

Data Collection and Preprocessing Phase

Date	20th June 2024
Team ID	SWTID1720080161
Project Title	Revolutionizing Liver Care : Predicting Liver Cirrhosis Using Advanced Machine Learning Techniques
Maximum Marks	6 Marks

Data Exploration and Preprocessing Template

Identifies data sources, assesses quality issues like missing values and duplicates, and implements resolution plans to ensure accurate and reliable analysis.

Section

Description

Dimensions : 950 x 42

Shape : (950,42)

df.shape

(950, 42)

Head:

s.no	Age	Gender	Place(location where the patient lives)	Duration of alcohol consumption(years)	Quantity of alcohol consumption (quarters/day)	Type of alcohol consumed	Hepatitis B infection	Hepatitis C infection	Diabetes Result	...	Indirect (mg/dl)	Total Protein (g/dl)	Albumin (g/dl)	Globulin (g/dl)	A/G Ratio	AL.Phosphatase (U/L)	SGOT/AST (U/L)	SGPT/ALT (U/L)	
0	1	55	male	rural	12	2	branded liquor	negative	negative	YES	...	3.0	6.0	3.0	4.0	0.75	150.0	56	34
1	2	55	male	rural	12	2	branded liquor	negative	negative	YES	...	3.0	6.0	3.0	4.0	0.75	150.0	56	34
2	3	55	male	rural	12	2	branded liquor	negative	negative	YES	...	3.0	6.0	3.0	4.0	0.75	150.0	56	34
3	4	55	male	rural	12	2	branded liquor	negative	negative	NO	...	3.0	6.0	3.0	4.0	0.75	150.0	56	34
4	5	55	female	rural	12	2	branded liquor	negative	negative	YES	...	3.0	6.0	3.0	4.0	0.75	150.0	56	34

5 rows x 42 columns

Overview of columns:

Data columns (total 42 columns):

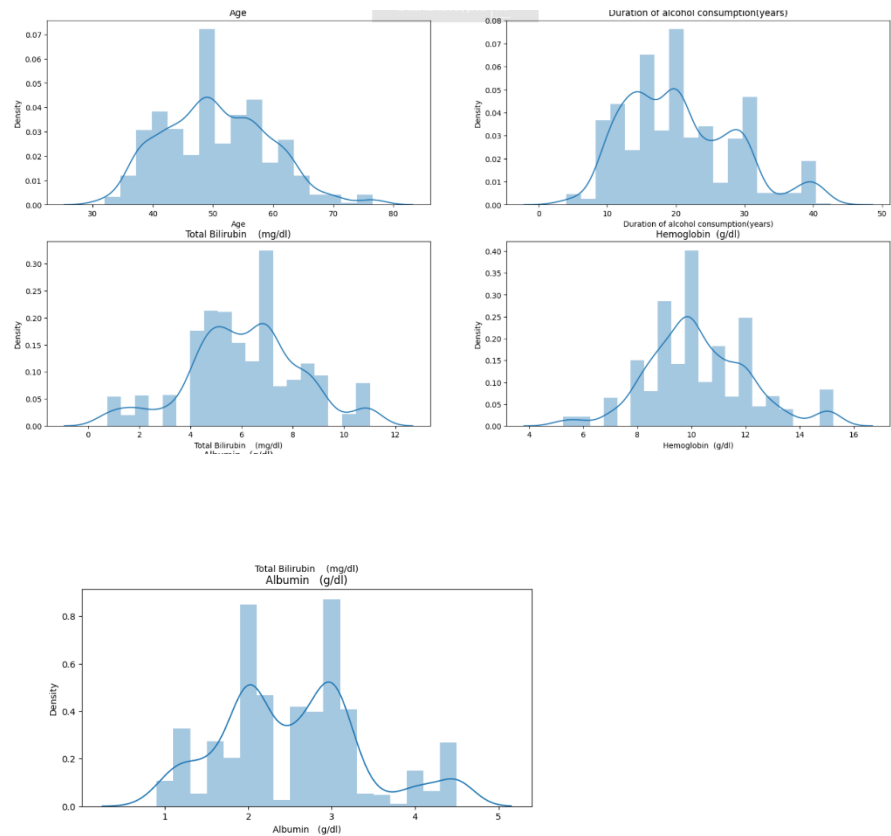
#	Column	Non-Null Count	Dtype
0	S.NO	1250 non-null	float64
1	Age	1250 non-null	float64
2	Gender	1250 non-null	object
3	Place(location where the patient lives)	1116 non-null	object
4	Duration of alcohol consumption(years)	1250 non-null	float64
5	Quantity of alcohol consumption (quarters/day)	1250 non-null	float64
6	Type of alcohol consumed	1250 non-null	object
7	Hepatitis B infection	1250 non-null	object
8	Hepatitis C infection	1250 non-null	object
9	Diabetes Result	1250 non-null	object
10	Blood pressure (mmhg)	1250 non-null	object
11	Obesity	1250 non-null	object
12	Family history of cirrhosis/ hereditary	1250 non-null	object
13	TCH	591 non-null	float64
14	TG	591 non-null	object
15	LDL	591 non-null	object
16	HDL	582 non-null	float64
17	Hemoglobin (g/dl)	1250 non-null	float64
18	PCV (%)	1220 non-null	float64
19	RBC (million cells/microliter)	698 non-null	float64
20	MCV (femtoliters/cell)	1241 non-null	float64
21	MCH (picograms/cell)	592 non-null	float64
22	MCHC (grams/deciliter)	578 non-null	float64
23	Total Count	1240 non-null	float64
24	Polymorphs (%)	1250 non-null	float64
25	Lymphocytes (%)	1250 non-null	float64
26	Monocytes (%)	1241 non-null	float64
27	Eosinophils (%)	1242 non-null	float64
28	Basophils (%)	1201 non-null	float64
29	Platelet Count (lakhs/mm)	1250 non-null	float64
30	Total Bilirubin (mg/dl)	1250 non-null	object
31	Direct (mg/dl)	1250 non-null	float64
32	Indirect (mg/dl)	1195 non-null	float64
33	Total Protein (g/dl)	1189 non-null	float64
34	Albumin (g/dl)	1241 non-null	float64
35	Globulin (g/dl)	1221 non-null	float64
36	A/G Ratio	785 non-null	object
37	AL.Phosphatase (U/L)	1240 non-null	float64
38	SGOT/AST (U/L)	1250 non-null	float64
39	SGPT/ALT (U/L)	1250 non-null	float64
40	USG Abdomen (diffuse liver or not)	1250 non-null	object
41	Predicted Value(Out Come-Patient suffering from liver cirrosis or not)	1196 non-null	object

dtypes: float64(27), object(15)

Data Overview

	<p>Duplicate rows:</p> <pre>[732] df.duplicated().sum()</pre> <p>↔ 0</p> <p>Target value to predict:</p> <p>Predicted Value(Out Come-Patient suffering from liver cirrosis or not)</p> <table> <tr> <td>YES</td> <td>876</td> </tr> <tr> <td>no</td> <td>20</td> </tr> </table> <p>Object columns:</p> <pre>object_cols = df.select_dtypes(include='object').columns.tolist() for col in object_cols: print(col)</pre> <p>Gender Place(location where the patient lives) Type of alcohol consumed Hepatitis B infection Hepatitis C infection Diabetes Result Blood pressure (mmhg) Obesity Family history of cirrhosis/ hereditary TG LDL Total Bilirubin (mg/dl) A/G Ratio USG Abdomen (diffuse liver or not) Predicted Value(Out Come-Patient suffering from liver cirrosis or not)</p>	YES	876	no	20
YES	876				
no	20				
Univariate Analysis	<p>Exploration using Distplots:</p> <p>Code:</p> <pre>l=['Age','Duration of alcohol consumption(years)','Total Bilirubin (mg/dl)','Hemoglobin (g/dl)','Albumin (g/dl)'] plt.figure(figsize=(20, 15)) for i, col in enumerate(l): plt.subplot(3, 2, i + 1) sns.distplot(df[col]) plt.title(col) plt.show()</pre>				

Plots:



Inference:

Inferences from Density Plots

Age Distribution:

- The majority of patients fall within the 40-60 age range.
- There is a noticeable peak around the age of 50, indicating a higher frequency of patients in their early 50s.

2. Duration of Alcohol Consumption:

- The duration of alcohol consumption varies widely among patients.
- A significant proportion of patients have been consuming alcohol for around 15-25 years, with a peak at approximately 20 years.

3. Total Bilirubin:

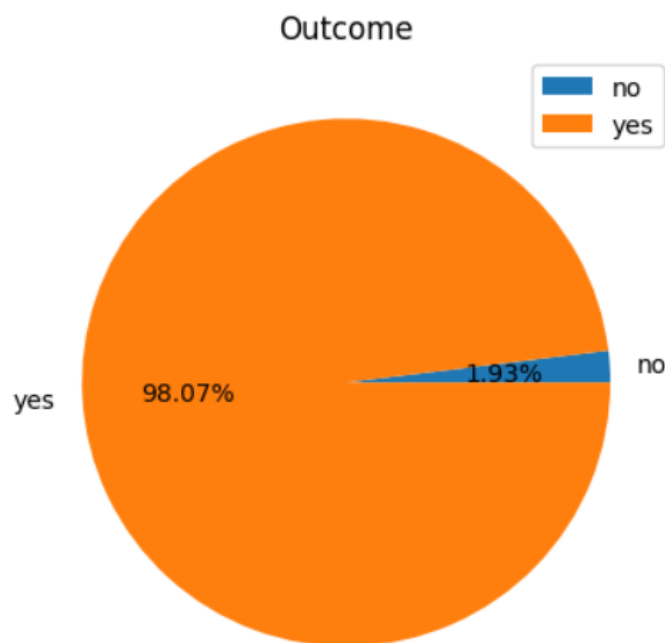
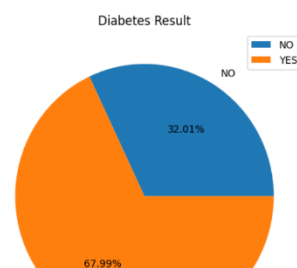
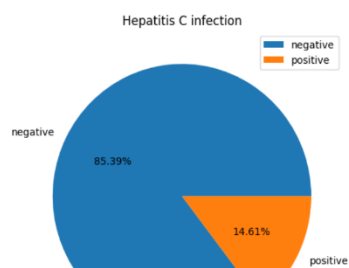
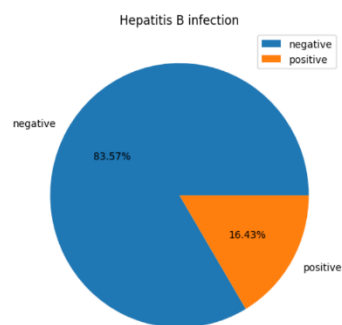
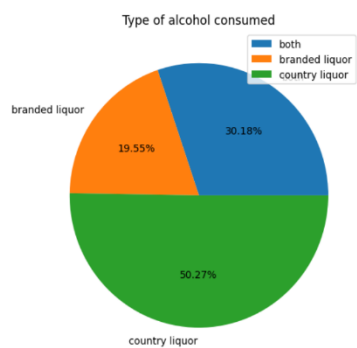
- The total bilirubin levels show a wide distribution, with a peak around 6 mg/dl.
- There are some patients with very high bilirubin levels, indicating possible liver dysfunction.

4. Hemoglobin Levels:

- Hemoglobin levels are generally distributed around a mean of approximately 10 g/dl.
- The distribution shows a peak around 10-12 g/dl, suggesting that most patients have moderate to normal hemoglobin levels.

Representing all the important categorical columns in pie chart

Pie charts:



Code:

```
fig, axes = plt.subplots(2, 2, figsize=(12, 10))

# Type of alcohol consumed
df.groupby("Type of alcohol consumed").size().plot(kind="pie", autopct="%.2f%%", ax=axes[0, 0], legend=True)
axes[0, 0].set_title("Type of alcohol consumed")

# Hepatitis B infection
df.groupby("Hepatitis B infection").size().plot(kind="pie", autopct="%.2f%%", ax=axes[0, 1], legend=True)
axes[0, 1].set_title("Hepatitis B infection")

# Hepatitis C infection
df.groupby("Hepatitis C infection").size().plot(kind="pie", autopct="%.2f%%", ax=axes[1, 0], legend=True)
axes[1, 0].set_title("Hepatitis C infection")

# Diabetes Result
df.groupby("Diabetes Result").size().plot(kind="pie", autopct="%.2f%%", ax=axes[1, 1], legend=True)
axes[1, 1].set_title("Diabetes Result")

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

Statistical analysis for individual variables:

	Age	Duration of alcohol consumption(years)	Quantity of alcohol consumption (quarters/day)	TCH	TG	LDL	HDL	Hemoglobin (g/dl)	PCV (%)	RBC (million cells/microliter)	...	Total Bilirubin (mg/dl)	Direct (mg/dl)	Indirect (mg/dl)	Total Protein (g/dl)
count	1182.000000	1182.000000	1182.000000	1182.000000	1182.0	1182.000000	1182.000000	1182.000000	1182.000000	1182.000000	...	1182.000000	1182.000000	1182.000000	1182.000000
mean	50.599225	17.857764	2.384987	196.498645	162.715736	106.0	35.331961	10.599428	35.178343	3.973412	...	4.990440	3.315440	2.336292	5.732175
std	8.820111	9.088443	0.839708	4.689123	6.334554	0.0	0.653258	1.866877	5.468803	0.177043	...	2.979027	2.064806	0.863999	1.211197
min	31.738678	3.639435	1.000000	188.683898	153.500000	106.0	34.270619	5.206250	21.500000	3.730220	...	0.300000	0.723012	0.391390	2.750000
25%	45.000000	10.000000	2.000000	194.000000	161.000000	106.0	35.000000	9.222500	32.000000	3.931788	...	2.000000	1.100000	1.956556	5.000000
50%	50.000000	17.000000	2.000000	197.544068	161.000000	106.0	35.486254	10.600000	36.000000	3.931788	...	5.200000	3.200000	2.124524	6.000000
75%	56.339932	25.000000	3.000000	197.544068	166.000000	106.0	35.486254	11.900000	39.000000	4.066167	...	7.000000	4.200000	3.000000	6.500000
max	73.349831	45.000000	4.500000	202.860169	173.500000	106.0	36.215636	15.900000	49.500000	4.267735	...	11.000000	8.850000	4.565166	8.300000

8 rows x 30 columns

Albumin (g/dl)	Globulin (g/dl)	A/G Ratio	AL.Phosphatase (U/L)	SGOT/AST (U/L)	SGPT/ALT (U/L)
182.000000	1182.000000	1182.000000	1182.000000	1182.000000	1182.000000
2.965578	3.130965	1.056125	124.464881	87.083213	61.483339
1.207149	0.910346	0.575430	30.762279	29.061998	22.207486
0.900000	1.000000	0.090000	50.771505	32.000000	23.000000
2.000000	2.500000	0.640000	104.730578	61.000000	43.000000
2.900000	3.000000	0.900000	119.656197	84.000000	60.000000
3.875198	3.800000	1.490000	146.000000	109.565245	74.212239
6.687995	5.750000	2.765000	206.000000	182.413113	121.030597

Mean of all numerical columns:

Age	50.588614
Duration of alcohol consumption(years)	20.552632
Quantity of alcohol consumption (quarters/day)	2.195489
TCH	195.816696
TG	163.541353
LDL	106.040279
HDL	34.914618
Hemoglobin (g/dl)	10.266305
PCV (%)	33.900873
RBC (million cells/microliter)	3.386582
MCV (femtoliters/cell)	87.434408
MCH (picograms/cell)	30.512111
MCHC (grams/deciliter)	31.907273
Total Count	8149.711704
Polymorphs (%)	66.932331
Lymphocytes (%)	26.006445
Monocytes (%)	3.633432
Eosinophils (%)	2.269037
Basophils (%)	0.469048
Platelet Count (lakhs/mm)	1.441933
Total Bilirubin (mg/dl)	6.118582
Direct (mg/dl)	3.704834
Indirect (mg/dl)	2.423035
Total Protein (g/dl)	5.595907
Albumin (g/dl)	2.529510
Globulin (g/dl)	3.225369
A/G Ratio	0.855725
AL.Phosphatase (U/L)	132.292207
SGOT/AST (U/L)	80.383459

Median:

Age	50.000000
Duration of alcohol consumption(years)	20.000000
Quantity of alcohol consumption (quarters/day)	2.000000
TCH	197.423932
TG	161.000000
LDL	106.000000
HDL	35.516464
Hemoglobin (g/dl)	10.000000
PCV (%)	35.000000
RBC (million cells/microliter)	3.386582
MCV (femtoliters/cell)	87.000000
MCH (picograms/cell)	30.512111
MCHC (grams/deciliter)	31.907273
Total Count	7500.000000
Polymorphs (%)	65.000000
Lymphocytes (%)	27.000000
Monocytes (%)	3.000000
Eosinophils (%)	2.000000
Basophils (%)	0.000000
Platelet Count (lakhs/mm)	1.400000
Total Bilirubin (mg/dl)	6.000000
Direct (mg/dl)	3.600000
Indirect (mg/dl)	2.400000
Total Protein (g/dl)	6.000000
Albumin (g/dl)	2.500000
Globulin (g/dl)	3.100000
A/G Ratio	0.780000
AL.Phosphatase (U/L)	130.000000
SGOT/AST (U/L)	74.000000
SGPT/ALT (U/L)	49.000000
dtype: float64	

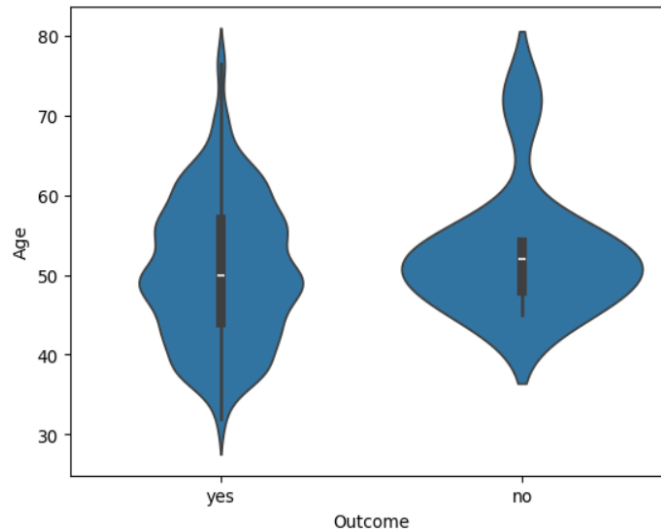
Bivariate Analysis

Violin Plots Between Two Variables:

✓ How does age vary with outcome

```
sns.violinplot(y=df["Age"],x=df["Outcome"])
```

```
<Axes: xlabel='Outcome', ylabel='Age'>
```



Inference:

Inferences from Violin Plot

The violin plot shows the age distribution for patients with and without liver cirrhosis.

- **Patients with Liver Cirrhosis (Yes):**
 - Broader age distribution with multiple peaks.
 - Concentration around 50-60 years.
- **Patients without Liver Cirrhosis (No):**
 - More uniform age distribution.
 - Noticeable peak around 50 years.

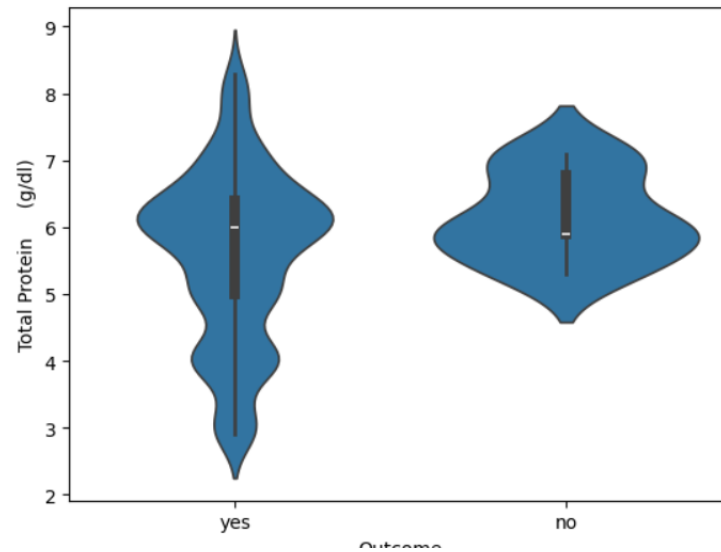
Conclusion

Liver cirrhosis affects a wider range of ages, especially 50-60 years, while the age distribution for patients without cirrhosis is more consistent.

✓ How does protein influence outcome

```
sns.violinplot(y=df["Total Protein (g/dl)",x=df["Outcome"]])
```

<Axes: xlabel='Outcome', ylabel='Total Protein (g/dl)'>



Inference:

Total Protein Distribution:

Patients with liver cirrhosis ("yes") have a wider distribution of total protein levels ranging from approximately 3 g/dl to 9 g/dl.

Patients without liver cirrhosis ("no") have a slightly narrower distribution, with total protein levels ranging from approximately 4.5 g/dl to 8 g/dl.

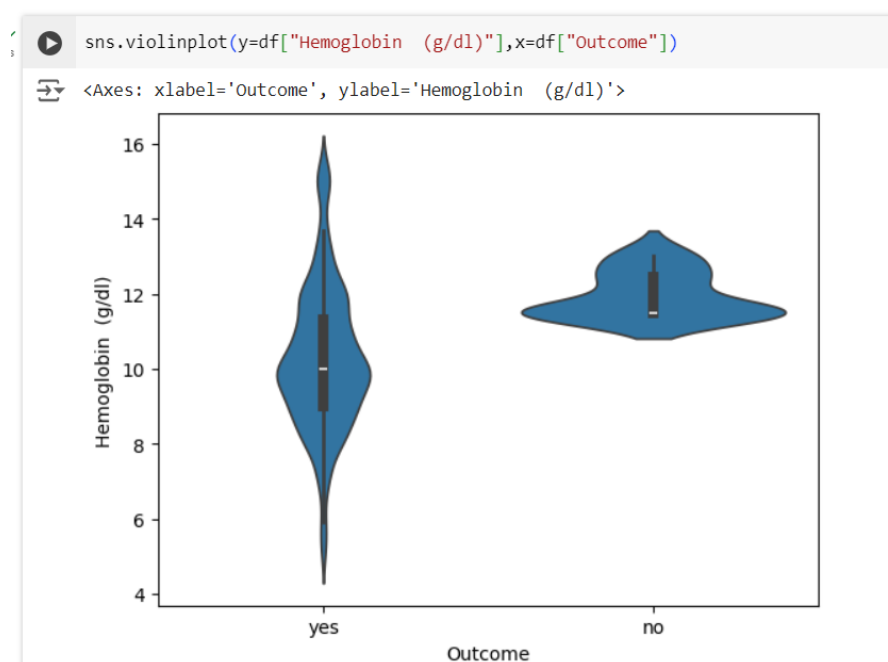
Median Total Protein Levels:

The median total protein level in patients with liver cirrhosis is slightly higher than in those without liver cirrhosis, as indicated by the white dot in the center of each violin.

Double-click (or enter) to edit

PROTEIN LEVEL HAS CONSIDERABLE EFFECT ON OUTCOME

✓ How does haemoglobin affect the outcome



Inference:

Distribution:

Cirrhosis ("yes"): Hemoglobin levels range broadly from approximately 4 g/dl to 16 g/dl.

No cirrhosis ("no"): Hemoglobin levels are more concentrated, ranging from about 11 g/dl to 14 g/dl. Median Levels:

Cirrhosis: The median hemoglobin level is around 10 g/dl.

No Cirrhosis: The median hemoglobin level is also around 11.5 g/dl.

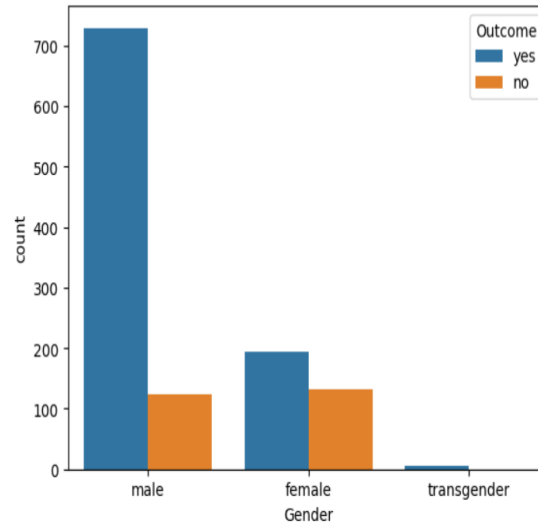
Comparison:

- Liver disease is associated with a wider range of hemoglobin levels.
- No liver disease shows more consistent hemoglobin levels centered around 11.5 g/dl.

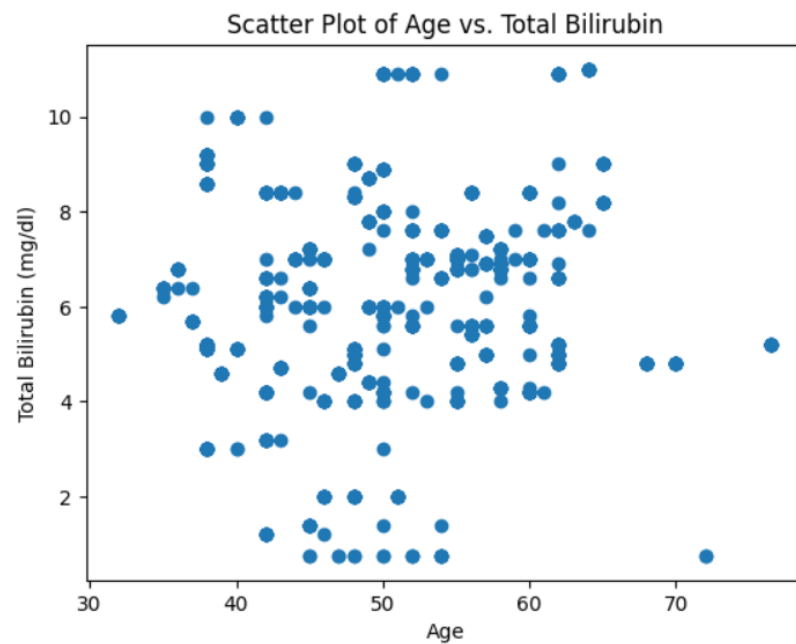
How does the distribution of gender affect the outcome

```
sns.countplot(data=df, x="Gender", hue="Outcome")
```

<Axes: xlabel='Gender', ylabel='count'>



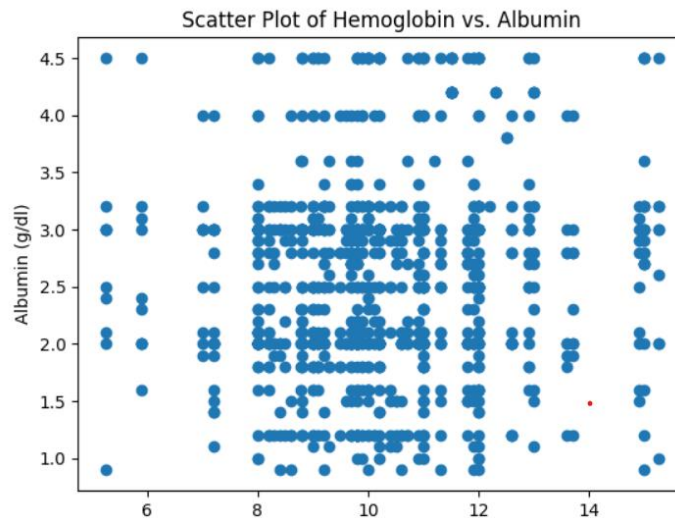
Scatter Plots:



Inference:

No Clear Trend:

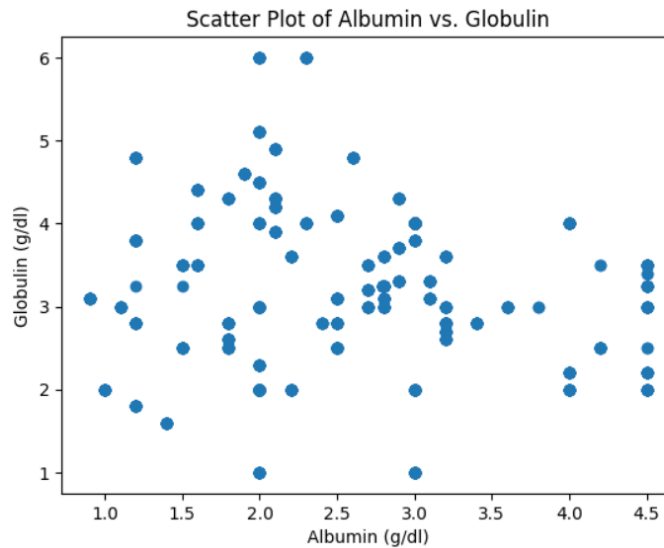
- There doesn't appear to be a clear linear relationship between age and Total Bilirubin levels.
- Total Bilirubin levels are spread across the age range without a consistent pattern.



Inference:

A large cluster of data points is concentrated around Haemoglobin levels of 8 to 12 g/dl and Albumin levels of 1.3 to 3 g/dl.

This suggests that most individuals in the dataset have Haemoglobin levels within this range.



Inference:

Inferences from the Scatter Plot of Albumin vs. Globulin:

1. No Strong Correlation:

- The scatter plot indicates no strong linear relationship between albumin and globulin levels. The data points are widely scattered, suggesting that variations in albumin levels do not directly predict changes in globulin levels.

2. Range of Values:

- Most albumin levels fall within the range of 2.0 to 4.0 g/dl, while globulin levels range from 2.0 to 5.0 g/dl. There are some outliers with higher globulin levels up to 6.0 g/dl and albumin levels up to 4.5 g/dl, indicating diverse liver function profiles among the patients.

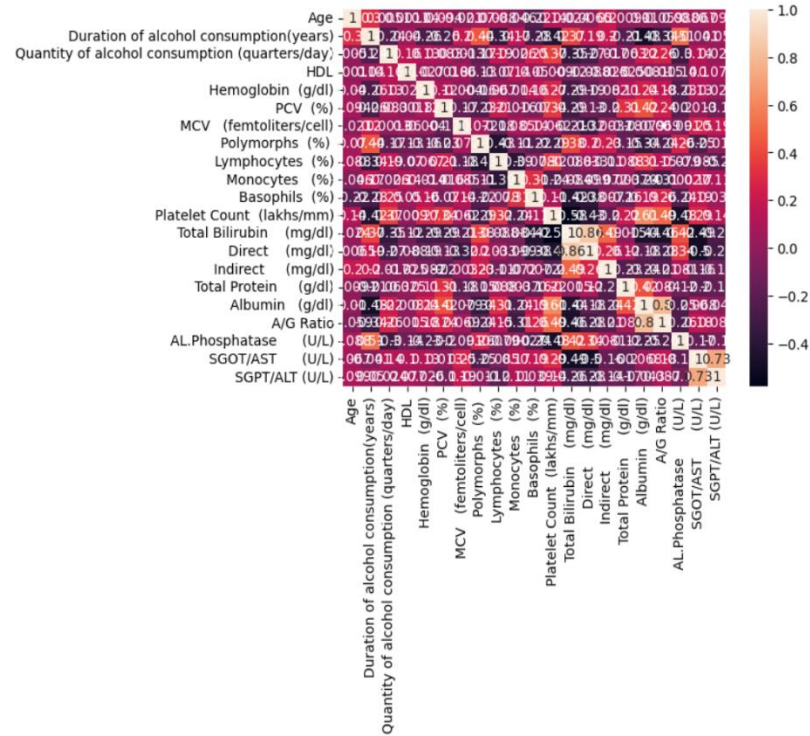
Correlation Matrix:

	Age	Duration of alcohol consumption(years)	Quantity of alcohol consumption (quarters/day)	HDL	Hemoglobin (g/dl)	PCV (%)	MCV (femtoliters/cell)	Polymorphs (%)	Lymphocytes (%)	Monocytes (%)	...	Platelet count (laks/mm)	Total Bilirubin (mg/dl)	Direct (mg/dl)	Indirect (mg/dl)
Age	1.000000	0.504880	-0.014838	0.027021	0.005643	0.097591	0.044536	0.102051	-0.051998	-0.017115	...	0.071371	0.111111	0.056810	0.241744
Duration of alcohol consumption(years)	0.504880	1.000000	0.013511	0.102488	-0.066525	-0.003214	0.275167	0.263651	-0.363089	0.199293	...	-0.093403	-0.180130	-0.250604	0.098370
Quantity of alcohol consumption (quarters/day)	-0.014838	0.013511	1.000000	0.087929	-0.028515	-0.106242	-0.003966	-0.001482	0.102467	-0.043940	...	0.111797	-0.058668	-0.070019	0.068496
HDL	0.027021	0.102488	0.087929	1.000000	-0.031386	-0.042923	-0.003529	-0.170594	-0.014607	0.114945	...	-0.145335	0.038456	-0.001202	0.038557
Hemoglobin (g/dl)	0.005643	-0.066525	-0.028515	-0.031386	1.000000	-0.006746	-0.026800	-0.023490	0.010444	-0.008577	...	0.021393	-0.046225	0.015173	-0.019270
PCV (%)	0.097591	-0.003214	-0.106242	-0.042923	-0.006746	1.000000	-0.215279	-0.061485	0.099363	-0.014051	...	0.260573	0.006346	0.124041	-0.147214
MCV (femtoliters/cell)	0.044536	0.275167	-0.003966	-0.003529	-0.026800	-0.215279	1.000000	0.096923	-0.223638	0.114024	...	0.029725	-0.301073	-0.408698	-0.007832
Polymorphs (%)	0.102051	0.263651	-0.001482	-0.170594	-0.023490	-0.061485	0.096923	1.000000	-0.479791	-0.128826	...	-0.095682	0.096292	-0.048245	0.163071
Lymphocytes (%)	-0.051998	-0.363089	0.102467	-0.014607	0.010444	0.099363	-0.223638	-0.479791	1.000000	-0.535430	...	0.382883	0.087118	0.220090	-0.092456
Monocytes (%)	-0.017115	0.199293	-0.043940	0.114945	-0.008577	-0.014051	0.114024	-0.128826	-0.535430	1.000000	...	-0.393730	-0.153523	-0.162125	-0.072557
Basophils (%)	-0.283272	-0.107265	0.139578	-0.072160	0.052103	-0.296938	0.119891	-0.069653	-0.180878	0.334910	...	-0.221665	-0.244269	-0.336547	0.084370
Platelet Count (laks/mm)	0.071371	-0.093403	0.111797	-0.145335	0.021393	0.260573	0.029725	-0.056582	0.382883	-0.393730	...	1.000000	-0.215804	-0.134197	-0.164128
Total Bilirubin (mg/dl)	0.111111	-0.180130	-0.058668	0.038456	-0.046225	0.006346	-0.301073	0.096292	0.087118	-0.153523	...	-0.215804	1.000000	0.860661	0.525814
Direct (mg/dl)	0.056810	-0.250604	-0.070019	-0.001202	0.015173	0.124041	-0.408698	-0.048245	0.220090	-0.162125	...	-0.134197	0.860661	1.000000	0.226658
Indirect (mg/dl)	0.241744	0.098370	0.068496	0.038557	-0.019270	-0.147214	-0.007832	0.163071	-0.092456	-0.072557	...	-0.164128	0.525814	0.226658	1.000000
Total Protein (g/dl)	0.061647	-0.127660	-0.176093	0.038159	0.036043	0.310499	-0.193946	-0.079210	0.180241	0.005474	...	0.165374	0.217946	0.357692	-0.214989
Albumin (g/dl)	-0.025472	-0.265224	-0.004464	-0.181625	0.069044	0.348276	-0.129655	-0.153799	0.387191	-0.344347	...	0.530975	-0.060116	0.085884	-0.020710
A/G Ratio	0.072670	-0.150173	0.128809	-0.173873	0.040801	0.120090	0.021159	-0.044456	0.197401	-0.391991	...	0.483932	-0.247892	-0.171140	-0.194788
AL Phosphatase (U/L)	0.117445	0.312634	-0.094731	-0.143857	-0.009615	0.003518	-0.043319	0.047370	0.006548	0.009877	...	-0.119343	0.030080	0.064650	-0.036866
SGOT/AST (U/L)	0.051609	0.305667	-0.062926	0.071819	-0.009007	-0.152265	0.278110	-0.100152	-0.215464	0.218727	...	0.037232	-0.345566	-0.372329	-0.115588

Multivariate Analysis

Heatmap:

<Axes: >



Columns having high correlation:

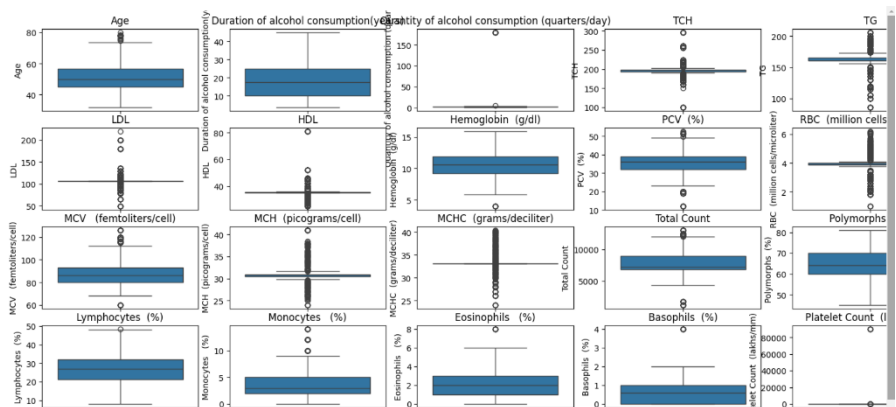
```
[450] correlation_matrix = df1.corr(numeric_only=True)
      high_correlation_pairs = []
      for i in range(len(correlation_matrix.columns)):
          for j in range(i + 1, len(correlation_matrix.columns)):
              if abs(correlation_matrix.iloc[i, j]) > 0.8:
                  high_correlation_pairs.append((correlation_matrix.columns[i], correlation_matrix.columns[j], correlation_matrix.iloc[i, j]))
      for pair in high_correlation_pairs:
          print(f"{pair[0]} and {pair[1]}: {pair[2] * 100:.2f}%")
```

Total Bilirubin (mg/dl) and Direct (mg/dl): 86.07%

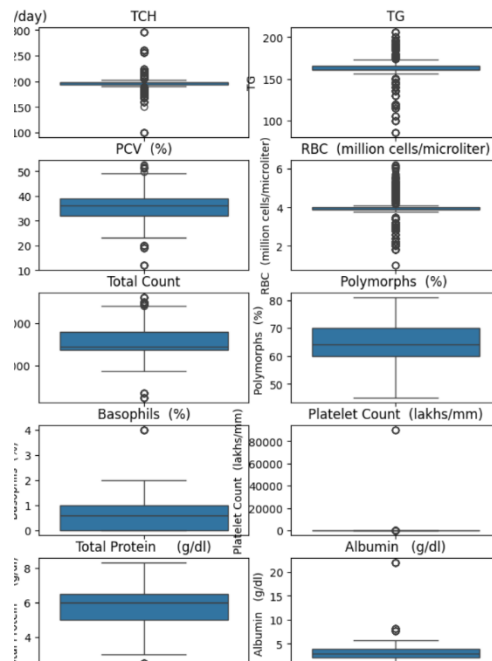
Identification using boxplot:

```
c=0
plt.figure(figsize=(20,15))
for i in df.columns:
    if(type(df[i][0])!=str):
        plt.subplot(7,5,c+1)
        # Attempt to convert the column to numeric, handling errors by coercing them to NaN
        sns.boxplot(df[i].apply(pd.to_numeric, errors='coerce'))
        plt.title(i)
        c=c+1
plt.show()
```

Outliers and
Anomalies



Removal

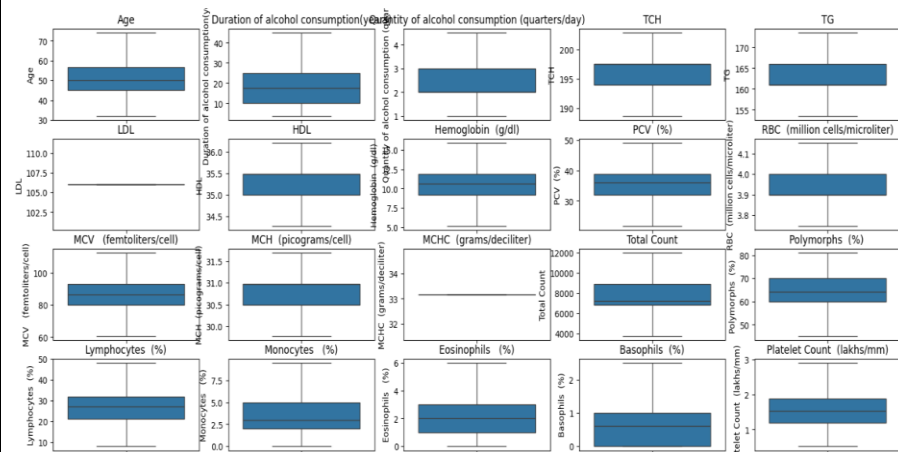


using IQR:

```
] def remove_outliers(df, columns):
    for col in columns:
        Q1 = df[col].quantile(0.25)
        Q3 = df[col].quantile(0.75)
        IQR = Q3 - Q1
        lower_bound = Q1 - 1.5 * IQR
        upper_bound = Q3 + 1.5 * IQR
        df[col] = np.where(df[col] < lower_bound, lower_bound, np.where(df[col] > upper_bound, upper_bound, df[col]))

numerical_columns = df.select_dtypes(include=['int64', 'float64']).columns
remove_outliers(df, numerical_columns)
```

After removing:



Data Preprocessing Code Screenshots

Loading Data

```
[890] df=pd.read_excel("HealthCareData.xlsx")
```

Handling Missing Data

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

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


Missing values in Data:

S.NO	0
Age	0
Gender	0
Place(location where the patient lives)	134
Duration of alcohol consumption(years)	0
Quantity of alcohol consumption (quarters/day)	0
Type of alcohol consumed	0
Hepatitis B infection	0
Hepatitis C infection	0
Diabetes Result	0
Blood pressure (mmhg)	0
Obesity	0
Family history of cirrhosis/ hereditary	0
TCH	359
TG	359
LDL	359
HDL	368
Hemoglobin (g/dl)	0
PCV (%)	30
RBC (million cells/microliter)	552
MCV (femtoliters/cell)	9
MCH (picograms/cell)	658
MCHC (grams/deciliter)	672
Total Count	10
Polymorphs (%)	0
Lymphocytes (%)	0
Monocytes (%)	9
Eosinophils (%)	8
Basophils (%)	49
Platelet Count (lakhs/mm)	0
Total Bilirubin (mg/dl)	0
Direct (mg/dl)	0
Indirect (mg/dl)	55
Total Protein (g/dl)	61
Albumin (g/dl)	9
Globulin (g/dl)	29
A/G Ratio	359
AL.Phosphatase (U/L)	10
SGOT/AST (U/L)	0
SGPT/ALT (U/L)	0
USG Abdomen (diffuse liver or not)	0
Predicted Value(Out Come-Patient suffering from liver cirrosis or not)	54

dtype: int64

Cleaning Numerical columns:

We can see TG LDL and Bilirubin are object type but they have numeric values

```
print(df["TG"].head(3))
print(df["LDL"].head(3))
print(df["Total Bilirubin (mg/dl)"].head(3))
```

```
0    115
1    115
2    115
Name: TG, dtype: object
0    120
1    120
2    120
Name: LDL, dtype: object
0     7
1     7
2     7
Name: Total Bilirubin (mg/dl), dtype: object
```

By using value_counts() we can notice that:

- TG contains a row - 130LDL
- LD contains a row - HDL
- Bilirubin contains a row - 0.4

```
[901] print(df["TG"].value_counts())
      print(df["LDL"].value_counts())
      print(df["Total Bilirubin (mg/dl)"].value_counts())
```

Dropping those rows

```
[902] df = df[df["TG"] != '130LDL']
      df = df[df["LDL"] != 'HDL']
      df = df[df["Total Bilirubin (mg/dl)"] != '0.4']
```

Converting into float

```
[903] df["TG"] = df["TG"].astype(float)
      df["LDL"] = df["LDL"].astype(float)
      df["Total Bilirubin (mg/dl)"] = df["Total Bilirubin (mg/dl)"].astype(float)
```

Filling numeric columns with mean:

Filling all numerical columns with their mean

```
[904] numerical_columns = df.select_dtypes(include=['int64', 'float64']).columns
      for col in numerical_columns:
          df[col].fillna(df[col].mean(), inplace=True)

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

S.NO	0
Age	0
Gender	0
Place(location where the patient lives)	133
Duration of alcohol consumption(years)	0
Quantity of alcohol consumption (quarters/day)	0
Type of alcohol consumed	0
Hepatitis B infection	0
Hepatitis C infection	0
Diabetes Result	0
Blood pressure (mmhg)	0
Obesity	0
Family history of cirrhosis/ hereditary	0
TCH	0
TG	0
LDL	0
HDL	0
Hemoglobin (g/dl)	0
PCV (%)	0
RBC (million cells/microliter)	0
MCV (femtoliters/cell)	0
MCH (picograms/cell)	0
MCHC (grams/deciliter)	0
Total Count	0
Polymorphs (%)	0
Lymphocytes (%)	0
Monocytes (%)	0
Eosinophils (%)	0
Basophils (%)	0
Platelet Count (lakhs/mm)	0
Total Bilirubin (mg/dl)	0
Direct (mg/dl)	0
Indirect (mg/dl)	0
Total Protein (g/dl)	0
Albumin (g/dl)	0
Globulin (g/dl)	0
A/G Ratio	437
AL.Phosphatase (U/L)	0
SGOT/AST (U/L)	0
SGPT/ALT (U/L)	0
USG Abdomen (diffuse liver or not)	0
Predicted Value(Out Come-Patient suffering from liver cirrosis or not)	54
dtype: int64	

Cleaning Abnormalities found in data:

Removing the abnormalities

```
✓ [403] df = df[df["Platelet Count (lakhs/mm)"] != 90000.000]
```

```
[399] df["Quantity of alcohol consumption (quarters/day)"].value_counts()
```

```
Quantity of alcohol consumption (quarters/day)
2      520
3      198
1      158
4       54
180     16
5         1
Name: count, dtype: int64
```

Removing the abnormalities

```
[400] df["Quantity of alcohol consumption (quarters/day)"] = df["Quantity of alcohol consumption (quarters/day)"].replace(180, 5)
```

```
[401] df["Quantity of alcohol consumption (quarters/day)"].value_counts()
```

```
Quantity of alcohol consumption (quarters/day)
2      520
3      198
1      158
4       54
5        17
Name: count, dtype: int64
```

```
df=df[df["Albumin (g/dl)"]!=22.0]
```

```
df=df[df["Globulin (g/dl)"]!=30.0]
```

Cleaning A/G Ratio:

Making it in the correct format

```
[907] df["A/G Ratio"] = round(df["Albumin (g/dl)"]/df["Globulin (g/dl)"],2)
```

```
[908] df["A/G Ratio"].value_counts()
```

```
A/G Ratio
1.00     99
0.75     87
0.67     49
0.43     30
0.50     30
..
1.46      1
1.11      1
1.84      1
1.29      1
2.08      1
Name: count, Length: 137, dtype: int64
```

```
[909] df["A/G Ratio"]=df["A/G Ratio"].astype(float)
```

```
[910] df["A/G Ratio"].fillna(df["A/G Ratio"].mean(), inplace=True)
```

Cleaning And Transforming Blood Pressure:

```
df["Blood pressure (mmhg)"] = df["Blood pressure (mmhg)"].str.replace('/', '/').str.split('/').apply(lambda x: float(x[0]) / float(x[1]))
```

[+ Code](#)
[+ Text](#)

Cleansing Categorical Columns:

✓ Viewing the spread of data in Categorical columns

```
for i in df.columns:
    if df[i].dtype == 'object' and i!="Blood pressure (mmhg)":
        print(df[i].value_counts())
        print("-"*50)
```

```
Gender
male      841
female    194
female     133
transgender 5
Name: count, dtype: int64
```

```
Place(location where the patient lives)
rural    566
urban    473
ocun      1
Name: count, dtype: int64
```

```
Type of alcohol consumed
country liquor    586
branded liquor    299
both              287
branded liquor     1
Name: count, dtype: int64
```

```
Hepatitis B infection
negative    909
Positive    263
positive     1
Name: count, dtype: int64
```

```
Hepatitis C infection
negative    920
Positive    251
positive     2
Name: count, dtype: int64
```

```
Diabetes Result
YES        647
NO         526
Name: count, dtype: int64
```

```
Obesity
no         624
yes        549
Name: count, dtype: int64
```

```
Family history of cirrhosis/ hereditary
no         984
yes        177
husband     12
Name: count, dtype: int64
```

```
USG Abdomen (diffuse liver or not)
YES        910
no         263
..         ..
```

Removing all the abnormalities:

Cleaning the Place column

```
[913] df = df[df['Place(location where the patient lives)'] != 'ocun']
```

Cleaning the Gender column

```
[914] df["Gender"].replace("female ", "female", inplace=True)
```



<ipython-input-914-fc8ed781fdc6>:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: <https://pandas.pydata.org/pandas-docs/stable>
df["Gender"].replace("female ", "female", inplace=True)

```
[915] df["Gender"].value_counts()
```



```
Gender
male      840
female    327
transgender    5
Name: count, dtype: int64
```

Cleaning alcohol consumption

```
[916] df["Type of alcohol consumed"].replace(" branded liquor", "branded liquor", inplace=True)
```



<ipython-input-916-54b9cbf74f34>:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
df["Type of alcohol consumed"].replace(" branded liquor", "branded liquor", inplace=True)

```
[917] df["Type of alcohol consumed"].value_counts()
```



```
Type of alcohol consumed
country liquor    586
branded liquor   300
both              286
Name: count, dtype: int64
```

Cleaning hepatitis column

```
[918] df["Hepatitis B infection"].replace("Positive", "positive", inplace=True)
df["Hepatitis C infection"].replace("Positive", "positive", inplace=True)
```

```
[919] df["Hepatitis B infection"].value_counts()
```



```
Hepatitis B infection
negative    908
positive    264
```

```
[920] df["Hepatitis C infection"].value_counts()
```

```
Hepatitis C infection
negative    919
positive    253
Name: count, dtype: int64
```

Cleaning family history column

```
[921] df["Family history of cirrhosis/ hereditary"].replace("husband", "yes", inplace=True)
df["Family history of cirrhosis/ hereditary"].value_counts()
```

```
Family history of cirrhosis/ hereditary
no      983
yes     189
Name: count, dtype: int64
```

Converting rest of columns to proper format

```
[922] df["Predicted Value(Out Come-Patient suffering from liver cirrosis or not)"].replace("YES", "yes", inplace=True)
df["Predicted Value(Out Come-Patient suffering from liver cirrosis or not)"].value_counts()
```

```
Predicted Value(Out Come-Patient suffering from liver cirrosis or not)
yes      874
no       244
Name: count, dtype: int64
```

After cleaning:

```
Gender
male      840
female    327
transgender    5
Name: count, dtype: int64
```

```
Place(location where the patient lives)
rural    566
urban    473
Name: count, dtype: int64
```

```
Type of alcohol consumed
country liquor    586
branded liquor    300
both              286
Name: count, dtype: int64
```

```
Hepatitis B infection
negative    908
positive    264
Name: count, dtype: int64
```

```
Hepatitis C infection
negative    919
positive    253
Name: count, dtype: int64
```

```
Diabetes Result
YES        647
NO         525
Name: count, dtype: int64
```

```
Obesity
no         623
yes        549
Name: count, dtype: int64
```

```
Family history of cirrhosis/ hereditary
no      983
yes     189
Name: count, dtype: int64
```

```
USG Abdomen (diffuse liver or not)
YES      910
no       262
Name: count, dtype: int64
```

Cleaning the outcome:

```
[50] df["Outcome"].value_counts()
```

```
Outcome
yes      859
no        18
Name: count, dtype: int64
```

```
df["Outcome"].isnull().sum()
```

```
54
```

Filling all null values of the column with yes

```
[52] df["Outcome"].fillna("yes", inplace=True)
```

Data Transformation

Encoding all the categorical columns:

```
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
for i in X.columns:
    if X[i].dtype == 'object':
        X[i] = le.fit_transform(X[i])
```

```
y_encoded = (le.fit_transform(y))
```

Encoded Data:

	Age	Quantity of alcohol consumption (quarters/day)	Diabetes Result	Blood pressure (mmhg)	Hemoglobin (g/dl)	PCV (%)	Polymorphs (%)	Lymphocytes (%)	Platelet count (lakhs/mm)	Total Bilirubin (mg/dl)	Indirect (mg/dl)	Total Protein (g/dl)	Albumin (g/dl)	Globulin (g/dl)
0	55.0	2.0	1	32	12.0	40.0	60.0	35.0	1.5	7.0	3.0	6.0	3.0	4.0
1	55.0	2.0	1	32	9.2	40.0	60.0	35.0	1.5	7.0	3.0	6.0	3.0	4.0
2	55.0	2.0	1	32	10.2	40.0	60.0	35.0	1.5	7.0	3.0	6.0	3.0	4.0
3	55.0	2.0	0	32	7.2	40.0	60.0	35.0	1.5	7.0	3.0	6.0	3.0	4.0
4	55.0	2.0	1	32	10.2	40.0	60.0	35.0	1.5	7.0	3.0	6.0	3.0	4.0

Feature Engineering

Feature Importance:

```
from sklearn.ensemble import RandomForestClassifier

model = RandomForestClassifier(n_estimators=100)
model.fit(X, y)
importances = model.feature_importances_

# Print feature importances
for feature, importance in zip(X.columns, importances):
    print(f"{feature}: {importance:.4f}")
```

```
Age: 0.0006
Gender: 0.0000
Duration of alcohol consumption(years): 0.1940
Quantity of alcohol consumption (quarters/day): 0.0206
Type of alcohol consumed: 0.0000
Hepatitis B infection: 0.0000
Hepatitis C infection: 0.0000
Diabetes Result: 0.0044
Blood pressure (mmhg): 0.0001
Obesity: 0.0000
Family history of cirrhosis/ hereditary: 0.0001
TCH: 0.0001
TG: 0.0001
LDL: 0.0002
HDL: 0.0003
Hemoglobin (g/dl): 0.0011
PCV (%): 0.0007
RBC (million cells/microliter): 0.0282
MCV (femtoliters/cell): 0.0007
MCH (picograms/cell): 0.0194
MCHC (grams/deciliter): 0.0534
Total Count: 0.0010
Polymorphs (%) : 0.0104
Lymphocytes (%): 0.0058
Monocytes (%): 0.0025
Eosinophils (%): 0.0000
Basophils (%): 0.0074
Platelet Count (lakhs/mm): 0.0203
Total Bilirubin (mg/dl): 0.1604
Direct (mg/dl): 0.1125
Indirect (mg/dl): 0.0092
Total Protein (g/dl): 0.0024
Albumin (g/dl): 0.0800
Globulin (g/dl): 0.0003
A/G Ratio: 0.0518
AL.Phosphatase (U/L): 0.0204
SGOT/AST (U/L): 0.0199
SGPT/ALT (U/L): 0.0114
USG Abdomen (diffuse liver or not): 0.1605
```

	<h3>Removing Unnecessary Features:</h3> <p>INFERENCE</p> <p>In the given output of feature importances from the RandomForestClassifier model, features have an importance score of 0 or very less features are:</p> <p>Gender</p> <p>Hepatitis B infection</p> <p>Hepatitis C infection</p> <p>Family history of cirrhosis/ hereditary</p> <p>TCH</p> <p>TG</p> <p>LDL</p> <p>HDL</p> <p>MCV (femtoliters/cell)</p> <p>DROPPING ALL UNECESSARY COLUMNS</p> <pre> 08 [953] drop_col=["Type of alcohol consumed", "Gender", "Direct (mg/dl)", "MCH (picograms/cell)", "MCHC (grams/deciliter)", "Ob 08 [954] for col in drop_col: 08 if col in X.columns: 08 X.drop(columns=[col], inplace=True) </pre>
Save Processed Data	<pre> X.to_csv('new_data1.csv', index=False) </pre>