Import Data and Libraries

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
df = pd.read_csv("heart_disease_uci.csv")
```

Column Descriptions

1. **id** → Unique id for each patient
2. **age** → Age of the patient in years
3. **origin** → Place of study
4. **sex** → Male/Female
5. **cp** → Chest pain type
   Values: [typical angina, atypical angina, non-anginal, asymptomatic]
6. **trestbps** → Resting blood pressure (in mm Hg on admission to the hospital)
7. **chol** → Serum cholesterol in mg/dl
8. **fbs** → Fasting blood sugar > 120 mg/dl
9. **restecg** → Resting electrocardiographic results
   Values: [normal, STT abnormality, LV hypertrophy]
10. **thalach** → Maximum heart rate achieved
11. **exang** → Exercise-induced angina (True/False)
12. **oldpeak** → ST depression induced by exercise relative to rest
13. **slope** → The slope of the peak exercise ST segment
14. **ca** → Number of major vessels (0-3) colored by fluoroscopy
15. **thal** → *Values*: [normal, fixed defect, reversible defect]
16. **num** → The predicted attribute

Data Exploration

In [3]:
```
df.sample(5)
```

Out[3]:

	id	age	sex	dataset	cp	trestbps	chol	fbs	res
661	662	57	Male	Switzerland	asymptomatic	110.0	0.0	NaN	abnorm
543	544	53	Male	Hungary	asymptomatic	120.0	246.0	False	nc
557	558	44	Male	Hungary	asymptomatic	130.0	290.0	False	nc
221	222	54	Female	Cleveland	non-anginal	108.0	267.0	False	hypertr
462	463	55	Male	Hungary	atypical angina	120.0	256.0	True	nc

In [4]:
```
# find out the dimensions of the data
df.shape
```

Out[4]: (920, 16)

In [5]:
```
# information about the data types and null values
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 920 entries, 0 to 919
Data columns (total 16 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   id        920 non-null    int64  
 1   age       920 non-null    int64  
 2   sex       920 non-null    object 
 3   dataset   920 non-null    object 
 4   cp        920 non-null    object 
 5   trestbps  861 non-null    float64
 6   chol      890 non-null    float64
 7   fbs       830 non-null    object 
 8   restecg   918 non-null    object 
 9   thalch    865 non-null    float64
 10  exang     865 non-null    object 
 11  oldpeak   858 non-null    float64
 12  slope     611 non-null    object 
 13  ca        309 non-null    float64
 14  thal      434 non-null    object 
 15  num       920 non-null    int64  
dtypes: float64(5), int64(3), object(8)
memory usage: 115.1+ KB
```

In [6]:
```
print(df.isna().sum())
```

```
id            0
age           0
sex           0
dataset       0
cp            0
trestbps     59
chol         30
fbs          90
restecg       2
thalch       55
exang        55
oldpeak      62
slope       309
ca          611
thal        486
num           0
dtype: int64
```

ca (major vessels), thal (thalassemia), and slope (ST segment slope) have a significant amount of missing data.

In [7]:
```
df.describe()
```

Out[7]:

	id	age	trestbps	chol	thalch	oldpeak
count	920.000000	920.000000	861.000000	890.000000	865.000000	858.000000
mean	460.500000	53.510870	132.132404	199.130337	137.545665	0.878788
std	265.725422	9.424685	19.066070	110.780810	25.926276	1.091226
min	1.000000	28.000000	0.000000	0.000000	60.000000	-2.600000
25%	230.750000	47.000000	120.000000	175.000000	120.000000	0.000000
50%	460.500000	54.000000	130.000000	223.000000	140.000000	0.500000
75%	690.250000	60.000000	140.000000	268.000000	157.000000	1.500000
max	920.000000	77.000000	200.000000	603.000000	202.000000	6.200000

In [8]:
```
# Locations involved in study
print(df.dataset.unique())
```

```
['Cleveland' 'Hungary' 'Switzerland' 'VA Long Beach']
```

Data Cleaning & Transformation

since ca (major vessels), thal (thalassemia), and slope (ST segment slope) have a lot of missing data, we'll drop those columns

In [9]:
```
df = df.drop(columns=['id'])  # Dropping the 'id' column
```

In [10]:
```
# Drop columns with significant amount of missing columns
df= df.drop(columns = ['ca', 'slope', 'thal'])
```

```
df.head()
```

Out[10]:

	age	sex	dataset	cp	trestbps	chol	fbs	restecg	tha
0	63	Male	Cleveland	typical angina	145.0	233.0	True	lv hypertrophy	15
1	67	Male	Cleveland	asymptomatic	160.0	286.0	False	lv hypertrophy	10
2	67	Male	Cleveland	asymptomatic	120.0	229.0	False	lv hypertrophy	12
3	37	Male	Cleveland	non-anginal	130.0	250.0	False	normal	18
4	41	Female	Cleveland	atypical angina	130.0	204.0	False	lv hypertrophy	17

In [32]:
```
# Fill missing values for numerical columns with the median
numerical_columns = ['trestbps', 'chol', 'thalch', 'oldpeak']
df[numerical_columns] = df[numerical_columns].fillna(df[numerical_columns].m

# Fill missing values of categorical columns with the most occurring value
categorical_columns = ['fbs', 'restecg', 'exang']
for col in categorical_columns:
    df[col] = df[col].astype(str).fillna(df[col].mode()[0])
```

In [12]:
```
# One-hot encoding on "sex" column
df = pd.get_dummies(df, columns=['sex'], drop_first=True)

# Display the first few rows of the dataframe to verify the result
df.head()
```

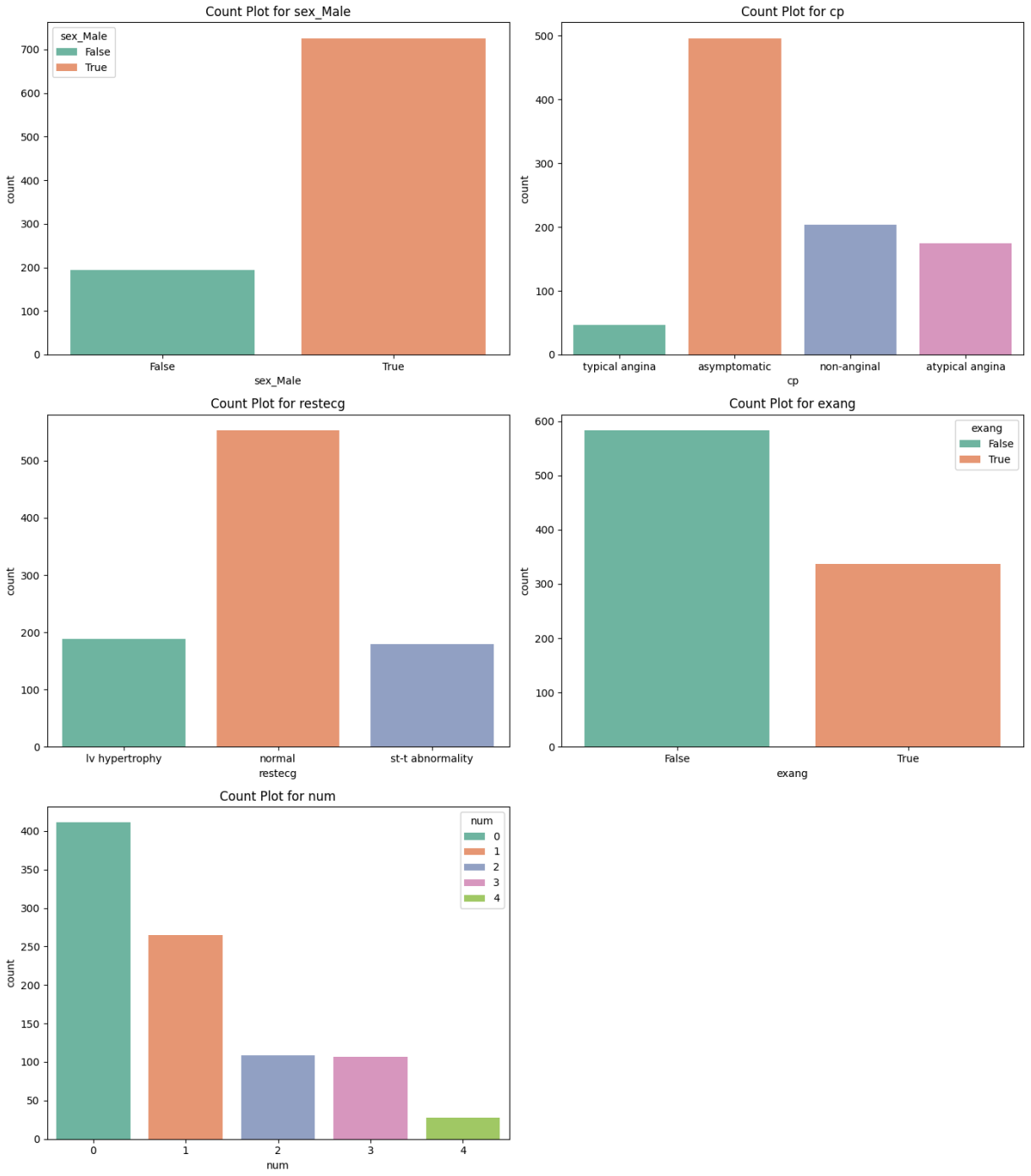
Out[12]:

	age	dataset	cp	trestbps	chol	fbs	restecg	thalch	exa
0	63	Cleveland	typical angina	145.0	233.0	True	lv hypertrophy	150.0	Fa
1	67	Cleveland	asymptomatic	160.0	286.0	False	lv hypertrophy	108.0	T
2	67	Cleveland	asymptomatic	120.0	229.0	False	lv hypertrophy	129.0	T
3	37	Cleveland	non-anginal	130.0	250.0	False	normal	187.0	Fa
4	41	Cleveland	atypical angina	130.0	204.0	False	lv hypertrophy	172.0	Fa

Univariate Analysis

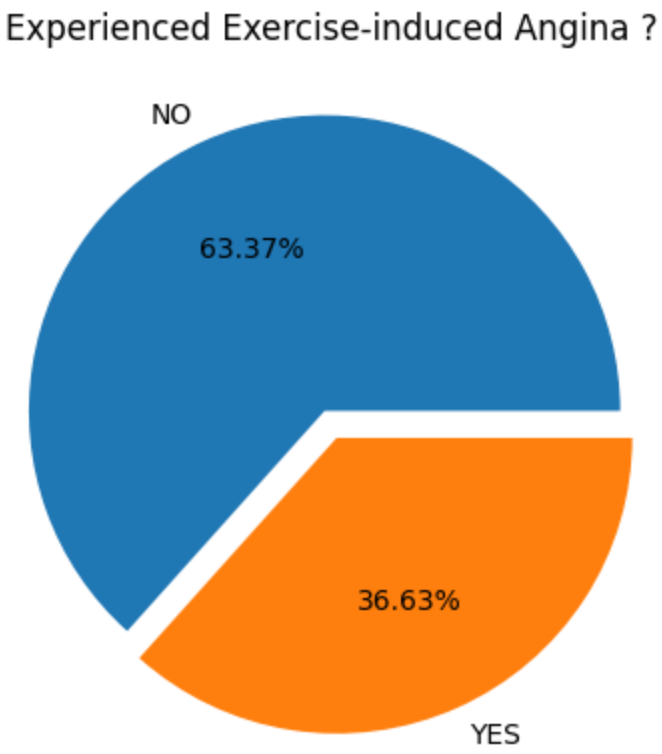
In [13]:
```
# List of categorical columns
categorical_columns = ['sex_Male', 'cp', 'restecg', 'exang', 'num']

