In [ ]:

In [133...
```python
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

What characteristics define a perfectly healthy individual?

In [104...
```python
df=pd.read_csv("heart1.csv")
print(df.head())
```

```
  Patient ID  Age     Sex  Cholesterol Blood Pressure  Heart Rate  Diabetes  \
0    BMW7812   67    Male          208         158/88          72         0
1    CZE1114   21    Male          389         165/93          98         1
2    BNI9906   21  Female          324         174/99          72         1
3    JLN3497   84    Male          383        163/100          73         1
4    GFO8847   66    Male          318          91/88          93         1

   Family History  Smoking  Obesity  ...  Income        BMI Triglycerides  \
0               0        1        0  ...  261404  31.251233           286
1               1        1        1  ...  285768  27.194973           235
2               0        0        0  ...  235282  28.176571           587
3               1        1        0  ...  125640  36.464704           378
4               1        1        1  ...  160555  21.809144           231

   Physical Activity Days Per Week  Sleep Hours Per Day    Country  \
0                                0                    6  Argentina
1                                1                    7     Canada
2                                4                    4     France
3                                3                    4     Canada
4                                1                    5   Thailand

       Continent           Hemisphere  Unnamed: 25  Heart Attack Risk
0  South America  Southern Hemisphere          NaN                  0
1  North America  Northern Hemisphere          NaN                  0
2         Europe  Northern Hemisphere          NaN                  0
3  North America  Northern Hemisphere          NaN                  0
4           Asia  Northern Hemisphere          NaN                  0

[5 rows x 27 columns]
```

In [105...
```python
#no of column no of row
print(df.info())
print(df.shape)
print(df.shape[1])
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8763 entries, 0 to 8762
Data columns (total 27 columns):
 #   Column                           Non-Null Count  Dtype  
---  ------                           --------------  -----  
 0   Patient ID                       8763 non-null   object 
 1   Age                              8763 non-null   int64  
 2   Sex                              8763 non-null   object 
 3   Cholesterol                      8763 non-null   int64  
 4   Blood Pressure                   8763 non-null   object 
 5   Heart Rate                       8763 non-null   int64  
 6   Diabetes                         8763 non-null   int64  
 7   Family History                   8763 non-null   int64  
 8   Smoking                          8763 non-null   int64  
 9   Obesity                          8763 non-null   int64  
 10  Alcohol Consumption              8763 non-null   int64  
 11  Exercise Hours Per Week          8763 non-null   float64
 12  Diet                             8763 non-null   object 
 13  Previous Heart Problems          8763 non-null   int64  
 14  Medication Use                   8763 non-null   int64  
 15  Stress Level                     8763 non-null   int64  
 16  Sedentary Hours Per Day          8763 non-null   float64
 17  Income                           8763 non-null   int64  
 18  BMI                              8763 non-null   float64
 19  Triglycerides                    8763 non-null   int64  
 20  Physical Activity Days Per Week  8763 non-null   int64  
 21  Sleep Hours Per Day              8763 non-null   int64  
 22  Country                          8763 non-null   object 
 23  Continent                        8763 non-null   object 
 24  Hemisphere                       8763 non-null   object 
 25  Unnamed: 25                      0 non-null      float64
 26  Heart Attack Risk                8763 non-null   int64  
dtypes: float64(4), int64(16), object(7)
memory usage: 1.8+ MB
None
(8763, 27)
27
```

check any null value

In [132…

```
df = df.drop(columns=['Unnamed: 25'])

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

```
Patient ID                         0
Age                                0
Sex                                0
Cholesterol                        0
Blood Pressure                     0
Heart Rate                         0
Diabetes                           0
Family History                     0
Smoking                            0
Obesity                            0
Alcohol Consumption                0
Exercise Hours Per Week            0
Diet                               0
Previous Heart Problems            0
Medication Use                     0
Stress Level                       0
Sedentary Hours Per Day            0
Income                             0
BMI                                0
Triglycerides                      0
Physical Activity Days Per Week    0
Sleep Hours Per Day                0
Country                            0
Continent                          0
Hemisphere                         0
Heart Attack Risk                  0
dtype: int64
```

In [ ]:

check any duplicate

In [107…
```
print(df.duplicated().sum())
```

```
0
```

check outlier

summary statistic help to check any outlier values in a column

column which lot of difference between minimum values and maxir value the outlier will present

min and max: If there's a big gap between them, check for outliers.

25%, 50%, 75%: These are quartiles. If the max is far above 75% (or far below 25%), it's a sign of potential outliers.

To check any outlier present in column

1.summary statistic help to check any outlier values in a column

2.column which lot of difference between minimum values and max value the outlier will present

3.min and max: If there's a big gap between them, check for outliers

4.25%, 50%, 75%: These are quartiles. If the max is far above 75% (or far below 25%), it's a sign of potential outliers.

In [108…

```
print(df.describe())
#all columns except dist code year state code must contain outlier
```

	Age	Cholesterol	Heart Rate	Diabetes	Family History
count	8763.000000	8763.000000	8763.000000	8763.000000	8763.000000
mean	53.707977	259.877211	75.021682	0.652288	0.492982
std	21.249509	80.863276	20.550948	0.476271	0.499979
min	18.000000	120.000000	40.000000	0.000000	0.000000
25%	35.000000	192.000000	57.000000	0.000000	0.000000
50%	54.000000	259.000000	75.000000	1.000000	0.000000
75%	72.000000	330.000000	93.000000	1.000000	1.000000
max	90.000000	400.000000	110.000000	1.000000	1.000000

	Smoking	Obesity	Alcohol Consumption	Exercise Hours Per Week
count	8763.000000	8763.000000	8763.000000	8763.000000
mean	0.896839	0.501426	0.598083	10.014284
std	0.304186	0.500026	0.490313	5.783745
min	0.000000	0.000000	0.000000	0.002442
25%	1.000000	0.000000	0.000000	4.981579
50%	1.000000	1.000000	1.000000	10.069559
75%	1.000000	1.000000	1.000000	15.050018
max	1.000000	1.000000	1.000000	19.998709

	Previous Heart Problems	Medication Use	Stress Level
count	8763.000000	8763.000000	8763.000000
mean	0.495835	0.498345	5.469702
std	0.500011	0.500026	2.859622
min	0.000000	0.000000	1.000000
25%	0.000000	0.000000	3.000000
50%	0.000000	0.000000	5.000000
75%	1.000000	1.000000	8.000000
max	1.000000	1.000000	10.000000

	Sedentary Hours Per Day	Income	BMI	Triglycerides
count	8763.000000	8763.000000	8763.000000	8763.000000
mean	5.993690	158263.181901	28.891446	417.677051
std	3.466359	80575.190806	6.319181	223.748137
min	0.001263	20062.000000	18.002337	30.000000
25%	2.998794	88310.000000	23.422985	225.500000
50%	5.933622	157866.000000	28.768999	417.000000
75%	9.019124	227749.000000	34.324594	612.000000
max	11.999313	299954.000000	39.997211	800.000000

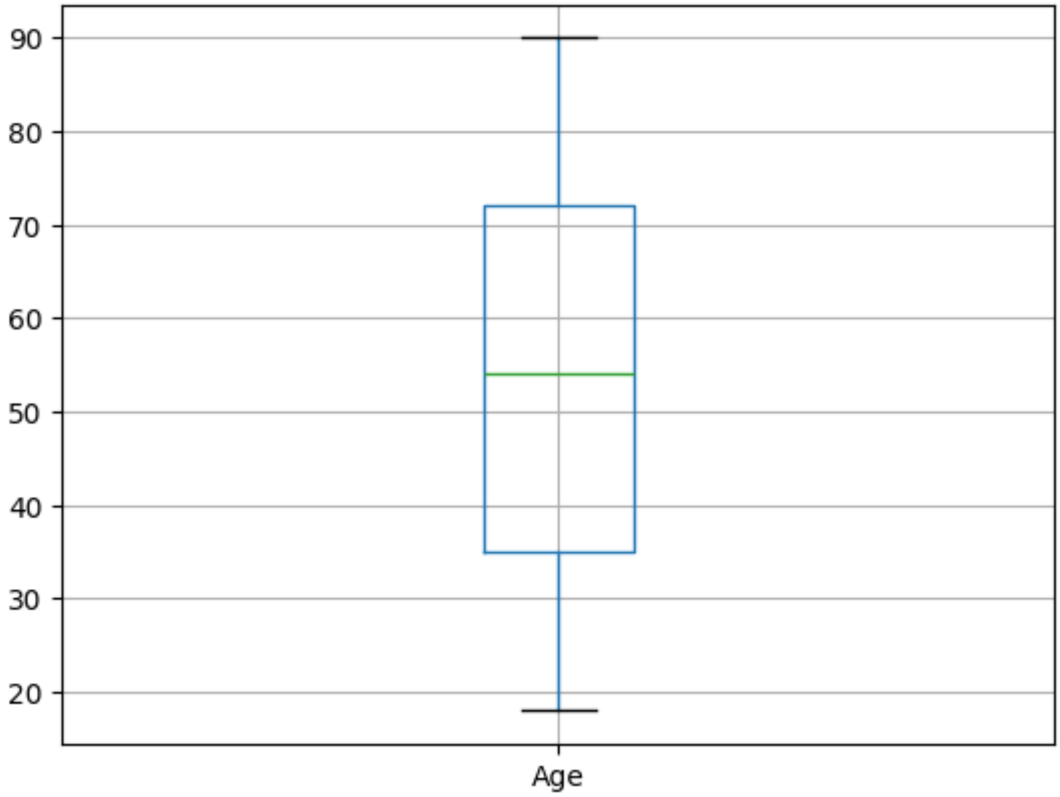
	Physical Activity Days Per Week	Sleep Hours Per Day	Unnamed: 25
count	8763.000000	8763.000000	0.0
mean	3.489672	7.023508	NaN
std	2.282687	1.988473	NaN
min	0.000000	4.000000	NaN
25%	2.000000	5.000000	NaN
50%	3.000000	7.000000	NaN
75%	5.000000	9.000000	NaN
max	7.000000	10.000000	NaN

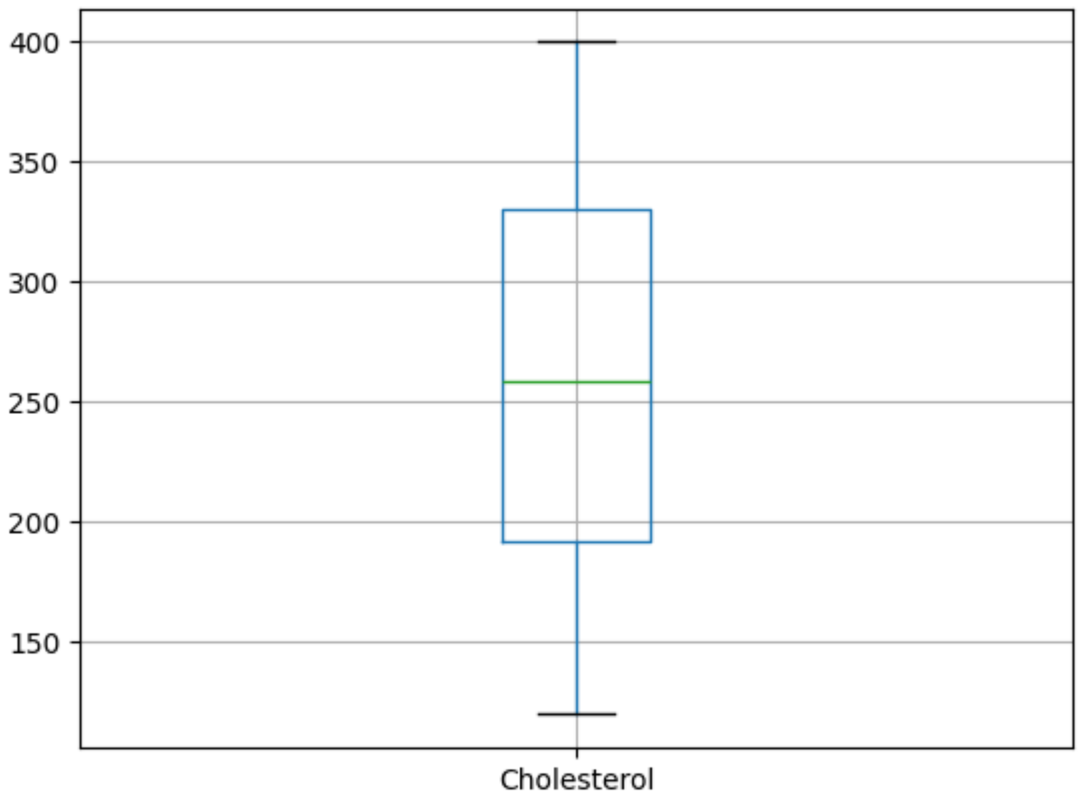
	Heart Attack Risk
count	8763.000000
mean	0.358211
std	0.479502
min	0.000000
25%	0.000000
50%	0.000000
75%	1.000000
max	1.000000

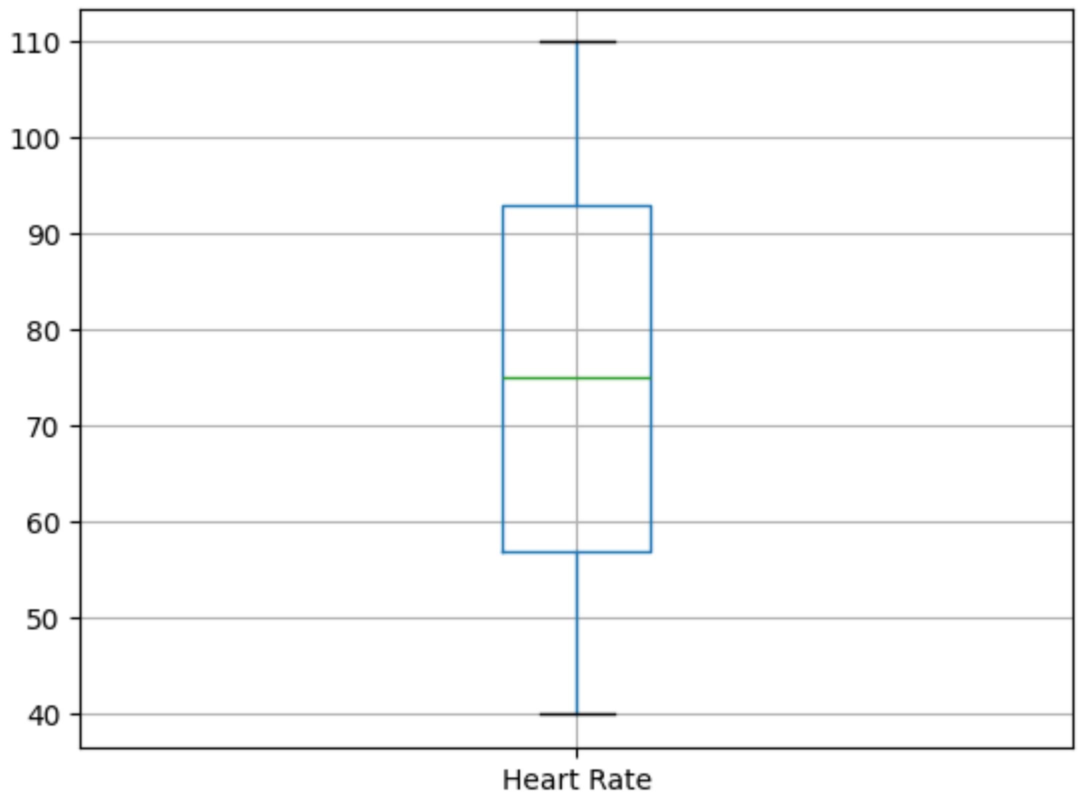
To check outlier use boxplot to check outlier

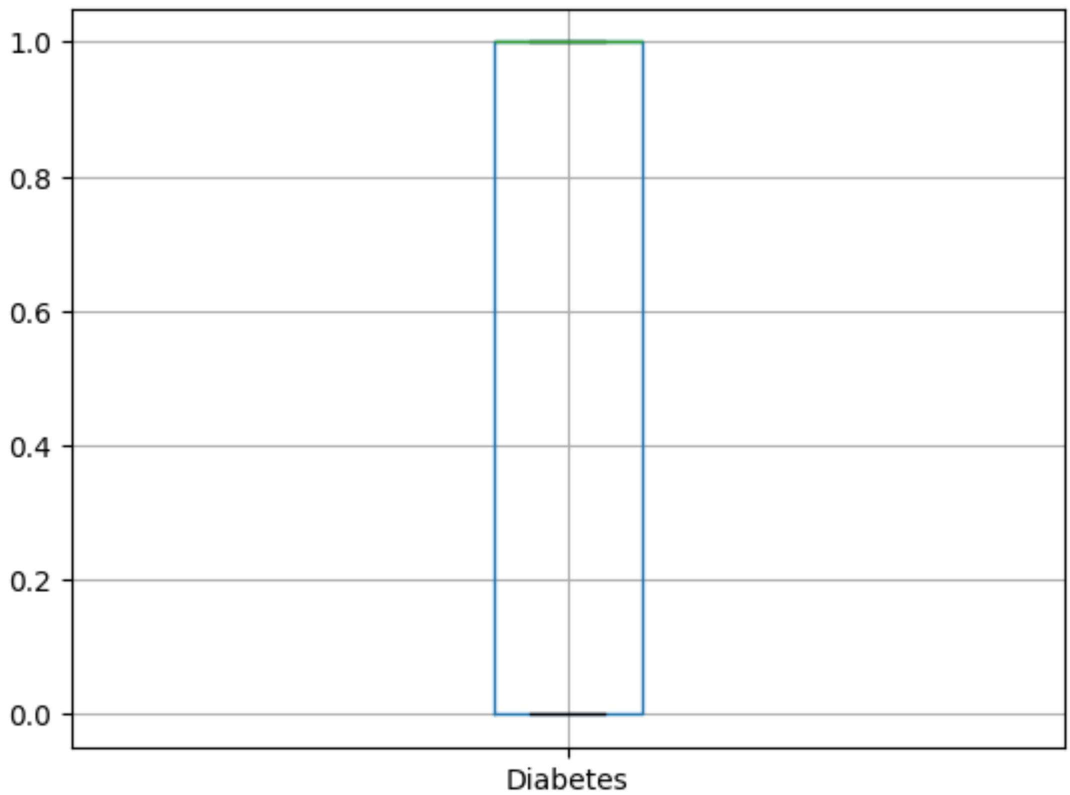
In [109…

```
# Step 1: Filter only numeric columns
numeric_cols = df.select_dtypes(include='number').columns

# Step 2: Choose top 75 (or however many you need)
#outlier_columns = numeric_cols[:75]



for i, n_col in enumerate(numeric_cols):
    df.boxplot(column=n_col)
    plt.show()
```

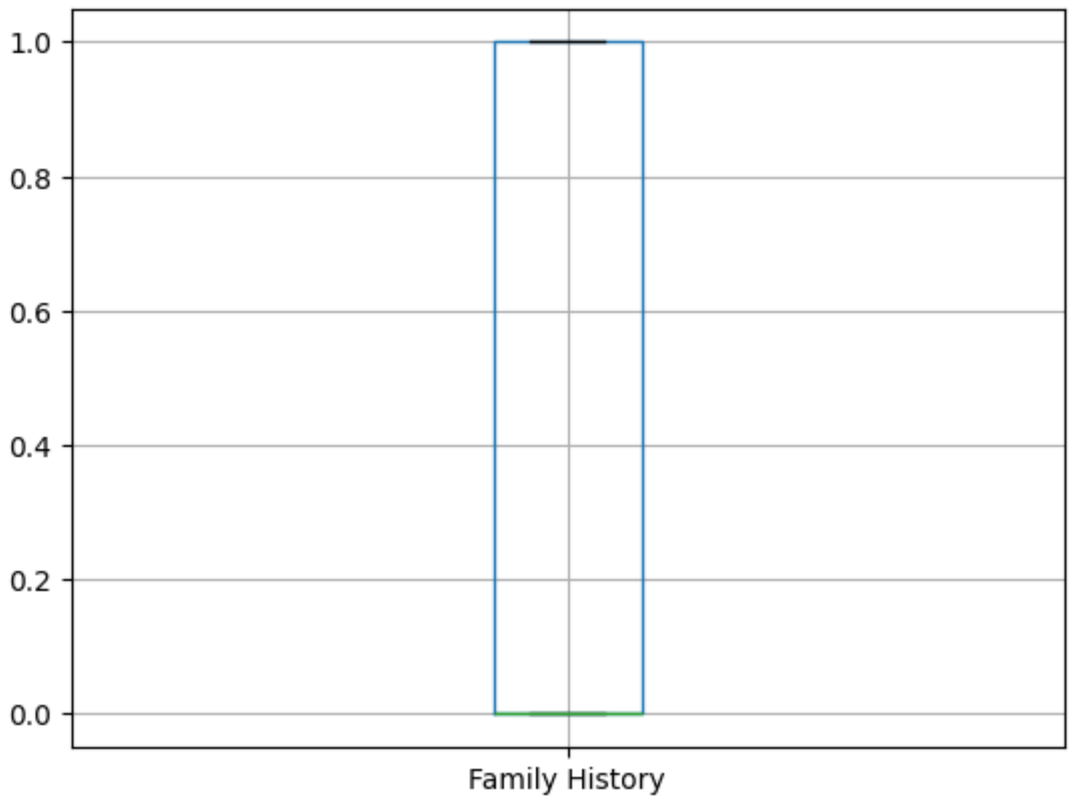



400
350
300
250
200
150
Cholesterol

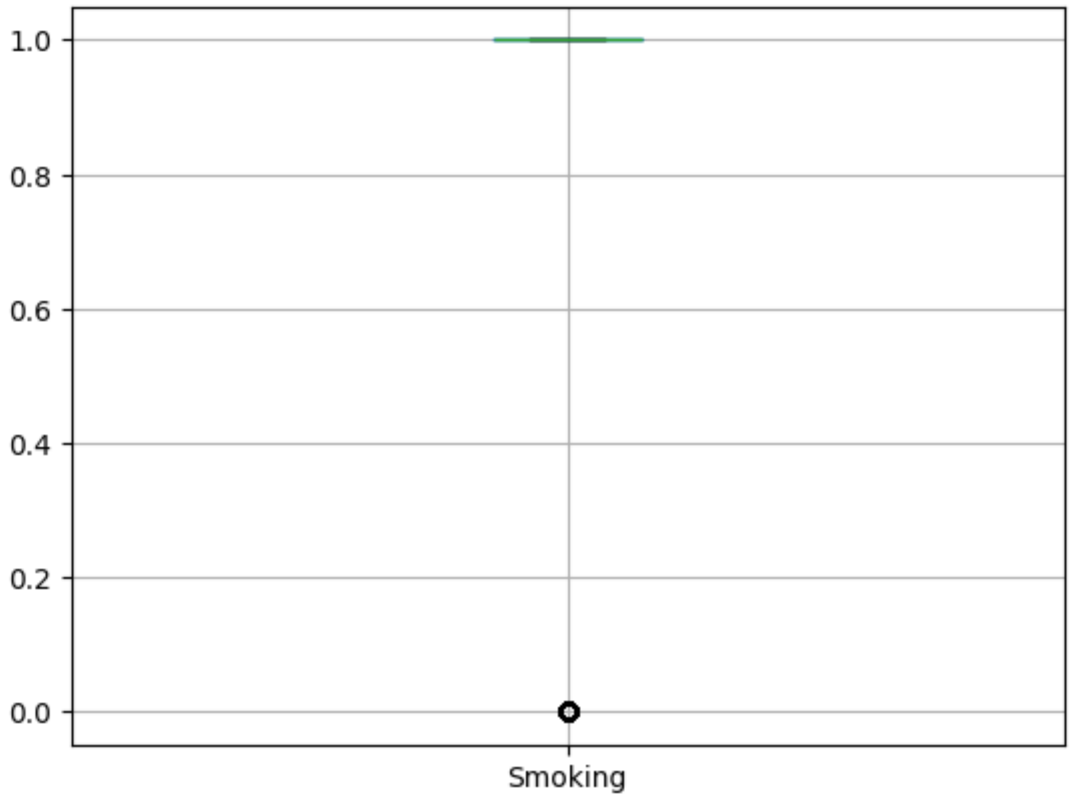

110
100
90
80
70
60
50
40
Heart Rate

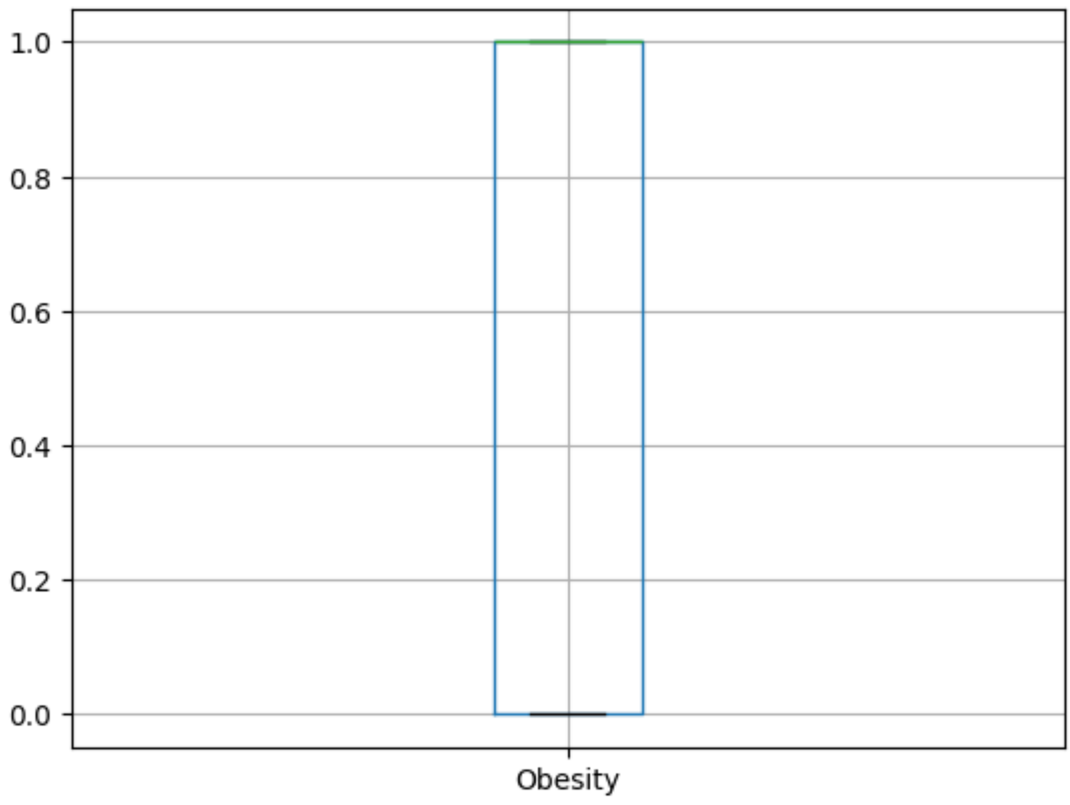


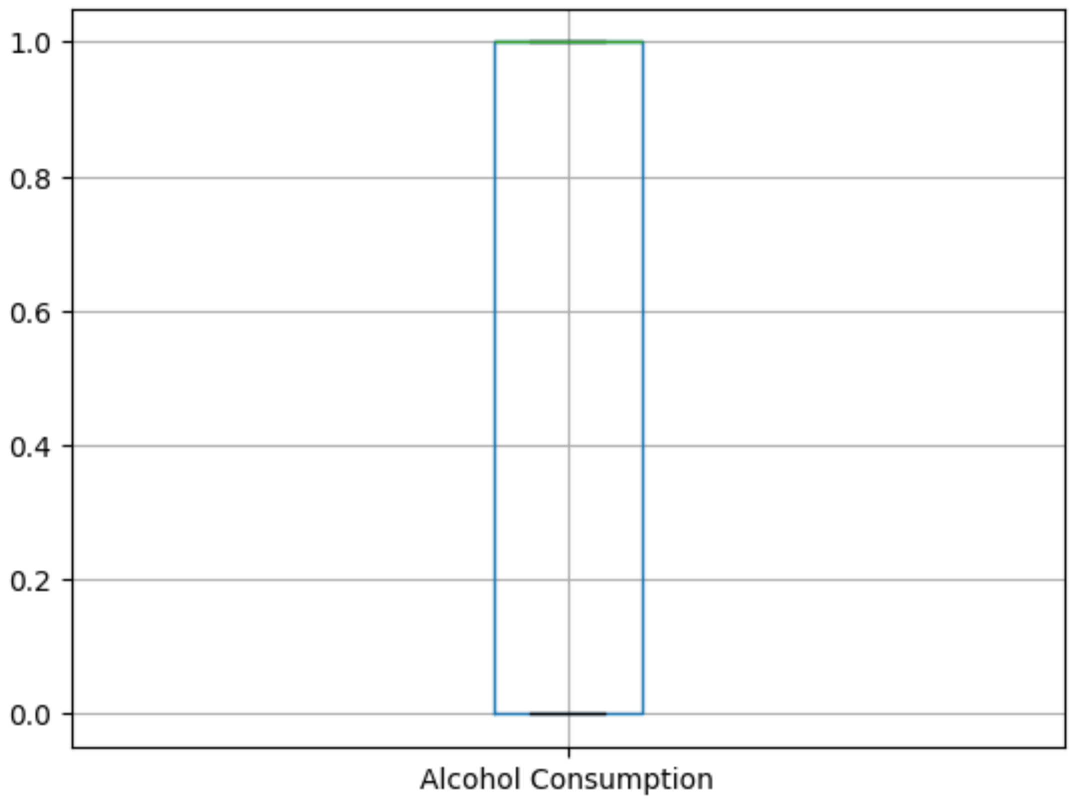
1.0
0.8
0.6
0.4
0.2
0.0
Diabetes

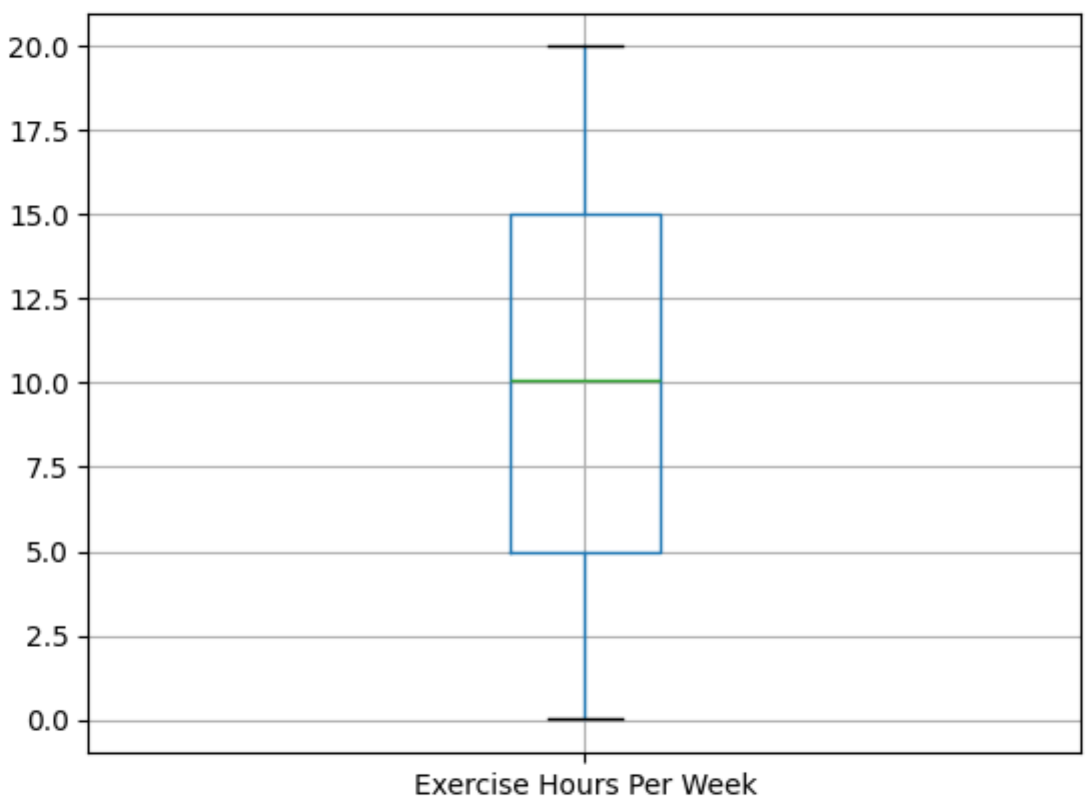


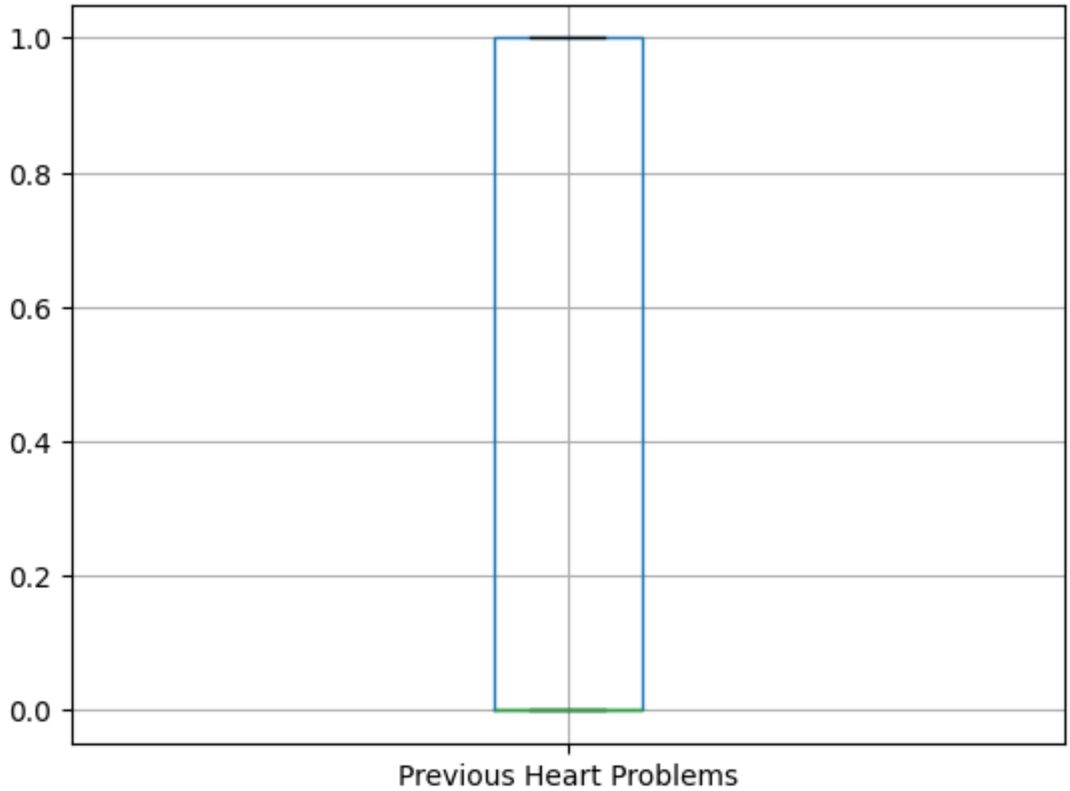
1.0
0.8
0.6
0.4
0.2
0.0
Family History

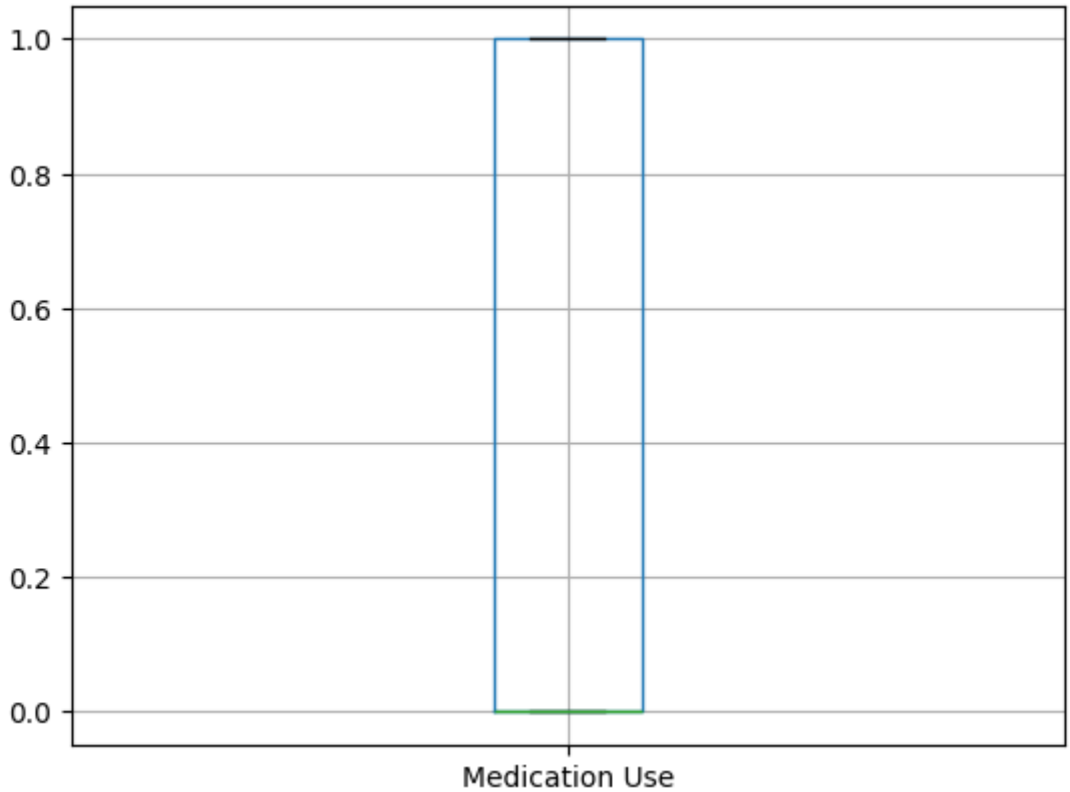

1.0
0.8
0.6
0.4
0.2
0.0
Smoking

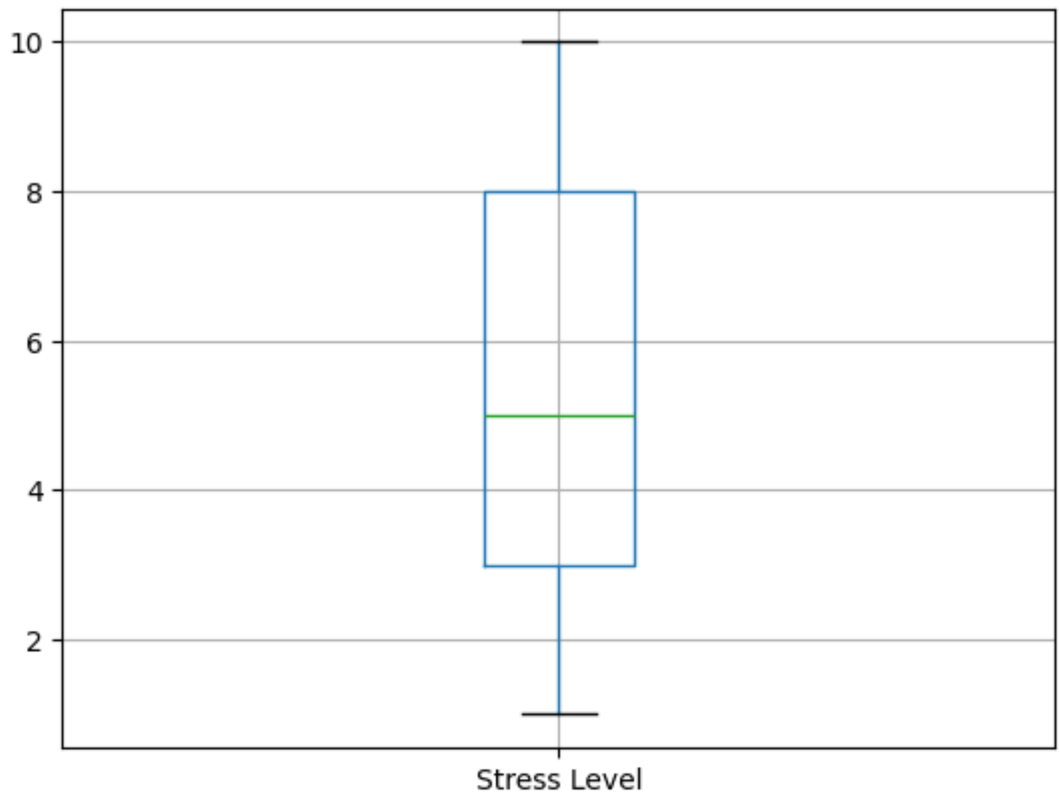

1.0
0.8
0.6
0.4
0.2
0.0
Obesity

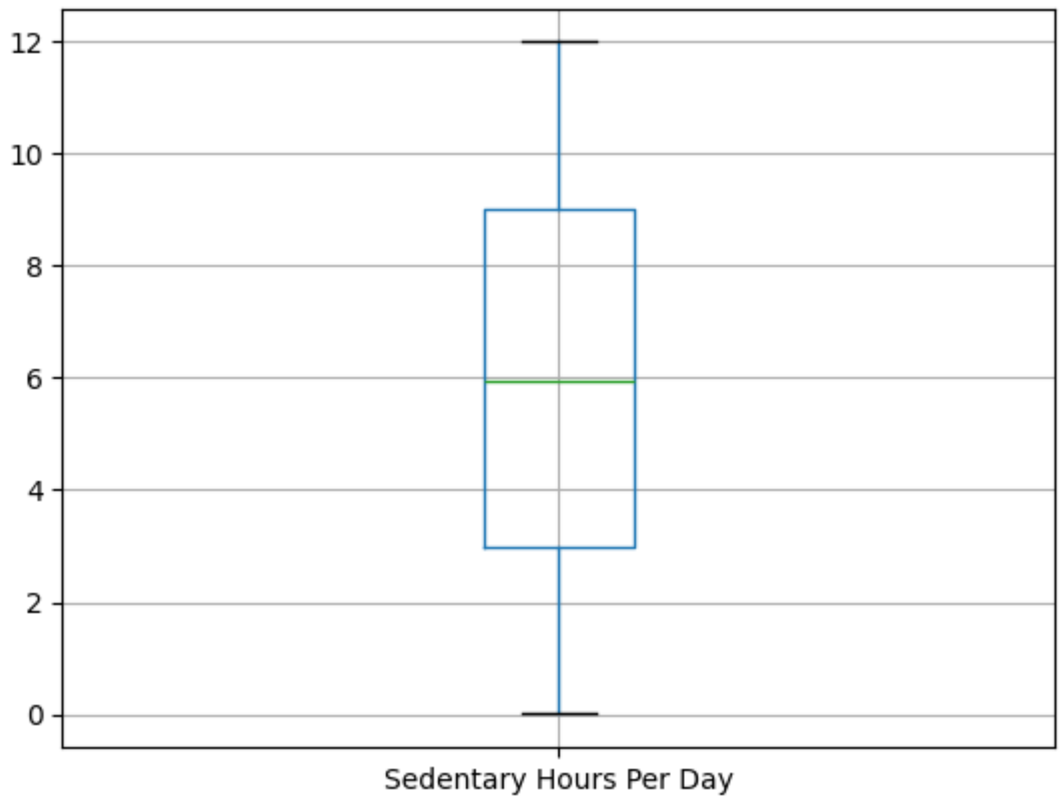

1.0
0.8
0.6
0.4
0.2
0.0
Alcohol Consumption

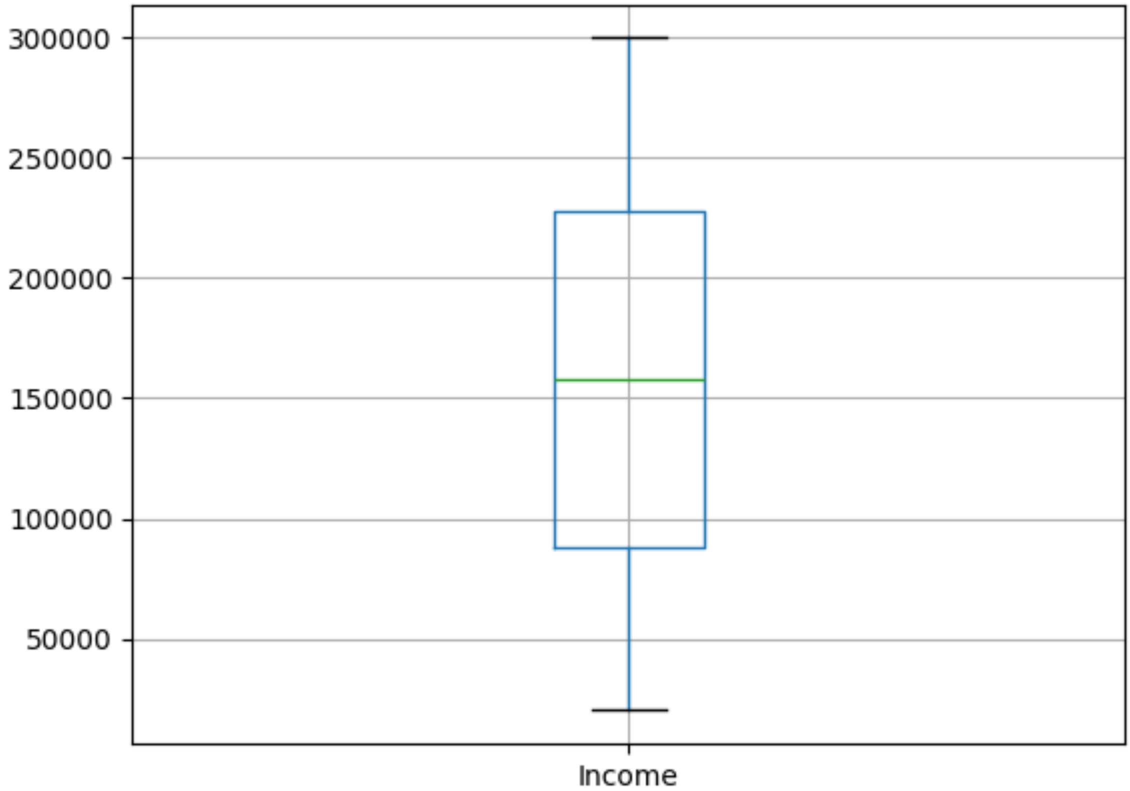

20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
Exercise Hours Per Week

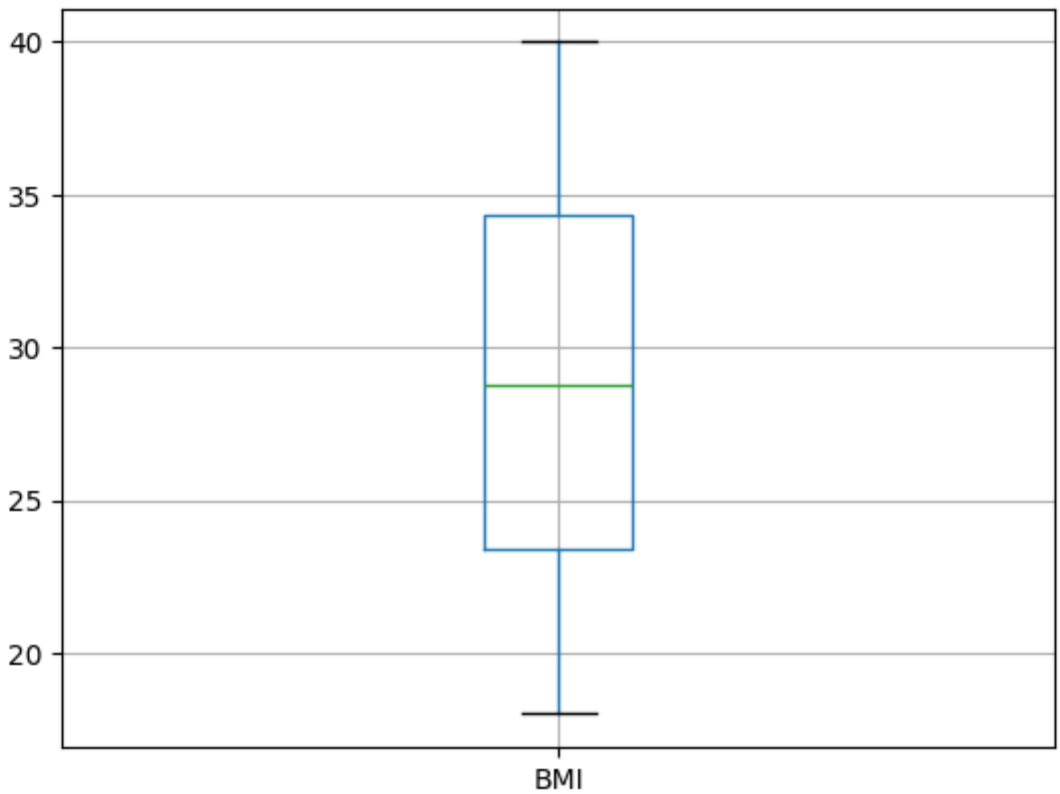

1.0
0.8
0.6
0.4
0.2
0.0
Previous Heart Problems

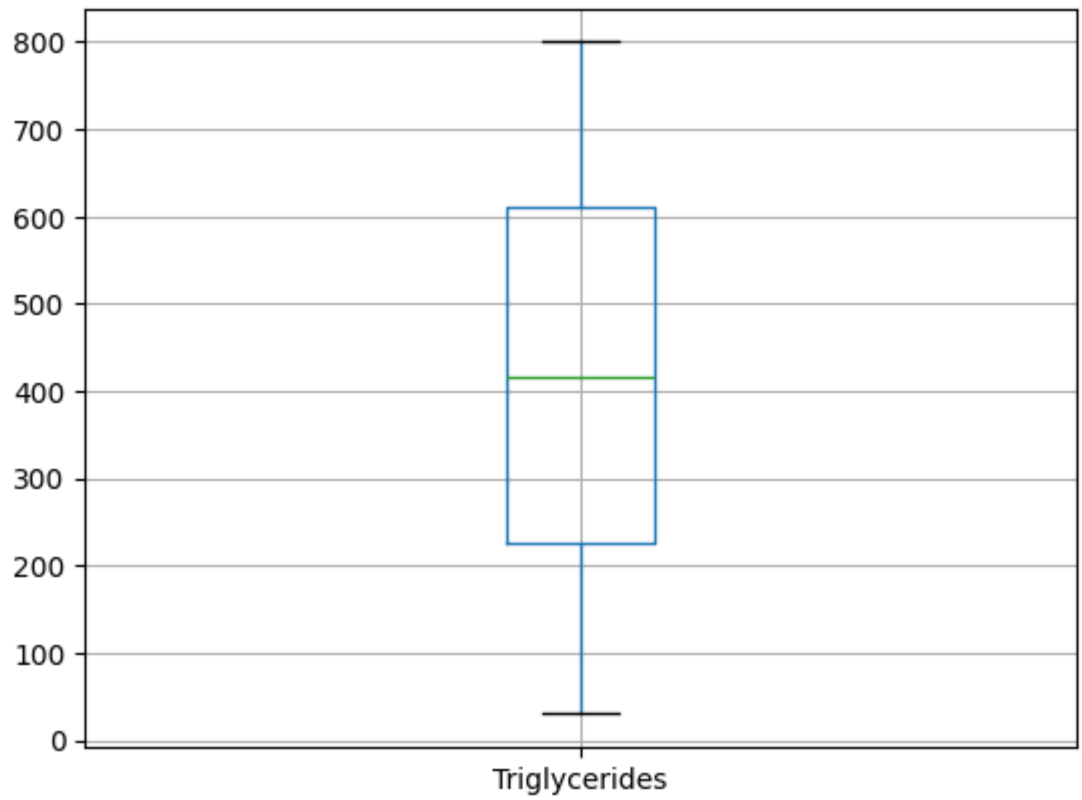

1.0
0.8
0.6
0.4
0.2
0.0
Medication Use

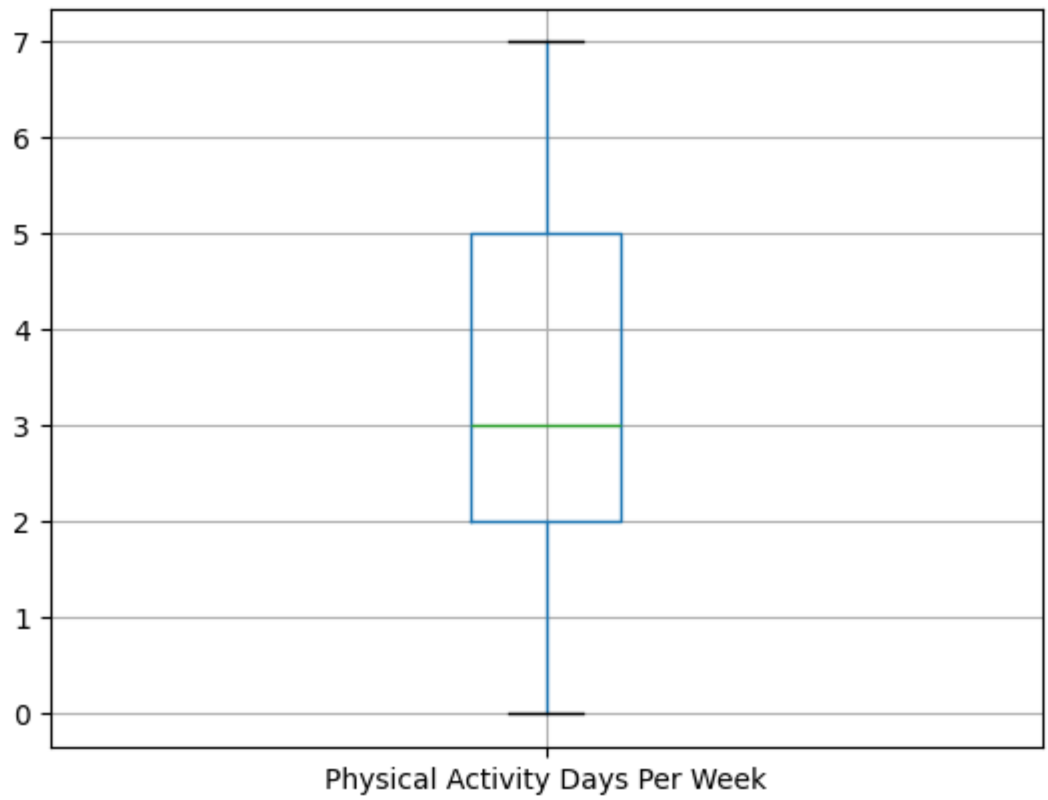

10
8
6
4
2
Stress Level

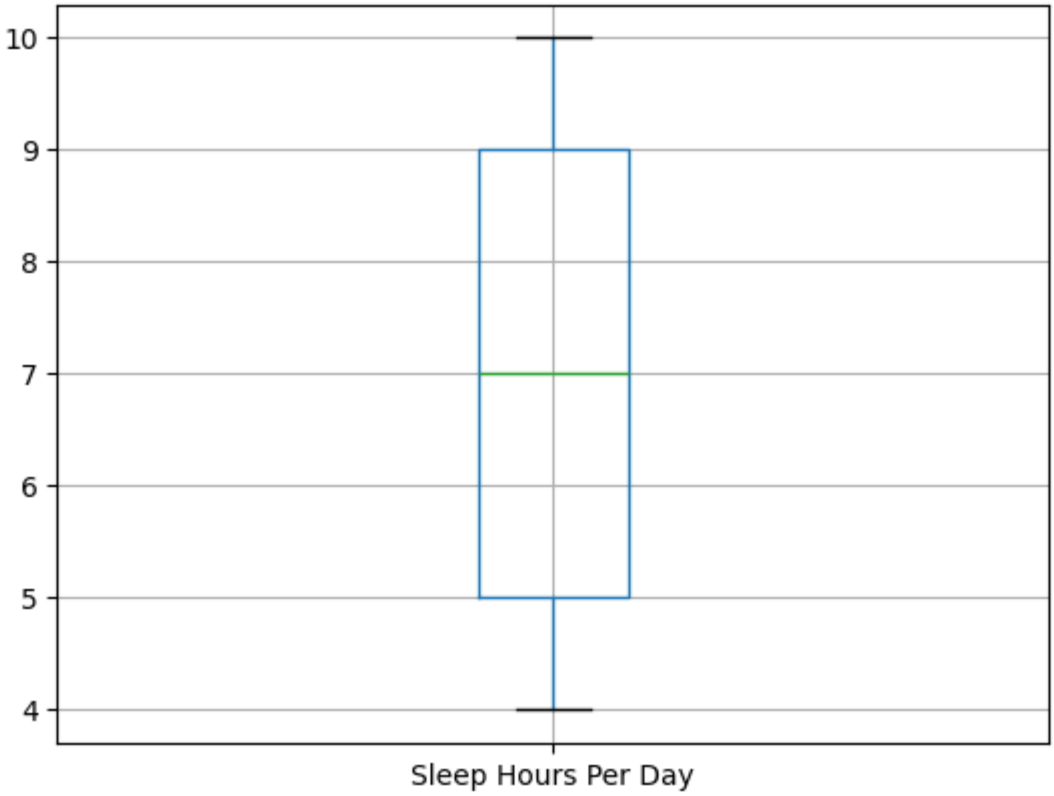

12
10
8
6
4
2
0
Sedentary Hours Per Day

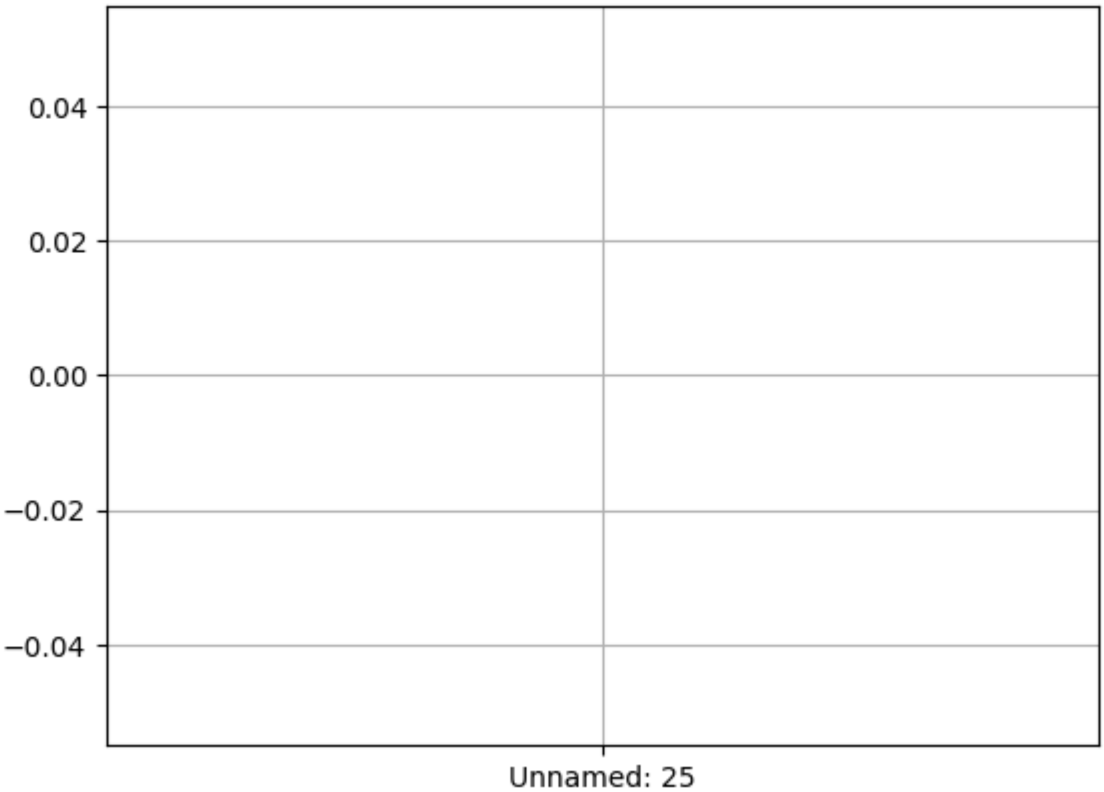

300000
250000
200000
150000
100000
50000
Income

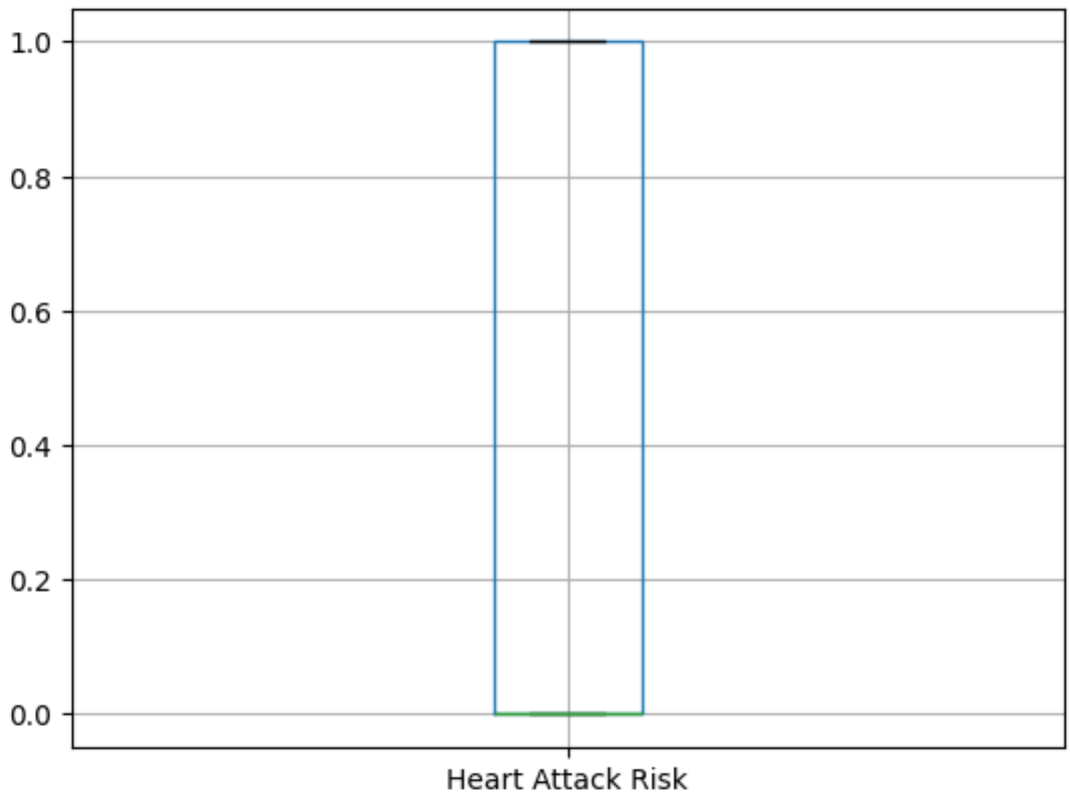

40
35
30
25
20
BMI


800
700
600
500
400
300
200
100
0
Triglycerides


7
6
5
4
3
2
1
0
Physical Activity Days Per Week


10
9
8
7
6
5
4
Sleep Hours Per Day


0.04
0.02
0.00
−0.02
−0.04
Unnamed: 25



In [110…

```
q1=df['Age'].quantile(0.25)
q2=df['Age'].quantile(0.75)
iqr=q2-q1
lower=q1-1.5*iqr
upper=q2+1.5*iqr
outlier=df.loc[(df['Age']>upper)|(df['Age']<lower)]
print(len(outlier))
```

```
0
```

In [ ]:

In [ ]:

check outlier in each column

In [62]:

```
numeric_col=df.select_dtypes(include='number').columns
for col in numeric_col:
    q1=df[col].quantile(0.25)
    q2=df[col].quantile(0.75)
    iqr=q2-q1
    lower=q1-1.5*iqr
    upper=q2+1.5*iqr
    outlier=df.loc[(df[col]>upper)|(df[col]<lower)]
    print(f"\nColumn: {col}")
    print(f"Number of outliers: {len(outlier)}")
```

```
Column: Age
Number of outliers: 0

Column: Cholesterol
Number of outliers: 0

Column: Heart Rate
Number of outliers: 0

Column: Diabetes
Number of outliers: 0

Column: Family History
Number of outliers: 0

Column: Smoking
Number of outliers: 904

Column: Obesity
Number of outliers: 0

Column: Alcohol Consumption
Number of outliers: 0

Column: Exercise Hours Per Week
Number of outliers: 0

Column: Previous Heart Problems
Number of outliers: 0

Column: Medication Use
Number of outliers: 0

Column: Stress Level
Number of outliers: 0

Column: Sedentary Hours Per Day
Number of outliers: 0

Column: Income
Number of outliers: 0

Column: BMI
Number of outliers: 0

Column: Triglycerides
Number of outliers: 0

Column: Physical Activity Days Per Week
Number of outliers: 0

Column: Sleep Hours Per Day
Number of outliers: 0

Column: Unnamed: 25
Number of outliers: 0

Column: Heart Attack Risk
Number of outliers: 0
```

Remove outlier in Smoking column

We can remove outliers by using

1.Z score method

2.IQR(Inter Quartile Range)

3.Clapping method: it replace the outlier with its nearest value

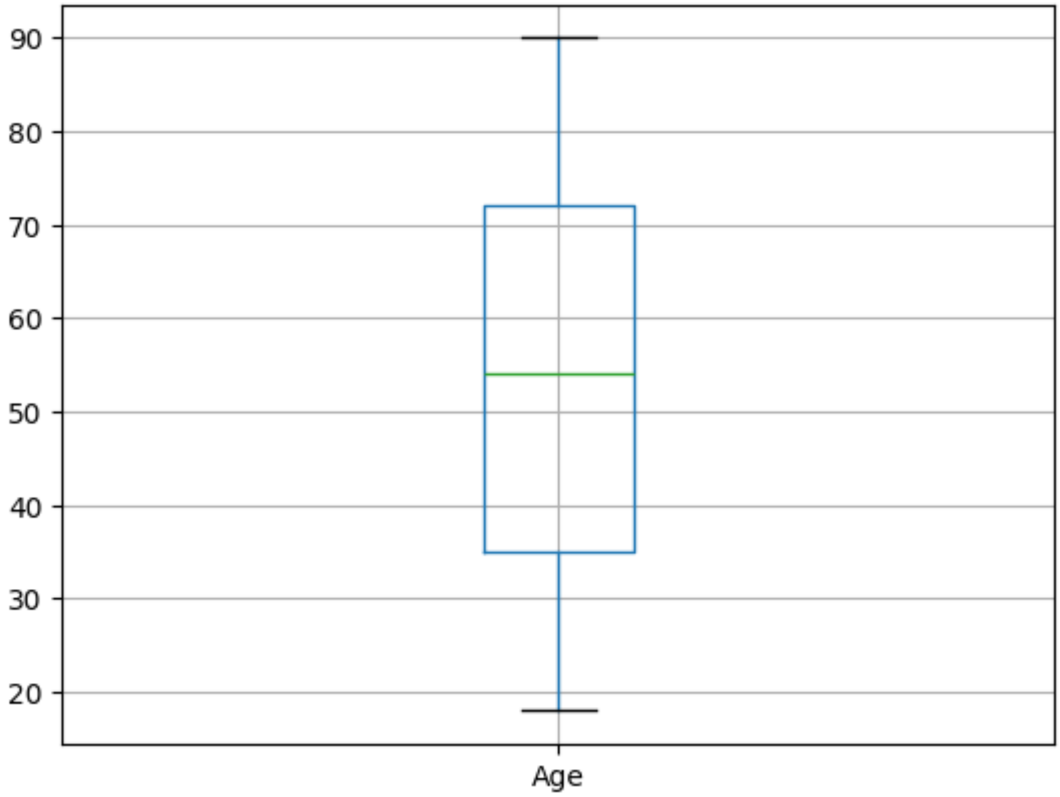
In [63]:
```
for col in numeric_col:
    q1 = df[col].quantile(0.25)
    q3 = df[col].quantile(0.75)
    iqr = q3 - q1
    lower = q1 - 1.5 * iqr
    upper = q3 + 1.5 * iqr


    df.loc[df[col] > upper, col] = upper
    df.loc[df[col] < lower, col] = lower

for col in numeric_col:
    q1=df[col].quantile(0.25)
    q3=df[col].quantile(0.75)
    iqr=q3-q1
    lower=q1-1.5*iqr
    upper=q3+1.5*iqr
    outlier=df.loc[(df[col]>upper)|(df[col]<lower)]
    print(f"\nColumn: {col}")
    print(f"Number of outliers: {len(outlier)}")
```

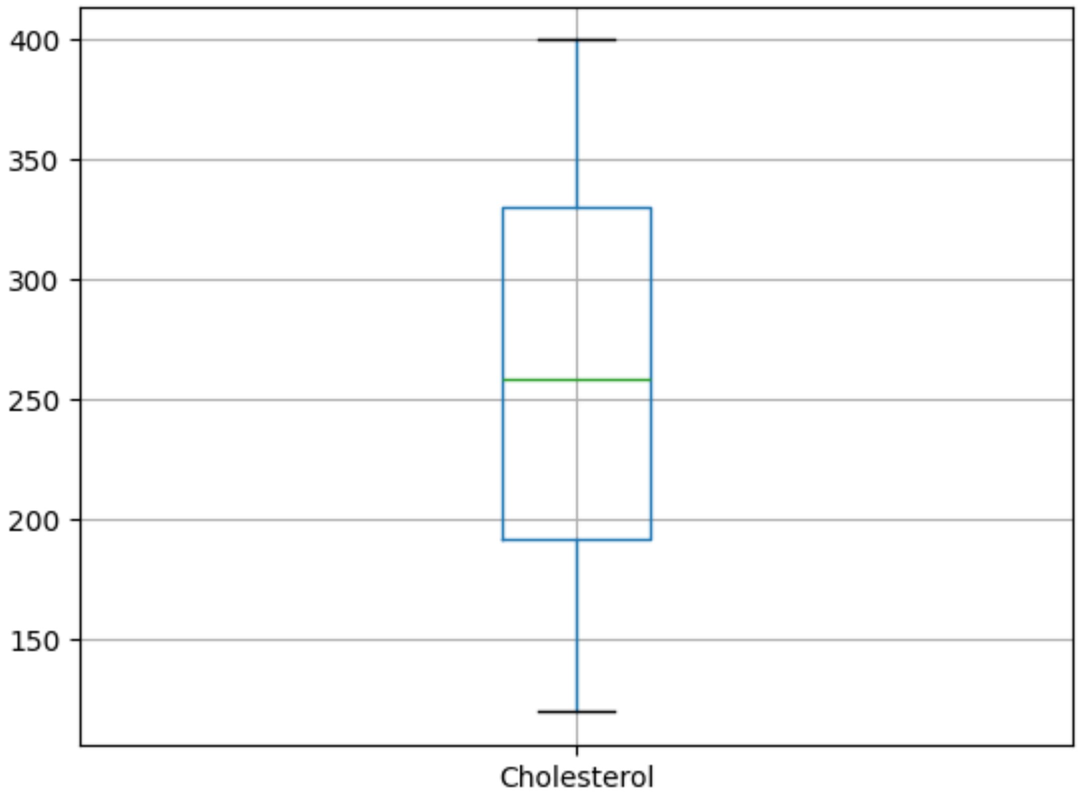
```
Column: Age
Number of outliers: 0

Column: Cholesterol
Number of outliers: 0

Column: Heart Rate
Number of outliers: 0

Column: Diabetes
Number of outliers: 0

Column: Family History
Number of outliers: 0

Column: Smoking
Number of outliers: 0

Column: Obesity
Number of outliers: 0

Column: Alcohol Consumption
Number of outliers: 0

Column: Exercise Hours Per Week
Number of outliers: 0

Column: Previous Heart Problems
Number of outliers: 0

Column: Medication Use
Number of outliers: 0

Column: Stress Level
Number of outliers: 0

Column: Sedentary Hours Per Day
Number of outliers: 0

Column: Income
Number of outliers: 0

Column: BMI
Number of outliers: 0

Column: Triglycerides
Number of outliers: 0

Column: Physical Activity Days Per Week
Number of outliers: 0

Column: Sleep Hours Per Day
Number of outliers: 0

Column: Unnamed: 25
Number of outliers: 0

Column: Heart Attack Risk
Number of outliers: 0
```

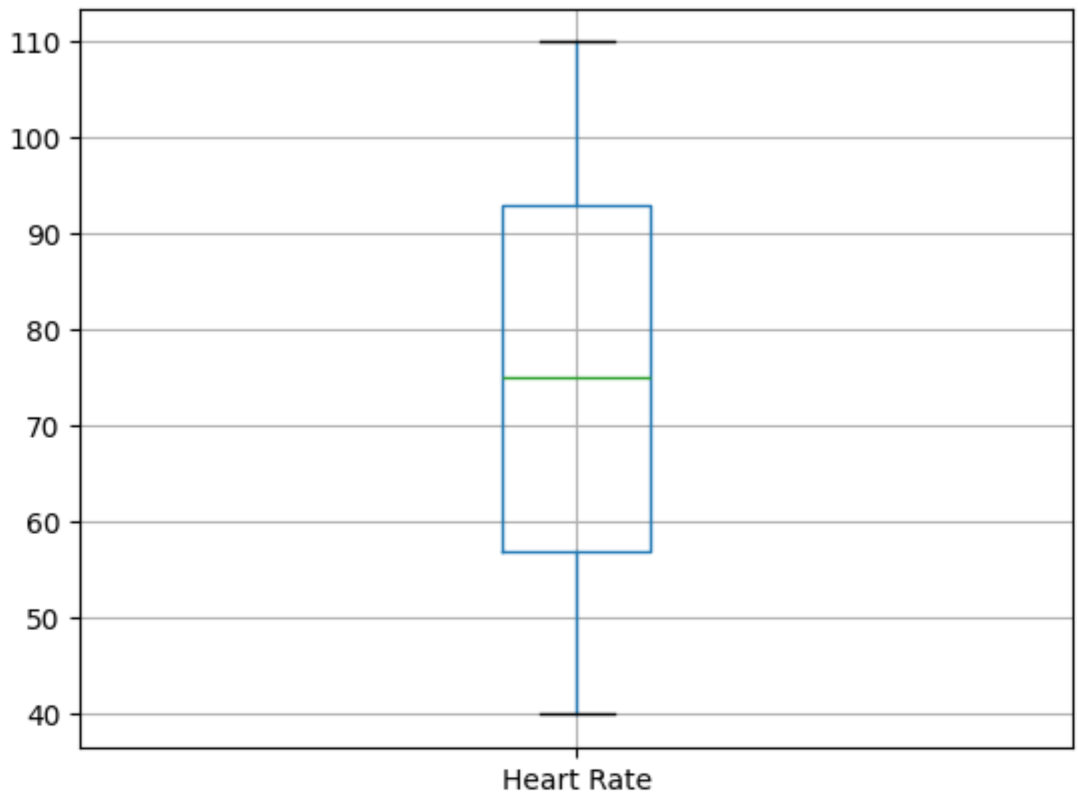
```
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '127.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '15.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '436907.5' has dtype incompatible with int64, please explicitly cast to
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '1191.75' has dtype incompatible with int64, please explicitly cast to
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '9.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\2885033268.py:10: FutureWarning: Set
an item of incompatible dtype is deprecated and will raise an error in a future versi
pandas. Value '2.5' has dtype incompatible with int64, please explicitly cast to a
compatible dtype first.
  df.loc[df[col] > upper, col] = upper
```

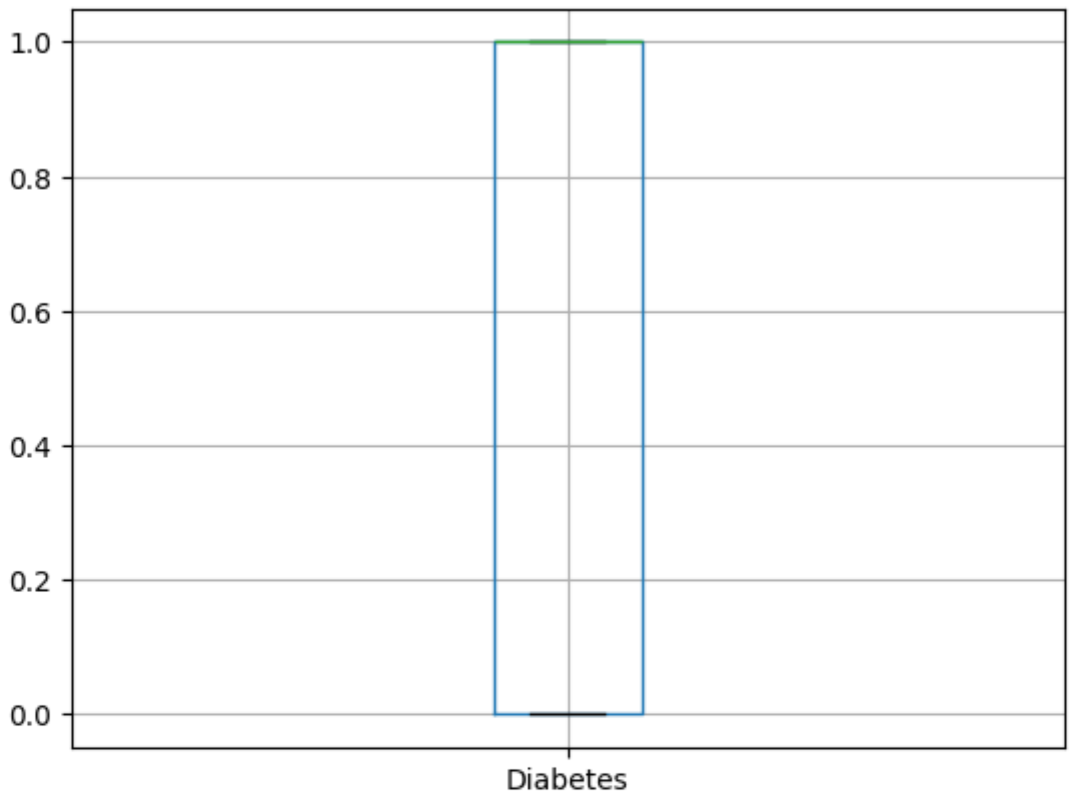
All outlier removed

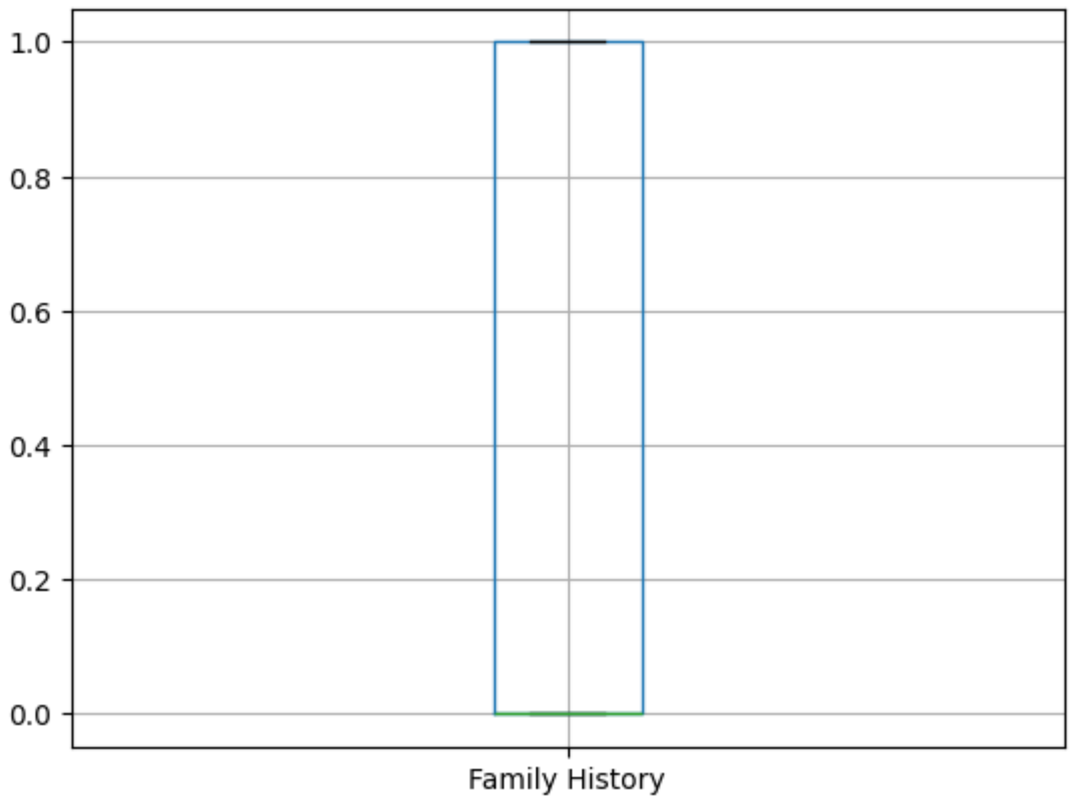
In [64]:
```
numeric_cols = df.select_dtypes(include='number').columns
for i, n_col in enumerate(numeric_cols):
    df.boxplot(column=n_col)
    plt.show()
```

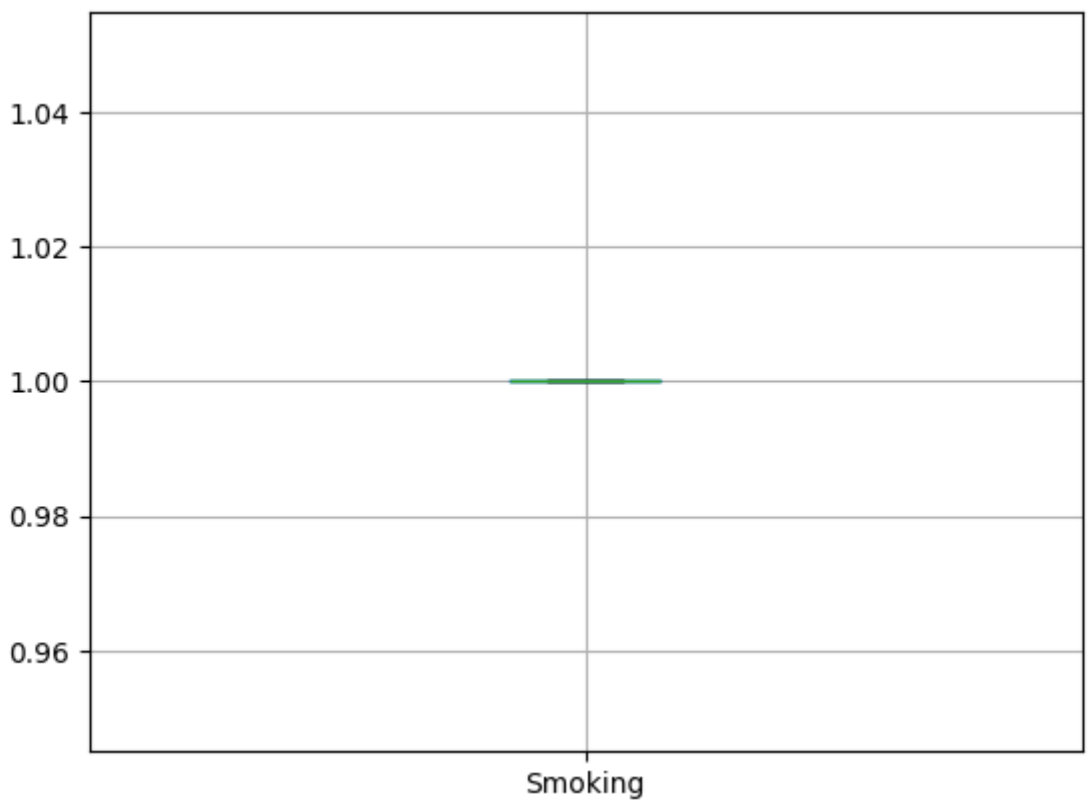


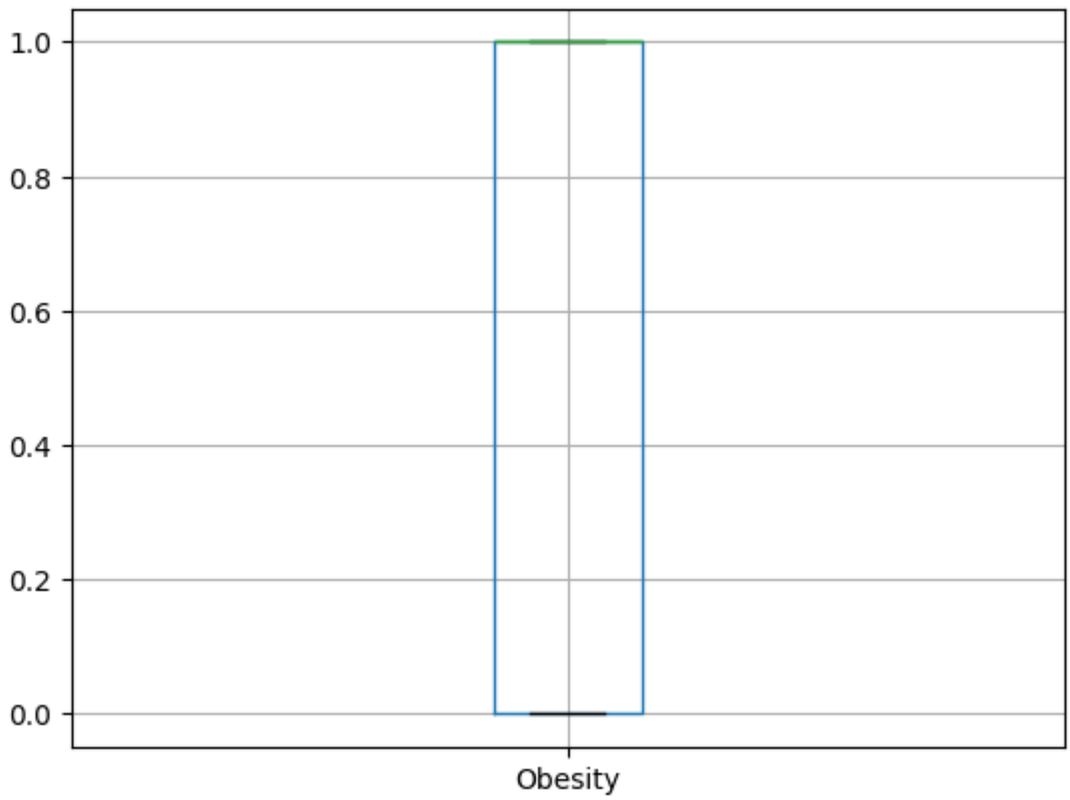


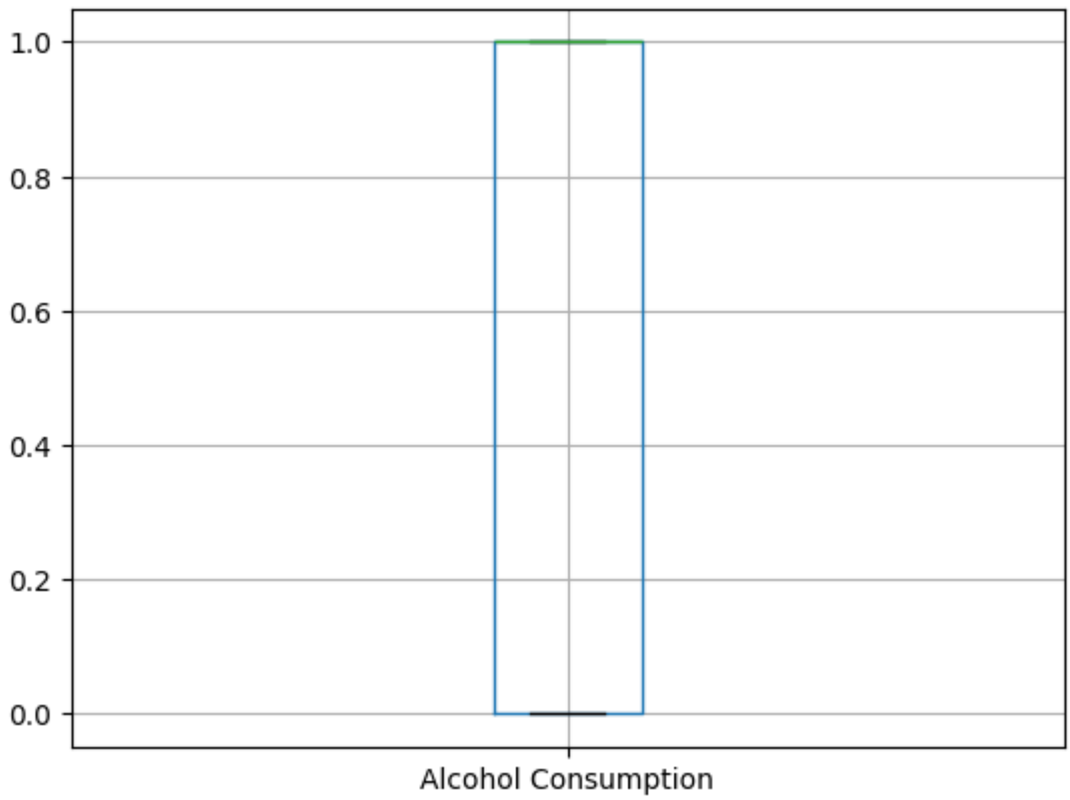

110
100
90
80
70
60
50
40
Heart Rate

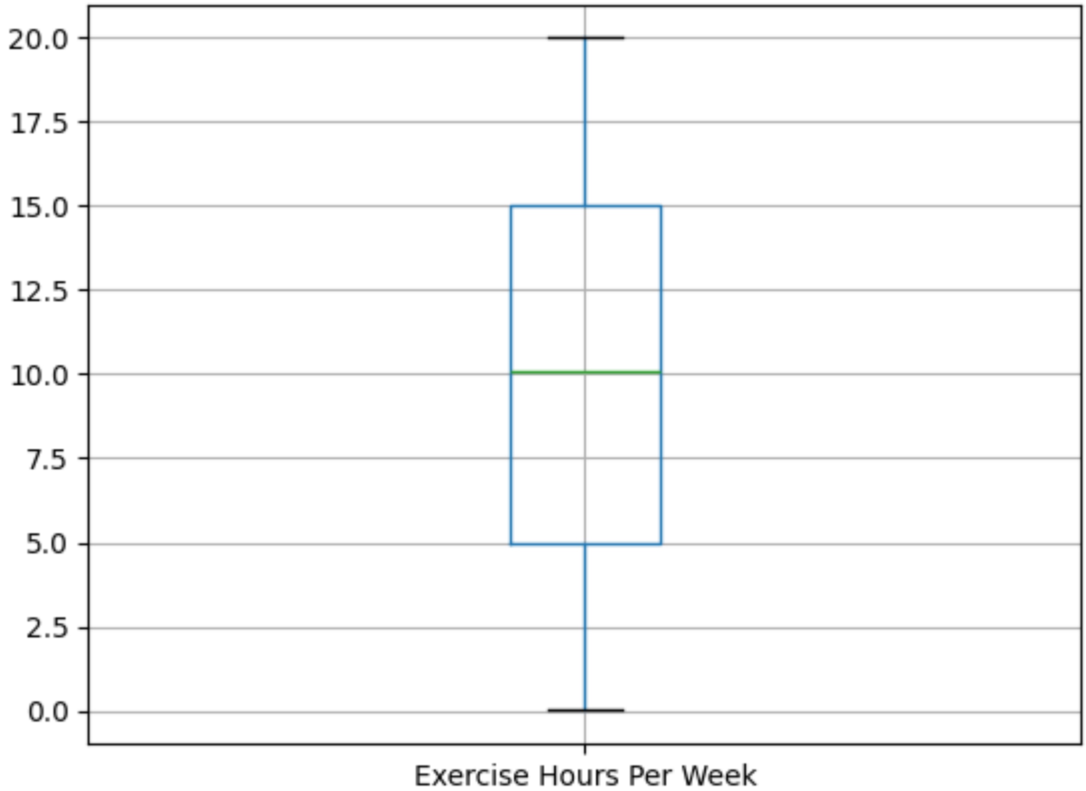

1.0
0.8
0.6
0.4
0.2
0.0
Diabetes

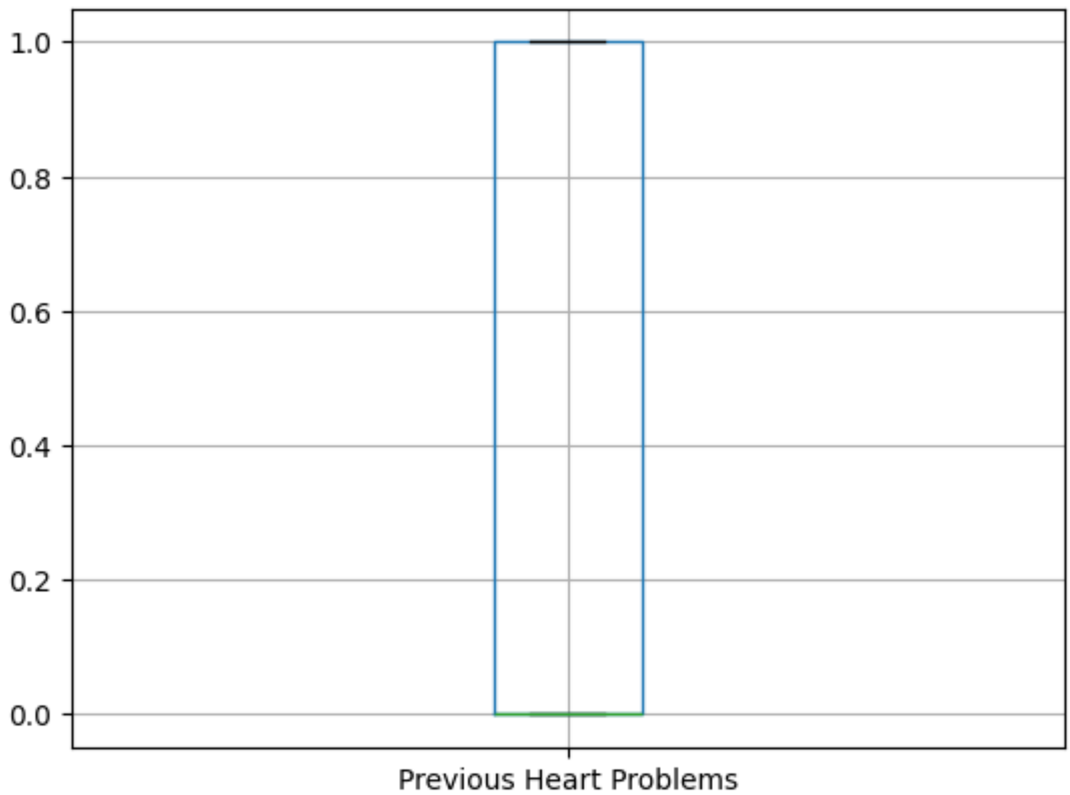

1.0
0.8
0.6
0.4
0.2
0.0
Family History

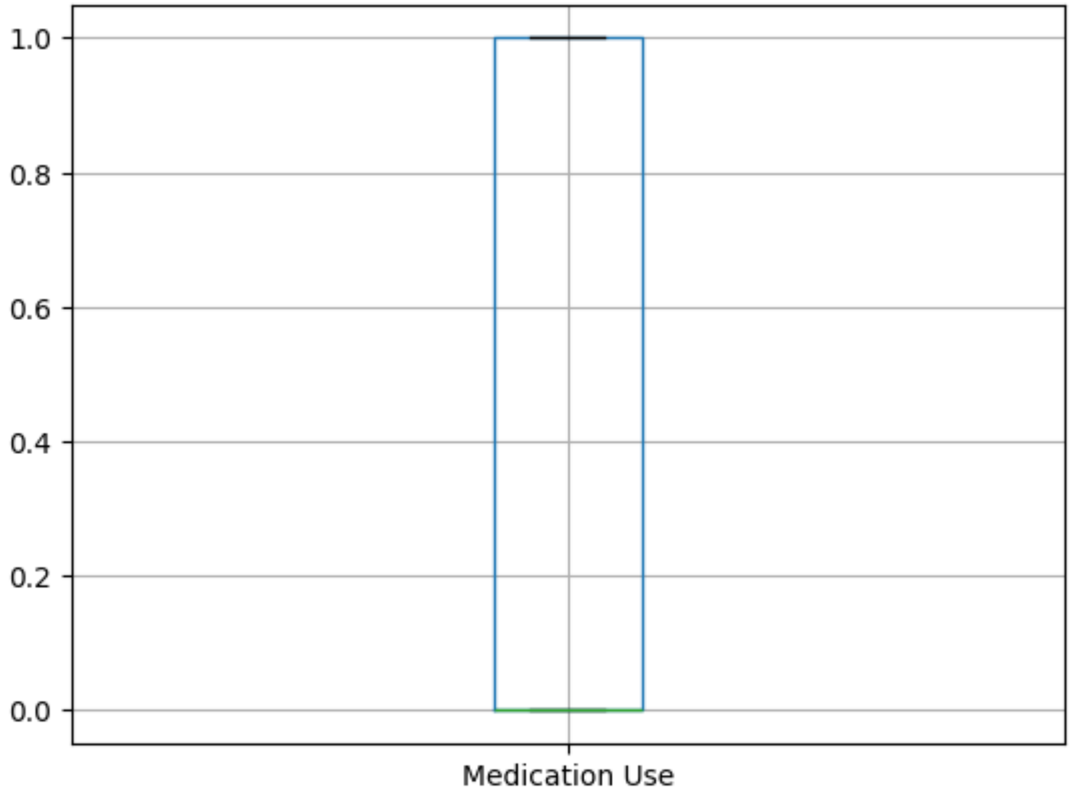

1.04
1.02
1.00
0.98
0.96
Smoking

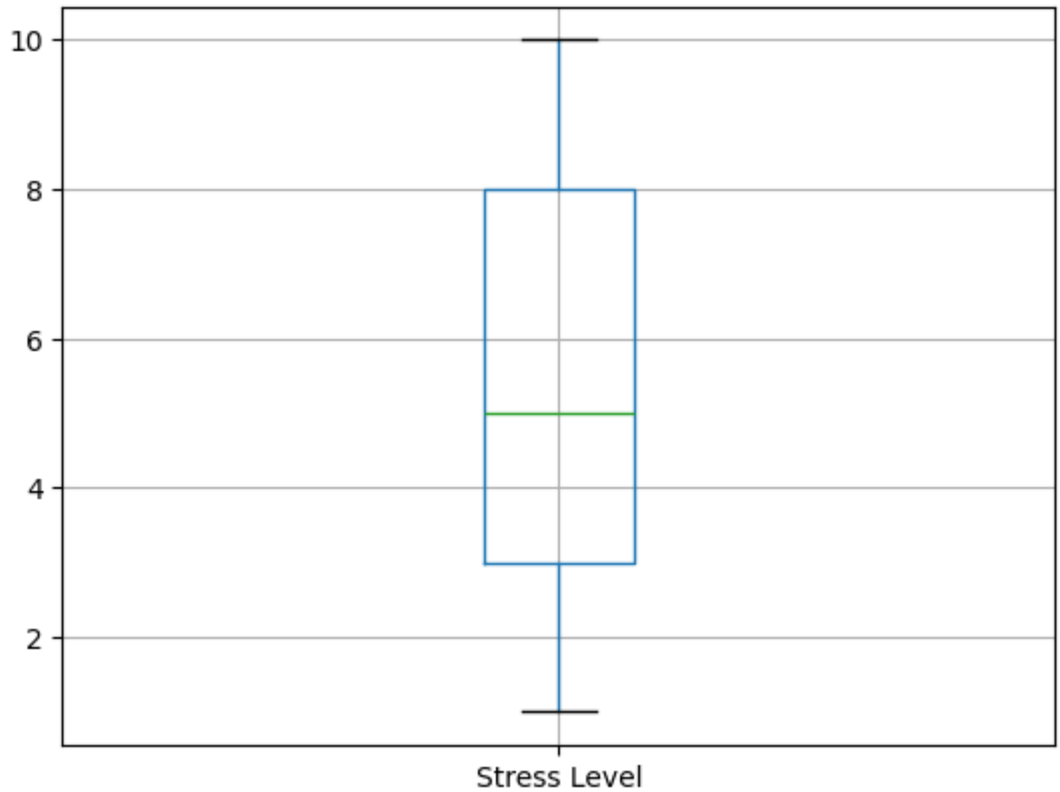

1.0
0.8
0.6
0.4
0.2
0.0
Obesity

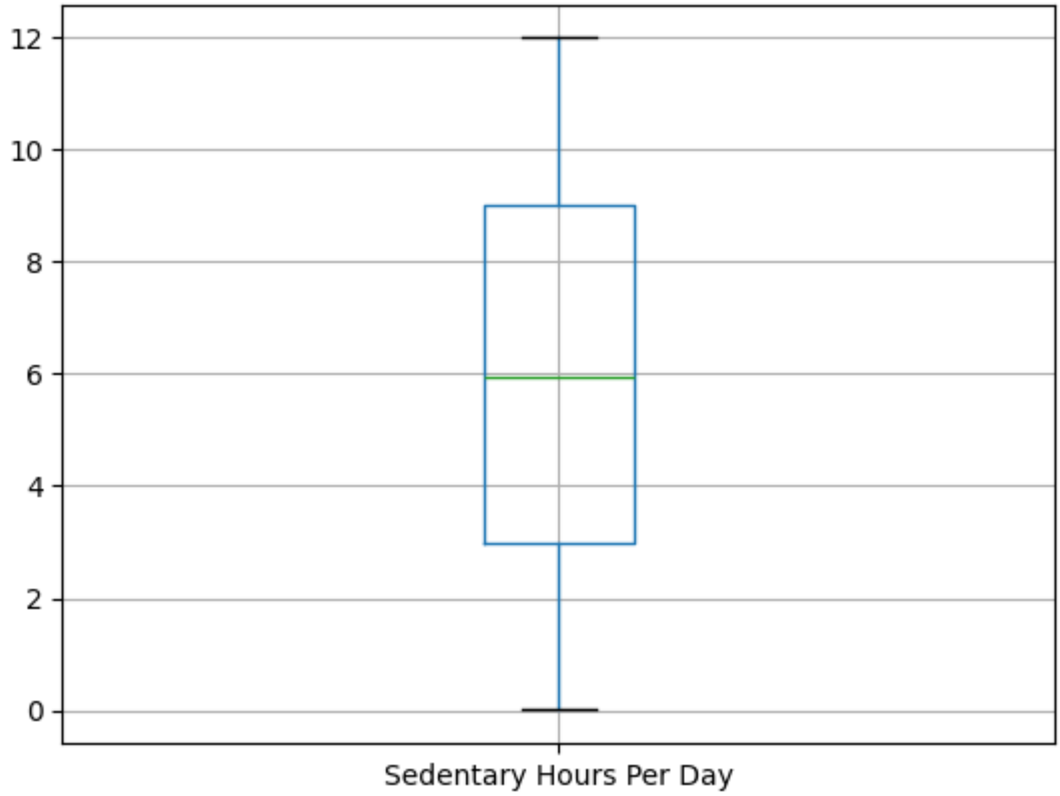

1.0
0.8
0.6
0.4
0.2
0.0
Alcohol Consumption

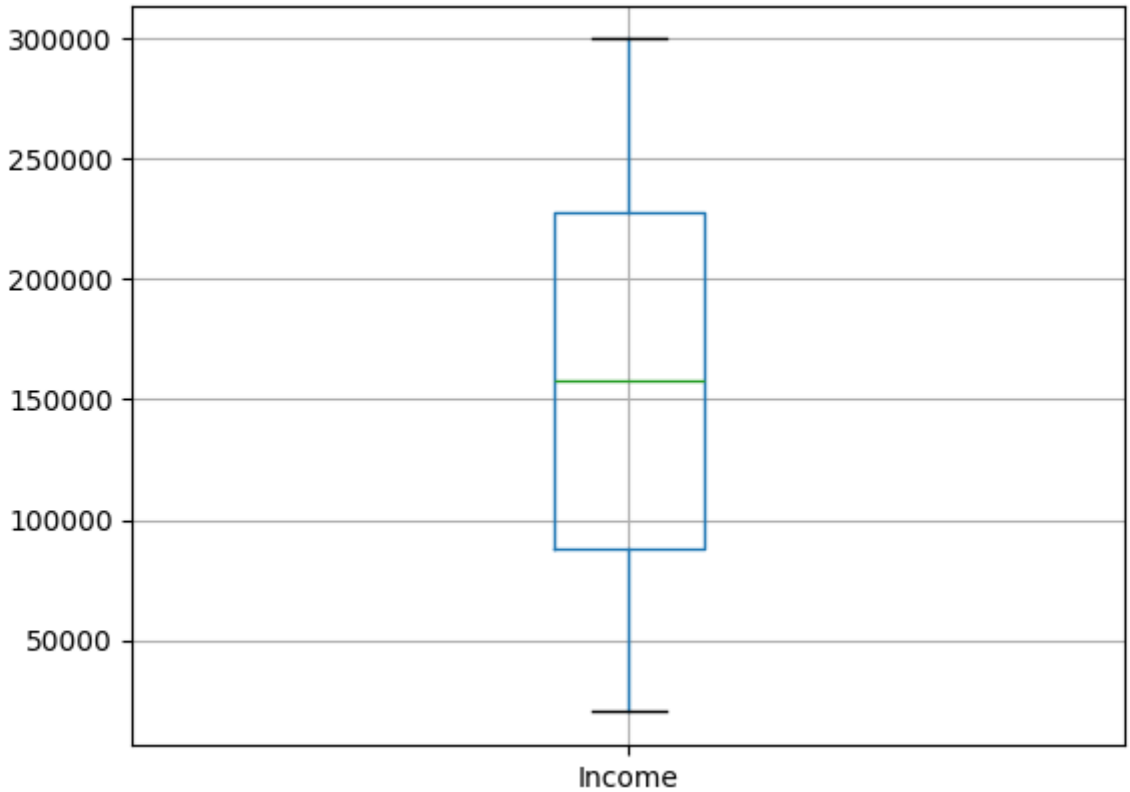

20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
Exercise Hours Per Week

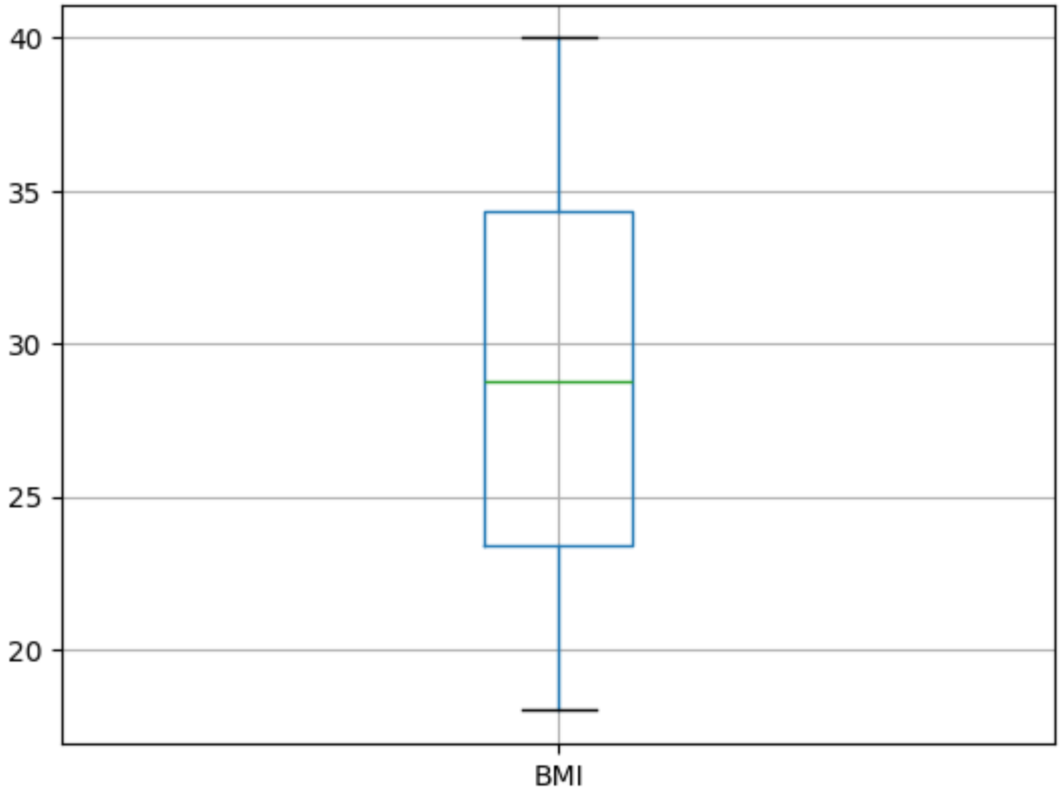

1.0
0.8
0.6
0.4
0.2
0.0
Previous Heart Problems

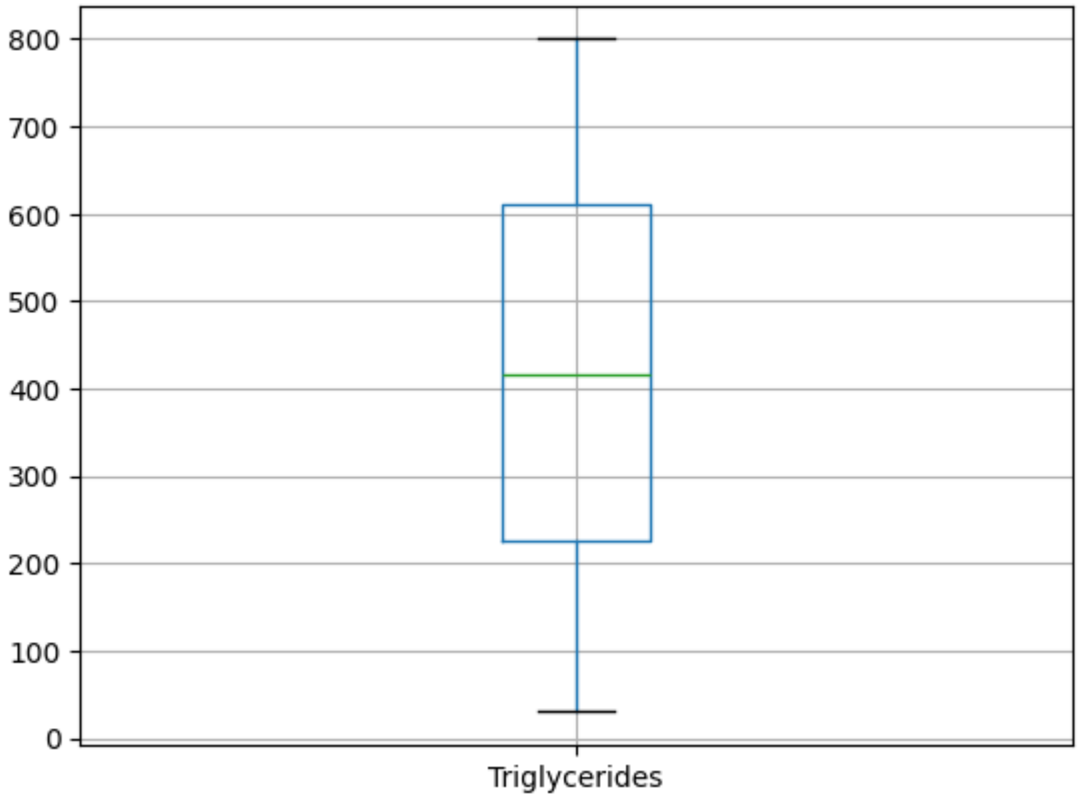

1.0
0.8
0.6
0.4
0.2
0.0
Medication Use

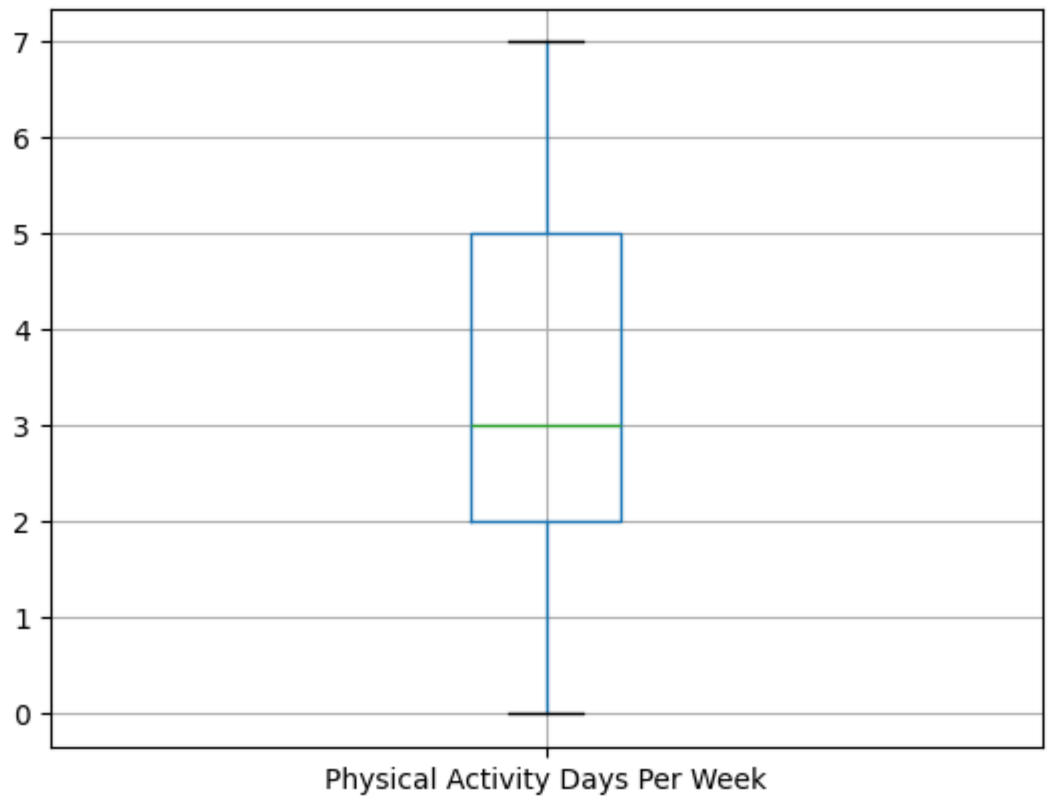

10
8
6
4
2
Stress Level


12
10
8
6
4
2
0
Sedentary Hours Per Day

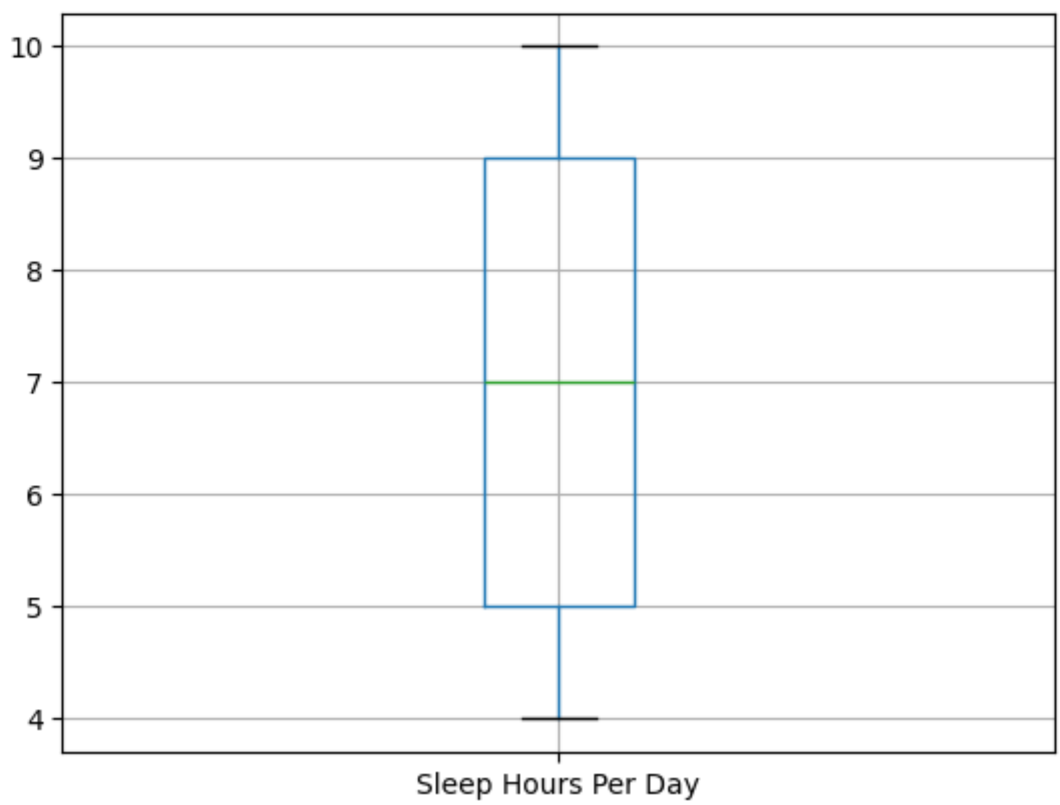

300000
250000
200000
150000
100000
50000
Income


40
35
30
25
20
BMI

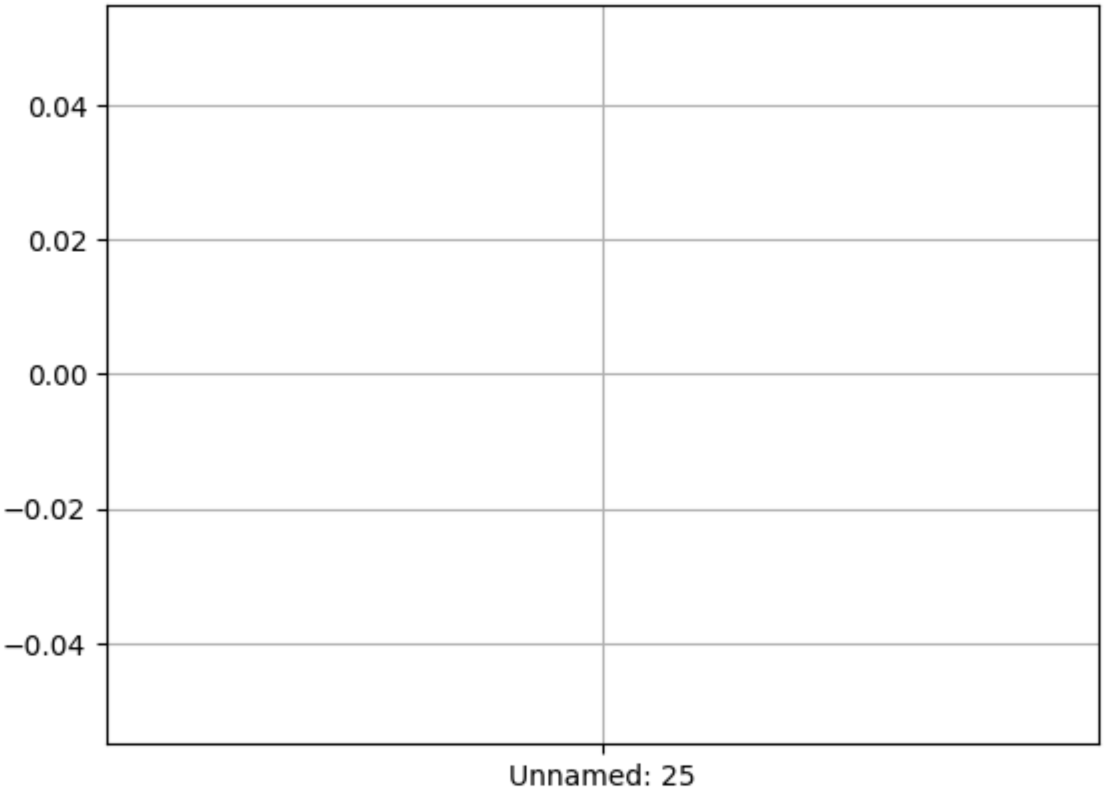

800
700
600
500
400
300
200
100
0
Triglycerides

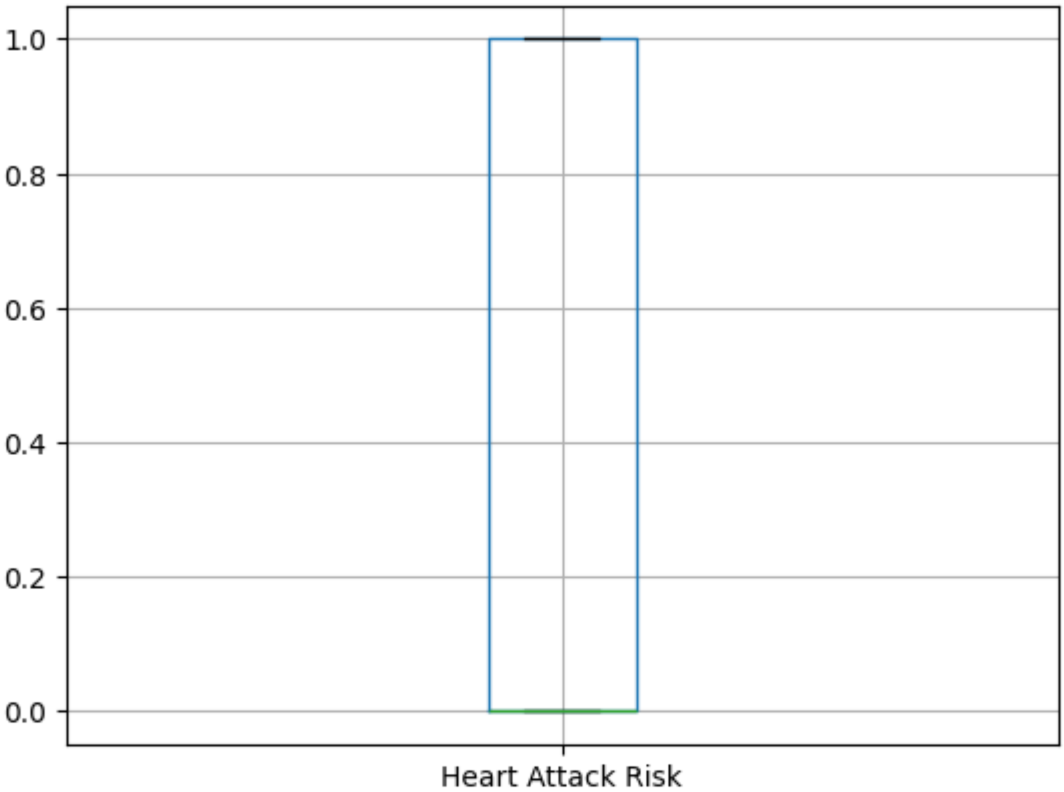


7
6
5
4
3
2
1
0
Physical Activity Days Per Week



10
9
8
7
6
5
4
Sleep Hours Per Day





Exploratory Data Analysis

In [65]:
```
#total patient in each continent
total_people=df.groupby("Continent")["Patient ID"].count()
print(total_people)
```

```
Continent
Africa            873
Asia             2543
Australia         884
Europe           2241
North America     860
South America    1362
Name: Patient ID, dtype: int64
```

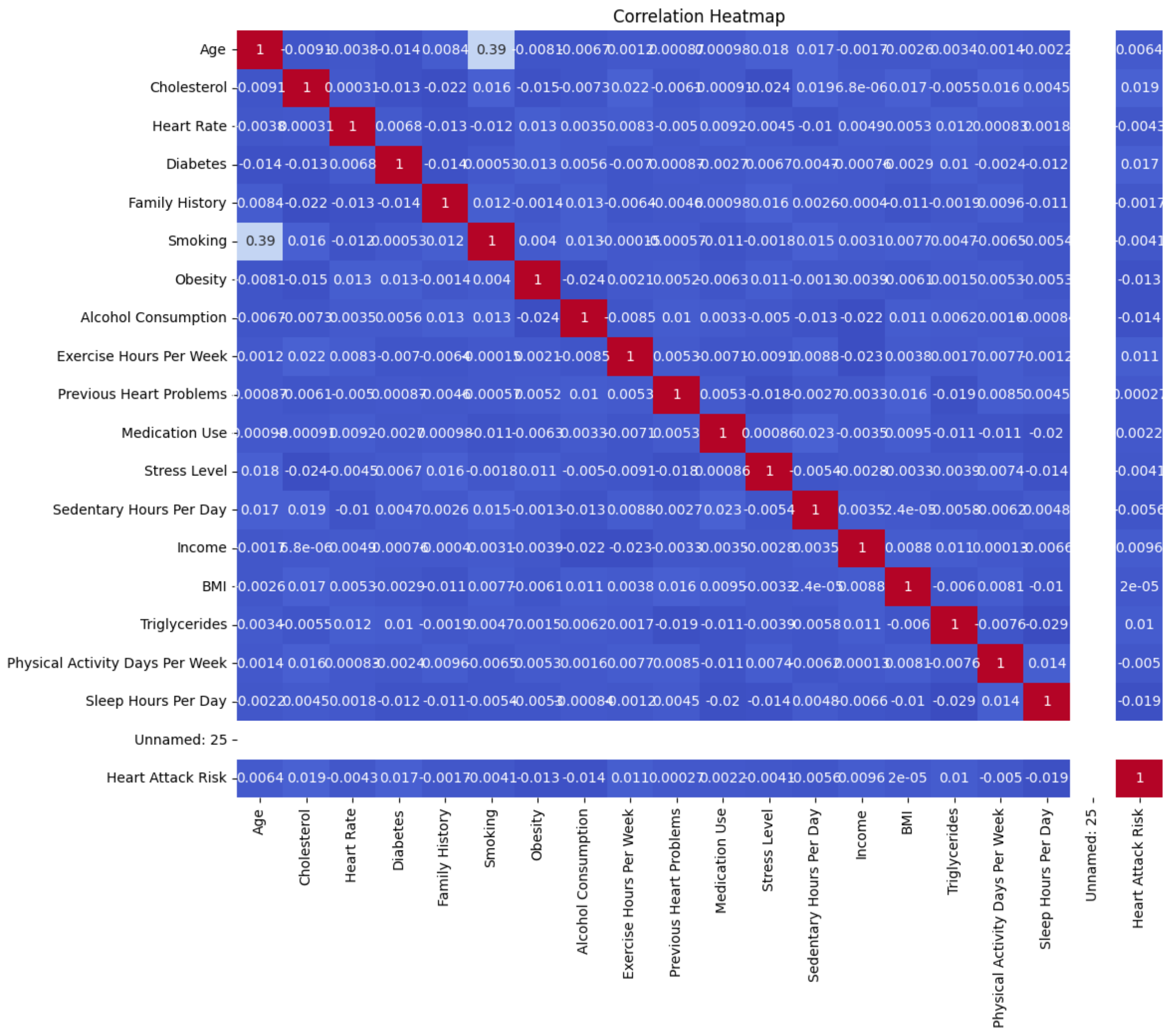
In [66]:

```
#total patient in each country
total=df.groupby("Country")["Patient ID"].count()
print(total.sort_values(ascending=False))
```

```
Country
Germany           477
Argentina         471
Brazil            462
United Kingdom    457
Australia         449
Nigeria           448
France            446
Canada            440
China             436
New Zealand       435
Japan             433
Italy             431
Spain             430
Colombia          429
Thailand          428
Vietnam           425
South Africa      425
United States     420
India             412
South Korea       409
Name: Patient ID, dtype: int64
```

In [115…

```
numeric=df.select_dtypes(include='number')
correlation=numeric.corr()

plt.figure(figsize=(15, 10))
sns.heatmap(correlation, annot=True, cmap='coolwarm')
plt.title('Correlation Heatmap')
plt.show()
```

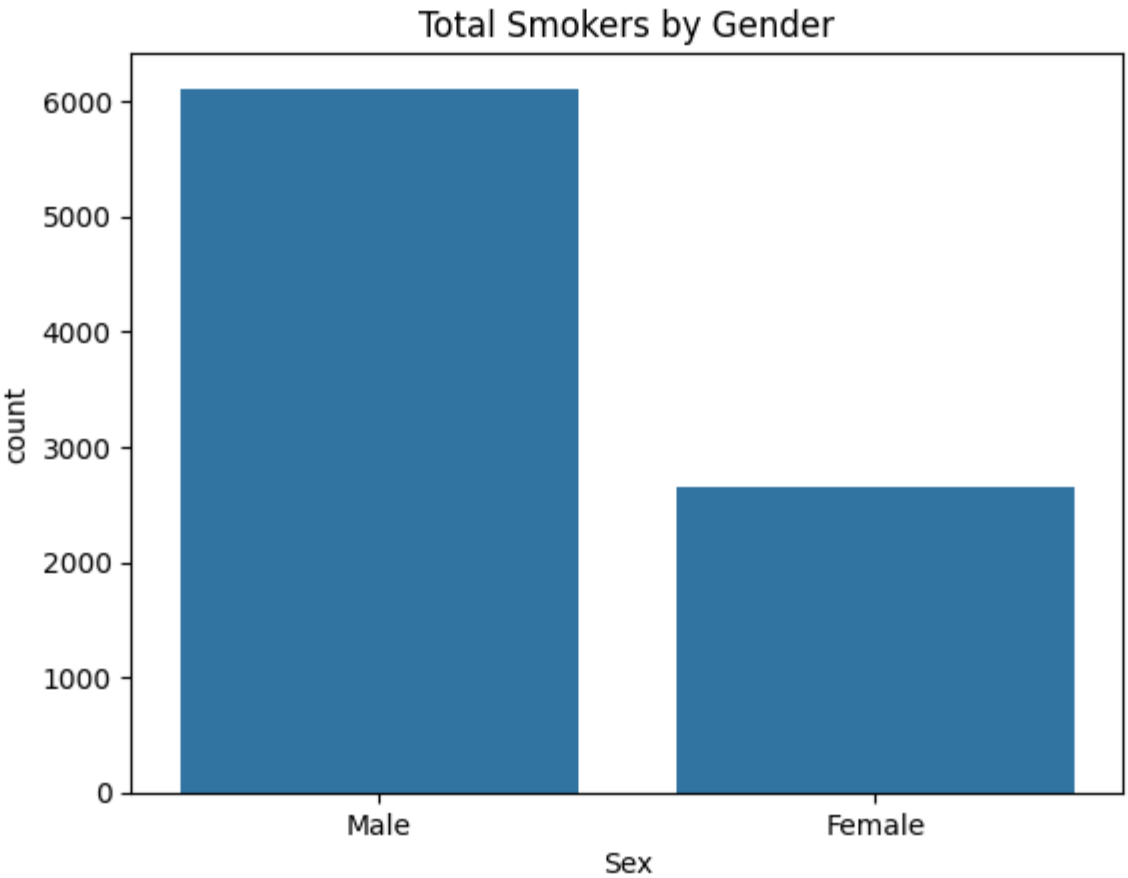


In [ ]:

In [67]:
```
#total smoking person male female
count=df[df['Smoking']==1].groupby('Sex')['Smoking'].count()
print(count)
sns.countplot(x='Sex', data=df)
plt.title("Total Smokers by Gender")
```

```
Sex
Female    2652
Male      6111
Name: Smoking, dtype: int64
```

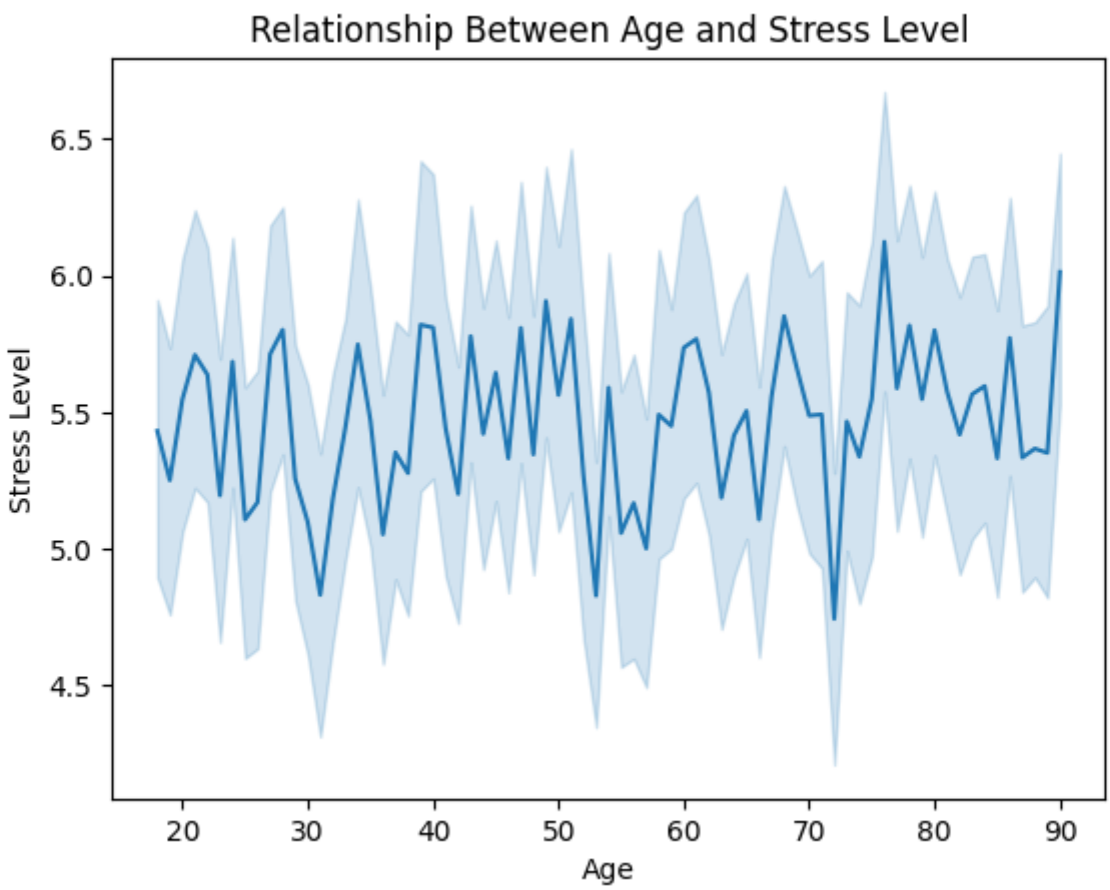
Out[67]: Text(0.5, 1.0, 'Total Smokers by Gender')



In [68]:
```
#Relation between Age column Stress column
#Age and Stress has no relation
#Very weak positive linear relationship.It's not strong enough to say "as age in
corr=df['Age'].corr(df['Stress Level'])
print(corr)
sns.lineplot(x='Age', y='Stress Level', data=df)
plt.title("Relationship Between Age and Stress Level")
plt.xlabel("Age")
plt.ylabel("Stress Level")
```

```
0.018306645661318687
```

Out[68]:
```
Text(0, 0.5, 'Stress Level')
```



In [69]:
```
#Create a new column BP range Blood Pressure Range
df["BP range"]=df['Blood Pressure'].apply(lambda x: round(eval(x), 2))
def applybp(r):
    if r<1.2:
        return 'low'
    elif r>1.2 and r<1.6:
        return 'medium'
    else:
        return 'high'

df['BP range']=df['BP range'].apply(applybp)
```

In [70]:
```
age=df.groupby(['Sex','Smoking','BP range'])['Exercise Hours Per Week'].count()
display(age)
```

```
Sex     Smoking  BP range
Female  1        high        1320
                 low          428
                 medium       904
Male    1        high        3030
                 low          993
                 medium      2088
Name: Exercise Hours Per Week, dtype: int64
```

In [ ]:

Cholosterol level of each group

In [71]:
```
#Cholosterol level of each group
bins = [0, 29, 39, 49, 59, 69, 120]  # Customize as needed
labels = ['<30', '30-39', '40-49', '50-59', '60-69', '70+']
df['AgeGroup'] = pd.cut(df['Age'], bins=bins, labels=labels, right=False)
```

```
average = df.groupby('AgeGroup')['Cholesterol'].mean()
print(average)
```

```
AgeGroup
<30      259.930403
30-39    263.412044
40-49    258.459848
50-59    258.903283
60-69    259.309504
70+      259.468593
Name: Cholesterol, dtype: float64
```

```
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\998015979.py:5: FutureWarning: The d
of observed=False is deprecated and will be changed to True in a future version of pa
Pass observed=False to retain current behavior or observed=True to adopt the future d
and silence this warning.
  average = df.groupby('AgeGroup')['Cholesterol'].mean()
```

Add one column Perfectly_Healthy for healthy or unheal

In [72]:

```
#add one column Perfectly_Healthy for healthy or unhealthy
df['Perfectly_Healthy'] = (
    (df['Diabetes'] == 0) &
    (df['Obesity'] == 0) &
    (df['BMI'] >= 18.5) & (df['BMI'] <= 24.9) &
    (df['Stress Level'] < 5) &
    (df['Exercise Hours Per Week'] >= 3) &
    (df['Sleep Hours Per Day'] >= 7) & (df['Sleep Hours Per Day'] <= 9) &
    (df['Cholesterol'] < 200) &
    (df['Triglycerides'] < 150) &
    (df['Previous Heart Problems'] == 0)
).astype(int)
```

Only 1 person was healthy 8762 person unhealthy

In [73]:

```
# What % of people are perfectly healthy
total=df.groupby('Perfectly_Healthy')['Patient ID'].count()
print(total)
```

```
Perfectly_Healthy
0    8762
1       1
Name: Patient ID, dtype: int64
```

Average of age, BMI, cholesterol of perfectly healthy peo vs others

In [74]:

```
# What is the average age, BMI, cholesterol of perfectly healthy people vs other
column_intrest=['Age','BMI','Cholesterol']
average_healthy=df.groupby('Perfectly_Healthy')[column_intrest].mean()
print(average_healthy)
```

```
                         Age        BMI  Cholesterol
Perfectly_Healthy
0                  53.704748  28.892206   259.886556
1                  82.000000  22.233594   178.000000
```

How Alcohol,Smoking releated to Healthy people and unhealthy people

In [75]:
```
column=['Smoking','Alcohol Consumption']
f=df.groupby('Perfectly_Healthy')[column].count()
print(f)
```

```
                   Smoking  Alcohol Consumption
Perfectly_Healthy
0                     8762                 8762
1                        1                    1
```

All unhealthy individuals (Perfectly_Healthy = 0) are botl smokers and alcohol consumers.

Stress Level Respected to Age Groups

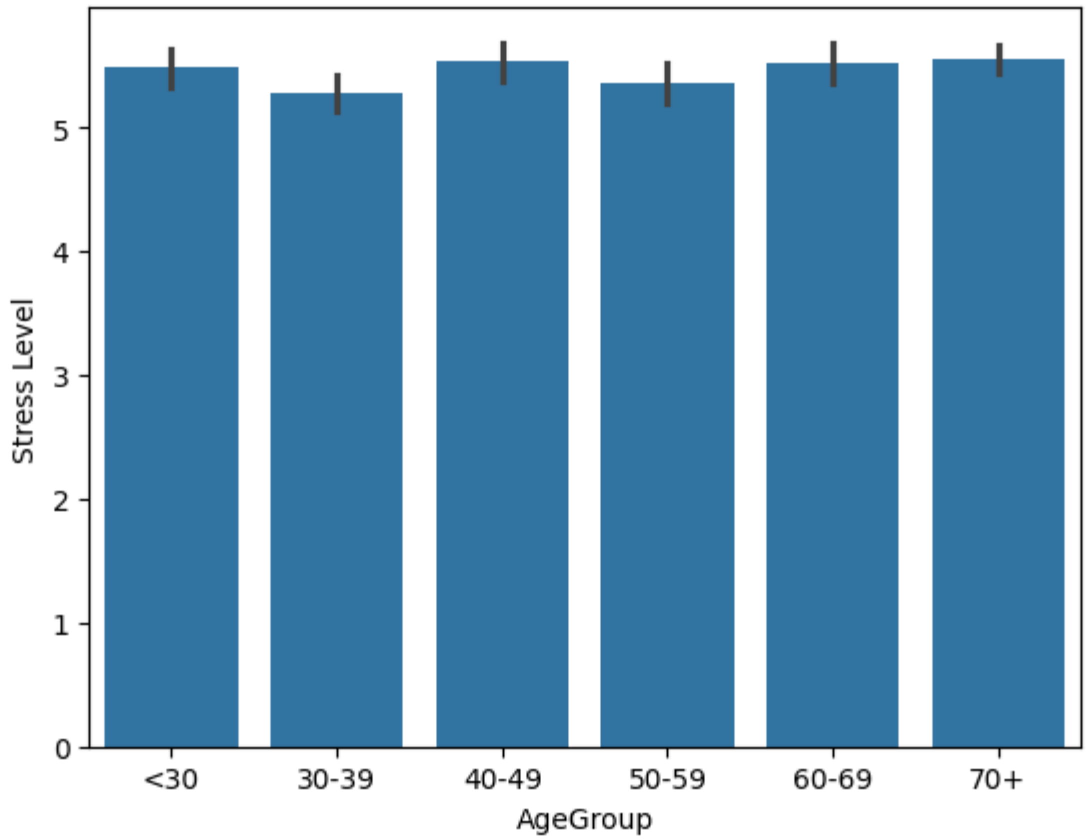
In [76]:
```
stress_level=df.groupby('AgeGroup')['Stress Level'].mean()
print(stress_level)
```

```
AgeGroup
<30      5.482784
30-39    5.275753
40-49    5.539307
50-59    5.366460
60-69    5.513404
70+      5.549518
Name: Stress Level, dtype: float64
```

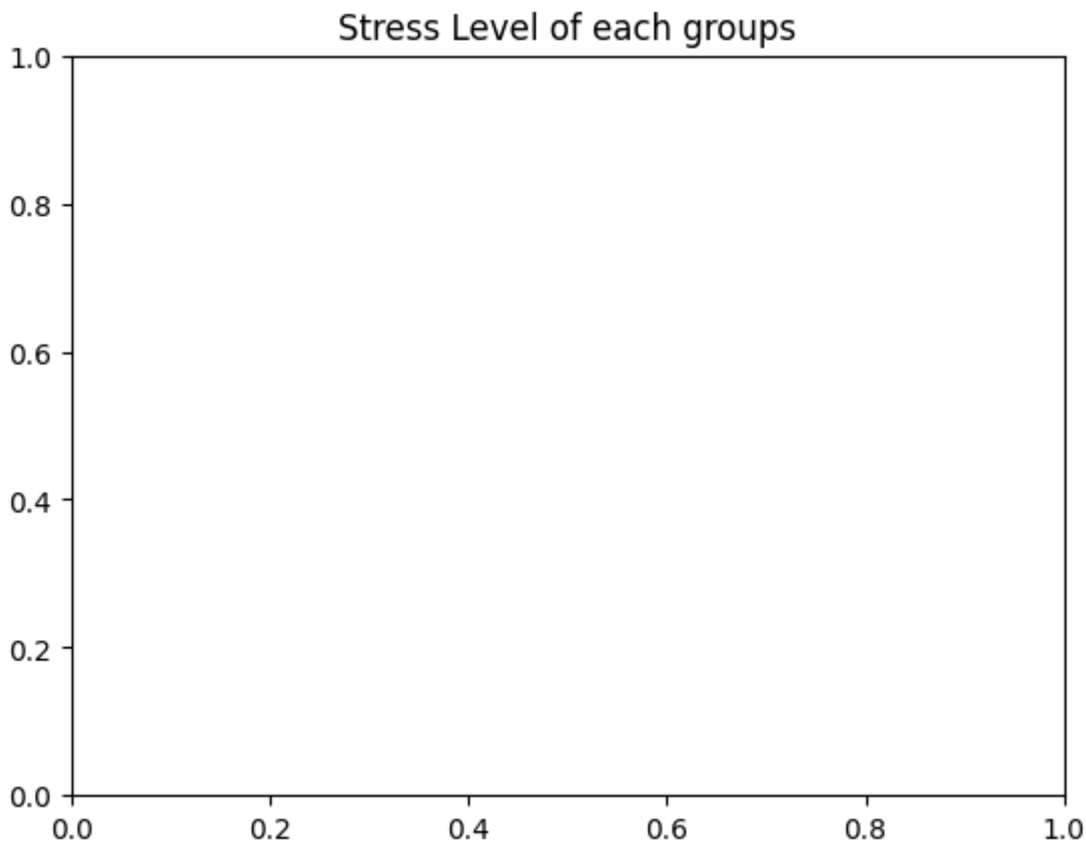
```
C:\Users\admin\AppData\Local\Temp\ipykernel_7900\4089233653.py:1: FutureWarning: The default of observed=False is deprecated and will be changed to True in a future versi pandas. Pass observed=False to retain current behavior or observed=True to adopt the default and silence this warning.
  stress_level=df.groupby('AgeGroup')['Stress Level'].mean()
```

Stress Level is same for all age groups

In [77]:
```
sns.barplot(x='AgeGroup',y='Stress Level',data=df,order=labels)
plt.show()
plt.title("Stress Level of each groups")
```



Out[77]: Text(0.5, 1.0, 'Stress Level of each groups')

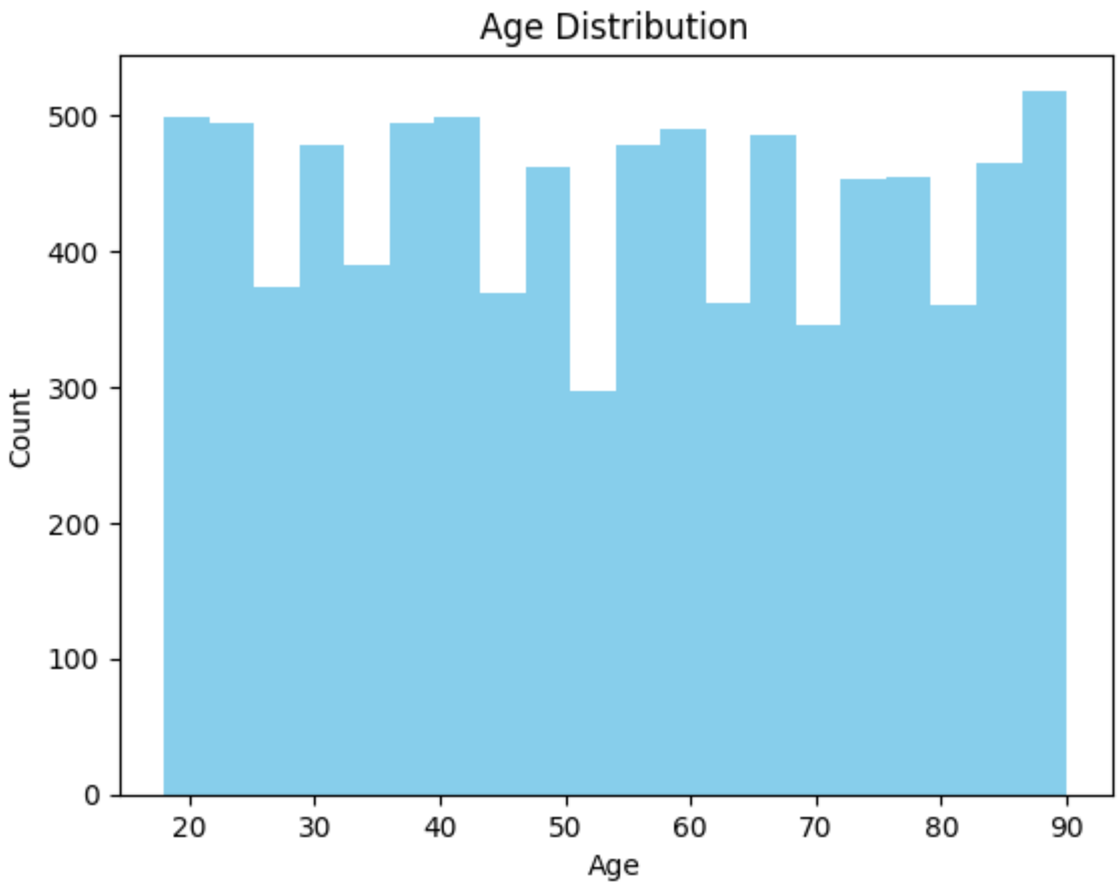


Histogram (Distribution of a Numeric Variable)

In [119…

```
plt.hist(df['Age'], bins=20, color='skyblue')
plt.title("Age Distribution")
plt.xlabel("Age")
```

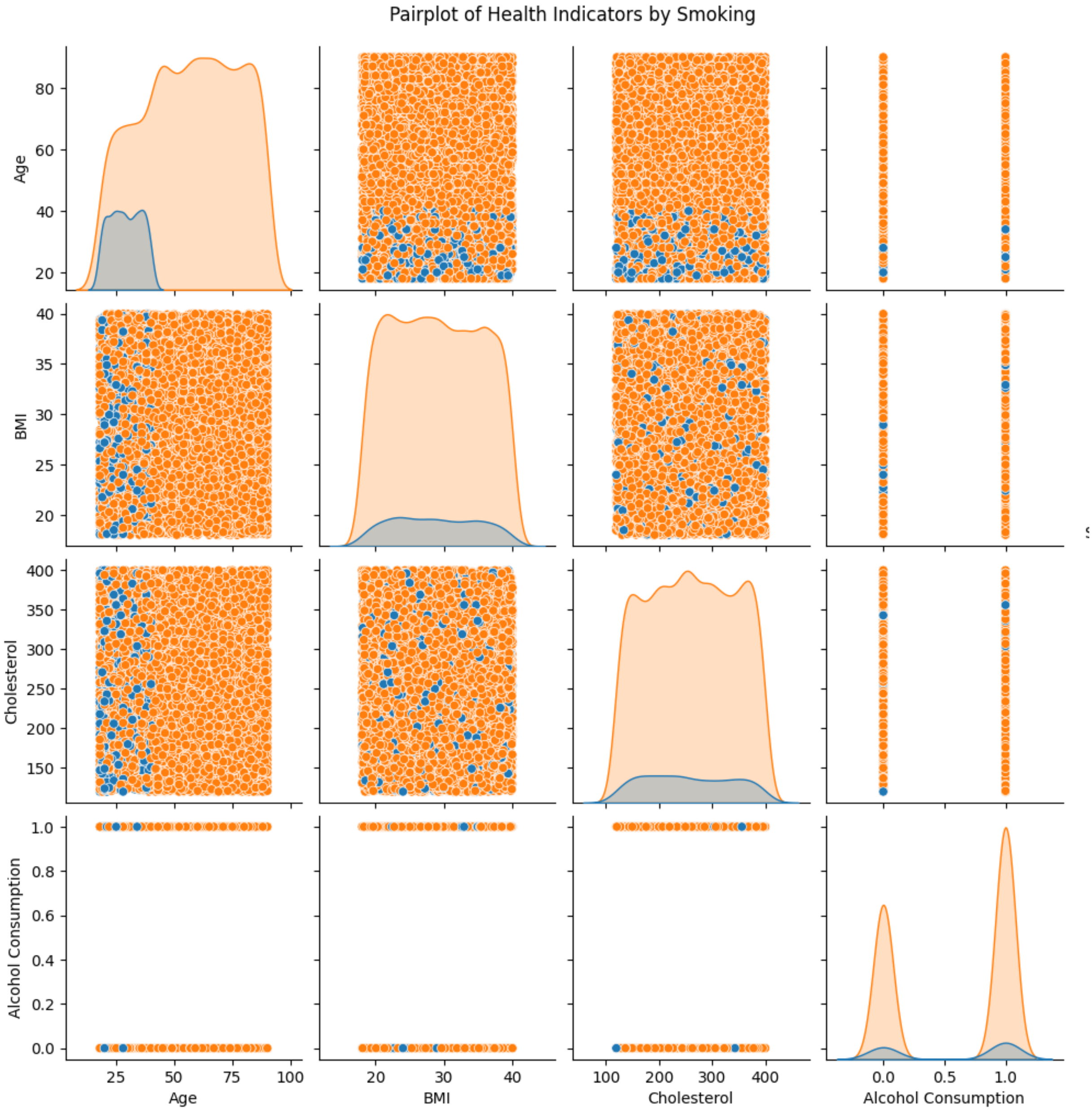
```
plt.ylabel("Count")
plt.show()
```



Bar Plot (Average of Feature by Category)

In [120…

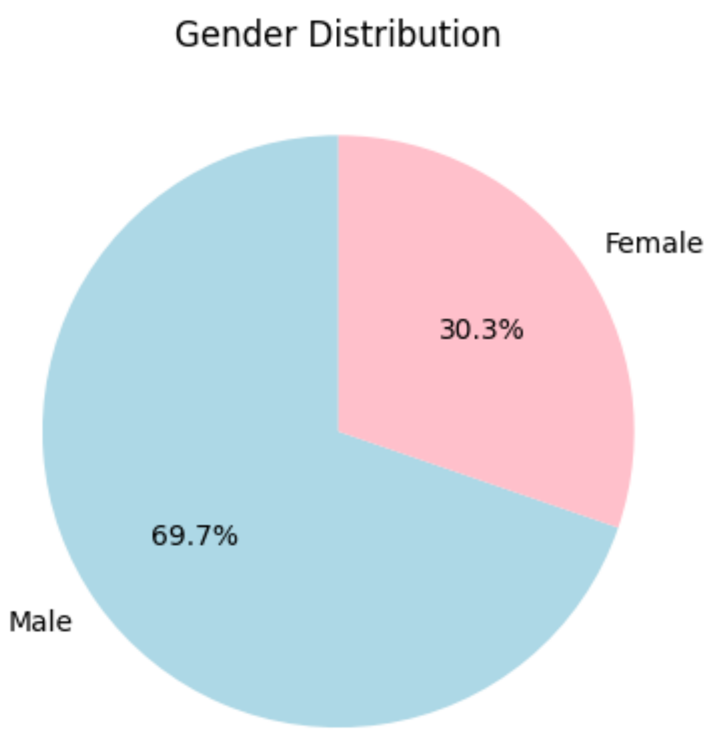
```
sns.pairplot(df[['Age', 'BMI', 'Cholesterol', 'Alcohol Consumption', 'Smoking']]
plt.suptitle("Pairplot of Health Indicators by Smoking", y=1.02)
plt.show()
```



Pie Chart (for Gender Distribution)

In [122…

```
df['Sex'].value_counts().plot.pie(autopct='%1.1f%%', startangle=90, colors=['lig
plt.title("Gender Distribution")
plt.ylabel('')
plt.show()
```



In [ ]:

To check the correlation between Age and BMI

Correlation: Correlation tells you how strongly variables are related — whether they move together, and in what direction

In [79]:
```
corre=df['Age'].corr(df['BMI'])
print(corre)
#As age increases or decreases, BMI doesn't consistently go up or down
```

```
-0.0026118461643639826
```

Is there a linear relationship between cholesterol and triglyceride le across the patient population? This helps us understand whether hi cholesterol is typically accompanied by high triglycerides

In [80]:
```
correlation=df['Cholesterol'].corr(df['Triglycerides'])
print(correlation)
#no correlation between Cholesterol,Triglycerides column
```

```
-0.0054537211761552075
```

In [81]:
```
# Correlation matrix
df.corr(numeric_only=True)

# Covariance matrix
#df.cov(numeric_only=True)
```

Out[81]:

	Age	Cholesterol	Heart Rate	Diabetes	Family History	Smoking	Obesity
Age	1.000000	-0.009107	-0.003844	-0.014105	0.008353	NaN	-0.008140
Cholesterol	-0.009107	1.000000	0.000315	-0.013428	-0.021608	NaN	-0.014843
Heart Rate	-0.003844	0.000315	1.000000	0.006764	-0.013470	NaN	0.012725
Diabetes	-0.014105	-0.013428	0.006764	1.000000	-0.013844	NaN	0.012866
Family History	0.008353	-0.021608	-0.013470	-0.013844	1.000000	NaN	-0.001444
Smoking	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Obesity	-0.008140	-0.014843	0.012725	0.012866	-0.001444	NaN	1.000000
Alcohol Consumption	-0.006666	-0.007261	0.003459	0.005551	0.012701	NaN	-0.024195
Exercise Hours Per Week	0.001206	0.021517	0.008276	-0.007014	-0.006378	NaN	0.002099
Previous Heart Problems	0.000868	-0.006070	-0.004956	0.000867	-0.004568	NaN	0.005159
Medication Use	0.000980	-0.000905	0.009244	-0.002656	0.000981	NaN	-0.006267
Stress Level	0.018307	-0.024487	-0.004547	0.006719	0.015637	NaN	0.010626
Sedentary Hours Per Day	0.017280	0.018914	-0.010232	0.004705	0.002561	NaN	-0.001333
Income	-0.001733	0.000007	0.004873	-0.000759	-0.000401	NaN	-0.003870
BMI	-0.002612	0.017292	0.005299	-0.002852	-0.011492	NaN	-0.006058
Triglycerides	0.003415	-0.005454	0.012244	0.010431	-0.001904	NaN	0.001467
Physical Activity Days Per Week	0.001384	0.016056	0.000834	-0.002411	0.009561	NaN	0.005337
Sleep Hours Per Day	-0.002185	0.004456	0.001811	-0.012457	-0.011199	NaN	-0.005314
Unnamed: 25	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Heart Attack Risk	0.006403	0.019340	-0.004251	0.017225	-0.001652	NaN	-0.013318
Perfectly_Healthy	0.014225	-0.010818	-0.006250	-0.014632	-0.010534	NaN	-0.010714

21 rows × 21 columns

Statistical Analyisis: Inferential Statistic

Before comparing BMI between different groups, we need to verify is normally distributed. Is the Body Mass Index (BMI) variable in this population normally distributed, or does it show signs of skewness multimodality

In [82]:

```
#Null hypothesis: BMI is normally distributed
#Alternate hypothesis: BMI is not nromally distributed
from scipy.stats import shapiro
data=df['BMI']
stat,p_value=shapiro(data)
print(p_value)
if(p_value<0.05):
    print("Alternate Hypothesis")
    print("BMI is not normally distributed")
```

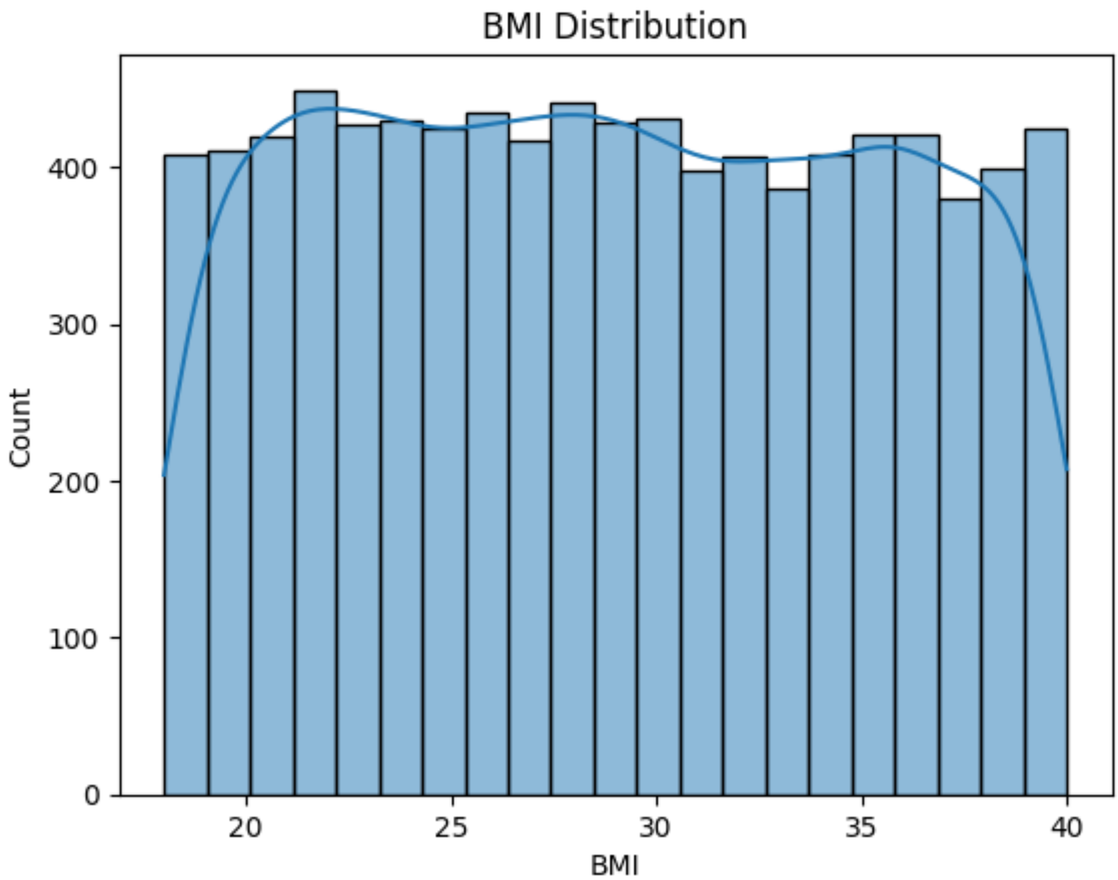
```
else:
    print("Null Hypothesis")
    print("BMI is normally distribucted")
```

```
3.1096630105816765e-45
Alternate Hypothesis
BMI is not normally distribucted
```

```
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\scipy\stats\_axis_nan_policy.py:586: UserWarning: scipy.stats.shapiro: For N
5000, computed p-value may not be accurate. Current N is 8763.
  res = hypotest_fun_out(*samples, **kwds)
```

Most people may have higher BMI (right skewed)

In [83]:
```
sns.histplot(df['BMI'], kde=True)
plt.title("BMI Distribution")
plt.show()
```



Is there a statistically significant difference in Body Mass Index (BM
between individuals labeled as 'perfectly healthy' and those who ar
This analysis will help identify if BMI plays a role in overall health st

In [84]:
```
# Null Hypothesis (H0): There is **no significant difference** in BMI between Pe
# Alternate Hypothesis (H1): There **is a significant difference** in BMI betwee


health_bmi=df[df['Perfectly_Healthy']==1]['BMI']
unhealth_bmi=df[df['Perfectly_Healthy']==0]['BMI']
from scipy.stats import ttest_ind
t_stat,p_value=ttest_ind(health_bmi,unhealth_bmi)
print(p_value)
if(p_value>0.05):
```

```
    print("Null Hypothesis")
    print("There is **no significant difference** in BMI between Perfectly Healt
else:
    print("Alternate Hypothesis")
    print("There **is a significant difference** in BMI between Perfectly Health
```

```
0.2920672958942085
Null Hypothesis
There is **no significant difference** in BMI between Perfectly Healthy and Unhealthy
people
```

Association Between Smoking and Health Status (Chi-Square Test)

Is there a significant association between smoking behavior and be classified as perfectly healthy? This will help determine whether smo prevalence differs among healthy and unhealthy individuals

In [85]:

```
#Null Hypothesis: There is no Significient relation between Smoking and Perfect
#Alternate Hypothesis: There is  Significient relation between Smoking and Perfe
from scipy.stats import chi2_contingency
data=['Smoking','Perfectly_Healthy']
fre=pd.crosstab(df['Smoking'],df['Perfectly_Healthy'])
chi2,p,dof,excpt=chi2_contingency(fre)
if(p>0.05):
    print("Null Hypothesis")
    print("There is no  Significient relation between Smoking and Perfect health
else:
    print("Alternate Hypothesis")
    print("here is Significient relation between Smoking and Perfect health")
```

```
Null Hypothesis
There is no  Significient relation between Smoking and Perfect health
```

Are higher income individuals more likely to be perfectly healthy

In [86]:

```
#Null Hypothesis (H0): There is NO significant difference in income between perf
#Alternate Hypothesis (H1): There IS a significant difference in income between

from scipy.stats import ttest_ind
healthy_income=df[df['Perfectly_Healthy']==1]['Income']
unhealthy_income=df[df['Perfectly_Healthy']==0]['Income']
t_stat,p_value=ttest_ind(healthy_income,unhealthy_income)
print(p_value)
if(p_value<0.05):
    print("Alternate Hypothesis")
    print("There IS a significant difference in income between perfectly healthy
else:
    print("Null Hypothesis")
    print("There is NO significant difference in income between perfectly health
```

```
0.4490003791470508
Null Hypothesis
There is NO significant difference in income between perfectly healthy and unhealthy
individuals
```

In [87]:

```
print(df)
```

```
     Patient ID   Age     Sex  Cholesterol Blood Pressure  Heart Rate  \
0       BMW7812  67.0    Male          208         158/88          72   
1       CZE1114  21.0    Male          389         165/93          98   
2       BNI9906  21.0  Female          324         174/99          72   
3       JLN3497  84.0    Male          383        163/100          73   
4       GFO8847  66.0    Male          318          91/88          93   
...         ...   ...     ...          ...            ...         ...   
8758    MSV9918  60.0    Male          121          94/76          61   
8759    QSV6764  28.0  Female          120        157/102          73   
8760    XKA5925  47.0    Male          250         161/75         105   
8761    EPE6801  36.0    Male          178         119/67          60   
8762    ZWN9666  25.0  Female          356         138/67          75   

      Diabetes  Family History  Smoking  Obesity  ...  \
0          0.0             0.0        1      0.0  ...   
1          1.0             1.0        1      1.0  ...   
2          1.0             0.0        1      0.0  ...   
3          1.0             1.0        1      0.0  ...   
4          1.0             1.0        1      1.0  ...   
...        ...             ...      ...      ...  ...   
8758       1.0             1.0        1      0.0  ...   
8759       1.0             0.0        1      1.0  ...   
8760       0.0             1.0        1      1.0  ...   
8761       1.0             0.0        1      0.0  ...   
8762       1.0             1.0        1      0.0  ...   

      Physical Activity Days Per Week  Sleep Hours Per Day         Country  \
0                                 0.0                    6       Argentina   
1                                 1.0                    7          Canada   
2                                 4.0                    4          France   
3                                 3.0                    4          Canada   
4                                 1.0                    5        Thailand   
...                               ...                  ...             ...   
8758                              7.0                    7        Thailand   
8759                              4.0                    9          Canada   
8760                              4.0                    4          Brazil   
8761                              2.0                    8          Brazil   
8762                              7.0                    4  United Kingdom   

          Continent           Hemisphere  Unnamed: 25  Heart Attack Risk  \
0     South America  Southern Hemisphere          NaN                0.0   
1     North America  Northern Hemisphere          NaN                0.0   
2            Europe  Northern Hemisphere          NaN                0.0   
3     North America  Northern Hemisphere          NaN                0.0   
4              Asia  Northern Hemisphere          NaN                0.0   
...             ...                  ...          ...                ...   
8758           Asia  Northern Hemisphere          NaN                0.0   
8759  North America  Northern Hemisphere          NaN                0.0   
8760  South America  Southern Hemisphere          NaN                1.0   
8761  South America  Southern Hemisphere          NaN                0.0   
8762         Europe  Northern Hemisphere          NaN                1.0   

      BP range  AgeGroup  Perfectly_Healthy  
0         high     60-69                  0  
1         high       <30                  0  
2         high       <30                  0  
3         high       70+                  0  
4          low     60-69                  0  
...        ...       ...                ...  
8758    medium     60-69                  0  
```

```
8759    medium      <30                   0
8760      high    40-49                   0
8761      high    30-39                   0
8762      high      <30                   0

[8763 rows x 30 columns]
```

Machile Learning

1. Problem Statement: What do you want to predict/classify?

2. Data Collection: Get relevant data

3. Data Cleaning: Handle nulls, remove outliers, encode values

4. Feature Selection: Choose important columns

5. Train-Test Split: Split into training and testing data

6. Model Training: Fit an algorithm to training data

7. Model Testing: Predict and evaluate using test data

8. Model Improvement: Tune parameters, try other models

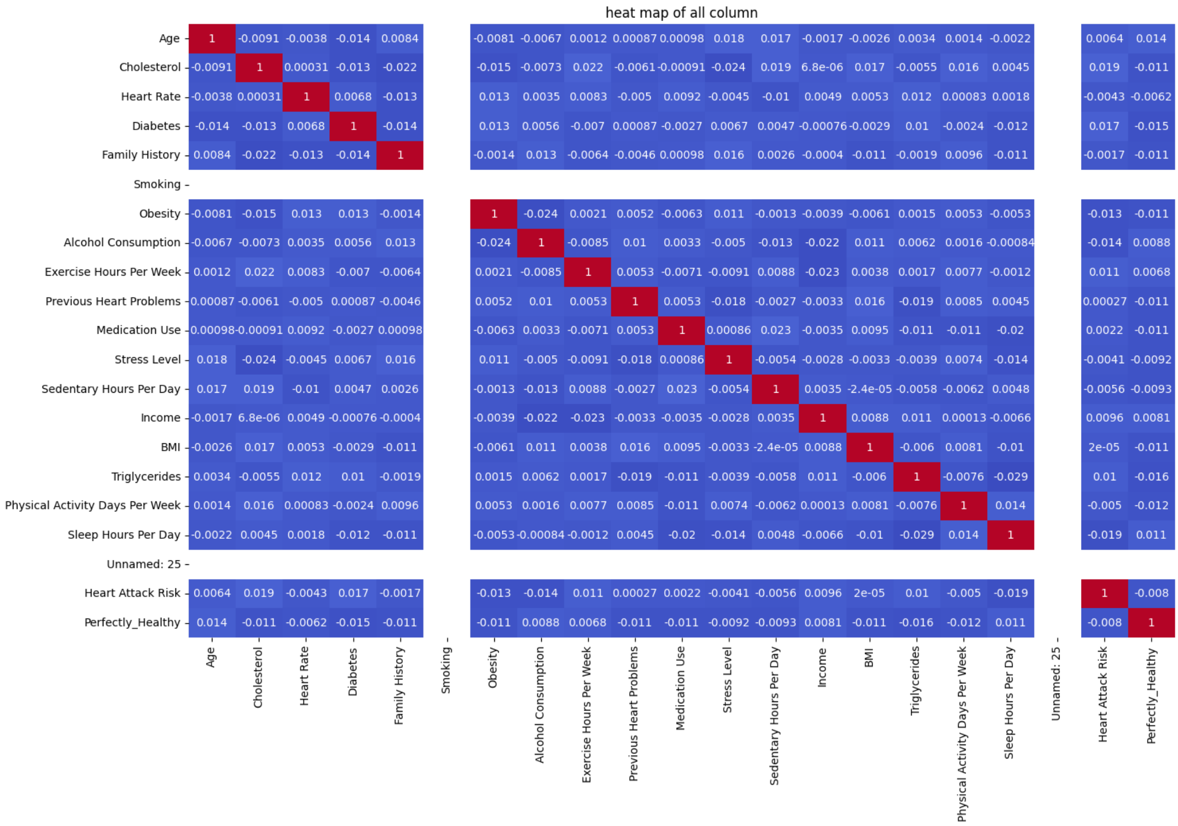
9. Deployment (optional) Use the model in a real app or website

1.Predict whether a person consumes alcohol or not bas on their lifestyle and health indicators

Features such as age, gender, smoking status, stress level, physical activity, sleep patterns, income, and diet quality, we aim to identify patterns that are strongly associated with alcohol consumption

In [88]:
```
numeric=df.select_dtypes(include='number')
f=numeric.corr()
plt.figure(figsize=(20, 10))
sns.heatmap(f,annot=True,cmap='coolwarm')
plt.title("heat map of all column")
```

Out[88]:
```
Text(0.5, 1.0, 'heat map of all column')
```



By calculate all correlation the dependent Alcohol Consumption ha more correlation with Heart Rate, Diabetes, Family History, Smoking,Medication use,Tringlycerides use these column to predict better Alcohol Consumption

Decision tree pre purning model

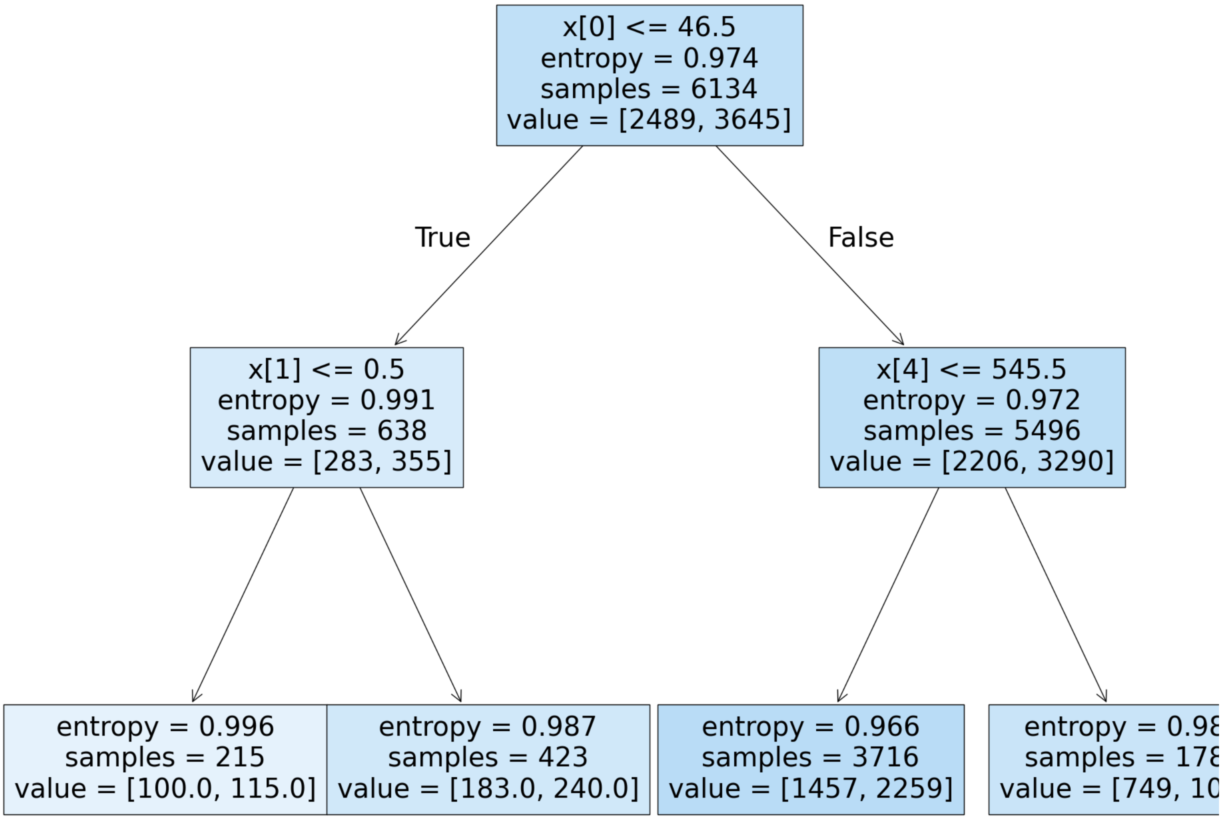
In [ ]:

In [89]:
```
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn import tree
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score,classification_report
le=LabelEncoder()
df['Sex']=le.fit_transform(df['Sex'])
df['Diet']=le.fit_transform(df['Diet'])
x =df[['Heart Rate', 'Diabetes', 'Smoking', 'Medication Use',
        'Triglycerides']]
y=df['Alcohol Consumption']
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.3,random_state=42
model1=DecisionTreeClassifier()

parameter= { 'criterion':['gini','entropy','log_loss'],
             'splitter':['best','random'],
             'max_depth':[1,2,3,4,5],
             'max_features':['sqrt','log2']
             }
cv=GridSearchCV(model1,parameter,cv=5,scoring='accuracy')
cv.fit(x_train,y_train)
print(cv.best_params_)
predict=cv.predict(x_test)
accuracy=accuracy_score(y_test,predict)
```

```
print(accuracy)
report=classification_report(y_test,predict)
print(report)
plt.figure(figsize=(25,20))
tree.plot_tree(cv.best_estimator_, filled=True)
plt.show()
```

```
{'criterion': 'entropy', 'max_depth': 2, 'max_features': 'log2', 'splitter': 'best'}
0.607074933434766
              precision    recall  f1-score   support

         0.0       0.00      0.00      0.00      1033
         1.0       0.61      1.00      0.76      1596

    accuracy                           0.61      2629
   macro avg       0.30      0.50      0.38      2629
weighted avg       0.37      0.61      0.46      2629
```

```
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\sklearn\metrics\_classification.py:1565: UndefinedMetricWarning: Precision i
defined and being set to 0.0 in labels with no predicted samples. Use `zero_division`
parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\sklearn\metrics\_classification.py:1565: UndefinedMetricWarning: Precision i
defined and being set to 0.0 in labels with no predicted samples. Use `zero_division`
parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\sklearn\metrics\_classification.py:1565: UndefinedMetricWarning: Precision i
defined and being set to 0.0 in labels with no predicted samples. Use `zero_division`
parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```



In [90]:
```
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn import tree
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score,classification_report
le=LabelEncoder()
df['Sex']=le.fit_transform(df['Sex'])
df['Diet']=le.fit_transform(df['Diet'])
x =df[['Heart Rate', 'Diabetes', 'Smoking', 'Medication Use',
        'Triglycerides']]
y=df['Alcohol Consumption']
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.3,random_state=42
model1=DecisionTreeClassifier()
cv.fit(x_train,y_train)
predict=cv.predict(x_test)
accuracy=accuracy_score(y_test,predict)
print(accuracy)
```

```
0.607074933434766
```

2.predict whether a person has diabetes (Yes=1, No=0) based on a set of independent health-related variables. dataset includes both original and derived features that reflect a person's lifestyle, biological metrics, and medica history

In [117…

```
import pandas as pd
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, accuracy_score




selected_features = [
    'BMI',
    'Income',
    'Exercise Hours Per Week',
    'Sedentary Hours Per Day',

    'Cholesterol',

    'Age',


    'Heart Rate'
]


# --------- Step 2: Create X and y ---------
X = df[selected_features]
y = df['Diabetes']

# Handle missing values (if any)
X = X.fillna(0)

# --------- Step 3: Train-test split ---------
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, random_state=42
)

# --------- Step 4: Random Forest Model with class_weight ---------
model = RandomForestClassifier(
    random_state=42,
    n_estimators=100,
    class_weight='balanced'
)
model.fit(X_train, y_train)

# --------- Step 5: Evaluation ---------
y_pred = model.predict(X_test)

print("Accuracy:", accuracy_score(y_test, y_pred))
print("\nClassification Report:\n", classification_report(y_test, y_pred))
```

```
Accuracy: 0.6520250998288648

Classification Report:
              precision    recall  f1-score   support

           0       0.41      0.05      0.09       595
           1       0.66      0.96      0.78      1158

    accuracy                           0.65      1753
   macro avg       0.53      0.51      0.44      1753
weighted avg       0.58      0.65      0.55      1753
```

3.Given a person's lifestyle and health indicators (such as age, exercise, diet, and heart health), can we accurately predict their Body Mass Index (BMI) using a machine learning model

Random Forest Regression Model

In [93]:

```python
import pandas as pd
from sklearn.ensemble import RandomForestRegressor
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error, r2_score

# Step 1: Fill missing values (optional: use df.isnull().sum() to check)


selected_features = [

    'Cholesterol',

]
X=df[selected_features]
y = df['BMI']

# Step 3: Convert categorical columns using one-hot encoding
X = pd.get_dummies(X, drop_first=True)

# Step 4: Split data
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.3, random_state=42
)

# Step 5: Train Random Forest model
rf = RandomForestRegressor(
    n_estimators=200,
    max_depth=10,
    min_samples_split=5,
    min_samples_leaf=3,
    random_state=42
)
rf.fit(X_train, y_train)

# Step 6: Predict
y_pred = rf.predict(X_test)

# Step 7: Evaluate
mse = mean_squared_error(y_test, y_pred)
```

```
r2 = r2_score(y_test, y_pred)

print("✅ MSE:", mse)
print("✅ R² Score:", r2)
```

```
✅ MSE: 39.8914700708232
✅ R² Score: -0.007354630272280449
```

5.Predicting Medication Usage Based on Health and Life Factors

Decision Tree Classifier

In [95]:

```
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, classification_report

# Define features and target
X = df[['BMI', 'Sedentary Hours Per Day', 'Age']]
y = df['Medication Use']

# Train/test split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_

# Model training
model = DecisionTreeClassifier()
model.fit(X_train, y_train)

# Prediction and evaluation
y_pred = model.predict(X_test)
accuracy = accuracy_score(y_test, y_pred)
cf = classification_report(y_test, y_pred)

print("Accuracy:", accuracy)
print("Classification Report:\n", cf)

# Correlation with Medication Use (only numeric columns)
```

```
✅ Accuracy: 0.5157854697603652
✅ Classification Report:
               precision    recall  f1-score   support

         0.0       0.53      0.51      0.52      1346
         1.0       0.50      0.52      0.51      1283

    accuracy                           0.52      2629
   macro avg       0.52      0.52      0.52      2629
weighted avg       0.52      0.52      0.52      2629
```

6.Predicting Smoking Status Based on Age

Random Forest Classifier

In [118…

```
X = df[['Age']]
y = df['Smoking']
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
```

```python
from sklearn.metrics import accuracy_score, classification_report

# Split
x_train, x_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_

# Train
model = RandomForestClassifier(n_estimators=100, random_state=42)
model.fit(x_train, y_train)

# Predict
y_pred = model.predict(x_test)

# Evaluate
print("Accuracy:", accuracy_score(y_test, y_pred))
print(classification_report(y_test, y_pred))
```

```
Accuracy: 0.899201217192849
              precision    recall  f1-score   support

           0       0.00      0.00      0.00       265
           1       0.90      1.00      0.95      2364

    accuracy                           0.90      2629
   macro avg       0.45      0.50      0.47      2629
weighted avg       0.81      0.90      0.85      2629
```

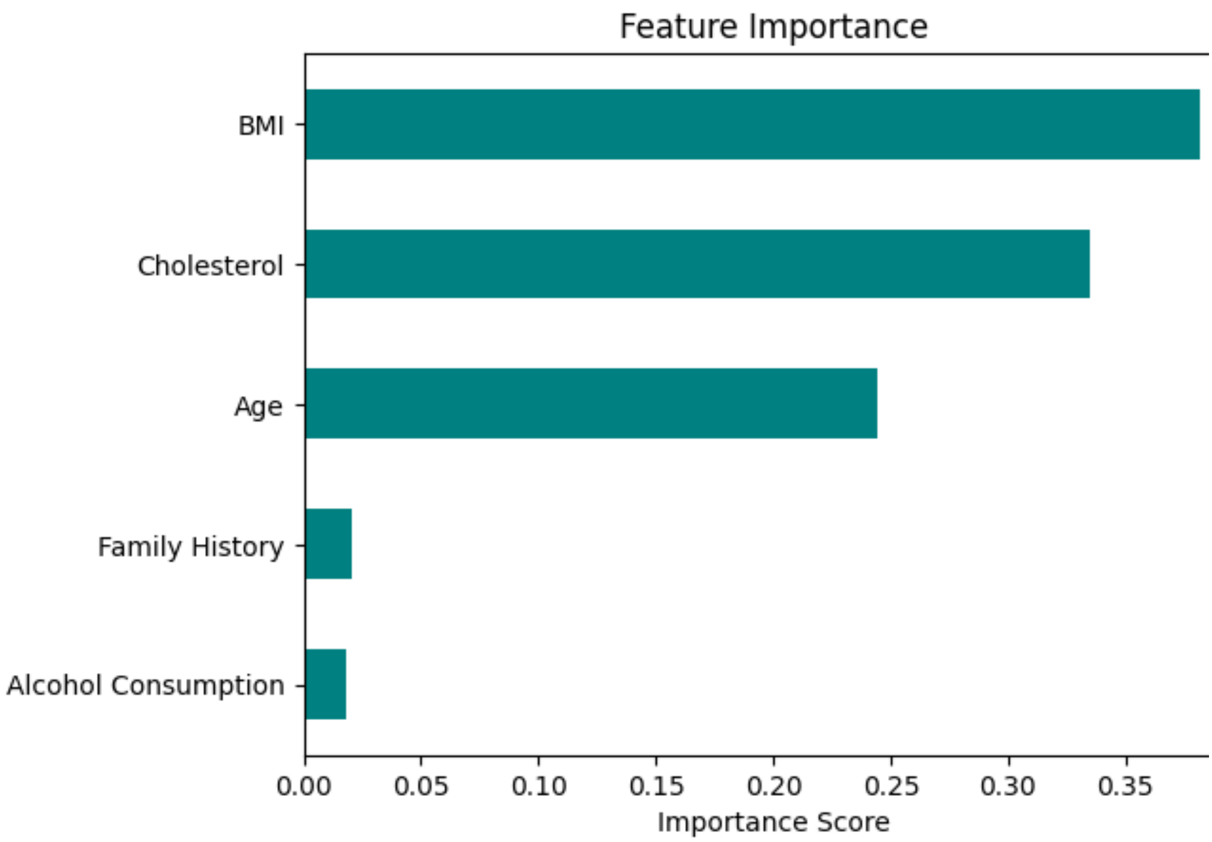
```
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\sklearn\metrics\_classification.py:1565: UndefinedMetricWarning: Precision i
defined and being set to 0.0 in labels with no predicted samples. Use `zero_division`
parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\sklearn\metrics\_classification.py:1565: UndefinedMetricWarning: Precision i
defined and being set to 0.0 in labels with no predicted samples. Use `zero_division`
parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
C:\Users\admin\AppData\Local\Programs\Python\Python313\Lib\site-
packages\sklearn\metrics\_classification.py:1565: UndefinedMetricWarning: Precision i
defined and being set to 0.0 in labels with no predicted samples. Use `zero_division`
parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```

In [128…

```python
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report, confusion_mat


X = df[['Age', 'BMI', 'Cholesterol', 'Alcohol Consumption', 'Family History']]
y = df['Heart Attack Risk']  # Target (0 or 1)


x_train, x_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_


model = RandomForestClassifier(n_estimators=100, random_state=42)
model.fit(x_train, y_train)


y_pred = model.predict(x_test)
```

```python
print("Accuracy:", accuracy_score(y_test, y_pred))
print("\nClassification Report:\n", classification_report(y_test, y_pred))
print("\nConfusion Matrix:\n", confusion_matrix(y_test, y_pred))


import matplotlib.pyplot as plt
import seaborn as sns

feat_importances = pd.Series(model.feature_importances_, index=X.columns)
feat_importances.sort_values().plot(kind='barh', color='teal')
plt.title("Feature Importance")
plt.xlabel("Importance Score")
plt.show()
```

```
Accuracy: 0.5956637504754659

Classification Report:
               precision    recall  f1-score   support

           0       0.64      0.84      0.73      1691
           1       0.35      0.16      0.22       938

    accuracy                           0.60      2629
   macro avg       0.50      0.50      0.48      2629
weighted avg       0.54      0.60      0.55      2629


Confusion Matrix:
 [[1413  278]
 [ 785  153]]
```



In [ ]:

Conclusion:

1.This project showcases how machine learning can support health
decisions by highlighting hidden patterns in patient data. The insig
derived from the model can assist doctors or public health professi
in:

2.Prioritizing high-risk individuals,

3.Advising lifestyle changes, and

4.Guiding preventive care strategies.

5.Our machine learning project analyzed a health dataset and prod
several important findings related to heart attack risk factors

6.Strong Correlation Between Smoking and Heart Attack Risk

7.Strong Correlation Between Age and Smoking

```
In [ ]:
```