In [1]:
```
# importing libraries
import pandas as pd
pd.set_option('display.max_columns', None)
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings("ignore")
from scipy import stats
from statsmodels.api import qqplot
```

In [2]:
```
#reading the dataset
df=pd.read_csv('Heart Disease data.csv')
```

In [3]:
```
#displaying first 5 rows
df.head()
```

Out[3]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	targ
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3	
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3	
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	

In [4]:
```
# obtaining how many rows and columns are present in the dataset(rows,colum
df.shape
```

Out[4]:
```
(1025, 14)
```

In [5]:
```
# basic information about data
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1025 entries, 0 to 1024
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       1025 non-null   int64  
 1   sex       1025 non-null   int64  
 2   cp        1025 non-null   int64  
 3   trestbps  1025 non-null   int64  
 4   chol      1025 non-null   int64  
 5   fbs       1025 non-null   int64  
 6   restecg   1025 non-null   int64  
 7   thalach   1025 non-null   int64  
 8   exang     1025 non-null   int64  
 9   oldpeak   1025 non-null   float64
 10  slope     1025 non-null   int64  
 11  ca        1025 non-null   int64  
 12  thal      1025 non-null   int64  
 13  target    1025 non-null   int64  
dtypes: float64(1), int64(13)
memory usage: 112.2 KB
```

In [6]:
```
# obtaining categorical features
category_features=[]
for i in df.columns:
    if(df[i].nunique()<10):
        category_features.append(i)
        print(i)
        print(df[i].value_counts())
```

```
sex
1    713
0    312
Name: sex, dtype: int64
cp
0    497
2    284
1    167
3     77
Name: cp, dtype: int64
fbs
0    872
1    153
Name: fbs, dtype: int64
restecg
1    513
0    497
2     15
Name: restecg, dtype: int64
exang
0    680
1    345
Name: exang, dtype: int64
slope
1    482
2    469
0     74
Name: slope, dtype: int64
ca
0    578
1    226
2    134
3     69
4     18
Name: ca, dtype: int64
thal
2    544
3    410
1     64
0      7
Name: thal, dtype: int64
target
1    526
0    499
Name: target, dtype: int64
```

In [7]:
```
category_features
```

Out[7]:
```
['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'thal', 'target']
```

In [8]:
```
df.cp.value_counts()
```

Out[8]:
```
0    497
2    284
1    167
3     77
Name: cp, dtype: int64
```

In [9]:
```
df.fbs.value_counts()
```

Out[9]:
```
0    872
1    153
Name: fbs, dtype: int64
```

In [10]:
```
df.restecg.value_counts()
```

Out[10]:
```
1    513
0    497
2     15
Name: restecg, dtype: int64
```

In [11]:
```
df.exang.value_counts()
```

Out[11]:
```
0    680
1    345
Name: exang, dtype: int64
```

In [12]:
```
df.slope.value_counts()
```

Out[12]:
```
1    482
2    469
0     74
Name: slope, dtype: int64
```

In [13]:
```
df.thal.value_counts()
```

Out[13]:
```
2    544
3    410
1     64
0      7
Name: thal, dtype: int64
```

In [14]:
```
# replacing numbers with different categories
df.sex.replace(to_replace={ 0:"F",  1:"M"}, inplace=True)
df.cp.replace(to_replace={0: "Typical angina",1: "Atypical angina",2:"Non-a
df.fbs.replace(to_replace={0: "True",1: "False"}, inplace=True)
df.exang.replace(to_replace={0: "No",1: "Yes"}, inplace=True)
df.slope.replace(to_replace={0: "Upsloping",1: "Flatsloping",2:"Downslopins

df.target.replace(to_replace={0:"Yes",1:"No"}, inplace=True)
df.head()
```

Out[14]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca
0	52	M	Typical angina	125	212	True	1	168	No	1.0	Downslopins	2
1	53	M	Typical angina	140	203	False	0	155	Yes	3.1	Upsloping	0
2	70	M	Typical angina	145	174	True	1	125	Yes	2.6	Upsloping	0
3	61	M	Typical angina	148	203	True	1	161	No	0.0	Downslopins	1
4	62	F	Typical angina	138	294	False	1	106	No	1.9	Flatsloping	3

In [15]:
```
df.describe().T
```

Out[15]:

	count	mean	std	min	25%	50%	75%	max
age	1025.0	54.434146	9.072290	29.0	48.0	56.0	61.0	77.0
trestbps	1025.0	131.611707	17.516718	94.0	120.0	130.0	140.0	200.0
chol	1025.0	246.000000	51.592510	126.0	211.0	240.0	275.0	564.0
restecg	1025.0	0.529756	0.527878	0.0	0.0	1.0	1.0	2.0
thalach	1025.0	149.114146	23.005724	71.0	132.0	152.0	166.0	202.0
oldpeak	1025.0	1.071512	1.175053	0.0	0.0	0.8	1.8	6.2
ca	1025.0	0.754146	1.030798	0.0	0.0	0.0	1.0	4.0
thal	1025.0	2.323902	0.620660	0.0	2.0	2.0	3.0	3.0

EDA

In [16]:
```
## checking for null values
df.isnull().sum()
```

Out[16]:
```
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
```

In [17]:
```
## checking for duplicates if any
df.duplicated().any()
```

Out[17]:
```
True
```

In [18]:
```
df.shape
```

Out[18]:
```
(1025, 14)
```

In [19]:
```
## droping duplicates
df.drop_duplicates(inplace=True)
df.shape
```

Out[19]:
```
(302, 14)
```

In [20]:
```
# obtaining numerical features
numerical_features=[]
for i in df.columns:
    if(df[i].nunique()>10):
        numerical_features.append(i)
numerical_features
```

Out[20]:
```
['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
```

In [21]:
```
category_features
```

Out[21]:
```
['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'thal', 'target']
```

Data Visualization`

In [22]:
```
# function takes a single dataframe column name as argument and
# plots a 1 x 2 subplot contains (pie plot and bar plot)
def plot_categorial(col_name):
    fig, ax = plt.subplots(
        nrows=1, ncols=2, figsize=(14, 5)
    )  # sets 1 x 2 subplots with figure size of (14,5)
    df[col_name].value_counts().plot.pie(
        autopct="%.0f%%",
        labels=df[col_name].unique(),
        shadow=True,
        startangle=180,
        ax=ax[0],
    )  # plots pie chart of given column with % percentage

    df[col_name].value_counts().plot.bar(
        ax=ax[1]
    )

    fig.suptitle(col_name.title())  # set plot's title
    plt.show()  # shows the plot
```

In [23]:
```
# function takes a single dataframe column name as argument and
# plots a 2 x 2 subplot contains (histogram, quantile-quantile plot, kernel
def plot_distribution(col_name):
    fig, axes = plt.subplots(
        2, 2, figsize=(15, 10)
    )  # sets 2 x 2 subplots with figure size of (14,10)
    sns.histplot(
        x=col_name, data=df, ax=axes[0][0], bins=20
    )  # displays histogram of the given dataframe column
    qqplot(
        data=df[col_name], ax=axes[0][1], line="45", fit=True, dist=stats.n
    )  # displays quantile-quantile plot of the given dataframe column
    sns.kdeplot(
        x=col_name, data=df, ax=axes[1][0], fill=True
    )  # displays kernel density estimate plot of the given dataframe colum
    sns.kdeplot(
        x=col_name, data=df, ax=axes[1][1], fill=True, cumulative=True
    )  # displays cumulative density plot of the given dataframe column
    plt.suptitle(
        "Distribution of " + col_name
    )  # sets the title for the subplot as "Distribution of <column name>"
    plt.show()  # shows the plot
```

In [24]:
```
# function takes a single dataframe column name as argument and
# plots a 2 x 2 subplot contains (histogram, quantile-quantile plot, kernel
def plot_distribution(col_name):
    fig, axes = plt.subplots(
        2, 2, figsize=(15, 10)
    )  # sets 2 x 2 subplots with figure size of (14,10)
    sns.histplot(
        x=col_name, data=df, ax=axes[0][0], bins=20
    )  # displays histogram of the given dataframe column
    qqplot(
        data=df[col_name], ax=axes[0][1], line="45", fit=True, dist=stats.n
    )  # displays quantile-quantile plot of the given dataframe column
    sns.kdeplot(
        x=col_name, data=df, ax=axes[1][0], fill=True
    )  # displays kernel density estimate plot of the given dataframe colum
    sns.kdeplot(
        x=col_name, data=df, ax=axes[1][1], fill=True, cumulative=True
    )  # displays cumulative density plot of the given dataframe column
    plt.suptitle(
        "Distribution of " + col_name
    )  # sets the title for the subplot as "Distribution of <column name>"
    plt.show()  # shows the plot
```

