In [165]:

```
# This Python 3 environment comes with many helpful analytics libraries installed
# It is defined by the kaggle/python Docker image: https://github.com/kaggle/docker-python
# For example, here's several helpful packages to load
import warnings
warnings.filterwarnings("ignore")
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import matplotlib.pyplot as plt
import seaborn as sns


# Input data files are available in the read-only "../input/" directory
# For example, running this (by clicking run or pressing Shift+Enter) will list all files under the input directory

import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))

# You can write up to 20GB to the current directory (/kaggle/working/) that gets preserved as output when you create a version using "Save & Run All"
# You can also write temporary files to /kaggle/temp/, but they won't be saved outside of the current session
```

```
/kaggle/input/heart-disease-dataset/heart.csv
```

In [ ]:

Step 1: Load the dataset into a Pandas DataFrame.

In [166]:

```
df=pd.read_csv("/kaggle/input/heart-disease-dataset/heart.csv")
df.head()
```

Out[166]:

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

Step 2: Explore the dataset.

In [167]:

```
df.shape
```

Out[167]:

```
(1025, 14)
```

In [168]:

```
df.describe()
```

Out[168]:

	age	sex	cp	trestbps	chol	fbs	restecg
count	1025.000000	1025.000000	1025.000000	1025.000000	1025.00000	1025.000000	1025.000000
mean	54.434146	0.695610	0.942439	131.611707	246.00000	0.149268	0.529756
std	9.072290	0.460373	1.029641	17.516718	51.59251	0.356527	0.527878
min	29.000000	0.000000	0.000000	94.000000	126.00000	0.000000	0.000000
25%	48.000000	0.000000	0.000000	120.000000	211.00000	0.000000	0.000000
50%	56.000000	1.000000	1.000000	130.000000	240.00000	0.000000	1.000000
75%	61.000000	1.000000	2.000000	140.000000	275.00000	0.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	564.00000	1.000000	2.000000

In [169]:

```
df.isnull().sum()
```

Out[169]:

```
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 [170]: df_heart_disease = df[df['target'] == 1]['chol']
          df_heart_disease
```

```
Out[170]: 5       248
          10      149
          12      210
          15      210
          16      308
                 ...
          1011    308
          1014    141
          1019    204
          1020    221
          1023    254
          Name: chol, Length: 526, dtype: int64
```

```
In [171]: df
```

Out[171]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	targe
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	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	
1020	59	1	1	140	221	0	1	164	1	0.0	2	0	2	
1021	60	1	0	125	258	0	0	141	1	2.8	1	1	3	
1022	47	1	0	110	275	0	0	118	1	1.0	1	1	2	
1023	50	0	0	110	254	0	0	159	0	0.0	2	0	2	
1024	54	1	0	120	188	0	1	113	0	1.4	1	1	3	

1025 rows × 14 columns

In [172]:

```
df_no_heart_disease = df[df['target'] == 0]['chol']
df_no_heart_disease
```

Out[172]:

```
0       212
1       203
2       174
3       203
4       294
       ...
1017    282
1018    172
1021    258
1022    275
1024    188
Name: chol, Length: 499, dtype: int64
```

In [173]:

```
df_heart_disease_mean = df_heart_disease.mean()
df_heart_disease_mean
```

Out[173]:

```
240.97908745247148
```

In [174]:

```
df_no_heart_disease_mean = df_no_heart_disease.mean()
df_no_heart_disease_mean
```

