5))
cmap = sns.diverging_palette(255, 10, as_cmap=True)
sns.heatmap(df.corr(), mask=mask, annot=True, square=True, cmap=cmap, vmin=-1, vmax=1, ax=ax)

bottom, top = ax.get_ylim()
ax.set_ylim(bottom+0.5, top-0.5)

Out[ ]: (6.5, -0.5)
```



- ‘cp’, ‘thalach’, ‘slope’ shows good positive correlation with target
- ‘oldpeak’, ‘exang’, ‘ca’, ‘thal’, ‘sex’, ‘age’ shows a good negative correlation with target
- ‘fbs’ ‘chol’, ‘trestbps’, ‘restecg’ has low correlation with our target