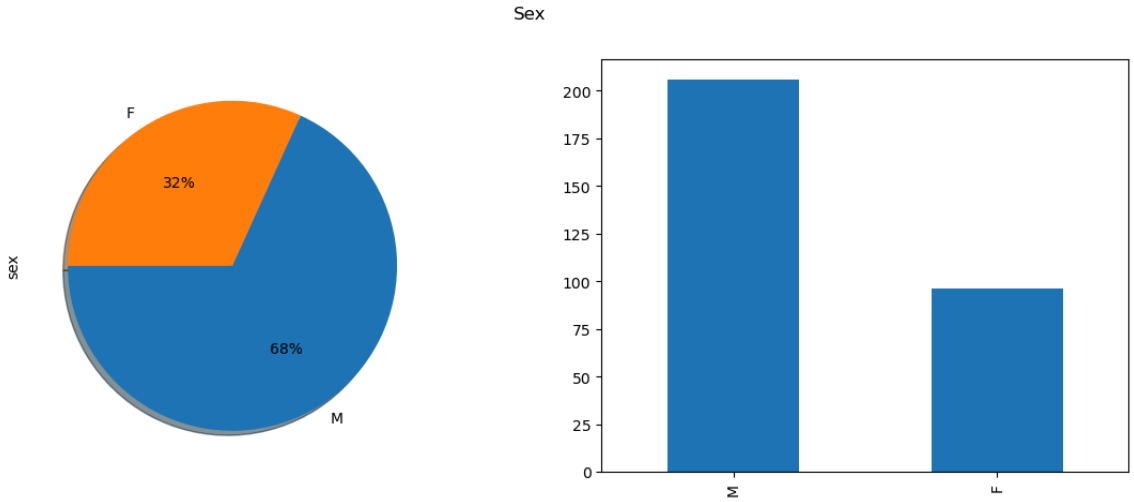
In [25]:
```
# function takes a single dataframe column name as argument and
# plots a 2 x 2 subplot contains (boxplot, violinplot, swarmplot and barplo
def plot_stats(col_name):
    fig, axes = plt.subplots(
        2, 2, figsize=(15, 10)
    )  # sets 2 x 2 subplots with figure size of (14,10)
    sns.boxplot(
        y=col_name, x="target", data=df, ax=axes[0][0], palette="viridis_r"
    )  # displays boxplot of the given dataframe column
    sns.violinplot(
        y=col_name, x="target", data=df, ax=axes[0][1], split=True, palette
    )  # displays violinplot of the given dataframe column
    sns.swarmplot(
        y=col_name, x="target", data=df, ax=axes[1][0], palette="viridis_r"
    )  # displays swarmplot of the given dataframe columns
    sns.barplot(
        x=col_name, y="target", data=df, hue="target", palette="viridis_r"
    )  # displays barplot of the given dataframe column respect to 'HeartDi
    plt.suptitle(
        "Statistics of " + col_name
    )  # sets the title for the subplot as "Statistics of <column name>"
    plt.show()  # shows the plot
```

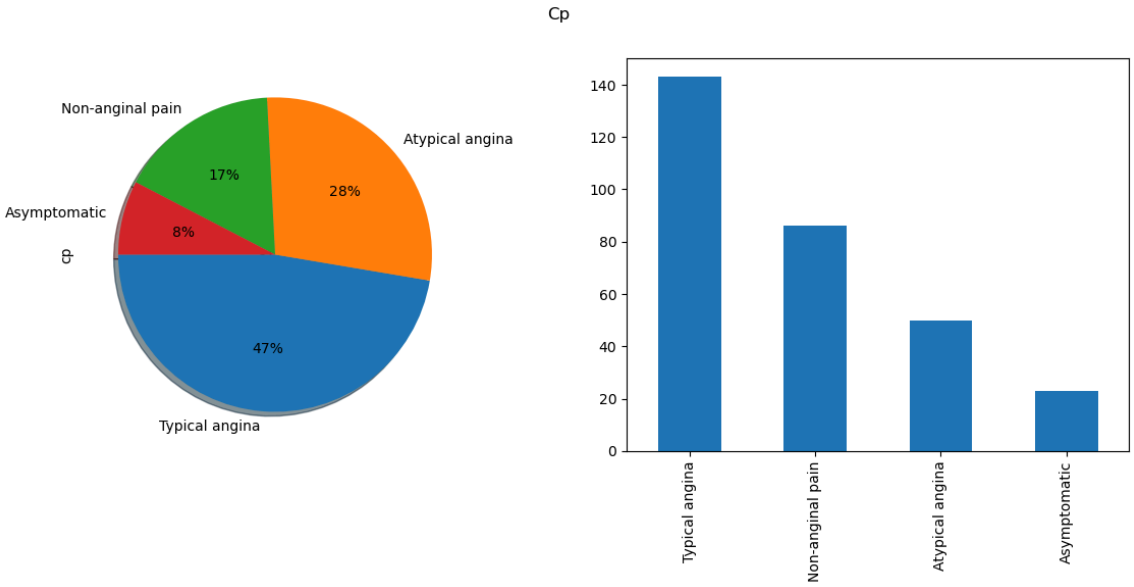
In [26]:

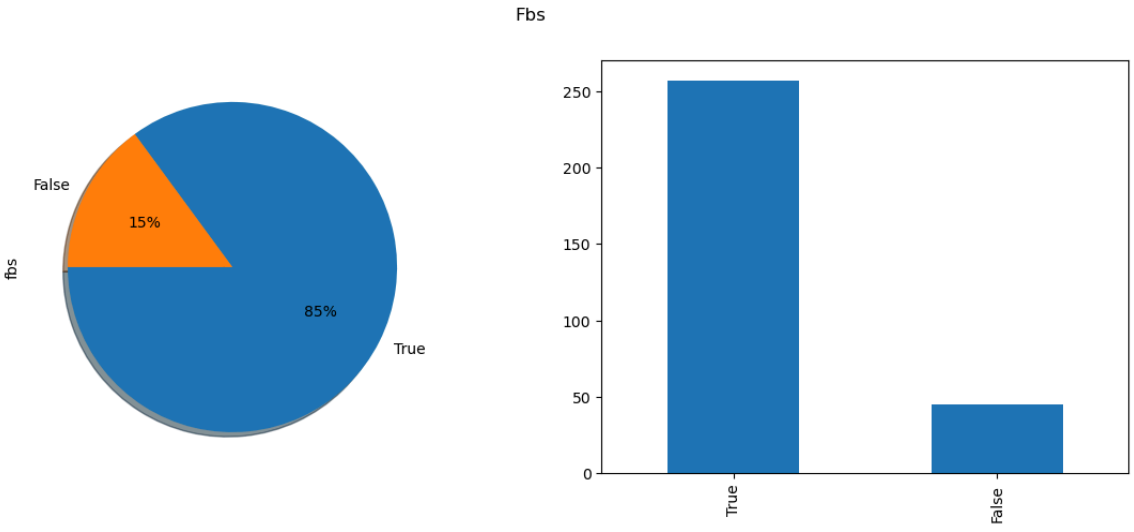
```
# function takes a single dataframe column name as argument and
# plots a single plot contains kernel density estimate plot
def plot_kde(col_name):
    facet = sns.FacetGrid(
        df, hue="target", aspect=4, palette="bright"
    )  # sets a seaborn FacetGrid with hue = "Outcome" and palette as "brig
    facet.map(
        sns.kdeplot, col_name, shade=True
    )  # kernel density plot of the given dataframe column respect to the d
    facet.set(
        xlim=(0, df[col_name].max())
    )  # sets the x axis from 0 to maximum value of the column
    facet.add_legend()  # add legend to the plot
    plt.title(
        col_name + " respect to Outcome"
    )  # sets the title for the plot as "<column name> respect to Outcome"
    plt.show()  # shows the plot
```

plots a 1 x 2 subplot contains (pie plot and bar plot) for each numerical columns

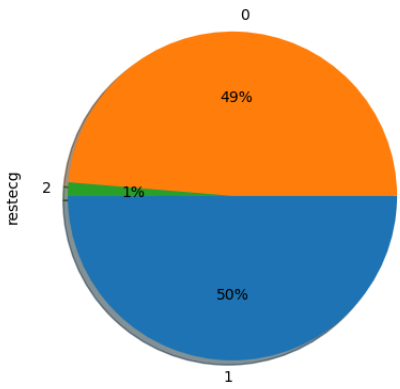
In [27]:
```
for i in category_features:
    plot_categorial(i)
```

