CA4 - Liver Disease Prediction

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Imports

```
# Importing Libaries
# ========================
import matplotlib.pyplot as plt
from sklearn.metrics import ConfusionMatrixDisplay
import pandas as pd
import numpy as np
import seaborn as sns
from sklearn.impute import SimpleImputer

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score

from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC

from sklearn.decomposition import PCA
from sklearn.model_selection import GridSearchCV
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline
from sklearn.metrics import confusion_matrix
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
as LDA

from sklearn.metrics import roc_curve, auc
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import cross_val_predict
```

Reading data

```
# Loading the dataset
# ========================
df_train = pd.read_csv('train.csv', index_col=0)
df_test = pd.read_csv('test.csv', index_col=0)
```

Data exploration and visualisation

```
#Cheking for missing data
# =========================
null_counts = df_train.isnull().sum().sum()
print(f'Total Missing values: {null_counts}' )

Total Missing values: 0

# Checking the info of the dataset
# ==================================
df_train.info()

<class 'pandas.core.frame.DataFrame'>
Index: 703 entries, 0 to 702
Data columns (total 32 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   index                        703 non-null    int64
 1   AFP (ng/mL)                  703 non-null    float64
 2   ALP (U/L)                    703 non-null    float64
 3   ALT (U/L)                    703 non-null    float64
 4   AST (U/L)                    703 non-null    float64
 5   Age                          703 non-null    int64
 6   Albumin (g/dL)               703 non-null    float64
 7   Alcohol_Use (yes/no)         703 non-null    object
 8   Bilirubin (mg/dL)            703 non-null    float64
 9   CRP (mg/L)                   703 non-null    float64
 10  Diabetes (yes/no)            703 non-null    object
 11  Fibroscan (kPa)              703 non-null    float64
 12  GGT (U/L)                    703 non-null    float64
 13  Gender                       703 non-null    object
 14  Hemoglobin (g/dL)            703 non-null    float64
 15  IL-6 (pg/mL)                 703 non-null    float64
 16  Obesity (yes/no)             703 non-null    object
 17  PT/INR                       703 non-null    float64
 18  Platelets (10^9/L)           703 non-null    float64
 19  RBC (10^12/L)                703 non-null    float64
 20  Serum_Ammonia (μmol/L)       703 non-null    float64
 21  Serum_Copper (μg/dL)         703 non-null    float64
 22  Serum_Creatinine (mg/dL)     703 non-null    float64
 23  Serum_Iron (μg/dL)           703 non-null    float64
 24  Serum_Lactate (mmol/L)       703 non-null    float64
 25  Serum_Urea (mg/dL)           703 non-null    float64
 26  Serum_Zinc (μg/dL)           703 non-null    float64
 27  TIBC (μg/dL)                 703 non-null    float64
 28  Transferrin_Saturation (%)   703 non-null    float64
 29  WBC (10^9/L)                 703 non-null    float64
 30  pH                           703 non-null    float64
 31  Diagnosis                    703 non-null    object
dtypes: float64(25), int64(2), object(5)
memory usage: 181.2+ KB
```

```
# Printing the first 10 rows of the dataframe with head(10)
# ==========================================================
df_train.head(10)
```

```
   index  AFP (ng/mL)    ALP (U/L)   ALT (U/L)  AST (U/L)  Age  \
0   1124    13.571425  1653.138489   40.405592  45.598427    4
1   1188    13.649342  1940.518305   21.336986  34.064095   55
2    530    10.898943  1557.369920   29.665496  16.044488   30
3    686    13.872275  1273.840525  142.418649  64.204257    0
4    296    10.102457  1461.622515   22.437303  23.940205   59
5    663     5.824125  1921.018155   83.136847  39.372095   64
6     40    12.476249  2182.137388   97.396622  98.221842   29
7    889    11.157910  1804.807405   25.813858  59.671478   34
8    785     9.174636  1229.834674   27.789897  37.531030    3
9   1171    10.889718  1314.998314   33.851749  22.029857   50

   Albumin (g/dL) Alcohol_Use (yes/no)  Bilirubin (mg/dL)  CRP (mg/L)
...  \
0        4.477126                  yes           0.541997    1.002121
...
1        3.190724                  yes           1.199063    0.582746
...
2        4.506351                   no           0.740952    1.670375
...
3        3.665655                  yes           1.939879    1.220646
...
4        4.005109                   no           0.769535    0.139863
...
5        3.471696                   no           0.557283    8.021424
...
6        4.112928                   no           1.670063    1.209236
...
7        3.739201                  yes           0.549854    0.980465
...
8        4.359691                  yes           0.749890    3.311809
...
9        3.581977                  yes           0.833413    1.065233
...

  Serum_Creatinine (mg/dL)  Serum_Iron (µg/dL)  Serum_Lactate (mmol/L)
\
0                 2.569954           97.242495                2.923385

1                 3.024642          128.597676                2.719966

2                 2.219844           98.026938                3.267757

3                 1.704282           63.105133                1.937625

4                 2.656926           89.966713                1.979801
```

```
5                 2.770285           96.542657                  4.784693

6                 2.801148          152.299112                  1.687116

7                 1.855184           72.934571                  2.610542

8                 3.953037          125.110690                  2.343232

9                 2.329074           40.899839                  1.986068


  Serum_Urea (mg/dL)  Serum_Zinc (µg/dL)  TIBC (µg/dL)  \
0          26.696110           96.124260    315.439318
1          23.021218           50.554650    268.492437
2          20.123808           82.900681    312.107620
3          36.436855           72.360010    182.506010
4          20.036074           63.216136    212.261519
5          27.760083           80.140859    304.210829
6           7.641927           70.282273    341.402911
7          16.227916           85.302620    201.170284
8          18.905484           81.647554    296.340915
9          20.626322           62.711051    339.683427

  Transferrin_Saturation (%)  WBC (10^9/L)        pH  \
0                  30.827639      4.180007  6.163600
1                  47.896200      4.590995  5.244266
2                  31.408057      4.524580  5.769592
3                  34.577016      4.234483  5.982228
4                  42.384844      4.306892  4.837404
5                  31.735444      4.275489  5.187919
6                  44.609787      8.069525  7.183443
7                  36.255141      4.693278  7.304284
8                  42.218500      4.526654  6.785159
9                  12.040575      4.393664  5.718308

                   Diagnosis
0                    Healthy
1                  Cirrhosis
2                    Healthy
3  Drug-induced Liver Injury
4                    Healthy
5        Fatty Liver Disease
6                  Hepatitis
7        Fatty Liver Disease
8                    Healthy
9                    Healthy

[10 rows x 32 columns]
```

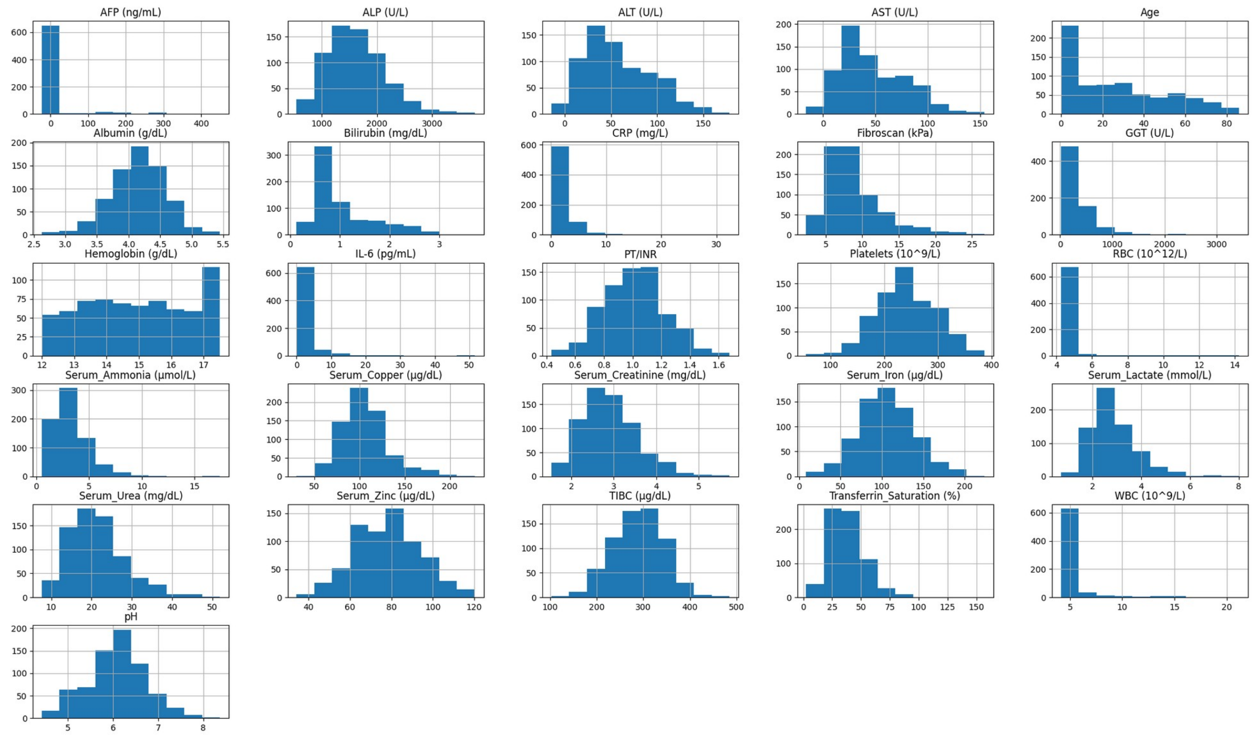
```
# Dropping the first column
# ===========================
df_train = df_train.drop('index', axis=1)

# Shwowing descriptive statistics of the dataset
# ================================================
df_train.describe()
```

```
       AFP (ng/mL)    ALP (U/L)   ALT (U/L)   AST (U/L)         Age  \
count   703.000000   703.000000  703.000000  703.000000  703.000000
mean     23.804227  1624.337402   58.262199   46.855946   27.206259
std      54.938736   517.367426   36.372428   30.838523   23.632185
min     -22.836893   546.609117  -14.313734  -16.215535    0.000000
25%       8.029213  1229.735749   29.939330   24.163363    5.000000
50%      10.195074  1553.771408   48.857238   38.720602   23.000000
75%      12.656547  1931.433883   84.583900   70.023374   45.000000
max     449.925304  3769.332343  178.226798  154.173314   86.000000

       Albumin (g/dL)  Bilirubin (mg/dL)  CRP (mg/L)  Fibroscan (kPa)  
\
count      703.000000         703.000000  703.000000       703.000000

mean         4.155568           1.056841    2.021190         8.899789

std          0.432317           0.617223    2.638333         3.822241

min          2.625845           0.130291    0.075035         2.323530

25%          3.880943           0.634089    0.651623         6.273365

50%          4.166995           0.801903    1.238123         7.966800

75%          4.437957           1.396853    2.449216        10.588808

max          5.447072           3.712815   32.356076        26.691648


         GGT (U/L)  ...  Serum_Copper (µg/dL)  Serum_Creatinine
(mg/dL)  \
count   703.000000  ...            703.000000
703.000000
mean    347.457426  ...            105.754889
2.901900
std     371.157528  ...             26.159403
0.647559
min      17.056568  ...             30.099096
1.525736
25%     131.695741  ...             88.632128
2.441051
50%     244.400101  ...            102.842960
2.844621
```

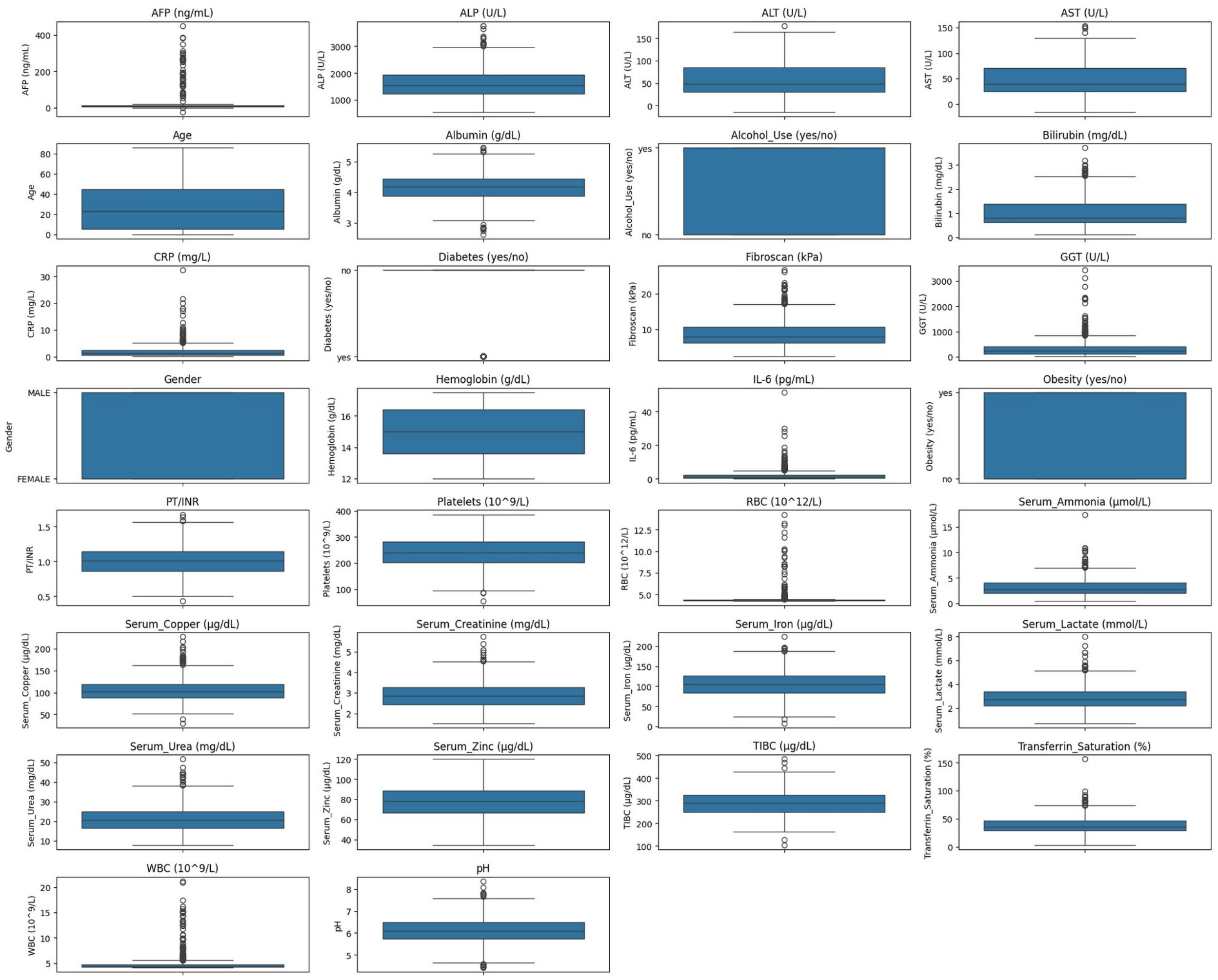
```
75%     419.660403  ...           118.722674
3.275906
max    3426.981860  ...           227.617474
5.729147

       Serum_Iron (µg/dL)  Serum_Lactate (mmol/L)  Serum_Urea (mg/dL)
\
count          703.000000              703.000000          703.000000

mean           105.901892                2.867523           21.440875

std             33.699054                0.936050            6.946169

min              8.328732                0.711997            7.641927

25%             84.737590                2.211484           16.422281

50%            104.670558                2.700933           20.668951

75%            125.937089                3.393898           25.096926

max            223.915730                8.010270           51.875943


       Serum_Zinc (µg/dL)  TIBC (µg/dL)  Transferrin_Saturation (%)  \
count          703.000000    703.000000                  703.000000
mean            78.021500    288.708468                   38.220427
std             15.826557     54.223207                   15.438507
min             34.170231    102.896996                    2.496813
25%             66.617374    248.832647                   28.598082
50%             78.024893    290.278094                   35.617342
75%             88.452369    326.508987                   46.630605
max            120.279580    484.581225                  156.858874

       WBC (10^9/L)          pH
count    703.000000  703.000000
mean       5.000254    6.072044
std        2.025527    0.642783
min        4.129884    4.416868
25%        4.243197    5.724293
50%        4.331605    6.085019
75%        4.762898    6.485114
max       21.195702    8.368522

[8 rows x 26 columns]
```

Histogram

```
# Plotting histograms for all columns in the dataset
# ====================================================
df_train.hist(bins=10, figsize=(26, 15))
plt.show()
```

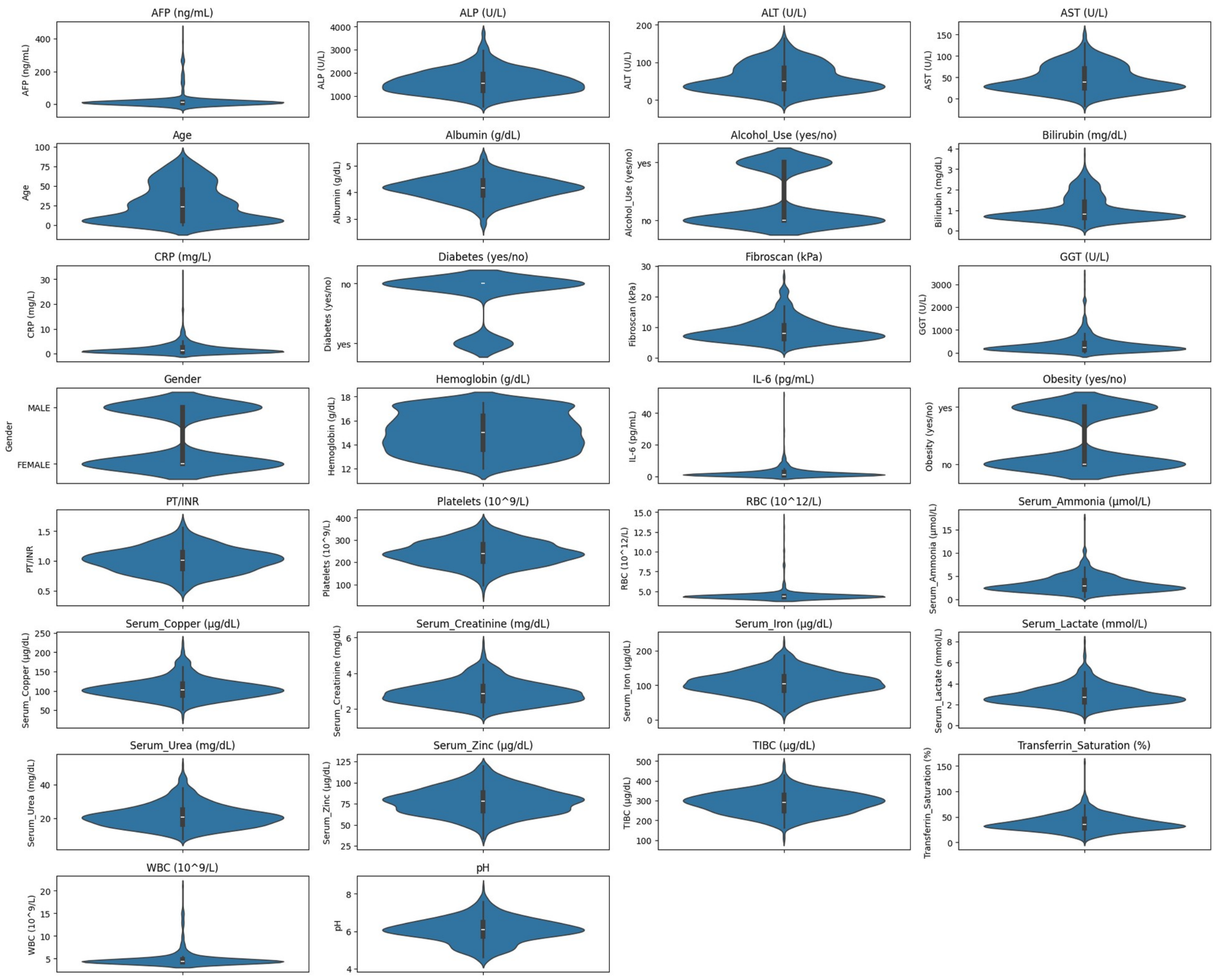


```
# Removing the target variable
# ==============================
features = df_train.columns[:-1]

plt.figure(figsize=(20, 60))

for i, column in enumerate(features):
    plt.subplot(len(features), 4, i + 1)
    sns.boxplot(y=df_train[column])
    plt.title(column)
    plt.tight_layout()

plt.show()
```



Violin Plots

```
# Removing the target variable
# ==============================
features = df_train.columns[:-1]

plt.figure(figsize=(20, 60))

for i, column in enumerate(features):
    plt.subplot(len(features), 4, i + 1)
    sns.violinplot(y=df_train[column])
    plt.title(column)

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



Data cleaning

```
# Coping the dataset
# ==================
df_train_copy = df_train.copy()

# printing the columns of the dataset
# ===================================
df_train_copy.info()

<class 'pandas.core.frame.DataFrame'>
Index: 703 entries, 0 to 702
Data columns (total 31 columns):
 #   Column                        Non-Null Count  Dtype
---  ------                        --------------  -----
 0   AFP (ng/mL)                   703 non-null    float64
 1   ALP (U/L)                     703 non-null    float64
 2   ALT (U/L)                     703 non-null    float64
 3   AST (U/L)                     703 non-null    float64
 4   Age                           703 non-null    int64
 5   Albumin (g/dL)                 703 non-null    float64
 6   Alcohol_Use (yes/no)           703 non-null    object
 7   Bilirubin (mg/dL)              703 non-null    float64
 8   CRP (mg/L)                     703 non-null    float64
 9   Diabetes (yes/no)              703 non-null    object
 10  Fibroscan (kPa)                703 non-null    float64
 11  GGT (U/L)                      703 non-null    float64
 12  Gender                         703 non-null    object
 13  Hemoglobin (g/dL)              703 non-null    float64
 14  IL-6 (pg/mL)                   703 non-null    float64
 15  Obesity (yes/no)               703 non-null    object
 16  PT/INR                         703 non-null    float64
 17  Platelets (10^9/L)             703 non-null    float64
 18  RBC (10^12/L)                  703 non-null    float64
 19  Serum_Ammonia (µmol/L)         703 non-null    float64
 20  Serum_Copper (µg/dL)           703 non-null    float64
 21  Serum_Creatinine (mg/dL)       703 non-null    float64
 22  Serum_Iron (µg/dL)             703 non-null    float64
 23  Serum_Lactate (mmol/L)         703 non-null    float64
 24  Serum_Urea (mg/dL)             703 non-null    float64
 25  Serum_Zinc (µg/dL)             703 non-null    float64
 26  TIBC (µg/dL)                   703 non-null    float64
 27  Transferrin_Saturation (%)     703 non-null    float64
 28  WBC (10^9/L)                   703 non-null    float64
 29  pH                             703 non-null    float64
 30  Diagnosis                      703 non-null    object
dtypes: float64(25), int64(1), object(5)
memory usage: 175.8+ KB
```

Handling Catagorical Features

```
# Storing item of Diagnosis columns
# =================================
diagonosis = df_train_copy['Diagnosis'].unique()

# Creating dictionary from array for diagnosis
# ============================================
diagonosis_dict = dict(zip(diagonosis, range(len(diagonosis))))

# Encoding the class label(Diagnosis) to integers
# ===============================================
df_train_copy['Diagnosis'] =
df_train_copy['Diagnosis'].map(diagonosis_dict)

# Converting the catagorical data to numerical data
# =================================================
df_dummies = pd.get_dummies(df_train_copy, drop_first=True)
```

```
# Checking the info of the dataset
# ================================
df_dummies.info()

<class 'pandas.core.frame.DataFrame'>
Index: 703 entries, 0 to 702
Data columns (total 31 columns):
 #   Column                      Non-Null Count  Dtype  
---  ------                      --------------  -----  
 0   AFP (ng/mL)                 703 non-null    float64
 1   ALP (U/L)                   703 non-null    float64
 2   ALT (U/L)                   703 non-null    float64
 3   AST (U/L)                   703 non-null    float64
 4   Age                         703 non-null    int64  
 5   Albumin (g/dL)              703 non-null    float64
 6   Bilirubin (mg/dL)           703 non-null    float64
 7   CRP (mg/L)                  703 non-null    float64
 8   Fibroscan (kPa)             703 non-null    float64
 9   GGT (U/L)                   703 non-null    float64
 10  Hemoglobin (g/dL)           703 non-null    float64
 11  IL-6 (pg/mL)                703 non-null    float64
 12  PT/INR                      703 non-null    float64
 13  Platelets (10^9/L)          703 non-null    float64
 14  RBC (10^12/L)               703 non-null    float64
 15  Serum_Ammonia (µmol/L)      703 non-null    float64
 16  Serum_Copper (µg/dL)        703 non-null    float64
 17  Serum_Creatinine (mg/dL)    703 non-null    float64
 18  Serum_Iron (µg/dL)          703 non-null    float64
 19  Serum_Lactate (mmol/L)      703 non-null    float64
 20  Serum_Urea (mg/dL)          703 non-null    float64
 21  Serum_Zinc (µg/dL)          703 non-null    float64
 22  TIBC (µg/dL)                703 non-null    float64
 23  Transferrin_Saturation (%)  703 non-null    float64
 24  WBC (10^9/L)                703 non-null    float64
 25  pH                          703 non-null    float64
 26  Diagnosis                   703 non-null    int64  
 27  Alcohol_Use (yes/no)_yes    703 non-null    bool   
 28  Diabetes (yes/no)_yes       703 non-null    bool   
 29  Gender_MALE                 703 non-null    bool   
 30  Obesity (yes/no)_yes        703 non-null    bool   
dtypes: bool(4), float64(25), int64(2)
memory usage: 156.5 KB

# Moving the target variable to the last column
# =============================================
df_dummies = df_dummies[[col for col in df_dummies.columns if col !=
'Diagnosis'] + ['Diagnosis']]
df_dummies.head()
```

```
   AFP (ng/mL)    ALP (U/L)   ALT (U/L)  AST (U/L)  Age  Albumin 
(g/dL)  \
0    13.571425  1653.138489   40.405592  45.598427    4          
4.477126   
1    13.649342  1940.518305   21.336986  34.064095   55          
3.190724   
2    10.898943  1557.369920   29.665496  16.044488   30          
4.506351   
3    13.872275  1273.840525  142.418649  64.204257    0          
3.665655   
4    10.102457  1461.622515   22.437303  23.940205   59          
4.005109   

   Bilirubin (mg/dL)  CRP (mg/L)  Fibroscan (kPa)   GGT (U/L)  ...  \
0           0.541997    1.002121         5.501881  311.253072  ...   
1           1.199063    0.582746        13.902151  264.586392  ...   
2           0.740952    1.670375         6.961641   66.247224  ...   
3           1.939879    1.220646         9.193268   78.838414  ...   
4           0.769535    0.139863        11.827885  246.940466  ...   

   Serum_Zinc (µg/dL)  TIBC (µg/dL)  Transferrin_Saturation (%)  WBC 
(10^9/L)  \
0           96.124260    315.439318                   30.827639      
4.180007   
1           50.554650    268.492437                   47.896200      
4.590995   
2           82.900681    312.107620                   31.408057      
4.524580   
3           72.360010    182.506010                   34.577016      
4.234483   
4           63.216136    212.261519                   42.384844      
4.306892   

         pH  Alcohol_Use (yes/no)_yes  Diabetes (yes/no)_yes  
Gender_MALE  \
0  6.163600                      True                  False        
True   
1  5.244266                      True                  False        
True   
2  5.769592                     False                  False       
False   
3  5.982228                      True                  False        
True   
4  4.837404                     False                  False       
False   

   Obesity (yes/no)_yes  Diagnosis  
0                  True          0  
1                  True          1  
2                  True          0  
```

```
3                    False          2
4                     True          0

[5 rows x 31 columns]
```

Removing Outliers

```
# Removing the outliers from the dataset using IQR method only for
numerical data
#
======================================================================
==========
# Taking only the numerical columns
df_numerical = df_dummies.select_dtypes(include=[np.number])
# Excluding the target variable
df_numerical = df_numerical.drop('Diagnosis', axis=1)
# Calculating the IQR
Q1 = df_numerical.quantile(0.25)
Q3 = df_numerical.quantile(0.75)
IQR = Q3 - Q1
# Removing the outliers
df_numerical_2 = df_numerical[~((df_numerical < (Q1 - 1.5 * IQR)) |
(df_numerical > (Q3 + 1.5 * IQR))).any(axis=1)]
df_numerical_2.info()

<class 'pandas.core.frame.DataFrame'>
Index: 309 entries, 0 to 701
Data columns (total 26 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   AFP (ng/mL)                  309 non-null    float64
 1   ALP (U/L)                    309 non-null    float64
 2   ALT (U/L)                    309 non-null    float64
 3   AST (U/L)                    309 non-null    float64
 4   Age                          309 non-null    int64
 5   Albumin (g/dL)               309 non-null    float64
 6   Bilirubin (mg/dL)            309 non-null    float64
 7   CRP (mg/L)                   309 non-null    float64
 8   Fibroscan (kPa)              309 non-null    float64
 9   GGT (U/L)                    309 non-null    float64
 10  Hemoglobin (g/dL)            309 non-null    float64
 11  IL-6 (pg/mL)                 309 non-null    float64
 12  PT/INR                       309 non-null    float64
 13  Platelets (10^9/L)           309 non-null    float64
 14  RBC (10^12/L)                309 non-null    float64
 15  Serum_Ammonia (µmol/L)       309 non-null    float64
 16  Serum_Copper (µg/dL)         309 non-null    float64
 17  Serum_Creatinine (mg/dL)     309 non-null    float64
 18  Serum_Iron (µg/dL)           309 non-null    float64
 19  Serum_Lactate (mmol/L)       309 non-null    float64
 20  Serum_Urea (mg/dL)            309 non-null    float64
 21  Serum_Zinc (µg/dL)            309 non-null    float64
 22  TIBC (µg/dL)                  309 non-null    float64
 23  Transferrin_Saturation (%)    309 non-null    float64
 24  WBC (10^9/L)                  309 non-null    float64
 25  pH                            309 non-null    float64
dtypes: float64(25), int64(1)
memory usage: 65.2 KB
```

Using IQR method almost half of the data is getting eliminated so this method doesn't seems good one.

In the below I tried the z-score method to clean the data

```
# Detecting the outliers using the z-score (With the help of lecture
note)
#
=======================================================================
===
for column in df_numerical.columns:
    # Calculating the Z-scores for each column
    z_scores = (df_numerical[column] - df_numerical[column].mean()) /
df_numerical[column].std()

    # Detecting outliers using the absolute value of the Z-scores
(threshold of 2)
    outliers = (np.abs(z_scores) > 2)

    print(f"Number of outliers in {column}: {outliers.sum()}")
```

```
Number of outliers in AFP (ng/mL): 36
Number of outliers in ALP (U/L): 28
Number of outliers in ALT (U/L): 21
Number of outliers in AST (U/L): 24
Number of outliers in Age: 27
Number of outliers in Albumin (g/dL): 33
Number of outliers in Bilirubin (mg/dL): 45
Number of outliers in CRP (mg/L): 25
Number of outliers in Fibroscan (kPa): 40
Number of outliers in GGT (U/L): 26
Number of outliers in Hemoglobin (g/dL): 0
Number of outliers in IL-6 (pg/mL): 21
Number of outliers in PT/INR: 32
Number of outliers in Platelets (10^9/L): 28
Number of outliers in RBC (10^12/L): 19
Number of outliers in Serum_Ammonia (µmol/L): 28
Number of outliers in Serum_Copper (µg/dL): 35
Number of outliers in Serum_Creatinine (mg/dL): 33
Number of outliers in Serum_Iron (µg/dL): 36
Number of outliers in Serum_Lactate (mmol/L): 31
Number of outliers in Serum_Urea (mg/dL): 33
Number of outliers in Serum_Zinc (µg/dL): 29
Number of outliers in TIBC (µg/dL): 27
Number of outliers in Transferrin_Saturation (%): 29
Number of outliers in WBC (10^9/L): 29
Number of outliers in pH: 35

# Printing information of the dataset with numerical columns
# ============================================================
df_numerical.info()

<class 'pandas.core.frame.DataFrame'>
Index: 703 entries, 0 to 702
Data columns (total 26 columns):
 #   Column                      Non-Null Count  Dtype  
---  ------                      --------------  -----  
 0   AFP (ng/mL)                 703 non-null    float64
 1   ALP (U/L)                   703 non-null    float64
 2   ALT (U/L)                   703 non-null    float64
 3   AST (U/L)                   703 non-null    float64
 4   Age                         703 non-null    int64  
 5   Albumin (g/dL)              703 non-null    float64
 6   Bilirubin (mg/dL)           703 non-null    float64
 7   CRP (mg/L)                  703 non-null    float64
 8   Fibroscan (kPa)             703 non-null    float64
 9   GGT (U/L)                   703 non-null    float64
 10  Hemoglobin (g/dL)           703 non-null    float64
 11  IL-6 (pg/mL)                703 non-null    float64
 12  PT/INR                      703 non-null    float64
 13  Platelets (10^9/L)          703 non-null    float64
 14  RBC (10^12/L)               703 non-null    float64
 15  Serum_Ammonia (µmol/L)      703 non-null    float64
 16  Serum_Copper (µg/dL)        703 non-null    float64
 17  Serum_Creatinine (mg/dL)    703 non-null    float64
 18  Serum_Iron (µg/dL)          703 non-null    float64
 19  Serum_Lactate (mmol/L)      703 non-null    float64
 20  Serum_Urea (mg/dL)          703 non-null    float64
 21  Serum_Zinc (µg/dL)          703 non-null    float64
 22  TIBC (µg/dL)                703 non-null    float64
 23  Transferrin_Saturation (%)  703 non-null    float64
 24  WBC (10^9/L)                703 non-null    float64
 25  pH                          703 non-null    float64
dtypes: float64(25), int64(1)
memory usage: 148.3 KB

# Removing the outliers from the dataset using Z-score method only for
numerical data (With the help of lecture note)
#
======================================================================
=============================================
for column in df_numerical.columns:
    # Calculate the z-scores for each column
    z_scores = (df_numerical[column] - df_numerical[column].mean()) /
df_numerical[column].std()

    # Only keep rows in dataframe where the z-score is less than 2
standard deviations
    df_numerical_3 = df_numerical[np.abs(z_scores) < 2]

# Checking the information of the dataset
df_numerical_3.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 668 entries, 0 to 702
Data columns (total 26 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   AFP (ng/mL)                668 non-null    float64
 1   ALP (U/L)                  668 non-null    float64
 2   ALT (U/L)                  668 non-null    float64
 3   AST (U/L)                  668 non-null    float64
 4   Age                        668 non-null    int64
 5   Albumin (g/dL)             668 non-null    float64
 6   Bilirubin (mg/dL)          668 non-null    float64
 7   CRP (mg/L)                 668 non-null    float64
 8   Fibroscan (kPa)            668 non-null    float64
 9   GGT (U/L)                  668 non-null    float64
 10  Hemoglobin (g/dL)          668 non-null    float64
 11  IL-6 (pg/mL)               668 non-null    float64
 12  PT/INR                     668 non-null    float64
 13  Platelets (10^9/L)         668 non-null    float64
 14  RBC (10^12/L)              668 non-null    float64
 15  Serum_Ammonia (μmol/L)     668 non-null    float64
 16  Serum_Copper (μg/dL)       668 non-null    float64
 17  Serum_Creatinine (mg/dL)   668 non-null    float64
 18  Serum_Iron (μg/dL)         668 non-null    float64
 19  Serum_Lactate (mmol/L)     668 non-null    float64
 20  Serum_Urea (mg/dL)         668 non-null    float64
 21  Serum_Zinc (μg/dL)         668 non-null    float64
 22  TIBC (μg/dL)               668 non-null    float64
 23  Transferrin_Saturation (%) 668 non-null    float64
 24  WBC (10^9/L)               668 non-null    float64
 25  pH                         668 non-null    float64
dtypes: float64(25), int64(1)
memory usage: 140.9 KB
```

This seems little bit more promising than the IQR. In the next steps both datasets with outliers and without outliers will be used.

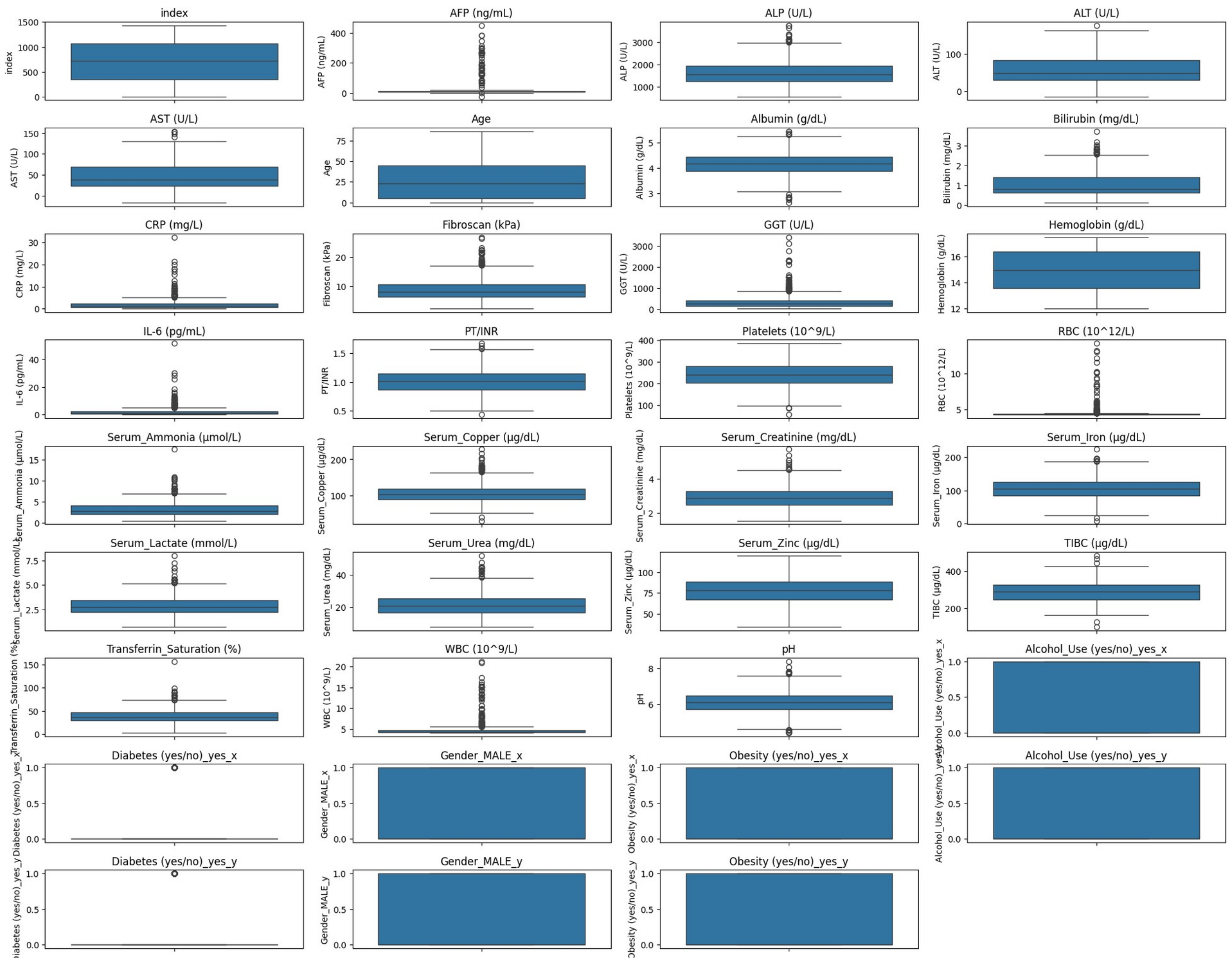
```
# Merging the numerical columns with the catagorical columns based on
the index column
#
======================================================================
==============
rest_columns = ['Alcohol_Use (yes/no)_yes', 'Diabetes (yes/no)_yes',
                    'Gender_MALE', 'Obesity (yes/no)_yes',
'Diagnosis']
df_cleaned = pd.merge(df_numerical_3, df_dummies[rest_columns],
left_index=True, right_index=True)
df_cleaned.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 668 entries, 0 to 702
Data columns (total 31 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   AFP (ng/mL)                  668 non-null    float64
 1   ALP (U/L)                    668 non-null    float64
 2   ALT (U/L)                    668 non-null    float64
 3   AST (U/L)                    668 non-null    float64
 4   Age                          668 non-null    int64
 5   Albumin (g/dL)               668 non-null    float64
 6   Bilirubin (mg/dL)            668 non-null    float64
 7   CRP (mg/L)                   668 non-null    float64
 8   Fibroscan (kPa)              668 non-null    float64
 9   GGT (U/L)                    668 non-null    float64
 10  Hemoglobin (g/dL)            668 non-null    float64
 11  IL-6 (pg/mL)                 668 non-null    float64
 12  PT/INR                       668 non-null    float64
 13  Platelets (10^9/L)           668 non-null    float64
 14  RBC (10^12/L)                668 non-null    float64
 15  Serum_Ammonia (µmol/L)       668 non-null    float64
 16  Serum_Copper (µg/dL)         668 non-null    float64
 17  Serum_Creatinine (mg/dL)     668 non-null    float64
 18  Serum_Iron (µg/dL)           668 non-null    float64
 19  Serum_Lactate (mmol/L)       668 non-null    float64
 20  Serum_Urea (mg/dL)           668 non-null    float64
 21  Serum_Zinc (µg/dL)           668 non-null    float64
 22  TIBC (µg/dL)                 668 non-null    float64
 23  Transferrin_Saturation (%)   668 non-null    float64
 24  WBC (10^9/L)                 668 non-null    float64
 25  pH                           668 non-null    float64
 26  Alcohol_Use (yes/no)_yes     668 non-null    bool
 27  Diabetes (yes/no)_yes        668 non-null    bool
 28  Gender_MALE                  668 non-null    bool
 29  Obesity (yes/no)_yes         668 non-null    bool
 30  Diagnosis                    668 non-null    int64
```

```
dtypes: bool(4), float64(25), int64(2)
memory usage: 148.7 KB
```

Visualizing after cleaning

```
# Removing the target variable
# ==============================
features = df_cleaned.columns[:-1]

plt.figure(figsize=(20, 60))

for i, column in enumerate(features):
    plt.subplot(len(features), 4, i + 1)
    sns.boxplot(y=df_cleaned[column])
    plt.title(column)
    plt.tight_layout()

plt.show()
```



Still shows a lot of Outliers.

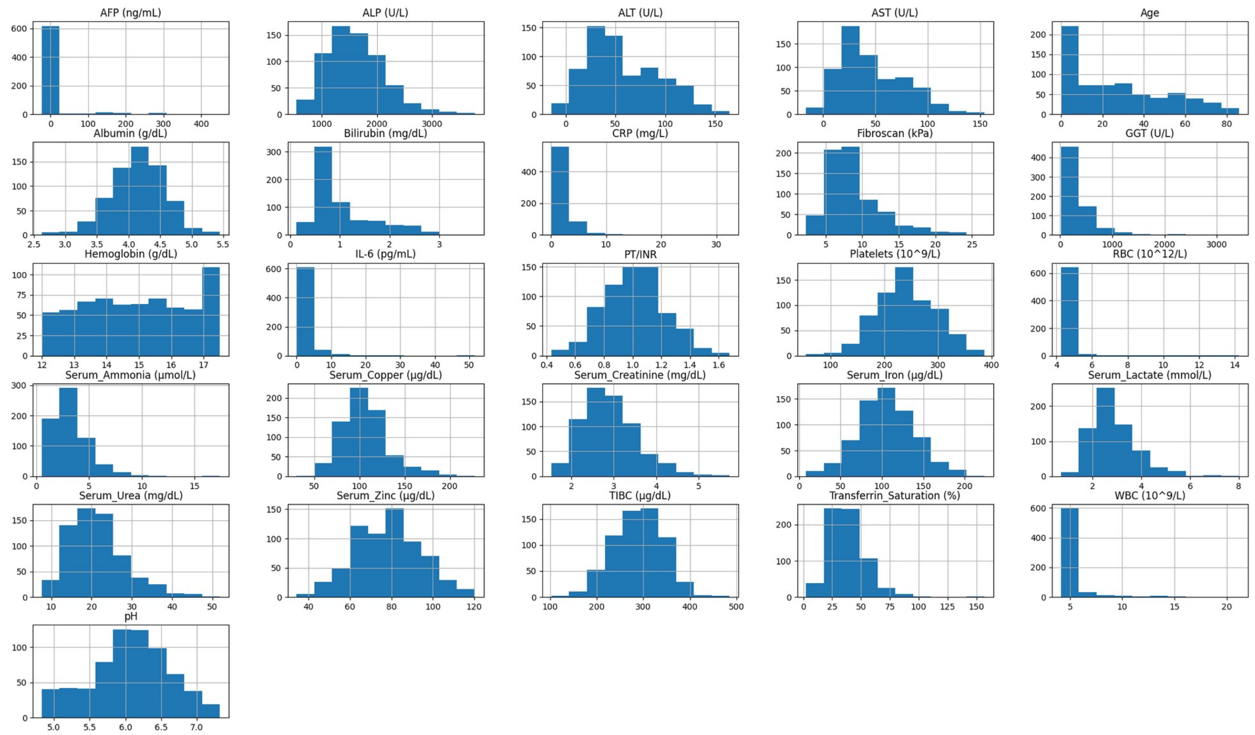
Data preprocessing and visualisation

Splitting the Dataset

```
#--------------------------------------------------
# Spliting the cleaned dataset into test and train
#--------------------------------------------------
X_cleaned = df_cleaned.drop('Diagnosis', axis=1)
y_cleaned = df_cleaned['Diagnosis']

X_train_cleaned, X_test_cleaned, y_train_cleaned, y_test_cleaned =
train_test_split(X_cleaned, y_cleaned, test_size=0.2, random_state=42)

#-------------------------------------------------------
# Spliting the dataset with outlier into test and train
#-------------------------------------------------------
X = df_dummies.drop('Diagnosis', axis=1)
y = df_dummies['Diagnosis']

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

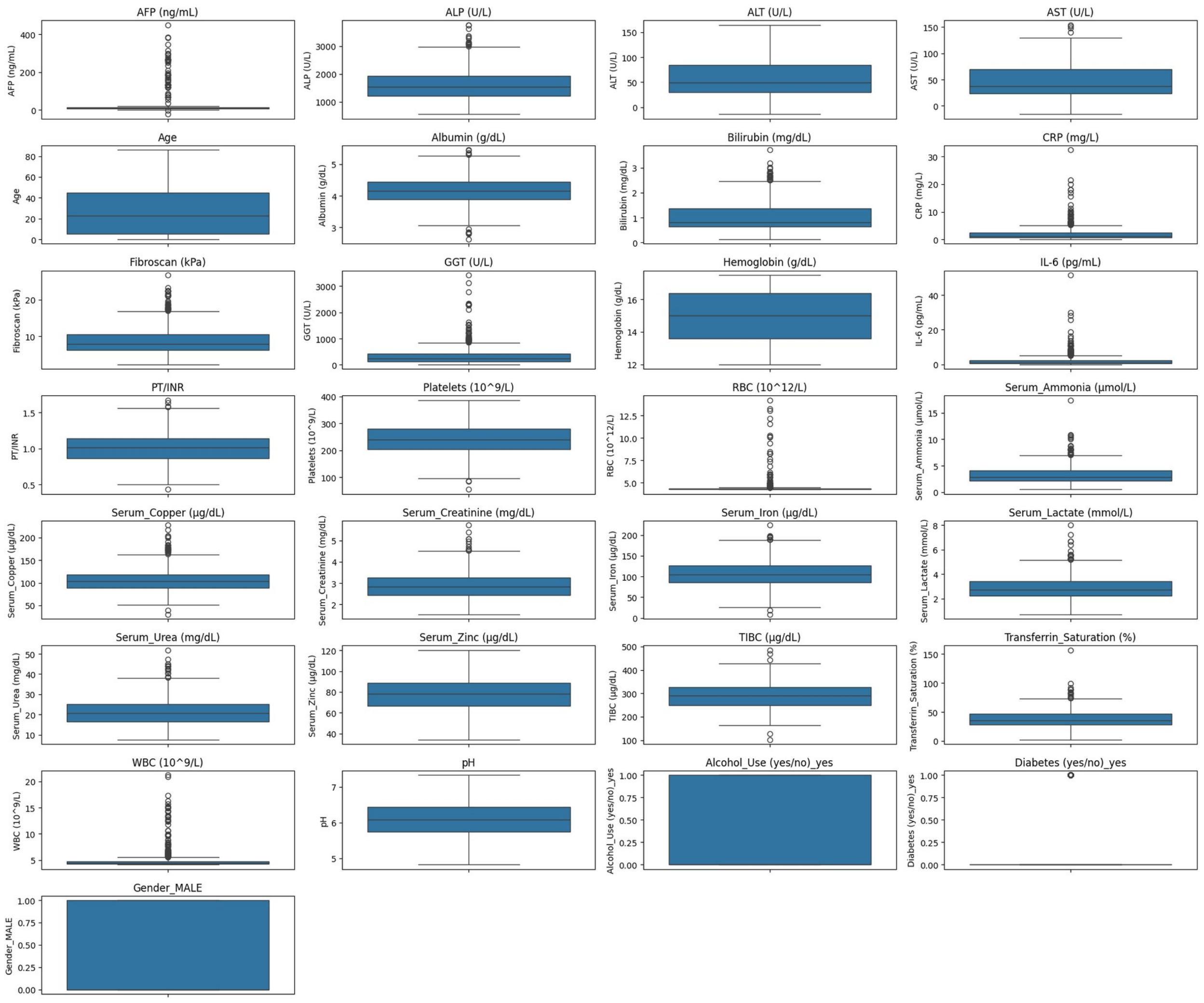
Exploring training data after cleaning and splitting

```
X_cleaned.info()

<class 'pandas.core.frame.DataFrame'>
Index: 668 entries, 0 to 702
Data columns (total 30 columns):
 #   Column                        Non-Null Count  Dtype  
---  ------                        --------------  -----  
 0   AFP (ng/mL)                   668 non-null    float64
 1   ALP (U/L)                     668 non-null    float64
 2   ALT (U/L)                     668 non-null    float64
 3   AST (U/L)                     668 non-null    float64
 4   Age                           668 non-null    int64  
 5   Albumin (g/dL)                668 non-null    float64
 6   Bilirubin (mg/dL)             668 non-null    float64
 7   CRP (mg/L)                    668 non-null    float64
 8   Fibroscan (kPa)               668 non-null    float64
 9   GGT (U/L)                     668 non-null    float64
 10  Hemoglobin (g/dL)             668 non-null    float64
 11  IL-6 (pg/mL)                  668 non-null    float64
 12  PT/INR                        668 non-null    float64
 13  Platelets (10^9/L)            668 non-null    float64
 14  RBC (10^12/L)                 668 non-null    float64
 15  Serum_Ammonia (μmol/L)        668 non-null    float64
 16  Serum_Copper (μg/dL)          668 non-null    float64
 17  Serum_Creatinine (mg/dL)      668 non-null    float64
 18  Serum_Iron (µg/dL)           668 non-null    float64
 19  Serum_Lactate (mmol/L)       668 non-null    float64
 20  Serum_Urea (mg/dL)           668 non-null    float64
 21  Serum_Zinc (µg/dL)           668 non-null    float64
 22  TIBC (µg/dL)                 668 non-null    float64
 23  Transferrin_Saturation (%)   668 non-null    float64
 24  WBC (10^9/L)                 668 non-null    float64
 25  pH                           668 non-null    float64
 26  Alcohol_Use (yes/no)_yes     668 non-null    bool
 27  Diabetes (yes/no)_yes        668 non-null    bool
 28  Gender_MALE                  668 non-null    bool
 29  Obesity (yes/no)_yes         668 non-null    bool
dtypes: bool(4), float64(25), int64(1)
memory usage: 143.5 KB

# Plotting histograms for all columns in the dataset
# ====================================================
X_cleaned.hist(bins=10, figsize=(26, 15))
plt.show()
```



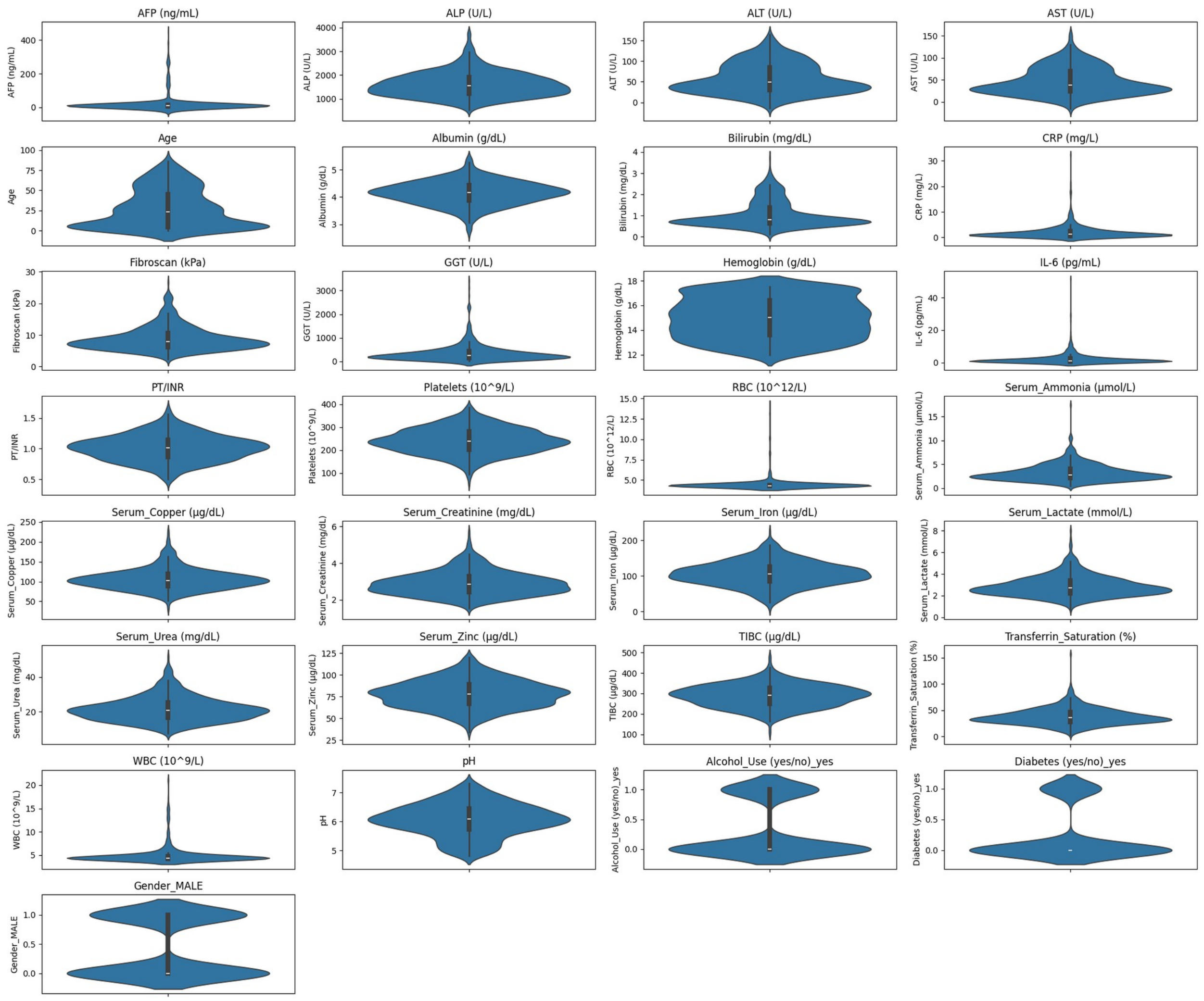
```
# Plotting the Boxplot for the cleaned dataset i.e
X_train_cleaned_sc_df
#
==================================================================
features = X_cleaned.columns[:-1]

plt.figure(figsize=(20, 60))
```

```python
for i, column in enumerate(features):
    plt.subplot(len(features), 4, i + 1)
    sns.boxplot(y=X_cleaned[column])
    plt.title(column)
    plt.tight_layout()

plt.show()
```



```python
# Plotting the Violin plot for the cleaned dataset i.e
X_train_cleaned_sc_df
#
=======================================================================
====
features = X_cleaned.columns[:-1]

plt.figure(figsize=(20, 60))
```

```python
for i, column in enumerate(features):
    plt.subplot(len(features), 4, i + 1)
    sns.violinplot(y=X_cleaned[column])
    plt.title(column)

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



Modelling

Pipelining with Kernel

```python
# Defining the pipeline with kernel(SVC) and pca
# ===============================================
pipe_svc_pca = Pipeline([
    ('scaler', StandardScaler()),
    ('pca', PCA()),
    ('classifier', SVC())
])

# Defining the parameters for the grid search
# ============================================
param_grid_svc_pca = {
    'pca__n_components': [0.9, 0.95, 0.99],
    'classifier__C': [0.1, 1, 10],
    'classifier__kernel': ['linear', 'poly', 'rbf', 'sigmoid']
}

# Defining the grid search
# ========================
grid_search_svc_pca = GridSearchCV(estimator=pipe_svc_pca,
param_grid=param_grid_svc_pca, scoring='f1_macro', cv=5)

# Fitting the grid search
# =======================
grid_search_svc_pca.fit(X_train_cleaned, y_train_cleaned)
```

```
GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('scaler', StandardScaler()),
                                       ('pca', PCA()), ('classifier',
SVC())]),
             param_grid={'classifier__C': [0.1, 1, 10],
                         'classifier__kernel': ['linear', 'poly',
'rbf',
                                                'sigmoid'],
                         'pca__n_components': [0.9, 0.95, 0.99]},
             scoring='f1_macro')
```

```
# Printing the best parameters
# ============================
print(f"Best parameters: {grid_search_svc_pca.best_params_}")

# Printing the best score
# ========================
print(f"Best score: {grid_search_svc_pca.best_score_}")
```

```
Best parameters: {'classifier__C': 1, 'classifier__kernel': 'sigmoid',
'pca__n_components': 0.95}
Best score: 0.7424156305547781
```

```
# Defining the pipeline with kernel(SVC) and lda
# ==============================================
pipe_svc_lda = Pipeline([
    ('scaler', StandardScaler()),
    ('lda', LDA()),
    ('classifier', SVC())
])

# Defining the parameters for the grid search
# ===========================================
param_grid_svc_lda= {
    'lda__n_components': [1, 2],
    'classifier__C': [0.1, 1, 10],
    'classifier__kernel': ['linear', 'poly', 'rbf', 'sigmoid']
}

# Defining the grid search
# ========================
grid_search_svc_lda = GridSearchCV(estimator=pipe_svc_lda,
param_grid=param_grid_svc_lda, scoring='f1_macro', cv=5)

# Fitting the grid search
# =======================
grid_search_svc_lda.fit(X_train_cleaned, y_train_cleaned)
```

```
GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('scaler', StandardScaler()),
                                       ('lda',
LinearDiscriminantAnalysis()),
                                       ('classifier', SVC())]),
             param_grid={'classifier__C': [0.1, 1, 10],
                         'classifier__kernel': ['linear', 'poly',
'rbf',
                                                'sigmoid'],
                         'lda__n_components': [1, 2]},
             scoring='f1_macro')
```

```
# Printing the best parameters
# ============================
print(f"Best parameters: {grid_search_svc_lda.best_params_}")

# Printing the best score
# ========================
print(f"Best score: {grid_search_svc_lda.best_score_}")
```

```
Best parameters: {'classifier__C': 10, 'classifier__kernel': 'linear',
'lda__n_components': 2}
Best score: 0.4884996676523051
```

Pipelining with Regularization

```
# Defining the pipeline with Regulization(LogisticRegression) and pca
# ====================================================================
pipe_lr_pca = Pipeline([
    ('scaler', StandardScaler()),
    ('pca', PCA()),
    ('classifier', LogisticRegression())
])

# Defining the parameters for the grid search
# ==========================================
param_grid_lr_pca = {
    'pca__n_components': [0.9, 0.95, 0.99],
    'classifier__C': [0.1, 1, 10],
    'classifier__penalty': ['l1', 'l2']
}

# Defining the grid search
# ========================
grid_search_lr_pca = GridSearchCV(estimator=pipe_lr_pca,
param_grid=param_grid_lr_pca, scoring='f1_macro', cv=5)

# Fitting the grid search
# =======================
grid_search_lr_pca.fit(X_train_cleaned, y_train_cleaned)
```

```
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/model_selection/_validation.py:542: FitFailedWarning:

45 fits failed out of a total of 90.
The score on these train-test partitions for these parameters will be
set to nan.
If these failures are not expected, you can try to debug them by
setting error_score='raise'.

Below are more details about the failures:
----------------------------------------------------------------------
----------
45 fits failed with the following error:
Traceback (most recent call last):
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/model_selection/_validation.py", line 890, in
_fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/base.py", line 1351, in wrapper
    return fit_method(estimator, *args, **kwargs)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/pipeline.py", line 475, in fit
    self._final_estimator.fit(Xt, y, **last_step_params["fit"])
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/base.py", line 1351, in wrapper
    return fit_method(estimator, *args, **kwargs)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py", line 1172, in fit
    solver = _check_solver(self.solver, self.penalty, self.dual)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py", line 67, in _check_solver
    raise ValueError(
ValueError: Solver lbfgs supports only 'l2' or None penalties, got l1
```

```
penalty.

  warnings.warn(some_fits_failed_message, FitFailedWarning)
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/model_selection/_search.py:1051: UserWarning: One or
more of the test scores are non-finite: [        nan         nan
nan 0.73142056 0.73013276 0.74056691
        nan        nan        nan 0.70825524 0.70806467 0.71615276
        nan        nan        nan 0.68664242 0.6847317  0.69363941]
  warnings.warn(

GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('scaler', StandardScaler()),
                                       ('pca', PCA()),
                                       ('classifier',
LogisticRegression())]),
             param_grid={'classifier__C': [0.1, 1, 10],
                         'classifier__penalty': ['l1', 'l2'],
                         'pca__n_components': [0.9, 0.95, 0.99]},
             scoring='f1_macro')

# Printing the best parameters
# ============================
print(f"Best parameters: {grid_search_lr_pca.best_params_}")

# Printing the best score
# ========================
print(f"Best score: {grid_search_lr_pca.best_score_}")

Best parameters: {'classifier__C': 0.1, 'classifier__penalty': 'l2',
'pca__n_components': 0.99}
Best score: 0.7405669117166076

# Defining the pipeline with Regulization(LogisticRegression) and lda
# ===================================================================
pipe_lr_lda = Pipeline([
    ('scaler', StandardScaler()),
    ('lda', LDA()),
    ('classifier', LogisticRegression())
])

# Defining the parameters for the grid search
# ===========================================
param_grid_lr_lda = {
    'lda__n_components': [1, 2],
    'classifier__C': [0.001, 0.01, 0.1, 1, 10, 100],
    'classifier__penalty': ['l1', 'l2']
}

# Defining the grid search
# ========================
grid_search_lr_lda = GridSearchCV(estimator=pipe_lr_lda,
param_grid=param_grid_lr_lda, scoring='f1_macro', cv=5)

# Fitting the grid search
# =======================
grid_search_lr_lda.fit(X_train_cleaned, y_train_cleaned)
```

```
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/model_selection/_validation.py:542: FitFailedWarning:

60 fits failed out of a total of 120.
The score on these train-test partitions for these parameters will be
set to nan.
If these failures are not expected, you can try to debug them by
setting error_score='raise'.

Below are more details about the failures:
----------------------------------------------------------------------
----------
60 fits failed with the following error:
Traceback (most recent call last):
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/model_selection/_validation.py", line 890, in
_fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/base.py", line 1351, in wrapper
    return fit_method(estimator, *args, **kwargs)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/pipeline.py", line 475, in fit
    self._final_estimator.fit(Xt, y, **last_step_params["fit"])
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/base.py", line 1351, in wrapper
    return fit_method(estimator, *args, **kwargs)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py", line 1172, in fit
    solver = _check_solver(self.solver, self.penalty, self.dual)
  File "/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py", line 67, in _check_solver
    raise ValueError(
ValueError: Solver lbfgs supports only 'l2' or None penalties, got l1
penalty.

  warnings.warn(some_fits_failed_message, FitFailedWarning)
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/model_selection/_search.py:1051: UserWarning: One or
more of the test scores are non-finite: [       nan        nan
0.20646821 0.22460156        nan        nan
 0.25982519 0.37231984        nan        nan 0.29688083 0.47922055
        nan        nan 0.30158403 0.49746643        nan        nan
 0.31018654 0.50354344        nan        nan 0.30933998 0.50567583]
  warnings.warn(

GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('scaler', StandardScaler()),
                                       ('lda',
LinearDiscriminantAnalysis()),
                                       ('classifier',
LogisticRegression())]),
             param_grid={'classifier__C': [0.001, 0.01, 0.1, 1, 10,
100],
                         'classifier__penalty': ['l1', 'l2'],
                         'lda__n_components': [1, 2]},
             scoring='f1_macro')

# Printing the best parameters
# ==============================
print(f"Best parameters: {grid_search_lr_lda.best_params_}")

# Printing the best score
# ==========================
print(f"Best score: {grid_search_lr_lda.best_score_}")

Best parameters: {'classifier__C': 100, 'classifier__penalty': 'l2',
'lda__n_components': 2}
Best score: 0.50567582960442

# Defining the pipeline with RandomForestClassifier and pca
# ========================================================
pipe_rf_pca = Pipeline([
    ('scaler', StandardScaler()),
    ('pca', PCA()),
    ('classifier', RandomForestClassifier())
])

# Defining the parameters for the grid search with f1 macro average as
scoring
#
======================================================================
======
param_grid_rf_pca = {
    'pca__n_components': [0.9, 0.95, 0.99],
    'classifier__n_estimators': [100, 200, 300],
    'classifier__max_depth': [5, 10, 15, 20],
}

# Defining the grid search
# ==========================
grid_search_rf_pca = GridSearchCV(estimator=pipe_rf_pca,
param_grid=param_grid_rf_pca, scoring='f1_macro', cv=5)
```

```
# Fitting the grid search(for cleaned dataset)
# ============================================
grid_search_rf_pca.fit(X_train_cleaned, y_train_cleaned)
```

```
GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('scaler', StandardScaler()),
                                       ('pca', PCA()),
                                       ('classifier',
                                        RandomForestClassifier())]),
             param_grid={'classifier__max_depth': [5, 10, 15, 20],
                         'classifier__n_estimators': [100, 200, 300],
                         'pca__n_components': [0.9, 0.95, 0.99]},
             scoring='f1_macro')
```

```
# Printing the best parameters
# ============================
print(f"Best parameters: {grid_search_rf_pca.best_params_}")

# Printing the best score
# ========================
print(f"Best score: {grid_search_rf_pca.best_score_}")
```

```
Best parameters: {'classifier__max_depth': 20,
'classifier__n_estimators': 300, 'pca__n_components': 0.99}
Best score: 0.6654014631167522
```

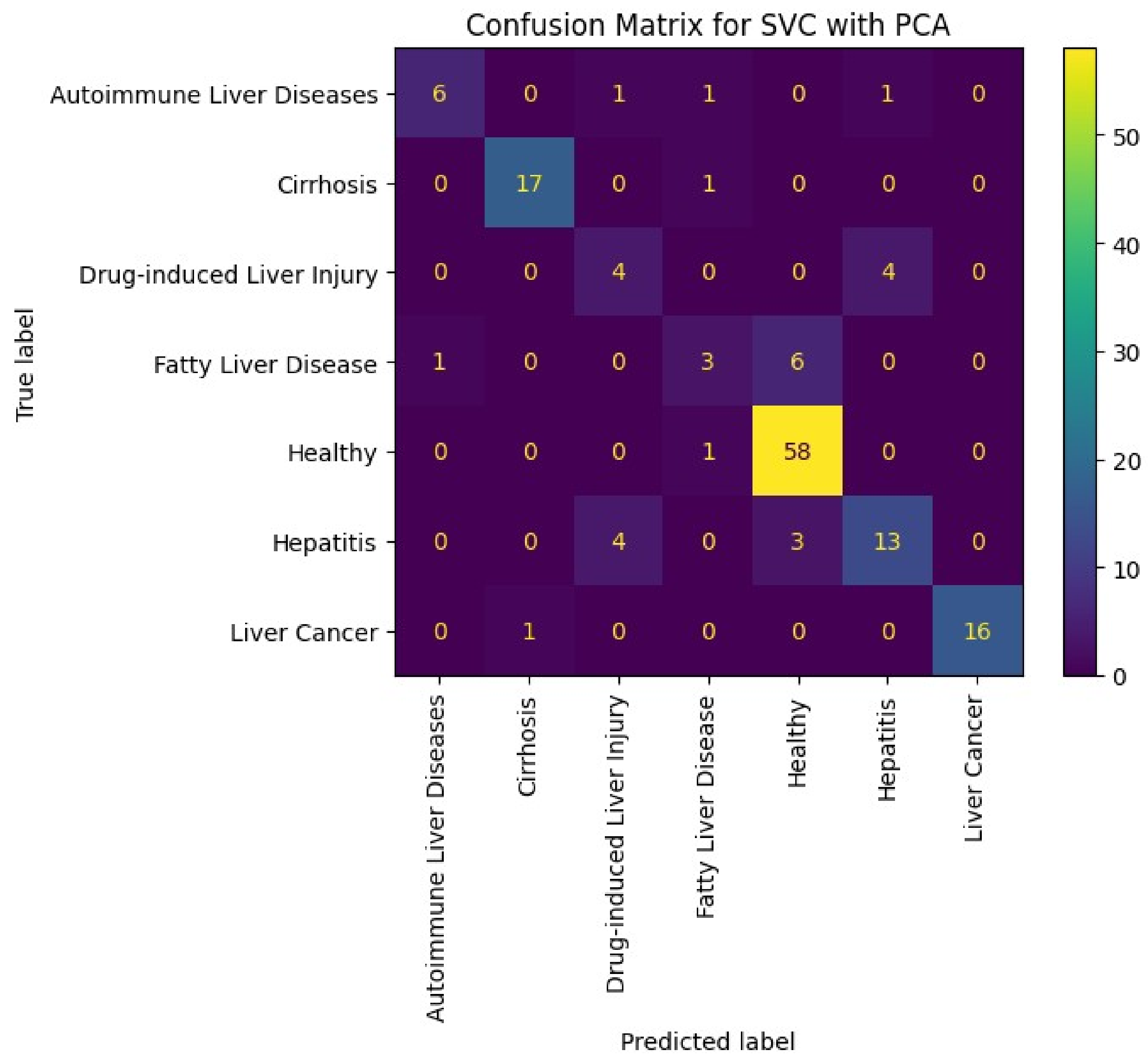
```
# Defining the pipeline with RandomForestClassifier and lda
# =========================================================
pipe_rf_lda = Pipeline([
    ('scaler', StandardScaler()),
    ('lda', LDA()),
    ('classifier', RandomForestClassifier())
])

# Defining the parameters for the grid search
# ===========================================
param_grid_rf_lda = {
    'lda__n_components': [1, 2],
    'classifier__n_estimators': [100, 200, 300],
    'classifier__max_depth': [5, 10, 15, 20]
}

# Defining the grid search
# ========================
grid_search_rf_lda = GridSearchCV(estimator=pipe_rf_lda,
param_grid=param_grid_rf_lda, scoring='f1_macro', cv=5)

# Fitting the grid search(for cleaned dataset)
# ============================================
grid_search_rf_lda.fit(X_train_cleaned, y_train_cleaned)
```

```
GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('scaler', StandardScaler()),
                                       ('lda',
LinearDiscriminantAnalysis()),
                                       ('classifier',
                                        RandomForestClassifier())]),
             param_grid={'classifier__max_depth': [5, 10, 15, 20],
                         'classifier__n_estimators': [100, 200, 300],
                         'lda__n_components': [1, 2]},
             scoring='f1_macro')

# Printing the best parameters
# ============================
print(f"Best parameters: {grid_search_rf_lda.best_params_}")

# Printing the best score
# ========================
print(f"Best score: {grid_search_rf_lda.best_score_}")

Best parameters: {'classifier__max_depth': 10,
'classifier__n_estimators': 200, 'lda__n_components': 2}
Best score: 0.5107671041902294

# Defining the pipeline with RandomForestClassifier
# ================================================
pipe_rf = Pipeline([
    ('scaler', StandardScaler()),
    ('classifier', RandomForestClassifier())
])

# Defining the parameters for the grid search
# ==========================================
param_grid_rf = {
    'classifier__n_estimators': [100, 200, 300],
    'classifier__max_depth': [5, 10, 15, 20]
}

# Defining the grid search
# ========================
grid_search_rf = GridSearchCV(estimator=pipe_rf,
param_grid=param_grid_rf, scoring='f1_macro', cv=5)

# Fitting the grid search(for cleaned dataset)
# ============================================
grid_search_rf.fit(X_train_cleaned, y_train_cleaned)

# Printing the best parameters
# ============================
print(f"Best parameters: {grid_search_rf.best_params_}")

# Printing the best score
# ========================
print(f"Best score: {grid_search_rf.best_score_}")
```

```
Best parameters: {'classifier__max_depth': 15,
'classifier__n_estimators': 300}
Best score: 0.7469526003955284
```

Confusion Matrix for the best model with 60-40 split

```
# Predicting the test data best model
# ===================================
X_train_c, X_test_c, y_train_c, y_test_c = train_test_split(X, y,
test_size=0.2, random_state=42)
best_model = grid_search_svc_pca.best_estimator_
best_model.fit(X_train_c, y_train_c)
y_pred = best_model.predict(X_test_c)

# Generating the confusion matrix (Taken from the lecture)
# ========================================================
ConfusionMatrixDisplay.from_predictions(y_test_c, y_pred)
plt.title('Confusion Matrix for SVC with PCA')
plt.xticks(rotation=90)
plt.show()
```



Final evaluation

```
# Dropping the first column from df_test
# =======================================
df_test = df_test.drop('index', axis=1)

# Converting the catagorical data to numerical data
# =================================================
df_test_dummies = pd.get_dummies(df_test, drop_first=True)

X_cleaned.info()

<class 'pandas.core.frame.DataFrame'>
Index: 668 entries, 0 to 702
Data columns (total 30 columns):
 #   Column                         Non-Null Count  Dtype
```

```
---  ------                          --------------  -----
 0   AFP (ng/mL)                     668 non-null    float64
 1   ALP (U/L)                       668 non-null    float64
 2   ALT (U/L)                       668 non-null    float64
 3   AST (U/L)                       668 non-null    float64
 4   Age                             668 non-null    int64
 5   Albumin (g/dL)                  668 non-null    float64
 6   Bilirubin (mg/dL)               668 non-null    float64
 7   CRP (mg/L)                      668 non-null    float64
 8   Fibroscan (kPa)                 668 non-null    float64
 9   GGT (U/L)                       668 non-null    float64
 10  Hemoglobin (g/dL)               668 non-null    float64
 11  IL-6 (pg/mL)                    668 non-null    float64
 12  PT/INR                          668 non-null    float64
 13  Platelets (10^9/L)              668 non-null    float64
 14  RBC (10^12/L)                   668 non-null    float64
 15  Serum_Ammonia (µmol/L)          668 non-null    float64
 16  Serum_Copper (µg/dL)            668 non-null    float64
 17  Serum_Creatinine (mg/dL)        668 non-null    float64
 18  Serum_Iron (µg/dL)              668 non-null    float64
 19  Serum_Lactate (mmol/L)          668 non-null    float64
 20  Serum_Urea (mg/dL)              668 non-null    float64
 21  Serum_Zinc (µg/dL)              668 non-null    float64
 22  TIBC (µg/dL)                    668 non-null    float64
 23  Transferrin_Saturation (%)      668 non-null    float64
 24  WBC (10^9/L)                    668 non-null    float64
 25  pH                              668 non-null    float64
 26  Alcohol_Use (yes/no)_yes        668 non-null    bool
 27  Diabetes (yes/no)_yes           668 non-null    bool
 28  Gender_MALE                     668 non-null    bool
 29  Obesity (yes/no)_yes            668 non-null    bool
dtypes: bool(4), float64(25), int64(1)
memory usage: 143.5 KB
```

```
df_test_dummies.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 302 entries, 0 to 301
Data columns (total 30 columns):
 #   Column                          Non-Null Count  Dtype
---  ------                          --------------  -----
 0   AFP (ng/mL)                     302 non-null    float64
 1   ALP (U/L)                       302 non-null    float64
 2   ALT (U/L)                       302 non-null    float64
 3   AST (U/L)                       302 non-null    float64
 4   Age                             302 non-null    int64
 5   Albumin (g/dL)                  302 non-null    float64
 6   Bilirubin (mg/dL)               302 non-null    float64
 7   CRP (mg/L)                      302 non-null    float64
 8   Fibroscan (kPa)                 302 non-null    float64
 9   GGT (U/L)                      302 non-null    float64
 10  Hemoglobin (g/dL)              302 non-null    float64
 11  IL-6 (pg/mL)                   302 non-null    float64
 12  PT/INR                         302 non-null    float64
 13  Platelets (10^9/L)             302 non-null    float64
 14  RBC (10^12/L)                  302 non-null    float64
 15  Serum_Ammonia (µmol/L)         302 non-null    float64
 16  Serum_Copper (µg/dL)           302 non-null    float64
 17  Serum_Creatinine (mg/dL)       302 non-null    float64
 18  Serum_Iron (µg/dL)             302 non-null    float64
 19  Serum_Lactate (mmol/L)         302 non-null    float64
 20  Serum_Urea (mg/dL)             302 non-null    float64
 21  Serum_Zinc (µg/dL)             302 non-null    float64
 22  TIBC (µg/dL)                   302 non-null    float64
 23  Transferrin_Saturation (%)     302 non-null    float64
 24  WBC (10^9/L)                   302 non-null    float64
 25  pH                             302 non-null    float64
 26  Alcohol_Use (yes/no)_yes       302 non-null    bool
 27  Diabetes (yes/no)_yes          302 non-null    bool
 28  Gender_MALE                    302 non-null    bool
 29  Obesity (yes/no)_yes           302 non-null    bool
dtypes: bool(4), float64(25), int64(1)
memory usage: 64.9 KB

# Fitting the best model on the training data
# ============================================
best_model.fit(X_cleaned, y_cleaned)

# Predicting the test data
# ========================
y_pred_final = best_model.predict(df_test_dummies)
```

Kaggle submission

```
# Mapping the diagnosis back to the original values
# ================================================
diagonosis_dict_reverse = {v: k for k, v in diagonosis_dict.items()}
y_pred_final = pd.Series(y_pred_final).map(diagonosis_dict_reverse)

#----------------------------------------
# Creating csv file for Kaggle submission
#----------------------------------------
DF = pd.DataFrame(y_pred_final)
headers = ["Diagnosis"]
DF.columns = headers
DF.to_csv('predictions.csv', index_label='index', index=True)
```

ROC Curve for Binary Version of the Target variable

```
# Coverting the diagoniss column to 2 classes
# ==============================================
df_train_simplified = df_cleaned.copy()
df_train_simplified['Diagnosis'] =
df_train_simplified['Diagnosis'].apply(lambda x: 0 if x == 0 else 1)

X_simplified = df_train_simplified.drop('Diagnosis', axis=1)
y_simplified = df_train_simplified['Diagnosis']

# Defining the classifier
# ========================
lr = LogisticRegression()
# Producing the probabilities for each class
y_prob = cross_val_predict(lr, X_simplified, y_simplified, cv=5,
method='predict_proba')
fpr, tpr, thresholds = roc_curve(y_simplified, y_prob[:, 1])

# Plotting the ROC curve
# ======================
plt.plot(fpr, tpr)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.show()
```

```
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning:
lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as
shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:

https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning:
lbfgs failed to converge (status=1):
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Increase the number of iterations (max_iter) or scale the data as
shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:

https://scikit-learn.org/stable/modules/linear_model.html#logistic-
```

```
regression
  n_iter_i = _check_optimize_result(
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning:
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/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning:
lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as
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    https://scikit-learn.org/stable/modules/preprocessing.html
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  n_iter_i = _check_optimize_result(
/Users/jony/opt/anaconda3/envs/dat200_env/lib/python3.10/site-
packages/sklearn/linear_model/_logistic.py:469: ConvergenceWarning:
lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as
shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:

https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(
```

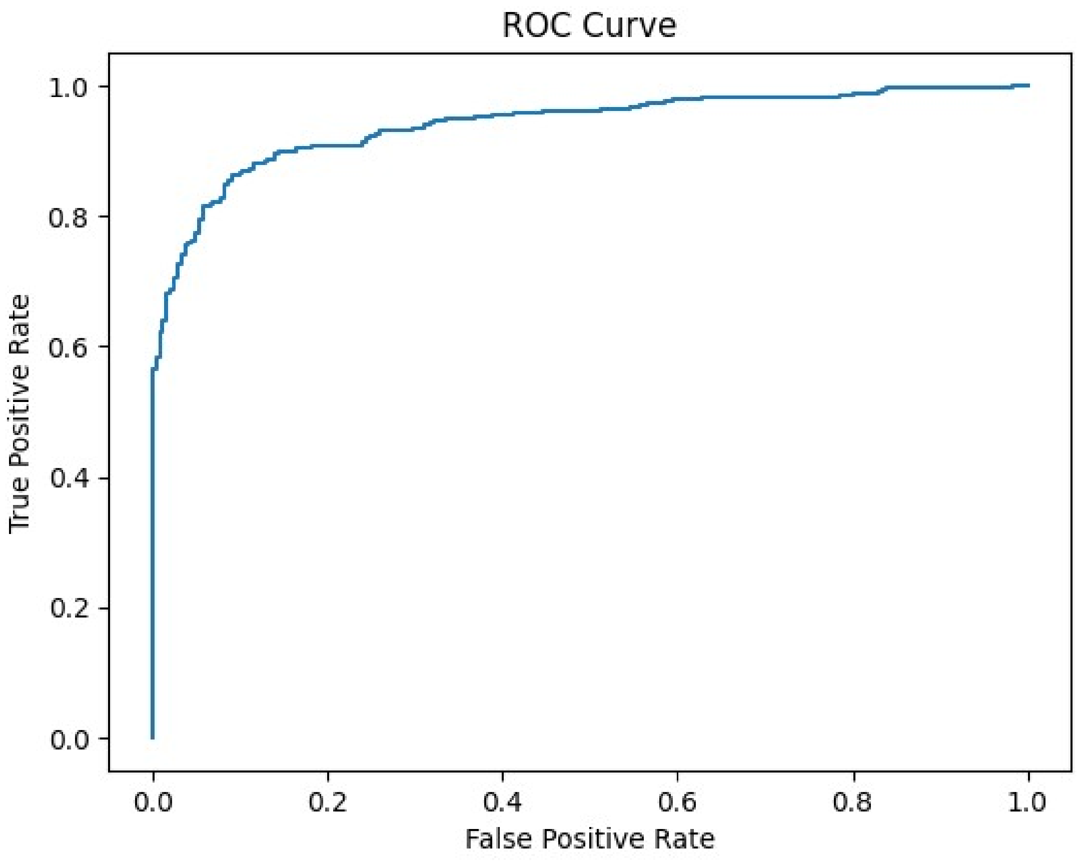
ROC Curve
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0