IMPORT DATASET

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix, roc_auc_score, auc, accuracy_score, precision_score, recall_score, f1_s
import warnings
warnings.filterwarnings('ignore')
```

LOADING THE CSV FILE (DATASET)

In [2]:
```
df= pd.read_csv('Heart_data.csv')
df.head()
```

Out[2]:

	index	id	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio
0	0	0	18393	2	168	62.0	110	80	1	1	0	0	1	0
1	1	1	20228	1	156	85.0	140	90	3	1	0	0	1	1
2	2	2	18857	1	165	64.0	130	70	3	1	0	0	0	1
3	3	3	17623	2	169	82.0	150	100	1	1	0	0	1	1
4	4	4	17474	1	156	56.0	100	60	1	1	0	0	0	0

DATA PREPROCESSING: DATA CLEARNING AND FEATURE ENGINEERING

1. Remove id, and index column
2. Add BMI, Substance used and new age as the new feature

3. Only medically realistic range for blood pressure and ensuring range for blood pressure and enuring systolic >= diastolic

In [3]:
```
#Create BMI column
df = df.drop('index', axis=1)
df = df.drop(columns=['id'])
df['bmi'] = df['weight'] / (df['height']/100)**2
df['age'] = (df['age'] / 365).astype(int)
df['substance used'] = (df['alco'] + df['smoke'])
```

In [4]:
```
# Blood Pressure Cleaning

df = df[(df['ap_hi'] >= 80) & (df['ap_hi'] <= 250)]
df = df[(df['ap_lo'] >= 50) & (df['ap_lo'] <= 200)]

#Ensure systolic >= diastolic
df = df[df['ap_hi'] >= df['ap_lo']]

print("Remaining rows after blood pressure cleaning:", df.shape[0])
```

```
Remaining rows after blood pressure cleaning: 68652
```

In [5]:
```
df.columns
```

Out[5]:
```
Index(['age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo', 'cholesterol',
       'gluc', 'smoke', 'alco', 'active', 'cardio', 'bmi', 'substance used'],
      dtype='object')
```

In [6]:
```
df.shape
```

Out[6]:
```
(68652, 14)
```

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

```
<class 'pandas.core.frame.DataFrame'>
Index: 68652 entries, 0 to 69999
Data columns (total 14 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   age             68652 non-null  int32  
 1   gender          68652 non-null  int64  
 2   height          68652 non-null  int64  
 3   weight          68652 non-null  float64
 4   ap_hi           68652 non-null  int64  
 5   ap_lo           68652 non-null  int64  
 6   cholesterol     68652 non-null  int64  
 7   gluc            68652 non-null  int64  
 8   smoke           68652 non-null  int64  
 9   alco            68652 non-null  int64  
 10  active          68652 non-null  int64  
 11  cardio          68652 non-null  int64  
 12  bmi             68652 non-null  float64
 13  substance used  68652 non-null  int64  
dtypes: float64(2), int32(1), int64(11)
memory usage: 7.6 MB
```

In [8]:
```
df.head()
```

Out[8]:

	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio	bmi	substance used
0	50	2	168	62.0	110	80	1	1	0	0	1	0	21.967120	0
1	55	1	156	85.0	140	90	3	1	0	0	1	1	34.927679	0
2	51	1	165	64.0	130	70	3	1	0	0	0	1	23.507805	0
3	48	2	169	82.0	150	100	1	1	0	0	1	1	28.710479	0
4	47	1	156	56.0	100	60	1	1	0	0	0	0	23.011177	0

In [9]:
```
df.tail()
```

Out[9]:

	age	gender	height	weight	ap_hi	ap_lo	cholesterol	gluc	smoke	alco	active	cardio	bmi	substance used
69995	52	2	168	76.0	120	80	1	1	1	0	1	0	26.927438	1
69996	61	1	158	126.0	140	90	2	2	0	0	1	1	50.472681	0
69997	52	2	183	105.0	180	90	3	1	0	1	0	1	31.353579	1
69998	61	1	163	72.0	135	80	1	2	0	0	0	1	27.099251	0
69999	56	1	170	72.0	120	80	2	1	0	0	1	0	24.913495	0

In [10]:

```
df.describe().T
```

Out[10]:

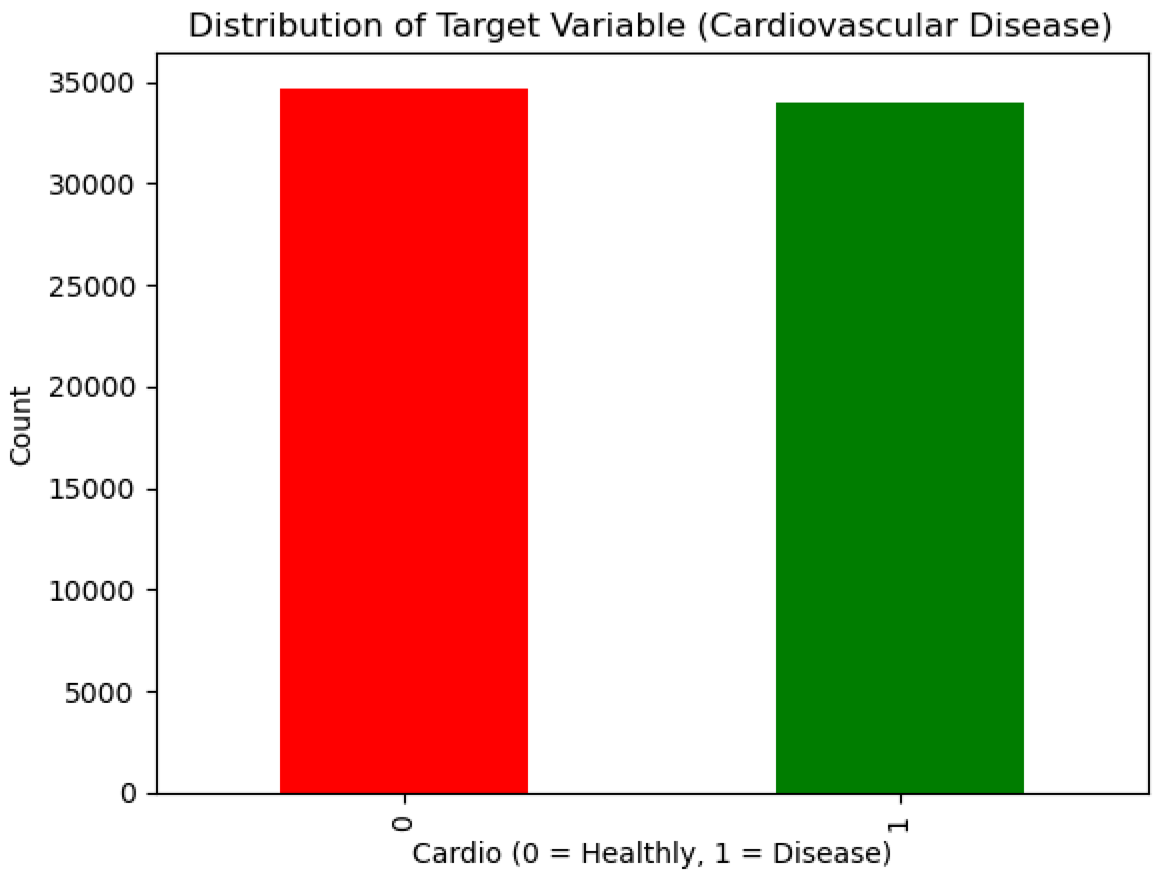
	count	mean	std	min	25%	50%	75%	max
age	68652.0	52.829371	6.768919	29.000000	48.000000	53.000000	58.000000	64.000000
gender	68652.0	1.348686	0.476558	1.000000	1.000000	1.000000	2.000000	2.000000
height	68652.0	164.362830	8.183262	55.000000	159.000000	165.000000	170.000000	250.000000
weight	68652.0	74.121230	14.331623	11.000000	65.000000	72.000000	82.000000	200.000000
ap_hi	68652.0	126.677198	16.686610	80.000000	120.000000	120.000000	140.000000	240.000000
ap_lo	68652.0	81.320457	9.430504	50.000000	80.000000	80.000000	90.000000	182.000000
cholesterol	68652.0	1.364651	0.678897	1.000000	1.000000	1.000000	2.000000	3.000000
gluc	68652.0	1.225689	0.571563	1.000000	1.000000	1.000000	1.000000	3.000000
smoke	68652.0	0.087965	0.283247	0.000000	0.000000	0.000000	0.000000	1.000000
alco	68652.0	0.053341	0.224715	0.000000	0.000000	0.000000	0.000000	1.000000
active	68652.0	0.803356	0.397464	0.000000	1.000000	1.000000	1.000000	1.000000
cardio	68652.0	0.494712	0.499976	0.000000	0.000000	0.000000	1.000000	1.000000
bmi	68652.0	27.522085	6.051969	3.471784	23.875115	26.346494	30.119376	298.666667
substance used	68652.0	0.141307	0.417219	0.000000	0.000000	0.000000	0.000000	2.000000

EXPLORATORY DATA ANALYSIS (EDA)

1. Target Distibution
2. Demographics (Age, Gender)
3. Anthropometrics (Height, Weight, BMI)
4. Medical Indicators (Blood Pressure, Cholesterol, Glucose)
5. Lifestyle Factors (Smoke, Alcohol, Activity)
6. Correlation
7. Feature Importance

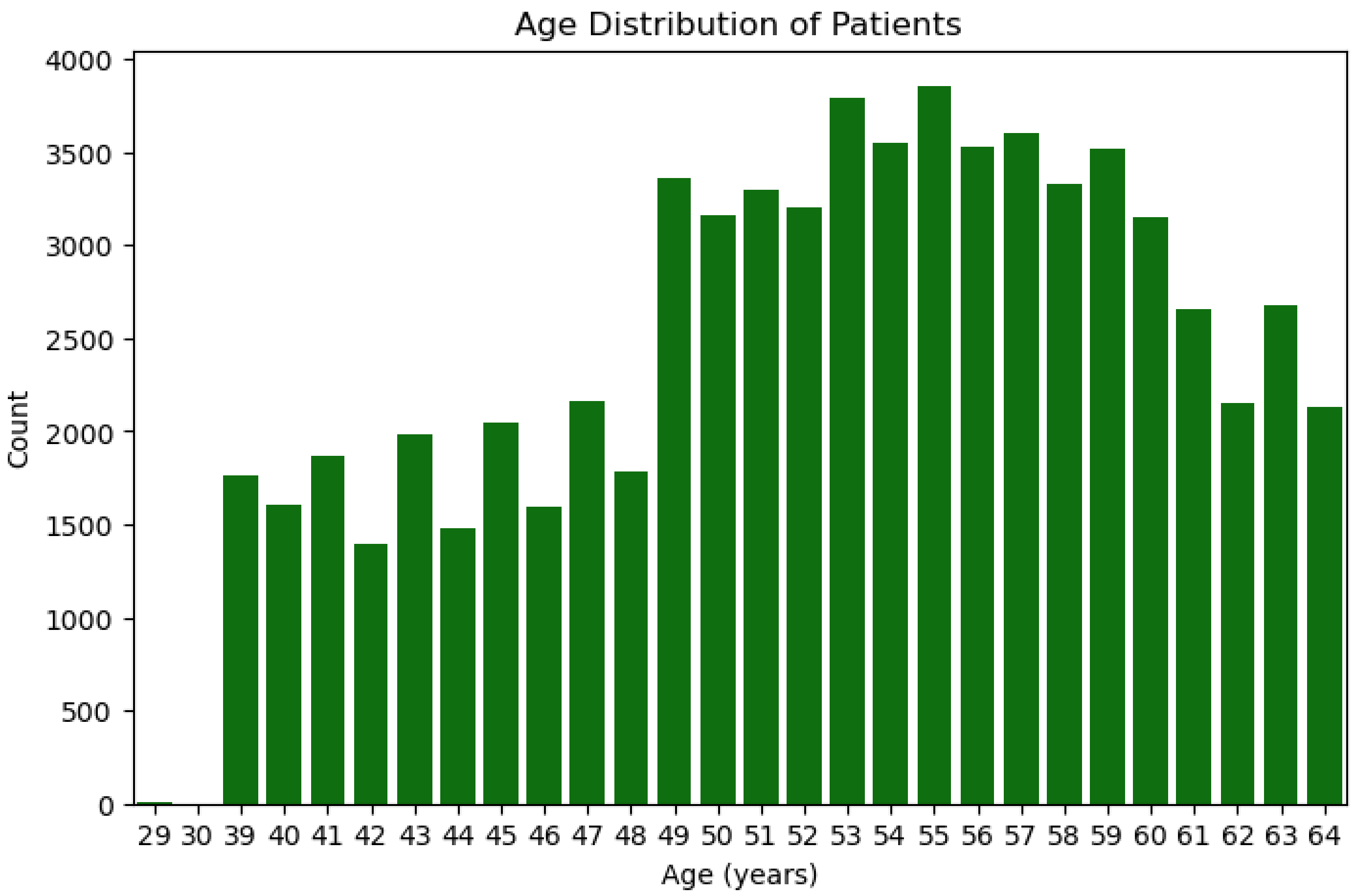
1. Target Variable Distribution

In [11]:
```
# Countplot of target variable
df['cardio'].value_counts().plot(kind='bar', color=['red','green'])
plt.title('Distribution of Target Variable (Cardiovascular Disease)')
plt.xlabel('Cardio (0 = Healthly, 1 = Disease)')
plt.ylabel('Count')
plt.show()
```



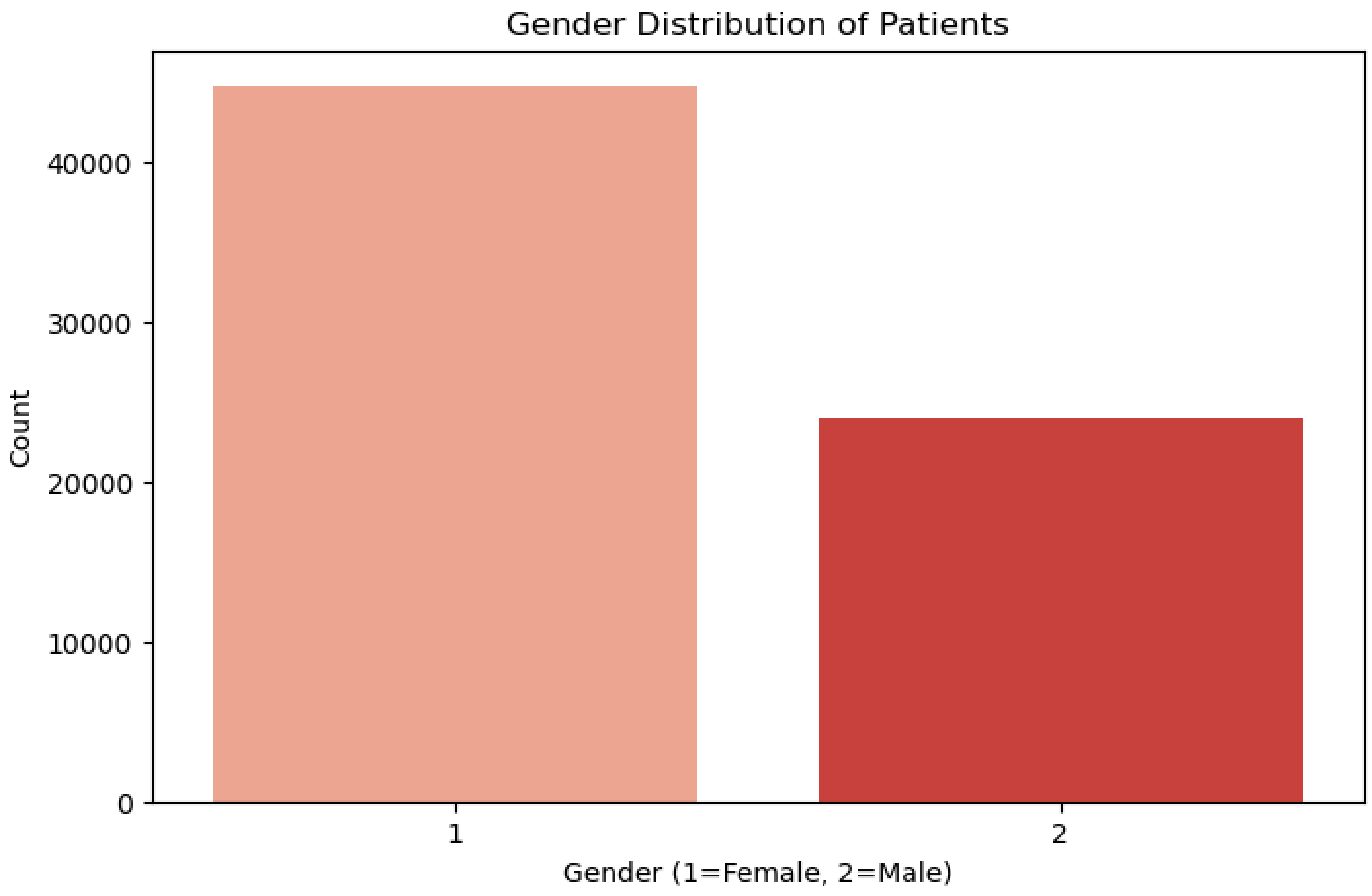
2. Demographics (Age, Gender)

In [12]:
```
#A: Age Distribution
# Plot age distribution
plt.figure(figsize=(8,5))
sns.countplot(x ='age', data=df, color='Green')
plt.title('Age Distribution of Patients')
plt.xlabel('Age (years)')
plt.ylabel('Count')
plt.show()
```



In [13]:
```
#B: Gender

# Plot age distribution
plt.figure(figsize=(8,5))
```

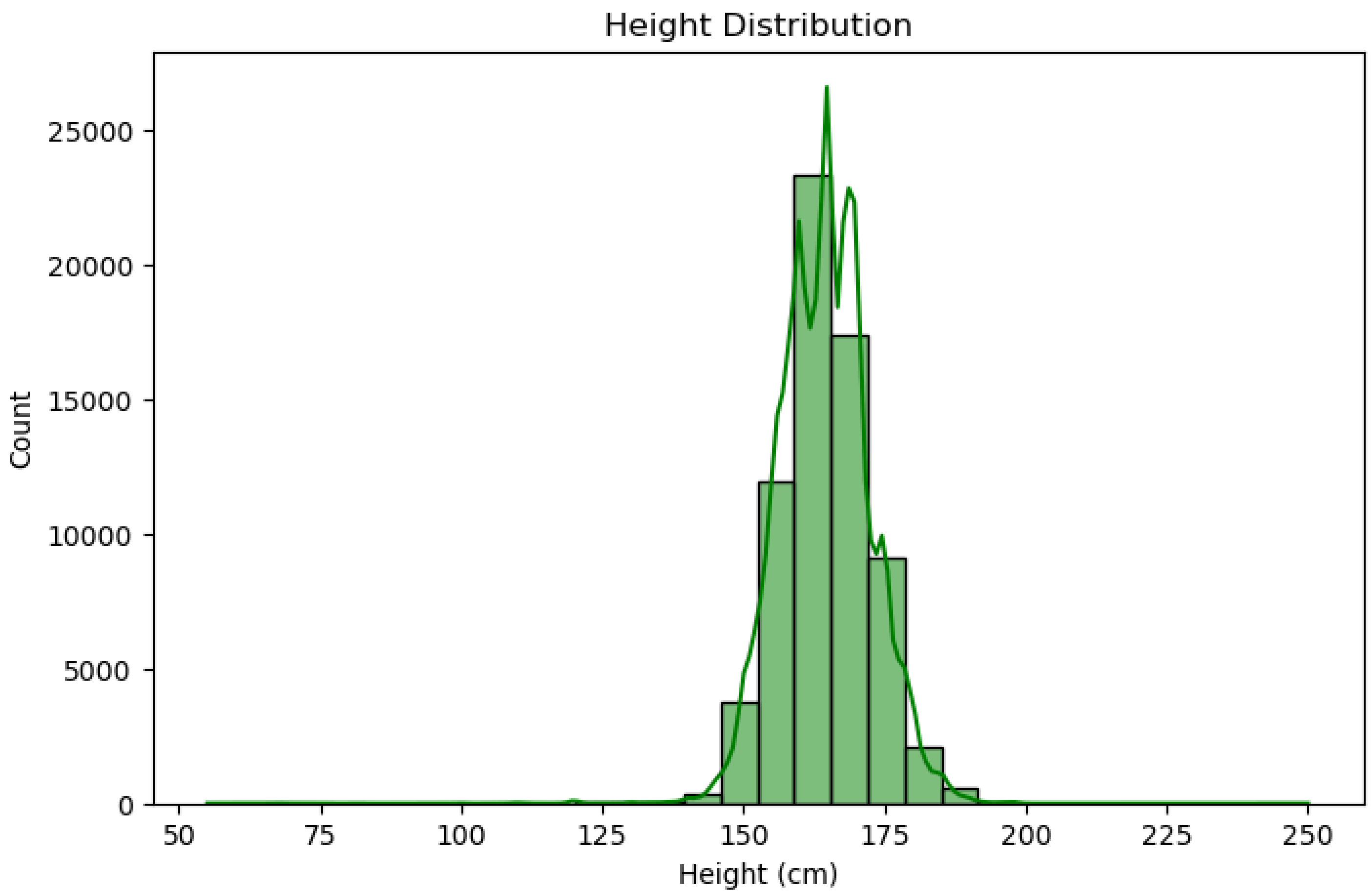
```python
sns.countplot(x ='gender', data=df, palette='Reds')
plt.title('Gender Distribution of Patients')
plt.xlabel('Gender (1=Female, 2=Male)')
plt.ylabel('Count')
plt.show()
```

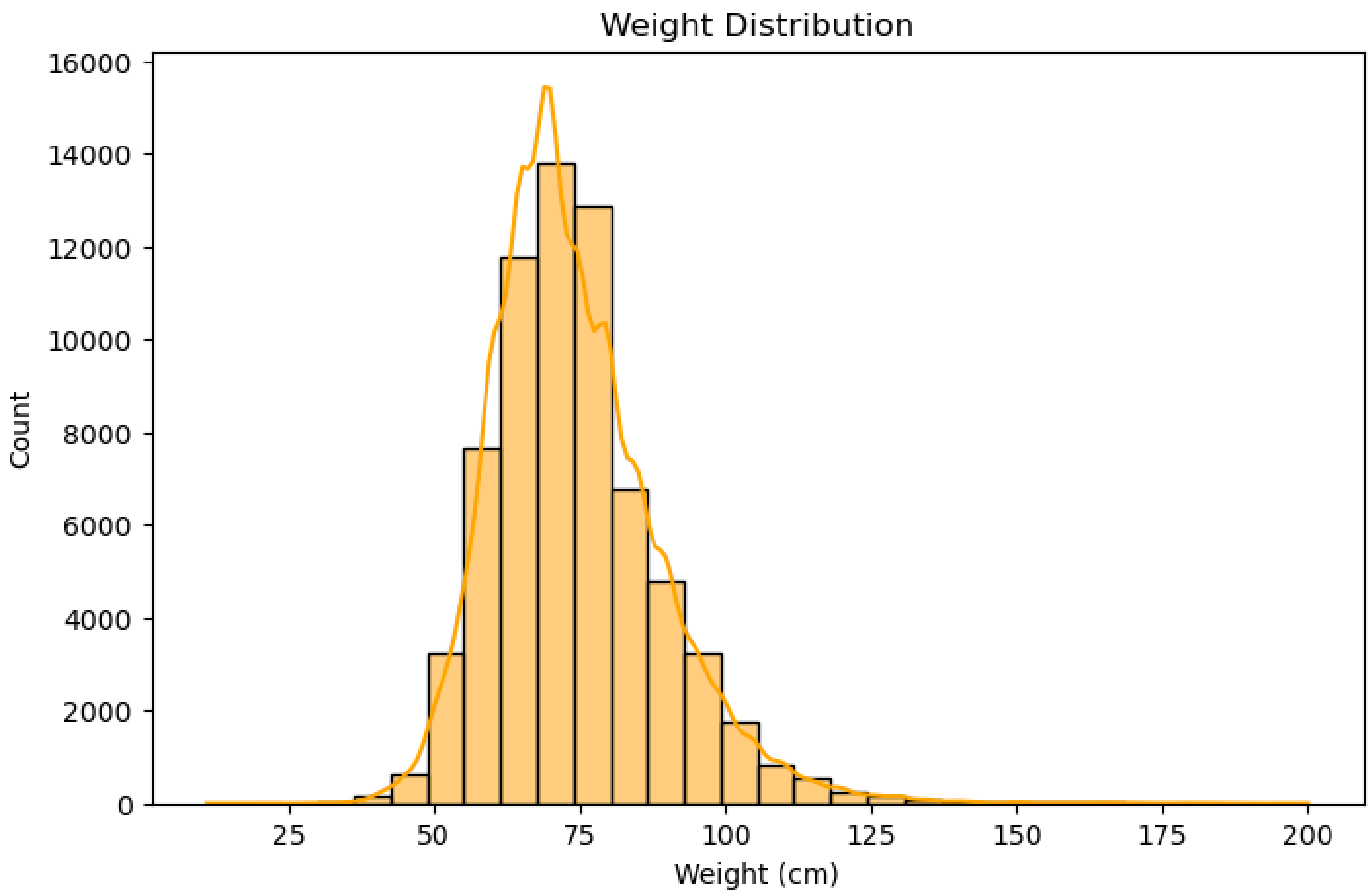


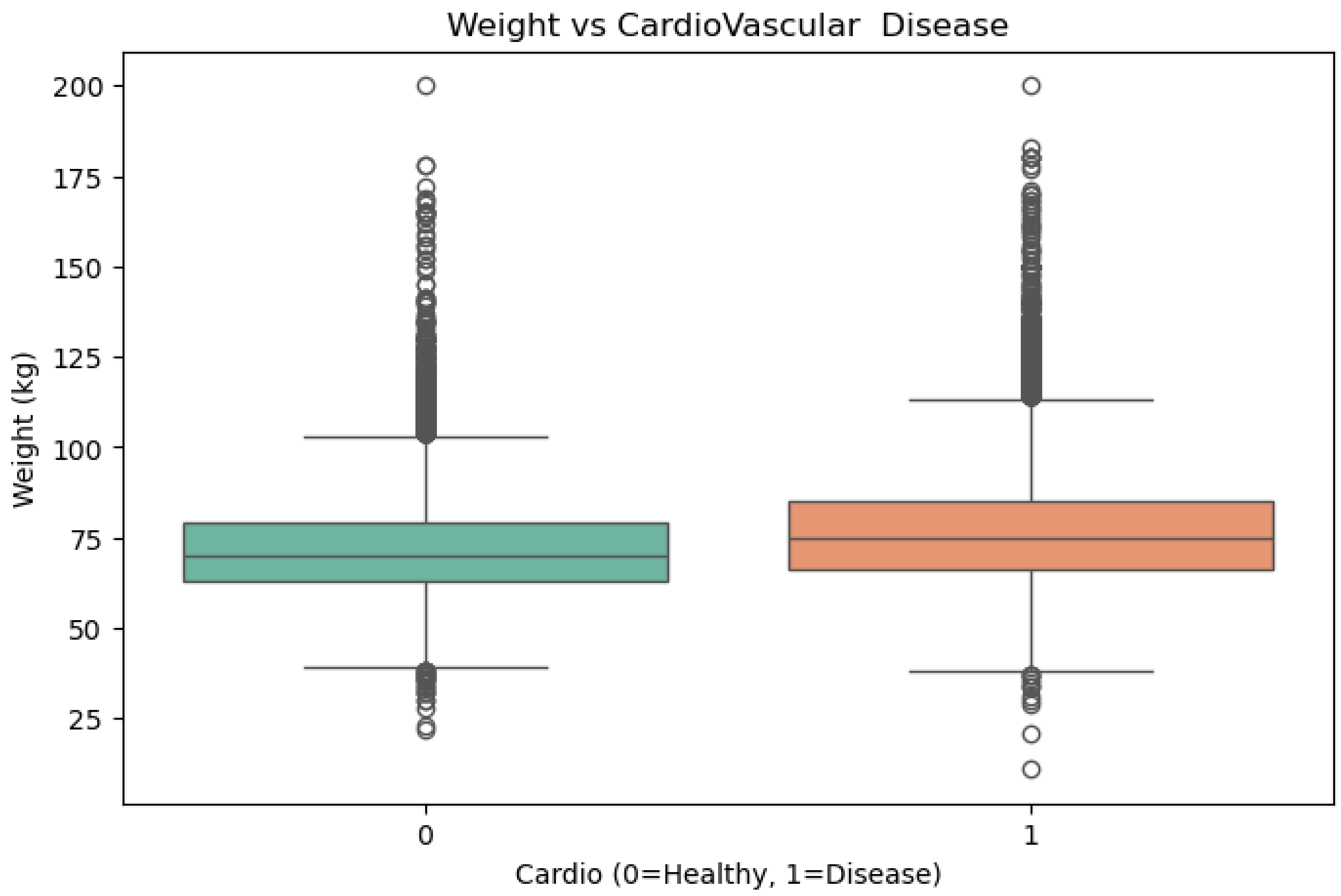
3. Anthropometrics (Height, Weight, BMI)

In [14]:
```python
#Height Distribution
plt.figure(figsize=(8,5))
sns.histplot(df['height'], bins=30, kde=True, color='green')
```

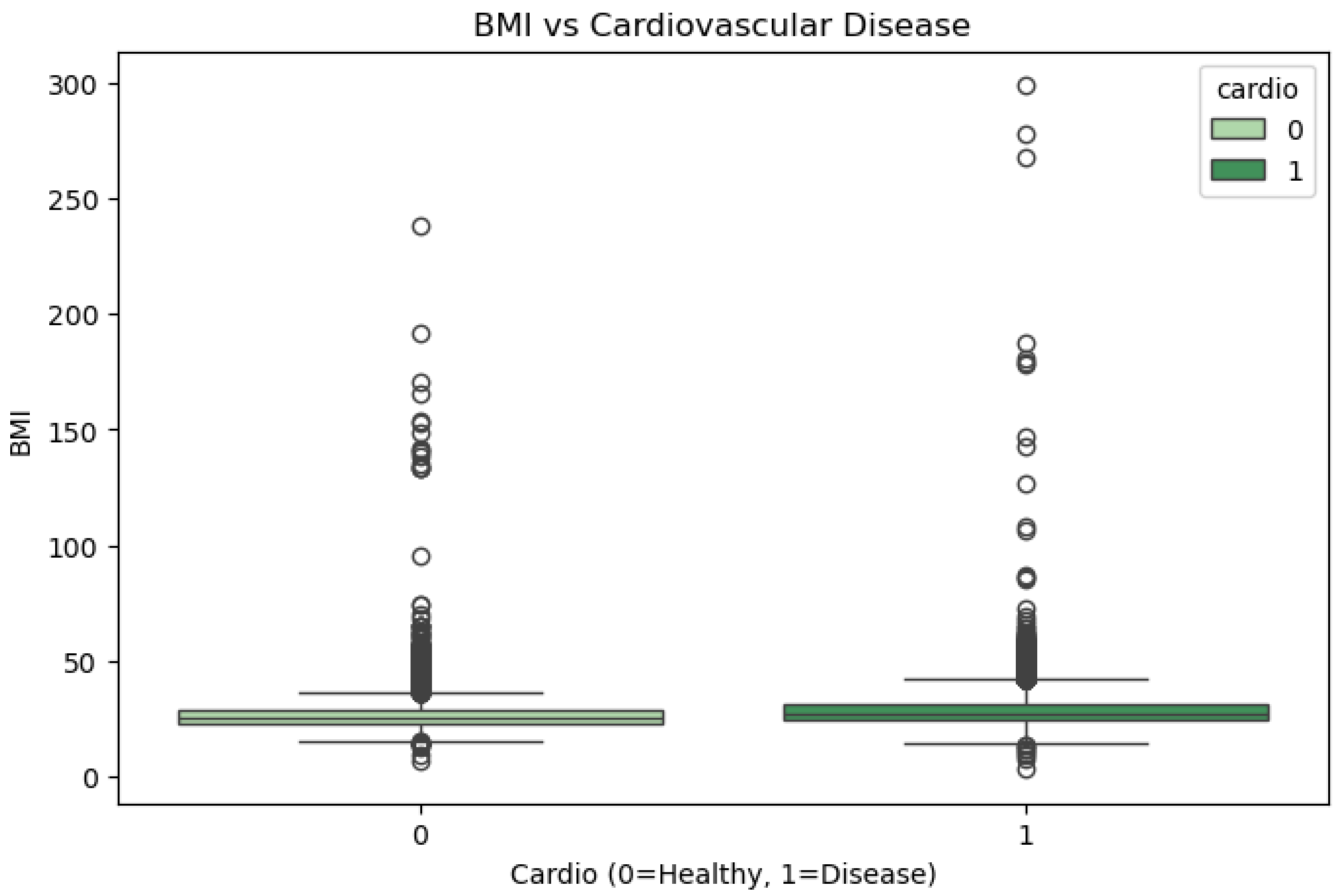
```
plt.title("Height Distribution")
plt.xlabel("Height (cm)")
plt.ylabel("Count")
plt.show()

#Weight Distribution
plt.figure(figsize=(8,5))
sns.histplot(df['weight'], bins=30, kde=True, color='orange')
plt.title("Weight Distribution")
plt.xlabel("Weight (cm)")
plt.ylabel("Count")
plt.show()

#Compare Weight vs Cardio
plt.figure(figsize=(8,5))
sns.boxplot(x='cardio', y="weight", data=df, palette='Set2')
plt.title("Weight vs CardioVascular  Disease")
plt.xlabel("Cardio (0=Healthy, 1=Disease)")
plt.ylabel("Weight (kg)")
plt.show()
```


Height Distribution
Count
25000
20000
15000
10000
5000
0
50
75
100
125
150
175
200
225
250
Height (cm)


Weight Distribution
16000
14000
12000
10000
8000
6000
4000
2000
0
Count
25
50
75
100
125
150
175
200
Weight (cm)



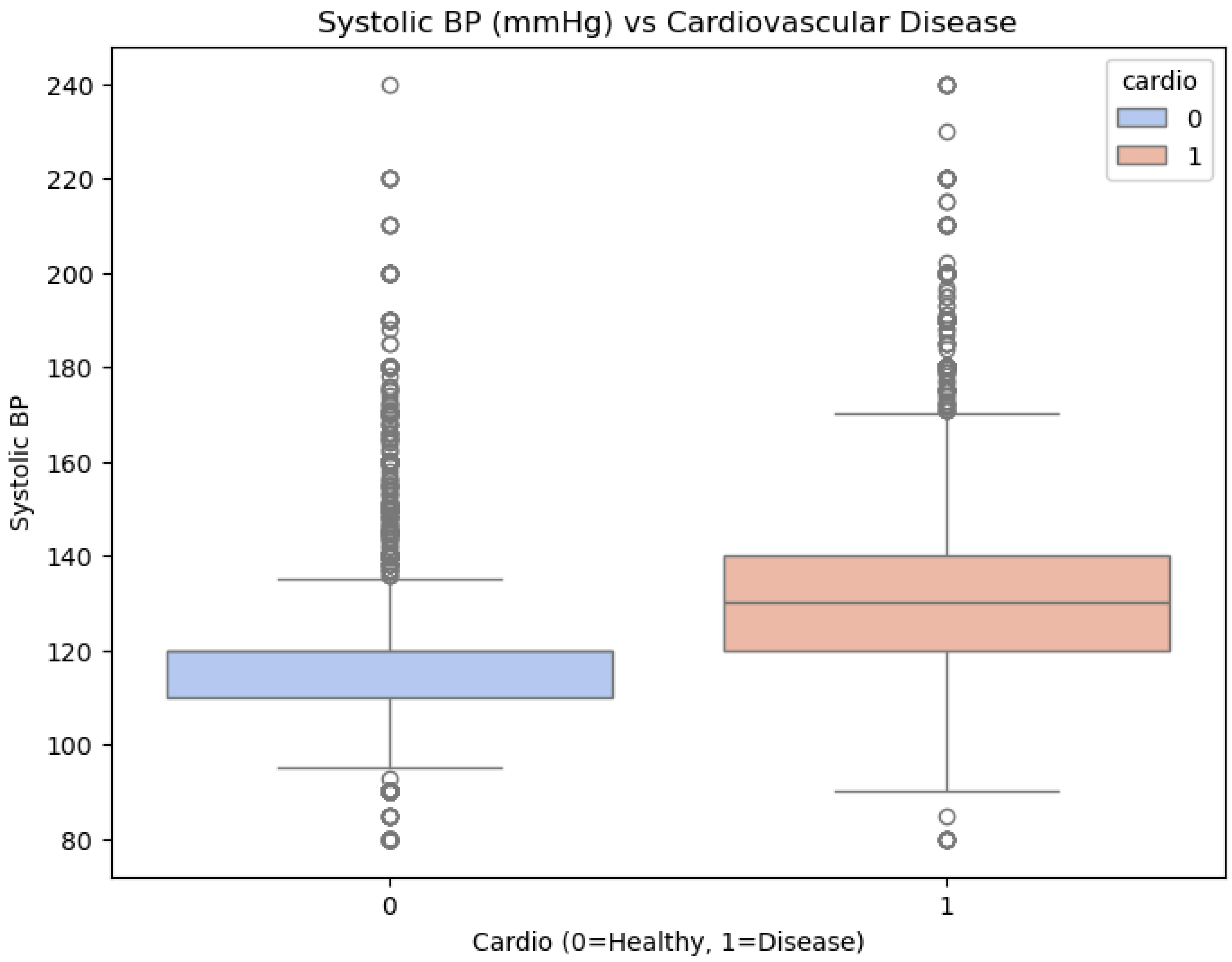
In [15]:
```
# Compare BMI by disease status
plt.figure(figsize=(8,5))
sns.boxplot(data= df, x='cardio', y='bmi', hue='cardio', palette='Greens')
plt.title("BMI vs Cardiovascular Disease")
plt.xlabel("Cardio (0=Healthy, 1=Disease)")
plt.ylabel("BMI")
plt.show()
```

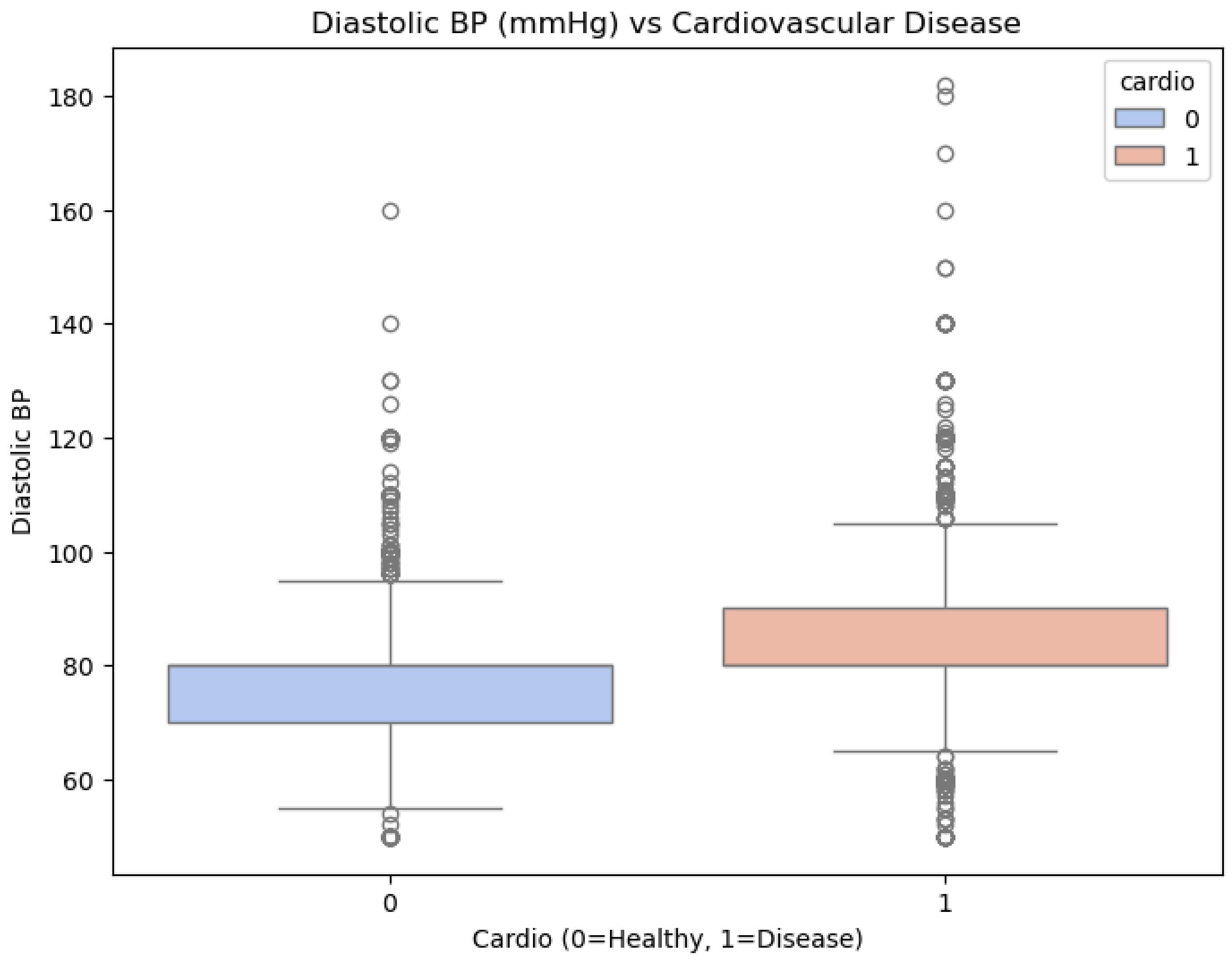


4. Medical Indicators (Blood Pressure, Cholesterol, Glucose)

In [16]:
```
# Compared Blood Pressure by Disease
plt.figure(figsize=(8,6))
sns.boxplot(data= df, x='cardio', y='ap_hi', hue='cardio', palette='coolwarm')
plt.title("Systolic BP (mmHg) vs Cardiovascular Disease")
plt.xlabel("Cardio (0=Healthy, 1=Disease)")
plt.ylabel("Systolic BP")
plt.show()

plt.figure(figsize=(8,6))
```

```
sns.boxplot(data= df, x='cardio', y='ap_lo', hue='cardio', palette='coolwarm')
plt.title("Diastolic BP (mmHg) vs Cardiovascular Disease")
plt.xlabel("Cardio (0=Healthy, 1=Disease)")
plt.ylabel("Diastolic BP")
plt.show()
```

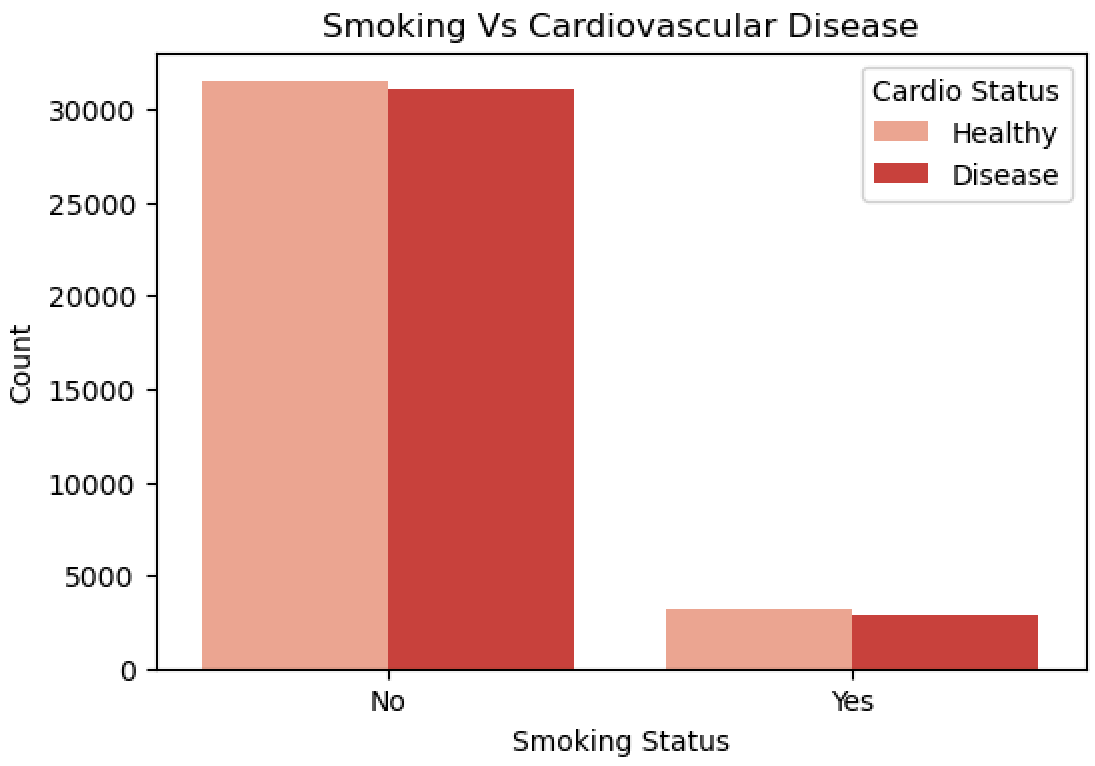


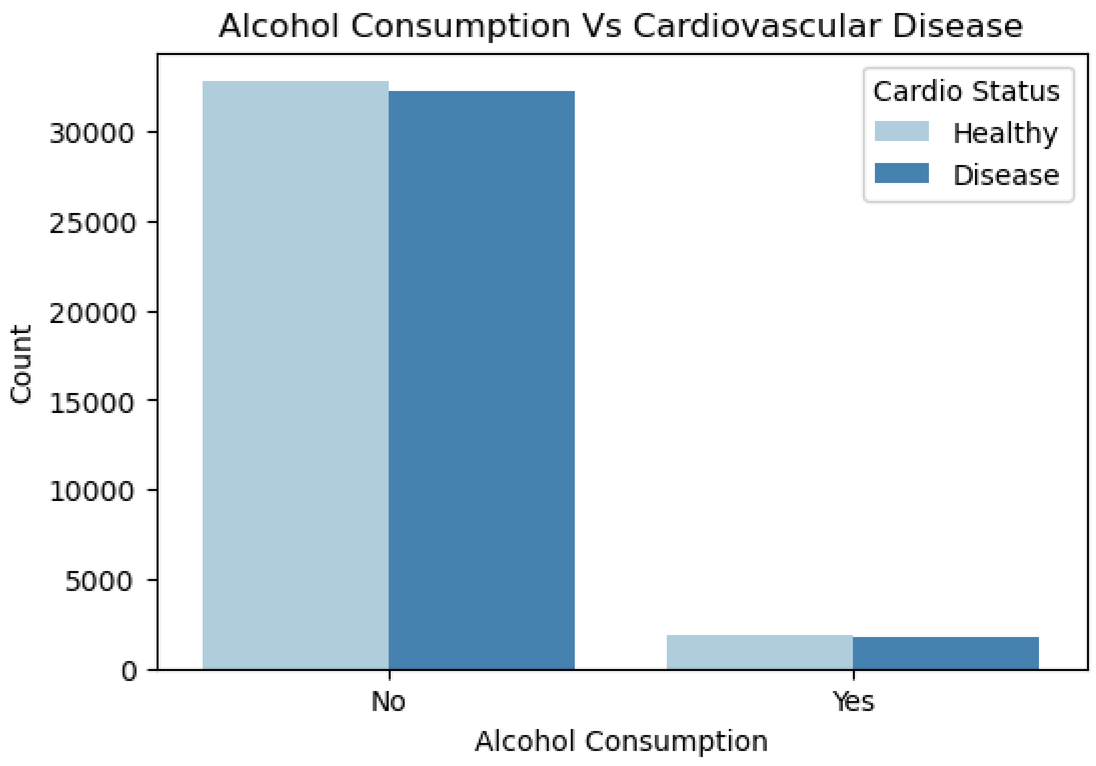


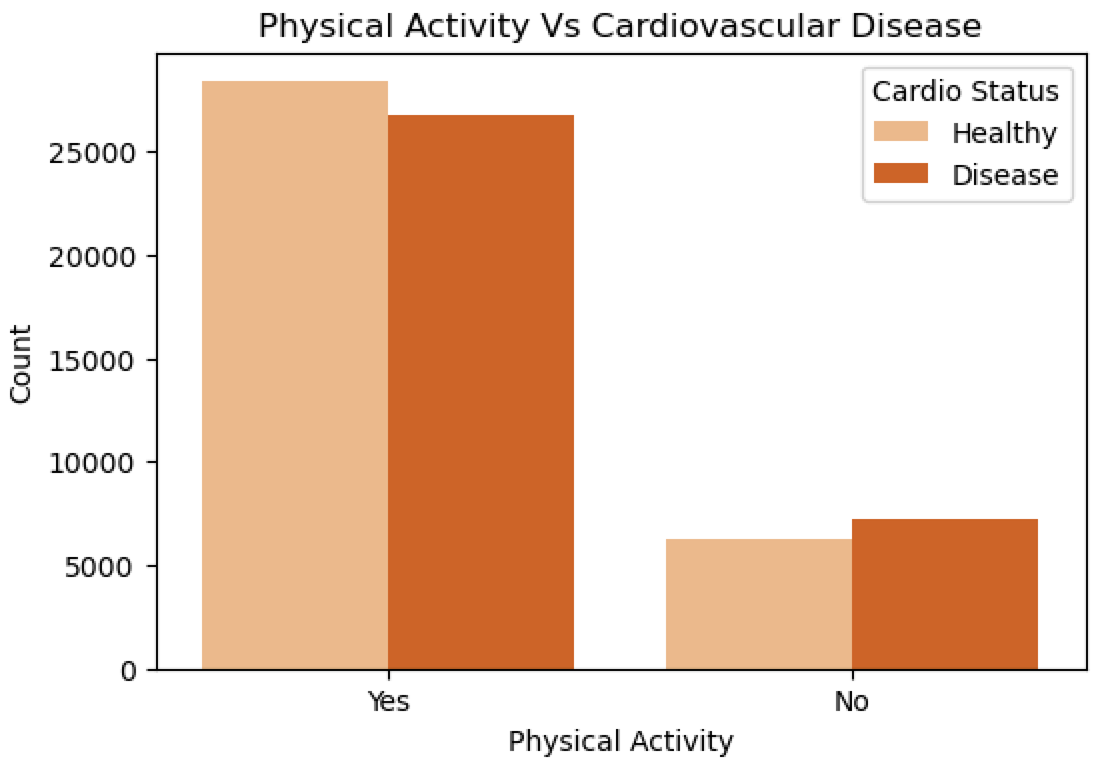
5. Lifestyle Factors (Smoke, Alcohol, Activity)

In [17]:
```
#Smoking vs Disease
#Create a temporary dataframe for plotting
df_plot = df.copy()
df_plot['smoke'] = df_plot['smoke'].map({0: "No", 1: "Yes"})
df_plot['cardio'] = df_plot['cardio'].map({0: "Healthy", 1: "Disease"})
```

```python

#Smoking vs Disease
plt.figure(figsize=(6,4))
sns.countplot(x='smoke', hue='cardio', data=df_plot, palette='Reds')
plt.title("Smoking Vs Cardiovascular Disease")
plt.xlabel("Smoking Status")
plt.ylabel("Count")
plt.legend(title="Cardio Status")
plt.show()


#Alcohol vs Disease
#Create a temporary dataframe for plotting
df_plot = df.copy()
df_plot['alco'] = df_plot['alco'].map({0: "No", 1: "Yes"})
df_plot['cardio'] = df_plot['cardio'].map({0: "Healthy", 1: "Disease"})

#Alcohol vs Disease
plt.figure(figsize=(6,4))
sns.countplot(x='alco', hue='cardio', data=df_plot, palette='Blues')
plt.title("Alcohol Consumption Vs Cardiovascular Disease")
plt.xlabel("Alcohol Consumption")
plt.ylabel("Count")
plt.legend(title="Cardio Status")
plt.show()


#Physical Activity vs Disease
df_plot['active'] = df_plot['active'].map({0: "No", 1: "Yes"})

#Physical Activity vs Disease
plt.figure(figsize=(6,4))
sns.countplot(x='active', hue='cardio', data=df_plot, palette='Oranges')
plt.title("Physical Activity Vs Cardiovascular Disease")
plt.xlabel("Physical Activity")
plt.ylabel("Count")
plt.legend(title="Cardio Status")
plt.show()
```

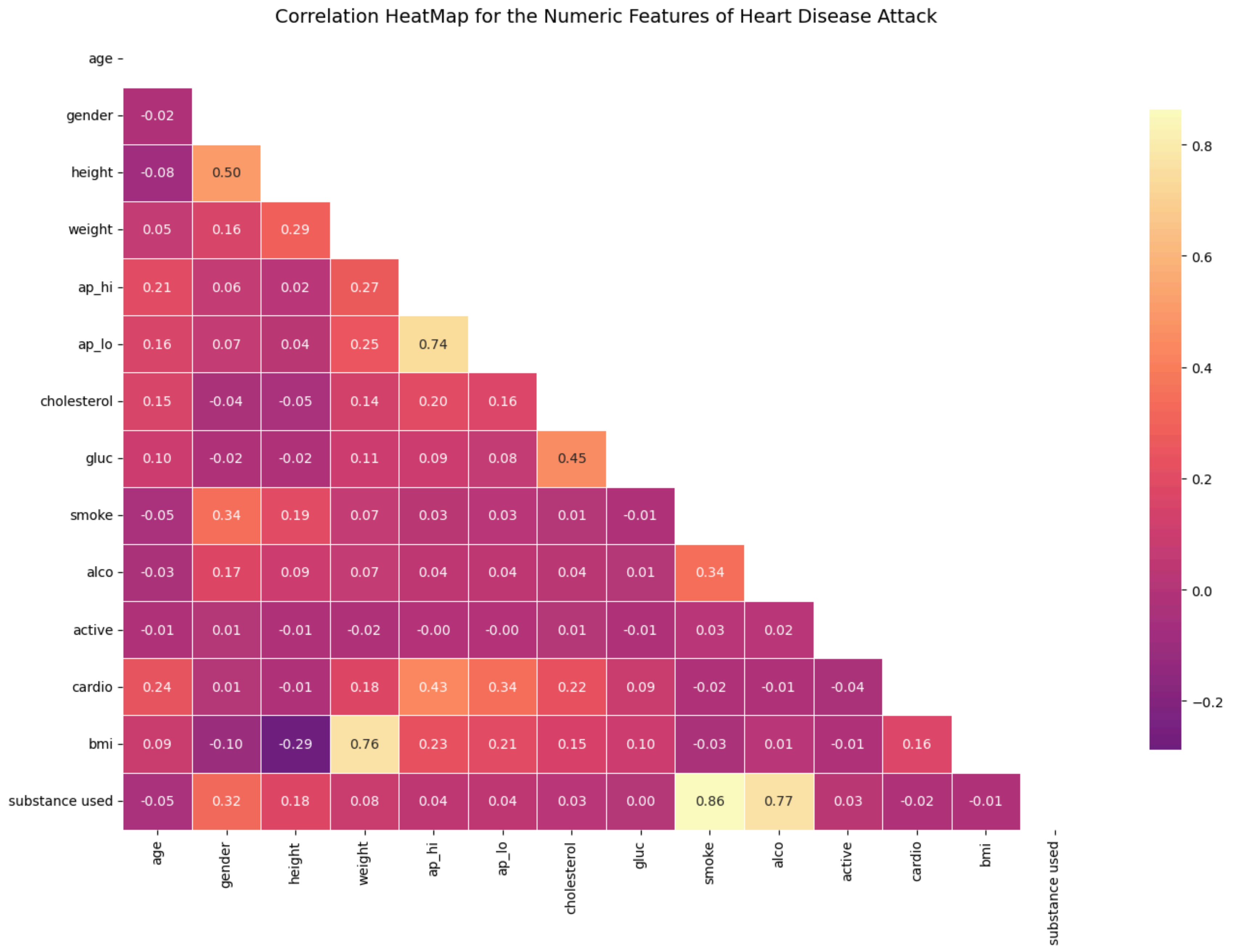

Smoking Vs Cardiovascular Disease
Count
30000
25000
20000
15000
10000
5000
0
No
Yes
Smoking Status
Cardio Status
Healthy
Disease


Alcohol Consumption Vs Cardiovascular Disease
Cardio Status
Healthy
Disease
Count
30000
25000
20000
15000
10000
5000
0
No
Yes
Alcohol Consumption



6. Correlation

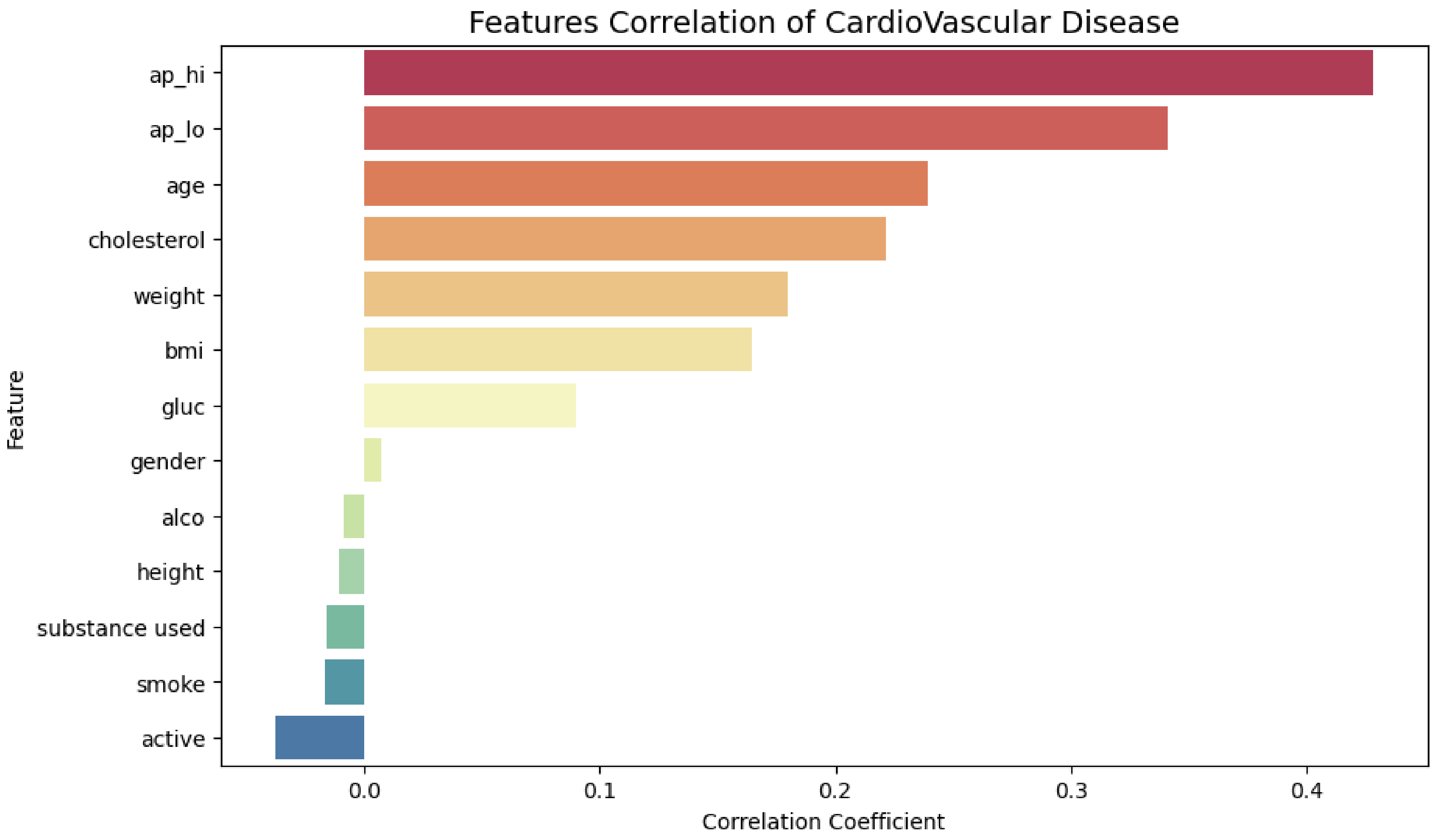
In [18]:
```
# ---  Correlation Heatmap -
plt.figure(figsize=(14,10))
 # Select only numeric columns for correlation
corr = df.select_dtypes(include=['number']).corr()
 # Focus on stronger correlations only
mask = np.triu(np.ones_like(corr, dtype=bool))  # mask upper triangle
sns.heatmap(
    corr,
    mask=mask,
    cmap="magma",
    center=0,
    annot=True,
    fmt=".2f",
    linewidths= 0.5,
    cbar_kws={"shrink": 0.8}
    )
plt.title("Correlation HeatMap for the Numeric Features of Heart Disease Attack", fontsize=14)
plt.tight_layout()
plt.show()

#Show correlation of features with target 'cardio'
target_corr = corr['cardio'].sort_values(ascending=False)
print("Correlation of Features with Target (cardio):\n")
print(target_corr)
```


Correlation HeatMap for the Numeric Features of Heart Disease Attack
age
gender -0.02
height -0.08 0.50
weight 0.05 0.16 0.29
ap_hi 0.21 0.06 0.02 0.27
ap_lo 0.16 0.07 0.04 0.25 0.74
cholesterol 0.15 -0.04 -0.05 0.14 0.20 0.16
gluc 0.10 -0.02 -0.02 0.11 0.09 0.08 0.45
smoke -0.05 0.34 0.19 0.07 0.03 0.03 0.01 -0.01
alco -0.03 0.17 0.09 0.07 0.04 0.04 0.04 0.01 0.34
active -0.01 0.01 -0.01 -0.02 -0.00 -0.00 0.01 -0.01 0.03 0.02
cardio 0.24 0.01 -0.01 0.18 0.43 0.34 0.22 0.09 -0.02 -0.01 -0.04
bmi 0.09 -0.10 -0.29 0.76 0.23 0.21 0.15 0.10 -0.03 0.01 -0.01 0.16
substance used -0.05 0.32 0.18 0.08 0.04 0.04 0.03 0.00 0.86 0.77 0.03 -0.02 -0.01
age gender height weight ap_hi ap_lo cholesterol gluc smoke alco active cardio bmi substance used
0.8
0.6
0.4
0.2
0.0
−0.2

```
Correlation of Features with Target (cardio):

cardio            1.000000
ap_hi             0.427838
ap_lo             0.341166
age               0.239069
cholesterol       0.221410
weight            0.179623
bmi               0.164265
gluc              0.089658
gender            0.007127
alco             -0.008639
height           -0.010773
substance used   -0.015656
smoke            -0.016207
active           -0.037558
Name: cardio, dtype: float64
```

7. Feature Importance

In [19]:
```
#Sorted Correlated with target
numeric_df = df.select_dtypes(include=['number'])
target_corr = (numeric_df.corr()["cardio"]
   .drop('cardio')
   .sort_values(ascending=False)
   )
# --- Visualize correlation strength --
plt.figure(figsize=(10, 6))
sns.barplot(x=target_corr, y=target_corr.index, palette='Spectral')
plt.title("Features Correlation of CardioVascular Disease", fontsize=14)
plt.xlabel("Correlation Coefficient")
plt.ylabel('Feature')
plt.show()
```



SPLITTING THE DATASET INTO TRAINING AND TESTING DATASET

In [20]:
```
#Seperate features (X) and target (y)

X = df.drop(columns='cardio')
y = df['cardio']

#Splitting the dataset into training (80%) and testing (20%)
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state = 42, stratify=y)
```

IMPORTING MODEL

In [21]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from xgboost import XGBClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
```

In [22]:

```
lr = LogisticRegression(max_iter=500)
dt = DecisionTreeClassifier(random_state=42)
rf = RandomForestClassifier(random_state=42)
xgb = XGBClassifier(use_label_encoder=False, eval_metric='logloss', random_state=42)
knn = KNeighborsClassifier()
gnb = GaussianNB()


models = {'Logistic Regression': lr, 'Decision Tree':dt, 'Random Forest': rf, "XGBoost": xgb, "KNeighborsClassifier"
         'Naive-Bayes': gnb}

for name, model in models.items():
    model.fit(X_train, y_train)
    print(f'{name} trained.')
```

```
Logistic Regression trained.
Decision Tree trained.
Random Forest trained.
XGBoost trained.
KNeighborsClassifier trained.
Naive-Bayes trained.
```

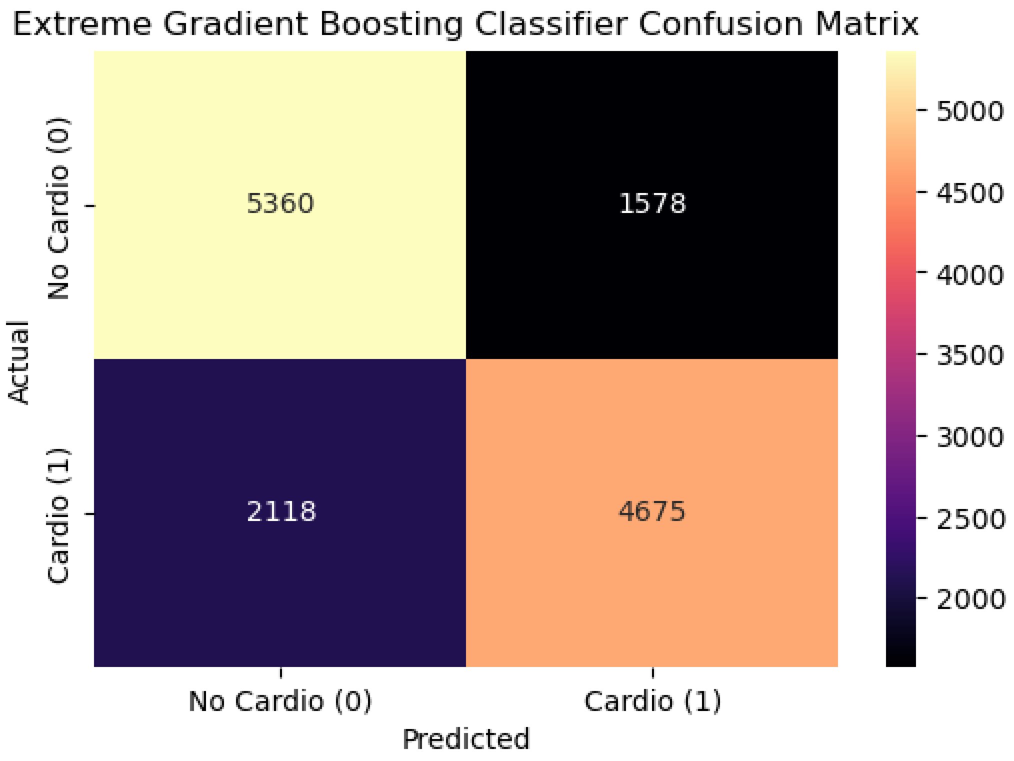
Model Evaluation Use Metrics: Accuracy, Precision, Recall, F1_Score and AUC_ROC

In [23]:
```
for name, model in models.items():
    y_pred = model.predict(X_test)
    print(f'{name}:')
    print(f'Accuracy: {accuracy_score(y_test, y_pred):.3f}')
    print(f'Precision: {precision_score(y_test, y_pred):.3f}')
    print(f'Recall: {recall_score(y_test, y_pred):.3f}')
    print(f'F1 Score: {f1_score(y_test, y_pred):.3f}')
    print(f'AUC-ROC: {roc_auc_score(y_test, model.predict_proba(X_test)[:,1]):.3f}\n')
```

```
Logistic Regression:
Accuracy: 0.724
Precision: 0.748
Recall: 0.668
F1 Score: 0.706
AUC-ROC: 0.785

Decision Tree:
Accuracy: 0.635
Precision: 0.634
Recall: 0.621
F1 Score: 0.628
AUC-ROC: 0.637

Random Forest:
Accuracy: 0.703
Precision: 0.704
Recall: 0.689
F1 Score: 0.696
AUC-ROC: 0.763

XGBoost:
Accuracy: 0.731
Precision: 0.748
Recall: 0.688
F1 Score: 0.717
AUC-ROC: 0.793

KNeighborsClassifier:
Accuracy: 0.688
Precision: 0.691
Recall: 0.668
F1 Score: 0.679
AUC-ROC: 0.735

Naive-Bayes:
Accuracy: 0.707
Precision: 0.753
Recall: 0.606
F1 Score: 0.671
AUC-ROC: 0.772
```

CONFUSION MATRIX

In [24]:
```
model_xgb = xgb

#Confusion Matrix
y_pred_xgb = model_xgb.predict(X_test)
cm = confusion_matrix(y_test, y_pred_xgb)

plt.figure(figsize=(6,4))
sns.heatmap(cm, annot=True, fmt='d', cmap='magma', xticklabels=['No Cardio (0)', 'Cardio (1)'],
            yticklabels=['No Cardio (0)', 'Cardio (1)'])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Extreme Gradient Boosting Classifier Confusion Matrix')
plt.show()
```



1. True Positives (4675): These are individuals who were correctly identified as having cardiovascular disease. The organization can take appropriate steps like offering medical attention, lifestyle interventions, or further screening.
2. False Positives (1578): These individuals were incorrectly flagged as having the condition when they are actually healthy. This could lead to unnecessary follow-ups or concern but ensures caution.
3. False Negative(2118): These individuals actually have the condition, but the model failed to detect it. This is the most concerning group, as they may go untreated. Reducing this number is essential to prevent serious health outcomes.
4. True Negative (5360): These are healthy individuals correctly identified as such. No action is needed, helping focus resources where they are truly needed.

APPLY STREAMLIT

In [25]:
```
import joblib
#save the trained model
joblib.dump(lr, 'best_model_lr.pkl')
print('Logistic Regression model saved as best_model_lr.pkl')
```

```
Logistic Regression model saved as best_model_lr.pkl
```

In [26]:
```
import joblib
#save the trained model
joblib.dump(xgb, 'best_model_xgb.pkl')
print('Extreme Gradient Boosting Classifier model saved as best_model_xgb.pkl')
```

```
Extreme Gradient Boosting Classifier model saved as best_model_xgb.pkl
```