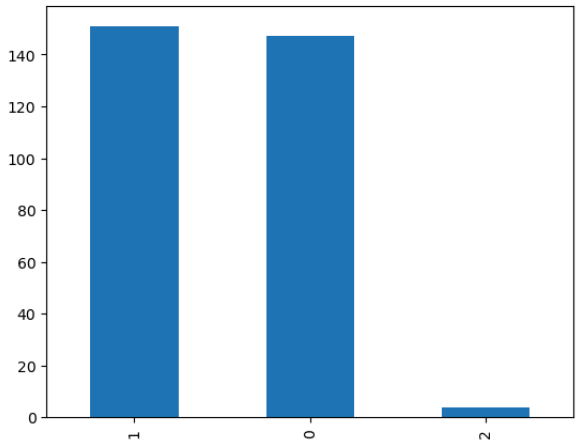




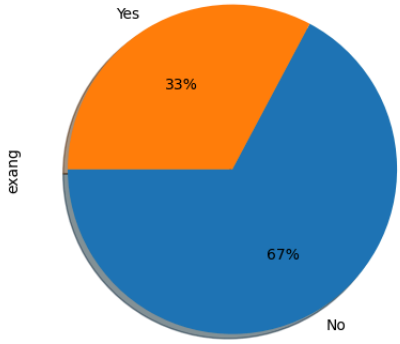


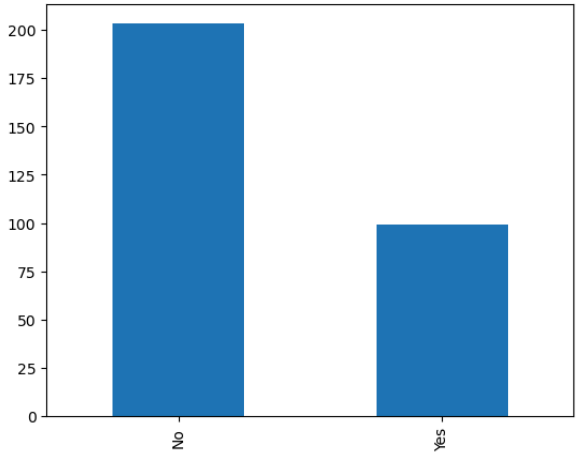
Restecg



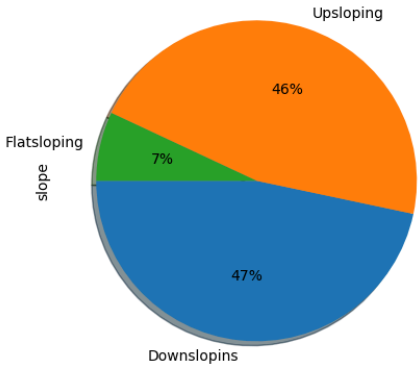


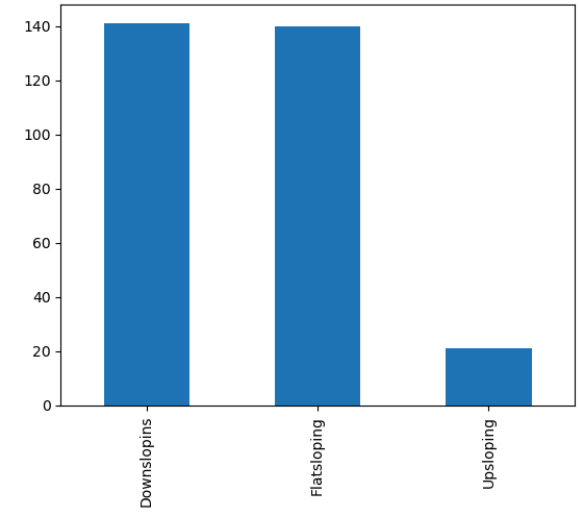
Exang



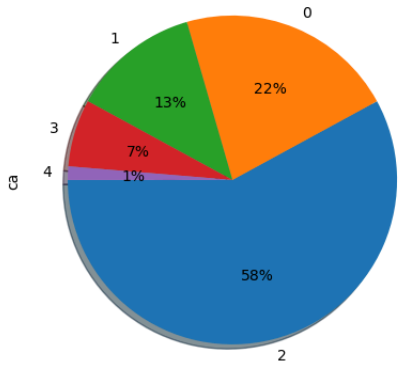


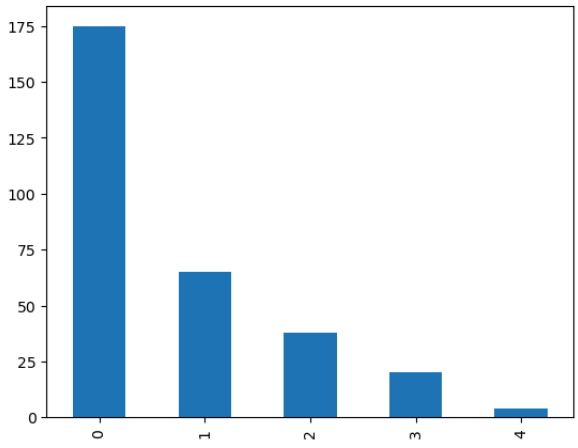
Slope



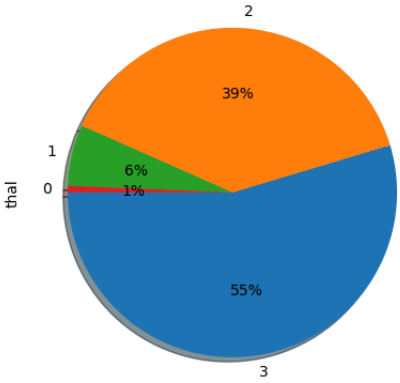


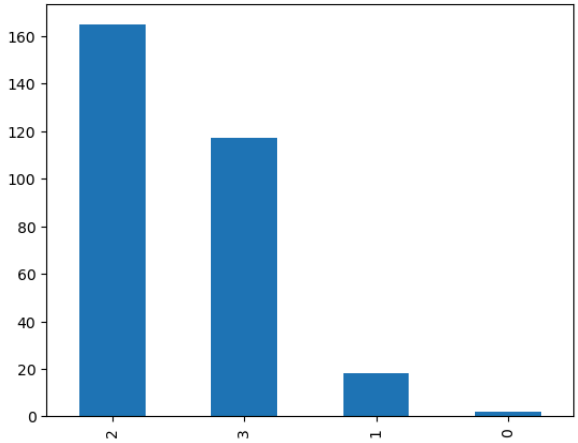
Ca



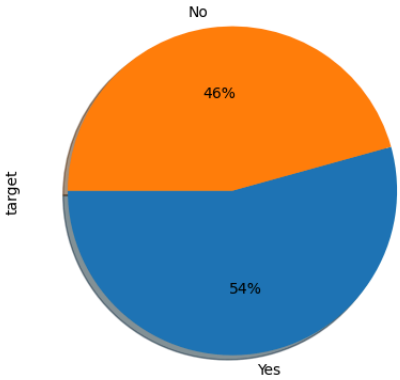


