# heart-disease-analysis

October 27, 2024

# 1 Heart Disease Analysis

## 1.1 1. Import the libraries and dataset

[24]:

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# Download the heart disease dataset from Kaggle (if not already downloaded)
!wget https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset/
 ↪download?version=1 -O heart.csv

# Read the CSV file into a pandas DataFrame
data = pd.read_csv("/content/drive/MyDrive/Data Analysis/Python Project/Heart␣
 ↪Disease/heart.csv")
```

```
--2024-10-27 17:35:44--  https://www.kaggle.com/datasets/johnsmith88/heart-
disease-dataset/download?version=1
Resolving www.kaggle.com (www.kaggle.com)… 35.244.233.98
Connecting to www.kaggle.com (www.kaggle.com)|35.244.233.98|:443… connected.
HTTP request sent, awaiting response… 302 Found
Location: /account/login?titleType=dataset-downloads&showDatasetDownloadSkip=Fal
se&messageId=datasetsWelcome&returnUrl=%2Fdatasets%2Fjohnsmith88%2Fheart-
disease-dataset%3Fresource%3Ddownload [following]
--2024-10-27 17:35:45--  https://www.kaggle.com/account/login?titleType=dataset-
downloads&showDatasetDownloadSkip=False&messageId=datasetsWelcome&returnUrl=%2Fd
atasets%2Fjohnsmith88%2Fheart-disease-dataset%3Fresource%3Ddownload
Reusing existing connection to www.kaggle.com:443.
HTTP request sent, awaiting response… 200 OK
Length: unspecified [text/html]
Saving to: ‘heart.csv’

heart.csv               [ <=>                ]   4.84K  --.-KB/s    in 0s

2024-10-27 17:35:45 (11.4 MB/s) - ‘heart.csv’ saved [4961]
```

*We import the necessary libraries: pandas for data manipulation, matplotlib.pyplot for basic plotting, and seaborn for advanced visualizations.* We download the heart disease dataset from Kaggle using wget (assuming you have it installed). If you already have the dataset, replace the wget command with the path to your CSV file. *We read the CSV data into a DataFrame

named data.

#Displaying Top and Last Rows

```
[25]: print("Top 5 rows:")
      data.head(5)
```

```
      Top 5 rows:

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

         ca  thal  target
      0   2     3       0
      1   0     3       0
      2   0     3       0
      3   1     3       0
      4   3     2       0
```

```
[26]: print("\nLast 5 rows:")
      data.tail(5)
```

```

      Last 5 rows:

[26]:       age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  \
      1020   59    1   1       140   221    0        1      164      1      0.0
      1021   60    1   0       125   258    0        0      141      1      2.8
      1022   47    1   0       110   275    0        0      118      1      1.0
      1023   50    0   0       110   254    0        0      159      0      0.0
      1024   54    1   0       120   188    0        1      113      0      1.4

            slope  ca  thal  target
      1020      2   0     2       1
      1021      1   1     3       0
      1022      1   1     2       0
      1023      2   0     2       1
      1024      1   1     3       0
```

- Top 5 Rows:
- This provides a glimpse into the initial data points. We can observe:

- Age: Ranging from 52 to 62.
- Sex: Primarily male (1).
- Chest Pain Type (CP): All instances are 0, indicating typical angina.
- Resting Blood Pressure (trestbps): Values between 125 and 148 mmHg.
- Cholesterol (chol): Levels ranging from 203 to 294 mg/dl.
- Fasting Blood Sugar (fbs): Most are 0, indicating fasting blood sugar is less than 120 mg/dl.
- Resting Electrocardiographic Results (restecg): Primarily 1, suggesting ST-T wave abnormality.
- Maximum Heart Rate Achieved (thalach): Values between 106 and 168 bpm.
- Exercise-Induced Angina (exang): Mostly 0, indicating no exercise-induced angina. ST Depression Induced by Exercise
- Relative to Rest (oldpeak): Values between 0 and 3.1. Slope of the Peak Exercise ST Segment (slope): Values 1 and 2.
- Number of Major Vessels (ca): Ranging from 0 to 3.
- Thalassemia (thal): Primarily 3, indicating normal.
- Target: All 0, suggesting a lower chance of heart attack.
- Last 5 Rows:
- A look at the final data points reveals:
- Sex: Both male and female are present.
- Chest Pain Type (CP): A mix of 0 and 1.
- Resting Blood Pressure (trestbps):
- Values between 110 and 140 mmHg.
- Cholesterol (chol): Levels ranging from 188 to 275 mg/dl.
- Fasting Blood Sugar (fbs): All 0.
- Resting Electrocardiographic Results (restecg): A mix of 0 and 1.
- Maximum Heart Rate Achieved (thalach):
- Values between 113 and 164 bpm.
- Exercise-Induced Angina (exang): Both 0 and 1 are present.
- ST Depression Induced by Exercise
- Relative to Rest (oldpeak): Values between 0 and 2.8. Slope of the Peak Exercise ST Segment (slope): Values 1 and 2.
- Number of Major Vessels (ca): Ranging from 0 to 1.
- Thalassemia (thal): Values 2 and 3.

- Target: A mix of 0 and 1, indicating both lower and higher chances of heart attack.
- Overall Observations:
- The dataset appears to contain a mix of individuals with varying heart health conditions.
- There's a range of values for key factors like age, blood pressure, cholesterol, heart rate, and exercise-induced angina.
- The target variable (heart attack risk) seems to be influenced by a combination of these factors.
- Further analysis and modeling can help identify the most significant predictors of heart disease risk.

#Finding Dataset Shape

[27]:

```python
print("Dataset shape:", data.shape)
print("Number of rows:", data.shape[0])
print("Number of columns:", data.shape[1])
```

```
Dataset shape: (1025, 14)
Number of rows: 1025
Number of columns: 14
```

#Getting Dataset Information

[28]:

```python
data.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
```

#Checking for Null Values

[29]:

```
print("Number of missing values in each column:")
data.isnull().sum()

# If there are missing values, handle them (e.g., impute or drop rows)
```

```
Number of missing values in each column:
```

[29]:

```
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
```

#Checking for Duplicate Data

[30]:

```
has_duplicates = data.duplicated().any()
print("Dataset contains duplicates:", has_duplicates)

if has_duplicates:
    # Remove duplicates
    data = data.drop_duplicates()
    print("Removed duplicates. New shape:", data.shape)
```

```
Dataset contains duplicates: True
Removed duplicates. New shape: (302, 14)
```

#Calculating Descriptive Statistics

[31]:

```
data.describe()
```

[31]:

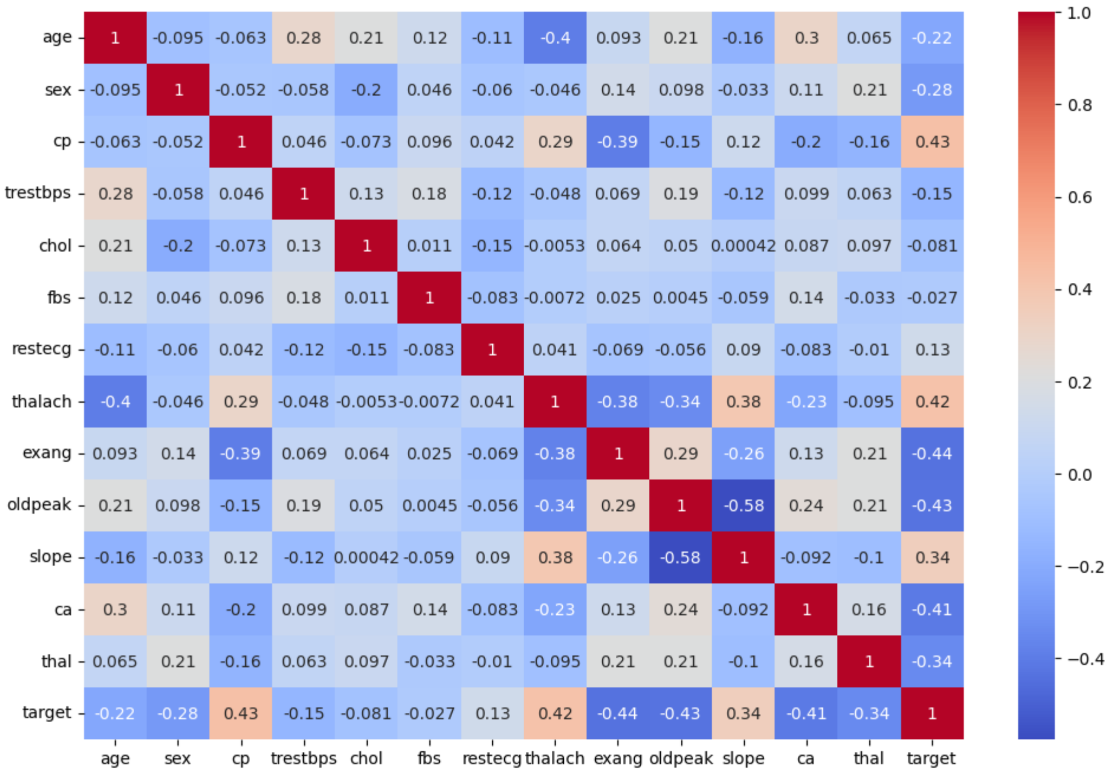
```
             age         sex          cp    trestbps        chol         fbs  \
count  302.00000  302.000000  302.000000  302.000000  302.000000  302.000000
mean    54.42053    0.682119    0.963576  131.602649  246.500000    0.149007
std      9.04797    0.466426    1.032044   17.563394   51.753489    0.356686
min     29.00000    0.000000    0.000000   94.000000  126.000000    0.000000
25%     48.00000    0.000000    0.000000  120.000000  211.000000    0.000000
50%     55.50000    1.000000    1.000000  130.000000  240.500000    0.000000
75%     61.00000    1.000000    2.000000  140.000000  274.750000    0.000000
```

```
max     77.00000    1.000000    3.000000  200.000000  564.000000    1.000000

         restecg     thalach       exang     oldpeak       slope          ca  \
count 302.000000  302.000000  302.000000  302.000000  302.000000  302.000000
mean    0.526490  149.569536    0.327815    1.043046    1.397351    0.718543
std     0.526027   22.903527    0.470196    1.161452    0.616274    1.006748
min     0.000000   71.000000    0.000000    0.000000    0.000000    0.000000
25%     0.000000  133.250000    0.000000    0.000000    1.000000    0.000000
50%     1.000000  152.500000    0.000000    0.800000    1.000000    0.000000
75%     1.000000  166.000000    1.000000    1.600000    2.000000    1.000000
max     2.000000  202.000000    1.000000    6.200000    2.000000    4.000000

            thal      target
count 302.000000  302.000000
mean    2.314570    0.543046
std     0.613026    0.498970
min     0.000000    0.000000
25%     2.000000    0.000000
50%     2.000000    1.000000
75%     3.000000    1.000000
max     3.000000    1.000000
```

#Correlation Matrix

[32]:

```
plt.figure(figsize=(12, 8))
sns.heatmap(data.corr(), annot=True, cmap="coolwarm")
plt.show()
```

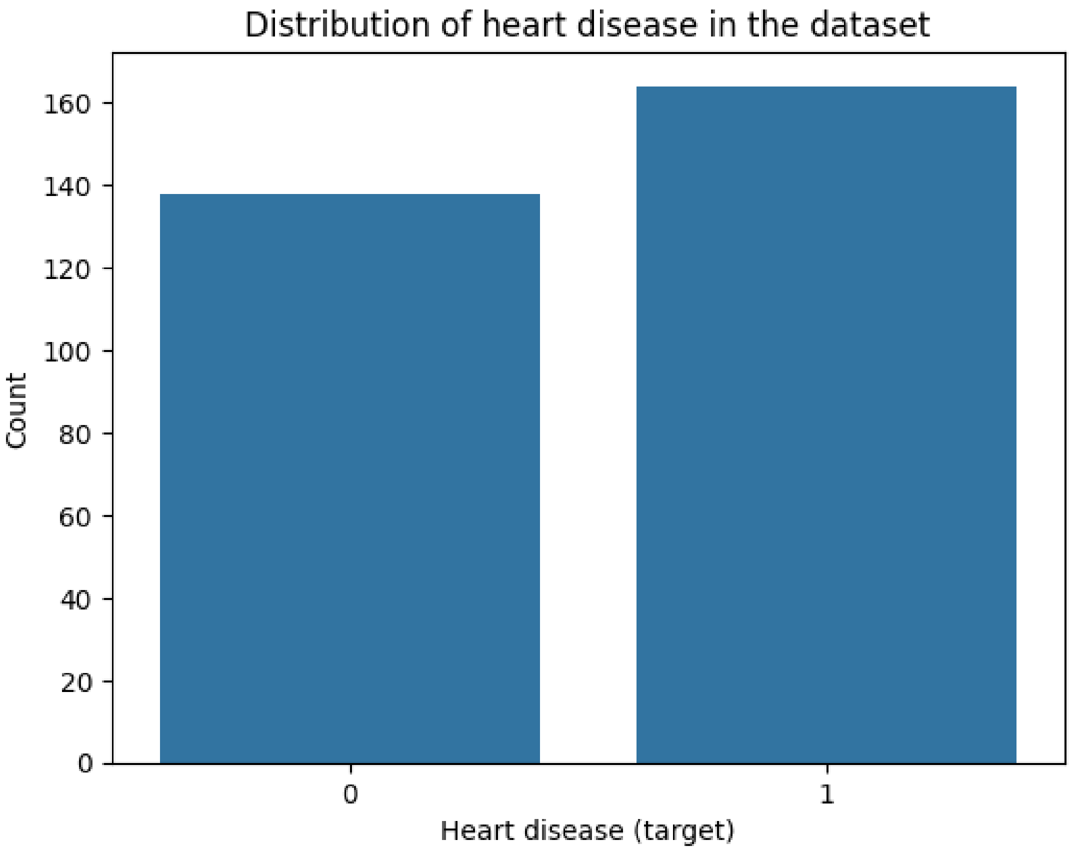


- We create a heatmap using seaborn to visualize the correlation coefficients between all numerical columns in the dataset.
- The heatmap shows the strength and direction of the relationships between variables, which can be helpful for feature selection and model building.

#Number of People with/without Heart Disease

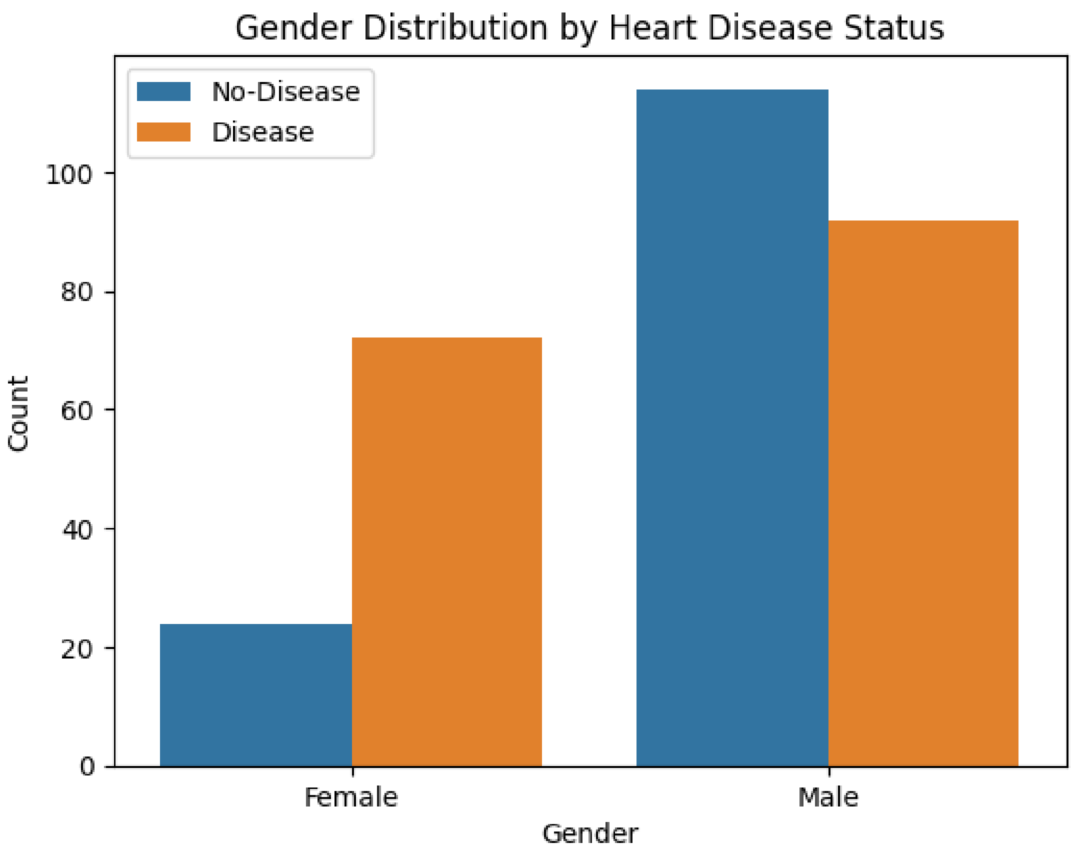
[40]:
```
print("Number of people with heart disease (target=1):", data["target"].
  ↪value_counts()[1])
print("Number of people without heart disease (target=0):", data["target"].
  ↪value_counts()[0])

# Alternatively, visualize with a count plot
sns.countplot(x="target", data=data)
plt.xlabel("Heart disease (target)")
plt.ylabel("Count")
plt.title("Distribution of heart disease in the dataset")
plt.show()
```

```
Number of people with heart disease (target=1): 164
Number of people without heart disease (target=0): 138
```



#Find Gender Distribution According to The Target Variable

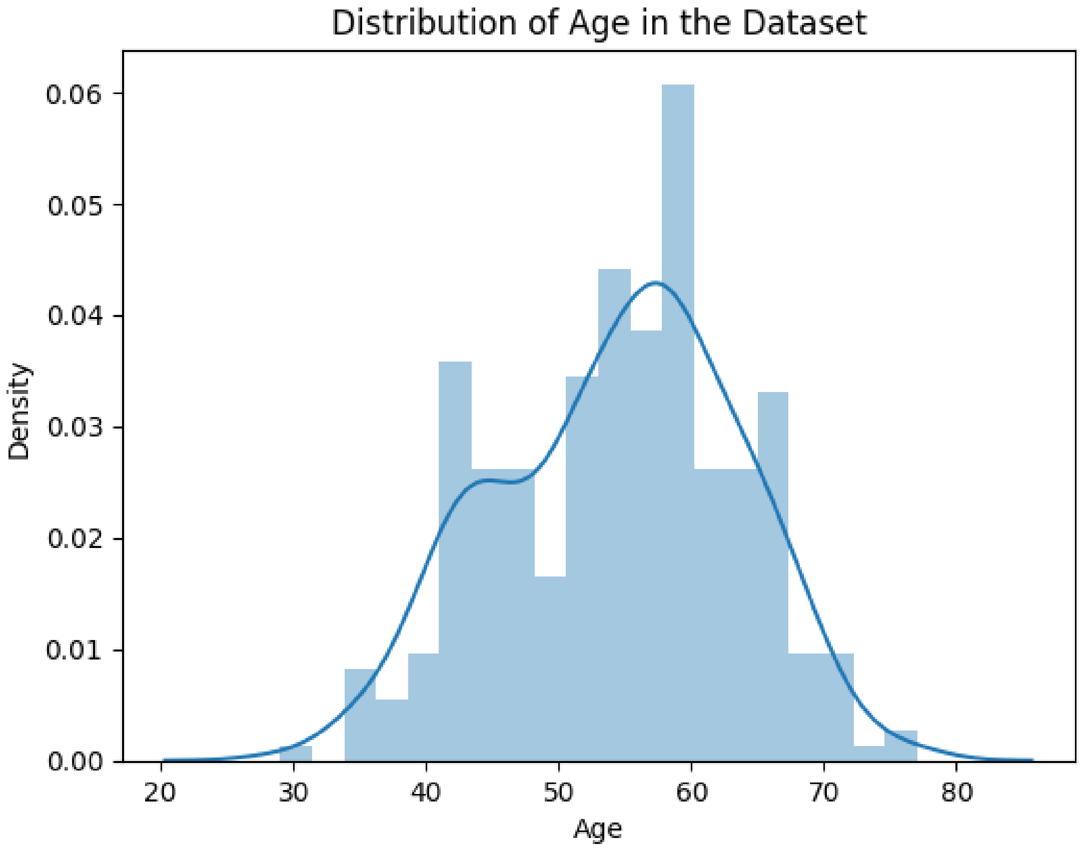
```
[34]: sns.countplot(x='sex', hue='target', data=data)
plt.xticks([1, 0], ['Male', 'Female'])
plt.legend(labels=['No-Disease', 'Disease'])
plt.xlabel("Gender")
plt.ylabel("Count")
plt.title("Gender Distribution by Heart Disease Status")
plt.show()
```



#Check Age Distribution In The Dataset

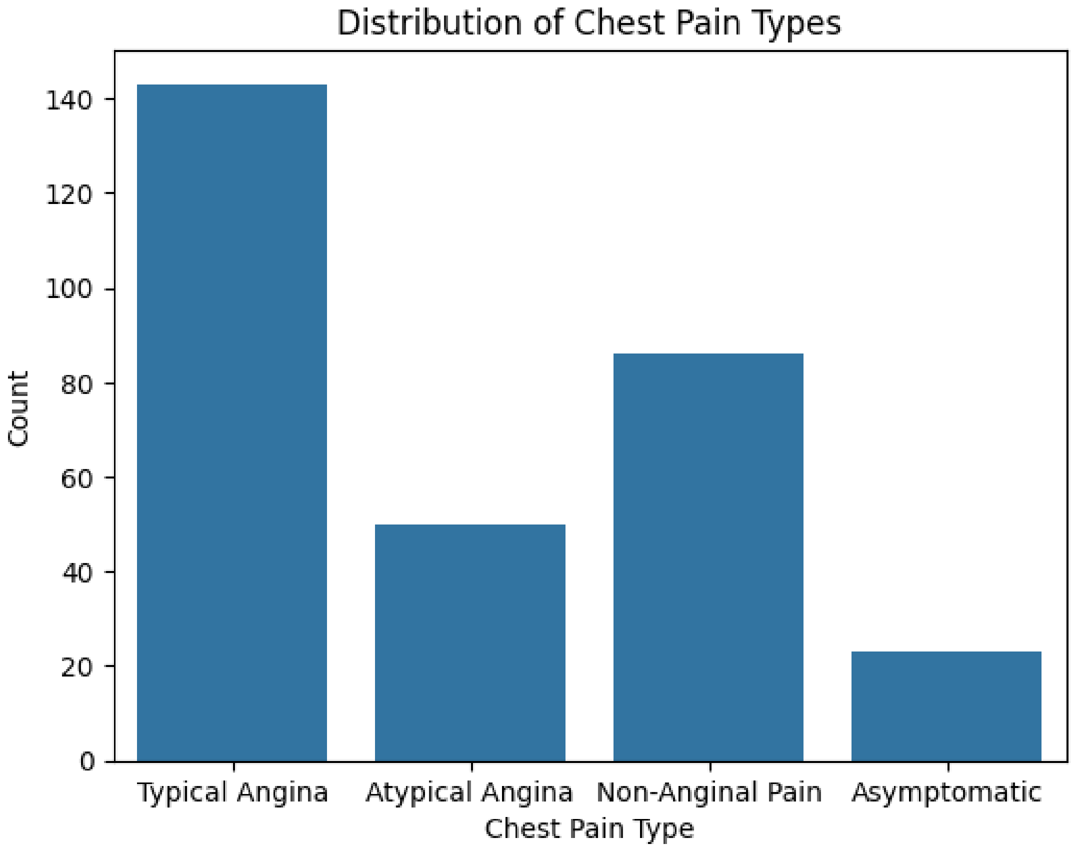
```
[41]: sns.distplot(data['age'], bins=20)
      plt.xlabel("Age")
      plt.ylabel("Density")
      plt.title("Distribution of Age in the Dataset")
      plt.show()
```

```
<ipython-input-41-71c185254c74>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(data['age'], bins=20)
```



#Which Check Chest Pain Type is More Common

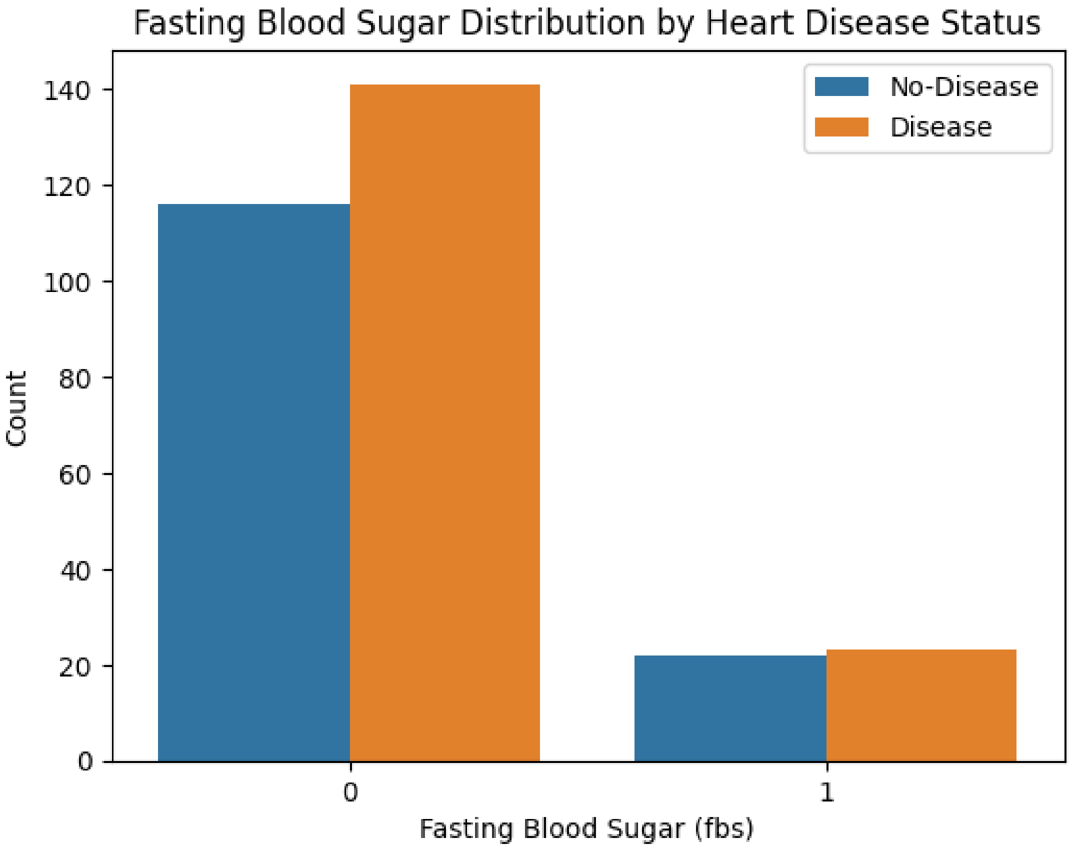
```
[42]: sns.countplot(x=data['cp'])
      plt.xticks([0, 1, 2, 3], ["Typical Angina", "Atypical Angina", "Non-Anginal␣
       ↪Pain", "Asymptomatic"])
      plt.xticks(rotation=0)
      plt.xlabel("Chest Pain Type")
      plt.ylabel("Count")
      plt.title("Distribution of Chest Pain Types")
      plt.show()
```



#Show The Chest Pain Distribution As Per Target Variable

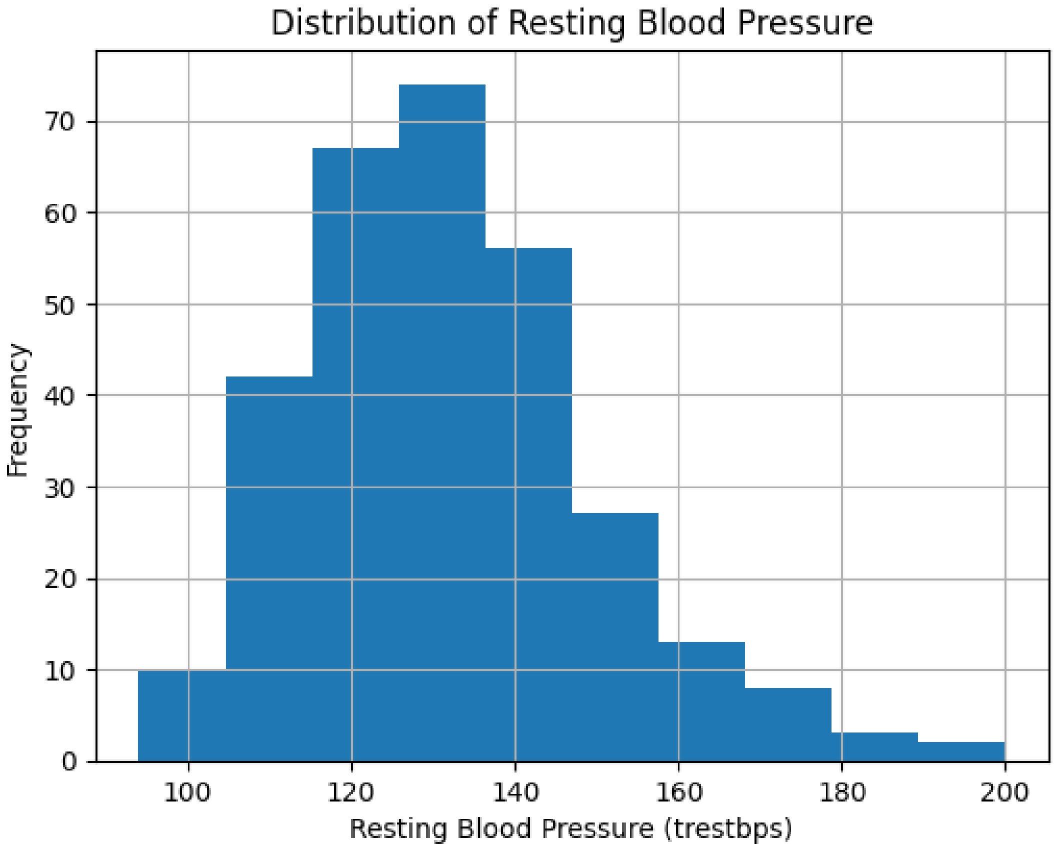
[43]:

```
sns.countplot(x='fbs', hue='target', data=data)
plt.legend(labels=['No-Disease', 'Disease'])
plt.xlabel("Fasting Blood Sugar (fbs)")
plt.ylabel("Count")
plt.title("Fasting Blood Sugar Distribution by Heart Disease Status")
plt.show()
```



#Check Resting Blood Pressure Distribution

[44]:
```
data['trestbps'].hist()
plt.xlabel("Resting Blood Pressure (trestbps)")
plt.ylabel("Frequency")
plt.title("Distribution of Resting Blood Pressure")
plt.show()
```

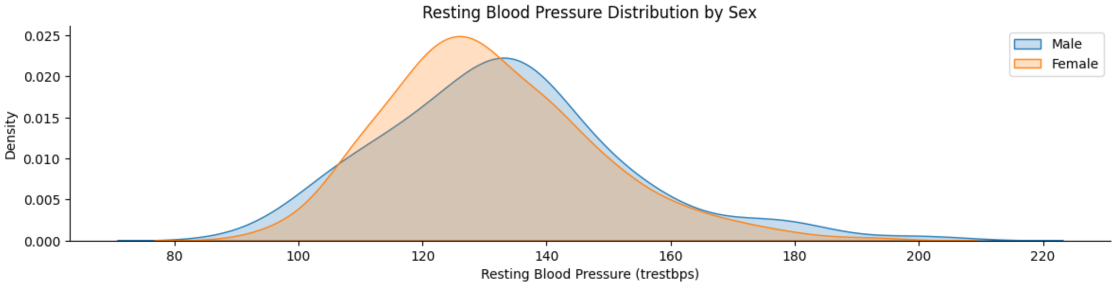


#Compare Resting Blood Pressure As Per Sex Column

```
[45]: g = sns.FacetGrid(data, hue="sex", aspect=4)
g.map(sns.kdeplot, 'trestbps', shade=True)
plt.legend(labels=['Male', 'Female'])
plt.xlabel("Resting Blood Pressure (trestbps)")
plt.ylabel("Density")
plt.title("Resting Blood Pressure Distribution by Sex")
plt.show()
```

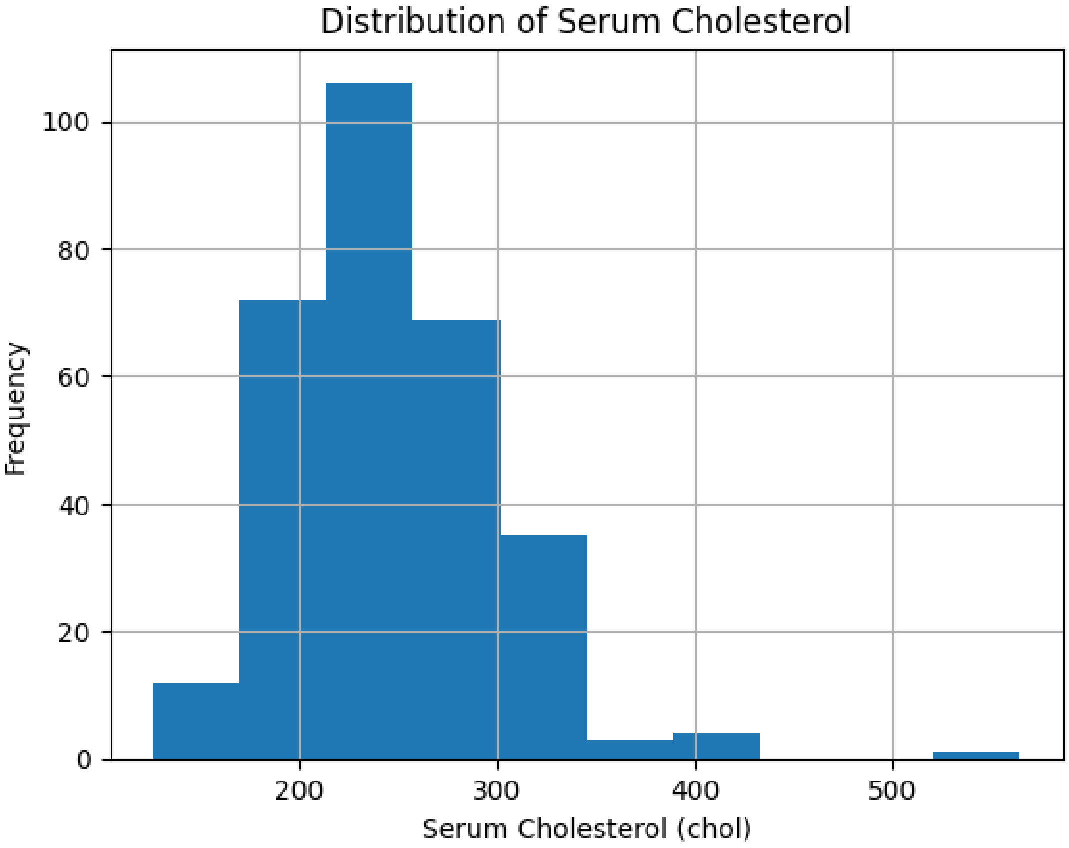
```
/usr/local/lib/python3.10/dist-packages/seaborn/axisgrid.py:854: FutureWarning:

`shade` is now deprecated in favor of `fill`; setting `fill=True`.
This will become an error in seaborn v0.14.0; please update your code.

  func(*plot_args, **plot_kwargs)
/usr/local/lib/python3.10/dist-packages/seaborn/axisgrid.py:854: FutureWarning:

`shade` is now deprecated in favor of `fill`; setting `fill=True`.
This will become an error in seaborn v0.14.0; please update your code.
```

```
func(*plot_args, **plot_kwargs)
```



#Show Distribution of Serum Cholesterol

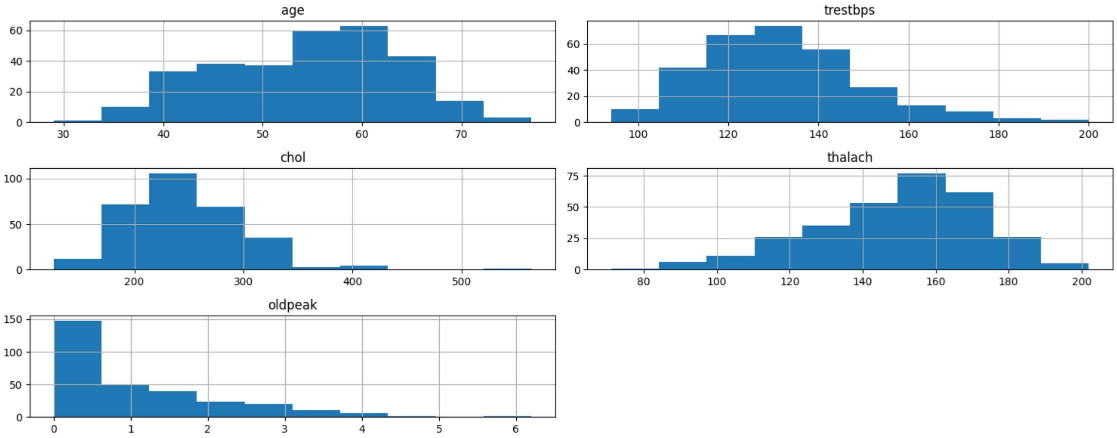
```
[46]: data['chol'].hist()
plt.xlabel("Serum Cholesterol (chol)")
plt.ylabel("Frequency")
plt.title("Distribution of Serum Cholesterol")
plt.show()
```



#Plot Continuous Variables

[47]:

```
categorical_cols = [col for col in data.columns if data[col].nunique() <= 10]
continuous_cols = [col for col in data.columns if col not in categorical_cols]

data.hist(continuous_cols, figsize=(15, 6))
plt.tight_layout()
plt.show()
```


age
trestbps
chol
thalach
oldpeak