Out[174]:

```
251.2925851703407
```

Step 3: Explore the distribution of variables and relationships between them

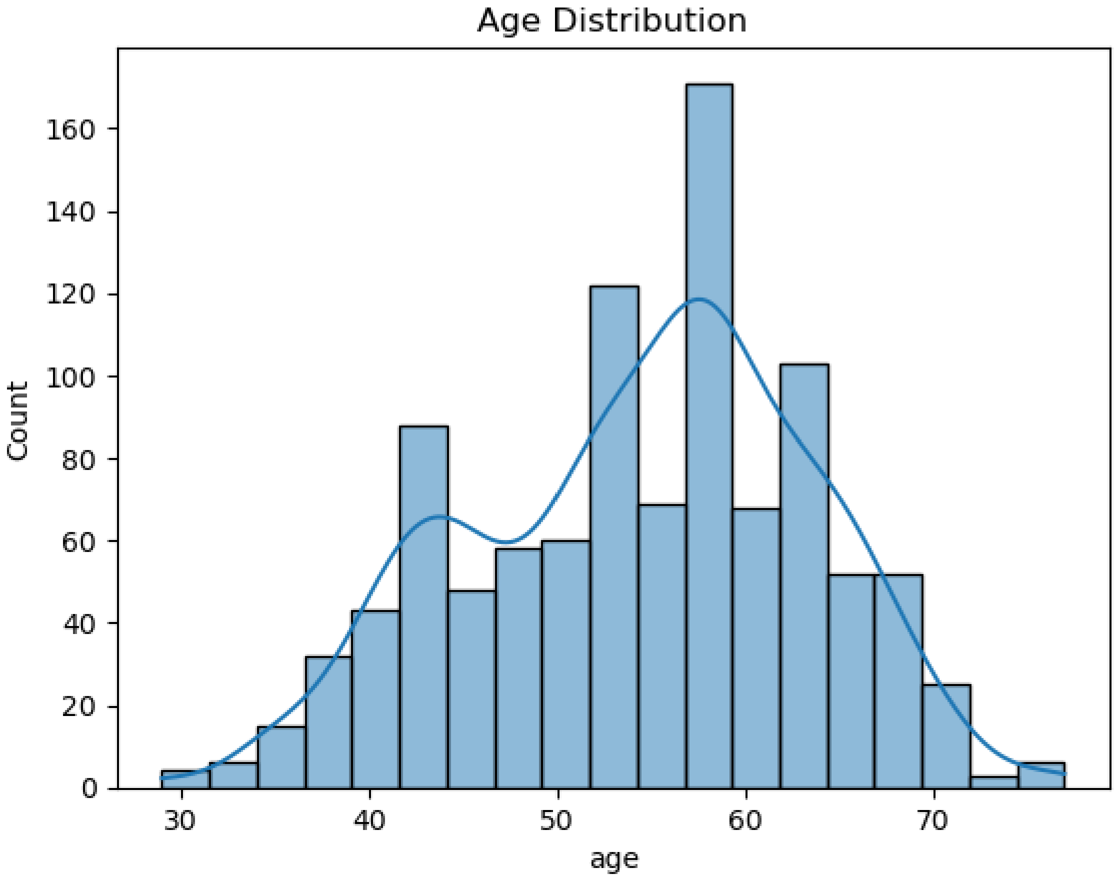
In [175]:

```
df.corr()
```

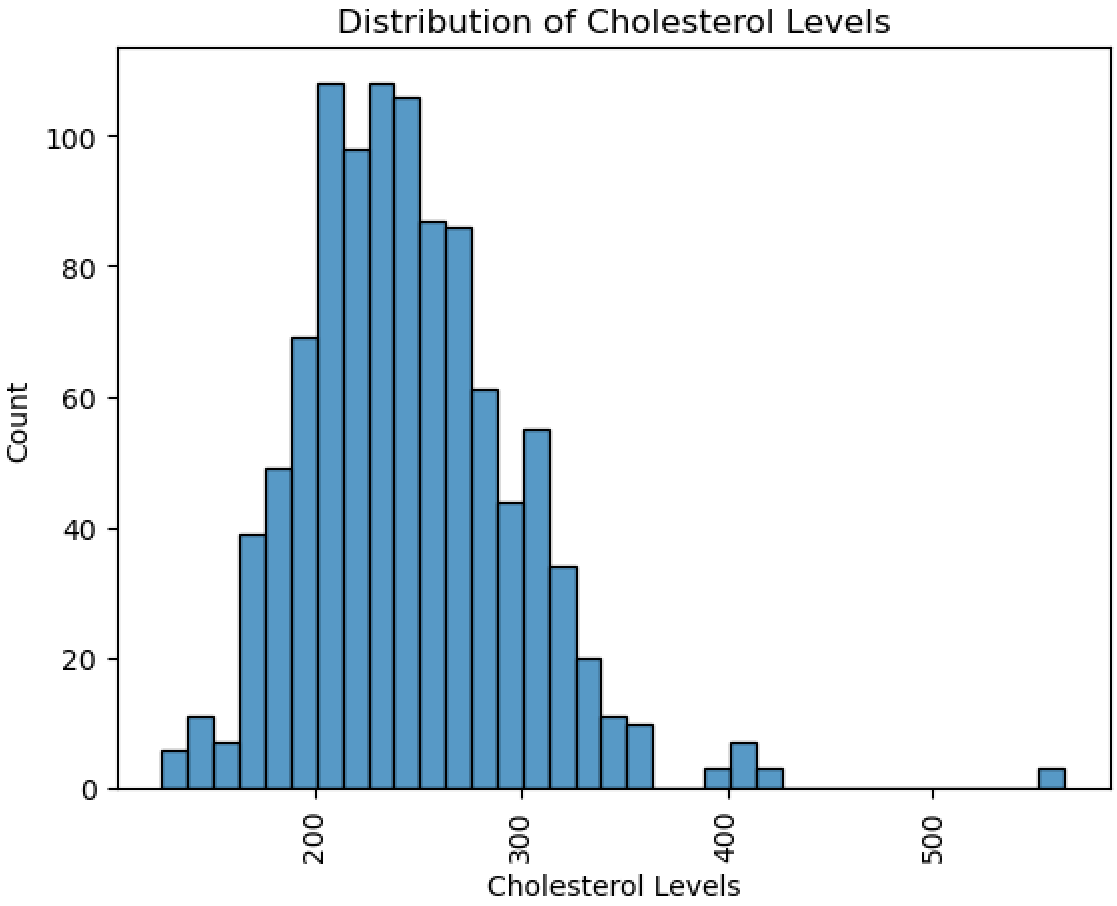
Out[175]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	
age	1.000000	-0.103240	-0.071966	0.271121	0.219823	0.121243	-0.132696	-0.390227	0
sex	-0.103240	1.000000	-0.041119	-0.078974	-0.198258	0.027200	-0.055117	-0.049365	0
cp	-0.071966	-0.041119	1.000000	0.038177	-0.081641	0.079294	0.043581	0.306839	-0
trestbps	0.271121	-0.078974	0.038177	1.000000	0.127977	0.181767	-0.123794	-0.039264	0
chol	0.219823	-0.198258	-0.081641	0.127977	1.000000	0.026917	-0.147410	-0.021772	0
fbs	0.121243	0.027200	0.079294	0.181767	0.026917	1.000000	-0.104051	-0.008866	0
restecg	-0.132696	-0.055117	0.043581	-0.123794	-0.147410	-0.104051	1.000000	0.048411	-0
thalach	-0.390227	-0.049365	0.306839	-0.039264	-0.021772	-0.008866	0.048411	1.000000	-0
exang	0.088163	0.139157	-0.401513	0.061197	0.067382	0.049261	-0.065606	-0.380281	1
oldpeak	0.208137	0.084687	-0.174733	0.187434	0.064880	0.010859	-0.050114	-0.349796	0
slope	-0.169105	-0.026666	0.131633	-0.120445	-0.014248	-0.061902	0.086086	0.395308	-0
ca	0.271551	0.111729	-0.176206	0.104554	0.074259	0.137156	-0.078072	-0.207888	0
thal	0.072297	0.198424	-0.163341	0.059276	0.100244	-0.042177	-0.020504	-0.098068	0
target	-0.229324	-0.279501	0.434854	-0.138772	-0.099966	-0.041164	0.134468	0.422895	-0

```
In [176]: # Example of plotting some variables for EDA
          sns.histplot(df['age'], kde=True)
          plt.title('Age Distribution')
          plt.show()
```

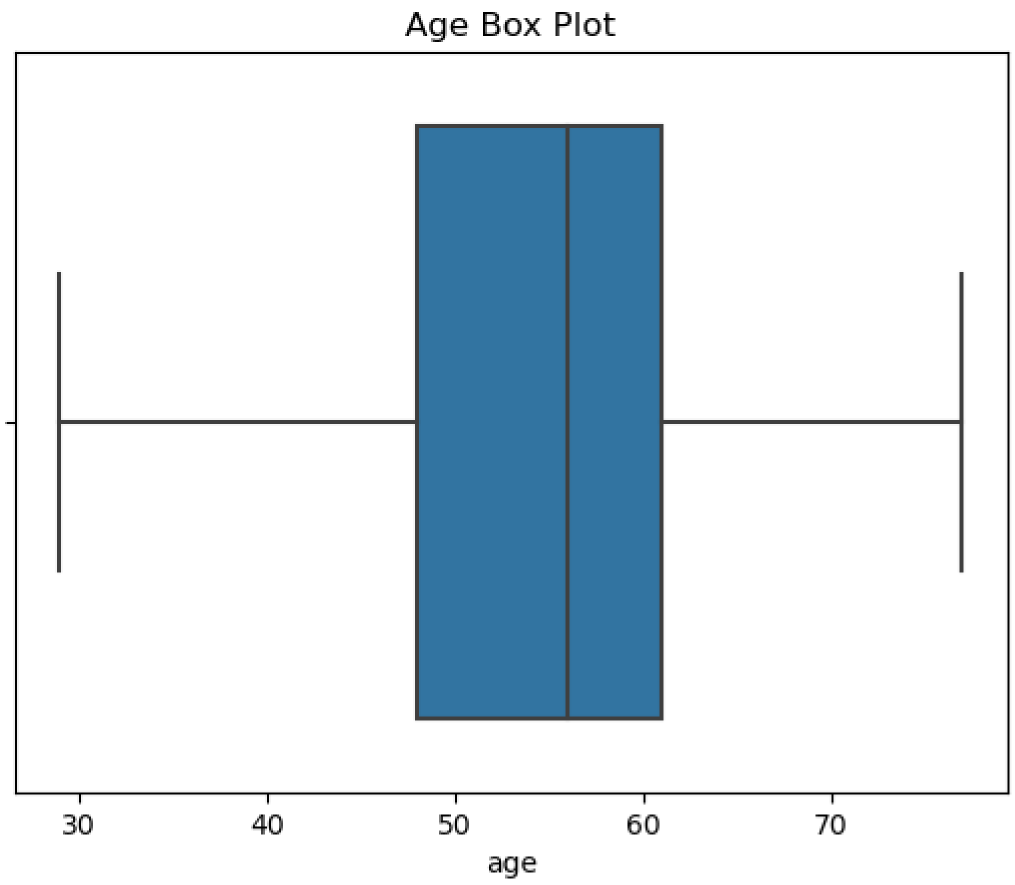


In [177]:
```
sns.histplot(x='chol', data=df)
plt.title('Distribution of Cholesterol Levels')
plt.xlabel('Cholesterol Levels')
plt.xticks(rotation=90)
plt.show()
```



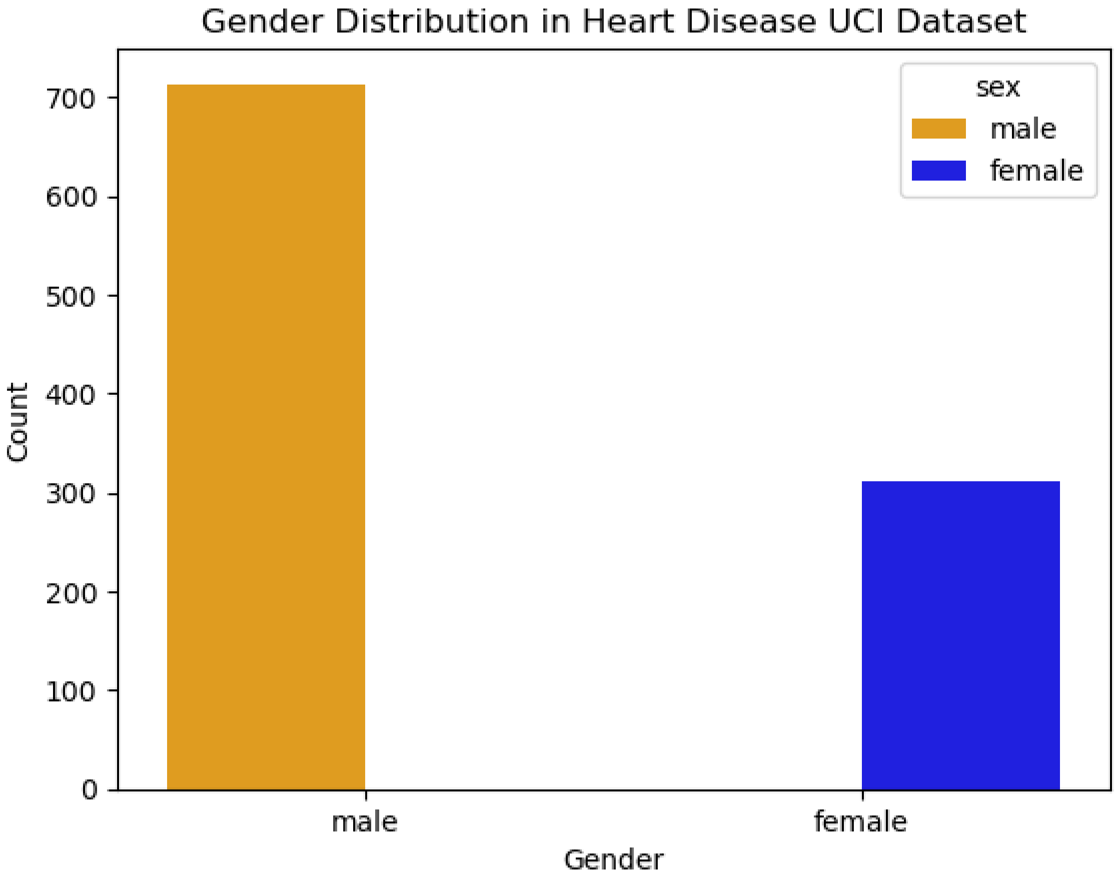
In [178]:

```
sns.boxplot(x='age', data=df)
plt.title('Age Box Plot')
plt.show()
```