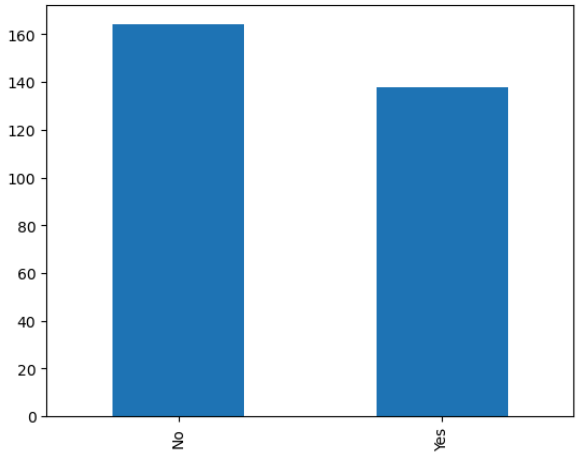
Thal





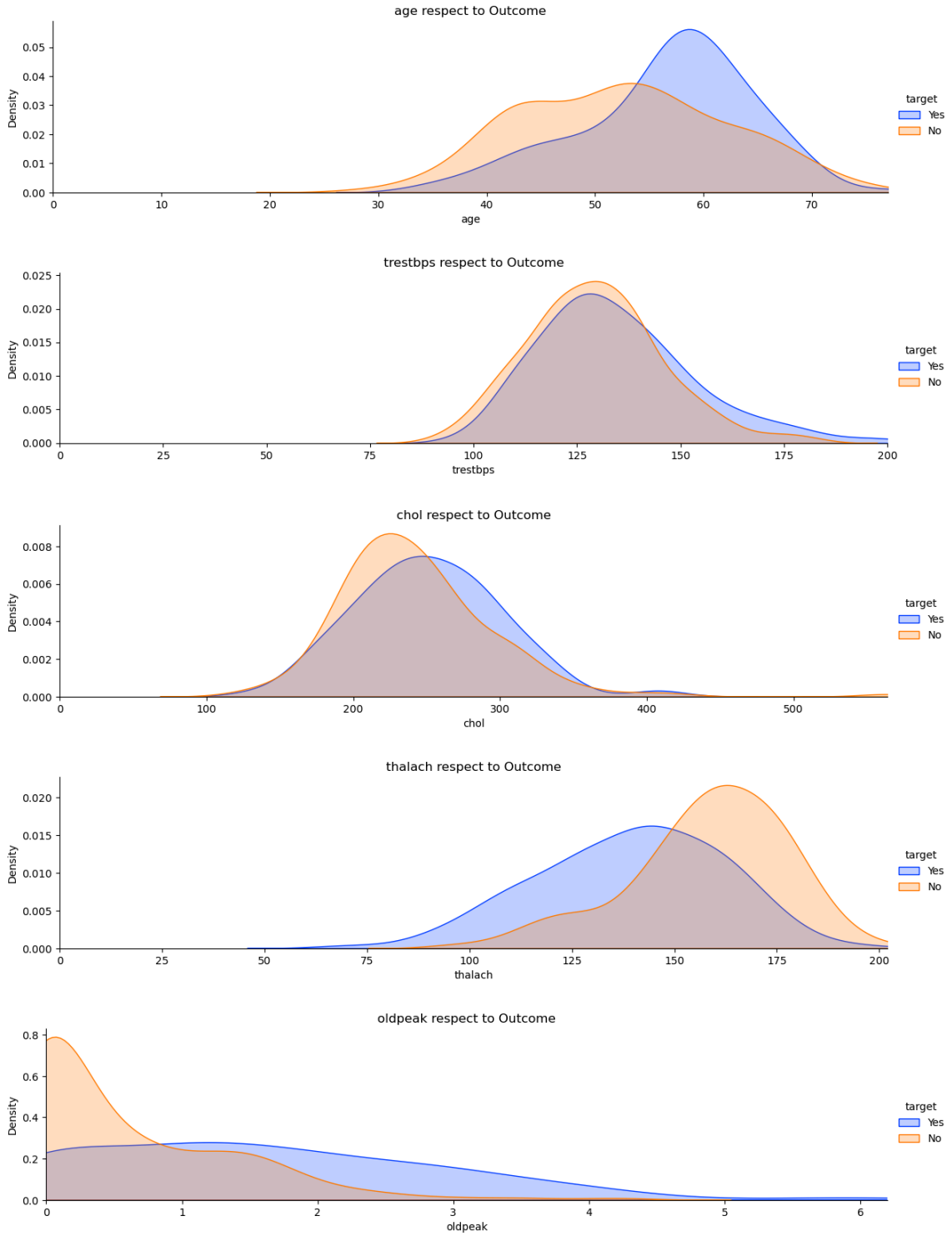
Target





Kernel density estimate plot for each numerical features

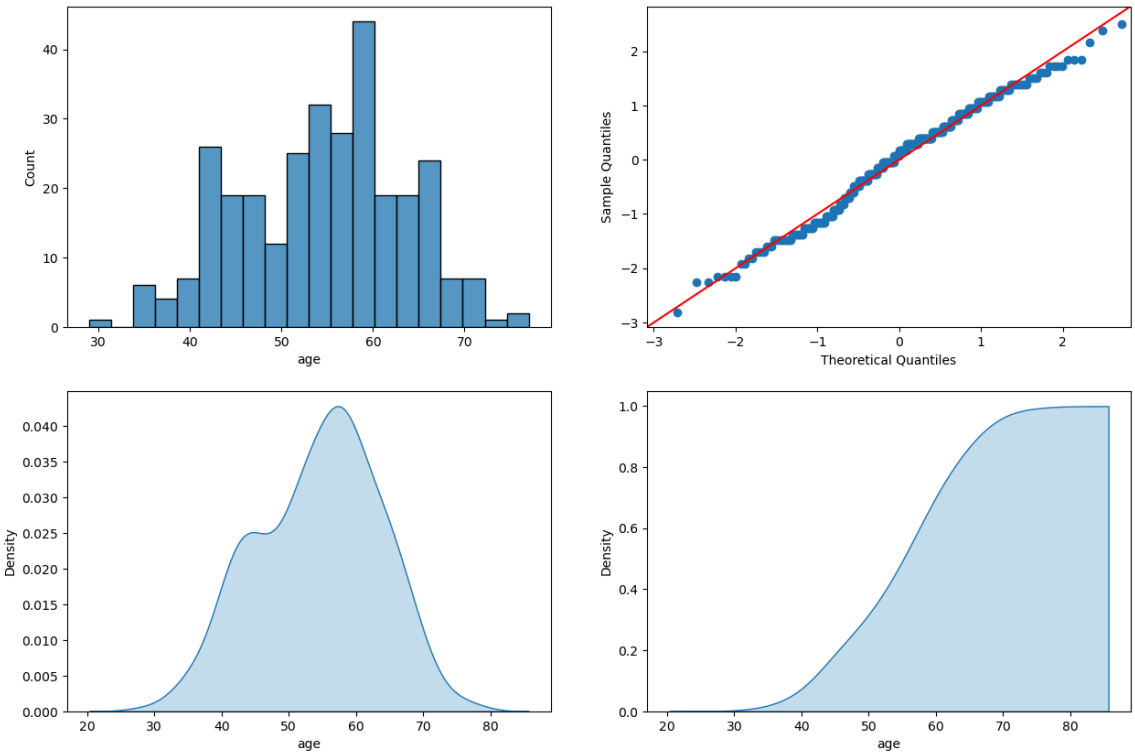
In [28]:
```
for i in numerical_features:
    plot_kde(i)
```



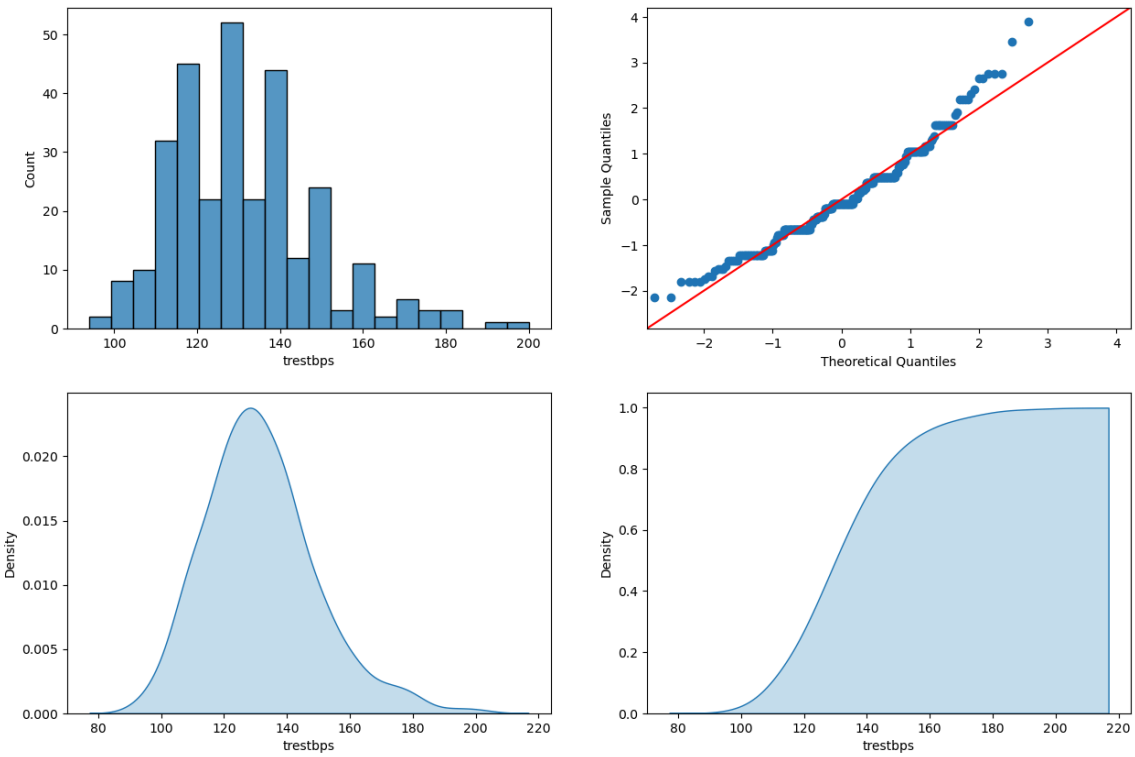
plots a 2 x 2 subplot contains (histogram, quantile-quantile plot, kernel density estimate plot and cumulative density plot) for each numerical feature

In [29]:
```
for i in numerical_features:
    plot_distribution(i)
```

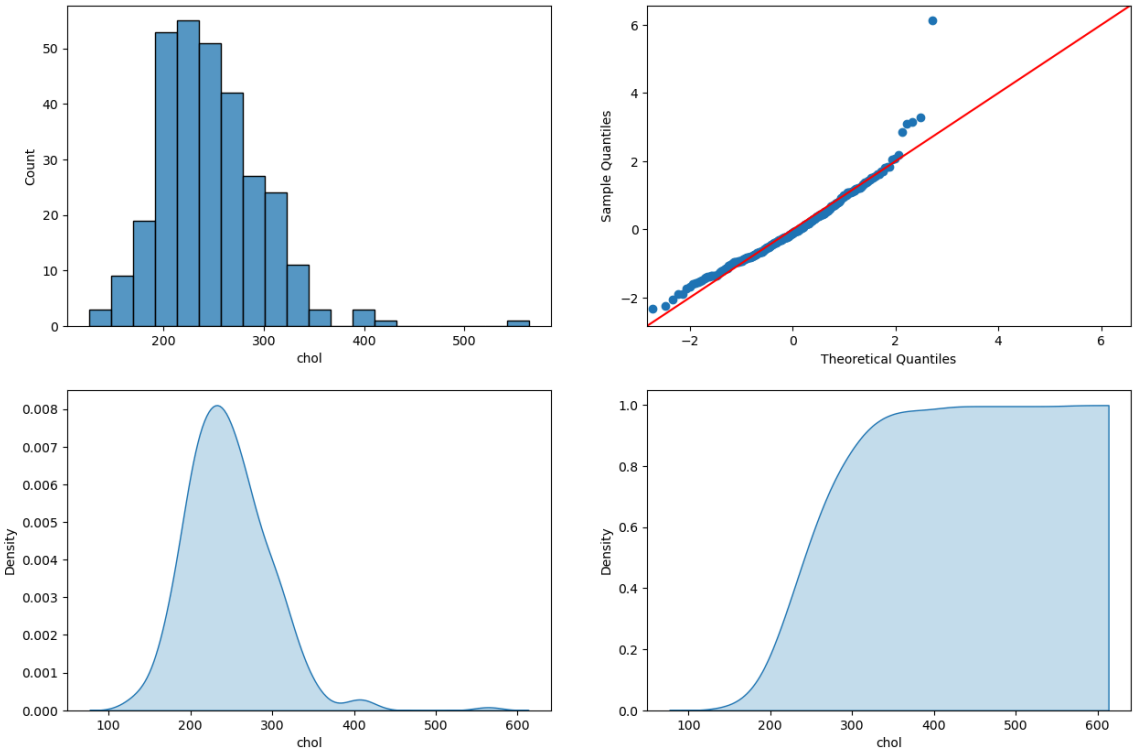
Distribution of age



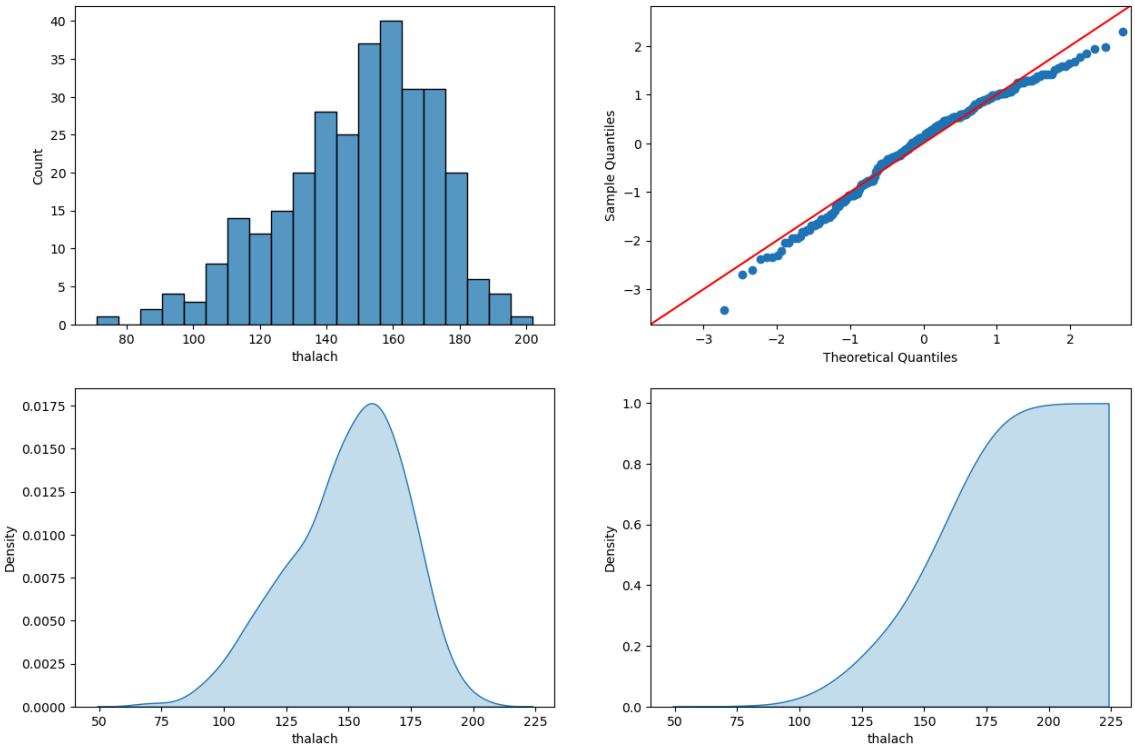
Distribution of trestbps



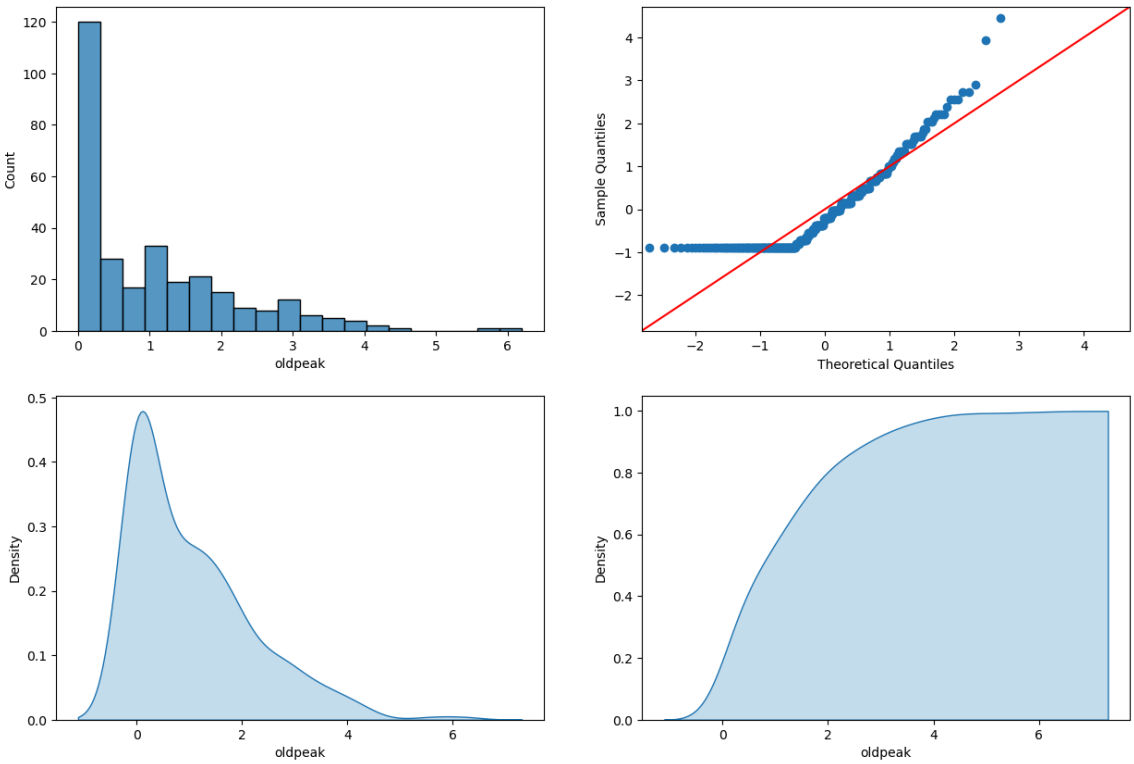
