Bio-Signal Analysis for Smoking

Agenda

01 Importing the Libraries

02 Loading the Data

03 Data Cleaning

04 One Hot Encoding

05 Feature Selection

06 Bagging Algorithms

Problem Statement

You are working as a data scientist in a global company. Over the years, the company has collected details and gathered a lot of information about individuals. The management wants to build an intelligent system from the data to determine the presence or absence of smoking in a person through bio-signals. Given a person's information, build a machine learning model that can classify the presence or absence of smoking.

Dataset Information

This dataset is a collection of basic health biological signal data which contains around 55K record with 27 attributes.

Dataset Information

Attributes	Description
ID	index
gender	gender of a person (M or F)
age	age of a person (5-years gap)
height(cm)	height of a person
weight(kg)	weight of a person
waist(cm)	waist circumference length
eyesight(left)	left eyesight
eyesight(right)	right eyesight
hearing(left)	hearing pulse in left ear
hearing(right)	hearing pulse in right ear
systolic	Blood pressure

Dataset Information

Attributes	Description
relaxation	Blood pressure
fasting blood sugar	Blood test
Cholesterol	total
triglyceride	Lipid found in blood
HDL	cholesterol type
LDL	cholesterol type
hemoglobin	Transporting oxygen in blood
Urine protein	Excess of bloodborne proteins in urine
serum creatinine	Amount of creatinine in blood
AST	glutamic oxaloacetic transaminase type
ALT	glutamic oxaloacetic transaminase type

Dataset Information

Attributes	Description
Gtp	γ-GTP
oral	Oral Examination status
dental caries	Tooth decay
tartar	tartar status
smoking	Smoker (0 or 1)

Importing the Libraries

We start off this project by importing all the necessary libraries that will be required for the process.

```
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
```

Loading the Data

Loading the data and removing the irrelevant columns.

```
df=pd.read_csv("smoking.csv")
df= df.drop(columns=["ID","oral"])
df.head()
```

	gender	age	height(cm)	weight(kg)	waist(cm)	eyesight(left)	eyesight(right)	hearing(left)	hearing(right)	systolic	...	LDL	hemoglobin
0	F	40	155	60	81.3	1.2	1.0	1.0	1.0	114.0	...	126.0	12.9
1	F	40	160	60	81.0	0.8	0.6	1.0	1.0	119.0	...	127.0	12.7
2	M	55	170	60	80.0	0.8	0.8	1.0	1.0	138.0	...	151.0	15.8
3	M	40	165	70	88.0	1.5	1.5	1.0	1.0	100.0	...	226.0	14.7
4	F	40	155	60	86.0	1.0	1.0	1.0	1.0	120.0	...	107.0	12.5

5 rows × 25 columns

Loading the Data

Checking the shape of a dataframe and datatypes of all columns along with calculating the statistical data.

```
df.shape
df.info()
df.describe()
```

```
(55692, 25)
```

```
gender                 55692 non-null  object
age                    55692 non-null  int64
height(cm)             55692 non-null  int64
weight(kg)             55692 non-null  int64
waist(cm)              55692 non-null  float64
eyesight(left)         55692 non-null  float64
eyesight(right)        55692 non-null  float64
hearing(left)          55692 non-null  float64
hearing(right)         55692 non-null  float64
systolic               55692 non-null  float64
relaxation             55692 non-null  float64
fasting blood sugar    55692 non-null  float64
Cholesterol            55692 non-null  float64
triglyceride           55692 non-null  float64
HDL                    55692 non-null  float64
LDL                    55692 non-null  float64
hemoglobin             55692 non-null  float64
Urine protein          55692 non-null  float64
serum creatinine       55692 non-null  float64
AST                    55692 non-null  float64
ALT                    55692 non-null  float64
Gtp                    55692 non-null  float64
dental caries          55692 non-null  int64
tartar                 55692 non-null  object
smoking                55692 non-null  int64
```

Loading the Data

	age	height(cm)	weight(kg)	waist(cm)	eyesight(left)	eyesight(right)	hearing(left)	hearing(right)	systolic	relaxation	...
count	55692.000000	55692.000000	55692.000000	55692.000000	55692.000000	55692.000000	55692.000000	55692.000000	55692.000000	55692.000000	...
mean	44.182917	164.649321	65.864936	82.046418	1.012623	1.007443	1.025587	1.026144	121.494218	76.004830	...
std	12.071418	9.194597	12.820306	9.274223	0.486873	0.485964	0.157902	0.159564	13.675989	9.679278	...
min	20.000000	130.000000	30.000000	51.000000	0.100000	0.100000	1.000000	1.000000	71.000000	40.000000	...
25%	40.000000	160.000000	55.000000	76.000000	0.800000	0.800000	1.000000	1.000000	112.000000	70.000000	...
50%	40.000000	165.000000	65.000000	82.000000	1.000000	1.000000	1.000000	1.000000	120.000000	76.000000	...
75%	55.000000	170.000000	75.000000	88.000000	1.200000	1.200000	1.000000	1.000000	130.000000	82.000000	...
max	85.000000	190.000000	135.000000	129.000000	9.900000	9.900000	2.000000	2.000000	240.000000	146.000000	...

