```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import  seaborn as sns
import warnings
warnings.filterwarnings('ignore')


from sklearn.tree import  DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from xgboost import XGBClassifier
from sklearn.ensemble import  RandomForestClassifier,AdaBoostClassifier
from sklearn.svm import  SVC
from sklearn.neighbors import KNeighborsClassifier
import xgboost as xg
from sklearn.model_selection import  train_test_split,GridSearchCV



from sklearn.preprocessing import  LabelEncoder, Normalizer , StandardScaler

from sklearn.metrics import accuracy_score,mean_squared_error,r2_score
```

Problem

Drinking has been proven to negatively affect health in a multiple ways.

1. Smoking has been found to harm nearly every organ of the body.
2. It is a cause of many diseases.
3. Reduces the life expectancy.
4. In 2018, smoking had been considered the leading cause of preventable morbidity and mortality in the world.

How a prediction model can help to solve this problem?

Providing a prediction model might be a favourable in a way to understand the chance of quitting smoking for each individual smoker

EDA

```
df = pd.read_csv('data/smoking.csv')


## For testing the model take a small subset of the dataset( Do not forget to comment it down)
df = df.iloc[:9000,:]


len(df)
```

```
9000
```

```
df.head()
```

	sex	age	height	weight	waistline	sight_left	sight_right	hear_left	hear_right	SBP	...	LDL_chole	triglyceride	hemoglobin
0	Male	35	170	75	90.0	1.0	1.0	1.0	1.0	120.0	...	126.0	92.0	17.1
1	Male	30	180	80	89.0	0.9	1.2	1.0	1.0	130.0	...	148.0	121.0	15.8
2	Male	40	165	75	91.0	1.2	1.5	1.0	1.0	120.0	...	74.0	104.0	15.8
3	Male	50	175	80	91.0	1.5	1.2	1.0	1.0	145.0	...	104.0	106.0	17.6
4	Male	50	165	60	80.0	1.0	1.2	1.0	1.0	138.0	...	117.0	104.0	13.8

5 rows × 24 columns

Understanding of columns

1. sex- gener of the person
2. age - Its age in years
3. Height - Height in cm
4. Weight - Weight in kg
5. waistline - Waist circumference length
6. sight_left - eyesight of left eye
7. sight_right - eyesight of right eye
8. hear_left - hearing of left ear
9. hear_right - hearing of right ear
10. SBP - systolic Blood Pressure (Force produced buy heart when it pumps blood out the body
11. DBP - Diastolic Blood Pressure(Pressure in blood vessels when the heart is at rest)
12. BLDS
13. tot_chole - Total Cholesterol
14. HDL_chole - High density Lipoprotein (Good cholesterol)(+)
15. LDL_chose - Low density Lipoprotein (Bad cholesterol)(-)
16. triglyceride - Triglycerides are a type of fat. They are the most common type of fat in your body. They come from foods, especially butter, oils, and other fats you eat. (+ or -)
17. Hemoglobin - Protein in red blood cells carries oxygen to body's organs(+)
18. Urine_protein - Protein in urine
19. serum_creatinine - creatinine level
20. SGOT_AST - Serum glutamic-oxaloacetic transaminase(Aspartate transaminase)
21. SGOT_ALT - "" "" (Alanine transaminase) These above two enzymes AST and ALT found inliver cells that leak out of cells and mix in blood when liver cells get injured
22. gamma_GTP - y-glutamyl transpepetidase (Test is used to detect diseases of the liver or bile ducts. This is similar tests like ALT, AST, ALP)
23. Smoking state,-

- 1 - never
- 2 - used to smoke but quit
- 3 - still smoke

24. DRK_YN - Drinker or Not - (Output)

- 1 - drink
- 0 - does not drink

```
df.head()
```

	sex	age	height	weight	waistline	sight_left	sight_right	hear_left	hear_right	SBP	...	LDL_chole	triglyceride	hemoglobin
0	Male	35	170	75	90.0	1.0	1.0	1.0	1.0	120.0	...	126.0	92.0	17.1
1	Male	30	180	80	89.0	0.9	1.2	1.0	1.0	130.0	...	148.0	121.0	15.8
2	Male	40	165	75	91.0	1.2	1.5	1.0	1.0	120.0	...	74.0	104.0	15.8
3	Male	50	175	80	91.0	1.5	1.2	1.0	1.0	145.0	...	104.0	106.0	17.6
4	Male	50	165	60	80.0	1.0	1.2	1.0	1.0	138.0	...	117.0	104.0	13.8

5 rows × 24 columns

Things to be done in EDA

check Missing values Check duplicates Check data type Check the number of unique values of each column Check Statistics of data set Check various categories present in the different categorical column

```
dataset_length_before_removing_dulicates = len(df)
```

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

```
0
```

- Zero missing values in dataset

```
df[df.duplicated()]
```

	sex	age	height	weight	waistline	sight_left	sight_right	hear_left	hear_right	SBP	...	LDL_chole	triglyceride	hemoglobin	uri

0 rows × 24 columns

- Total 26 dulicates rows present in dataset

```
df.drop_duplicates(inplace=True)
```

```
data_length_after_removing_duplicates = len(df)
```

```
print('Old data length {}'.format(dataset_length_before_removing_dulicates))
print('New data length {}'.format(data_length_after_removing_duplicates))
```

```
Old data length 9000
New data length 9000
```

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9000 entries, 0 to 8999
Data columns (total 24 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   sex               9000 non-null   object 
 1   age               9000 non-null   int64  
 2   height            9000 non-null   int64  
 3   weight            9000 non-null   int64  
 4   waistline         9000 non-null   float64
 5   sight_left        9000 non-null   float64
 6   sight_right       9000 non-null   float64
 7   hear_left         9000 non-null   float64
 8   hear_right        9000 non-null   float64
 9   SBP               9000 non-null   float64
 10  DBP               9000 non-null   float64
 11  BLDS              9000 non-null   float64
 12  tot_chole         9000 non-null   float64
 13  HDL_chole         9000 non-null   float64
 14  LDL_chole         9000 non-null   float64
 15  triglyceride      9000 non-null   float64
 16  hemoglobin        9000 non-null   float64
 17  urine_protein     9000 non-null   float64
 18  serum_creatinine  9000 non-null   float64
 19  SGOT_AST          9000 non-null   float64
 20  SGOT_ALT          9000 non-null   float64
 21  gamma_GTP         9000 non-null   float64
 22  SMK_stat_type_cd  9000 non-null   float64
 23  DRK_YN            9000 non-null   object 
dtypes: float64(19), int64(3), object(2)
memory usage: 1.6+ MB
```

- 1- string
- 3 - integer
- 6 - float

- We can observe the dataset that we have 1 categorical feature named 'sex' and remaining all are continuous features

```
df.describe()
```

	age	height	weight	waistline	sight_left	sight_right	hear_left	hear_right	SBP	DBP	...
count	9000.000000	9000.000000	9000.000000	9000.000000	9000.000000	9000.000000	9000.000000	9000.000000	9000.000000	9000.000000	...
mean	47.561111	162.297222	63.311111	81.254089	0.981056	0.988056	1.029889	1.029333	122.759222	76.313667	...
std	14.143968	9.292567	12.605501	9.706305	0.604377	0.647287	0.170290	0.168748	14.675356	10.007751	...
min	20.000000	135.000000	35.000000	49.000000	0.100000	0.100000	1.000000	1.000000	75.000000	46.000000	

- In waistline feature max value is way greater than the mean and median(50%), may 'waistline' contains some outliers,
- same scenerio for both eyesights, BLDS, tol_chole , HDL_chole, LDL_chole, triglyceride , SGOT_AST, SGOT_ALT

Checking multicollinearity

What is Variance Inflation factor(VIF)? *VIF is a measure of amount of multicollinearity in the independent featurse in the dataset.*

What is multicollinearity? *High correlation between independent features. Having high correlation between the independent features can increase the complexity of the model since the model can not be able to detect the pattern in those features because of multicollinearity*

How multicollinearity affects the model's capability to capture the influence of a independent feature on dependent feature *consider this example - *A two feature regression equation is given below Y = W0+W1X1+W2X2*

here, Y - Output variable X1,X2 - Independent features W1,W2 - Slopes (coefficient of independent feautures) W0 - Intercept

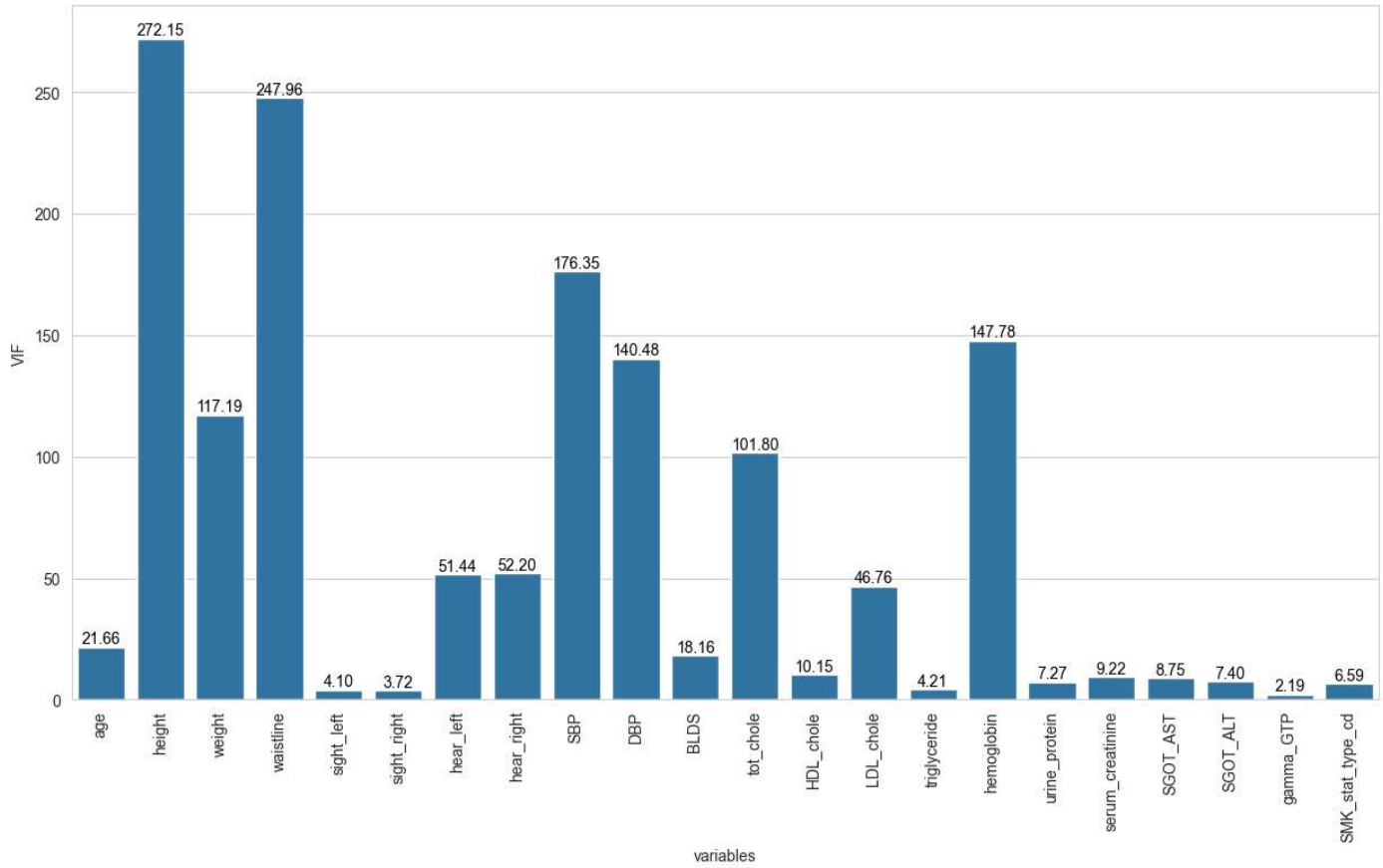
Coefficient W1 is the increase in Y for a unit increase in X1 while keeping X2 constant. But since X1 and X2 are highly correlated, ***changes in X1 would also cause changes in X2, and we would not be able to see their individual effect on Y.***

```
from statsmodels.stats.outliers_influence import variance_inflation_factor

def calc_vif(X):
    # Check for missing or non-finite values in the input data
    # if X.isnull().values.any() or not np.isfinite(X).all():
    #     raise ValueError("Input data contains missing or non-finite values.")

    # Calculating VIF
    vif = pd.DataFrame()
    vif["variables"] = X.columns
    vif["VIF"] = [variance_inflation_factor(X.values, i) for i in range(X.shape[1])]

    return vif


calc_vif(df.drop(['sex','DRK_YN'],axis=1))
```

	variables	VIF
0	age	21.662001
1	height	272.147022
2	weight	117.185055
3	waistline	247.961763
4	sight_left	4.095456
5	sight_right	3.719158

Visuals of VIF

```
fig = plt.figure(figsize=(15, 8))
ax = sns.barplot(
    data=calc_vif(df.drop(['sex', 'DRK_YN'], axis=1)), x='variables', y='VIF'
)

# Rotate the x-axis labels by 90 degrees
ax.set_xticklabels(labels=ax.get_xticklabels(), rotation=90)

# Add labels to the bars
for p in ax.patches:
    ax.annotate(f'{p.get_height():.2f}', (p.get_x() + p.get_width() / 2., p.get_height()),
                ha='center', va='center', fontsize=10, color='black', xytext=(0, 5),
                textcoords='offset points')

plt.show()
```



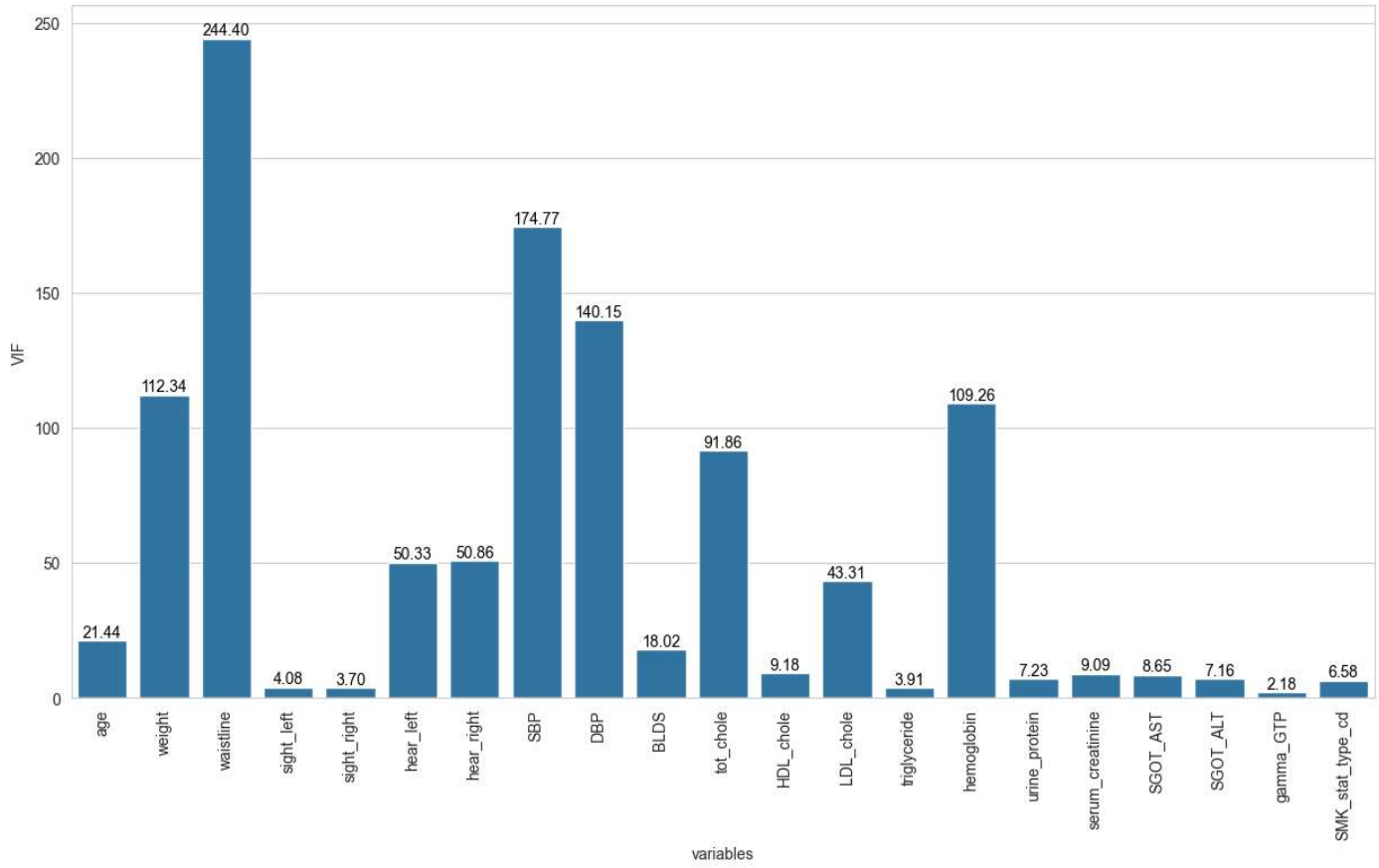
Conclusion

- Here Vif of the features are seems to be highly correlated, for e.g. SBP and DBP these two features shows high vif
- Same with 'hear_left' and 'hear_right' features

Lets remove some columns causing multicollinearity

```
df.drop(['height'],axis=1,inplace = True)
```

```
fig = plt.figure(figsize=(15, 8))
ax = sns.barplot(
    data=calc_vif(df.drop(['sex', 'DRK_YN'], axis=1)), x='variables', y='VIF'
)

# Rotate the x-axis labels by 90 degrees
ax.set_xticklabels(labels=ax.get_xticklabels(), rotation=90)

# Add labels to the bars
for p in ax.patches:
    ax.annotate(f'{p.get_height():.2f}', (p.get_x() + p.get_width() / 2., p.get_height()),
                ha='center', va='center', fontsize=10, color='black', xytext=(0, 5),
                textcoords='offset points')
```

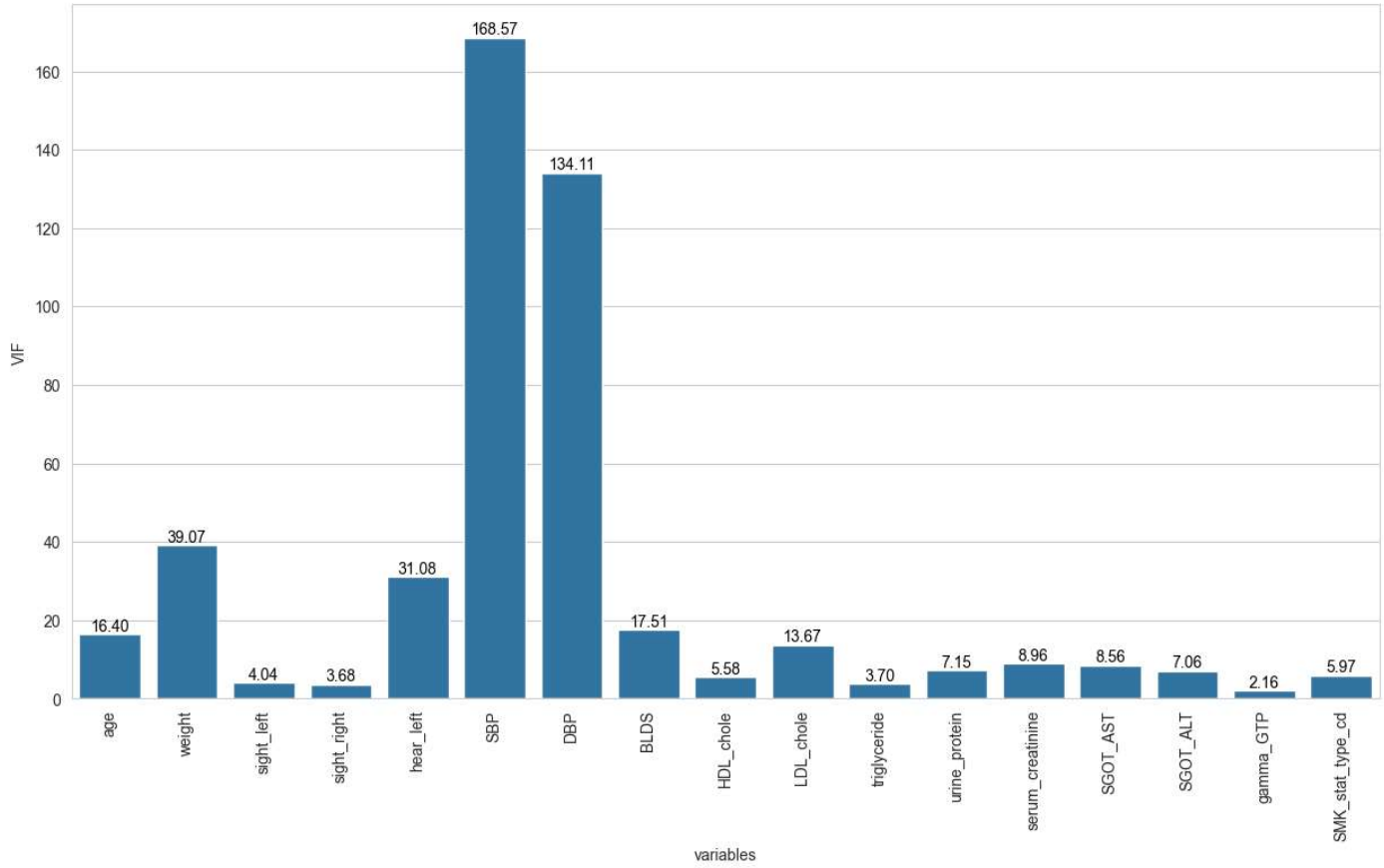


Conclusion

- By removing one feature, VIF of other features decreases with the same extent at which the deleted feature was corrleted

```
## Lets remove a couple of  features and see the effect
df.drop(['hear_right','waistline','tot_chole','hemoglobin'],axis=1,inplace=True)
fig = plt.figure(figsize=(15, 8))
ax = sns.barplot(
    data=calc_vif(df.drop(['sex', 'DRK_YN'], axis=1)), x='variables', y='VIF'
```

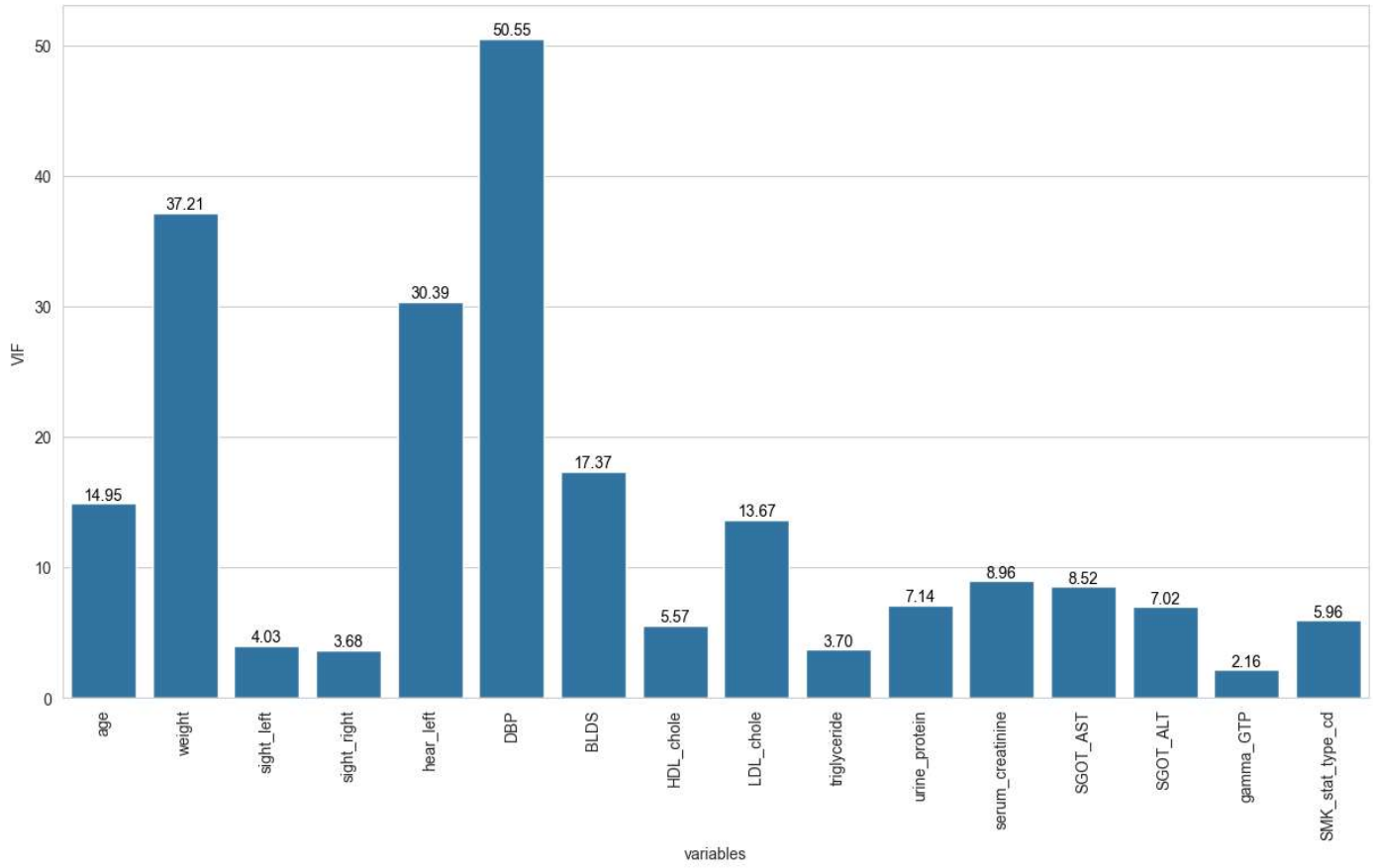
```
)

# Rotate the x-axis labels by 90 degrees
ax.set_xticklabels(labels=ax.get_xticklabels(), rotation=90)

# Add labels to the bars
for p in ax.patches:
    ax.annotate(f'{p.get_height():.2f}', (p.get_x() + p.get_width() / 2., p.get_height()),
                ha='center', va='center', fontsize=10, color='black', xytext=(0, 5),
                textcoords='offset points')
```



Conclusion

- By removing high related features, there is sharp decrement in the vif of other features, for e.g. weigt from 117 to 39 and LDL_chole from 46 to 13

```
df.drop(['SBP'],axis=1,inplace=True)
fig = plt.figure(figsize=(15, 8))
ax = sns.barplot(
    data=calc_vif(df.drop(['sex', 'DRK_YN'], axis=1)), x='variables', y='VIF'
)

# Rotate the x-axis labels by 90 degrees
ax.set_xticklabels(labels=ax.get_xticklabels(), rotation=90)

# Add labels to the bars
for p in ax.patches:
    ax.annotate(f'{p.get_height():.2f}', (p.get_x() + p.get_width() / 2., p.get_height()),
                ha='center', va='center', fontsize=10, color='black', xytext=(0, 5),
                textcoords='offset points')
```



Conclusion

- Now vif is ok
- Further dropping the columns can cause loss of information

```
df.head()
```

	sex	age	weight	sight_left	sight_right	hear_left	DBP	BLDS	HDL_chole	LDL_chole	triglyceride	urine_protein	serum_creatinine
0	Male	35	75	1.0	1.0	1.0	80.0	99.0	48.0	126.0	92.0	1.0	1.0
1	Male	30	80	0.9	1.2	1.0	82.0	106.0	55.0	148.0	121.0	1.0	0.9
2	Male	40	75	1.2	1.5	1.0	70.0	98.0	41.0	74.0	104.0	1.0	0.9
3	Male	50	80	1.5	1.2	1.0	87.0	95.0	76.0	104.0	106.0	1.0	1.1
4	Male	50	60	1.0	1.2	1.0	82.0	101.0	61.0	117.0	104.0	1.0	0.8

Separate categorical and continuous columns

```
categorical_columns = [i for i in df.columns if df[i].dtypes == 'O']
continuous_columns = [i for i in df.columns if df[i].dtypes == 'int64' or df[i].dtypes == 'float64' or df[i].dtypes == 'int32']
```

```
print('Categorical columns')
for i in categorical_columns:
    print(i,end= '\t')
```

```
Categorical columns
sex     DRK_YN
```

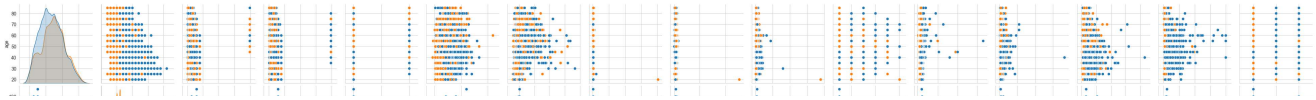
```
print('Continuous columns')
for i in continuous_columns:
    print(i,end= '\t')
```

```
Continuous columns
age	weight	sight_left	sight_right	hear_left	DBP	BLDS	HDL_chole	LDL_chole	triglyceride	urine_pr
```

Visualizations

```
plt.figure(figsize=(15,8))
sns.pairplot(
    data = df , hue='sex'
)
```

```
<seaborn.axisgrid.PairGrid at
0x194139515d0>Error in callback <function _draw_all_if_interactive at 0x00000193C55D2840> (for post_execute):

KeyboardInterrupt

<Figure size 1500x800 with 0 Axes>
```

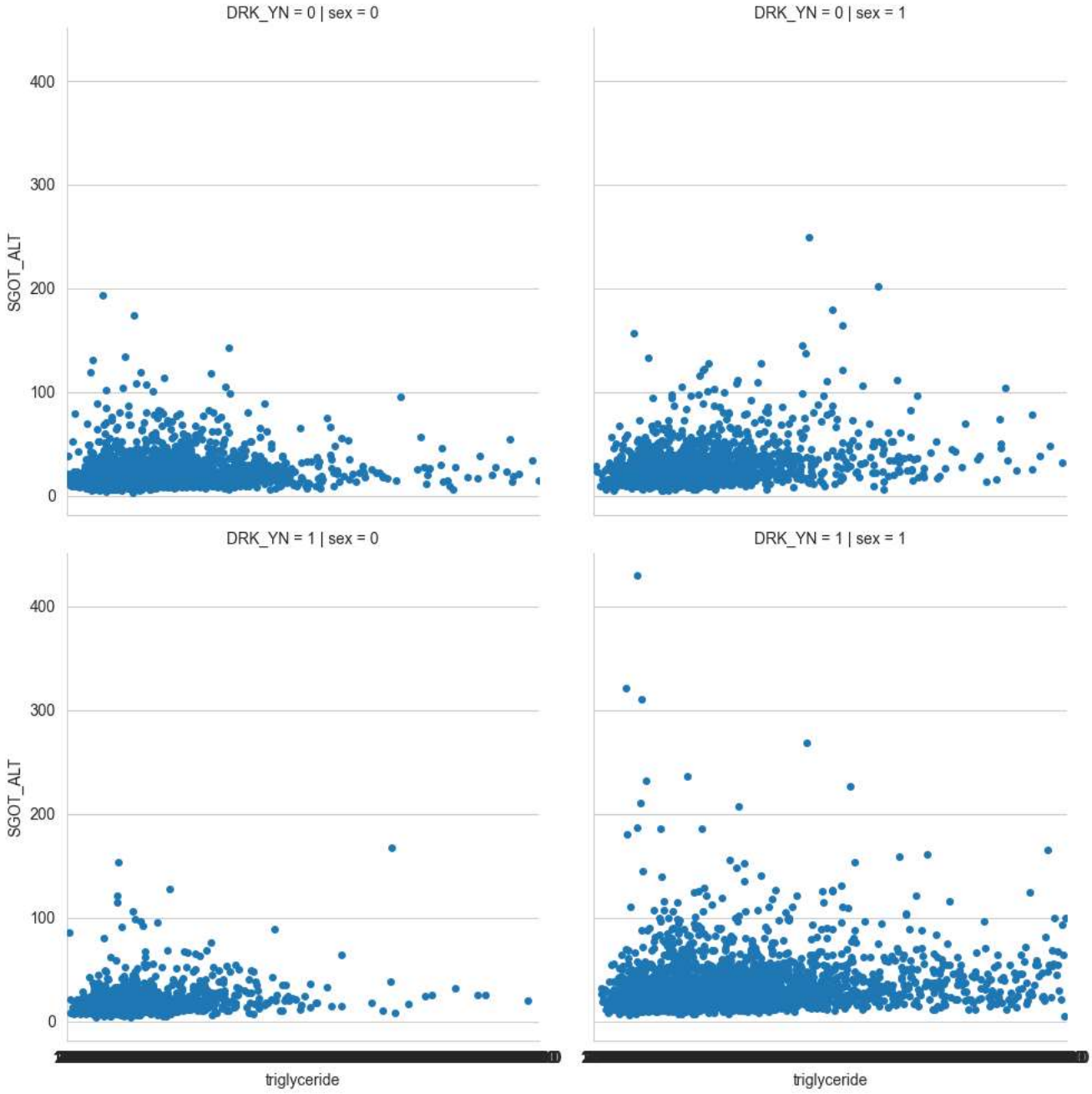


Conclusion

- Clear images of Dominating factor of male over female in Drinking/Smoking
- In all the factors (tyiglyceride , Blood pressure , etc..) males are showing high presence of it


```
sns.catplot(
    data  =df ,x = 'triglyceride',y= 'SGOT_ALT', col= 'sex',row='DRK_YN'
)
```

```
<seaborn.axisgrid.FacetGrid at 0x1942925d950>
```



Interpretations

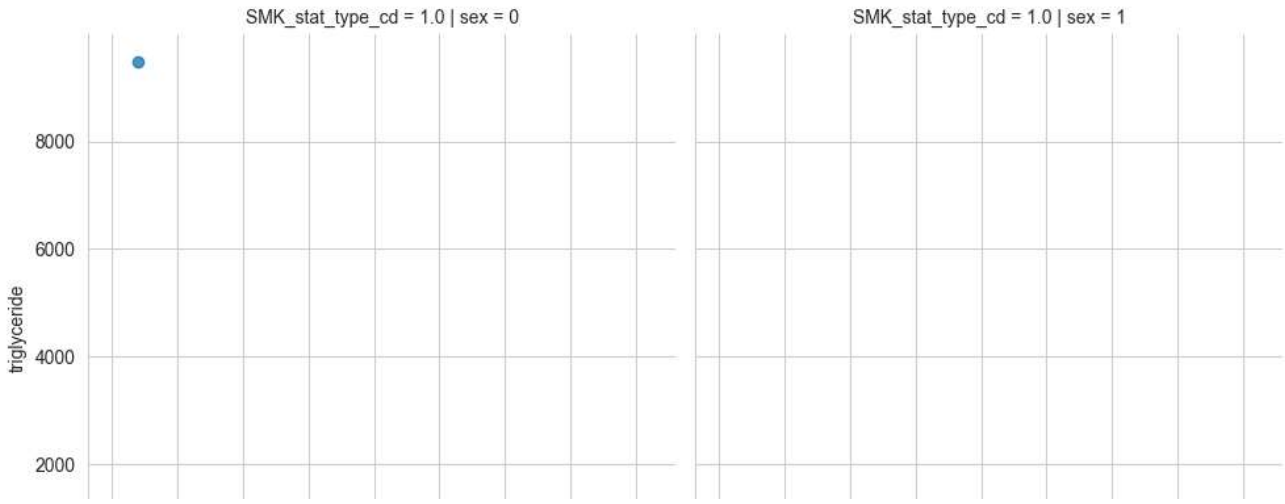
- Drinkers SGOT_ALT is high in male then female
- In non drinkers presence of SGOT_ALT is almost same

```
print('Total columns')
for colum in df.columns:
    print(colum, end = '\t')
```

```
Total columns
sex	age	weight	sight_left	sight_right	hear_left	DBP	BLDS	HDL_chole	LDL_chole	triglyceride
```

```
  # Bivariate analysis
sns.lmplot(
        data = df , x = 'serum_creatinine' ,y = 'triglyceride', col='sex' , hue='DRK_YN' , row='SMK_stat_type_cd'
    )
```

```
<seaborn.axisgrid.FacetGrid at 0x1940739a690>
```



Conclusion

- Analysis is not going good because of some outliers.
- It would be better to deal with outliers first

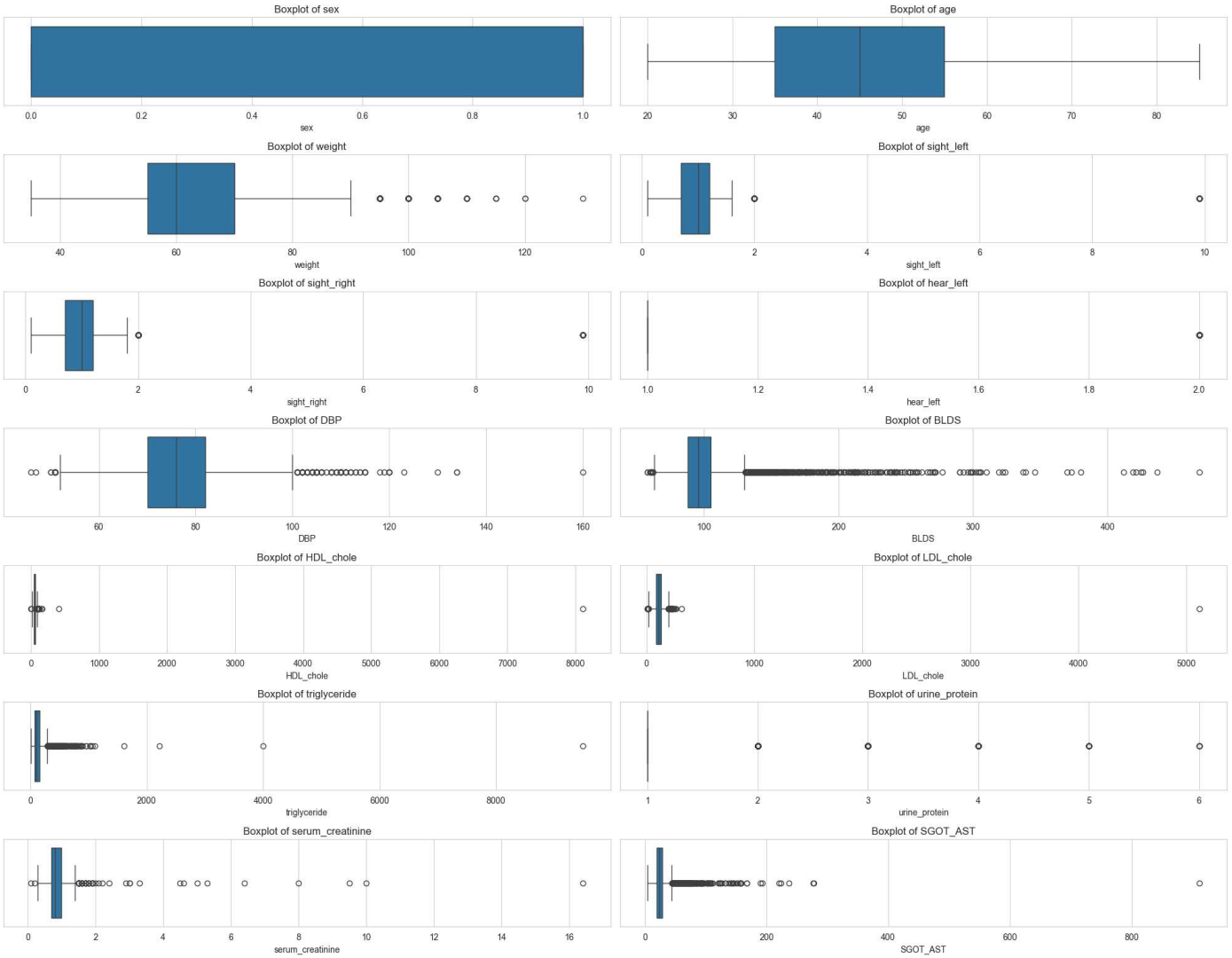
SMK_stat_type_cd = 2.0 | sex = 0 SMK_stat_type_cd = 2.0 | sex = 1

Dealing with Outliers

```
def plot_boxplots(dataframe):
    num_columns = dataframe.select_dtypes(include=['number']).columns
    print(num_columns)
    num_plots = len(num_columns)
    rows = (num_plots + 1) // 2

    fig, axes = plt.subplots(nrows=rows, ncols=2, figsize=(20, 20))

    for i, column in enumerate(num_columns):
        row = i // 2
        col = i % 2
        ax = axes[row, col]
        sns.boxplot(x=dataframe[column], ax=ax)
        ax.set_title(f"Boxplot of {column}")
        ax.set_xlabel(column)

    plt.tight_layout()
    plt.show()
```

```
plot_boxplots(df)
```

```
Index(['sex', 'age', 'weight', 'sight_left', 'sight_right', 'hear_left', 'DBP',
       'BLDS', 'HDL_chole', 'LDL_chole', 'triglyceride', 'urine_protein',
       'serum_creatinine', 'SGOT_AST', 'SGOT_ALT', 'gamma_GTP',
       'SMK_stat_type_cd', 'DRK_YN'],
      dtype='object')
```



What to remove

- Weights greater than 120
- sight_left >= 2 (same for sight_right)
- DBP > 120
- BLDS > 350
- HDL_chole, which is maximum
- LDL_chole, which is maximum
- triglyceride , >= 4th largest
- serum >=8
- SGOT_AST > 200 (same for SGOT_ALT)
- gamma_GTP > 600

Dropping outlier values at some extent(Not all)

Imp - Removing all outliers can significantly impact the model becuase of the Information loss

```
rows_before_drop = len(df)
print('Total rows before dropping outliers {}'.format(len(df)))
```

```
Total rows before dropping outliers 9000
```

Removing the outliers process begins

```
print('Total Rows before removing outliers {}'.format(len(df)))
df.drop(df['weight'].loc[df['weight'] >= 120].index,inplace=True)
print('Total Rows after removing outliers {}'.format(len(df)))
print(df.shape)
```

```
Total Rows before removing outliers 9000
Total Rows after removing outliers 8997
(8997, 18)
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['sight_right'].loc[df['sight_right'] >=2]))
df.drop(df['sight_right'].loc[df['sight_right'] >=2].index,inplace = True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8997
106
Total Rows after removing outliers 8891
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['sight_left'].loc[df['sight_left'] >=2]))
df.drop(df['sight_left'].loc[df['sight_left'] >=2].index ,inplace =True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8891
75
Total Rows after removing outliers 8816
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['DBP'].loc[df['DBP'] > 120]))
df.drop(df['DBP'].loc[df['DBP'] > 120].index, inplace=True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8816
5
Total Rows after removing outliers 8811
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['BLDS'].loc[df['BLDS'] > 350]))
df.drop(df['BLDS'].loc[df['BLDS'] > 350].index, inplace =True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8811
10
Total Rows after removing outliers 8801
```

```
max_value = df['LDL_chole'].loc[df['LDL_chole'].values.max()]
print(len(df['LDL_chole'].loc[df['LDL_chole'] == max_value]))
df.drop(df['LDL_chole'].loc[df['LDL_chole'] == max_value].index, inplace = True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
108
Total Rows after removing outliers 8693
```

```
max_value = df['HDL_chole'].loc[df['HDL_chole'].values.max()]
print(len(df['HDL_chole']))
print(len(df['HDL_chole'].loc[df['HDL_chole'] == max_value]))
df.drop(df['HDL_chole'].loc[df['HDL_chole'] == max_value].index, inplace = True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
8693
225
Total Rows after removing outliers 8468
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
df.drop(df.nlargest(4,'triglyceride').index,inplace = True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8468
Total Rows after removing outliers 8464
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['serum_creatinine'].loc[df['serum_creatinine'] >=8]))
df.drop(df['serum_creatinine'].loc[df['serum_creatinine'] >=8].index, inplace = True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8464
4
Total Rows after removing outliers 8460
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['SGOT_AST'].loc[df['SGOT_AST'] >= 200]))
df.drop(df['SGOT_AST'].loc[df['SGOT_AST'] >= 200].index,inplace =True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8460
6
Total Rows after removing outliers 8454
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['SGOT_ALT'].loc[df['SGOT_ALT'] >= 200]))
df.drop(df['SGOT_ALT'].loc[df['SGOT_ALT'] >= 200].index,inplace =True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8454
5
Total Rows after removing outliers 8449
```

```
print('Total Rows before removing outliers {}'.format(len(df)))
print(len(df['gamma_GTP'].loc[df['gamma_GTP'] > 600]))
df.drop(df['gamma_GTP'].loc[df['gamma_GTP'] > 600].index ,inplace = True)
print('Total Rows after removing outliers {}'.format(len(df)))
```

```
Total Rows before removing outliers 8449
8
Total Rows after removing outliers 8441
```

```
print('Total rows after removing the outliers {}'.format(len(df)))
rows_after_drop = len(df)
```

```
Total rows after removing the outliers 8441
```

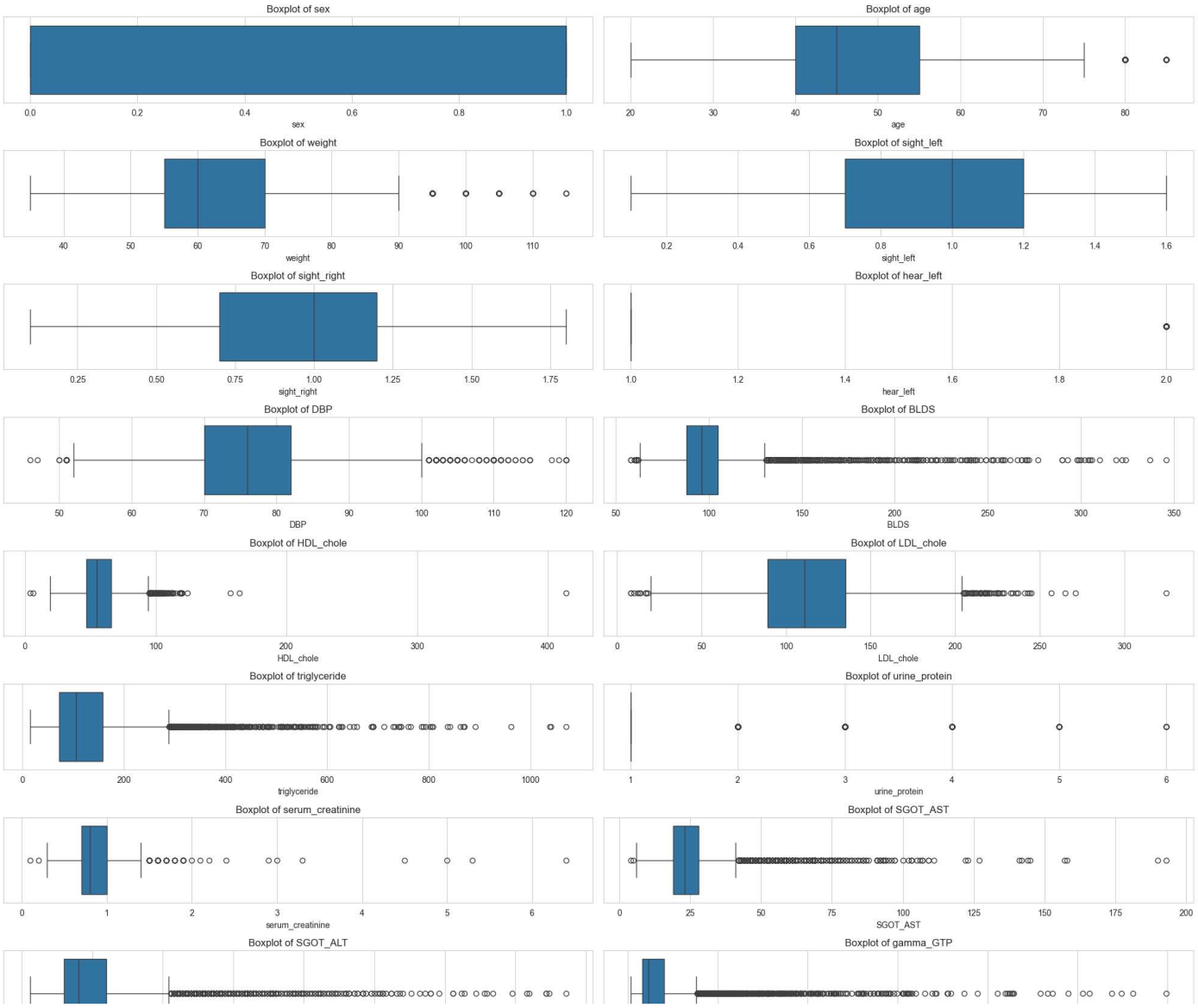
```
print('Toal {} row containing outliers are removed'.format(rows_before_drop - rows_after_drop))
```

```
Toal 559 row containing outliers are removed
```

Visuals after removing outliers

```
plot_boxplots(df)
```

```
Index(['sex', 'age', 'weight', 'sight_left', 'sight_right', 'hear_left', 'DBP',
       'BLDS', 'HDL_chole', 'LDL_chole', 'triglyceride', 'urine_protein',
       'serum_creatinine', 'SGOT_AST', 'SGOT_ALT', 'gamma_GTP',
       'SMK_stat_type_cd', 'DRK_YN'],
      dtype='object')
```

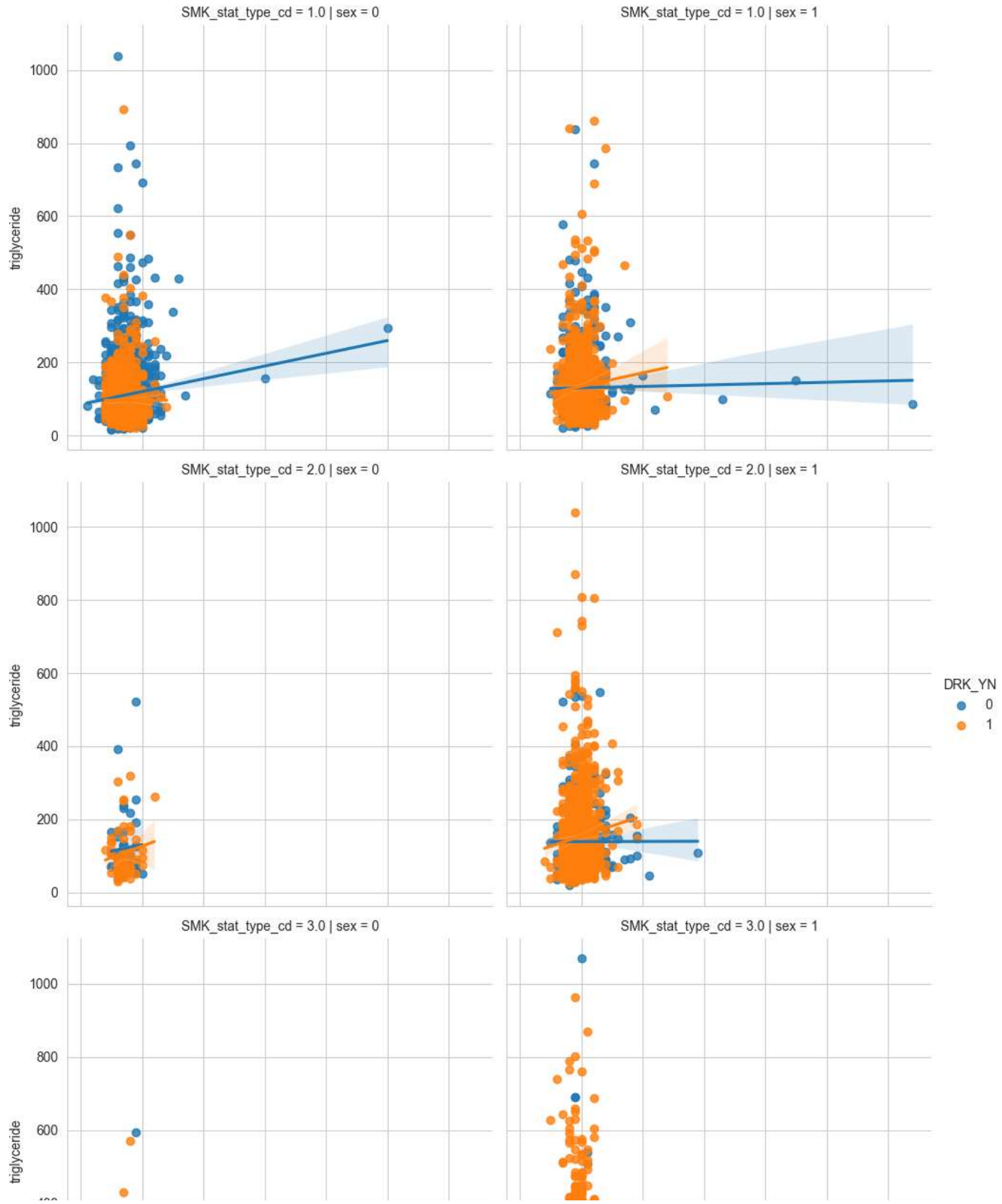


Interpretations

- Still some outliers are present in the dataset, Otherwise we would have lost the important information about dataset
- *Future operations**
- Will scaledown the values so that outliers effect can be reduced


```
# Bivariate analysis
sns.lmplot(
    data = df , x = 'serum_creatinine' ,y = 'triglyceride', col='sex' , hue='DRK_YN' , row='SMK_stat_type_cd'
)
```

```
<seaborn.axisgrid.FacetGrid at 0x19429255050>
```



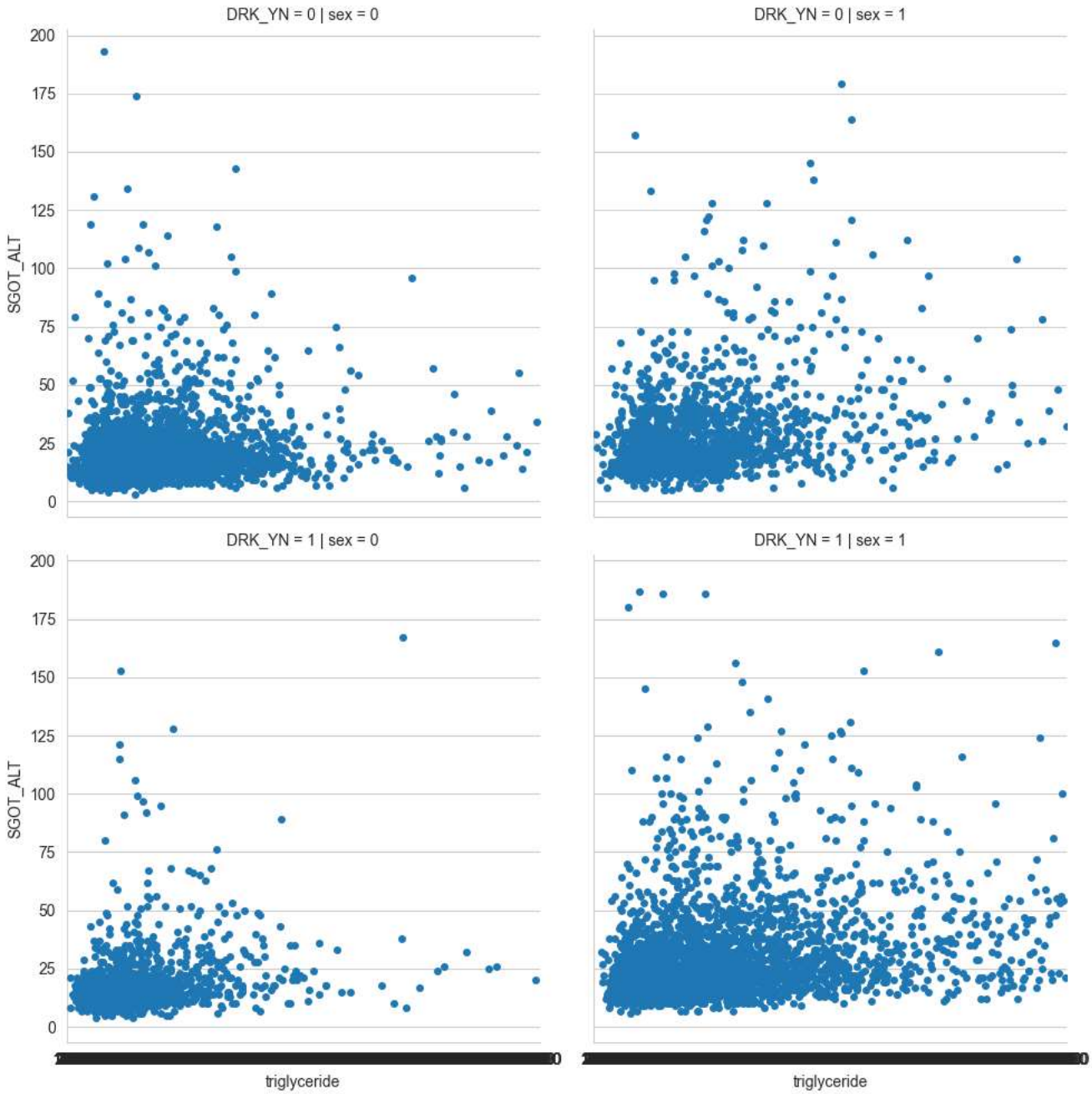
Interpretations

- According to report , "trend of **increased** cTG was observed in men with moderate and high alcohol intake after dinner and at bedtime (p for trend <0.001) which persisted after adjustment for age, smoking and body mass index"
- **What relationship creatinine holds with drinking habits?**
- Adults with a higher weekly alcohol consumption had significantly **lower** levels of creatine
- ** How smoking habit is associated with triglyceride ?

- According to reports, "We examined the relationships of cigarette smoking with fasting triglycerides, total cholesterol, and high-density lipoprotein cholesterol (HDL-C) levels among a group of 191 white women aged 20 to 40 years. The mean triglyceride level among current smokers was 100.0 mg/100 ml and among nonsmokers was 68.4 mg/dl (p less than 0.005). "
- **Some interpretations we can match with the actual reports are -**
- Females usually holds less concentration of triglyceride than males
- High triglyceride in smokers especially in male than female(fig, reference - [3,1])
- **Some authentic references of the quoted experiments are -**
- ref1 - "https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3875928/"
- ref2 - "https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6961205/#:~:text=Crucially%2C%20adults%20with%20a%20higher,deficit%20in%20their%20hippocampal%20metabolism."
- ref3 - "https://pubmed.ncbi.nlm.nih.gov/6829404/"
-

```
sns.catplot(
    data  =df ,x = 'triglyceride',y= 'SGOT_ALT', col= 'sex',row='DRK_YN'
)
```

```
<seaborn.axisgrid.FacetGrid at 0x1944f95a5d0>
```



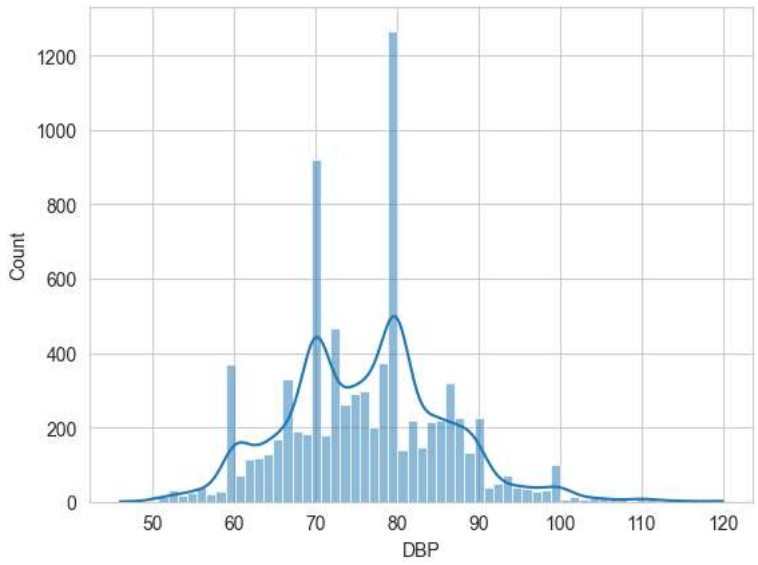
Interpretations

- High SGOT_ALT for the male then female
- And for Drinkers above interpretation holds more strongly
-

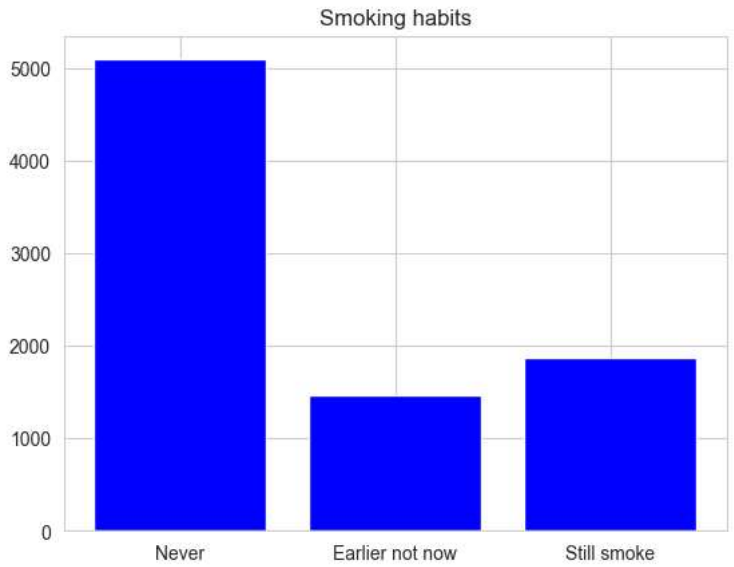
Frequency distributions of feaures

```
sns.histplot(
    data = df , x='DBP', kde =True , multiple='stack'
)
```

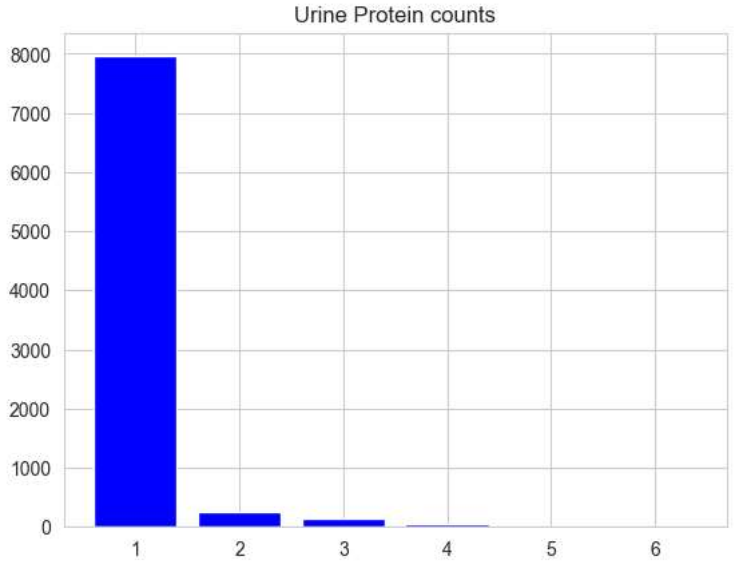
```
<Axes: xlabel='DBP', ylabel='Count'>
```




```
df['SMK_stat_type_cd'].value_counts()
x_axis = df['SMK_stat_type_cd'].value_counts().index
y_axis = df['SMK_stat_type_cd'].value_counts().values
category_labels  = {1.0 : 'Never', 2.0 : 'Earlier not now',3.0 : 'Still smoke'}
plt.bar(x_axis,y_axis, color = 'blue' , tick_label=[category_labels[x] for x in x_axis])
plt.title('Smoking habits')
legend_labels = [f'{int(x)}: {category_labels[x]}' for x in x_axis]
plt.show()
```

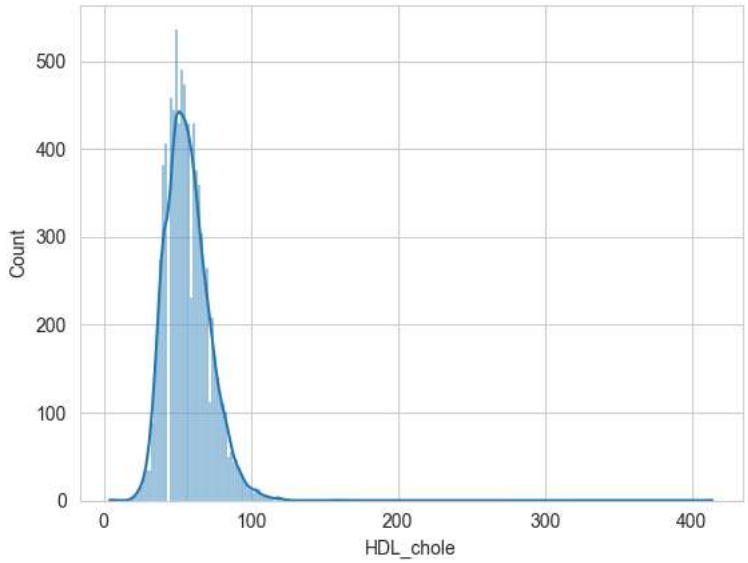


```
df['urine_protein'].value_counts()
x_axis = df['urine_protein'].value_counts().index
y_axis = df['urine_protein'].value_counts().values
plt.bar(x_axis,y_axis, color = 'blue')
plt.title('Urine Protein counts')
plt.show()
```



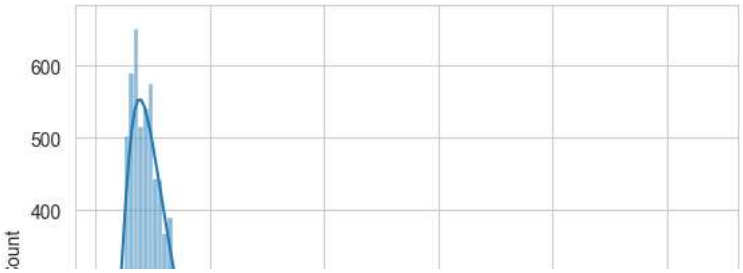

```
sns.histplot(
    data = df , x='HDL_chole', kde =True , multiple='stack'
)
```

```
<Axes: xlabel='HDL_chole', ylabel='Count'>
```




```
sns.histplot(
    data = df , x='triglyceride', kde =True , multiple='stack'
)
```

```
<Axes: xlabel='triglyceride', ylabel='Count'>
```



Conclusion

- There is obviously many outliers in the dataset

Feature scaling(Normalization) and Labelencoding

What is Feature scaling? What is the role of feature scaling in machine learning? *Before feeding data into the machine learning models, We need to make sure that data should be scaled properly. Process of scaling feature values is known as feature scaling Real-world datasets often contain features that are varying in degrees of magnitude, range, and units. Without scaling down the values , model can generate non accurate results.*

```
encoder = LabelEncoder()
## converting 'sex' feature into numerical
df['sex'] = encoder.fit_transform(df['sex'])
df['DRK_YN'] = encoder.fit_transform(df['DRK_YN'])

## Normalizing all the features
normalize = Normalizer()
normalized_without_output_feature = df.drop(['DRK_YN',],axis= 1)
normalize.fit(normalized_without_output_feature)
normalized = normalize.transform(normalized_without_output_feature)
X_normalized = pd.DataFrame(normalized,columns=df.columns[:-1])
```

How normalized data looks like

```
X_normalized
```

	sex	age	weight	sight_left	sight_right	hear_left	DBP	BLDS	HDL_chole	LDL_chole	triglyceride	urine_prote
0	0.004345	0.152076	0.325878	0.004345	0.004345	0.004345	0.347603	0.430158	0.208562	0.547474	0.399743	0.0043
1	0.003856	0.115667	0.308446	0.003470	0.004627	0.003856	0.316157	0.408691	0.212057	0.570625	0.466525	0.0038
2	0.004585	0.183402	0.343879	0.005502	0.006878	0.004585	0.320954	0.449336	0.187987	0.339294	0.476846	0.0045
3	0.004239	0.211948	0.339117	0.006358	0.005087	0.004239	0.368790	0.402702	0.322161	0.440853	0.449330	0.0042
4	0.004369	0.218451	0.262141	0.004369	0.005243	0.004369	0.358259	0.441271	0.266510	0.511175	0.454378	0.0043
...	...	...	...	...	...	...	...	...	...	...	...	
8995	0.000000	0.292736	0.209097	0.002091	0.002509	0.004182	0.271827	0.518561	0.242553	0.246735	0.602200	0.0041
8996	0.003089	0.138991	0.216208	0.003706	0.003706	0.003089	0.191498	0.284159	0.138991	0.509632	0.568317	0.0030
8997	0.000000	0.194023	0.155218	0.003880	0.003492	0.003880	0.353122	0.504460	0.275513	0.628634	0.271632	0.0038
8998	0.003858	0.135019	0.231461	0.004629	0.005787	0.003858	0.293184	0.432061	0.231461	0.246892	0.721387	0.0038
8999	0.002862	0.200312	0.228928	0.002575	0.002862	0.002862	0.197450	0.432101	0.120187	0.271852	0.752600	0.0085

9000 rows × 17 columns

```
y = df[['DRK_YN']]

print('Shape of X_normalized {}'.format(X_normalized.shape))
print('Shape of y(output feature) {}'.format(y.shape))
```

```
Shape of X_normalized (9000, 17)
Shape of y(output feature) (9000, 1)
```

```
print('dimension of X_normalized {}'.format(X_normalized.ndim))
print('Dimension of y(output feature) {}'.format(y.ndim))
```

```
dimension of X_normalized 2
Dimension of y(output feature) 2
```

Checks

- Checked missing(null) values ✅
- Checked duplicate values ✅
- Multicollinearity ✅
- Removed Unwanted features ✅
- Removed Outliers ✅
- Encoded 'sex' feature ✅
- Normalized dataset ✅

Splitting

```
X_train,X_test,y_train,y_test = train_test_split(X_normalized,y,random_state=42)
```

Approach -

1. Train all the models with normalized dataset
2. Check the accuracy of all the models
3. Compare all the models
4. Choose one which shows the best accuracy on test dataset
5. Repeat the same proces without normalized dataset

My first model | branch name - 'main (github link - 'https://github.com/codedestructed007/Drink_watch/tree/main')

Model 1. - Hypertuning on all the algorithms

```
# instantiating the models
def model_implementation_normalized_dataset(X_train,X_test,y_train,y_test):
    svc = SVC()
    dtc = DecisionTreeClassifier()
    ada_boost = AdaBoostClassifier()
    rfclf = RandomForestClassifier()
    Knn = KNeighborsClassifier()
    lr = LogisticRegression()
    xgb = XGBClassifier()

    classifiers = {
        'SVC': svc,
        'DecisionTreeClassifier': dtc,
        'AdaBoostClassifier': ada_boost,
        'RandomForestClassifier': rfclf,
        'KNeighborsClassifier': Knn,
        'LogisticRegression': lr,
        'XGBClassifier' : xgb
    }
    accuracy_score_train = []
    accuracy_score_test = []
    algorithms = []
    mse_train = []
    mse_test = []
    parameters = {
        'SVC' : {
            'C' : [0.7 , 1.0 , 1.3],
```

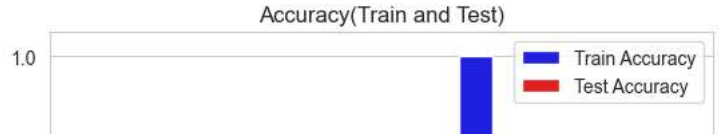
```
            'kernel' : ['linear','poly','rbf'],
            'gamma' : ['scale','auto']
        },
        'DecisionTreeClassifier' : {
            'criterion' : ['gini','entropy'],
            'splitter' : ['best','random'],
            'max_depth' : [1,3,5,8]
        },
        'AdaBoostClassifier' : {
            'n_estimators' : [50,80,100,120],
            'learning_rate' : [0.7 , 1.0 , 1.3],
            'algorithm' : ['SAMME','SAMME.R']
        },
        'RandomForestClassifier' : {
            'n_estimators' : [80,100,120],
            'criterion' : ['gini','entropy','log_loss'],
            'max_depth' : [3,5,7,8,None]
        },
        'KNeighborsClassifier' : {
            'n_neighbors' : [2,3,5,6,7],
            'weights' : ['uniform','distance'],
            'algorithm' : ['auto','ball_tree','kd_tree']
        },
        'LogisticRegression' : {
            'penalty' : ['l1','l2','elasticnet'],
            'C' : [0.6,0.9,1,1.3],

        },
        'XGBClassifier' : {
            'n_estimators' : [1,2,4,6],
            'max_depth' : [1,3,4,5],
            'learning_rate' : [0.7 , 1.0, 1.3]
        }
    }
    for obj, algos in classifiers.items():
        algorithms.append(obj)
        params = parameters[obj]

        ## Hypertuning begins
        clf = GridSearchCV(estimator=algos,param_grid=params,cv = 5,scoring='accuracy')
        clf.fit(X_train,y_train)
        best_parameters = clf.best_params_
        # Get the best parameters
        algos.set_params(**best_parameters)
        algos.fit(X_train,y_train)
        train_pred = algos.predict(X_train)
        test_pred = algos.predict(X_test)
        accuracy_score_train.append(accuracy_score(y_train,train_pred))
        accuracy_score_test.append(accuracy_score(y_test,test_pred))
        mse_train.append(mean_squared_error(y_train,train_pred))
        mse_test.append(mean_squared_error(y_test, test_pred))
    result_full_features = pd.DataFrame(
        {
            'Algorithm' : algorithms,
            'Accuracy(train)' : accuracy_score_train,
            'Accuracy(test)' : accuracy_score_test,
            'MSE(train)' : mse_train,
            'MSE(test)': mse_test
        }
    )
    return result_full_features


normalized_accuracy_result = model_implementation_normalized_dataset(X_train, X_test, y_train, y_test)


normalized_accuracy_result
```

	Algorithm	Accuracy(train)	Accuracy(test)	MSE(train)	MSE(test)
0	SVC	0.721037	0.710667	0.278963	0.289333
5	LogisticRegression	0.697481	0.691556	0.302519	0.308444

Conclusion

- RandomForestClassifer, SVC and AdaBoost performs better than remaining.
- KNeighborsClassifier is totally overfit model
- We should check without normalized dataset

```
import seaborn as sns
import matplotlib.pyplot as plt

# Assuming you have imported 'result_full_features' properly

# Create the figure and axes
fig, ax = plt.subplots()

# Set the width of each bar
bar_width = 0.35

# Create positions for the bars
x = range(len(normalized_accuracy_result['Algorithm']))

# Plot train accuracy
sns.barplot(
    x=x, y='Accuracy(train)', data=normalized_accuracy_result,
    color='blue', label='Train Accuracy', ax=ax, width=bar_width
)

# Plot test accuracy
sns.barplot(
    x=x, y='Accuracy(test)', data=normalized_accuracy_result,
    color='red', label='Test Accuracy', ax=ax, width=bar_width
)

# Set the plot title
ax.set_title('Accuracy(Train and Test)')

# Set x-axis labels and rotate them for better readability
ax.set_xticks(x)
ax.set_xticklabels(normalized_accuracy_result['Algorithm'], rotation=90)

# Show a legend
ax.legend()

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



without normalizing the dataset

Label encoding on output feature

```
df['DRK_YN'] = encoder.fit_transform(df['DRK_YN'])
```

```
df.head()
```

	sex	age	weight	sight_left	sight_right	hear_left	DBP	BLDS	HDL_chole	LDL_chole	triglyceride	urine_protein	serum_creatinine
0	1	35	75	1.0	1.0	1.0	80.0	99.0	48.0	126.0	92.0	1.0	1.0
1	1	30	80	0.9	1.2	1.0	82.0	106.0	55.0	148.0	121.0	1.0	0.9
2	1	40	75	1.2	1.5	1.0	70.0	98.0	41.0	74.0	104.0	1.0	0.9
3	1	50	80	1.5	1.2	1.0	87.0	95.0	76.0	104.0	106.0	1.0	1.1
4	1	50	60	1.0	1.2	1.0	82.0	101.0	61.0	117.0	104.0	1.0	0.8

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

```
0
```

```
df.duplicated().any()
```

```
False
```

```
df.info()
```

```
X,y = df.iloc[:,:-1],df[['DRK_YN']]
```

```
X.shape
```

```
(9000, 17)
```

```
y.shape
```

```
(9000, 1)
```

Checklist

- Missing values ✅
- Duplicate rows ✅
- No object datatype ✅
- Outliers removed ✅
- Then we are good to go 😊

Splitting into X_train,X_test, y_train,y_test

```
## Train test split
X_train,X_test,y_train,y_test= train_test_split(X,y,random_state=42)
```

```
# Create a list of dataset names
dataset_names = ['X_train', 'X_test', 'y_train', 'y_test']

# Create a list of your datasets
allsets = [X_train, X_test, y_train, y_test]
```

```
# Iterate over both the names and datasets
for name, dataset in zip(dataset_names, allsets):
    print(name)
    print('Total rows {} total columns {}'.format(len(dataset), len(dataset.columns)))
    print('Shape {}'.format(dataset.shape))
    print('Dimension {}'.format(dataset.ndim))
```

```
 X_train
 Total rows 6750 total columns 17
 Shape (6750, 17)
 Dimension 2
 X_test
 Total rows 2250 total columns 17
 Shape (2250, 17)
 Dimension 2
 y_train
 Total rows 6750 total columns 1
 Shape (6750, 1)
 Dimension 2
 y_test
 Total rows 2250 total columns 1
 Shape (2250, 1)
 Dimension 2
```

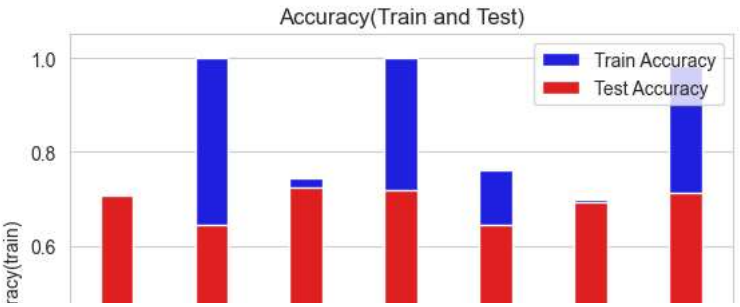
```
# instantiating the models
def model_implementation_without_normalized_dataset(X_train,X_test,y_train,y_test):
    svc = SVC()
    dtc = DecisionTreeClassifier()
    ada_boost = AdaBoostClassifier()
    rfclf = RandomForestClassifier()
    Knn = KNeighborsClassifier()
    lr = LogisticRegression()
    xgb = XGBClassifier()

    classifiers = {
        'SVC': svc,
        'DecisionTreeClassifier': dtc,
        'AdaBoostClassifier': ada_boost,
        'RandomForestClassifier': rfclf,
        'KNeighborsClassifier': Knn,
        'LogisticRegression': lr,
        'XGBClassifier' : xgb
    }
    accuracy_score_train = []
    accuracy_score_test = []
    algorithms = []
    mse_train = []
    mse_test = []

    for obj, algos in classifiers.items():
        algorithms.append(obj)
        algos.fit(X_train,y_train)
        train_pred = algos.predict(X_train)
        test_pred = algos.predict(X_test)
        accuracy_score_train.append(accuracy_score(y_train,train_pred))
        accuracy_score_test.append(accuracy_score(y_test,test_pred))
        mse_train.append(mean_squared_error(y_train,train_pred))
        mse_test.append(mean_squared_error(y_test, test_pred))
    result_full_features = pd.DataFrame(
        {
            'Algorithm' : algorithms,
            'Accuracy(train)' : accuracy_score_train,
            'Accuracy(test)' : accuracy_score_test,
            'MSE(train)' : mse_train,
            'MSE(test)': mse_test
        }
    )
    return result_full_features


result = model_implementation_without_normalized_dataset(X_train,X_test,y_train,y_test)


result
```

	Algorithm	Accuracy(train)	Accuracy(test)	MSE(train)	MSE(test)
0	SVC	0.709185	0.708444	0.290815	0.291556
1	DecisionTreeClassifier	1.000000	0.645778	0.000000	0.354222
2	AdaBoostClassifier	0.743407	0.723111	0.256593	0.276889
3	RandomForestClassifier	1.000000	0.720000	0.000000	0.280000
4	KNeighborsClassifier	0.761926	0.644444	0.238074	0.355556
5	LogisticRegression	0.697778	0.692000	0.302222	0.308000

Conclusion

- AdaBoostClassifier is giving the best model among all the others model
- Even LogisticRegression has shown its consistency in both train and in test score same with SV
- **Further move**
- Will go forward with AdaBoostClassifer and again see the accuracy after Hypertuning on this model

```
import seaborn as sns
import matplotlib.pyplot as plt

# Create the figure and axes
fig, ax = plt.subplots()

# Set the width of each bar
bar_width = 0.35

# Create positions for the bars
x = range(len(result['Algorithm']))

# Plot train accuracy
sns.barplot(
    x=x, y='Accuracy(train)', data=result,
    color='blue', label='Train Accuracy', ax=ax, width=bar_width
)

# Plot test accuracy
sns.barplot(
    x=x, y='Accuracy(test)', data=result,
    color='red', label='Test Accuracy', ax=ax, width=bar_width
)

# Set the plot title
ax.set_title('Accuracy(Train and Test)')

# Set x-axis labels and rotate them for better readability
ax.set_xticks(x)
ax.set_xticklabels(result['Algorithm'], rotation=90)

# Show a legend
ax.legend()

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



Hypertuning on AdaBoostClassifier

```
parameters  = {
    'n_estimators' : [50,70,80,100,120],
    'learning_rate' : [0.7 ,0.9, 1.0 ,1.15, 1.3],
    'algorithm' : ['SAMME','SAMME.R']
}
```

```
def hypertuned_ada(X_train,X_test,y_train,y_test):
    ada = AdaBoostClassifier()
    params = parameters
    clf = GridSearchCV(ada,params,cv=5,verbose=3,scoring='accuracy')
    clf.fit(X_train,y_train)
    ada = AdaBoostClassifier(**clf.best_params_)
    ada.fit(X_train,y_train)
    return ada


ada = hypertuned_ada(X_train,X_test,y_train,y_test)
```

```
Fitting 5 folds for each of 50 candidates, totalling 250 fits
[CV 1/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=50;, score=0.736 total time=   1.9s
[CV 2/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=50;, score=0.728 total time=   2.0s
[CV 3/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=50;, score=0.725 total time=   1.6s
[CV 4/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=50;, score=0.712 total time=   1.6s
[CV 5/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=50;, score=0.727 total time=   1.6s
[CV 1/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=70;, score=0.732 total time=   2.3s
[CV 2/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=70;, score=0.726 total time=   2.3s
[CV 3/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=70;, score=0.721 total time=   2.3s
[CV 4/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=70;, score=0.711 total time=   2.4s
[CV 5/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=70;, score=0.723 total time=   2.4s
[CV 1/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=80;, score=0.733 total time=   2.6s
[CV 2/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=80;, score=0.727 total time=   2.7s
[CV 3/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=80;, score=0.721 total time=   2.8s
[CV 4/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=80;, score=0.711 total time=   2.8s
[CV 5/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=80;, score=0.715 total time=   3.1s
[CV 1/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=100;, score=0.733 total time=   3.5s
[CV 2/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=100;, score=0.724 total time=   3.7s
[CV 3/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=100;, score=0.721 total time=   3.3s
[CV 4/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=100;, score=0.718 total time=   3.3s
[CV 5/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=100;, score=0.715 total time=   3.3s
[CV 1/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=120;, score=0.733 total time=   4.0s
[CV 2/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=120;, score=0.726 total time=   4.1s
[CV 3/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=120;, score=0.723 total time=   4.0s
[CV 4/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=120;, score=0.719 total time=   4.0s
[CV 5/5] END algorithm=SAMME, learning_rate=0.7, n_estimators=120;, score=0.709 total time=   4.1s
[CV 1/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=50;, score=0.737 total time=   1.6s
[CV 2/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=50;, score=0.725 total time=   1.7s
[CV 3/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=50;, score=0.727 total time=   1.6s
[CV 4/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=50;, score=0.710 total time=   1.6s
[CV 5/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=50;, score=0.723 total time=   1.6s
[CV 1/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=70;, score=0.731 total time=   2.3s
[CV 2/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=70;, score=0.726 total time=   2.3s
[CV 3/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=70;, score=0.728 total time=   2.4s
[CV 4/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=70;, score=0.710 total time=   2.3s
[CV 5/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=70;, score=0.718 total time=   2.3s
[CV 1/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=80;, score=0.731 total time=   2.7s
[CV 2/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=80;, score=0.726 total time=   2.7s
[CV 3/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=80;, score=0.733 total time=   2.7s
[CV 4/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=80;, score=0.715 total time=   2.6s
[CV 5/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=80;, score=0.716 total time=   2.6s
[CV 1/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=100;, score=0.732 total time=   3.6s
[CV 2/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=100;, score=0.726 total time=   3.4s
[CV 3/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=100;, score=0.728 total time=   3.3s
[CV 4/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=100;, score=0.716 total time=   3.4s
[CV 5/5] END algorithm=SAMME, learning_rate=0.9, n_estimators=100;, score=0.721 total time=   3.3s
```