Distribution of chol



Distribution of thalach



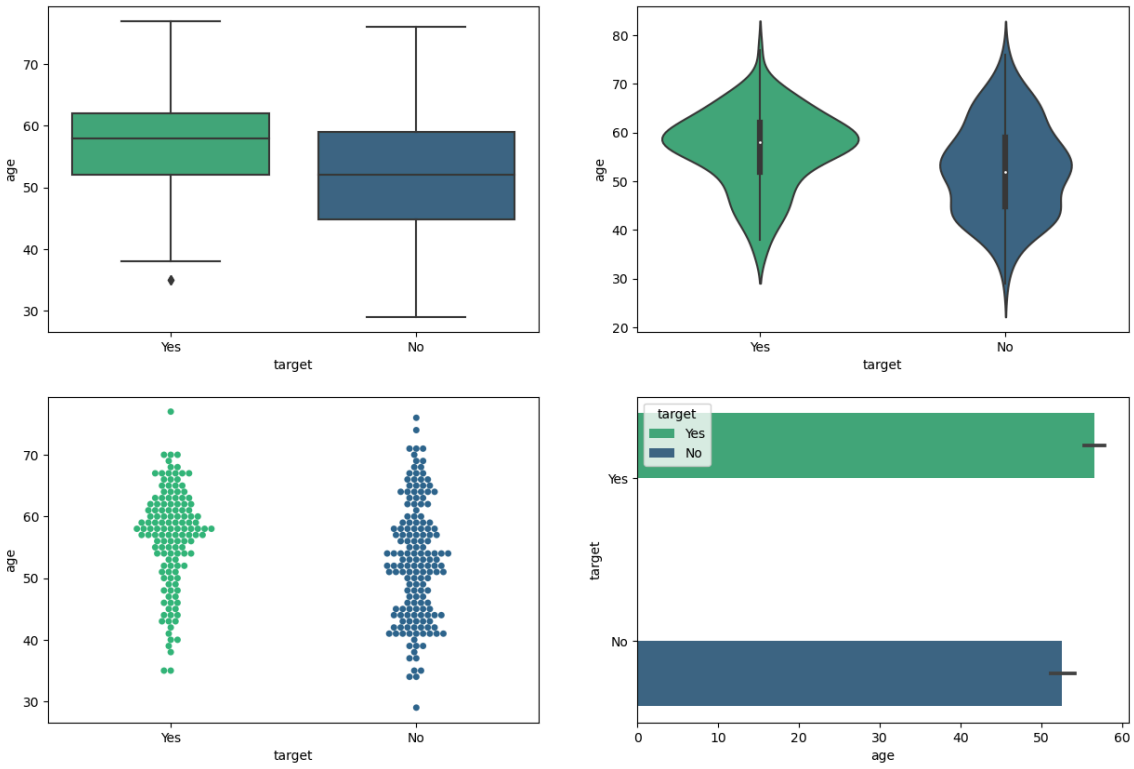
Distribution of oldpeak



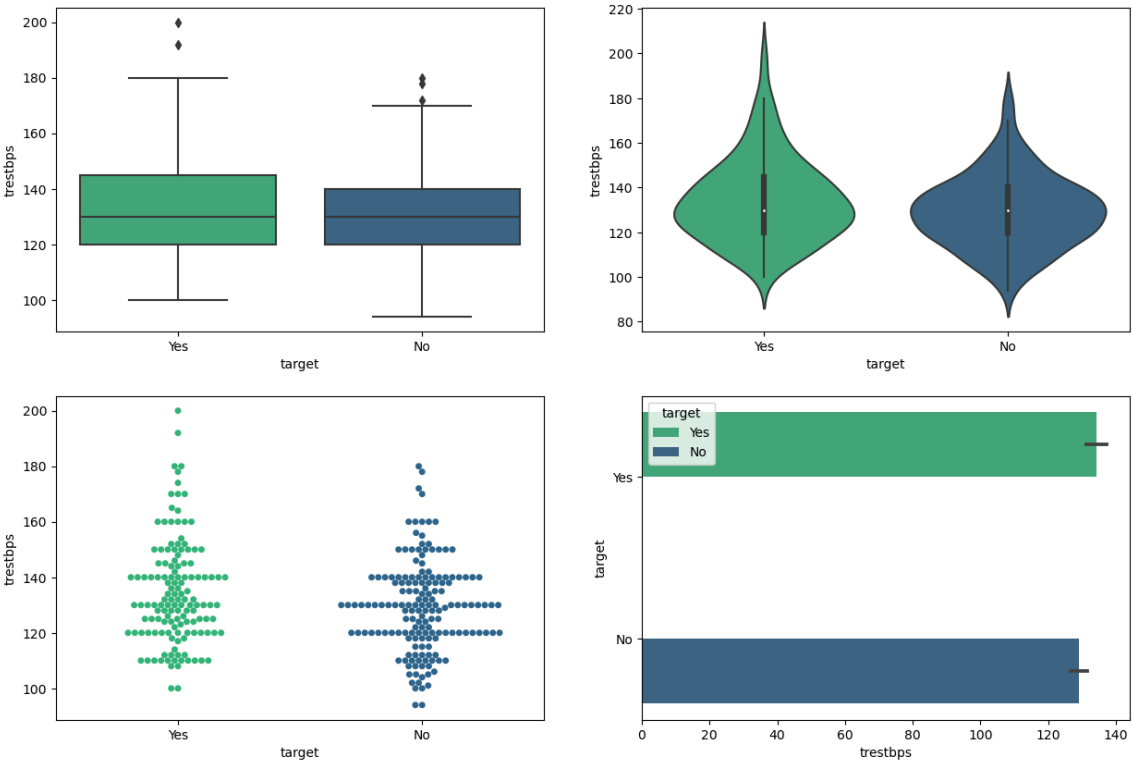
plots a 2 x 2 subplot contains (boxplot, violinplot, swarmplot and barplot) for each numerical features

In [30]:
```
for i in numerical_features:
    plot_stats(i)
```

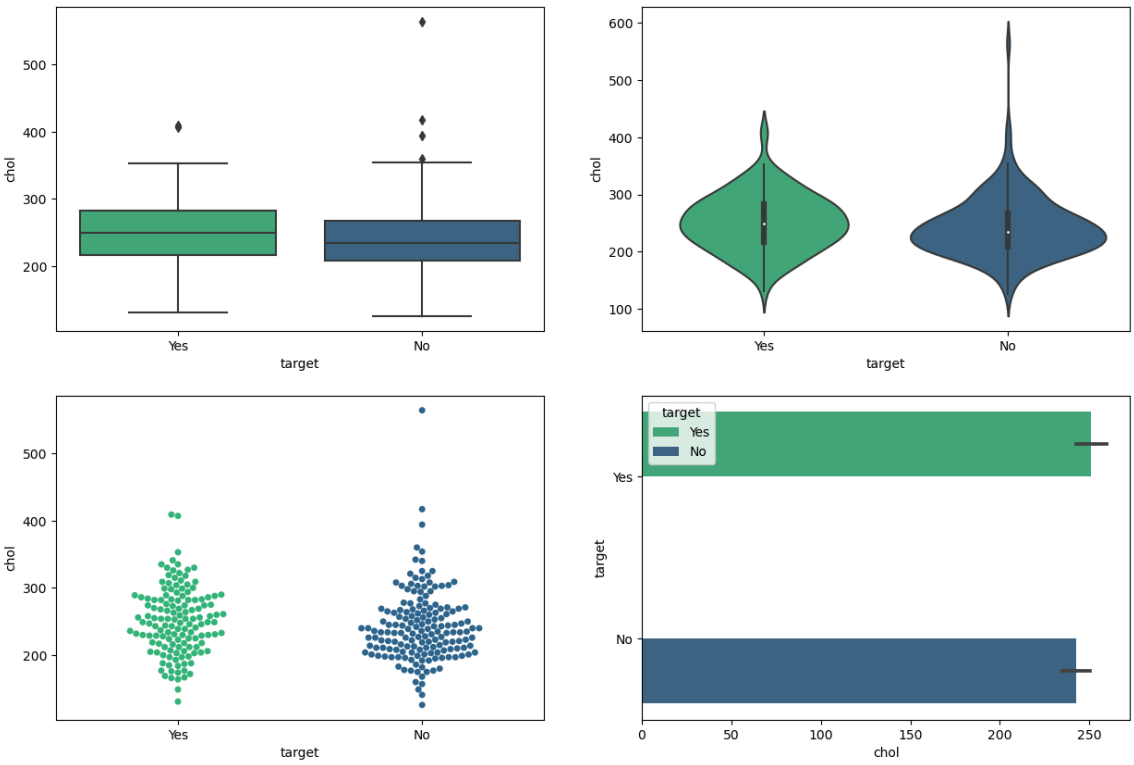
Statistics of age



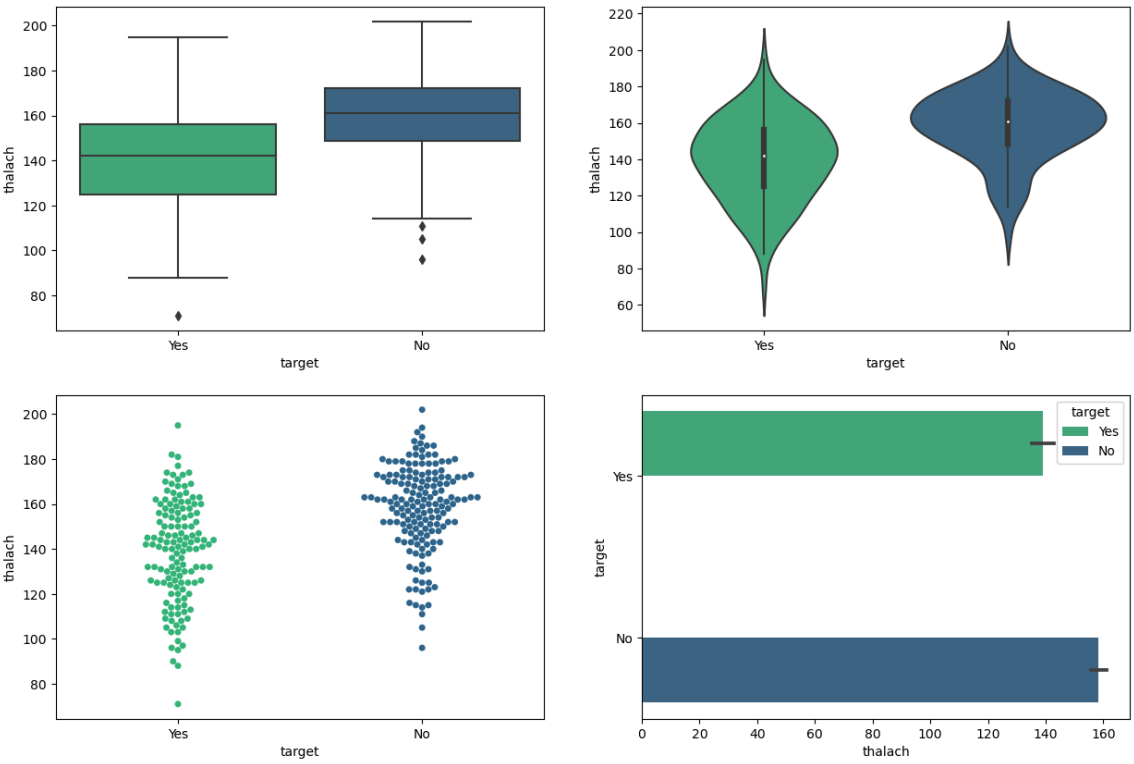
Statistics of trestbps

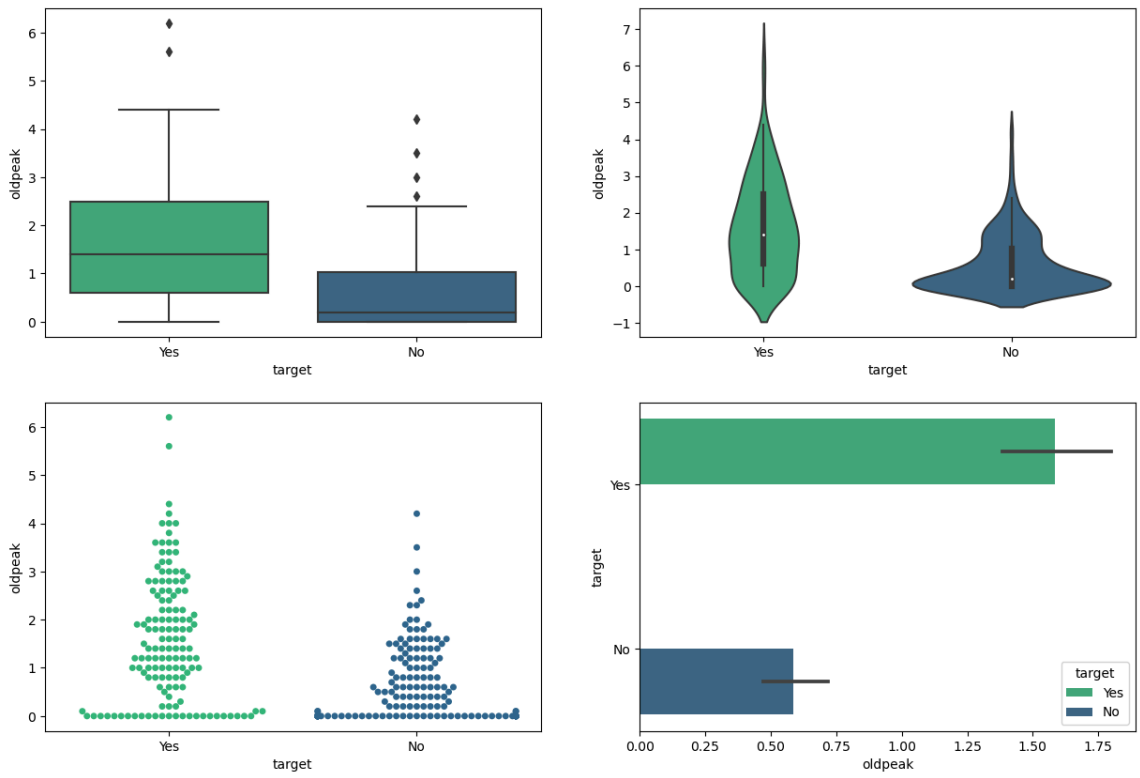


Statistics of chol



Statistics of thalach





PairPlot

In [31]:
```
## Features to change
features_to_change=[]
for i in df.columns:
    if(df[i].dtype=='object'):
        features_to_change.append(i)
features_to_change
```

Out[31]:
```
['sex', 'cp', 'fbs', 'exang', 'slope', 'target']
```

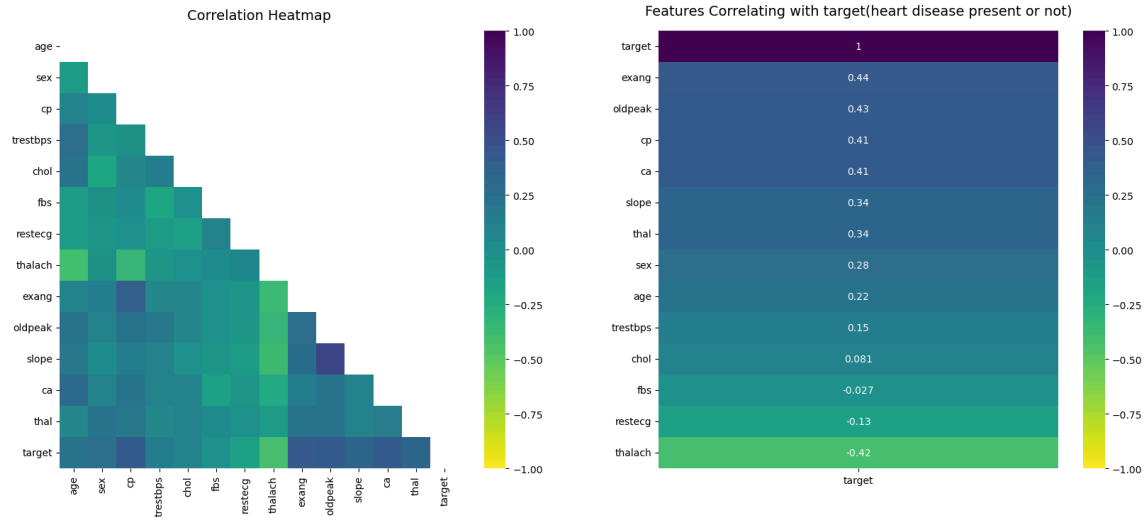
In [32]:
```
 ## transforming categorical features to numerical (using labelEncoding tec
from sklearn.preprocessing import LabelEncoder
df1=df.copy()
le=LabelEncoder()
for i in features_to_change:
    df1[i]=le.fit_transform(df[i])

df1.head()
```

Out[32]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	targ
0	52	1	3	125	212	1	1	168	0	1.0	0	2	3	
1	53	1	3	140	203	0	0	155	1	3.1	2	0	3	
2	70	1	3	145	174	1	1	125	1	2.6	2	0	3	
3	61	1	3	148	203	1	1	161	0	0.0	0	1	3	
4	62	0	3	138	294	0	1	106	0	1.9	1	3	2	