8 rows × 23 columns

Missing Values

Checking out the missing values in a dataframe

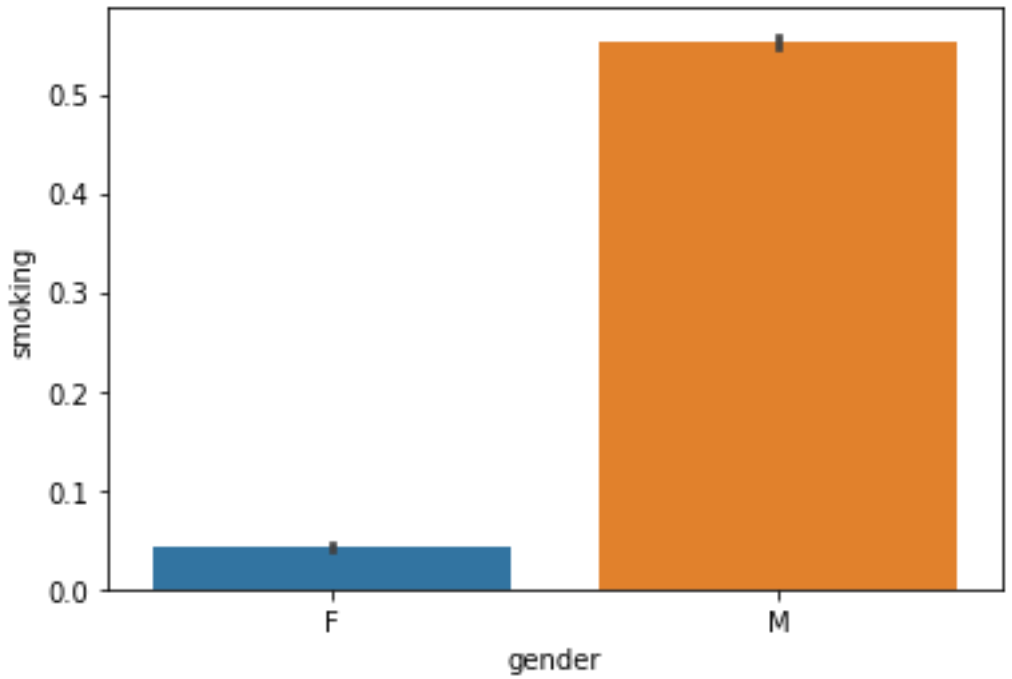
```
df.isnull().sum()
```

```
gender                0
age                   0
height(cm)            0
weight(kg)            0
waist(cm)             0
eyesight(left)        0
eyesight(right)       0
hearing(left)         0
hearing(right)        0
systolic              0
relaxation            0
fasting blood sugar   0
Cholesterol           0
triglyceride          0
HDL                   0
LDL                   0
hemoglobin            0
Urine protein         0
serum creatinine      0
AST                   0
ALT                   0
Gtp                   0
dental caries         0
tartar                0
smoking               0
dtype: int64
```

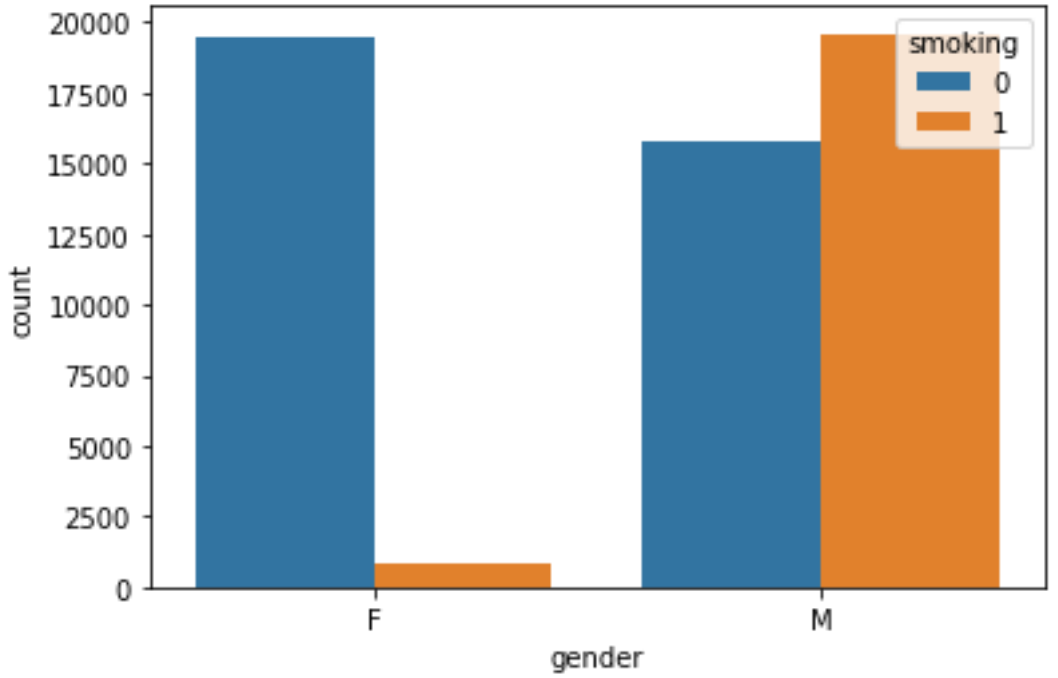
Data Visualization

We can clearly see from the below graph that most smokers are men

```
sns.barplot(x=df["gender"],y=df["smoking"])
plt.show()
```



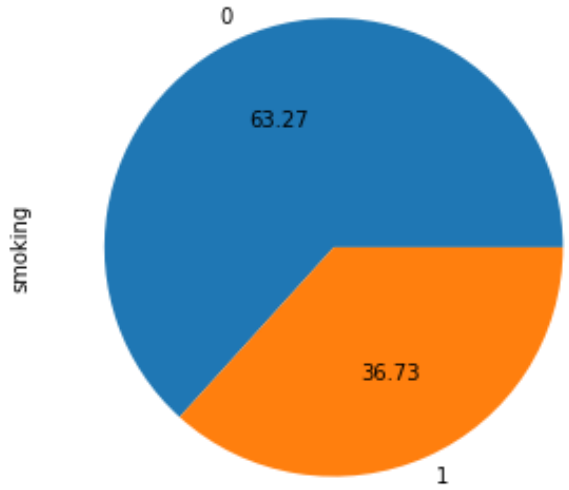

```
sns.countplot(df["gender"],hue=df["smoking"])
```



Data Visualization

There are 36.73 percent of the people who are smoking ciggarette.

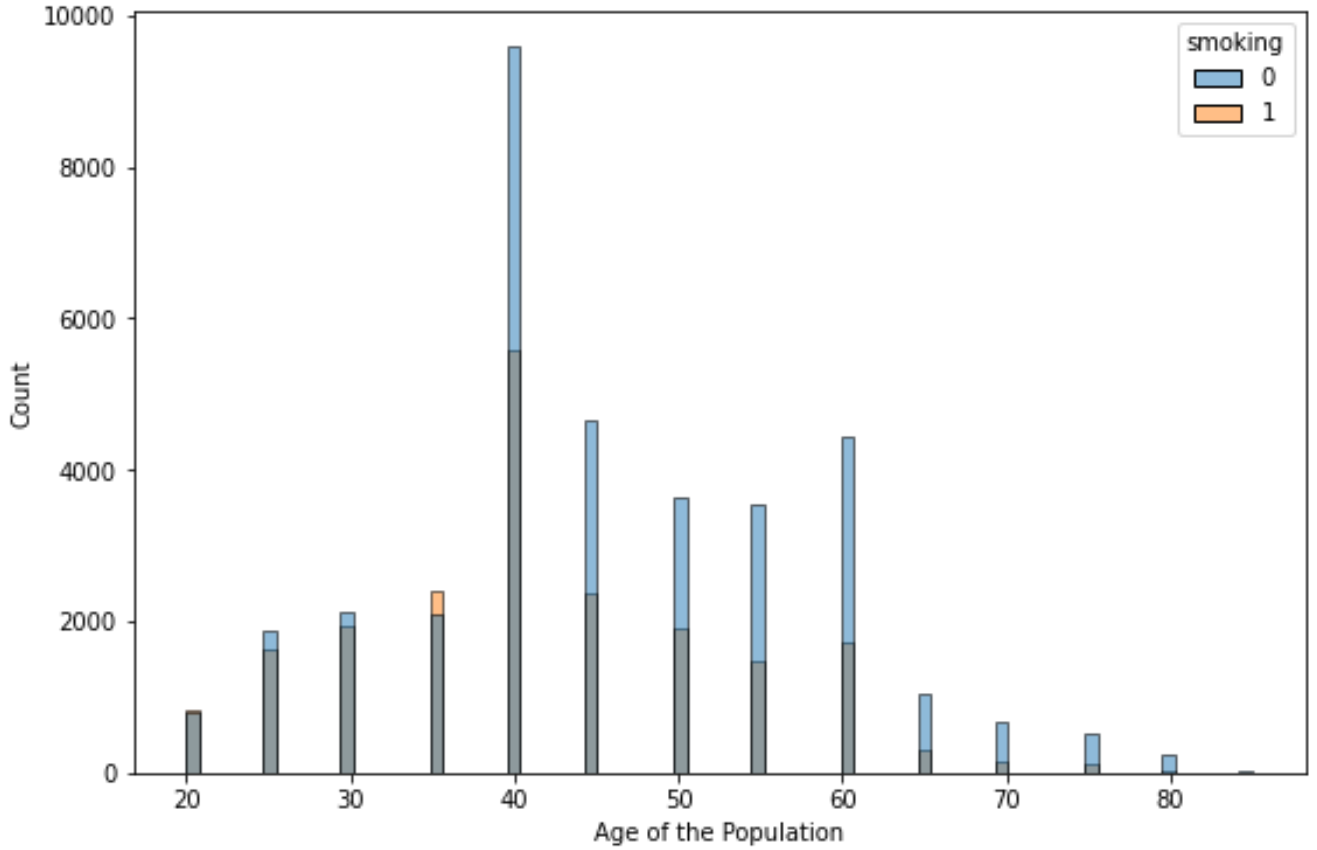
```
plt.figure(figsize=(10,5))
df["smoking"].value_counts().plot.pie(autopct='%0.2f')
```



Data Visualization

Most number of smokers are having the age 40

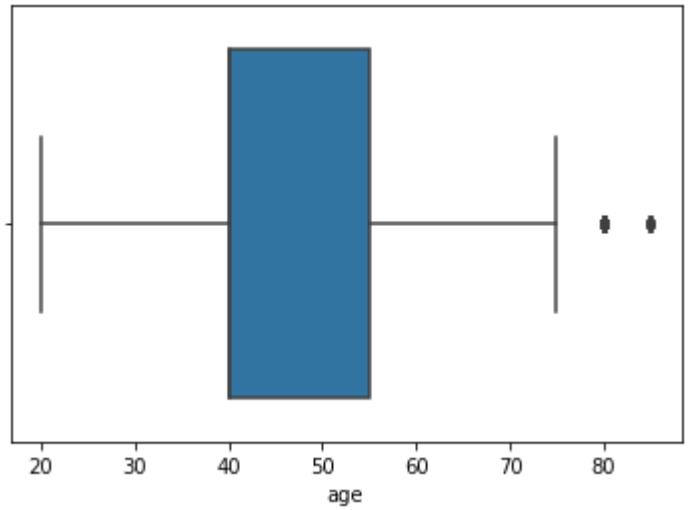
```
plt.figure(figsize=(9,6))
sns.histplot(x=df["age"],hue=df["smoking"])
plt.show()
```

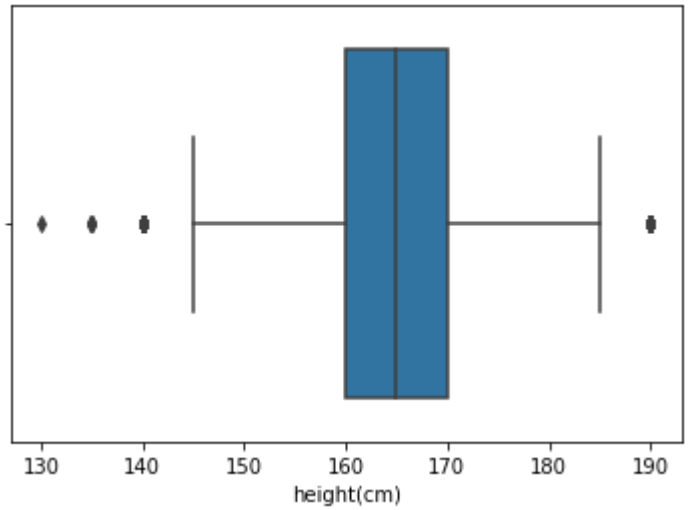


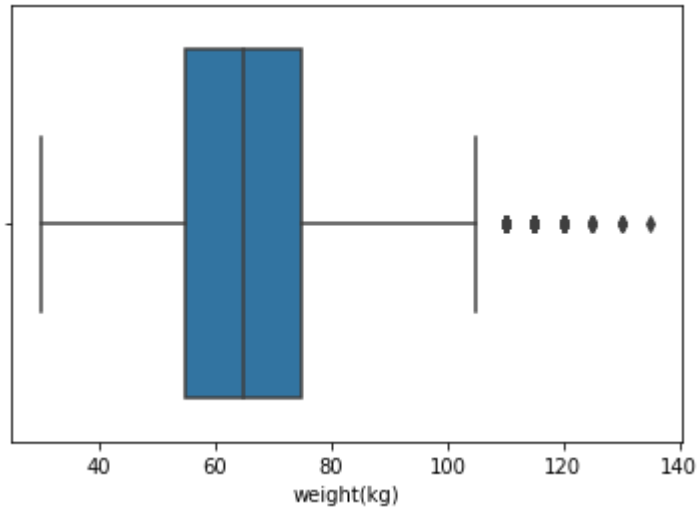
Data Visualization

Representation of columns using boxplot to detect outliers. Here outliers represent natural variations in the population, and they should be left as is in the dataset. These are called true outliers. Therefore for this dataset we will not remove outliers.

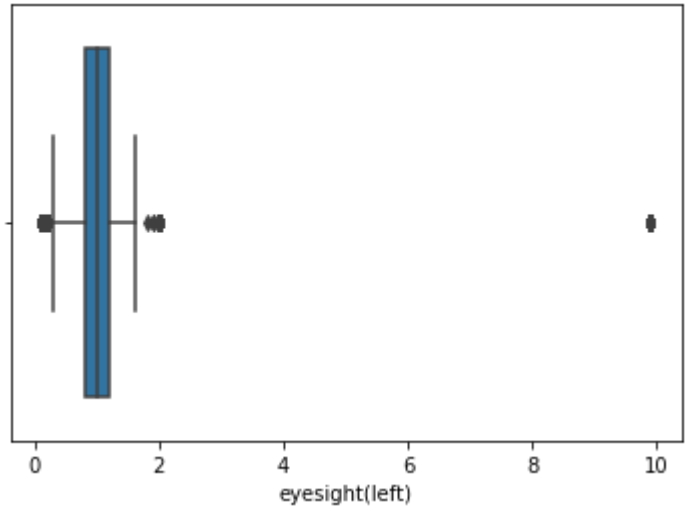
```
for i in df.columns:
  if(df[i].dtypes=='int64' or df[i].dtypes=='float64'):
    sns.boxplot(df[i])
    plt.show()
```

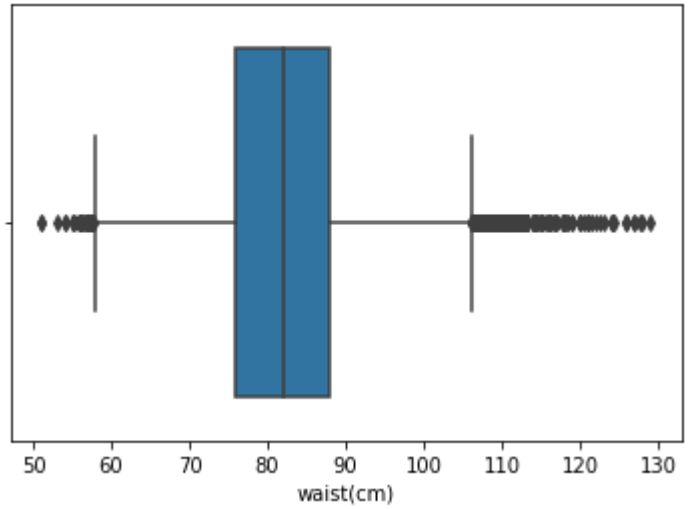


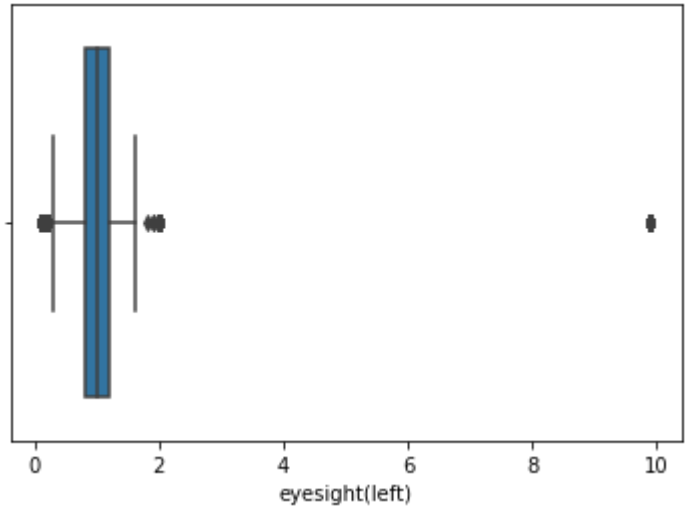


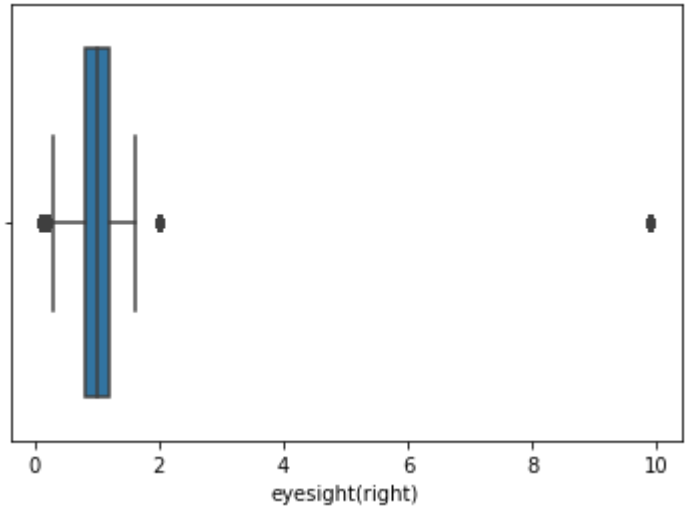


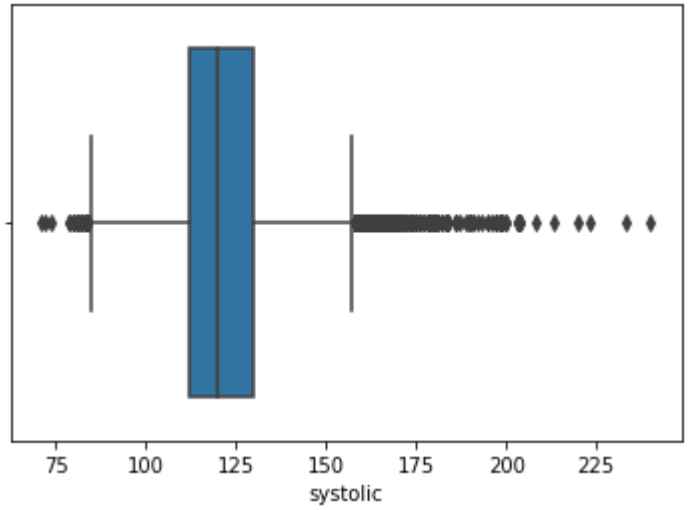
Data Visualization

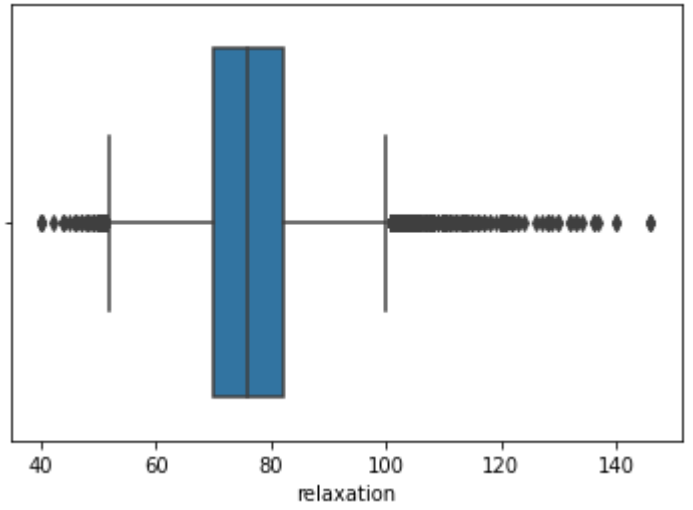




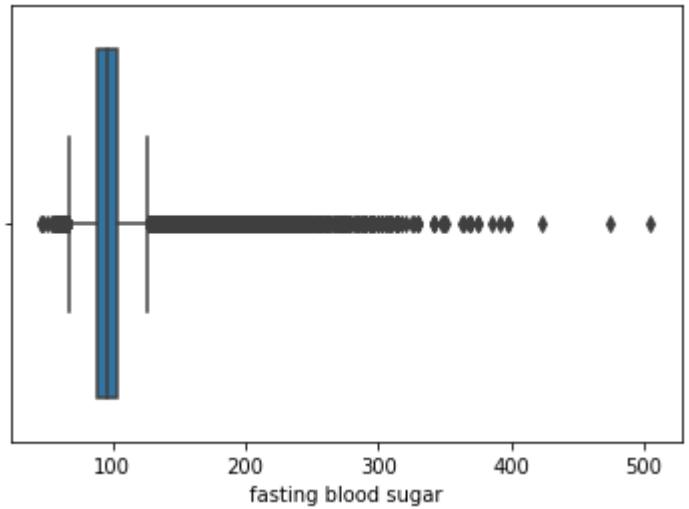


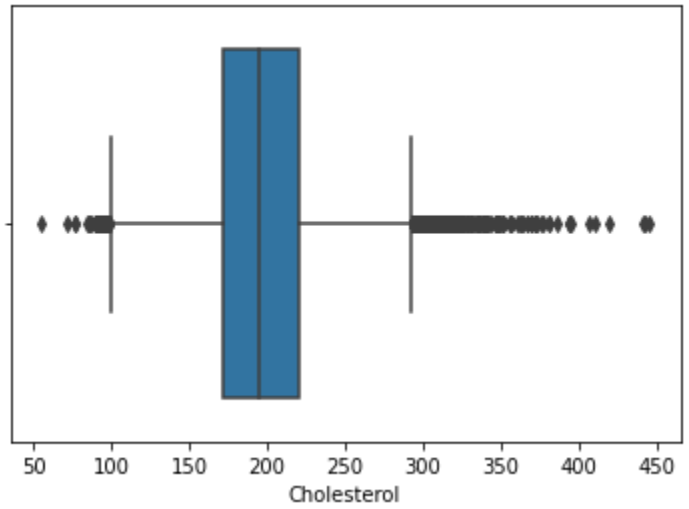


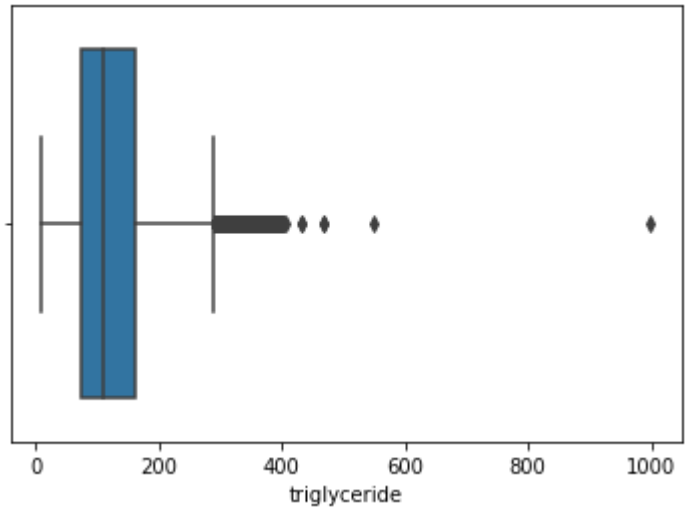


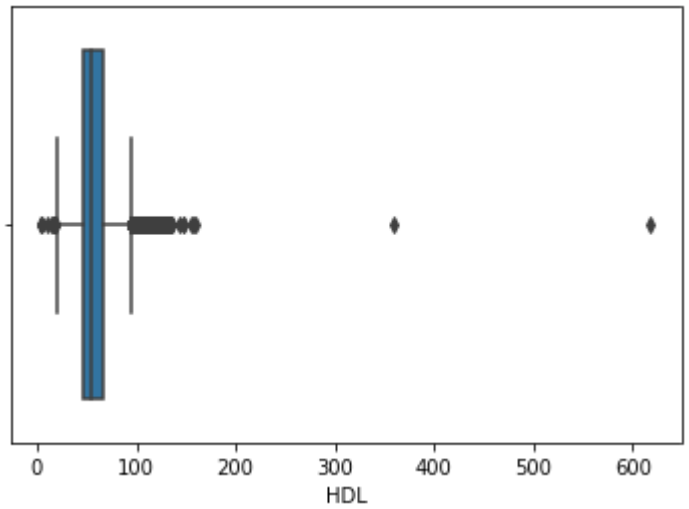


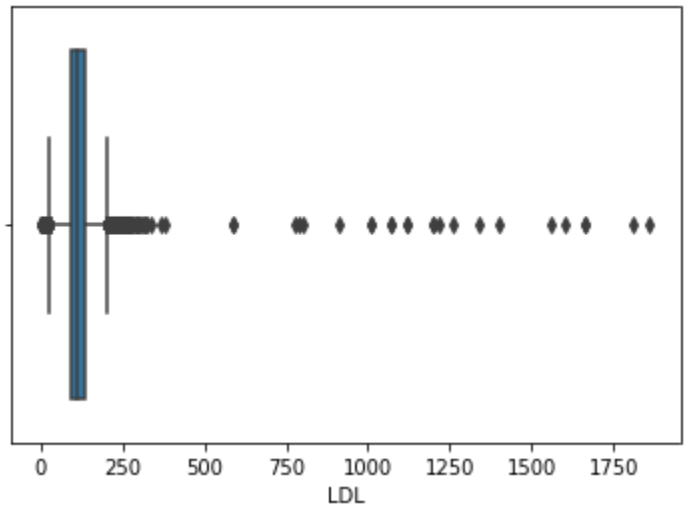
Data Visualization

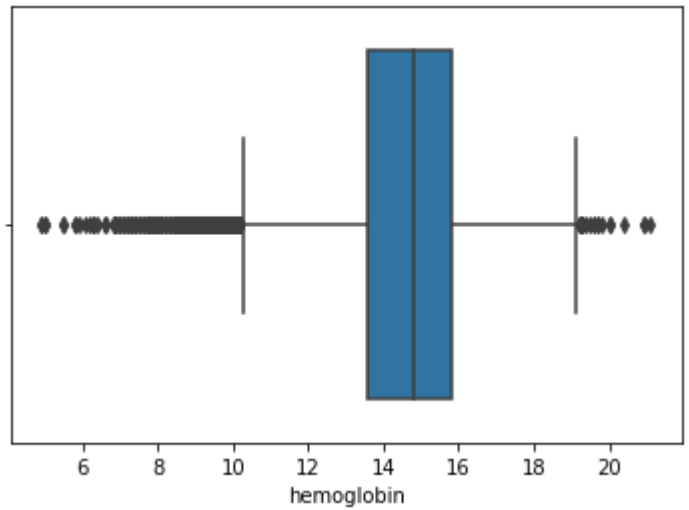




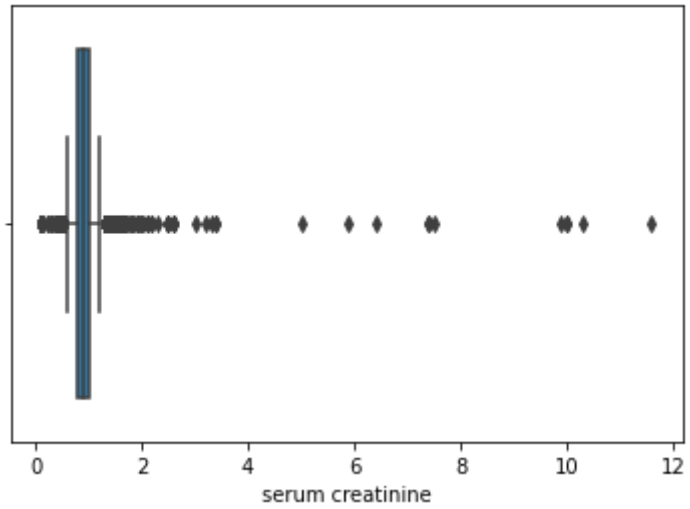


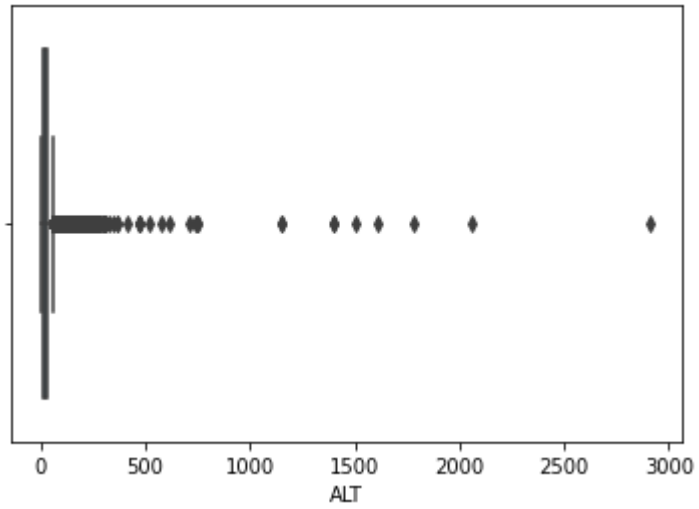


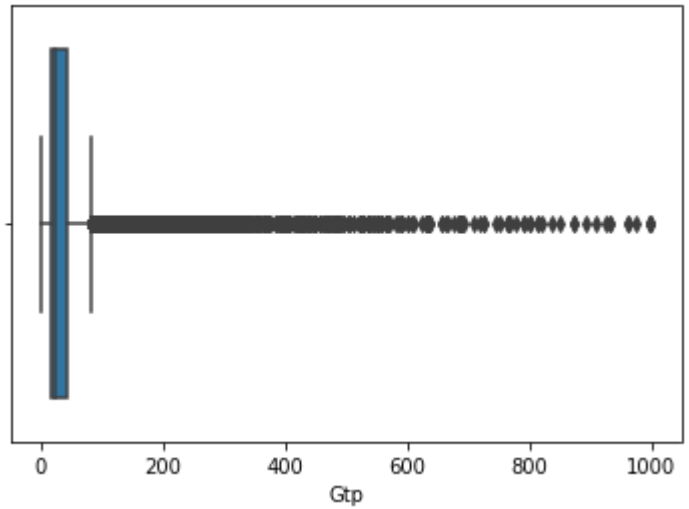


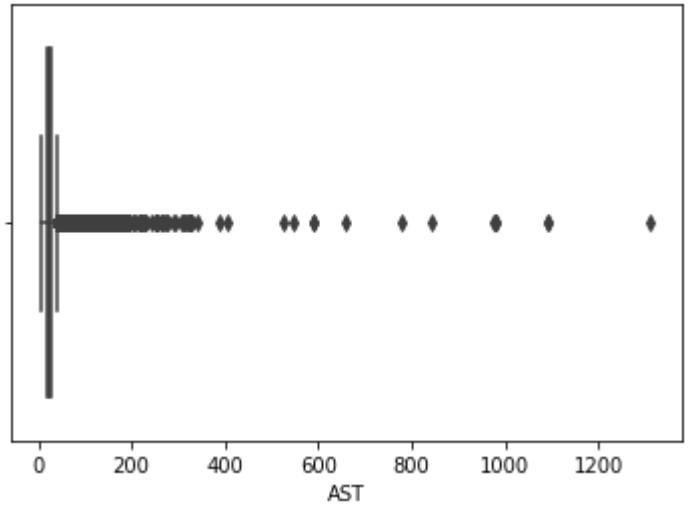


Data Visualization









Data Cleaning

```
from sklearn.preprocessing import LabelEncoder
le= LabelEncoder()
df["gender"]=le.fit_transform(df["gender"])
df["tartar"]=le.fit_transform(df["tartar"])
df["dental caries"]=le.fit_transform(df["dental caries"])
```

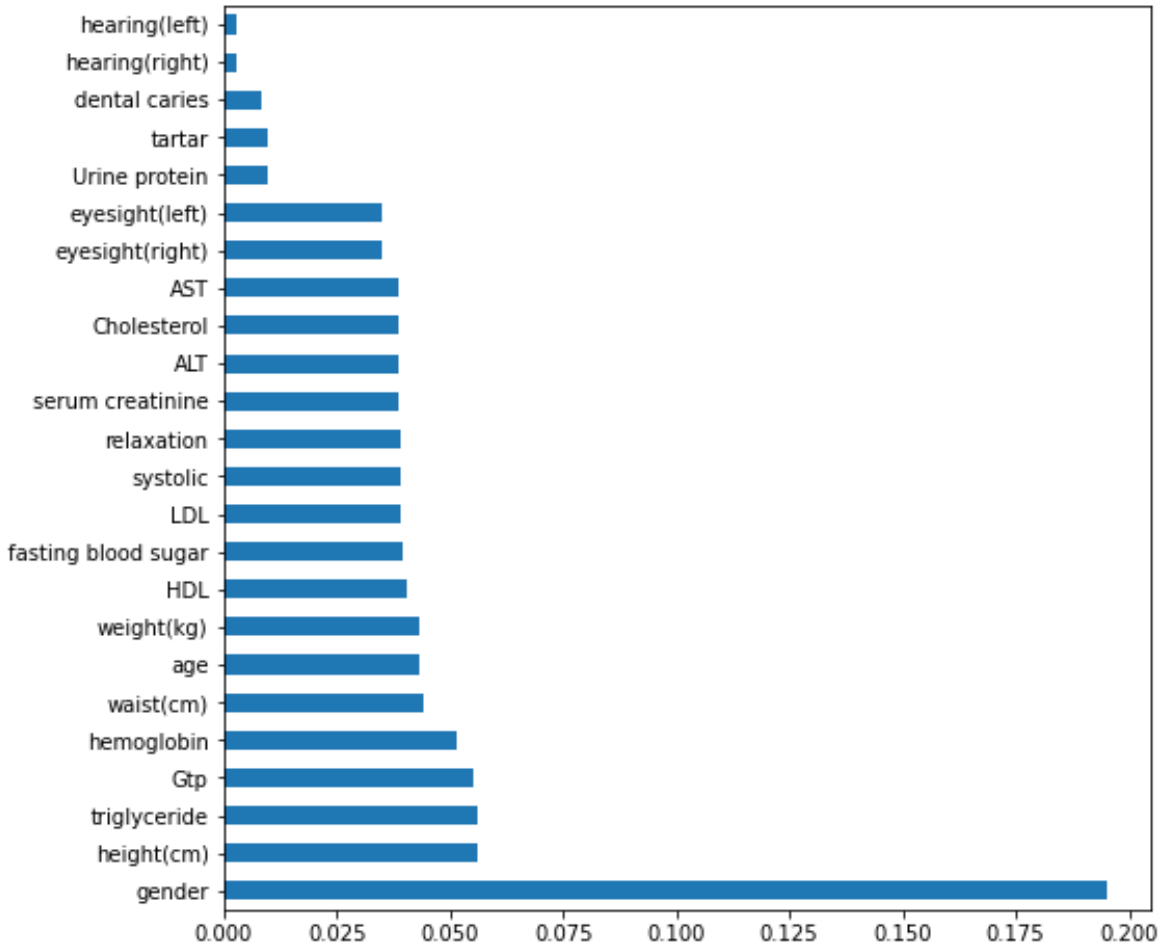
Performing One Hot Encoding for categorical features of a dataframe

```
gender               55692 non-null  int64
age                  55692 non-null  int64
height(cm)           55692 non-null  int64
weight(kg)           55692 non-null  int64
waist(cm)            55692 non-null  float64
eyesight(left)       55692 non-null  float64
eyesight(right)      55692 non-null  float64
hearing(left)        55692 non-null  float64
hearing(right)       55692 non-null  float64
systolic             55692 non-null  float64
relaxation           55692 non-null  float64
fasting blood sugar  55692 non-null  float64
Cholesterol          55692 non-null  float64
triglyceride         55692 non-null  float64
HDL                  55692 non-null  float64
LDL                  55692 non-null  float64
hemoglobin           55692 non-null  float64
Urine protein        55692 non-null  float64
serum creatinine     55692 non-null  float64
AST                  55692 non-null  float64
ALT                  55692 non-null  float64
Gtp                  55692 non-null  float64
dental caries        55692 non-null  int64
tartar               55692 non-null  int64
smoking              55692 non-null  int64
```

Feature selection using feature importance

```
X=df.iloc[:,:-1]
y=df["smoking"]
from sklearn.ensemble import ExtraTreesClassifier
model=ExtraTreesClassifier()
model.fit(X,y)
df1=pd.Series(model.feature_importances_,index= X.columns)
plt.figure(figsize=(8,8))
df1.nlargest(24).plot(kind='barh')
plt.show()
```

Feature importance is a technique that calculate a score for all the input features for a given model. So out of 24 features we will select the top 15 features based on the score.



Logistic Regression

```
X= df[["gender","height(cm)","Gtp","hemoglobin","triglyceride","age","weight(kg)","waist(cm)","HDL","serum creatinine",
"ALT","fasting blood sugar","relaxation","LDL","systolic"]]
y=df["smoking"]
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(X,y,test_size=0.2,random_state=42)
from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
x_train=sc.fit_transform(x_train)
x_test=sc.transform(x_test)
from sklearn.linear_model import LogisticRegression
lr=LogisticRegression()
lr.fit(x_train,y_train)
y_pred=lr.predict(x_test)
from sklearn.metrics import accuracy_score,classification_report
accuracy_score(y_test,y_pred)
classification_report(y_test,y_pred)
```

Calculating accuracy and generating the classification report of Logistic Regression

```
0.7347158631834096
```

	precision	recall	f1-score	support
0	0.81	0.76	0.78	7027
1	0.63	0.69	0.66	4112
accuracy			0.73	11139
macro avg	0.72	0.73	0.72	11139
weighted avg	0.74	0.73	0.74	11139

Decision Tree

The accuracy of the logistic regression model is 78 percentage

```
from sklearn.tree import DecisionTreeClassifier
dt=DecisionTreeClassifier()
dt.fit(x_train,y_train)
y_pred=dt.predict(x_test)
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.83      0.83      0.83      7027
           1       0.71      0.71      0.71      4112

    accuracy                           0.78     11139
   macro avg       0.77      0.77      0.77     11139
weighted avg       0.78      0.78      0.78     11139
```

Bagging Algorithm – Bagging Classifier

Bootstrap Aggregation or bagging involves taking multiple samples from the training dataset (with replacement) and training a model for each sample.

```
from sklearn.ensemble import BaggingClassifier
bagging_clf=BaggingClassifier(base_estimator=DecisionTreeClassifier(),n_estimators=1000)
bagging_clf.fit(x_train,y_train).score(x_test,y_test)
y_pred=bagging_clf.predict(x_test)
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.88      0.85      0.86      7027
           1       0.75      0.80      0.77      4112

    accuracy                           0.83     11139
   macro avg       0.82      0.82      0.82     11139
weighted avg       0.83      0.83      0.83     11139
```

Bagging Algorithm – Extra Trees

```
from sklearn.ensemble import ExtraTreesClassifier
et=ExtraTreesClassifier(n_estimators=1000,random_state=42)
et.fit(x_train,y_train)
y_pred=et.predict(x_test)
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.89      0.84      0.86      7027
           1       0.75      0.82      0.78      4112

    accuracy                           0.83     11139
   macro avg       0.82      0.83      0.82     11139
weighted avg       0.83      0.83      0.83     11139
```

Bagging Algorithm – Random Forest

```
from sklearn.ensemble import RandomForestClassifier
rfc= RandomForestClassifier(n_estimators=1000)
rfc.fit(x_train,y_train)
y_pred=rfc.predict(x_test)
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.88      0.85      0.86      7027
           1       0.75      0.80      0.78      4112

    accuracy                           0.83     11139
   macro avg       0.82      0.82      0.82     11139
weighted avg       0.83      0.83      0.83     11139
```