MLOps Assignment-1: Group 90

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Load and Prepare Dataset

We begin by loading the **processed Cleveland subset** of the UCI Heart Disease dataset. This step includes:

- Assigning column names for interpretability
- Handling missing values represented by `'?'`
- Dropping rows with missing data for this analysis
- Converting all features to numeric types

These preprocessing steps ensure the dataset is clean and ready for exploration and modeling.

In [1]:
```python
# EDA for UCI Heart Disease Dataset

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

# Load the processed Cleveland subset of the dataset
df = pd.read_csv("../data/processed/uci_heart_extracted/processed.cleveland.data", header=None)

# Assign standard column names based on dataset documentation
df.columns = [
    "age",       # age in years
    "sex",       # sex (1 = male; 0 = female)
    "cp",        # chest pain type (1-4)
    "trestbps",  # resting blood pressure (in mm Hg)
    "chol",      # serum cholesterol (mg/dl)
    "fbs",       # fasting blood sugar > 120 mg/dl (1 = true; 0 = false)
    "restecg",   # resting electrocardiographic results (0-2)
    "thalach",   # maximum heart rate achieved
    "exang",     # exercise-induced angina (1 = yes; 0 = no)
    "oldpeak",   # ST depression induced by exercise relative to rest
    "slope",     # slope of the peak exercise ST segment
    "ca",        # number of major vessels (0-3) colored by fluoroscopy
    "thal",      # thalassemia (3 = normal; 6 = fixed defect; 7 = reversible defect)
    "target"     # diagnosis of heart disease (0 = no, 1+ = yes)
]

# Replace '?' with pandas' NA marker (missing value)
df.replace("?", pd.NA, inplace=True)

# Drop any rows with missing data to ensure clean EDA
df = df.dropna()

# Convert all columns to numeric (float), required for visualizations and modeling
df = df.astype(float)
```

Dataset Overview and Target Distribution

We now examine the basic structure and statistical summary of the dataset:

- `df.info()` gives an overview of the columns, non-null counts, and data types.
- `df.describe()` provides statistical metrics such as mean, std, min, and quartiles.
- `df['target'].value_counts()` shows the distribution of the target variable.

This helps verify data integrity, understand feature scales, and assess class imbalance in the target.

In [2]:
```
# Display dataset structure and null count
df.info()

# Show descriptive statistics for numerical features
df.describe()

# Count distribution of target variable (0 = no disease, 1 = disease)
df['target'].value_counts()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 297 entries, 0 to 301
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       297 non-null    float64
 1   sex       297 non-null    float64
 2   cp        297 non-null    float64
 3   trestbps  297 non-null    float64
 4   chol      297 non-null    float64
 5   fbs       297 non-null    float64
 6   restecg   297 non-null    float64
 7   thalach   297 non-null    float64
 8   exang     297 non-null    float64
 9   oldpeak   297 non-null    float64
 10  slope     297 non-null    float64
 11  ca        297 non-null    float64
 12  thal      297 non-null    float64
 13  target    297 non-null    float64
dtypes: float64(14)
memory usage: 34.8 KB
```

Out[2]:
```
target
0.0    160
1.0     54
2.0     35
3.0     35
4.0     13
Name: count, dtype: int64
```

Class Distribution Visualization

To visually examine the balance of the target classes, we use a count plot:

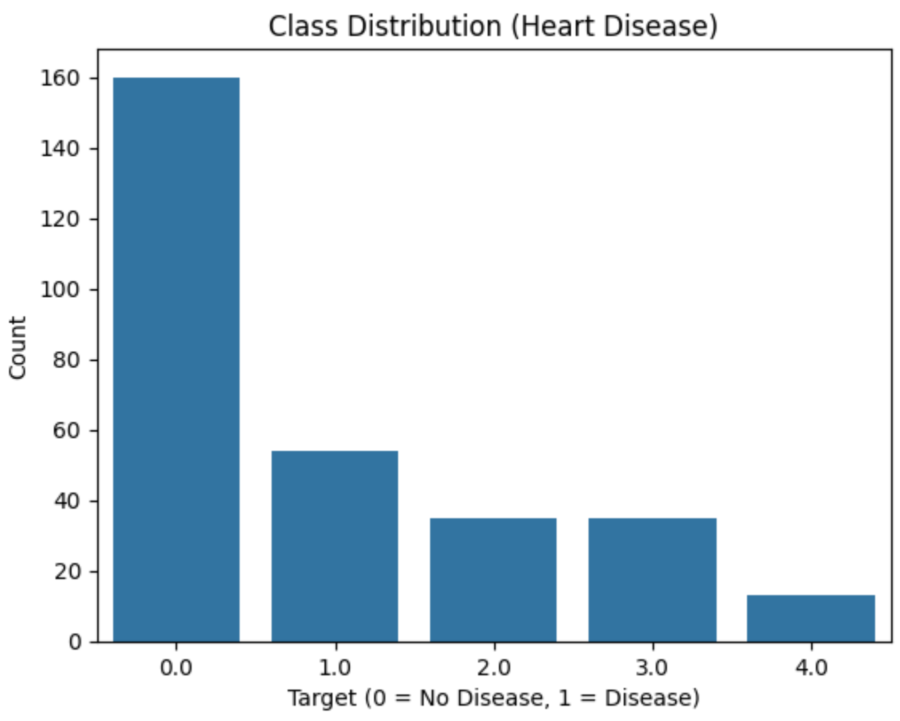
- The `target` variable indicates the presence (1) or absence (0) of heart disease.
- Class imbalance can impact model performance and influence the choice of evaluation metrics (e.g., ROC-AUC over accuracy).

This plot helps assess whether special handling (e.g., stratified sampling or resampling) may be needed during model development.

In [3]:
```
# Plot the class distribution of the target variable
sns.countplot(x='target', data=df)

# Add plot title and axis labels
plt.title("Class Distribution (Heart Disease)")
plt.xlabel("Target (0 = No Disease, 1 = Disease)")
plt.ylabel("Count")

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



Feature Distributions

We use histograms to visualize the distribution of each numerical feature in the dataset. This provides insights into:

- Skewness or outliers in continuous variables (e.g., `chol` , `trestbps`)
- Bimodal or uniform distributions
- Potential need for feature scaling or transformation

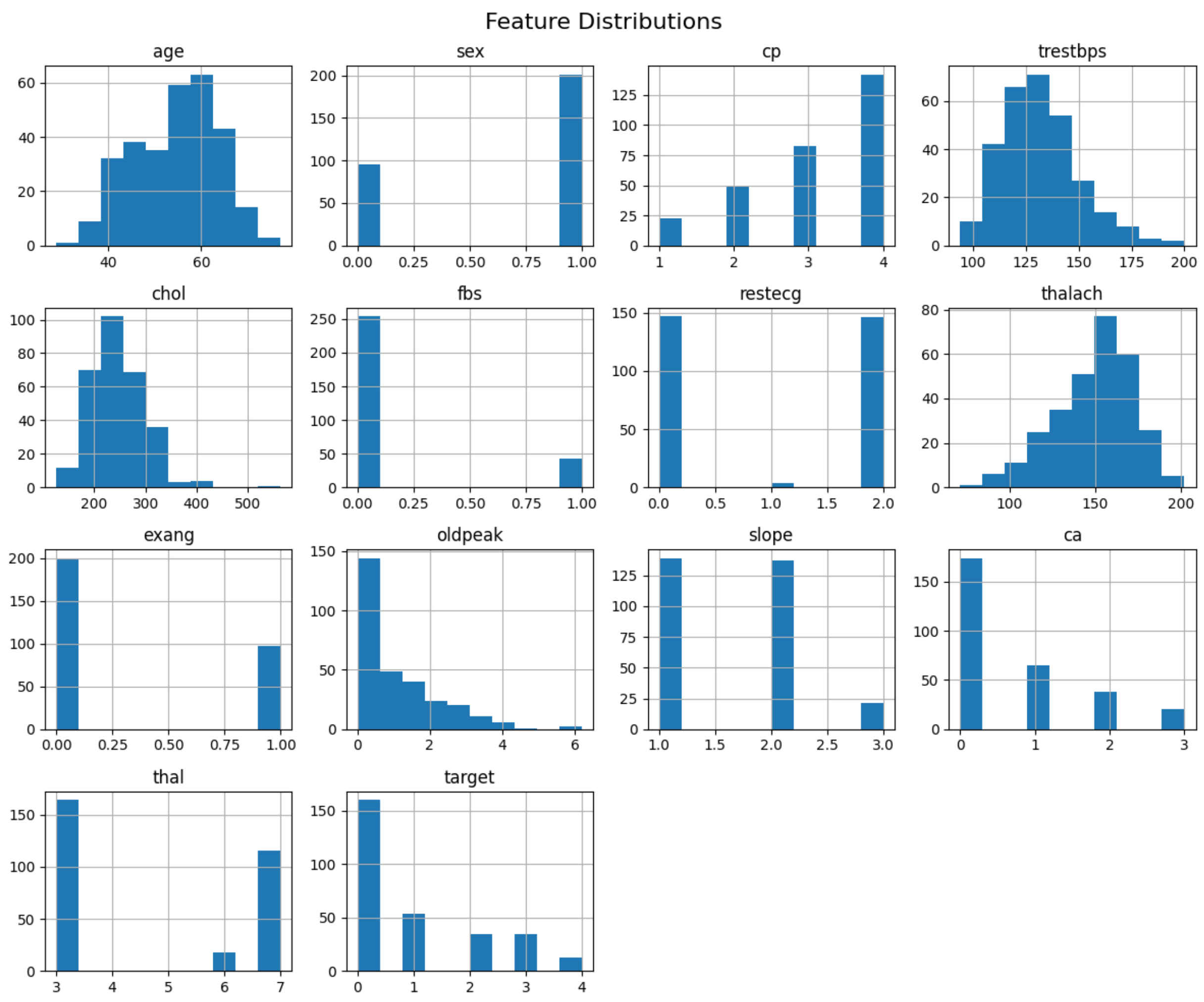
Understanding these patterns helps inform preprocessing and model assumptions.

In [4]:
```
# Plot histograms for each numerical feature in the dataset
df.hist(figsize=(12, 10))  # Set overall figure size

# Add a main title to the entire figure
plt.suptitle("Feature Distributions", fontsize=16)

# Adjust layout to prevent overlapping labels
plt.tight_layout()

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



Feature Correlation Heatmap

We compute and visualize the correlation matrix to:

- Identify relationships between input features
- Detect multicollinearity (highly correlated features like `thalach` and `age`)
- Understand how features relate to the target variable

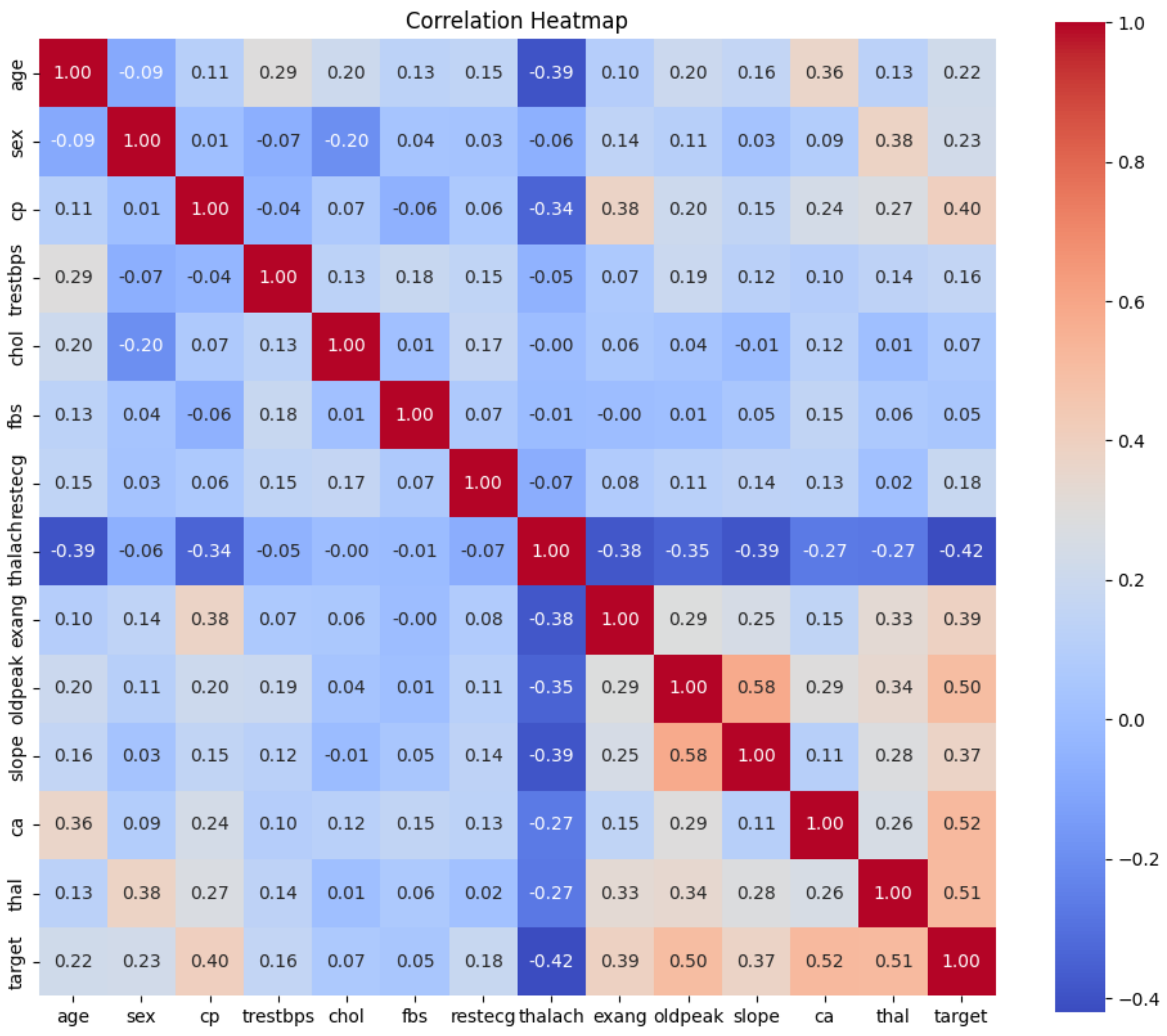
This can help in feature selection and understanding feature importance trends.

In [5]:
```
# Set up the plot size
plt.figure(figsize=(12, 10))

# Compute and plot the correlation heatmap
sns.heatmap(
    df.corr(),              # Compute correlation matrix
    annot=True,             # Display correlation coefficients
    fmt=".2f",              # Format to 2 decimal places
    cmap="coolwarm",        # Color scheme for clarity
    square=True             # Square cells for aesthetics
)

# Add title to the heatmap
plt.title("Correlation Heatmap")

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



Selected Feature Pairplot

We use a pairplot to visualize pairwise relationships between selected features, colored by the target class.

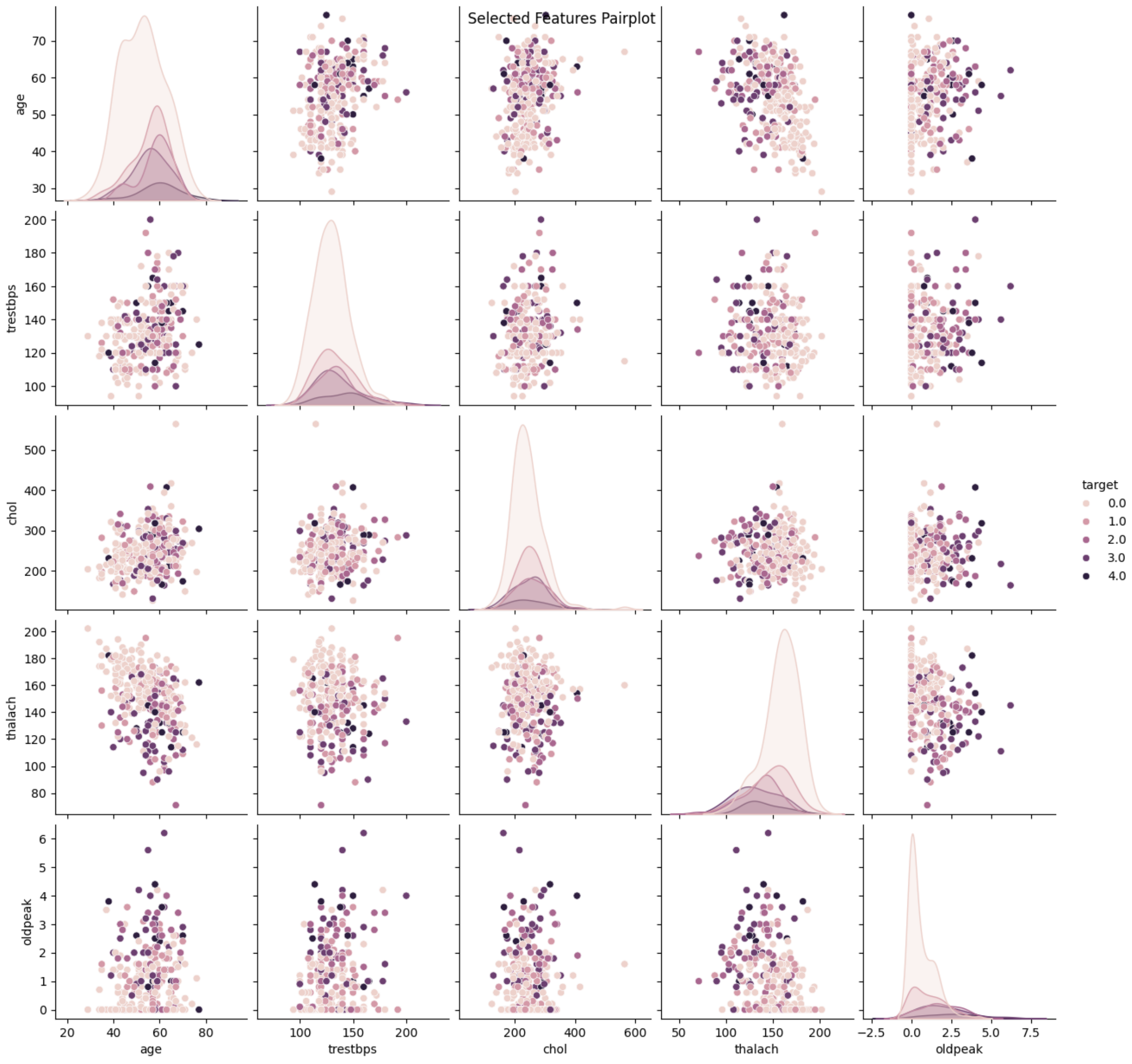
- This helps identify separability between classes in 2D feature space.
- Visual patterns may suggest useful feature interactions or transformations.
- For example, combinations like `age` vs `thalach` or `chol` vs `oldpeak` may show class clustering trends.

This plot supports informed feature engineering and model interpretability.

In [6]:
```
# Create a pairplot for selected features colored by target class
sns.pairplot(
    df[['age', 'trestbps', 'chol', 'thalach', 'oldpeak', 'target']],
    hue='target'  # Color code by class label
)

# Add an overall title
plt.suptitle("Selected Features Pairplot")

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



EDA Summary & Insights

- The dataset contains 14 features plus a binary `target` indicating heart disease presence.
- No missing values remain after cleaning (`?` entries were removed).
- Feature distributions vary widely:
  - `chol` , `trestbps` , and `thalach` show mild skewness.
  - Categorical variables like `cp` , `restecg` , and `thal` show discrete distributions.
- The target classes are **somewhat imbalanced**, with more samples in the "no disease" class.
- The correlation heatmap shows:
  - Strong negative correlation between `thalach` and `age`
  - Moderate positive correlation between `cp` and `target`
  - Most features have weak to moderate correlation with the target

These insights inform our preprocessing choices and model selection in the next stage.