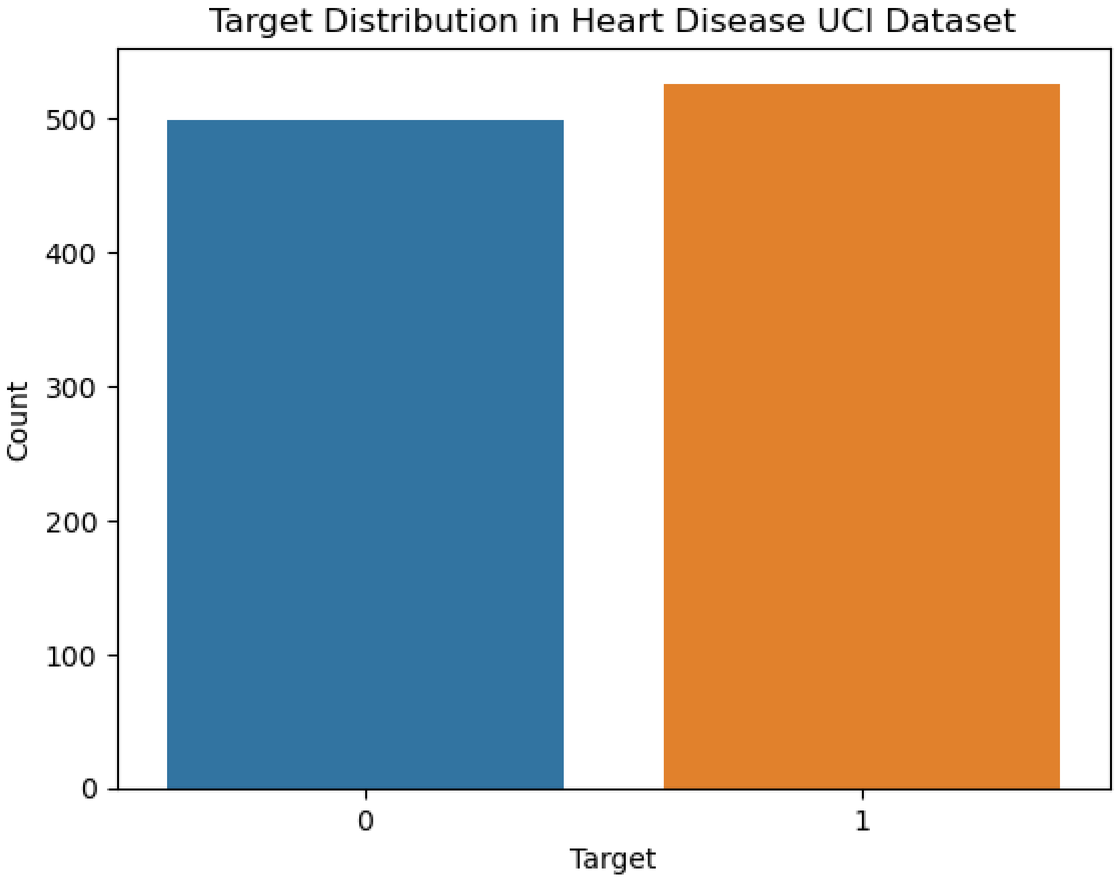
In [179]:

```
df['sex'] = df['sex'].map({0: 'female', 1: 'male'})
sns.countplot(x='sex', data=df, hue='sex', palette={'female': 'blue', 'male':
'orange'})
# Customize the plot
plt.title('Gender Distribution in Heart Disease UCI Dataset')
plt.xlabel('Gender')
plt.ylabel('Count')

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



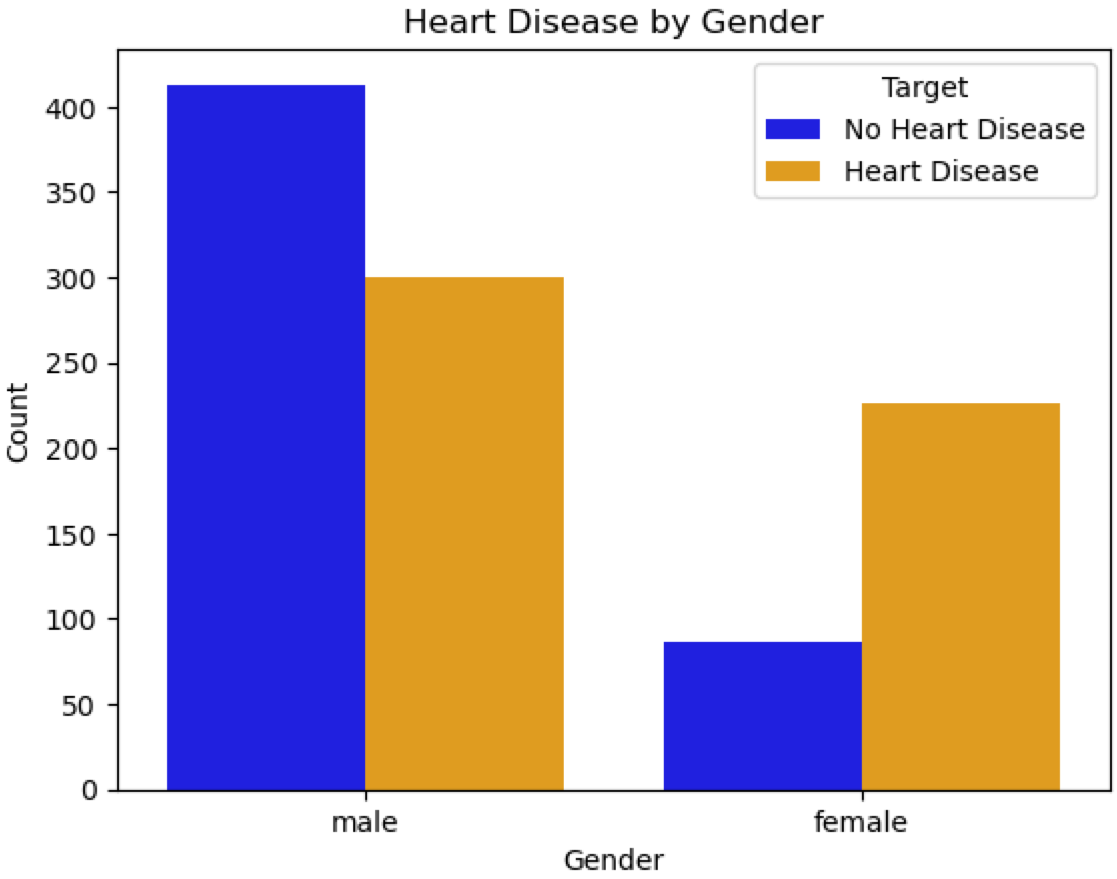
In [180]:

```
sns.countplot(x='target', data=df)

# Customize the plot
plt.title('Target Distribution in Heart Disease UCI Dataset')
plt.xlabel('Target')
plt.ylabel('Count')

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



In [181]:

```
# Use the countplot function and set 'sex' as the 'x' parameter, 'hue' to 'target'
sns.countplot(x='sex', hue='target', data=df, palette={0: 'blue', 1: 'orange'})

# Customize the plot
plt.title('Heart Disease by Gender')
plt.xlabel('Gender')
plt.ylabel('Count')
plt.legend(title='Target', labels=['No Heart Disease', 'Heart Disease'])

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



hypothesis

In [182]:

```
from scipy import stats
t_stat, p_value = stats.ttest_ind(df_heart_disease, df_no_heart_disease)
print("T-statistic:", t_stat)
print("P-value:", p_value)
```

```
T-statistic: -3.213433097179175
P-value: 0.0013525712504626976
```

In [183]:

```
print("P-value:", p_value)
if p_value < 0.05:
    print("There is a significant difference in cholesterol levels between patients with and without heart disease.")
else:
    print("There is no significant difference in cholesterol levels between patients with and without heart disease.")
```

```
P-value: 0.0013525712504626976
There is a significant difference in cholesterol levels between patients with
and without heart disease.
```

In [184]:

```
# Calculate confidence intervals for relevant variables (cholesterol levels)
confidence_interval_heart_disease = stats.t.interval(0.95, len(df_heart_disease) - 1, loc=df_heart_disease.mean(), scale=stats.sem(df_heart_disease))
confidence_interval_no_heart_disease = stats.t.interval(0.95, len(df_no_heart_disease) - 1, loc=df_no_heart_disease.mean(), scale=stats.sem(df_no_heart_disease))
```

In [185]:

```
confidence_interval_heart_disease
```

Out[185]:

```
(236.438435496363, 245.51973940857994)
```

In [186]:

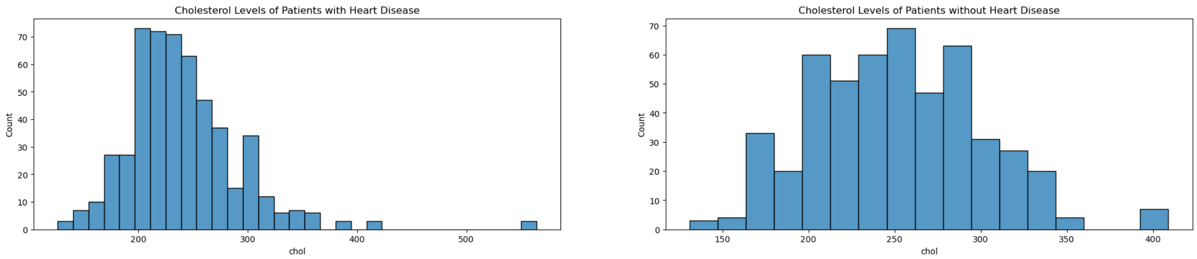
```
confidence_interval_no_heart_disease
```

Out[186]:

```
(246.9336896954613, 255.65148064522006)
```

In [187]:

```
plt.figure(figsize=(25, 10))
plt.subplot(2, 2, 1)
sns.histplot(df_heart_disease)
plt.title('Cholesterol Levels of Patients with Heart Disease')
plt.subplot(2, 2, 2)
sns.histplot(df_no_heart_disease)
plt.title('Cholesterol Levels of Patients without Heart Disease')
plt.show()
```



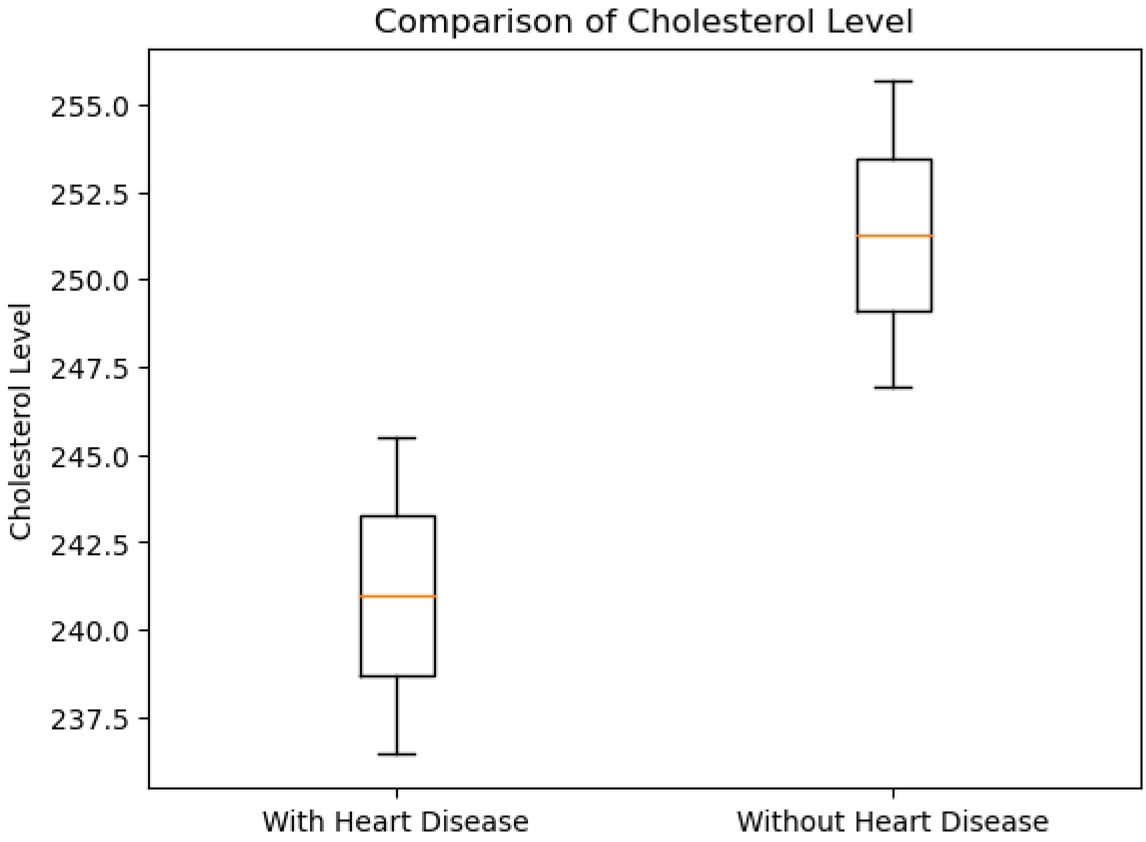
In [189]:

```python
# Summarize the findings
print("Hypothesis Test Results:")
print("T-statistic:", t_stat)
print("P-value:", p_value)

print("\nConfidence Intervals for Cholesterol Levels:")
print("Heart Disease Group:", confidence_interval_heart_disease)
print("No Heart Disease Group:", confidence_interval_no_heart_disease)
```

```
Hypothesis Test Results:
T-statistic: -3.213433097179175
P-value: 0.0013525712504626976

Confidence Intervals for Cholesterol Levels:
Heart Disease Group: (236.438435496363, 245.51973940857994)
No Heart Disease Group: (246.9336896954613, 255.65148064522006)
```

In [192]:

```python
plt.boxplot([confidence_interval_heart_disease,confidence_interval_no_heart_disease], labels=['With Heart Disease','Without Heart Disease'])
plt.ylabel('Cholesterol Level')
plt.title('Comparison of Cholesterol Level')
plt.show()
```



In [ ]: