Library Imports

```
# Imports
import numpy as np
import random
import matplotlib.pyplot as plt
import pandas as pd
from pandas.plotting import scatter_matrix
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.ensemble import BaggingClassifier
```

#Reading data and Generating our data set variant using our ids

```
# Load the CSV file
from google.colab import drive
drive.mount('/content/drive')

id_1 = 7487 #change to first student id
id_2 = 7597 #change to second student id
id_3 = 7409 #change to third student id "leave 0000 if team of 2"

random_seed = id_1+id_2+id_3
random.seed(random_seed)
data_path='/content/drive/MyDrive/Data.csv' #replace with data path
output_path='/content/drive/MyDrive/your_data.csv' #replace with
output data path

all_data=pd.read_csv(data_path)
all_columns = all_data.columns.tolist()

target_column = 'smoking'

all_columns.remove(target_column)

selected_columns = random.sample(all_columns, 10)

print(selected_columns) #MUST BE PRINTED
selected_columns = np.append(selected_columns, target_column)
data = all_data[selected_columns].copy()
```

```
Drive already mounted at /content/drive; to attempt to forcibly
remount, call drive.mount("/content/drive", force_remount=True).
['ALT', 'eyesight(left)', 'hemoglobin', 'age', 'waist(cm)',
'hearing(right)', 'id', 'height(cm)', 'systolic', 'HDL']
```

```
data.head()
```

```
   ALT  eyesight(left)  hemoglobin  age  waist(cm)  hearing(right)  id
\
0   25             0.5        16.5   55       81.0               1   0

1   23             0.6        16.2   70       89.0               2   1

2   31             0.4        17.4   20       81.0               1   2

3   27             1.5        15.9   35      105.0               1   3

4   13             1.5        15.4   30       80.5               1   4


   height(cm)  systolic  HDL  smoking
0         165       135   40        1
1         165       146   57        0
2         170       118   45        1
3         180       131   38        0
4         165       121   44        1

data = data.drop('id', axis=1)
```

since id attribute is an auto increment attribute used for indexing it's no good to use it

```
data.head()

   ALT  eyesight(left)  hemoglobin  age  waist(cm)  hearing(right)  \
0   25             0.5        16.5   55       81.0               1
1   23             0.6        16.2   70       89.0               2
2   31             0.4        17.4   20       81.0               1
3   27             1.5        15.9   35      105.0               1
4   13             1.5        15.4   30       80.5               1

   height(cm)  systolic  HDL  smoking
0         165       135   40        1
1         165       146   57        0
2         170       118   45        1
3         180       131   38        0
4         165       121   44        1

data.to_csv(output_path, index=False)   #From HERE YOU CAN SPLIT FOR
TRAIN ,VALID AND TEST
```

Data spliting

```
# Randomly splitting the dataset into (70% Training + 15% Testing +
15% Validation)
data_train, data_temp = train_test_split(data, test_size = 0.3)
```

```
data_test, data_validate = train_test_split(data_temp, test_size =
0.5)
```

Univariate Analysis

```
data_train.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 111479 entries, 112849 to 57617
Data columns (total 10 columns):
 #   Column           Non-Null Count   Dtype
---  ------           --------------   -----
 0   ALT              111479 non-null  int64
 1   eyesight(left)   111479 non-null  float64
 2   hemoglobin       111479 non-null  float64
 3   age              111479 non-null  int64
 4   waist(cm)        111479 non-null  float64
 5   hearing(right)   111479 non-null  int64
 6   height(cm)       111479 non-null  int64
 7   systolic         111479 non-null  int64
 8   HDL              111479 non-null  int64
 9   smoking          111479 non-null  int64
dtypes: float64(3), int64(7)
memory usage: 9.4 MB
```

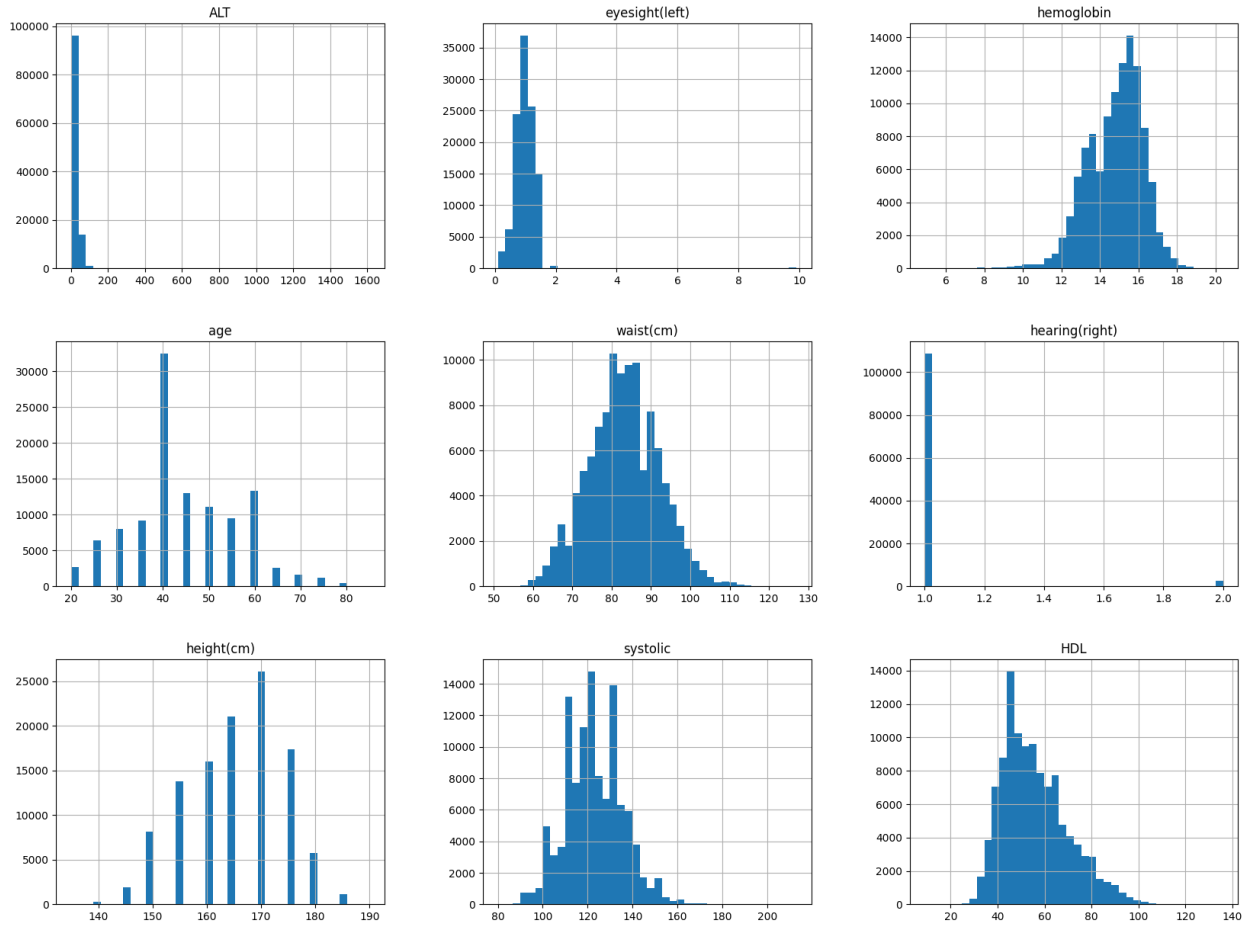
Central Tendency & Dispersion:

```
data_train.describe()
```

```
                ALT  eyesight(left)     hemoglobin            age  \
count  111479.000000   111479.000000  111479.000000  111479.000000
mean       26.539025        1.006102      14.793888      44.319145
std        16.019601        0.402362       1.434894      11.846594
min         1.000000        0.100000       4.900000      20.000000
25%        16.000000        0.800000      13.800000      40.000000
50%        22.000000        1.000000      15.000000      40.000000
75%        32.000000        1.200000      15.800000      55.000000
max      1612.000000        9.900000      20.400000      85.000000

          waist(cm)  hearing(right)     height(cm)       systolic  \
count  111479.000000   111479.000000  111479.000000  111479.000000
mean       82.993420        1.023753     165.246809     122.475166
std         8.956527        0.152280       8.828943      12.719375
min        51.000000        1.000000     135.000000      80.000000
25%        77.000000        1.000000     160.000000     114.000000
50%        83.000000        1.000000     165.000000     121.000000
75%        89.000000        1.000000     170.000000     130.000000
max       127.000000        2.000000     190.000000     213.000000
```

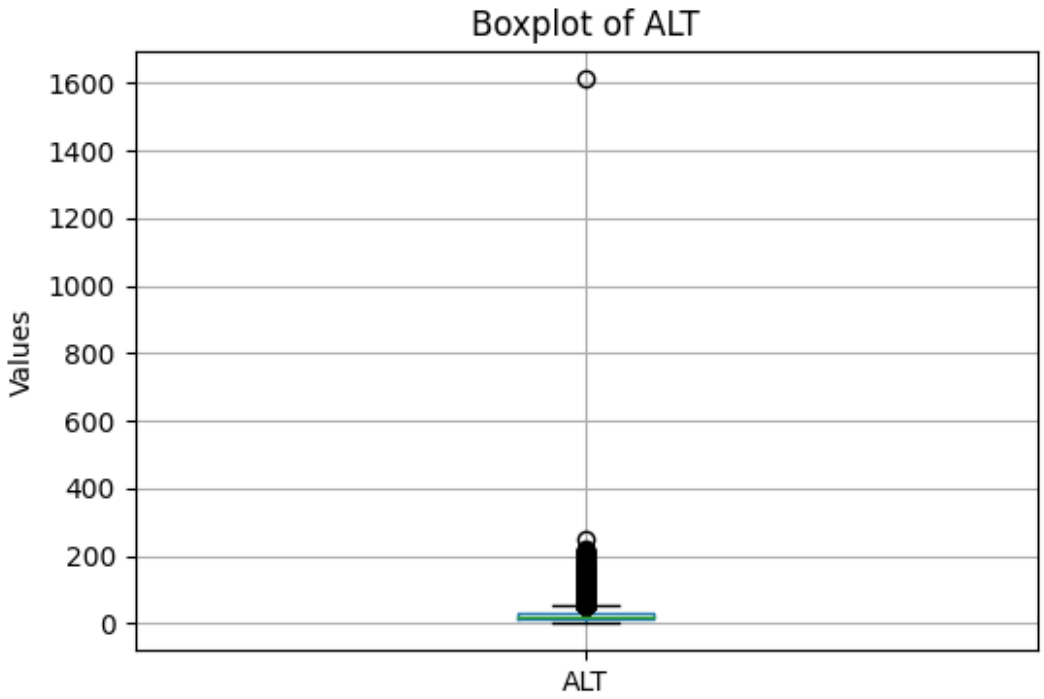
```
                HDL         smoking
count  111479.000000  111479.000000
mean       55.856673       0.437751
std        13.959852       0.496112
min         9.000000       0.000000
25%        45.000000       0.000000
50%        54.000000       0.000000
75%        64.000000       1.000000
max       136.000000       1.000000
```

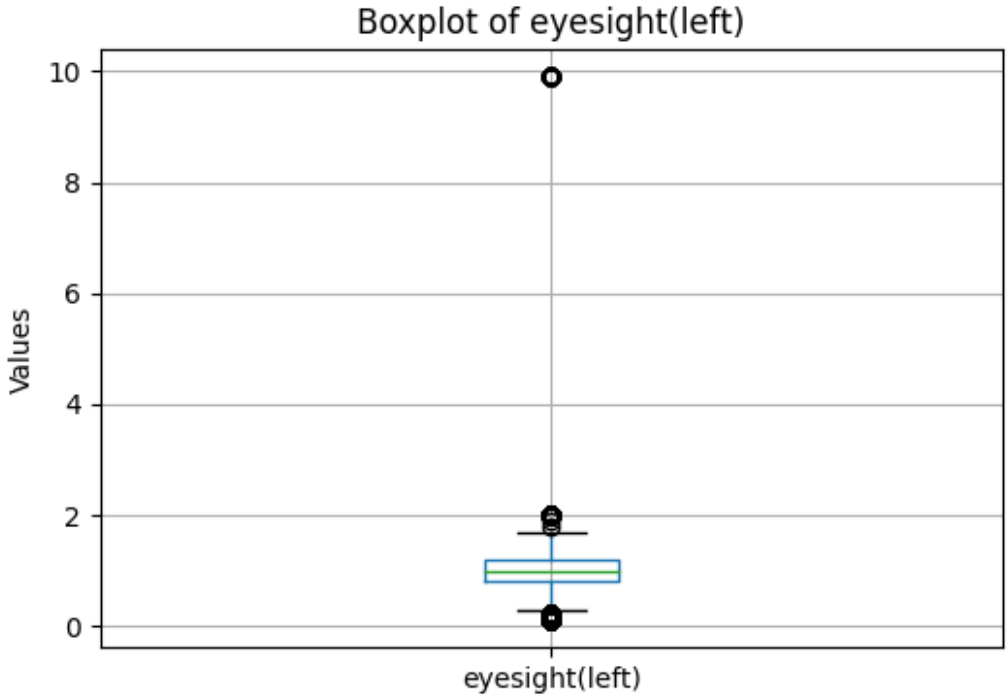
```
#data.hist(bins=50,figsize=(20,15))
data_train[['ALT','eyesight(left)','hemoglobin'  ,'age','waist(cm)','hearing(right)','height(cm)','systolic','HDL']].hist(bins=40,figsize=(20,15))
plt.show()
```

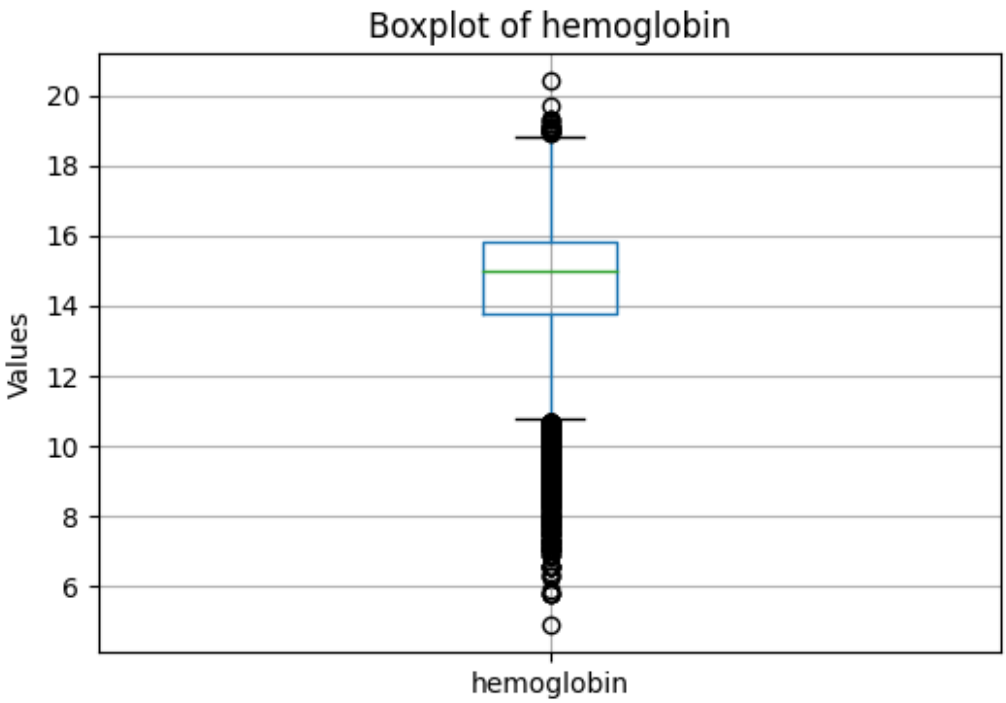


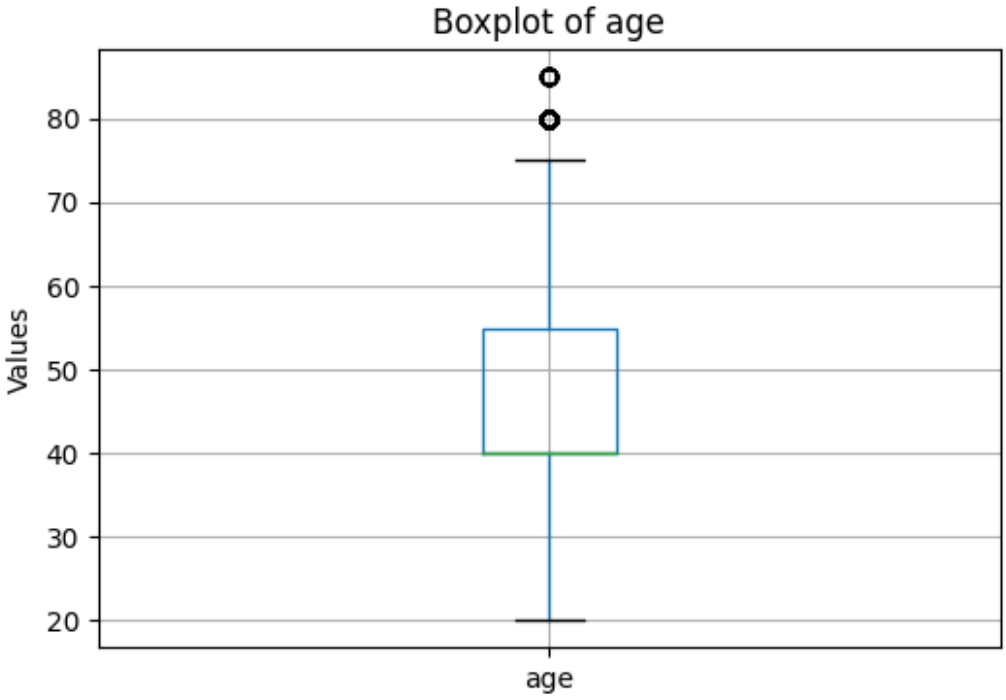

```
for column in data_train.columns:
    plt.figure(figsize=(6, 4))  # Adjust the figure size as needed
    data_train.boxplot(column=column)
    plt.title(f'Boxplot of {column}')
```

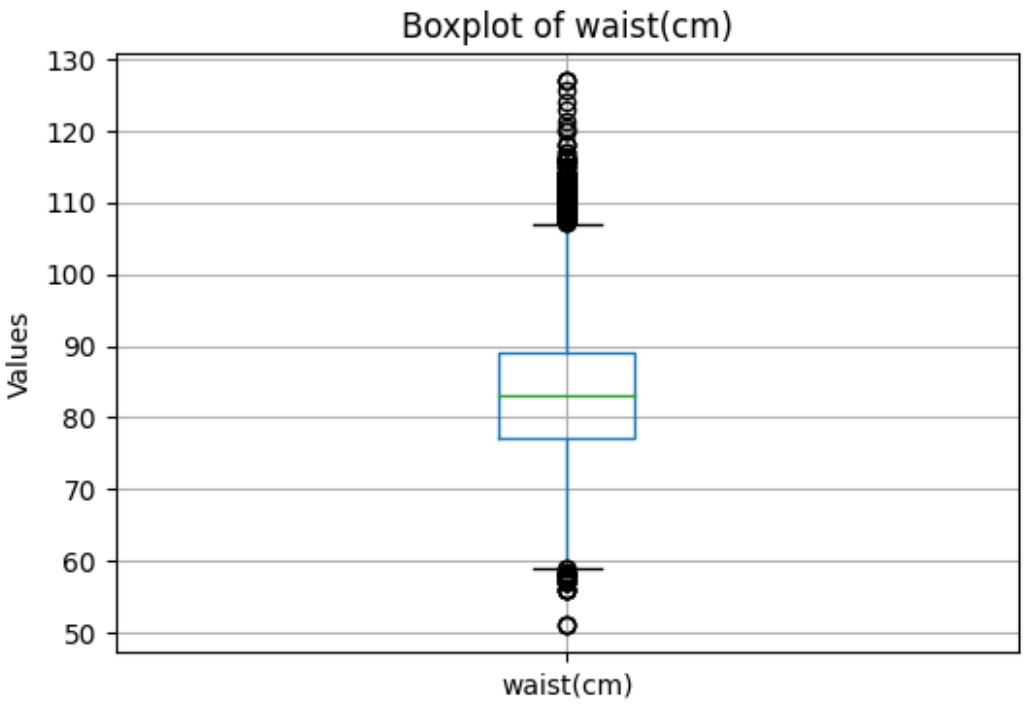
```
    plt.ylabel('Values')
    plt.show()
```

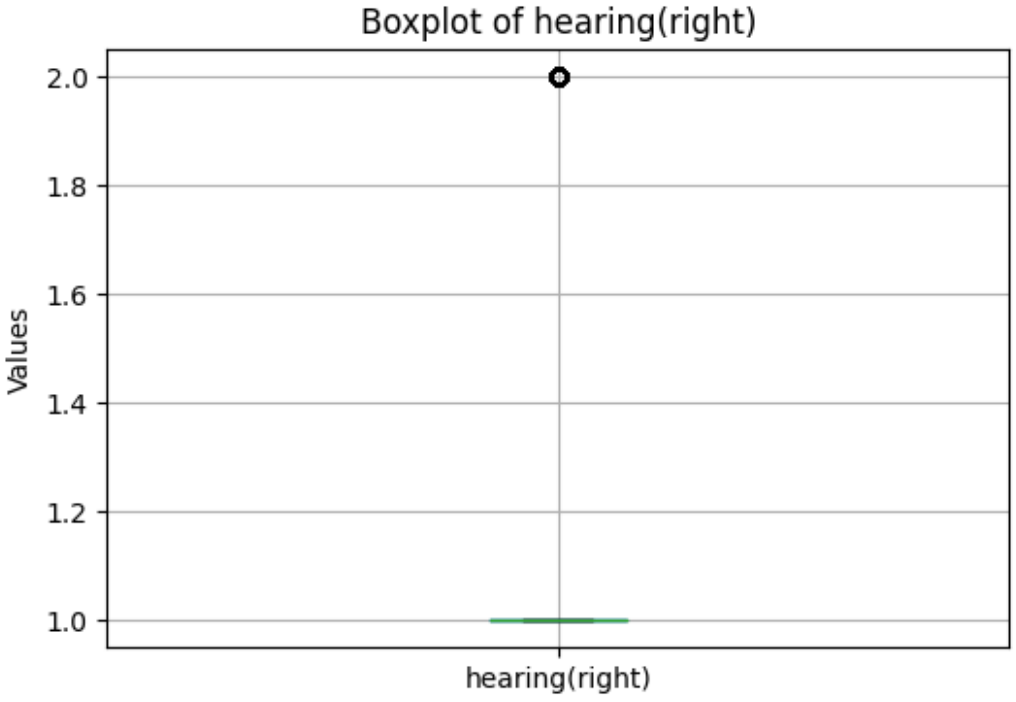


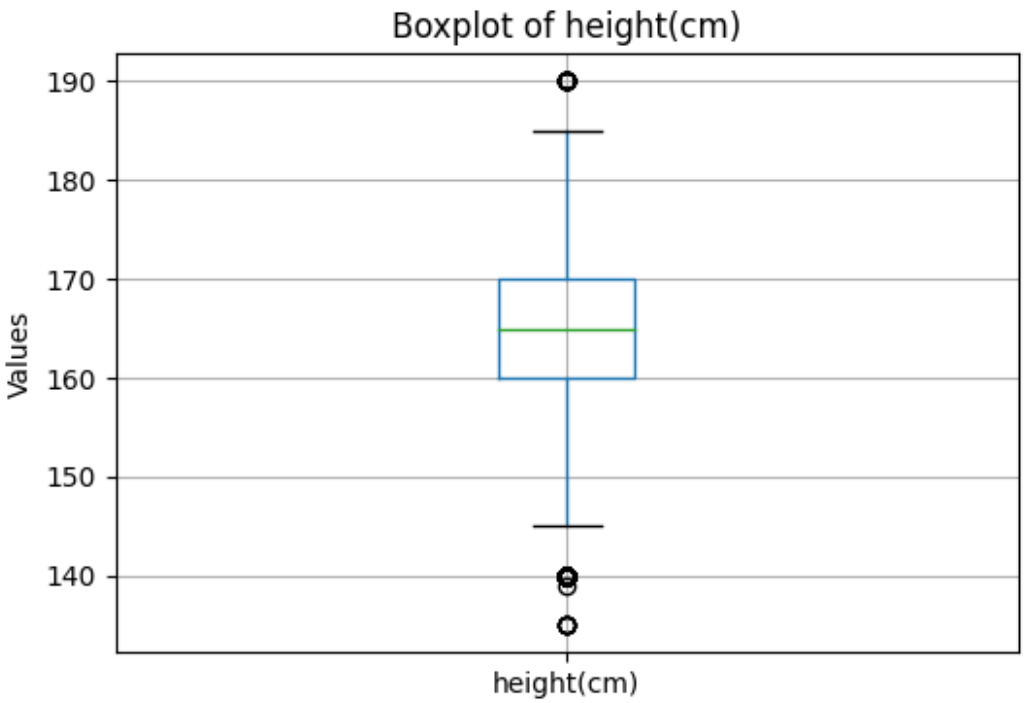


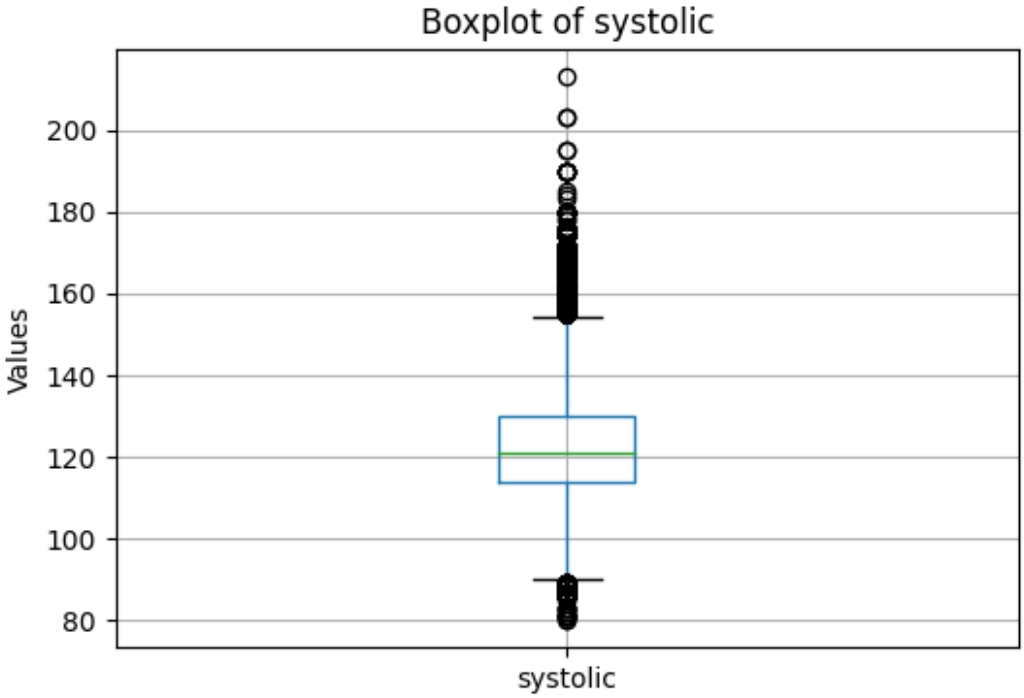

Boxplot of hemoglobin
Values
20
18
16
14
12
10
8
6
hemoglobin

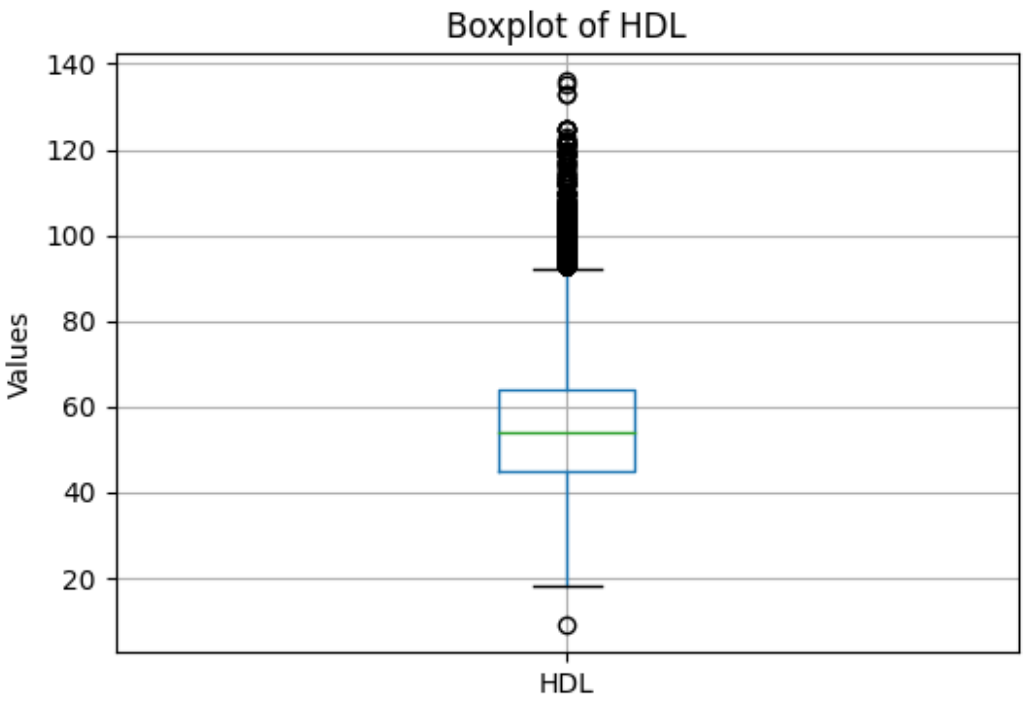

Boxplot of age
Values
80
70
60
50
40
30
20
age

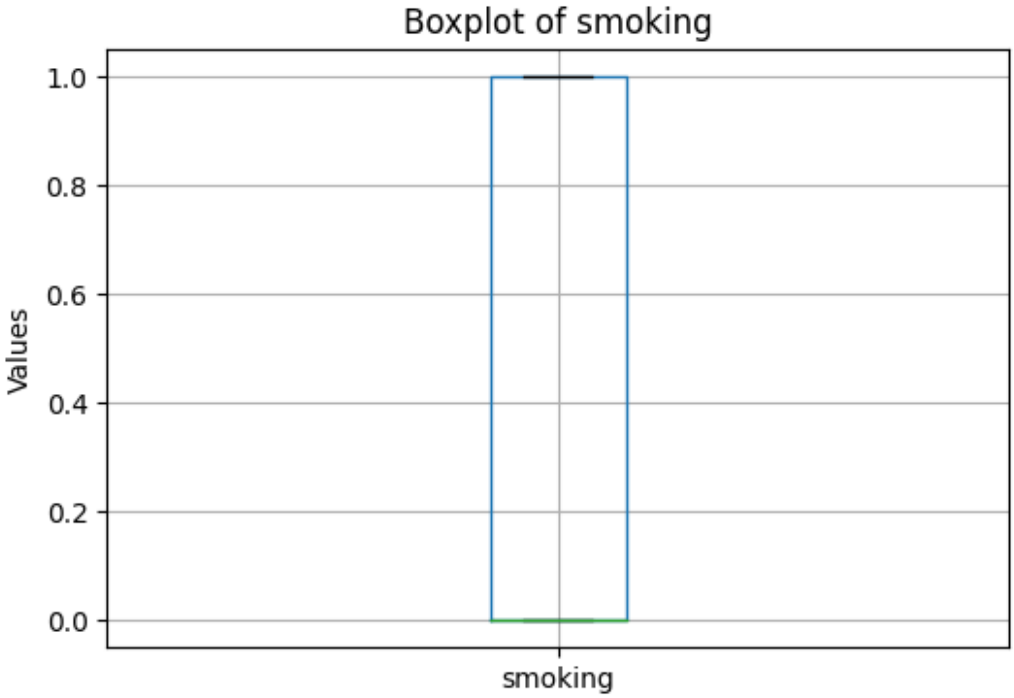

Boxplot of waist(cm)
130
120
110
100
90
80
70
60
50
Values
waist(cm)


Boxplot of hearing(right)
2.0
1.8
1.6
1.4
1.2
1.0
Values
hearing(right)


Boxplot of height(cm)
190
180
170
160
150
140
Values
height(cm)


Boxplot of systolic
200
180
160
140
120
100
80
Values
systolic


Boxplot of HDL
140
120
100
80
60
40
20
Values
HDL


Boxplot of smoking
1.0
0.8
0.6
0.4
0.2
0.0
Values
smoking

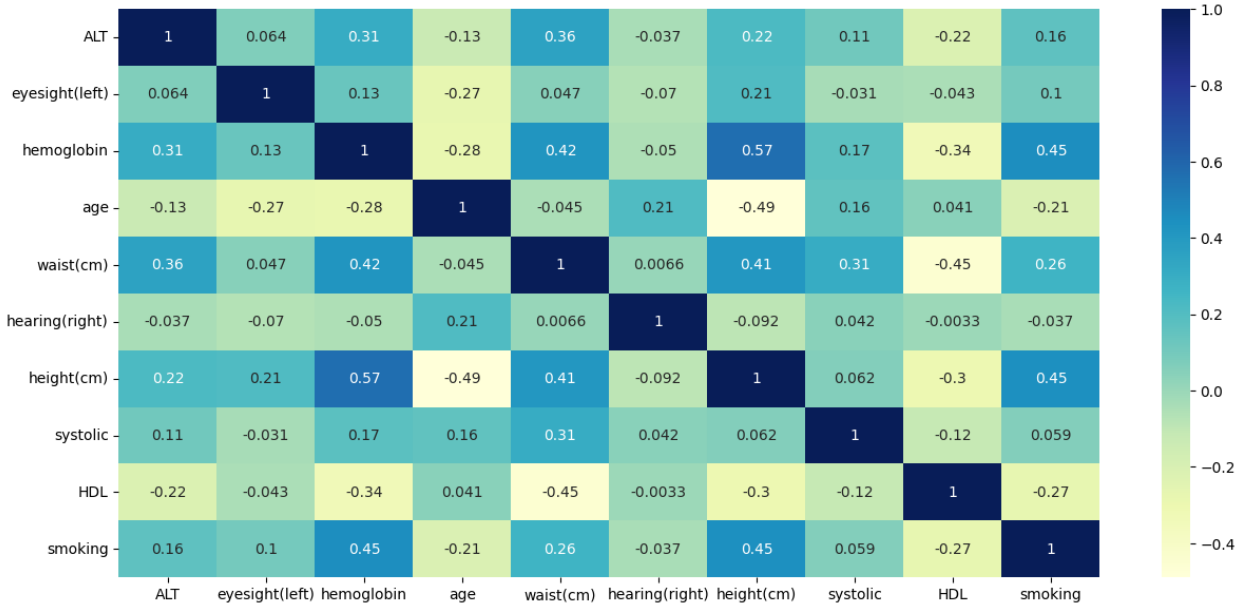
Bivariate Analysis

```
data_train.corr()
corr_matrix=data.corr()
corr_matrix["smoking"].sort_values(ascending=False)
```

```
smoking            1.000000
hemoglobin         0.450679
height(cm)         0.447111
waist(cm)          0.262715
ALT                0.163016
eyesight(left)     0.100420
systolic           0.058642
hearing(right)    -0.036858
age               -0.206033
HDL               -0.271186
Name: smoking, dtype: float64
```

```
plt.figure(figsize=(15,7))
sns.heatmap(corr_matrix, annot=True, cmap="YlGnBu")
```

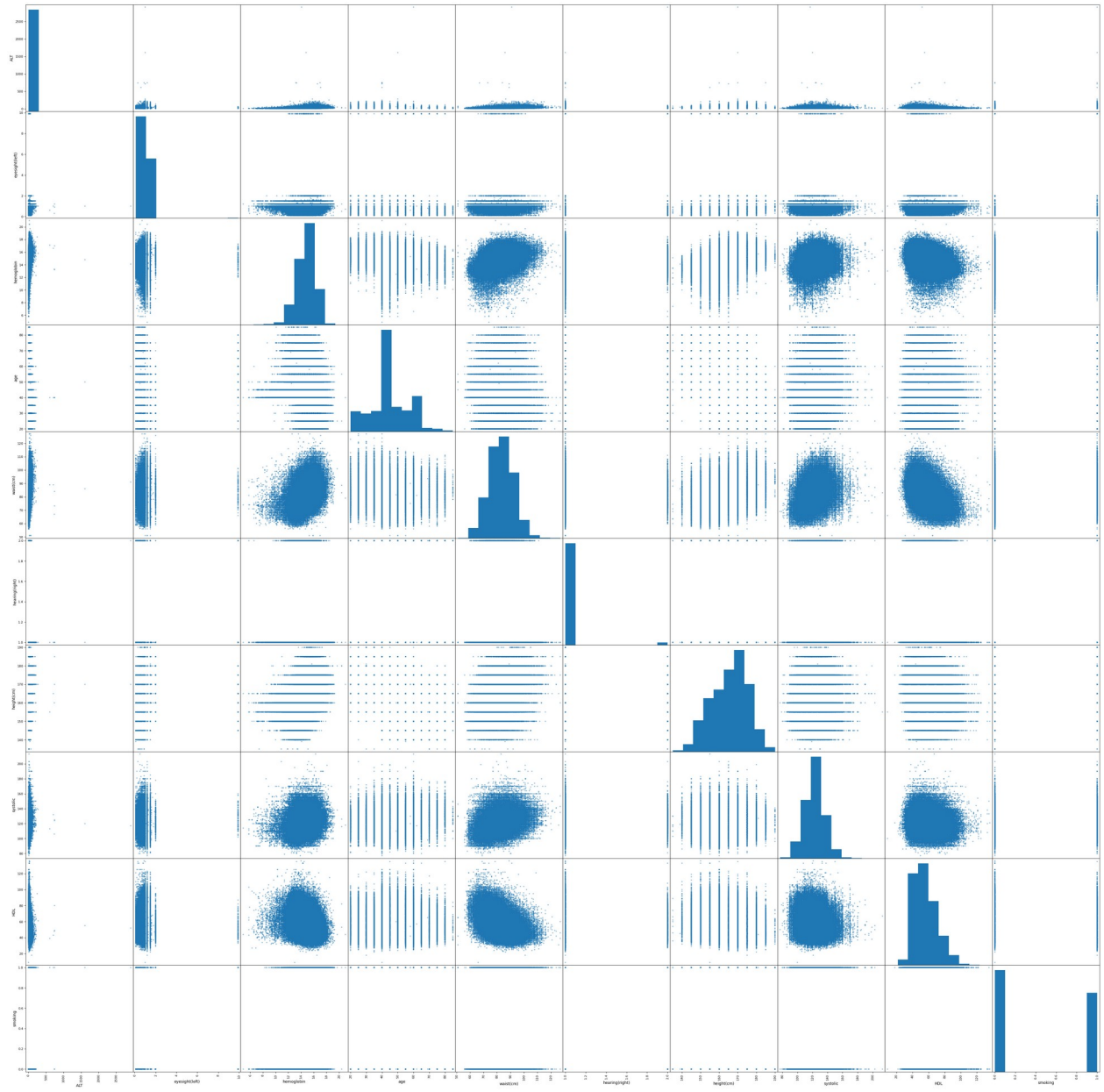
```
<Axes: >
```



Notes:

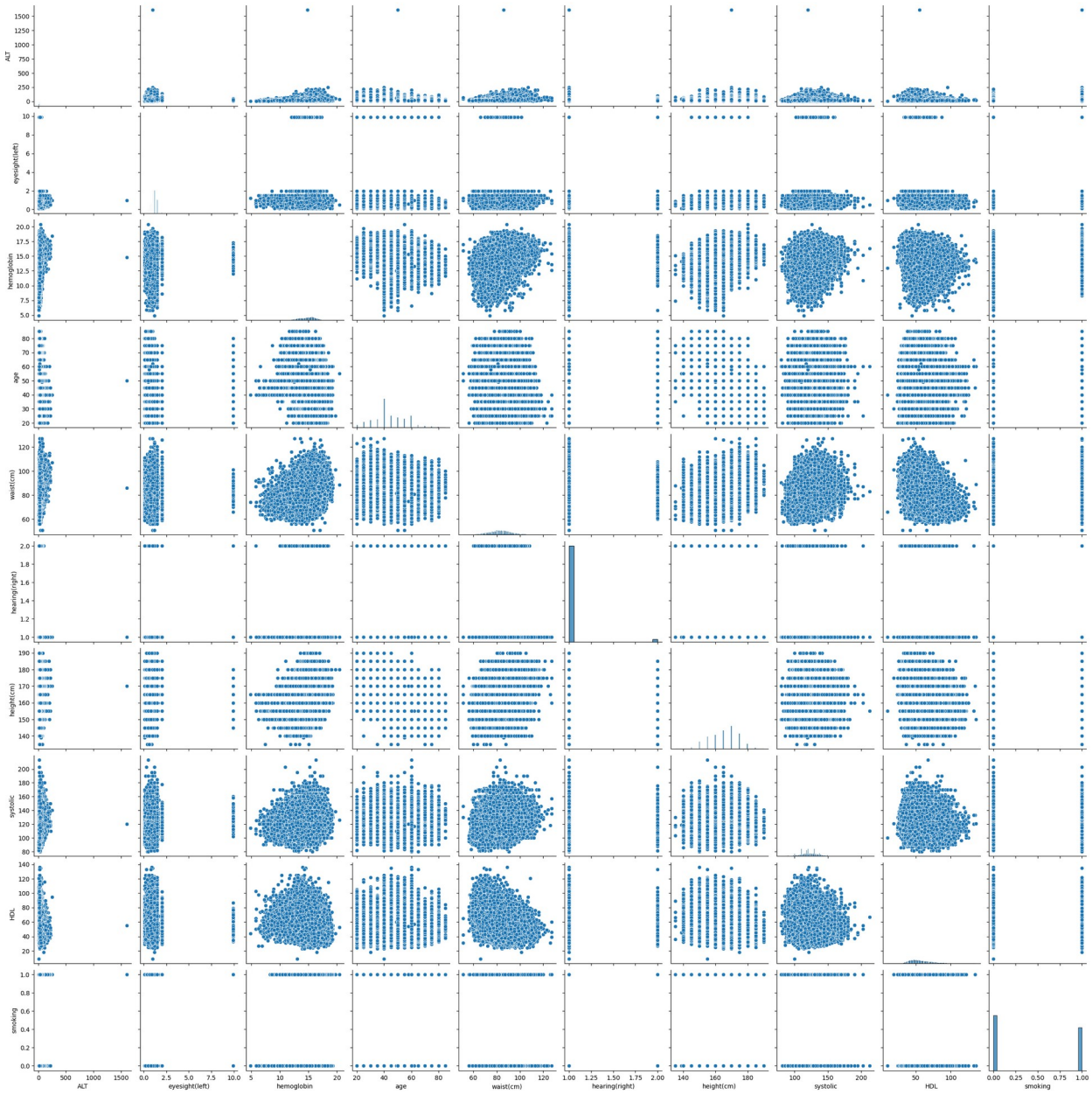
- hemoglibin -> animia
- ALT related to liver functions -wasit -> obese/fat ->bad health -height -> high direct correlation with smoking but inverse correlation with age therefore smokers tend to be older -HDL(High density fat) benefical -> good health inverse correlation with smoking

```
scatter_matrix(data, figsize=(50, 50))
plt.show()
```

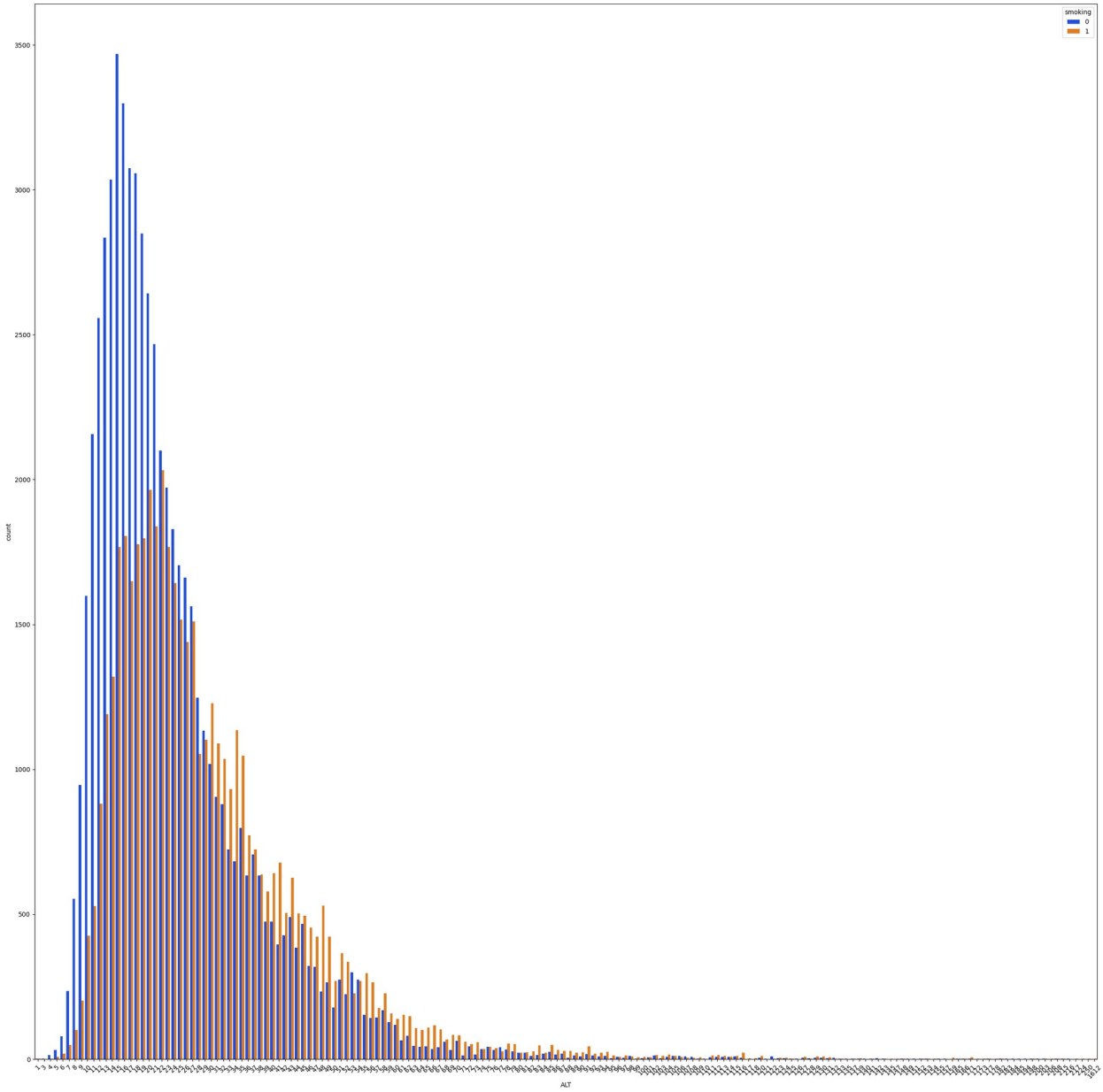


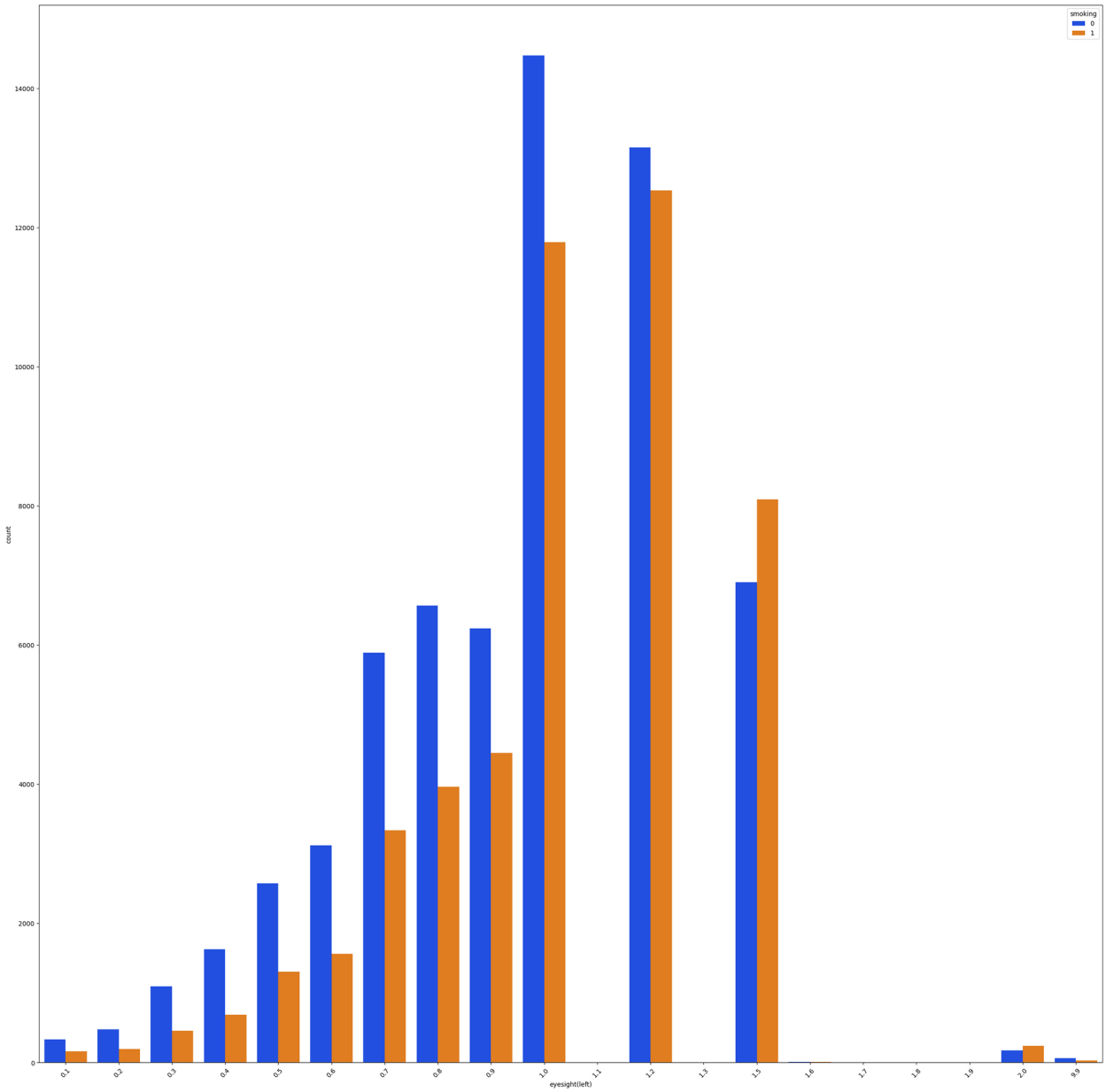
```
sns.pairplot(data_train)
```

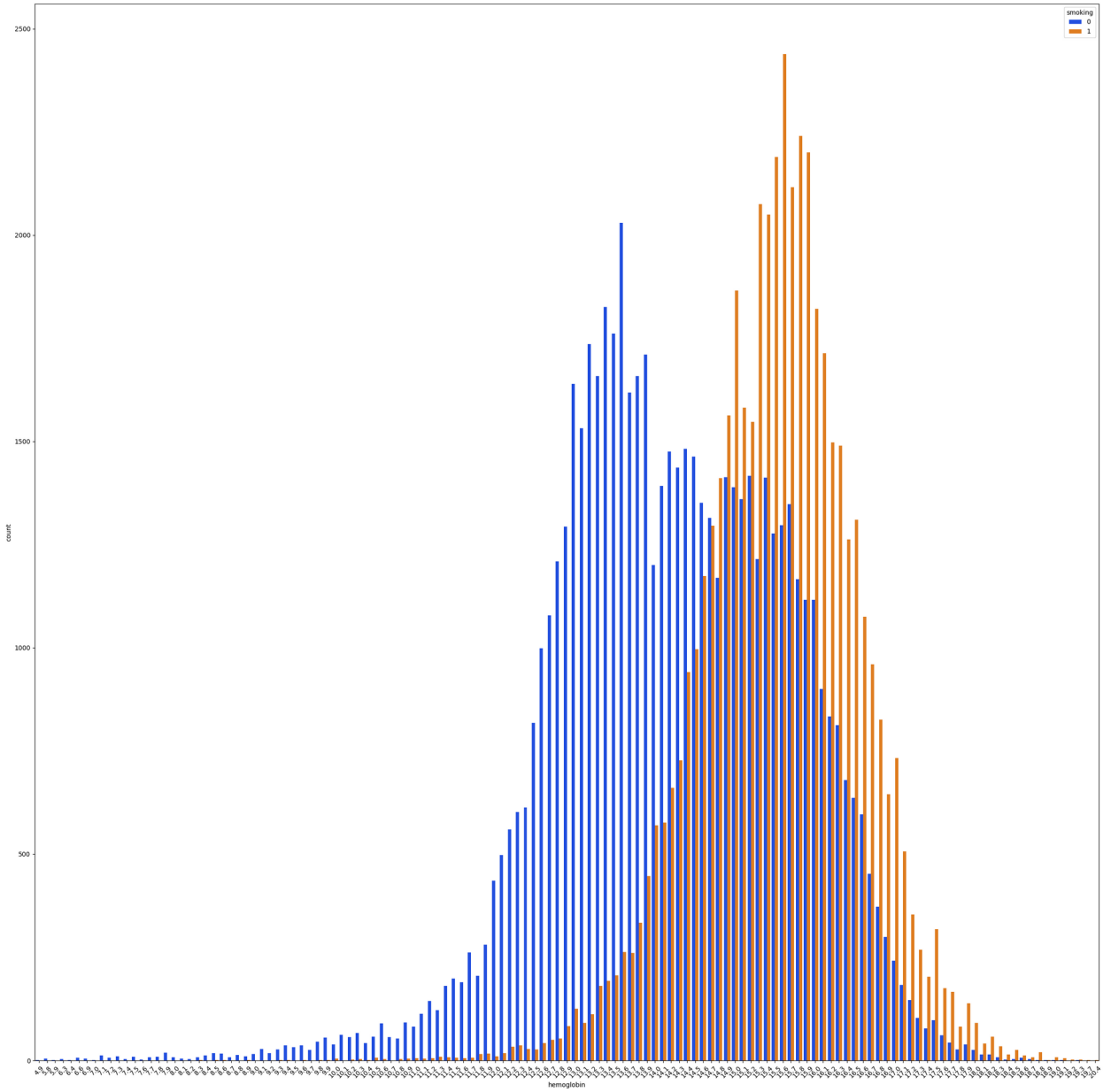
```
<seaborn.axisgrid.PairGrid at 0x7f3c3f9d4f70>
```

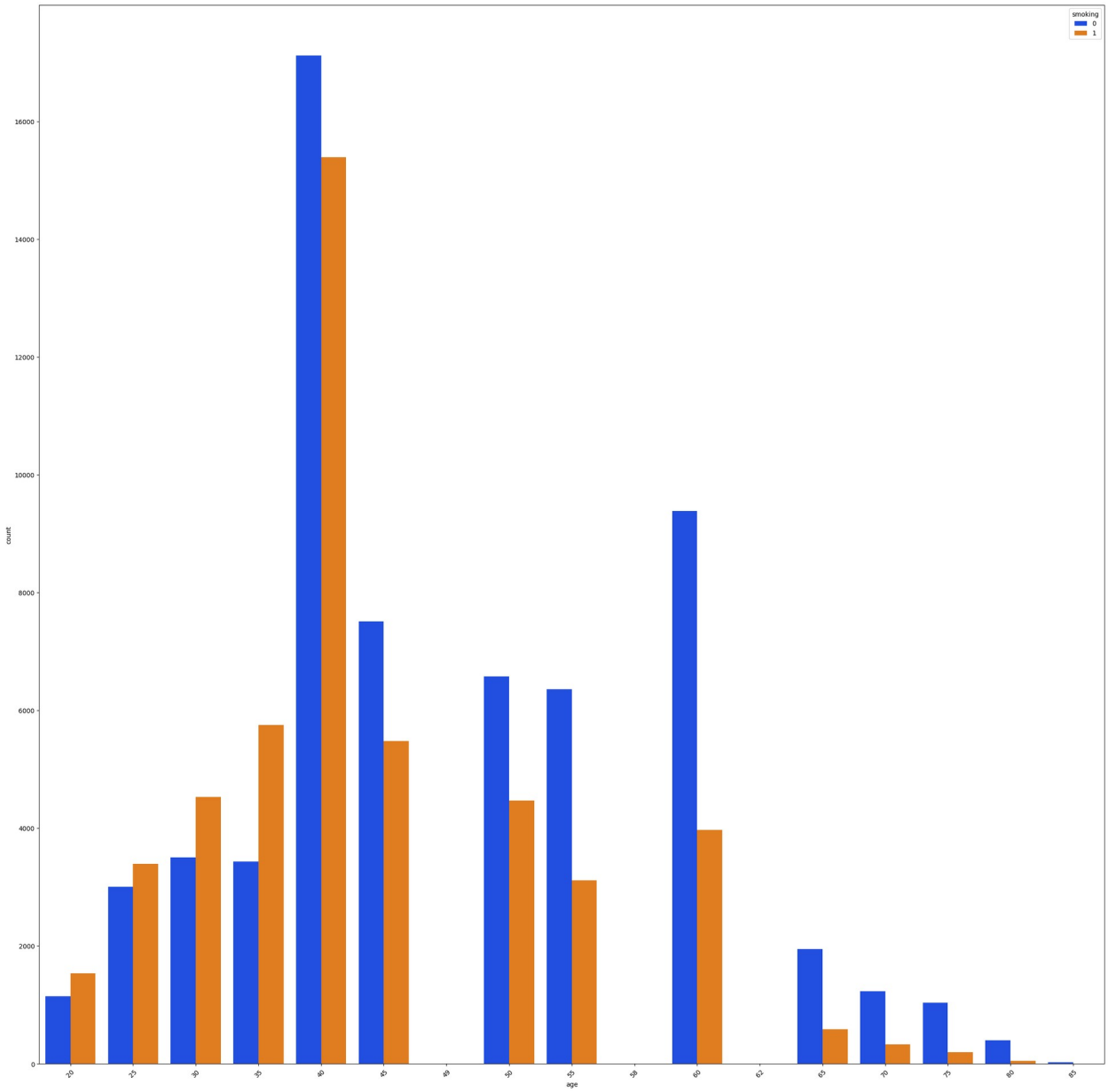


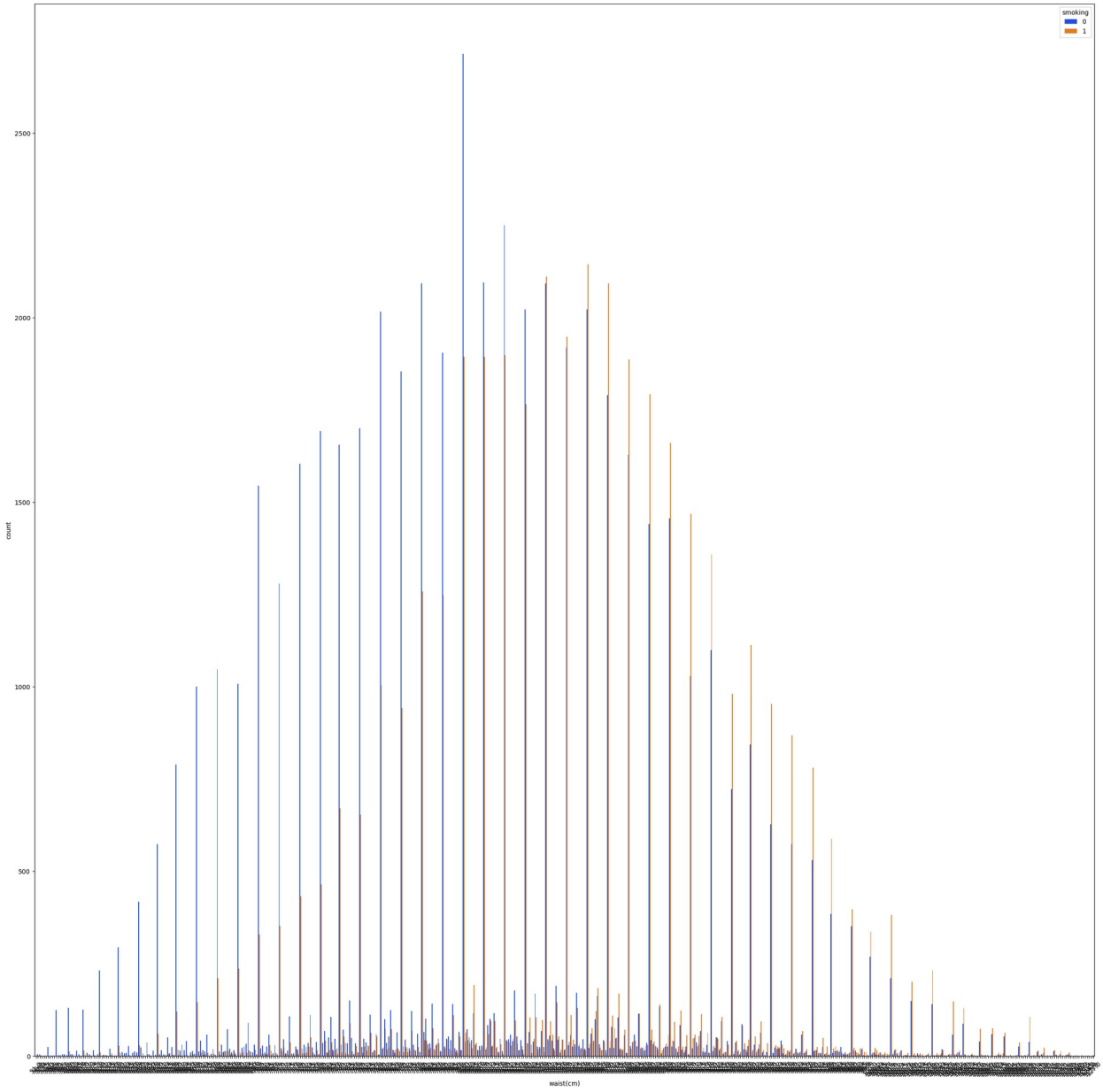

```
features =['ALT','eyesight(left)','hemoglobin'
      ,'age','waist(cm)','hearing(right)','height(cm)','systolic','HDL'
]

for feature in data_train.columns[:-1]:
  plt.figure(figsize = (30, 30))
  ax = sns.countplot(data=data_train, x=feature, hue='smoking',
palette='bright')
  #plt.tight_layout()  # Adjust layout to prevent overlapping
  plt.xticks(rotation=45)
  plt.show()
```

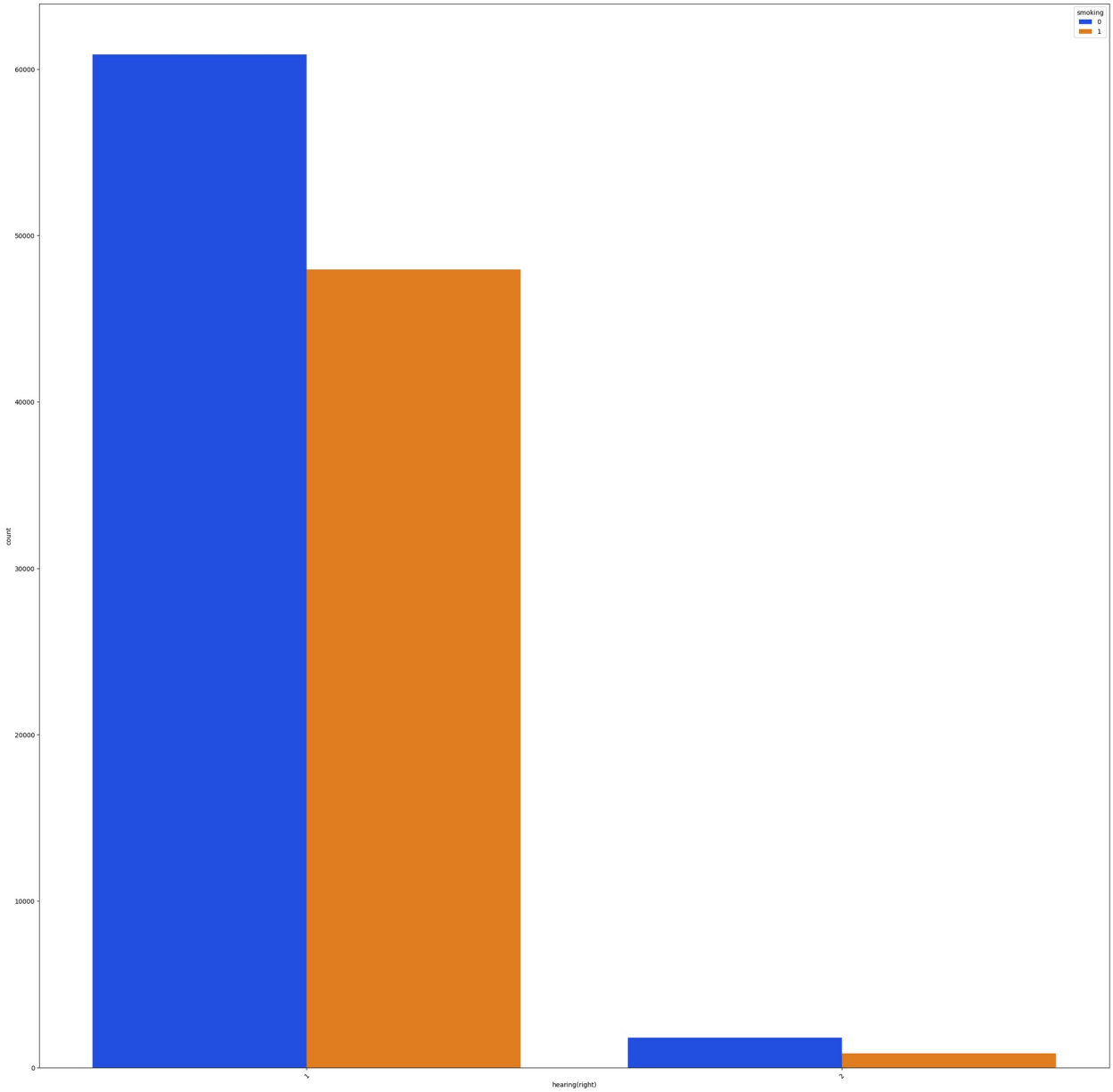

smoking
0
1
count
ALT
0
500
1000
1500
2000
2500
3000
3500

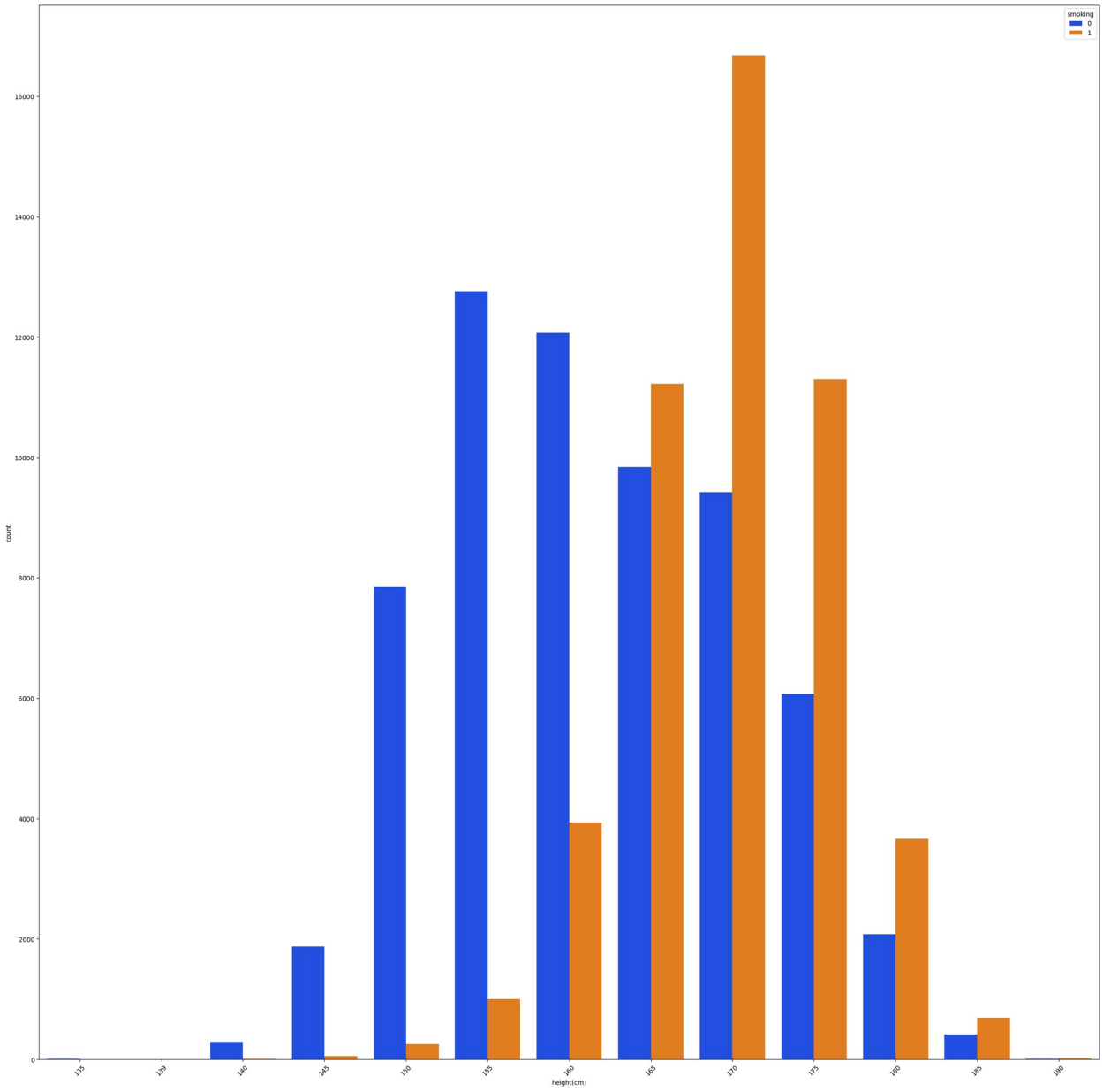

smoking
0
1
14000
12000
10000
8000
6000
4000
2000
0
count
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
1.2
1.3
1.5
1.6
1.7
1.8
1.9
2.0
9.9
eyesight(left)

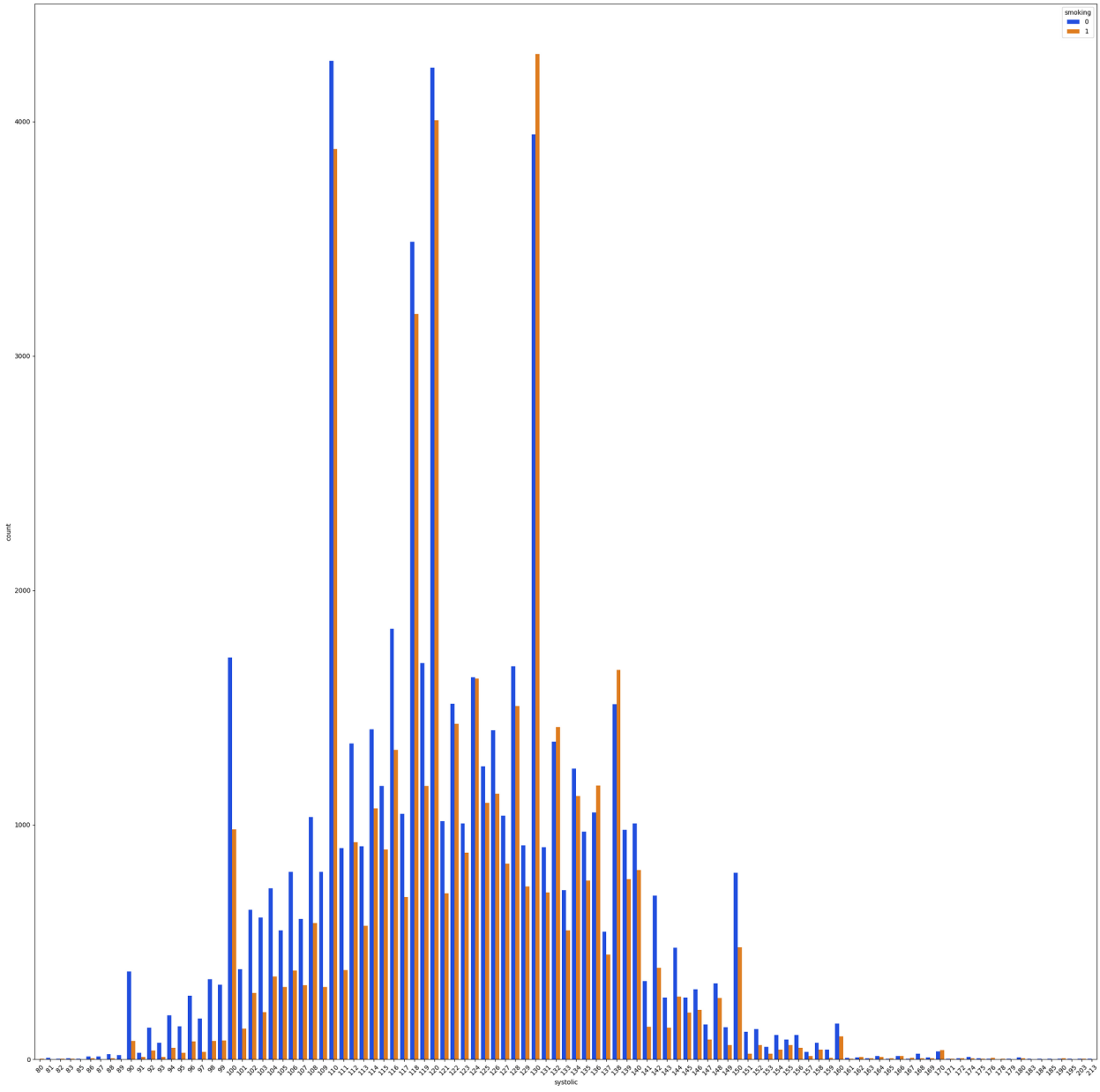

smoking
0
1
count
2500
2000
1500
1000
500
0
hemoglobin

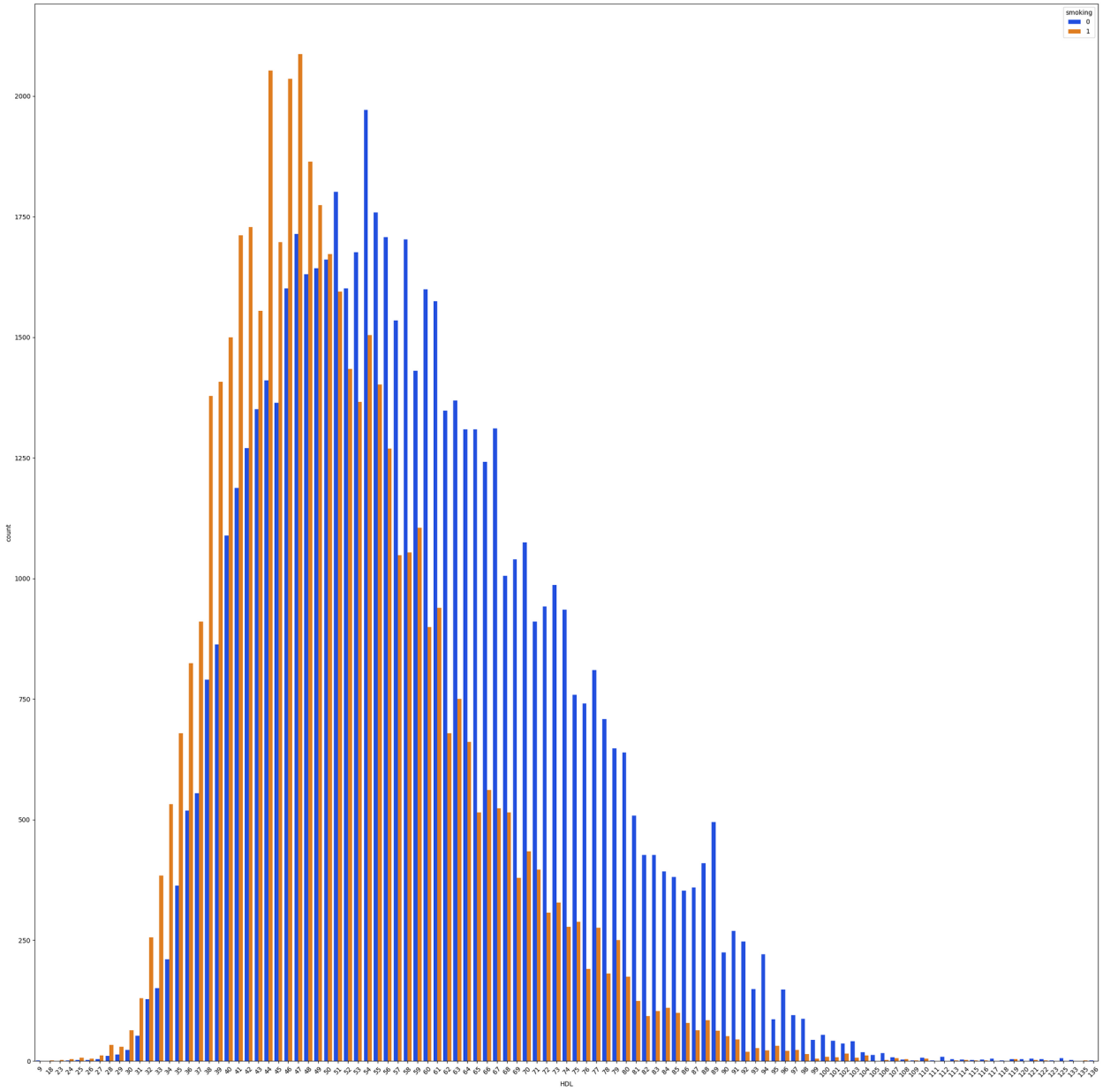

smoking
0
1
count
0
2000
4000
6000
8000
10000
12000
14000
16000
20
25
30
35
40
45
49
50
55
59
60
61
65
70
75
80
85
age


smoking
0
1
2500
2000
1500
1000
500
0
count
waist(cm)


smoking
0
1
60000
50000
40000
30000
20000
10000
0
count
1
2
hearing(right)


smoking
0
1
16000
14000
12000
10000
8000
6000
4000
2000
0
count
135
139
140
145
150
155
160
165
170
175
180
185
190
height(cm)

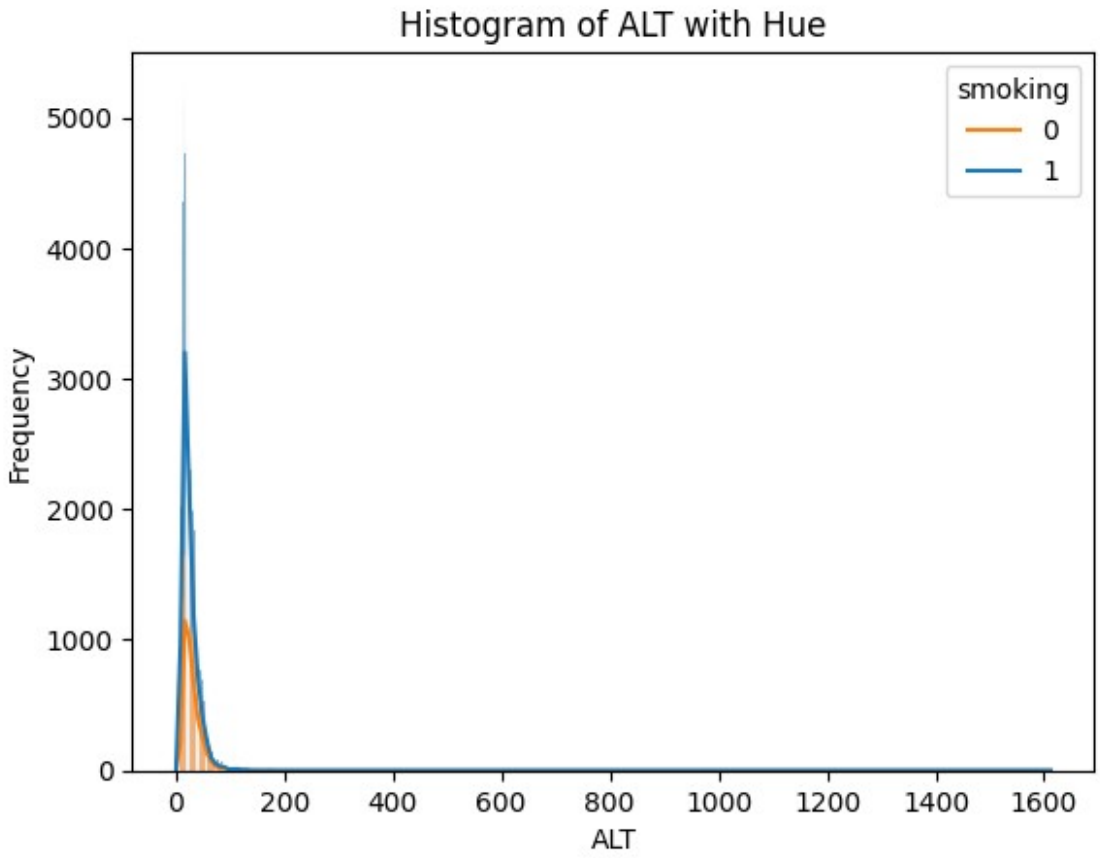

smoking
0
1
count
systolic
0
1000
2000
3000
4000

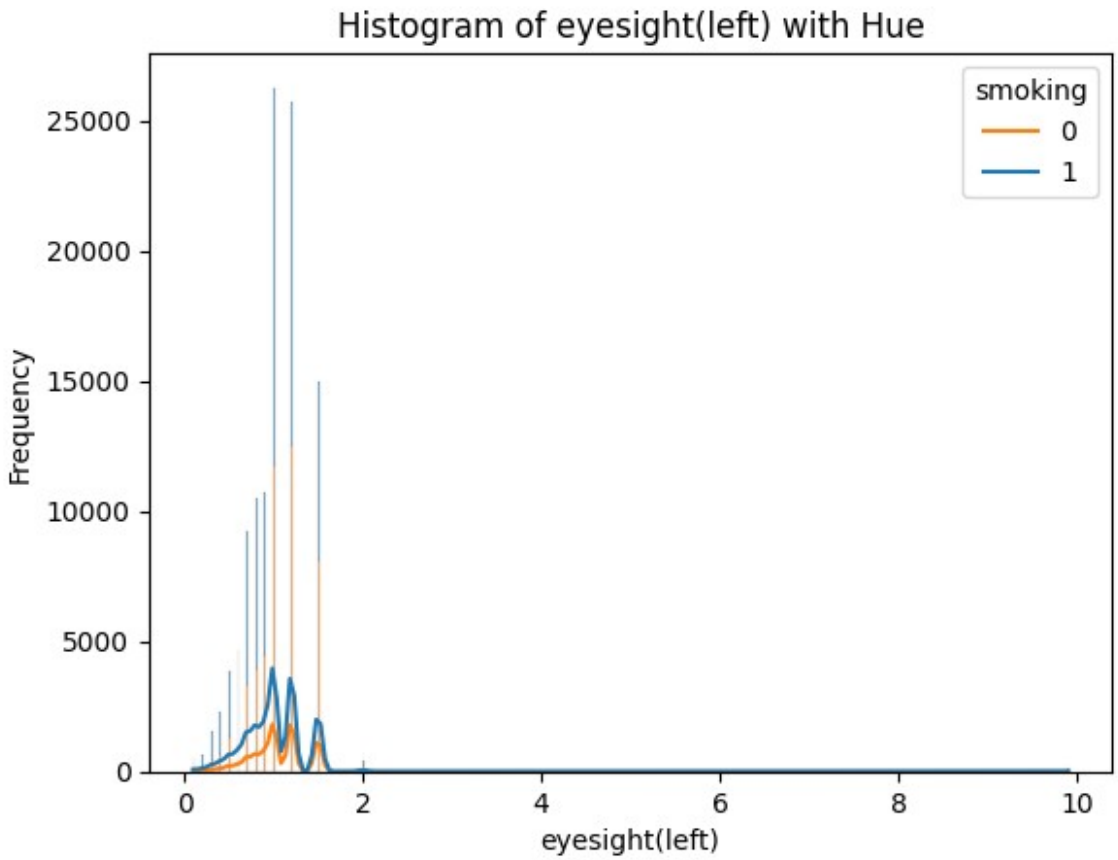


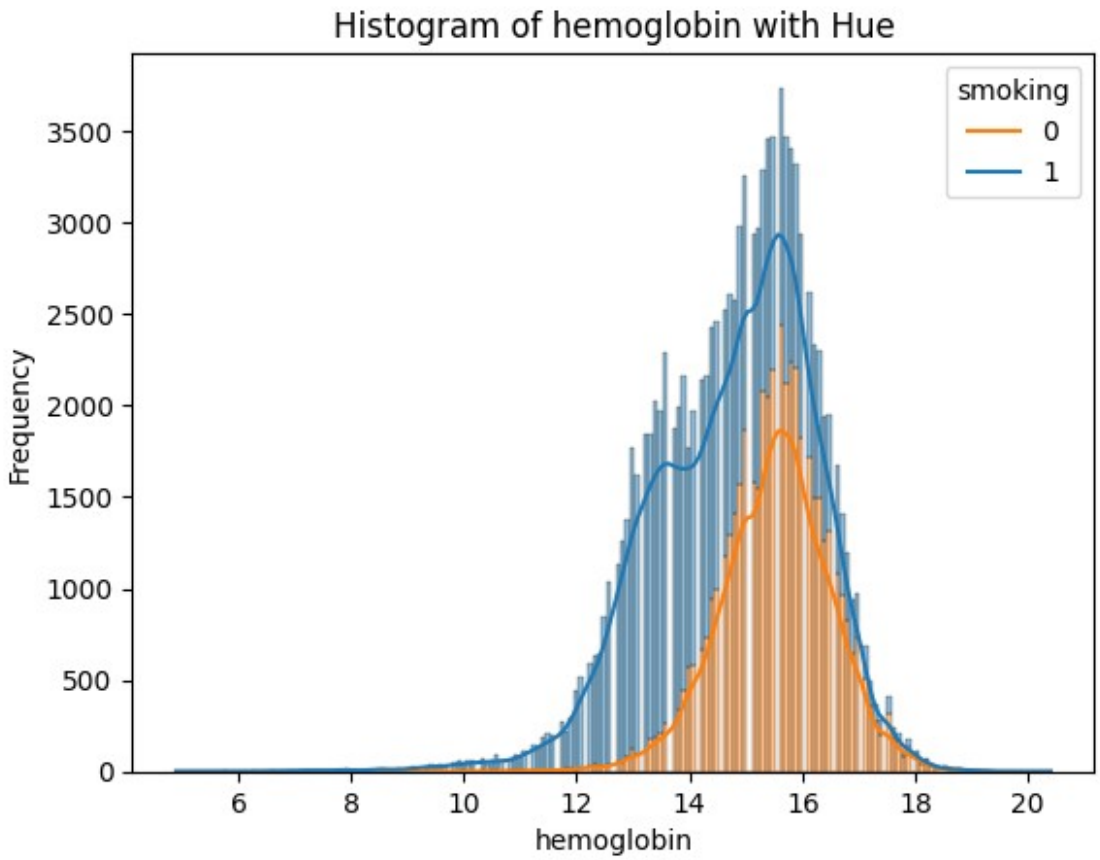
- Based on the height histogram above, we can conclude that the percentage of smokers compared to non-smokers is greater for people with a height above 170 cm. It can be seen that the majority of smokers (orange) have a height above 170cm. Because, in our opinion, people who are above 170cm tall are mostly adults. Therefore, we agree with the existing dataset because most smokers are adults. -From HDL diagram it can be seen that non smokers tend to have higher HDL which is healthy.
- According to healthline journal smoking is much more likely to lead to an increased hemoglobin count, which i shown in hemoglobin histogram

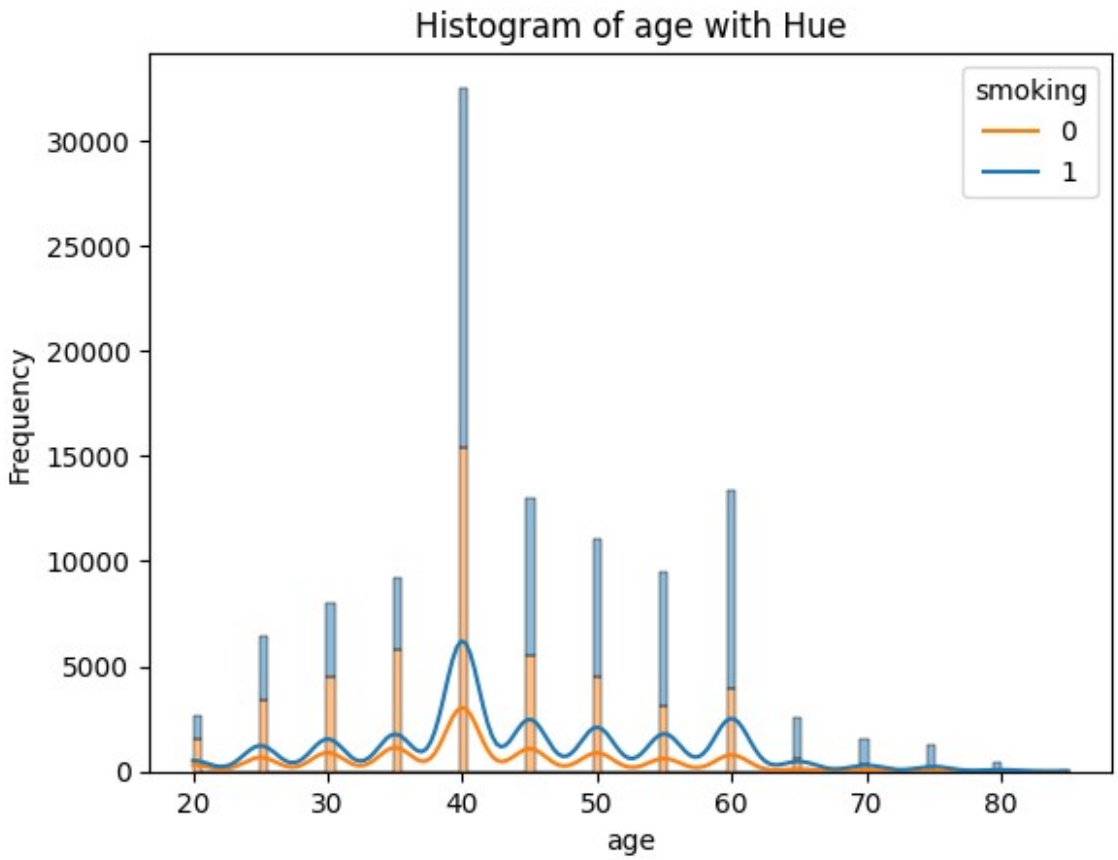
```
category_labels = {1: '1',0: '0'}

# Plotting histograms for all columns with hue and assigned labels in
legend
```

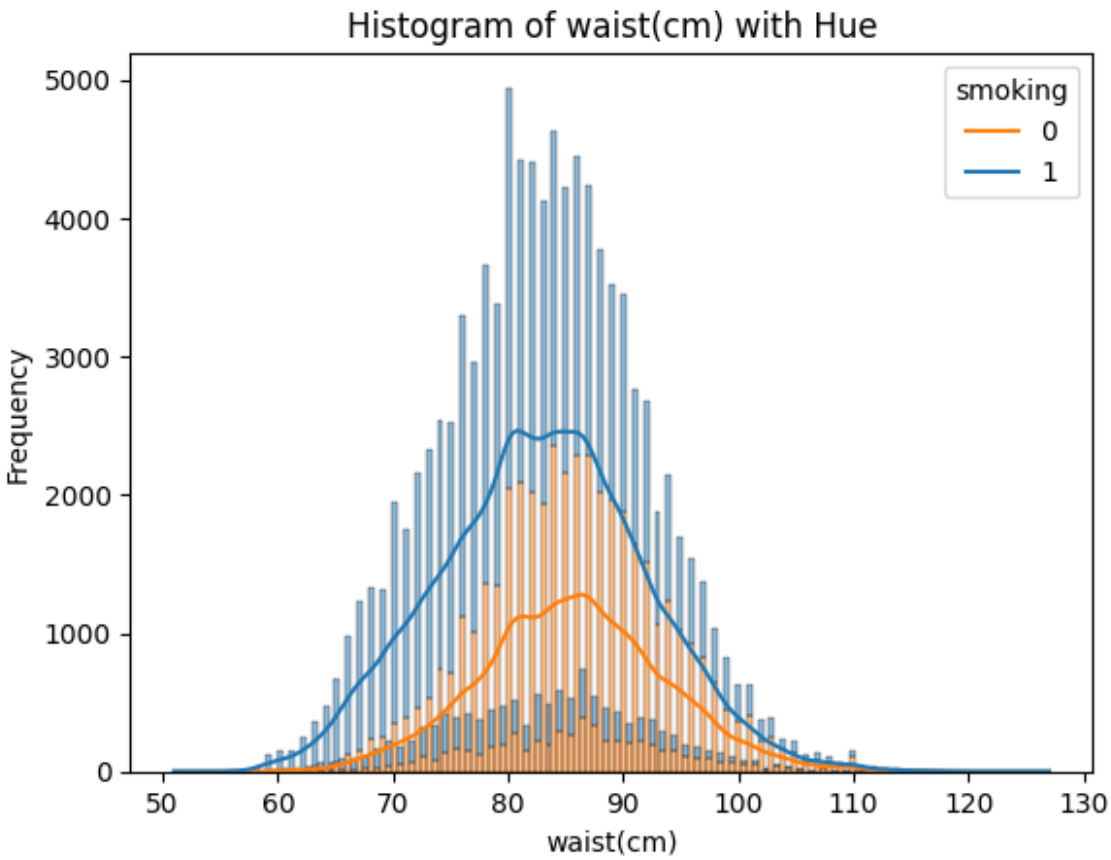
```
for column in data_train.columns[:-1]:  # Exclude the last column as it's the 'Category' column
    sns.histplot(data=data_train, x=column, hue='smoking', kde=True, multiple='stack', palette='tab10')
    plt.xlabel(column)
    plt.ylabel('Frequency')
    plt.title(f'Histogram of {column} with Hue')
    plt.legend(title='smoking', labels=[category_labels[0], category_labels[1]])
    plt.show()
```

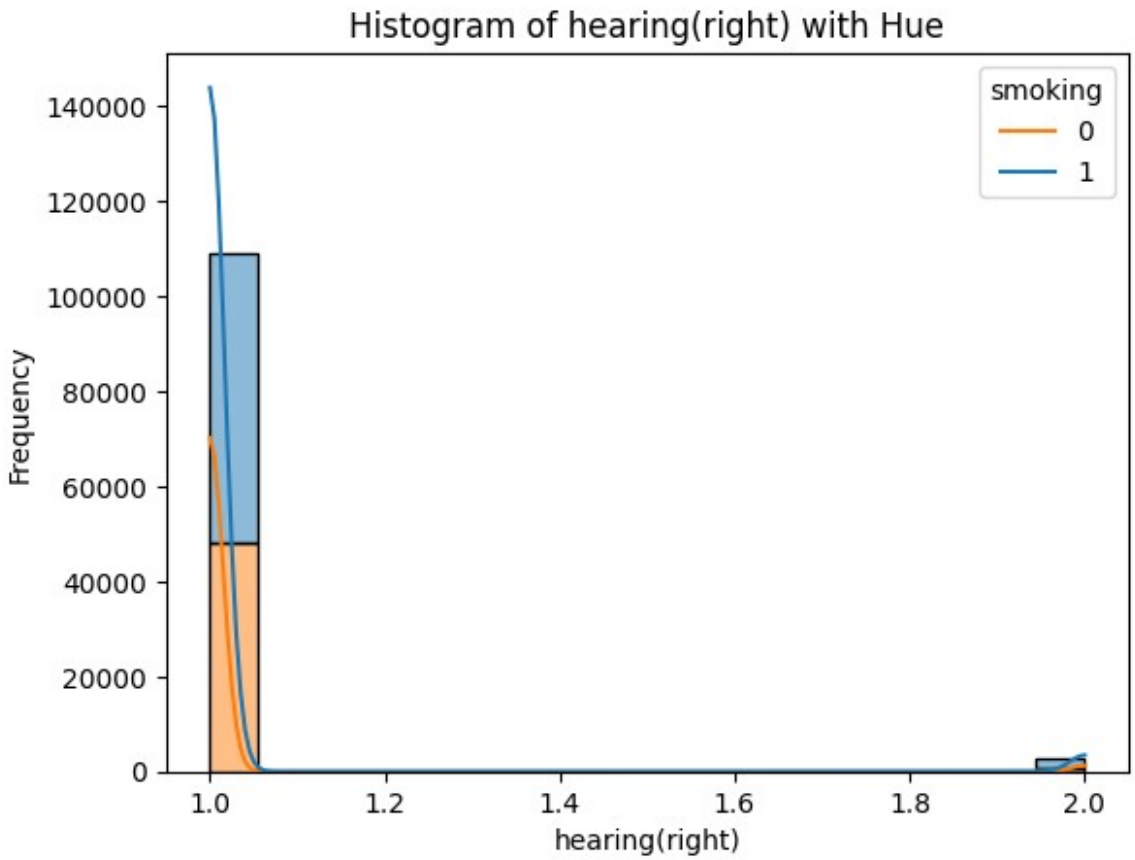


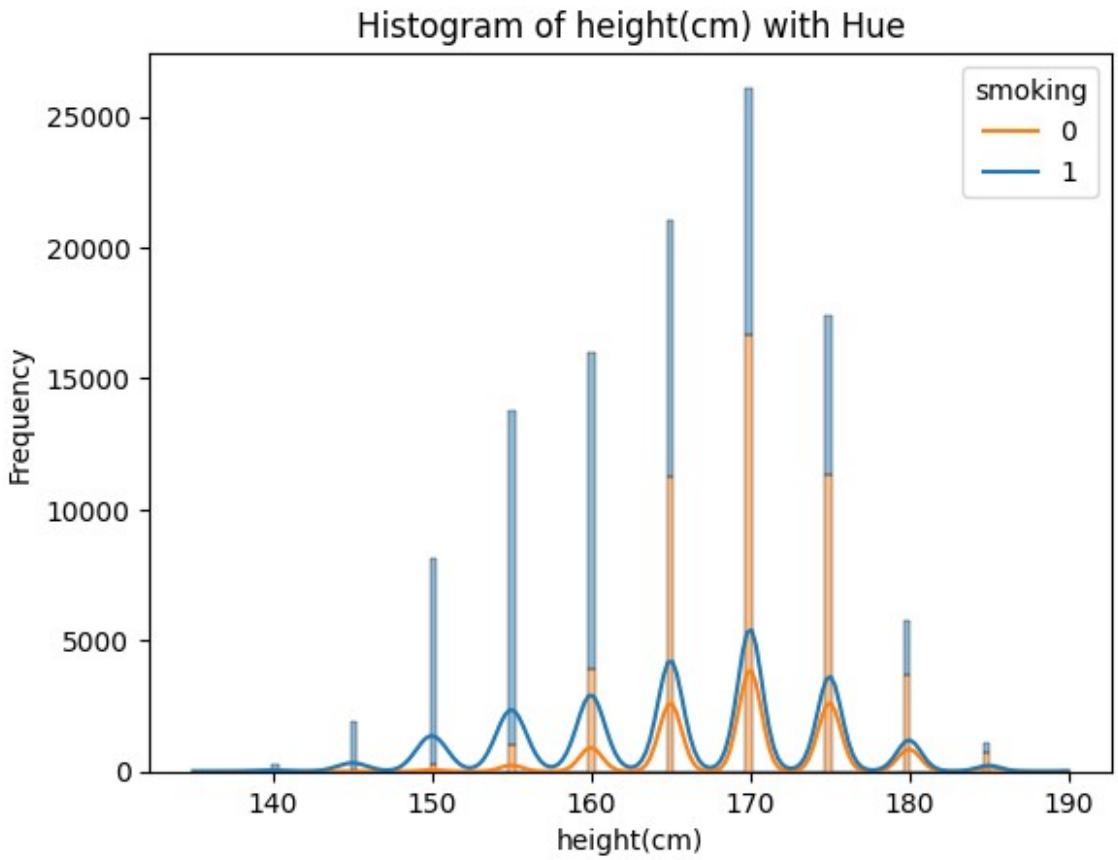

Histogram of eyesight(left) with Hue
smoking
0
1
Frequency
25000
20000
15000
10000
5000
0
0
2
4
6
8
10
eyesight(left)

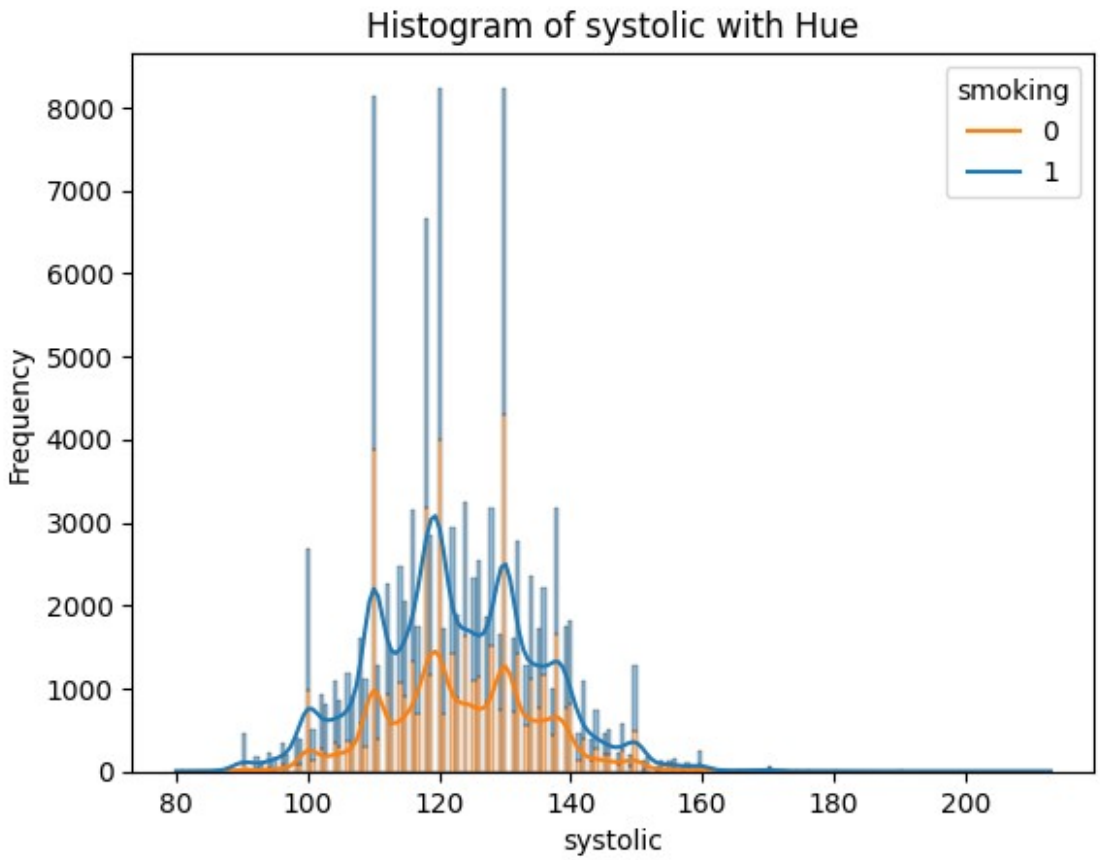

Histogram of hemoglobin with Hue
smoking
0
1
Frequency
3500
3000
2500
2000
1500
1000
500
0
6
8
10
12
14
16
18
20
hemoglobin

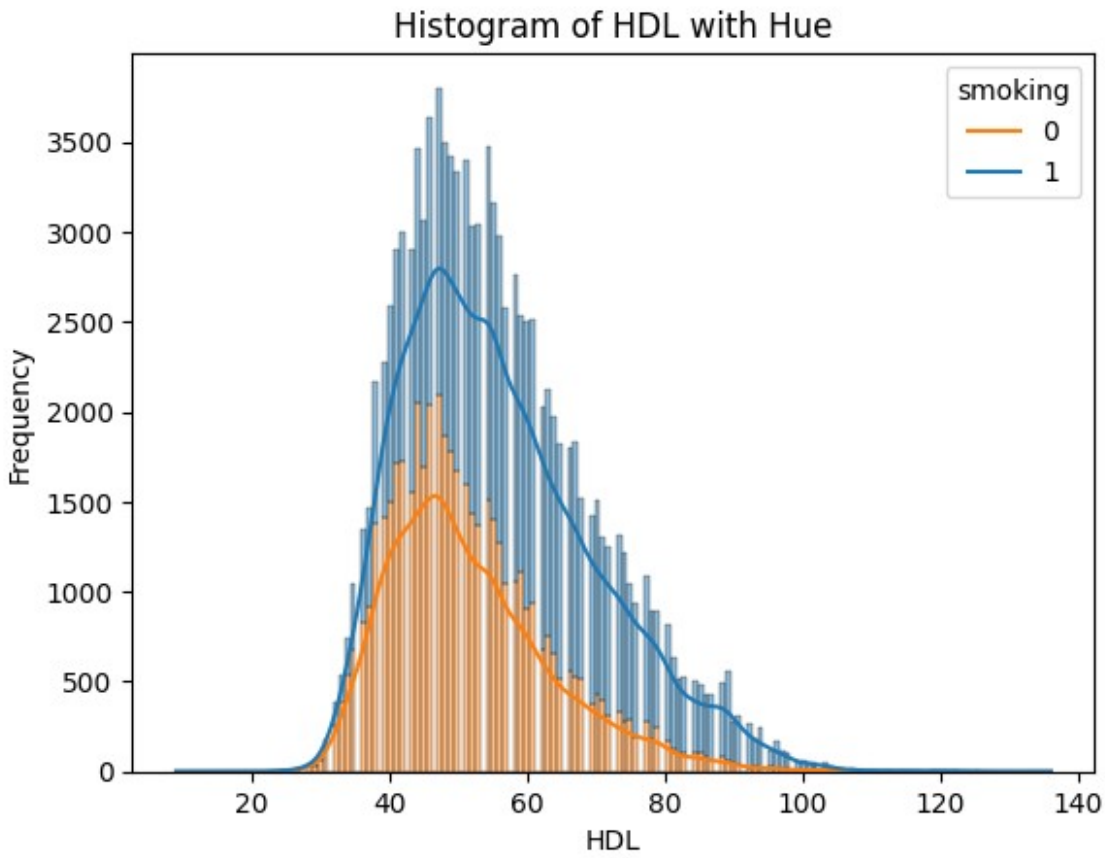

Histogram of age with Hue
smoking
0
1
Frequency
30000
25000
20000
15000
10000
5000
0
20
30
40
50
60
70
80
age


Histogram of waist(cm) with Hue
smoking
0
1
Frequency
5000
4000
3000
2000
1000
0
50
60
70
80
90
100
110
120
130
waist(cm)

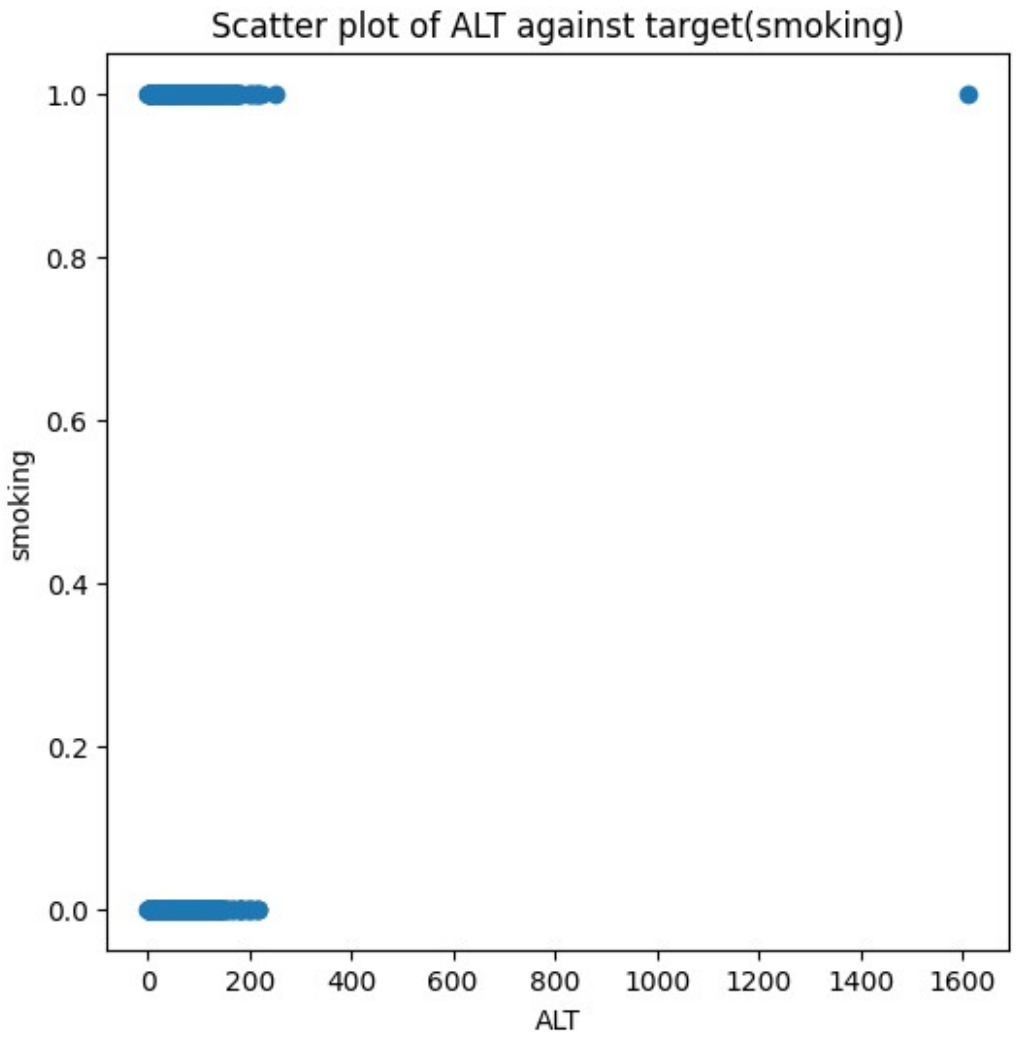

Histogram of hearing(right) with Hue
smoking
0
1
Frequency
140000
120000
100000
80000
60000
40000
20000
0
1.0
1.2
1.4
1.6
1.8
2.0
hearing(right)

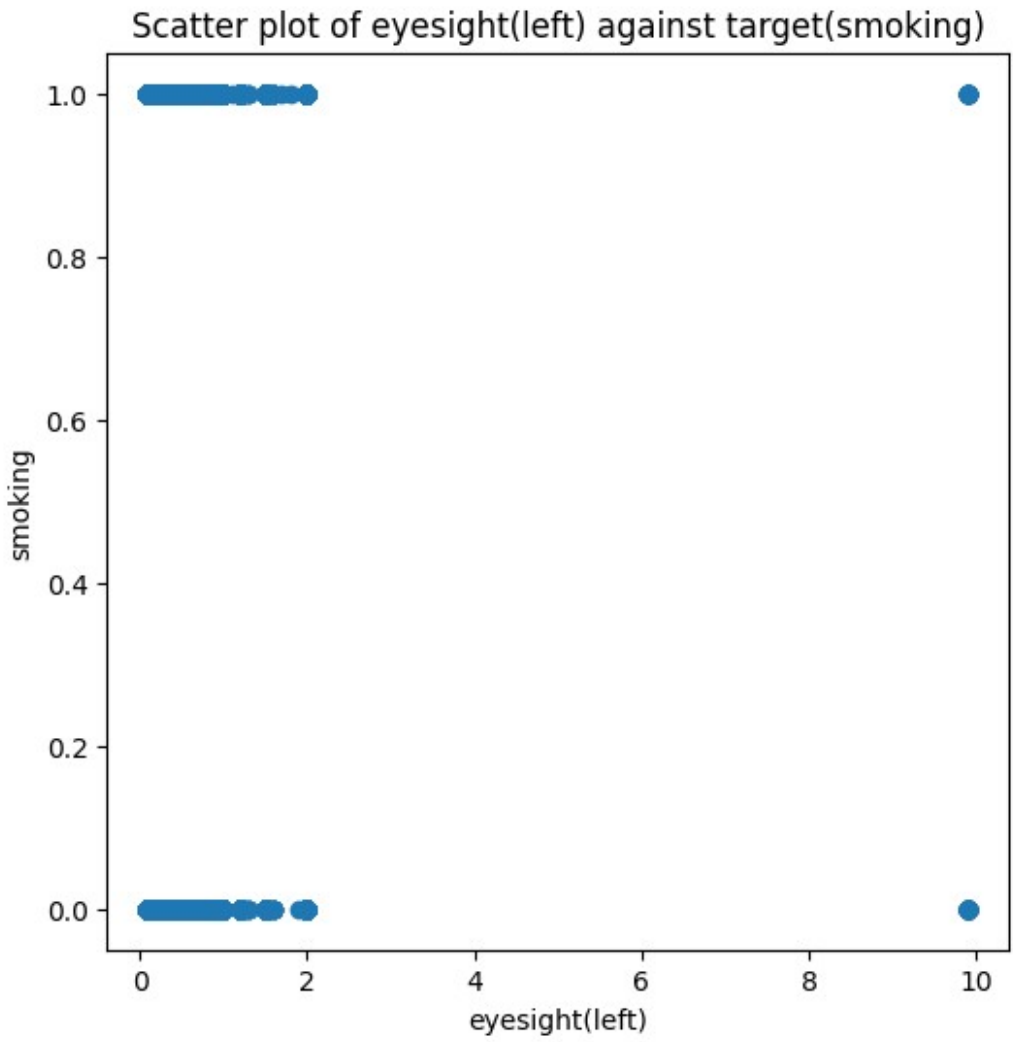

Histogram of height(cm) with Hue
smoking
0
1
Frequency
25000
20000
15000
10000
5000
0
140
150
160
170
180
190
height(cm)

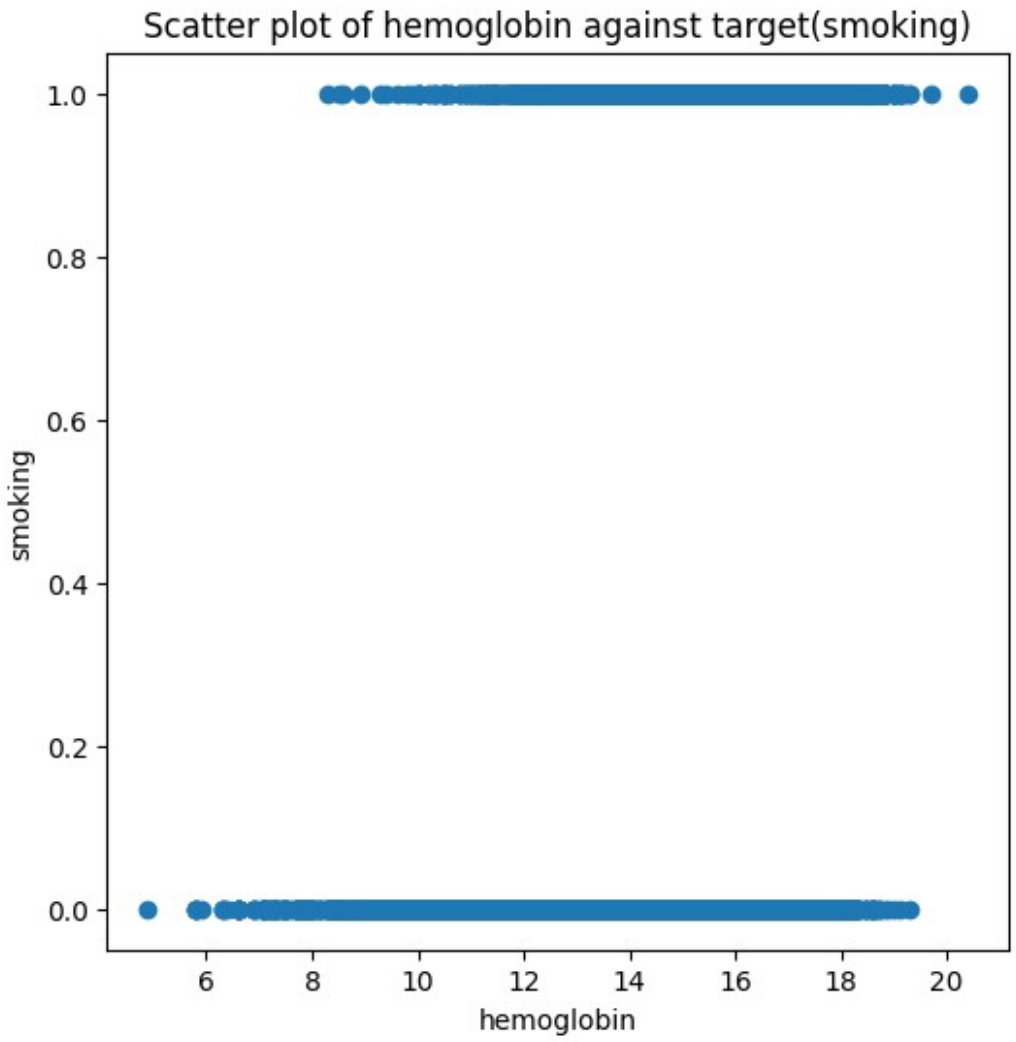

Histogram of systolic with Hue
smoking
0
1
Frequency
8000
7000
6000
5000
4000
3000
2000
1000
0
80
100
120
140
160
180
200
systolic

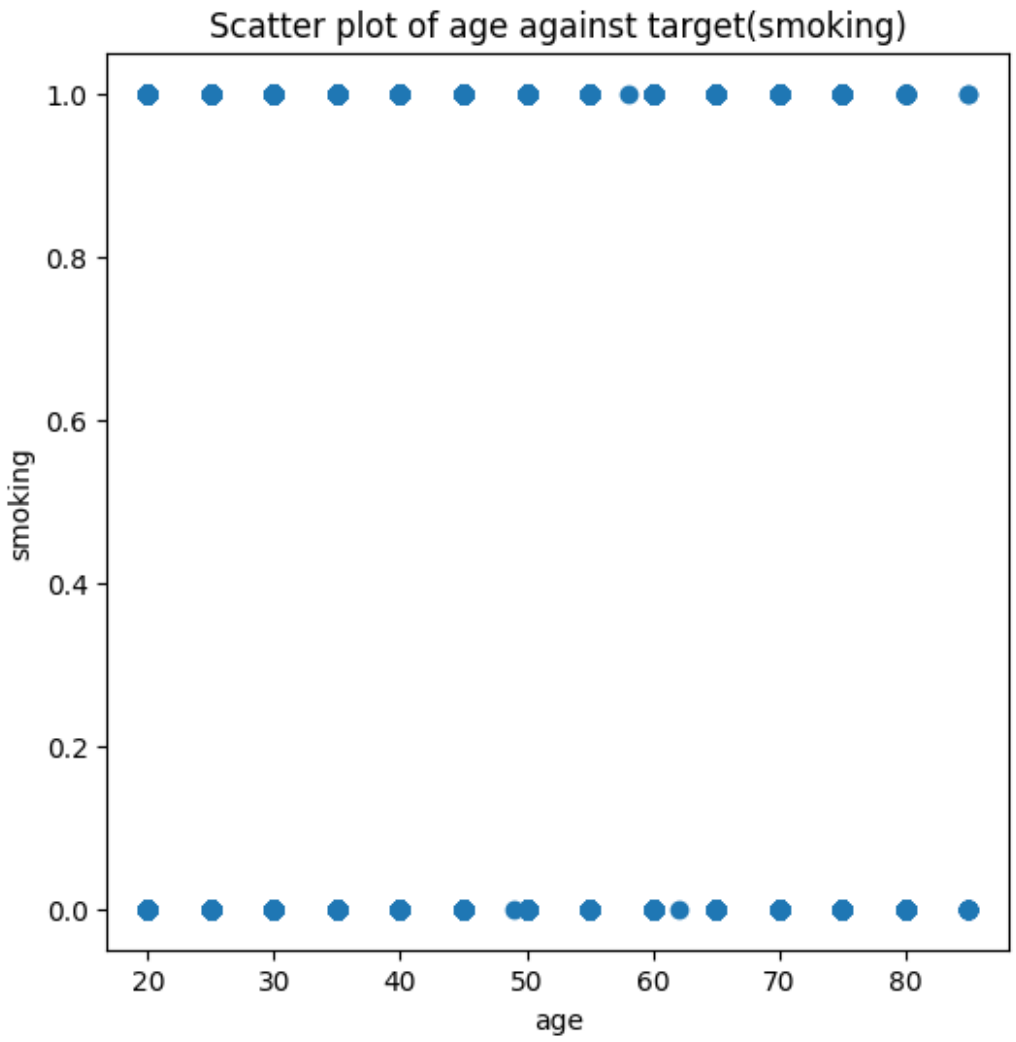


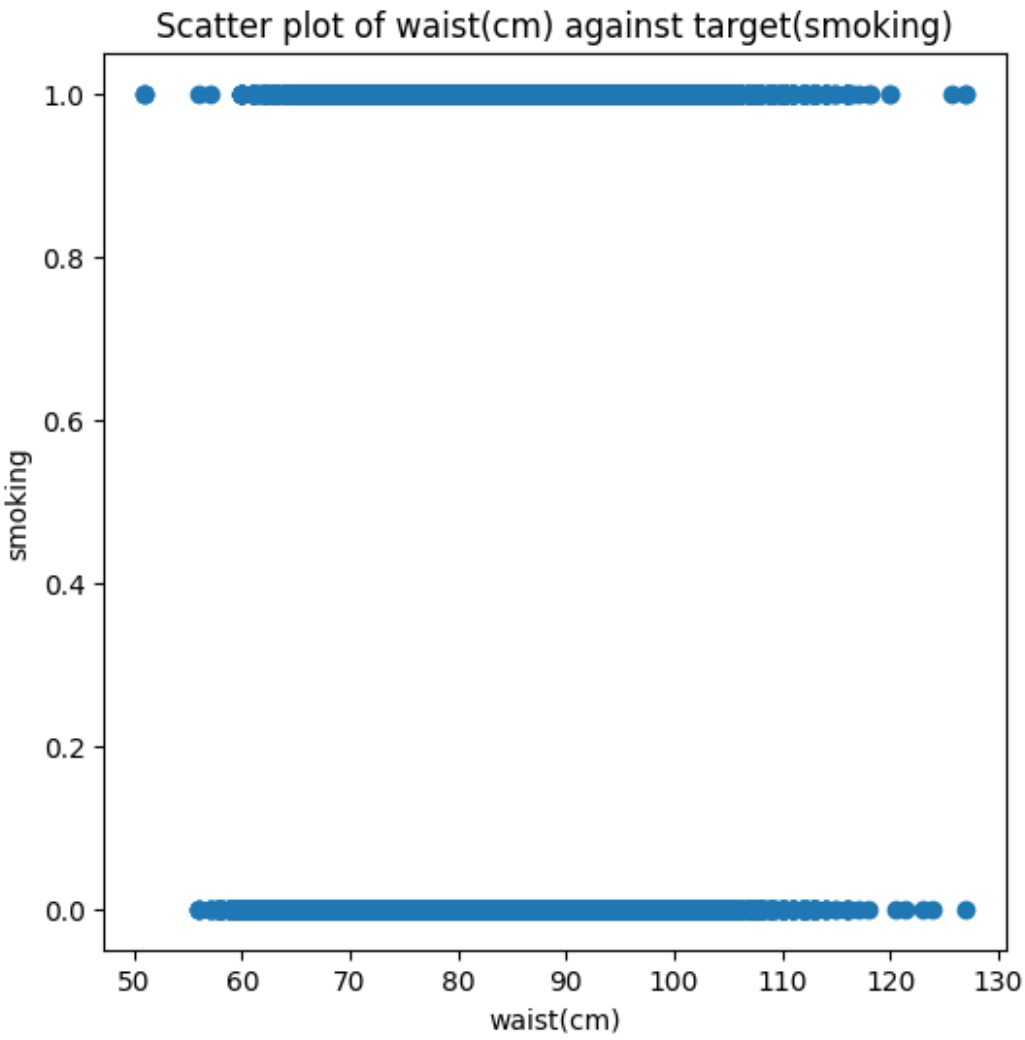

```
for feature in features:
   plt.figure(figsize=(6, 6))
   plt.scatter(data_train[feature], data_train['smoking'])
   plt.xlabel(feature)
   plt.ylabel('smoking')
   plt.title('Scatter plot of {} against
target(smoking)'.format(feature))
   plt.show()
```

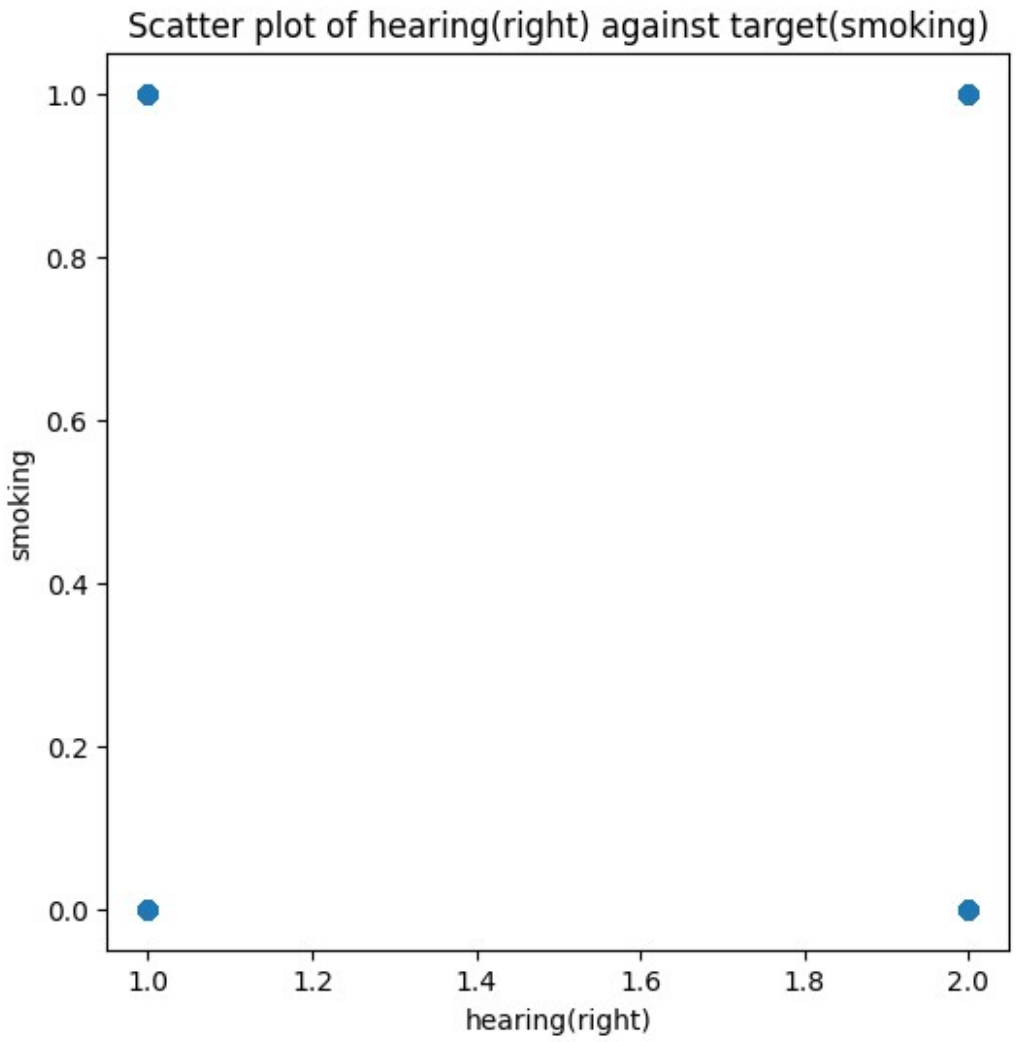

Scatter plot of ALT against target(smoking)
smoking
ALT
1.0
0.8
0.6
0.4
0.2
0.0
0
200
400
600
800
1000
1200
1400
1600

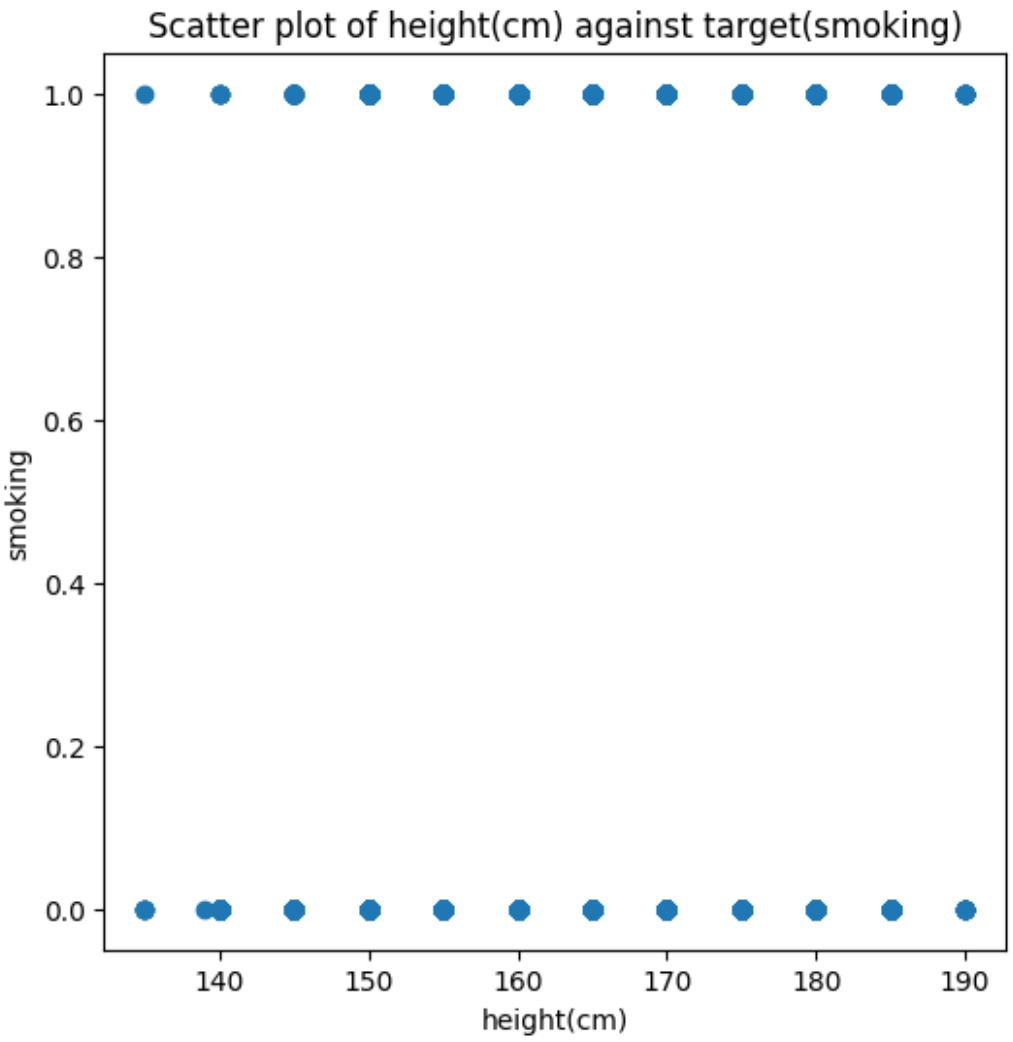

Scatter plot of eyesight(left) against target(smoking)
smoking
eyesight(left)
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10

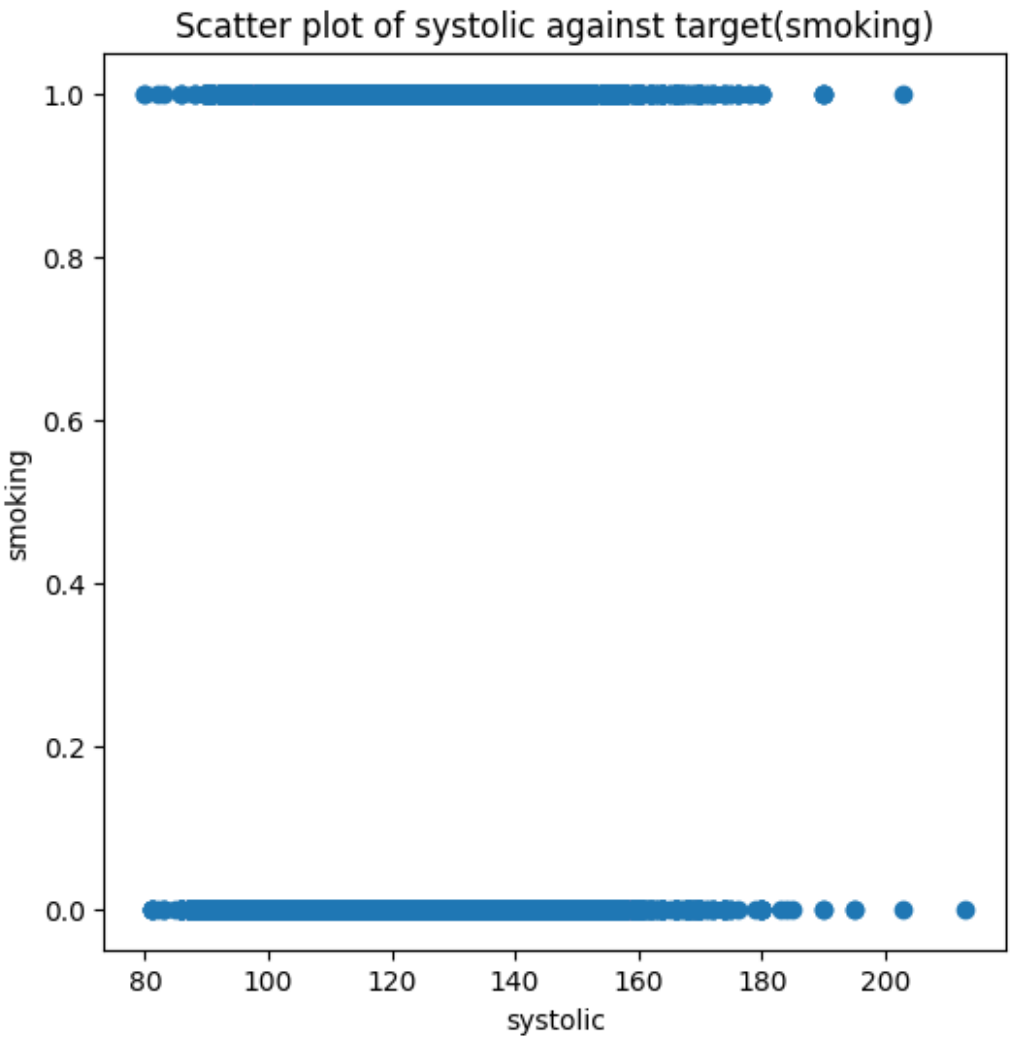

Scatter plot of hemoglobin against target(smoking)
smoking
hemoglobin
1.0
0.8
0.6
0.4
0.2
0.0
6
8
10
12
14
16
18
20

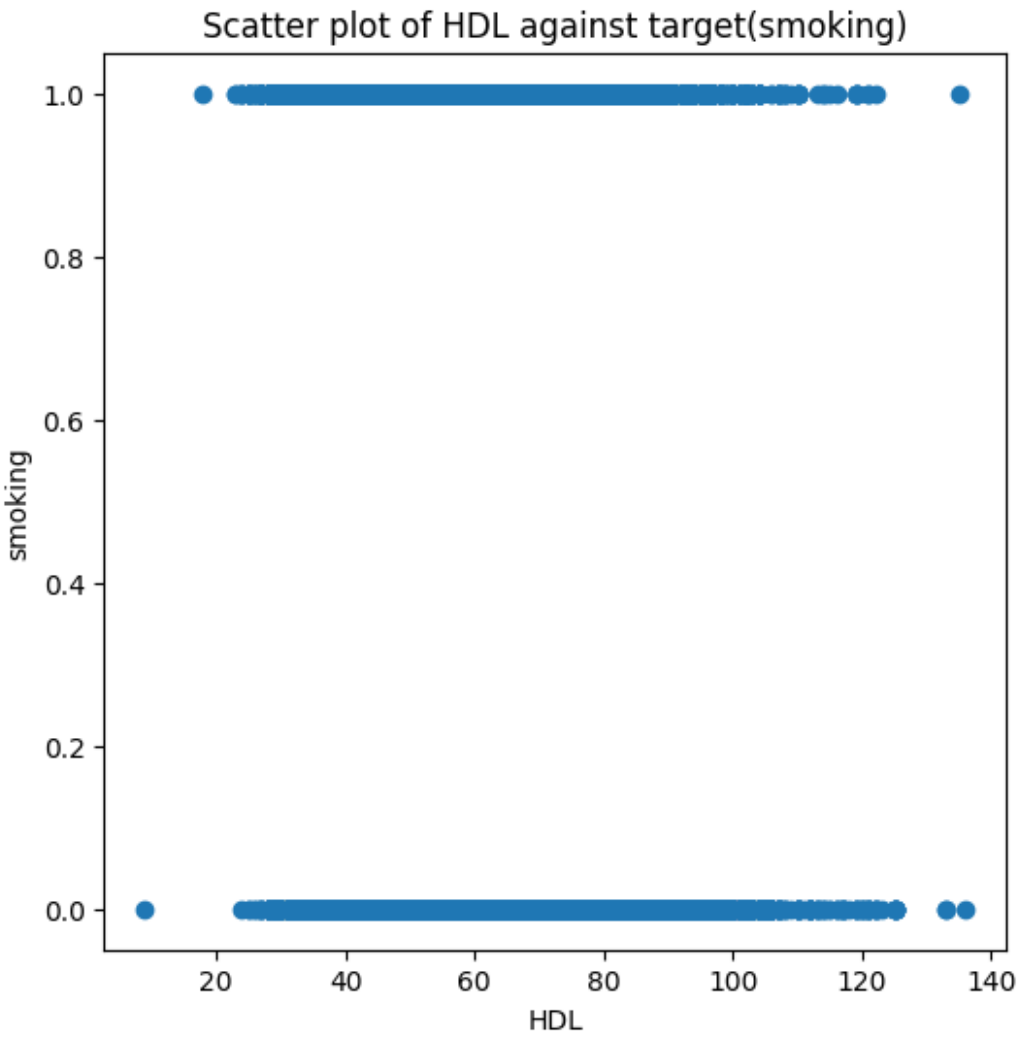

Scatter plot of age against target(smoking)
1.0
0.8
0.6
0.4
0.2
0.0
smoking
20
30
40
50
60
70
80
age

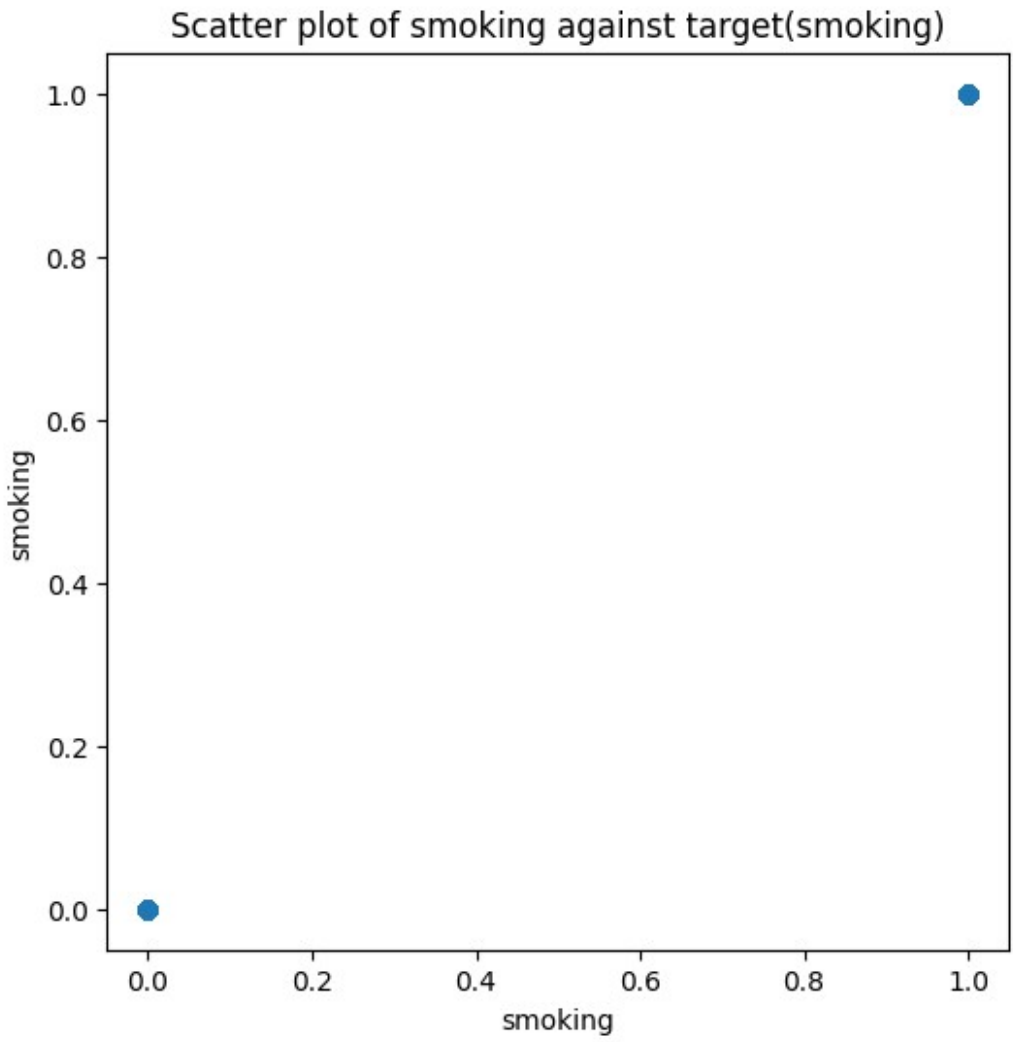

Scatter plot of waist(cm) against target(smoking)
smoking
waist(cm)
1.0
0.8
0.6
0.4
0.2
0.0
50
60
70
80
90
100
110
120
130


Scatter plot of hearing(right) against target(smoking)
smoking
hearing(right)
1.0
0.8
0.6
0.4
0.2
0.0
1.0
1.2
1.4
1.6
1.8
2.0


Scatter plot of height(cm) against target(smoking)
smoking
height(cm)
1.0
0.8
0.6
0.4
0.2
0.0
140
150
160
170
180
190


Scatter plot of systolic against target(smoking)
1.0
0.8
0.6
0.4
0.2
0.0
smoking
80
100
120
140
160
180
200
systolic


Scatter plot of HDL against target(smoking)
1.0
0.8
0.6
0.4
0.2
0.0
smoking
20
40
60
80
100
120
140
HDL



From the results of this data analysis, it can be concluded that there is a positive correlation between height and hemoglobin levels in the blood and the possibility of a person becoming a smoker. In particular, the level of smoking tendency tends to increase with increases in height and hemoglobin levels.

Multivariate Analysis

```
sns.pairplot(data_train, hue='smoking')
plt.legend(title='smoking', labels=[category_labels[0],
category_labels[1]])
plt.show()
```


ALT
eyesight(left)
hemoglobin
age
waist(cm)
hearing(right)
height(cm)
systolic
HDL
smoking
0
1