# Plotting count plots for each categorical variable
```

```
plt.figure(figsize=(14, 16))
for i, column in enumerate(categorical_columns, 1):
    plt.subplot(3, 2, i)
    sns.countplot(x=column, data=df, hue=column, palette="Set2")
    plt.title(f'Count Plot for {column}')
    plt.tight_layout()

plt.show()
```

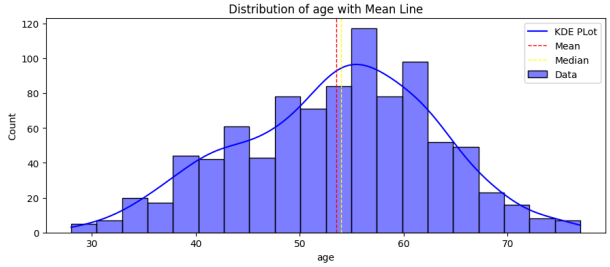


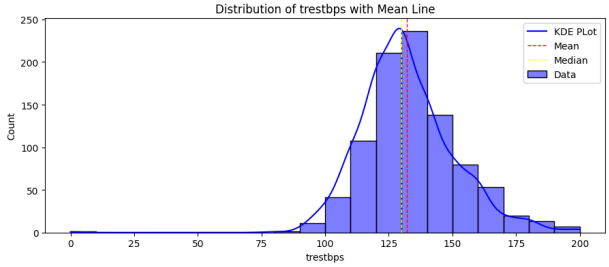
In [14]:
```
# Exercise-induced Angina

df.exang.value_counts().plot(kind='pie', explode=[0.05,0.05], labels=['NO',
autopct=lambda p: '{:.2f}%'.format(p), title = 'Experienced Exercise-induced
```

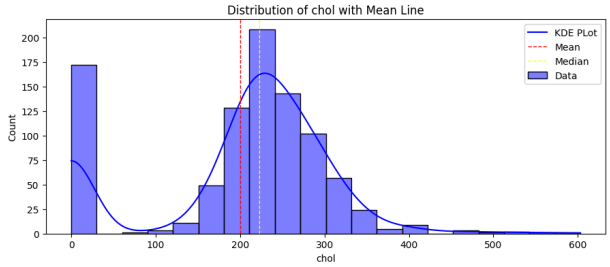
```
plt.ylabel('')
plt.show()
```

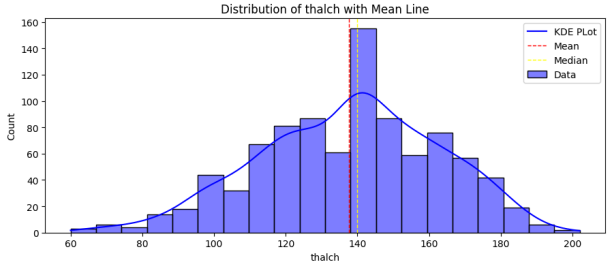


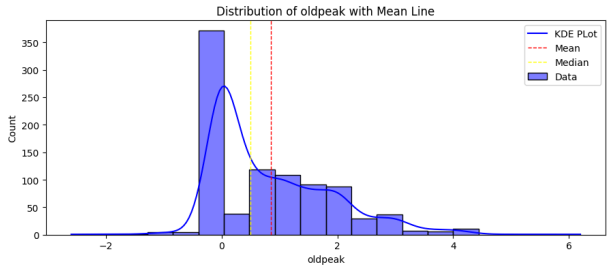
In [15]:
```
# List of numerical columns
numerical_columns = ['age', 'trestbps', 'chol', 'thalch', 'oldpeak']

# Plotting histograms for numerical variables
plt.figure(figsize=(18, 12))
for i, column in enumerate(numerical_columns, 1):
    plt.subplot(3, 2, i)
    sns.histplot(df[column], kde=True, color='blue', bins=20)
    plt.axvline(df[column].mean(), color='red', linestyle='dashed', linewidt
    plt.axvline(df[column].median(), color='yellow', linestyle='dashed', lir
    plt.title(f'Distribution of {column} with Mean Line')
    plt.tight_layout()
    plt.legend(['KDE PLot','Mean', 'Median','Data'])

plt.show()
```



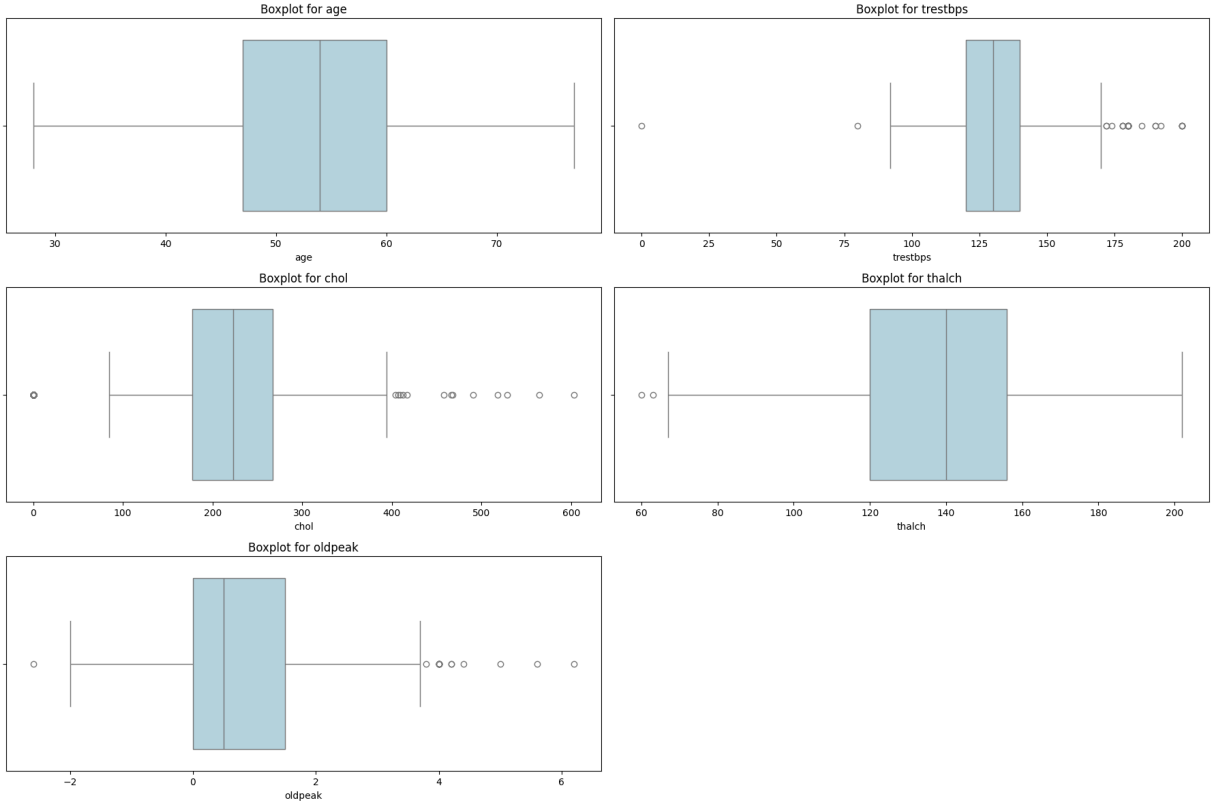




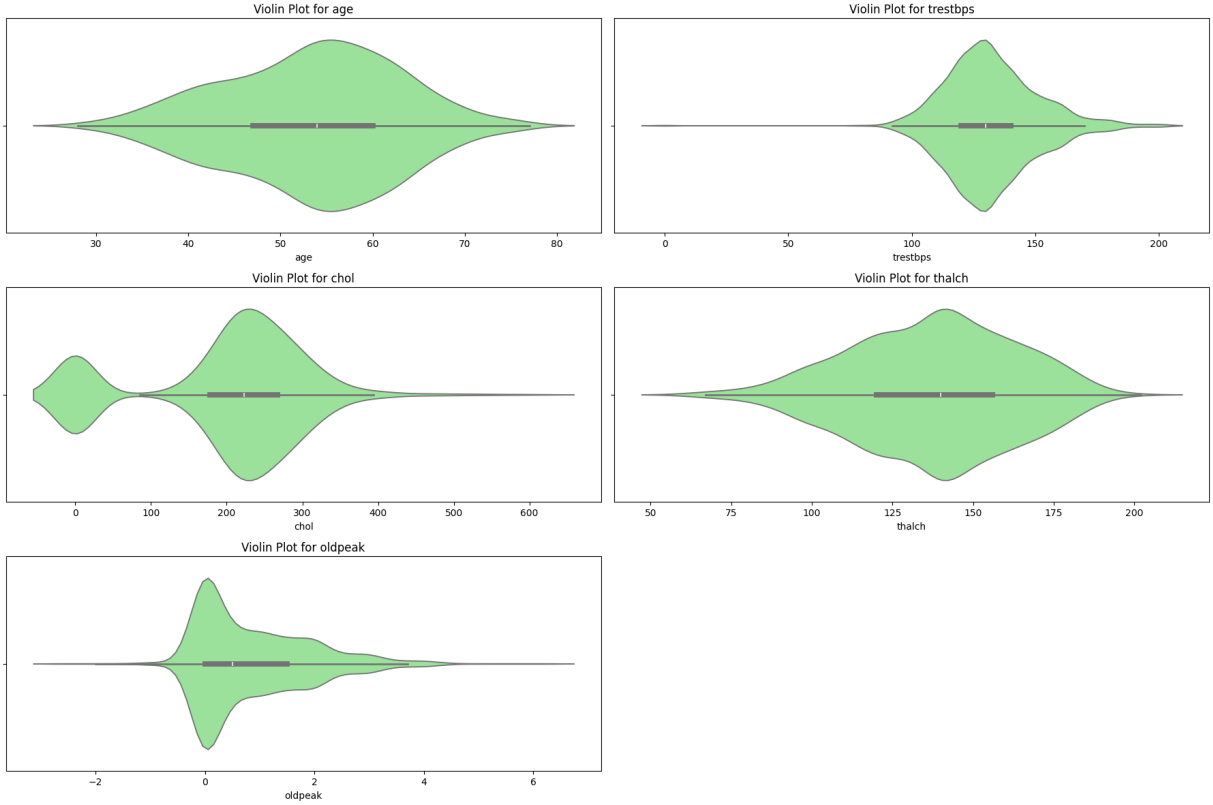




In [16]:
```python
# Boxplot for Numerical Variables
plt.figure(figsize=(18, 12))
for i, column in enumerate(numerical_columns, 1):
    plt.subplot(3, 2, i)
    sns.boxplot(x=df[column], color='lightblue')
    plt.title(f'Boxplot for {column}')
    plt.tight_layout()
plt.show()
```



In [17]:
```
# Violin plot for numericall variables
plt.figure(figsize=(18, 12))
for i, column in enumerate(numerical_columns, 1):
    plt.subplot(3, 2, i)
    sns.violinplot(x=df[column], color='lightgreen')
    plt.title(f'Violin Plot for {column}')
    plt.tight_layout()

plt.show()
```



Outlier detection

In [18]:
```
# Descriptive statistics for numerical variables
df[numerical_columns].describe()

# Calculate IQR for detecting outliers
Q1 = df[numerical_columns].quantile(0.25)
Q3 = df[numerical_columns].quantile(0.75)
IQR = Q3 - Q1
print(IQR)
```

```
age         13.00
trestbps    20.00
chol        89.25
thalch      36.00
oldpeak      1.50
dtype: float64
```

In [19]:
```
# Calculate outlier boundaries
lower_bound = Q1 - 1.5 * IQR
upper_bound = Q3 + 1.5 * IQR

# Identify outliers
outliers = (df[numerical_columns] < lower_bound) | (df[numerical_columns] >

# Display rows containing outliers
outlier_rows = df[outliers.any(axis=1)]
print(outlier_rows)
```

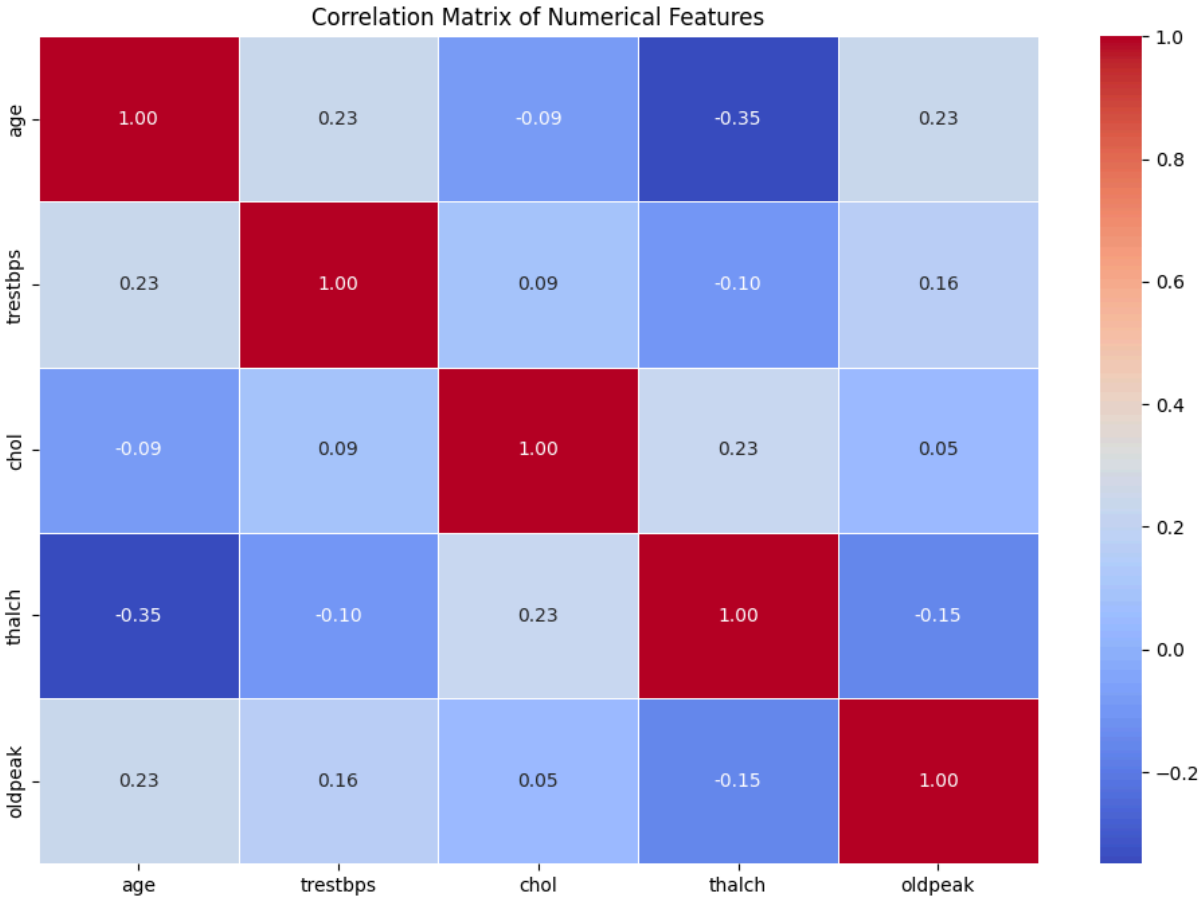
```
     age        dataset               cp  trestbps   chol    fbs  \
14    52      Cleveland      non-anginal     172.0  199.0   True
48    65      Cleveland      non-anginal     140.0  417.0   True
83    68      Cleveland      non-anginal     180.0  274.0   True
91    62      Cleveland     asymptomatic     160.0  164.0  False
121   63      Cleveland     asymptomatic     150.0  407.0  False
..   ...            ...              ...       ...    ...    ...
841   74  VA Long Beach     asymptomatic     150.0  258.0   True
854   55  VA Long Beach     asymptomatic     172.0  260.0  False
863   64  VA Long Beach     asymptomatic     134.0  273.0  False
889   57  VA Long Beach  atypical angina     180.0  285.0   True
896   61  VA Long Beach     asymptomatic     190.0  287.0   True

                restecg  thalch  exang  oldpeak  num  sex_Male
14               normal   162.0  False      0.5    0      True
48       lv hypertrophy   157.0  False      0.8    0     False
83       lv hypertrophy   150.0   True      1.6    3      True
91       lv hypertrophy   145.0  False      6.2    3     False
121      lv hypertrophy   154.0  False      4.0    4     False
..                  ...     ...    ...      ...  ...       ...
841  st-t abnormality   130.0   True      4.0    3      True
854            normal    73.0  False      2.0    3      True
863            normal   102.0   True      4.0    4      True
889  st-t abnormality   120.0  False      0.8    1      True
896      lv hypertrophy   150.0   True      2.0    4      True

[217 rows x 12 columns]
```

Since outliers can be useful for determining abnormal medical condition, we won't be removing them from our data.

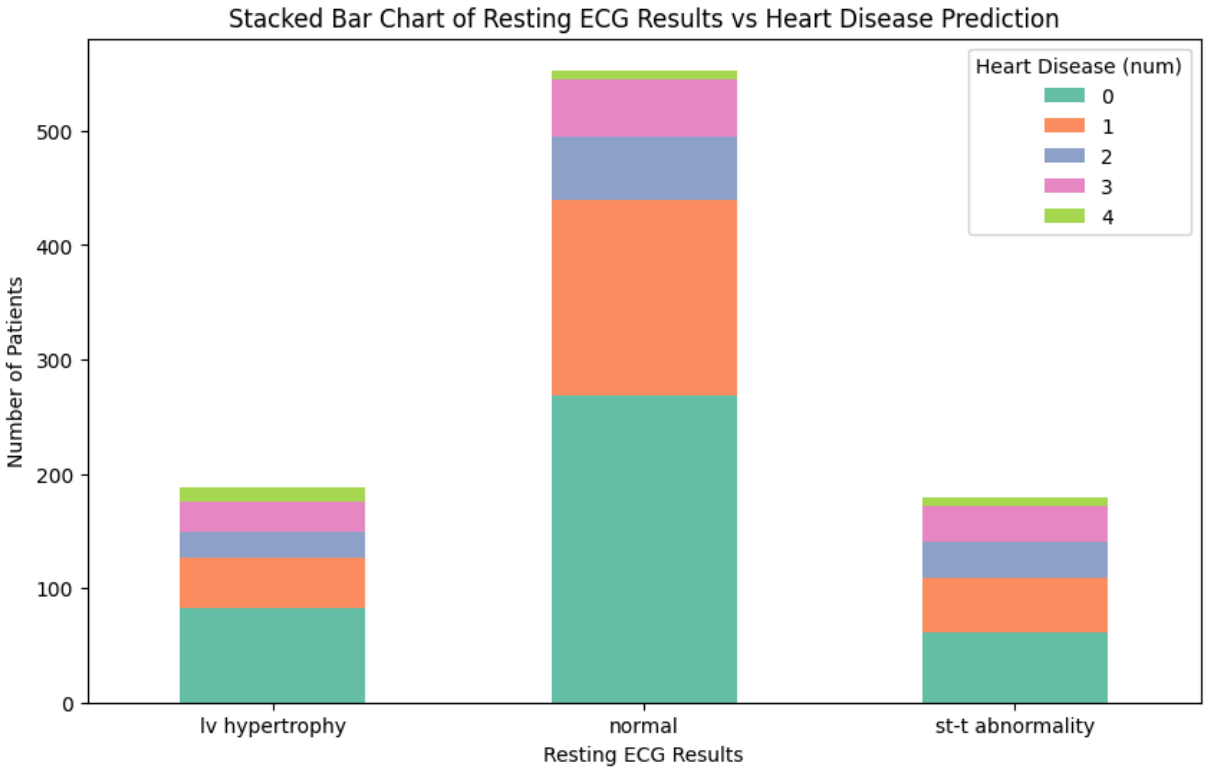
In [ ]:

Multivariate Analysis

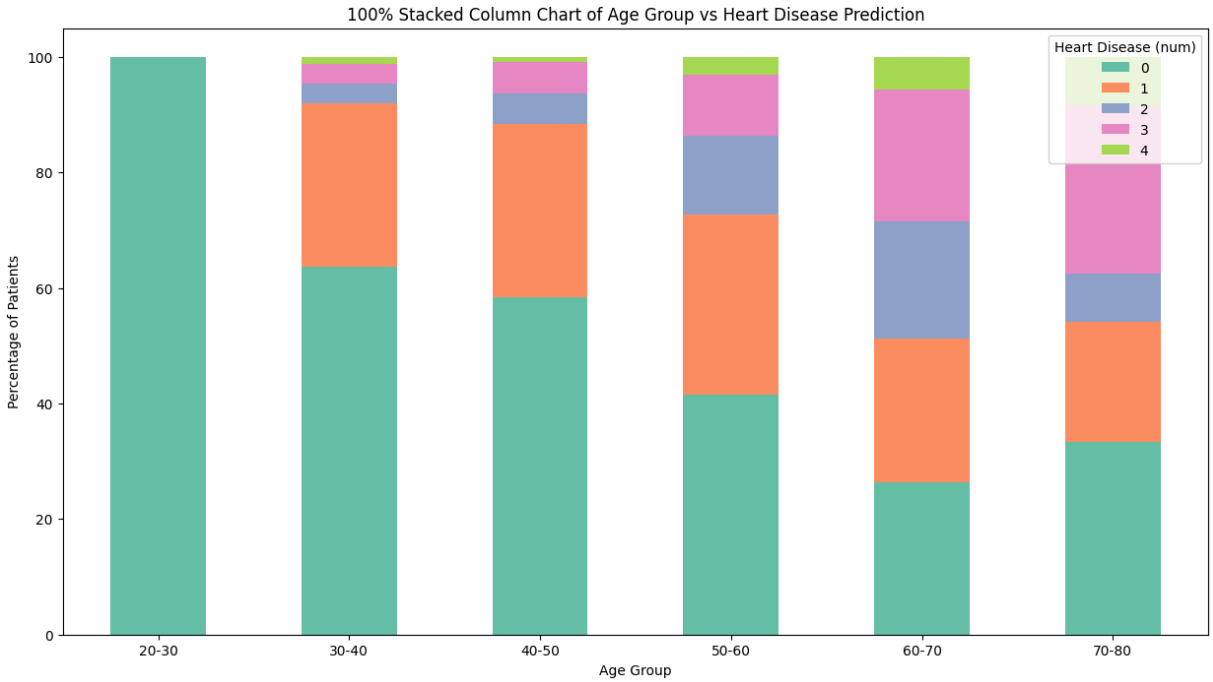
In [20]:
```
# Correlation matrix
corr_matrix = df[['age', 'trestbps', 'chol', 'thalch', 'oldpeak']].corr()

# Heatmap to visualize correlation matrix
plt.figure(figsize=(12, 8))
sns.heatmap(corr_matrix, annot=True, cmap="coolwarm", fmt='.2f', linewidths=
plt.title('Correlation Matrix of Numerical Features')
plt.show()
```



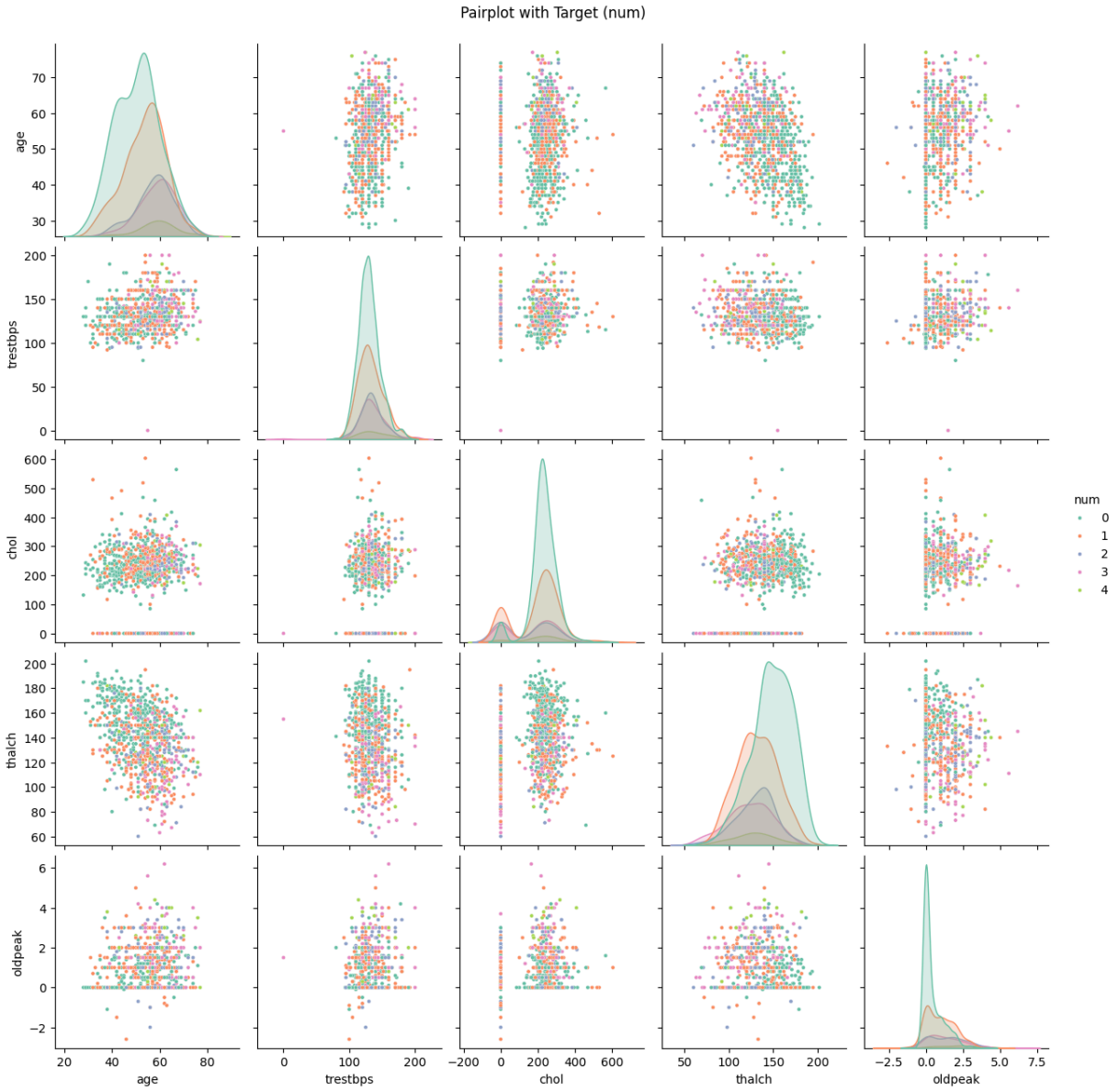
In [34]:
```
# Group by restecg and num to get counts
restecg_vs_num = df.groupby(['restecg', 'num']).size().unstack()

colors = sns.color_palette("Set2")
# Plot stacked column chart
restecg_vs_num.plot(kind='bar', stacked=True, figsize=(10, 6), color=colors)

# Add labels and title
plt.xlabel('Resting ECG Results')
plt.ylabel('Number of Patients')
plt.title('Stacked Bar Chart of Resting ECG Results vs Heart Disease Predict
plt.legend(title='Heart Disease (num)', loc='upper right')
plt.xticks(rotation=0)  # Ensure the x-axis labels are horizontal

# Display the chart
plt.show()
```



In [33]:
```
# import pandas as pd
# import matplotlib.pyplot as plt

# Bin the age column into intervals (e.g., 30-40, 40-50, etc.)
age_bins = [20, 30, 40, 50, 60, 70, 80]
age_labels = ['20-30', '30-40', '40-50', '50-60', '60-70', '70-80']
df['age_group'] = pd.cut(df['age'], bins=age_bins, labels=age_labels)

# Group by age group and num to get counts
age_vs_num = df.groupby(['age_group', 'num'], observed=False).size().unstack

# Convert to percentages (100% stacked)
age_vs_num_percentage = age_vs_num.div(age_vs_num.sum(axis=1), axis=0) * 100

# Plot the 100% stacked column chart
age_vs_num_percentage.plot(kind='bar', stacked=True, figsize=(15, 8), color=

# Add labels and title
plt.xlabel('Age Group')
plt.ylabel('Percentage of Patients')
plt.title('100% Stacked Column Chart of Age Group vs Heart Disease Predictio
plt.legend(title='Heart Disease (num)', loc='upper right')
plt.xticks(rotation=0)

# Display the chart
plt.show()
```

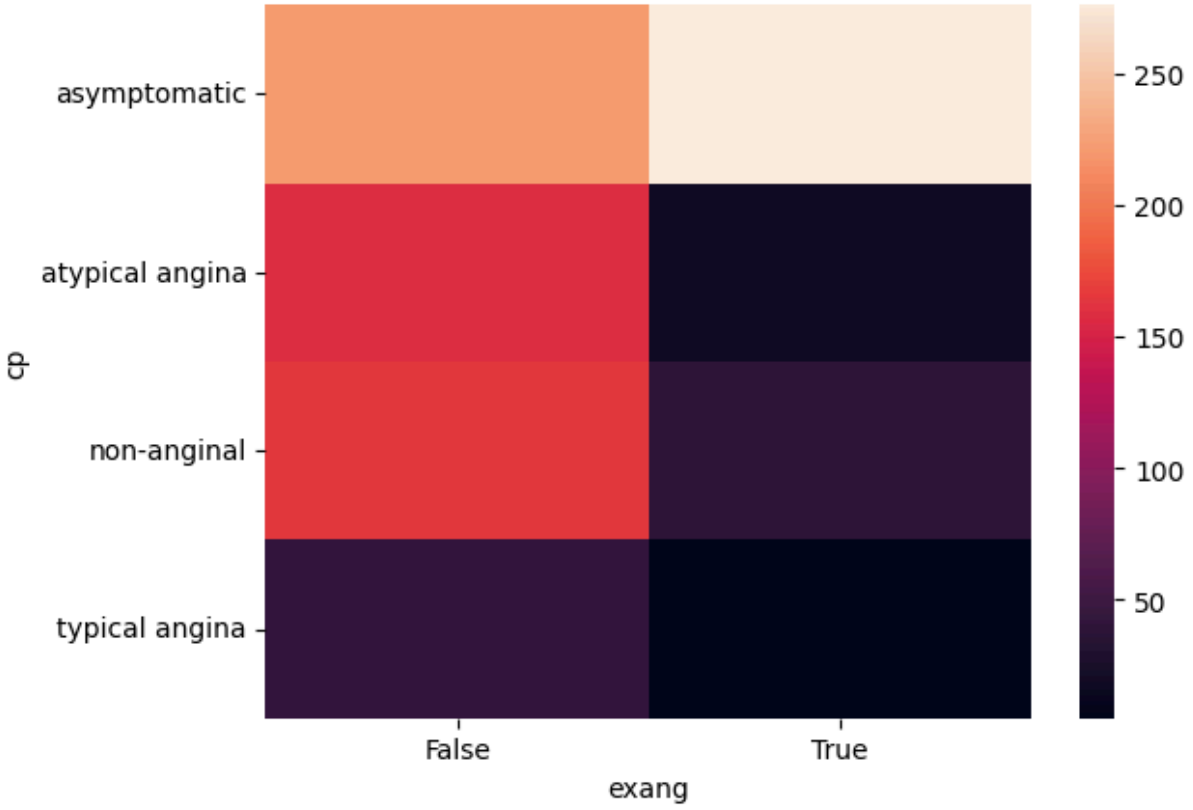


In [23]:
```
# Pairplot for selected features with 'num' as hue
sns.pairplot(df[['age', 'trestbps', 'chol', 'thalch', 'oldpeak', 'num']], hu
plt.suptitle('Pairplot with Target (num)', y=1.02)
plt.show()
```



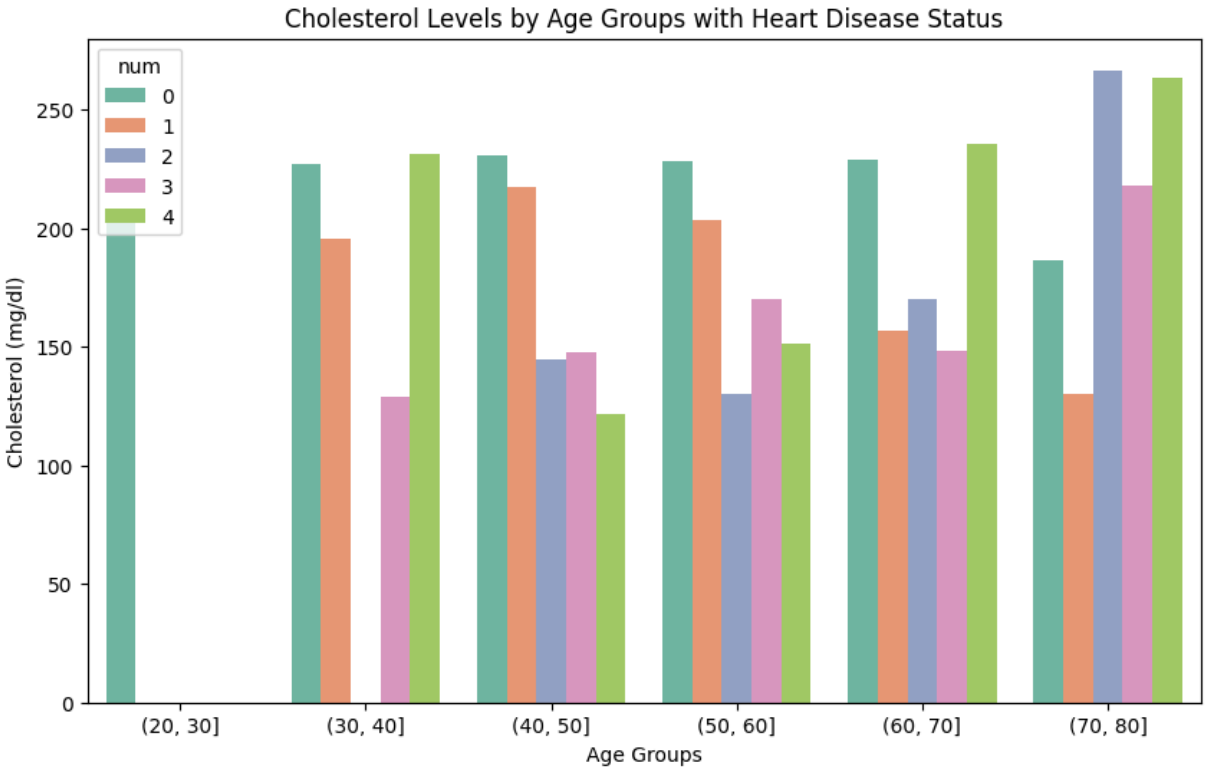
In [24]:
```
sns.heatmap(pd.crosstab(df.cp, df.exang))
```

Out[24]: <Axes: xlabel='exang', ylabel='cp'>



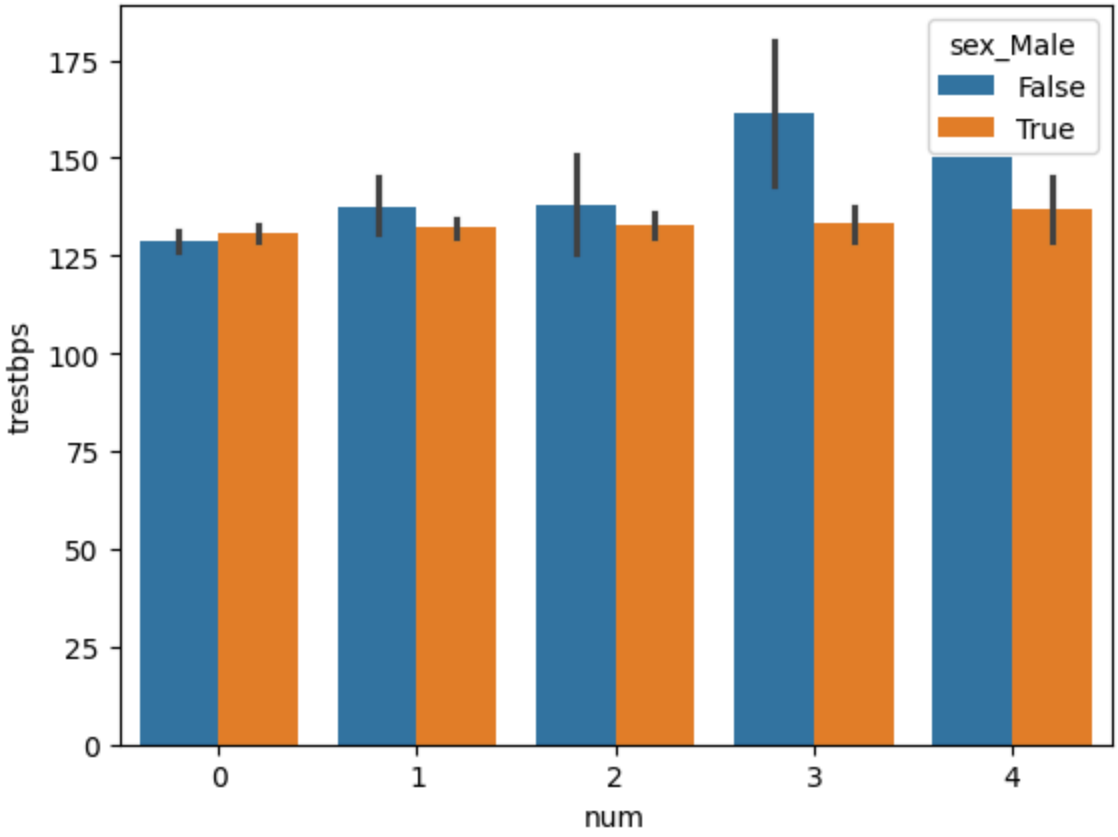
In [ ]:

In [35]:
```
# Create age bins
age_bins = pd.cut(df['age'], bins=[20, 30, 40, 50, 60, 70, 80])
df['age_bins'] = age_bins

# Plot bar chart of cholesterol vs age bins with hue as 'num'
plt.figure(figsize=(10, 6))
sns.barplot(x='age_bins', y='chol', hue='num', data=df, palette='Set2', erro

# Set plot labels and title
plt.title('Cholesterol Levels by Age Groups with Heart Disease Status')
plt.xlabel('Age Groups')
plt.ylabel('Cholesterol (mg/dl)')

# Show the plot
plt.show()
```

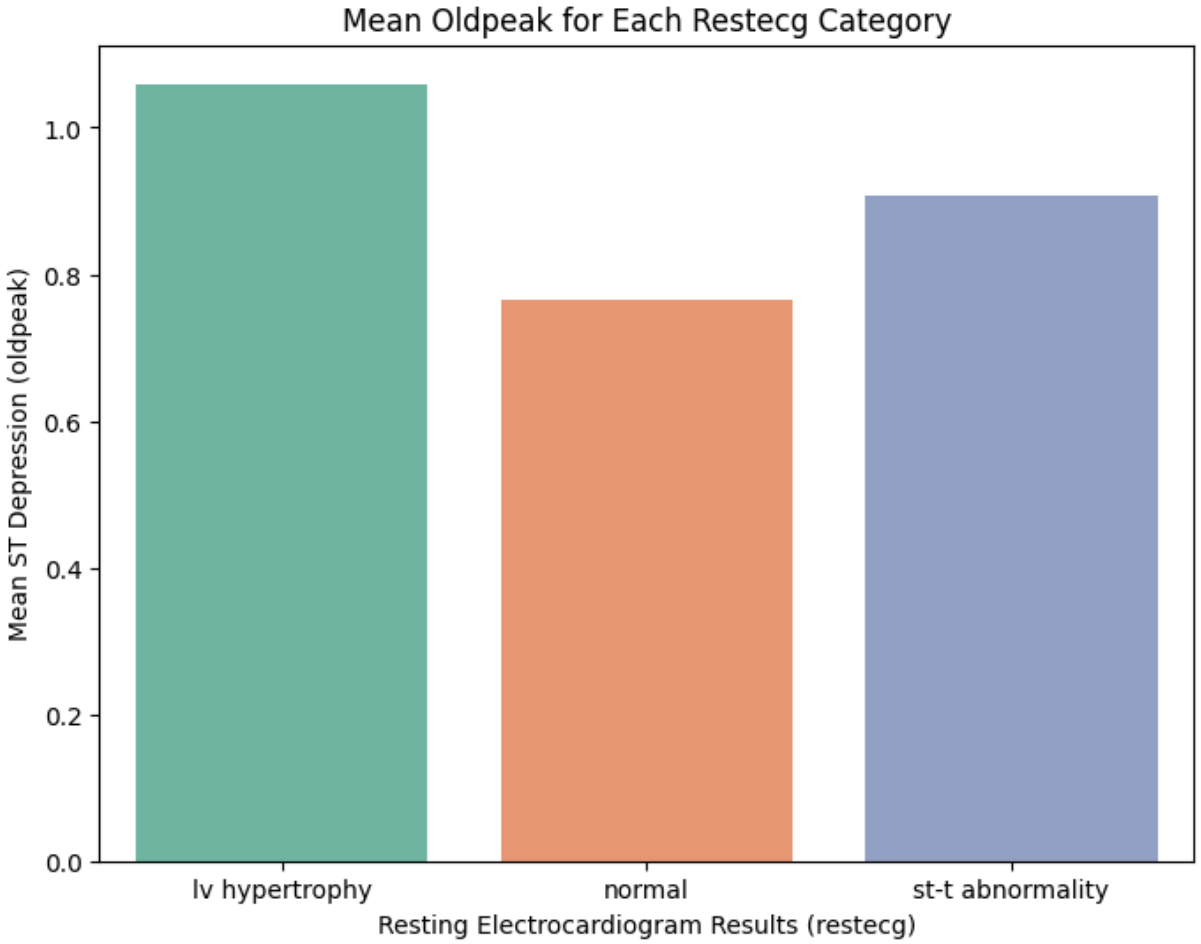


In [26]:
```
sns.barplot(data=df, x='num', y='trestbps', hue='sex_Male')
# plt.legend(labels=['Female','Male'])
```

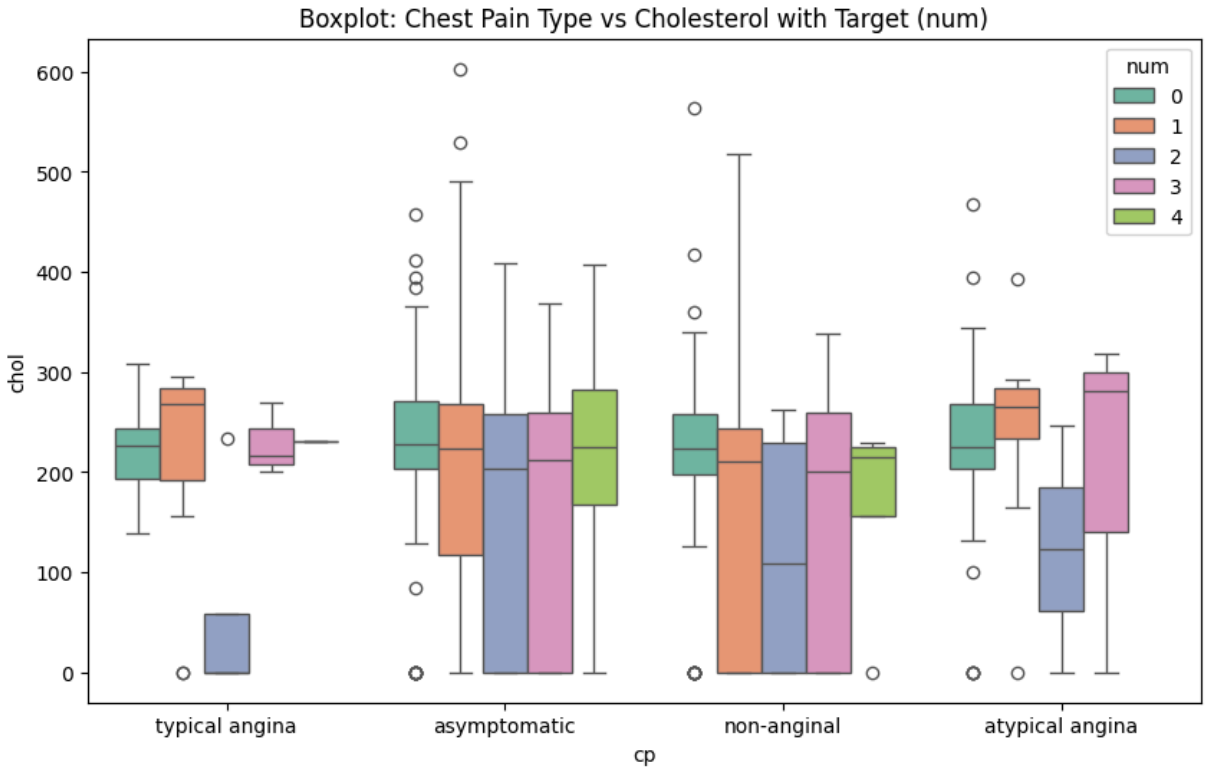
Out[26]: <Axes: xlabel='num', ylabel='trestbps'>



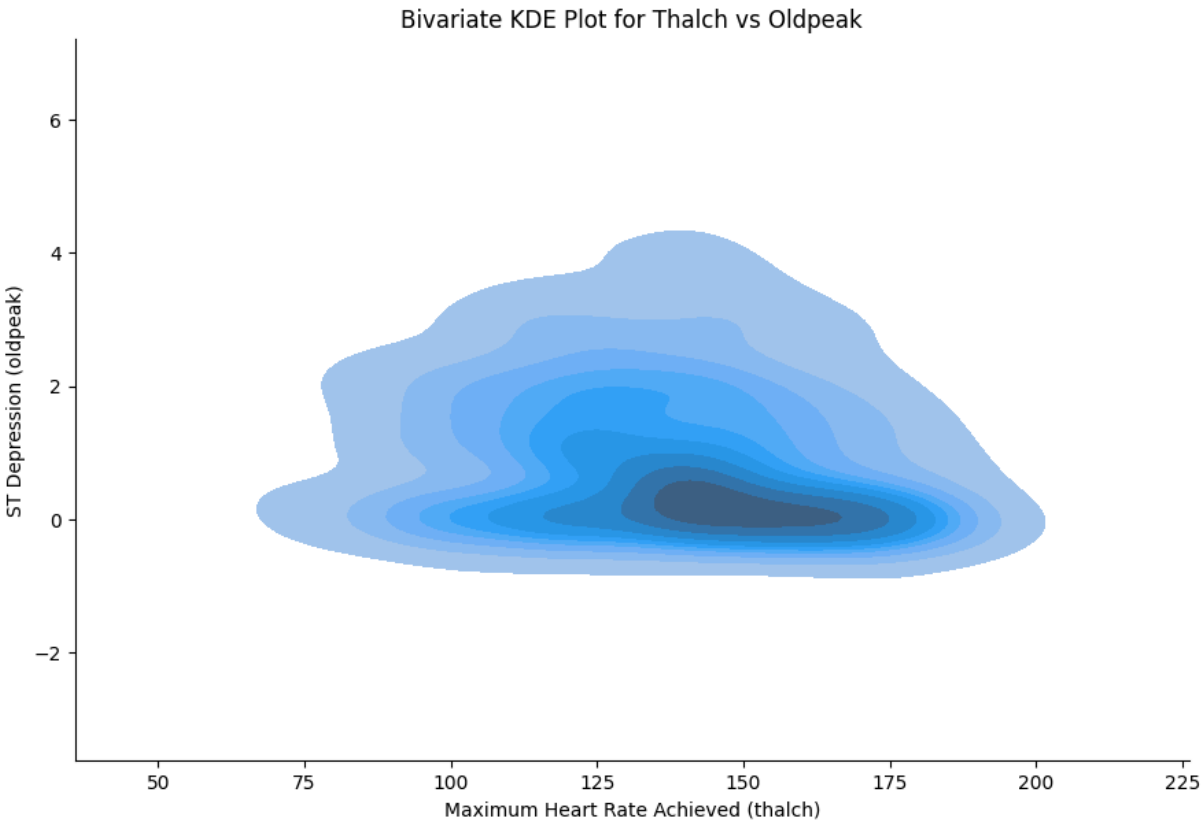
In [36]:
```
# Group the data by 'restecg' and calculate the mean of 'oldpeak'
mean_oldpeak = df.groupby('restecg')['oldpeak'].mean().reset_index()

# Plot a bar graph
plt.figure(figsize=(8, 6))
sns.barplot(x='restecg', y='oldpeak', hue='restecg', data=mean_oldpeak, pale

# Set plot labels and title
plt.title('Mean Oldpeak for Each Restecg Category')
plt.xlabel('Resting Electrocardiogram Results (restecg)')
plt.ylabel('Mean ST Depression (oldpeak)')

# Show the plot
plt.show()
```



In [28]:
```
# Boxplot of 'cp' vs 'chol' colored by 'num'
plt.figure(figsize=(10, 6))
sns.boxplot(x='cp', y='chol', hue='num', data=df, palette='Set2')
plt.title('Boxplot: Chest Pain Type vs Cholesterol with Target (num)')
plt.show()
```



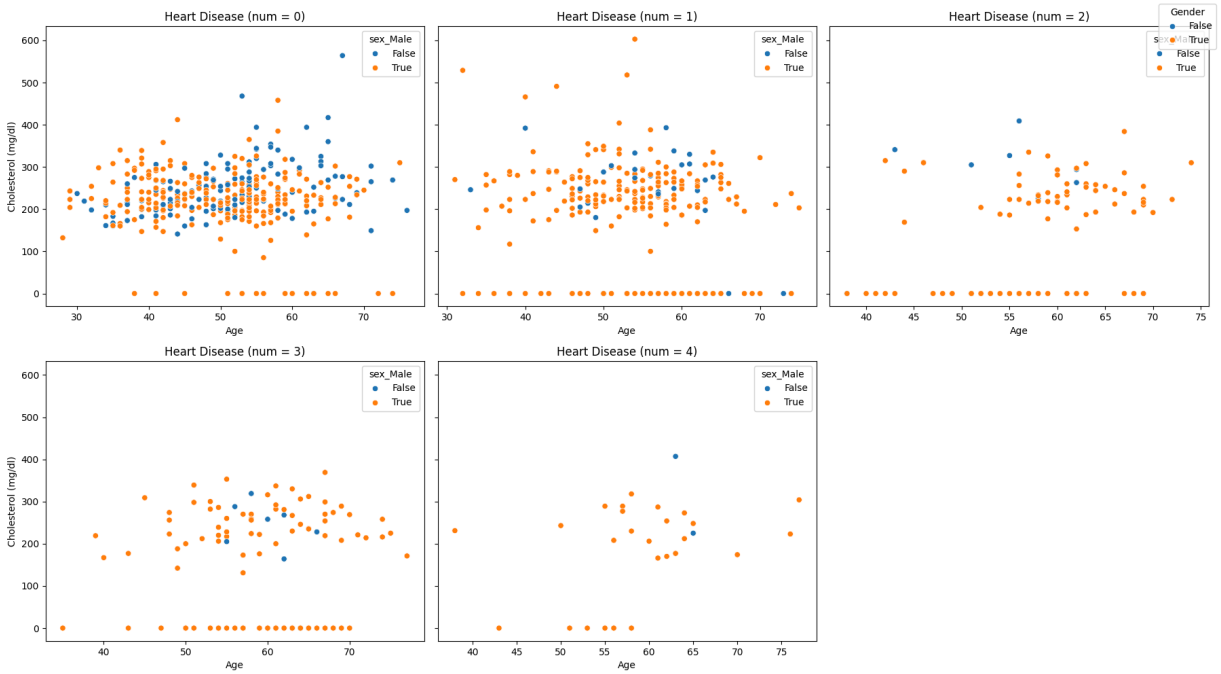
In [29]:
```
# Create a displot for thalch vs oldpeak using a bivariate KDE plot
sns.displot(df, x='thalch', y='oldpeak', kind='kde', aspect=1.5, height=6, f

# Set plot labels and title
plt.title('Bivariate KDE Plot for Thalch vs Oldpeak')
plt.xlabel('Maximum Heart Rate Achieved (thalch)')
plt.ylabel('ST Depression (oldpeak)')

# Show the plot
plt.show()
```



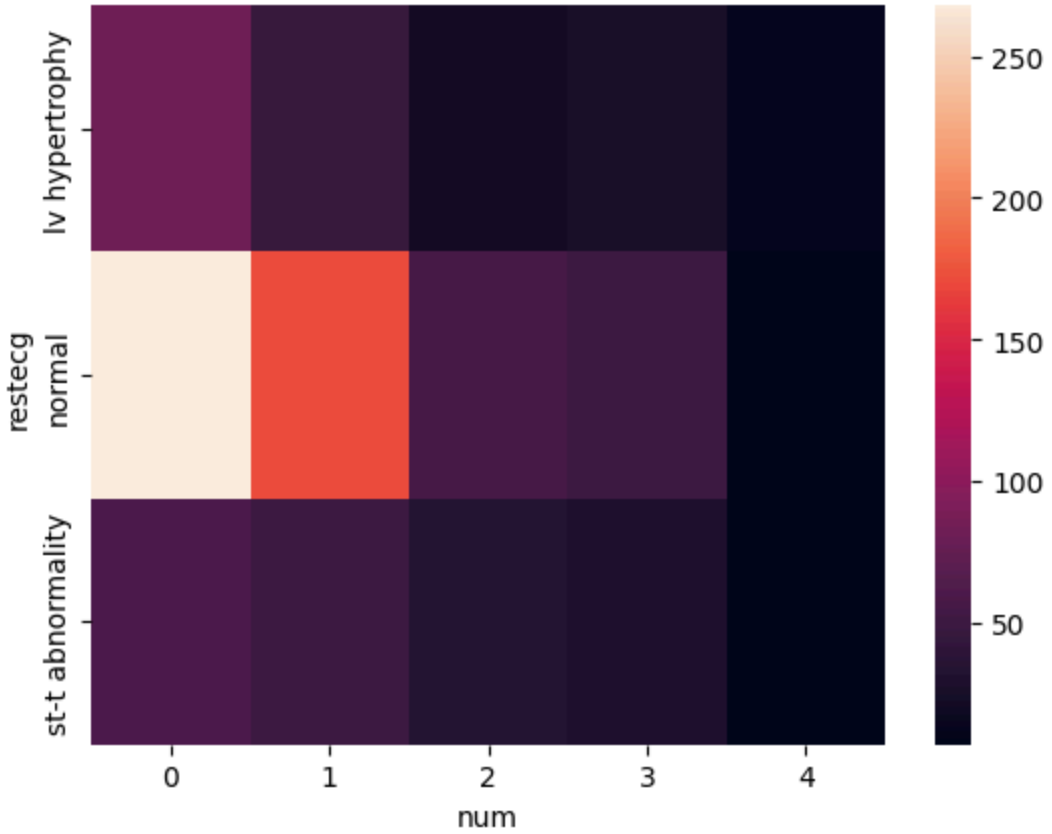
In [30]:

```python
# Create a figure and subplots (2 rows, 3 columns)
fig, axes = plt.subplots(2, 3, figsize=(18, 10), sharey=True)

# Define a color palette for gender
palette = {0: "#1f77b4", 1: "#ff7f0e"}  # Adjust for gender (e.g., 0: Female

# Flatten the axes for easier iteration
axes = axes.flatten()

# Loop through each 'num' value and create a subplot for each
for i, num_val in enumerate(sorted(df['num'].unique())):
    # Filter the data for the current num value
    subset = df[df['num'] == num_val]

    # Create the scatter plot for chol vs age, hue as gender
    sns.scatterplot(data=subset, x='age', y='chol', hue='sex_Male', palette=

    # Set the title for each subplot
    axes[i].set_title(f'Heart Disease (num = {num_val})')
    axes[i].set_xlabel('Age')
    axes[i].set_ylabel('Cholesterol (mg/dl)')

# Hide the last subplot (since we only have 5 plots but 6 spaces)
axes[-1].axis('off')

# Set a common legend for all subplots
handles, labels = axes[0].get_legend_handles_labels()
fig.legend(handles, labels, loc='upper right', title='Gender')

# Adjust layout
```

```
plt.tight_layout()

# Show the plot
plt.show()
```



In [31]:
```
sns.heatmap(pd.crosstab(df.restecg, df.num))
plt.show()
```



In [ ]:

Observed Patterns and Conclusions

- The age distribution shows that most patients with heart disease are middle-aged or elderly. Heart disease risk increases with age, with a noticeable concentration of cases in patients above 50 years old.
- Asymptomatic chest pain is the most prevalent type among heart disease patients, suggesting that many patients do not experience the classic symptoms of angina, and yet they have heart conditions.
- A notable portion of patients with heart disease experience exercise-induced angina, suggesting that physical exertion tends to bring out symptoms of heart disease. Patients who experience this are more likely to be in more advanced stages of heart disease.
- Both resting blood pressure and cholesterol levels show considerable variation, but the presence of outliers suggests some patients have abnormally high levels. Elevated blood pressure and cholesterol are well-known risk factors for heart disease.
- Higher cholesterol levels generally correlate with the presence of heart disease. While some patients with lower cholesterol levels also show signs of heart disease, most high-cholesterol patients in the dataset have heart disease.
- Patients with high resting blood pressure and exercise-induced angina are at a significantly increased risk for heart disease. These patients may require closer monitoring and more aggressive intervention to manage their heart conditions

In [ ]: