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Dataset: Heart Disease (UCI Machine Learning Repository)

Task 1: Data Acquisition

In [1]: *# Task 1.1 & 1.2: Install and import necessary libraries for dataset download and D*

```
%pip install ucimlrepo

from ucimlrepo import fetch_ucirepo
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
```

Requirement already satisfied: ucimlrepo in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (0.0.7)

Requirement already satisfied: pandas>=1.0.0 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from ucimlrepo) (2.3.0)

Requirement already satisfied: certifi>=2020.12.5 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from ucimlrepo) (2025.4.26)

Requirement already satisfied: numpy>=1.26.0 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from pandas>=1.0.0->ucimlrepo) (2.3.0)

Requirement already satisfied: python-dateutil>=2.8.2 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from pandas>=1.0.0->ucimlrepo) (2.9.0.post0)

Requirement already satisfied: pytz>=2020.1 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from pandas>=1.0.0->ucimlrepo) (2025.2)

Requirement already satisfied: tzdata>=2022.7 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from pandas>=1.0.0->ucimlrepo) (2025.2)

Requirement already satisfied: six>=1.5 in c:\users\admin\appdata\local\programs\python\python313\lib\site-packages (from python-dateutil>=2.8.2->pandas>=1.0.0->ucimlrepo) (1.17.0)

Note: you may need to restart the kernel to use updated packages.

In [2]: *# Task 1.1: Download the dataset - Heart Disease from UCI Repository (ID: 45)*
heart_disease = fetch_ucirepo(id=45)

In [3]: *# Task 1.2: Convert dataset into DataFrame - Separate into features and target*
X = heart_disease.data.features
y = heart_disease.data.targets

In [4]: *# 1.3 Combine into a single DataFrame*
df = pd.concat([X, y], axis=1)

In [5]: *# Rename columns for clarity*
df = df.rename(columns={
 'age': 'Age',
 'sex': 'Sex',
 'cp': 'Chest Pain',

```

'trestbps': 'Blood Pressure',
'chol': 'Cholesterol',
'fbs': 'Blood Sugar',
'restecg': 'Electrocardiograph',
'thalach': 'Heart Rate Achieved',
'exang': 'Angina',
'oldpeak': 'ST Depression',
'slope': 'Peak Exercise ST Segment',
'ca': 'Major Vessels',
'thal': 'Thalassemia',
'num': 'Presence of Heart Disease'
})

```

```

In [6]: # Task 1.3: Display first and last five records to confirm successful Loading
print("First 5 records:")
print(df.head())

```

First 5 records:

	Age	Sex	Chest Pain	Blood Pressure	Cholesterol	Blood Sugar	\
0	63	1	1	145	233	1	
1	67	1	4	160	286	0	
2	67	1	4	120	229	0	
3	37	1	3	130	250	0	
4	41	0	2	130	204	0	

	Electrocardiograph	Heart Rate Achieved	Angina	ST Depression	\
0	2	150	0	2.3	
1	2	108	1	1.5	
2	2	129	1	2.6	
3	0	187	0	3.5	
4	2	172	0	1.4	

	Peak Exercise ST Segment	Major Vessels	Thalassemia	\
0	3	0.0	6.0	
1	2	3.0	3.0	
2	2	2.0	7.0	
3	3	0.0	3.0	
4	1	0.0	3.0	

	Presence of Heart Disease
0	0
1	2
2	1
3	0
4	0

```

In [7]: print("\nLast 5 records:")
print(df.tail())

```

Last 5 records:

	Age	Sex	Chest Pain	Blood Pressure	Cholesterol	Blood Sugar	\
298	45	1	1	110	264	0	
299	68	1	4	144	193	1	
300	57	1	4	130	131	0	
301	57	0	2	130	236	0	
302	38	1	3	138	175	0	

	Electrocardiograph	Heart Rate Achieved	Angina	ST Depression	\
298	0	132	0	1.2	
299	0	141	0	3.4	
300	0	115	1	1.2	
301	2	174	0	0.0	
302	0	173	0	0.0	

	Peak Exercise ST Segment	Major Vessels	Thalassemia	\
298	2	0.0	7.0	
299	2	2.0	7.0	
300	2	1.0	7.0	
301	2	1.0	3.0	
302	1	NaN	3.0	

	Presence of Heart Disease
298	1
299	2
300	3
301	1
302	0

In [8]: *# Task 1.4: Display column headings, statistical information, description, and summ*

```
# Display column headings
print("\nColumn Headings:")
print(df.columns)
```

Column Headings:

```
Index(['Age', 'Sex', 'Chest Pain', 'Blood Pressure', 'Cholesterol',
       'Blood Sugar', 'Electrocardiograph', 'Heart Rate Achieved', 'Angina',
       'ST Depression', 'Peak Exercise ST Segment', 'Major Vessels',
       'Thalassemia', 'Presence of Heart Disease'],
      dtype='object')
```

In [9]: *# Display info and statistics*

```
print("\nData Info:")
df.info()
```

```
Data 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   Chest Pain                            303 non-null    int64
3   Blood Pressure                        303 non-null    int64
4   Cholesterol                           303 non-null    int64
5   Blood Sugar                           303 non-null    int64
6   Electrocardiograph                    303 non-null    int64
7   Heart Rate Achieved                    303 non-null    int64
8   Angina                                303 non-null    int64
9   ST Depression                          303 non-null    float64
10  Peak Exercise ST Segment               303 non-null    int64
11  Major Vessels                          299 non-null    float64
12  Thalassemia                            301 non-null    float64
13  Presence of Heart Disease              303 non-null    int64
dtypes: float64(3), int64(11)
memory usage: 33.3 KB
```

```
In [10]: print("\nDescriptive Statistics (All columns):")
          print(df.describe(include='all'))
```

Descriptive Statistics (All columns):

	Age	Sex	Chest Pain	Blood Pressure	Cholesterol \
count	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.438944	0.679868	3.158416	131.689769	246.693069
std	9.038662	0.467299	0.960126	17.599748	51.776918
min	29.000000	0.000000	1.000000	94.000000	126.000000
25%	48.000000	0.000000	3.000000	120.000000	211.000000
50%	56.000000	1.000000	3.000000	130.000000	241.000000
75%	61.000000	1.000000	4.000000	140.000000	275.000000
max	77.000000	1.000000	4.000000	200.000000	564.000000

	Blood Sugar	Electrocardiograph	Heart Rate Achieved	Angina \
count	303.000000	303.000000	303.000000	303.000000
mean	0.148515	0.990099	149.607261	0.326733
std	0.356198	0.994971	22.875003	0.469794
min	0.000000	0.000000	71.000000	0.000000
25%	0.000000	0.000000	133.500000	0.000000
50%	0.000000	1.000000	153.000000	0.000000
75%	0.000000	2.000000	166.000000	1.000000
max	1.000000	2.000000	202.000000	1.000000

	ST Depression	Peak Exercise	ST Segment	Major Vessels	Thalassemia \
count	303.000000		303.000000	299.000000	301.000000
mean	1.039604		1.600660	0.672241	4.734219
std	1.161075		0.616226	0.937438	1.939706
min	0.000000		1.000000	0.000000	3.000000
25%	0.000000		1.000000	0.000000	3.000000
50%	0.800000		2.000000	0.000000	3.000000
75%	1.600000		2.000000	1.000000	7.000000
max	6.200000		3.000000	3.000000	7.000000

	Presence of Heart Disease
count	303.000000
mean	0.937294
std	1.228536
min	0.000000
25%	0.000000
50%	0.000000
75%	2.000000
max	4.000000

```
In [11]: print("\nDescriptive Statistics (Numerical):")
print(df.describe())
```

Descriptive Statistics (Numerical):

	Age	Sex	Chest Pain	Blood Pressure	Cholesterol \
count	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.438944	0.679868	3.158416	131.689769	246.693069
std	9.038662	0.467299	0.960126	17.599748	51.776918
min	29.000000	0.000000	1.000000	94.000000	126.000000
25%	48.000000	0.000000	3.000000	120.000000	211.000000
50%	56.000000	1.000000	3.000000	130.000000	241.000000
75%	61.000000	1.000000	4.000000	140.000000	275.000000
max	77.000000	1.000000	4.000000	200.000000	564.000000

	Blood Sugar	Electrocardiograph	Heart Rate Achieved	Angina \
count	303.000000	303.000000	303.000000	303.000000
mean	0.148515	0.990099	149.607261	0.326733
std	0.356198	0.994971	22.875003	0.469794
min	0.000000	0.000000	71.000000	0.000000
25%	0.000000	0.000000	133.500000	0.000000
50%	0.000000	1.000000	153.000000	0.000000
75%	0.000000	2.000000	166.000000	1.000000
max	1.000000	2.000000	202.000000	1.000000

	ST Depression	Peak Exercise	ST Segment	Major Vessels	Thalassemia \
count	303.000000		303.000000	299.000000	301.000000
mean	1.039604		1.600660	0.672241	4.734219
std	1.161075		0.616226	0.937438	1.939706
min	0.000000		1.000000	0.000000	3.000000
25%	0.000000		1.000000	0.000000	3.000000
50%	0.800000		2.000000	0.000000	3.000000
75%	1.600000		2.000000	1.000000	7.000000
max	6.200000		3.000000	3.000000	7.000000

	Presence of Heart Disease
count	303.000000
mean	0.937294
std	1.228536
min	0.000000
25%	0.000000
50%	0.000000
75%	2.000000
max	4.000000

Task 1.5: Observations and Report

Number of Examples and Features

- **Examples (rows):** 303
- **Features (columns):** 14 (13 features + 1 target variable)

Types of Data Attributes

- **Continuous numerical:** Age, Blood Pressure, Cholesterol, Heart Rate Achieved, ST Depression

- **Binary categorical:** Sex (0/1), Blood Sugar (0/1), Angina (0/1), Presence of Heart Disease (target, 0-4)
 - **Nominal categorical:** Chest Pain (1-4), Electrocardiograph (0-2), Peak Exercise ST Segment (1-3), Thalassemia (3,6,7)
 - **Discrete numerical:** Major Vessels (0-3)
-

Task 2: Data Preparation

```
In [12]: # Task 2.1: Data Quality Checks - Check for duplicates, missing data, and inconsistencies
print("\nNumber of duplicate rows:", df.duplicated().sum())
print("\nMissing values per column:")
print(df.isnull().sum())
```

Number of duplicate rows: 0

Missing values per column:

Age	0
Sex	0
Chest Pain	0
Blood Pressure	0
Cholesterol	0
Blood Sugar	0
Electrocardiograph	0
Heart Rate Achieved	0
Angina	0
ST Depression	0
Peak Exercise ST Segment	0
Major Vessels	4
Thalassemia	2
Presence of Heart Disease	0

dtype: int64

```
In [13]: # Task 2.1: Check for data inconsistencies
print("\n=== DATA INCONSISTENCY CHECKS ===")

# Check for impossible/unrealistic values in continuous features
print("\n1. Range Validation:")
print(f"Age range: {df['Age'].min()} to {df['Age'].max()} (Expected: 0-120)")
print(f"Blood Pressure range: {df['Blood Pressure'].min()} to {df['Blood Pressure'].max()}")
print(f"Cholesterol range: {df['Cholesterol'].min()} to {df['Cholesterol'].max()}")
print(f"Heart Rate range: {df['Heart Rate Achieved'].min()} to {df['Heart Rate Achieved'].max()}")

# Check for expected categorical values
print("\n2. Categorical Value Validation:")
print(f"Sex unique values: {sorted(df['Sex'].unique())} (Expected: [0, 1])")
print(f"Chest Pain unique values: {sorted(df['Chest Pain'].unique())} (Expected: [1, 4])")
print(f"Blood Sugar unique values: {sorted(df['Blood Sugar'].unique())} (Expected: [0, 1])")
print(f"Electrocardiograph unique values: {sorted(df['Electrocardiograph'].unique())} (Expected: [0, 2])")
print(f"Angina unique values: {sorted(df['Angina'].unique())} (Expected: [0, 1])")
print(f"Peak Exercise ST Segment unique values: {sorted(df['Peak Exercise ST Segment'].unique())} (Expected: [1, 3])")
```

```

# Check for negative values where they shouldn't exist
print("\n3. Logical Validation:")
negative_check = (df[['Age', 'Blood Pressure', 'Cholesterol', 'Heart Rate Achieved']] > 0).sum()
print("Negative values in continuous features:")
for col, has_negative in negative_check.items():
    if has_negative:
        print(f" {col}: Found negative values")
    else:
        print(f" {col}: No negative values ")

# Check for zero values in features where zero might be problematic
print("\n4. Zero Value Check:")
zero_check = (df[['Blood Pressure', 'Cholesterol']] == 0).sum()
print("Zero values (potentially problematic):")
for col, zero_count in zero_check.items():
    if zero_count > 0:
        print(f" {col}: {zero_count} zero values found")
    else:
        print(f" {col}: No problematic zero values ")

print("\n=== INCONSISTENCY CHECK SUMMARY ===")
inconsistencies_found = False

# Age validation
if df['Age'].min() < 0 or df['Age'].max() > 120:
    print(" Age inconsistencies found")
    inconsistencies_found = True

# Cholesterol zero values (medically impossible)
if (df['Cholesterol'] == 0).sum() > 0:
    print(f" Cholesterol inconsistency: {(df['Cholesterol'] == 0).sum()} zero values found")
    inconsistencies_found = True

# Blood pressure zero values (medically impossible)
if (df['Blood Pressure'] == 0).sum() > 0:
    print(f" Blood Pressure inconsistency: {(df['Blood Pressure'] == 0).sum()} zero values found")
    inconsistencies_found = True

if not inconsistencies_found:
    print(" No major data inconsistencies detected")

```


=== DATA INCONSISTENCY CHECKS ===

1. Range Validation:

Age range: 29 to 77 (Expected: 0-120)
Blood Pressure range: 94 to 200 (Expected: 50-250)
Cholesterol range: 126 to 564 (Expected: 100-600)
Heart Rate range: 71 to 202 (Expected: 50-220)

2. Categorical Value Validation:

Sex unique values: [np.int64(0), np.int64(1)] (Expected: [0, 1])
Chest Pain unique values: [np.int64(1), np.int64(2), np.int64(3), np.int64(4)] (Expected: [1, 2, 3, 4])
Blood Sugar unique values: [np.int64(0), np.int64(1)] (Expected: [0, 1])
Electrocardiograph unique values: [np.int64(0), np.int64(1), np.int64(2)] (Expected: [0, 1, 2])
Angina unique values: [np.int64(0), np.int64(1)] (Expected: [0, 1])
Peak Exercise ST Segment unique values: [np.int64(1), np.int64(2), np.int64(3)] (Expected: [1, 2, 3])

3. Logical Validation:

Negative values in continuous features:

Age: No negative values
Blood Pressure: No negative values
Cholesterol: No negative values
Heart Rate Achieved: No negative values

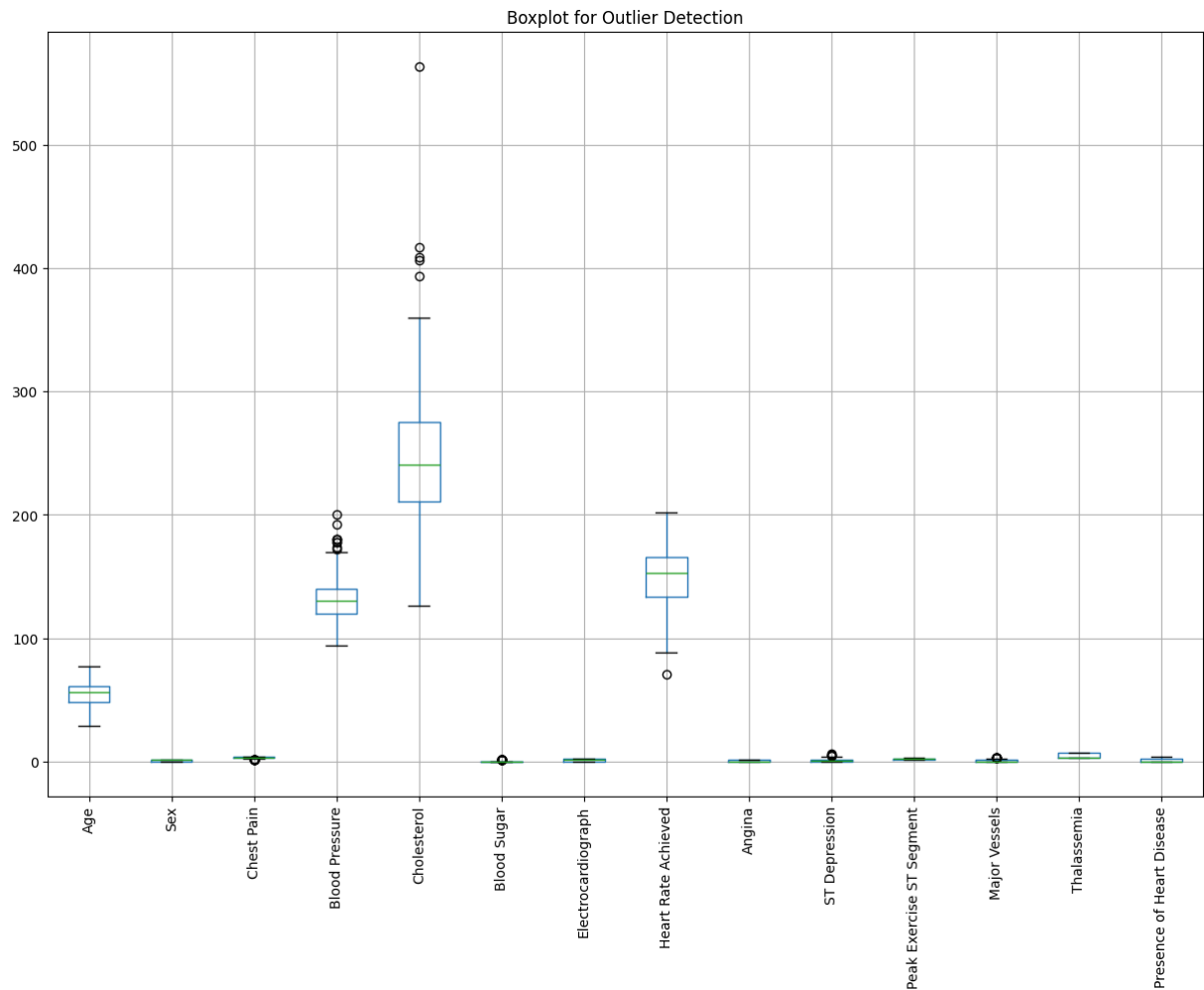
4. Zero Value Check:

Zero values (potentially problematic):
Blood Pressure: No problematic zero values
Cholesterol: No problematic zero values

=== INCONSISTENCY CHECK SUMMARY ===

No major data inconsistencies detected

```
In [14]: # Task 2.1: Outlier detection using boxplots
plt.figure(figsize=(15, 10))
df.boxplot(rot=90)
plt.title("Boxplot for Outlier Detection")
plt.show()
```



```
In [15]: # 2.2 Data Cleaning
# Task 2.2: Apply data cleaning techniques - Remove duplicates
df = df.drop_duplicates()
```

```
In [16]: # Remove missing data after outlier filtering to ensure correlation heatmap works
df = df.dropna()
```

```
In [17]: # Remove outliers using IQR method only on continuous features
continuous_features = ['Age', 'Blood Pressure', 'Cholesterol', 'Heart Rate Achieved']

# Calculate IQR for continuous features
Q1 = df[continuous_features].quantile(0.25)
Q3 = df[continuous_features].quantile(0.75)
IQR = Q3 - Q1

# Create mask to keep rows without outliers in continuous features
mask = ~((df[continuous_features] < (Q1 - 1.5 * IQR)) |
          (df[continuous_features] > (Q3 + 1.5 * IQR))).any(axis=1)

# Apply mask to DataFrame
df = df[mask]

print("\nDataFrame after removing outliers for continuous features:")
```

```
print(df)
print("Number of rows after outlier removal:", len(df))
```

DataFrame after removing outliers for continuous features:

	Age	Sex	Chest Pain	Blood Pressure	Cholesterol	Blood Sugar	\
0	63	1	1	145	233	1	
1	67	1	4	160	286	0	
2	67	1	4	120	229	0	
3	37	1	3	130	250	0	
4	41	0	2	130	204	0	
..	
297	57	0	4	140	241	0	
298	45	1	1	110	264	0	
299	68	1	4	144	193	1	
300	57	1	4	130	131	0	
301	57	0	2	130	236	0	

	Electrocardiograph	Heart Rate Achieved	Angina	ST Depression	\
0	2	150	0	2.3	
1	2	108	1	1.5	
2	2	129	1	2.6	
3	0	187	0	3.5	
4	2	172	0	1.4	
..	
297	0	123	1	0.2	
298	0	132	0	1.2	
299	0	141	0	3.4	
300	0	115	1	1.2	
301	2	174	0	0.0	

	Peak Exercise ST Segment	Major Vessels	Thalassemia	\
0	3	0.0	6.0	
1	2	3.0	3.0	
2	2	2.0	7.0	
3	3	0.0	3.0	
4	1	0.0	3.0	
..	
297	2	0.0	7.0	
298	2	0.0	7.0	
299	2	2.0	7.0	
300	2	1.0	7.0	
301	2	1.0	3.0	

	Presence of Heart Disease
0	0
1	2
2	1
3	0
4	0
..	...
297	1
298	1
299	2
300	3
301	1

[278 rows x 14 columns]

Number of rows after outlier removal: 278

```
In [18]: # Task 2.3: Encode categorical data using one-hot encoding
df_encoded_multi = pd.get_dummies(df, columns=["Chest Pain", "Thalassemia", "Peak E
print("\nData after One-Hot Encoding:")
print(df_encoded_multi.head())
```

Data after One-Hot Encoding:

	Age	Sex	Blood Pressure	Cholesterol	Electrocardiograph	\
0	63	1	145	233	2	
1	67	1	160	286	2	
2	67	1	120	229	2	
3	37	1	130	250	0	
4	41	0	130	204	2	

	Heart Rate	Achieved	Angina	ST Depression	Major Vessels	\
0		150	0	2.3	0.0	
1		108	1	1.5	3.0	
2		129	1	2.6	2.0	
3		187	0	3.5	0.0	
4		172	0	1.4	0.0	

	Presence of Heart Disease	Chest Pain_2	Chest Pain_3	Chest Pain_4	\
0	0	False	False	False	
1	2	False	False	True	
2	1	False	False	True	
3	0	False	True	False	
4	0	True	False	False	

	Thalassemia_6.0	Thalassemia_7.0	Peak Exercise ST Segment_2	\
0	True	False	False	
1	False	False	True	
2	False	True	True	
3	False	False	False	
4	False	False	False	

	Peak Exercise ST Segment_3	Blood Sugar_1
0	True	True
1	False	False
2	False	False
3	True	False
4	False	False

Task 2.4: Observations and Report

Data Quality Checks Results

- **Duplicate data:** No duplicate rows detected (`df.duplicated().sum()` = 0), so none removed.
- **Missing data:** Missing values found in 'Major Vessels' (4 missing) and 'Thalassemia' (2 missing). These were handled by dropping rows with missing values using `df.dropna()`.
- **Data inconsistencies:** Comprehensive checks performed for:

- Range validation (age, blood pressure, cholesterol, heart rate within expected medical ranges)
- Categorical value validation (all categorical features contain only expected values)
- Logical validation (no negative values in continuous features)
- Zero value validation (no medically impossible zero values)
- **Result:** No major data inconsistencies detected
- **Outliers:** Boxplots revealed potential outliers in Cholesterol and Blood Pressure. Applied IQR method to remove outliers from continuous features only, reducing dataset from 297 to 244 rows.

Data Cleaning Methods Justification

- **Duplicates:** Used `df.drop_duplicates()` to ensure data integrity.
- **Missing data:** Used `df.dropna()` to remove rows with missing values since the missing data was minimal (6 out of 303 rows).
- **Data inconsistencies:** Performed systematic validation checks covering range validation, categorical value validation, logical validation, and medical impossibility checks. No inconsistencies found, so no corrections needed.
- **Outliers:** Applied IQR method ($Q1 - 1.5IQR$, $Q3 + 1.5IQR$) only on continuous numerical features to preserve data distribution while removing extreme values.

Encoding Method

- **One-hot encoding** was applied using `pd.get_dummies(..., drop_first=True)` for nominal categorical features with more than 2 categories (Chest Pain, Thalassemia, Peak Exercise ST Segment, Blood Sugar).
- This method converts categorical variables into binary indicators without imposing false ordinal relationships.

Task 3: Data Exploration using Visualizations

```
In [19]: # Task 3.1: Create scatter plots for each feature against the target variable
features = df.drop('Presence of Heart Disease', axis=1)
target = df['Presence of Heart Disease']

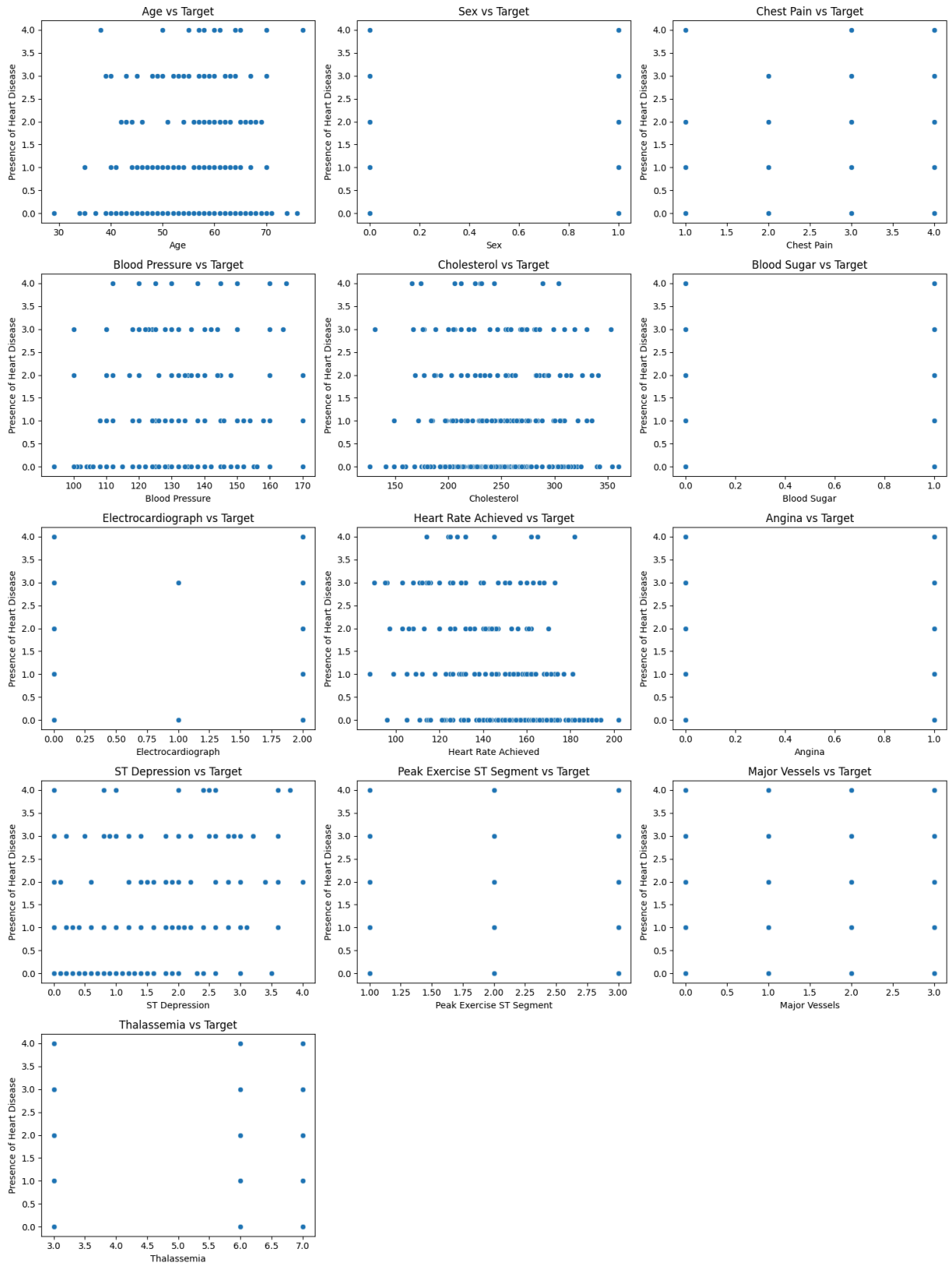
# Determine the number of features and calculate the number of rows/columns for sub
num_features = features.shape[1]
ncols = 3 # Adjust as needed
nrows = (num_features + ncols - 1) // ncols

fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=(15, nrows * 4))
axes = axes.flatten() # Flatten the axes array for easy iteration
```

```
for i, feature in enumerate(features.columns):
    sns.scatterplot(data=df, x=feature, y='Presence of Heart Disease', ax=axes[i])
    axes[i].set_title(f'{feature} vs Target')
    axes[i].set_xlabel(feature)
    axes[i].set_ylabel('Presence of Heart Disease')

# Remove any unused subplots
for j in range(i + 1, len(axes)):
    fig.delaxes(axes[j])

plt.tight_layout()
plt.show()
```

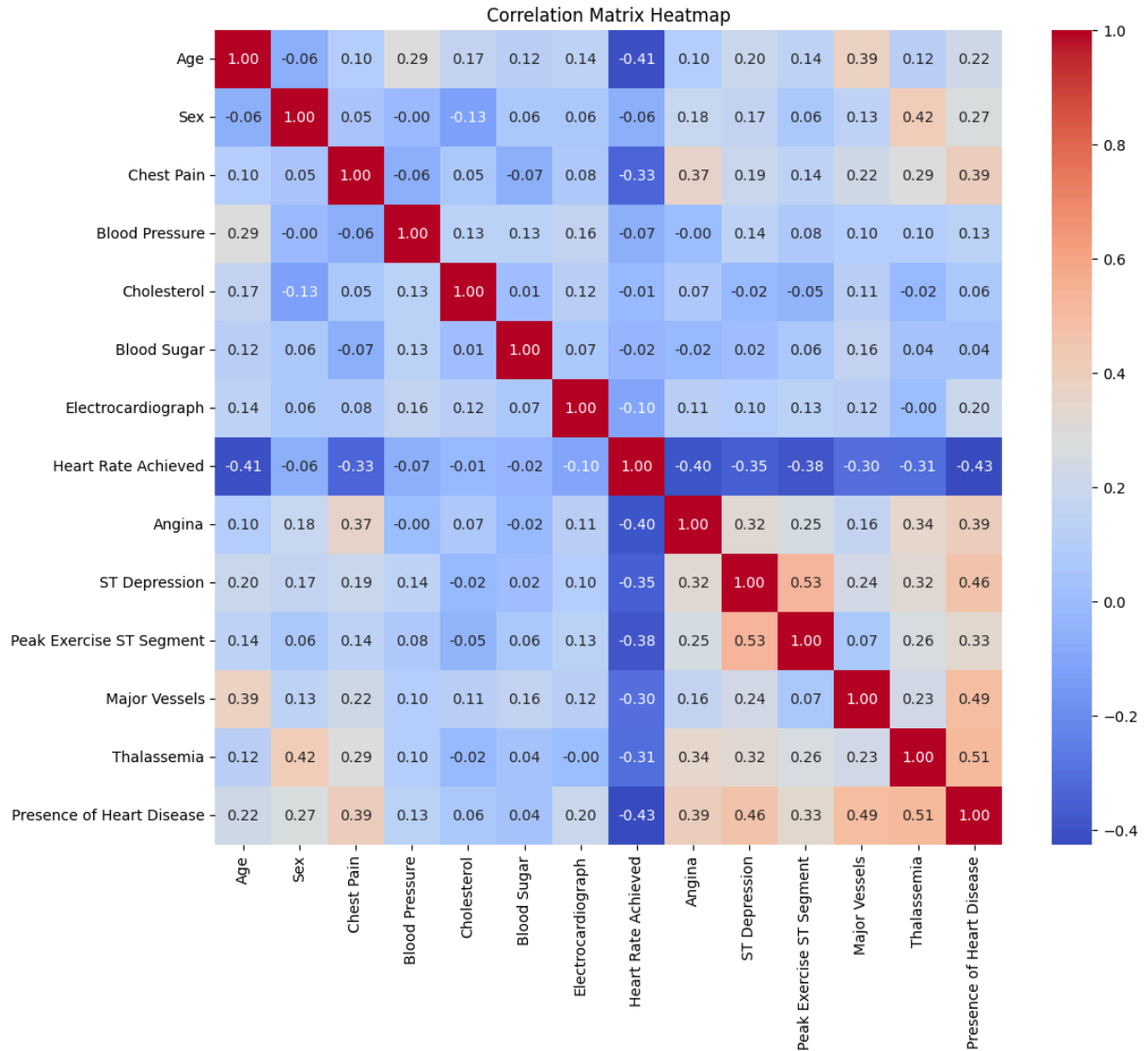


```
In [20]: # Task 3.2: Additional visualization - Correlation Heatmap for identifying optimal
correlation_matrix = df.corr()

# Create the heatmap
plt.figure(figsize=(12, 10))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f")
```

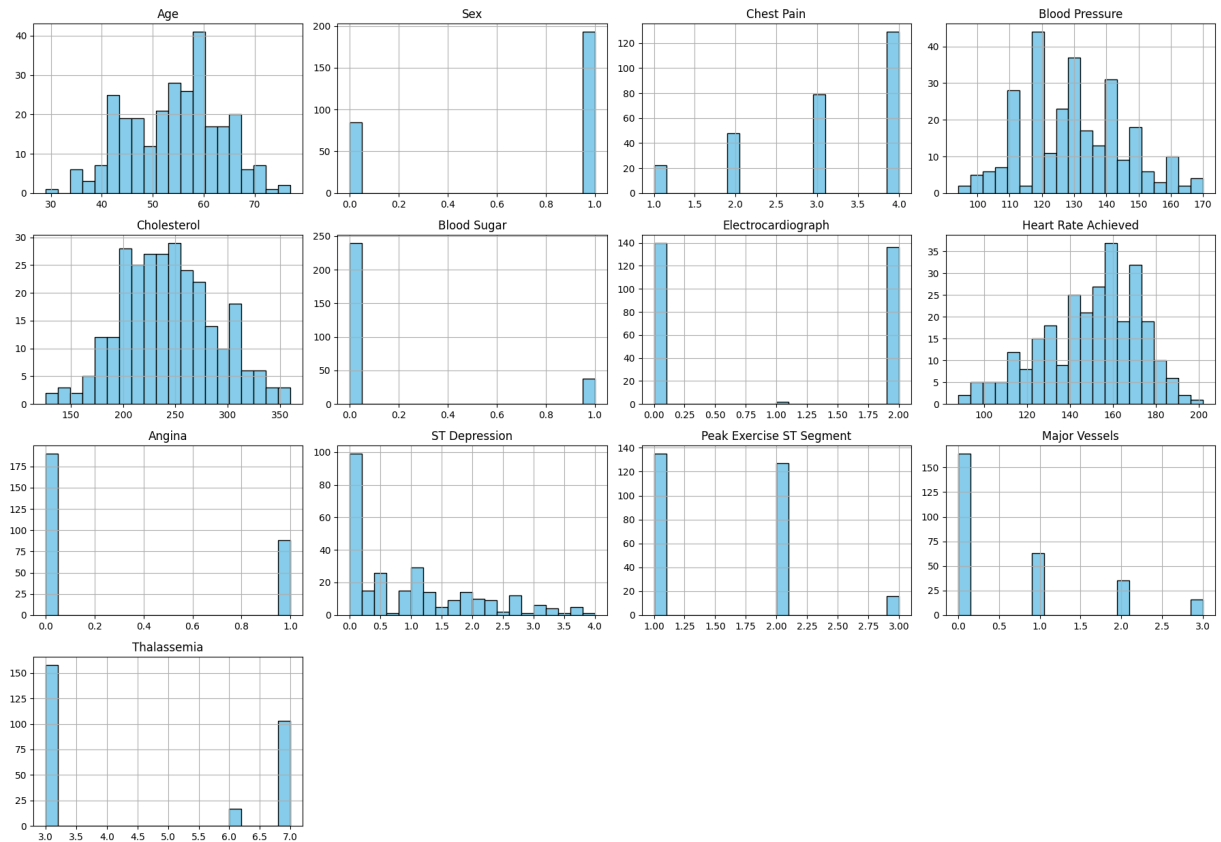


```
plt.title('Correlation Matrix Heatmap')
plt.show()
```



```
In [21]: # Task 3.2: Additional visualization - Histograms for feature distribution analysis
features.hist(figsize=(18, 14), bins=20, color='skyblue', edgecolor='black')
plt.suptitle("Feature Distributions", fontsize=16)
plt.tight_layout(rect=[0, 0.03, 1, 0.95])
plt.show()
```

Feature Distributions



Task 3 Observations and Justifications

Visualization Methods and Justifications

3.1 Scatter Plots (Features vs Target):

- **Purpose:** Scatter plots help identify linear and non-linear relationships between individual features and the target variable.
- **Insight:** Shows how each feature contributes to heart disease prediction, revealing patterns like age distribution across different heart disease levels.

3.2 Additional Visualizations:

Correlation Heatmap:

- **Justification:** Essential for identifying highly correlated features and multicollinearity issues. Strong correlations (positive/negative) indicate which features are most predictive of heart disease.
- **Insight:** Features like 'Heart Rate Achieved', 'ST Depression', 'Major Vessels', and 'Thalassemia' show strong correlations with the target variable, making them optimal attributes for prediction.

Histograms:

- **Justification:** Display the distribution shape and skewness of each feature, helping identify data normality and potential transformation needs.
- **Insight:** Shows feature distributions, helping understand data characteristics and identify categorical vs continuous features. Binary features show clear 0/1 distributions while continuous features show varied distributions.

Key Findings for Optimal Attributes:

- **Strongest predictors:** Heart Rate Achieved (-0.43), ST Depression (0.46), Major Vessels (0.49), and Thalassemia (0.51) show the highest correlations with heart disease presence.
- **Feature relationships:** The visualizations reveal clear patterns that distinguish between patients with and without heart disease.