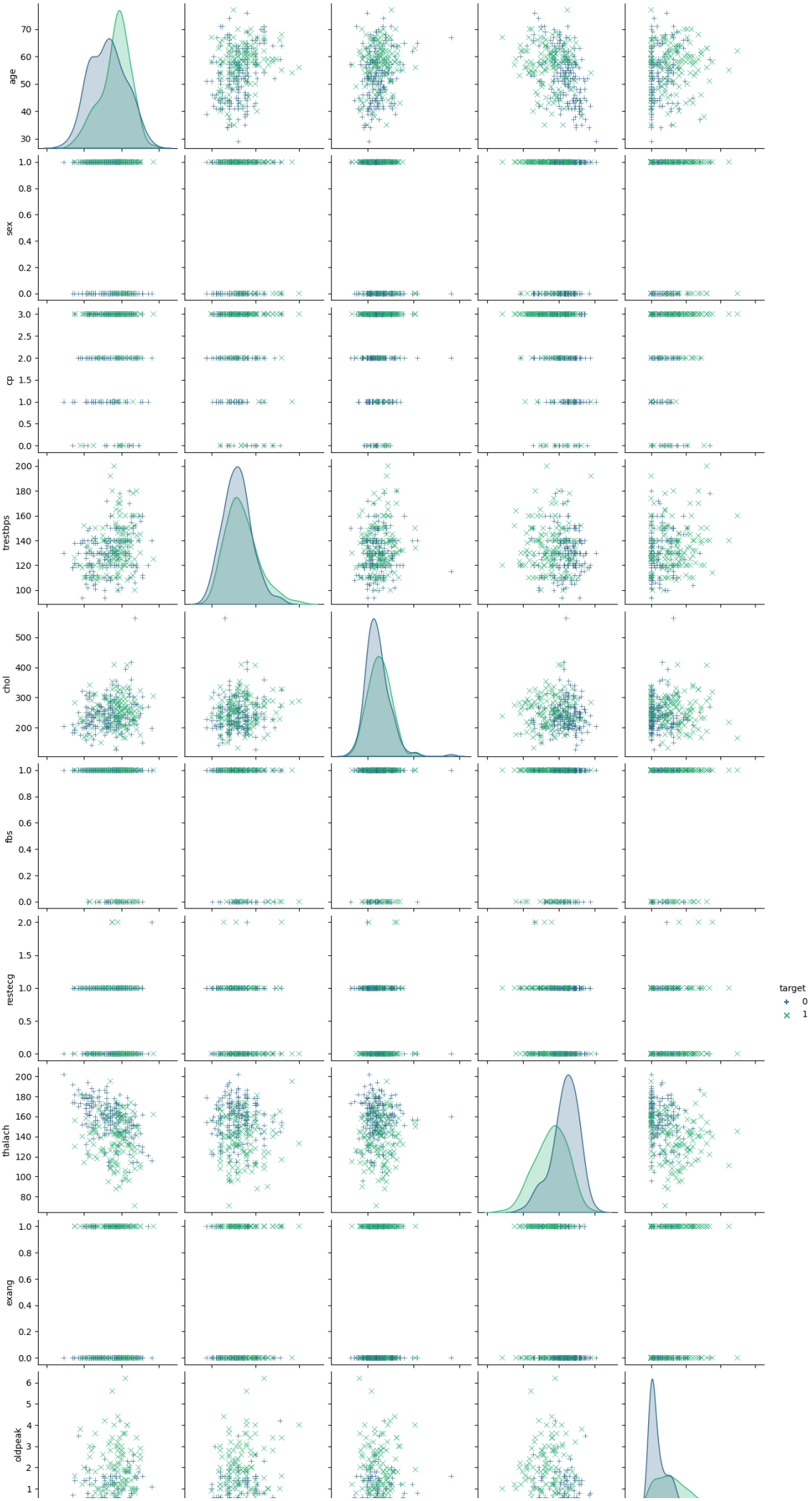
correlation

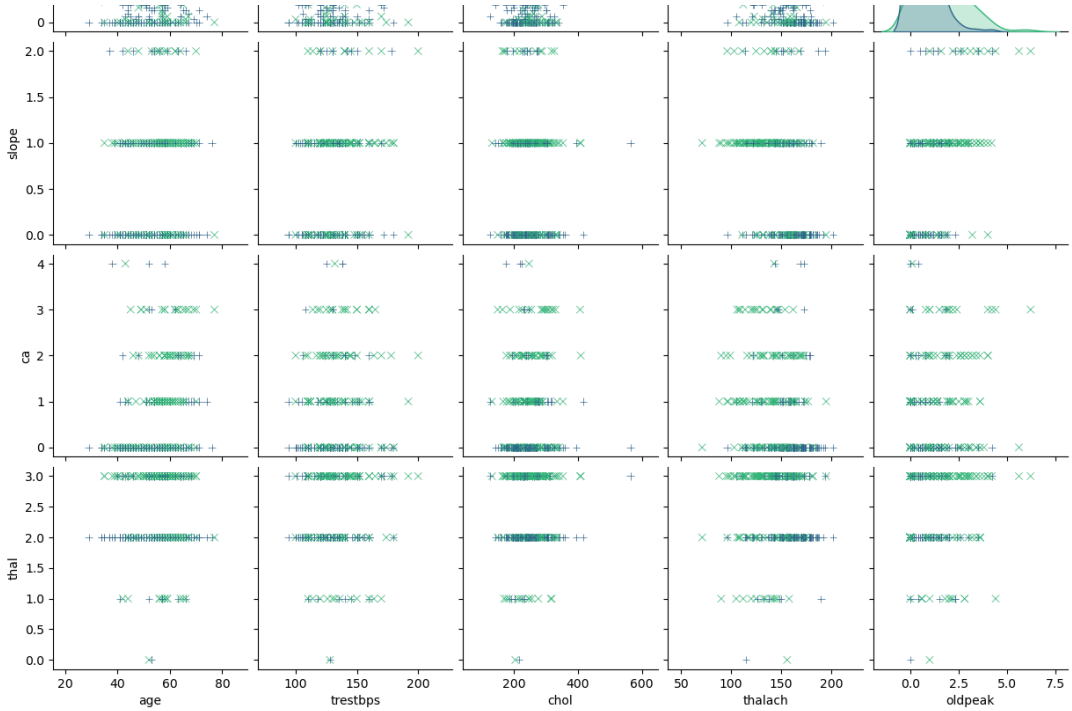
In [33]:
```
fig, ax = plt.subplots(ncols=2, figsize=(20, 8))  # create a 1 x 2 subplot
resign_corr = df1.corr()  # calculate correlation of the dataframe
mask = np.triu(np.ones_like(resign_corr, dtype=bool))
cat_heatmap = sns.heatmap(
    df1.corr(), mask=mask, vmin=-1, vmax=1, annot=False, ax=ax[0], cmap="vi
)  # cornor heatmap of the dataframe correlation
cat_heatmap.set_title(
    "Correlation Heatmap", fontdict={"fontsize": 14}, pad=12
)  # sets the title for the heatmap with font size 14 and padding 12

heatmap = sns.heatmap(
    resign_corr[["target"]].sort_values(by="target", ascending=False),
    vmin=-1,
    vmax=1,
    annot=True,
    ax=ax[1],
    cmap="viridis_r",
)  # create heatmap for features correlating with the dependant varibale 'H
heatmap.set_title(
    "Features Correlating with target(heart disease present or not)",
    fontdict={"fontsize": 14},
    pad=16,  # sets the title for the heatmap with font size 14 and padding
)
plt.show()  # shows the subplot
```



Pairplot

In [34]:
```
sns.pairplot(
    df1,
    hue="target",
    x_vars=numerical_features,
    markers=["+", "x"],
    palette="viridis",
)  # pairplot with given columns in x axis and all columns in y axis
plt.show()  # shows the plot
```


age
sex
cp
trestbps
chol
fbs
restecg
thalach
exang
oldpeak
target
0
1



In [ ]:

Observations after EDA:

1. Males are consistently more likely to have heart disease.
2. Most of heart disease Patients have age between 55 and 65.
3. Most patients with 0 oldpeak, don't have Heart disease
4. The cholesterol level slightly depends on heart disease. People with high cholesterol levels may have a higher risk of developing heart disease.
5. Maximum Heart Rate (thalach): Higher maximum heart rates are generally associated with a lower likelihood of having heart disease.
6. Resting Blood Pressure (trestbps): A resting blood pressure around 130 mm Hg is more commonly associated with heart disease.

In [ ]: