Data Collection and Preprocessing Phase

Data Exploration and Preprocessing Template

Dataset variables will be statistically analyzed to identify patterns and outliers, with Python employed for preprocessing tasks like normalization and feature engineering. Data cleaning will address missing values and outliers, ensuring quality for subsequent analysis and modeling, and forming a strong foundation for insights and predictions.

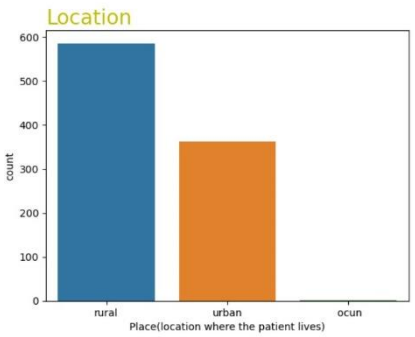
<table>
<tr><th>Section</th><th>Description</th></tr>
<tr><td>Data Overview</td><td><u>Dimension:</u>

949 rows × 39 columns

<u>Descriptive statistics:</u>

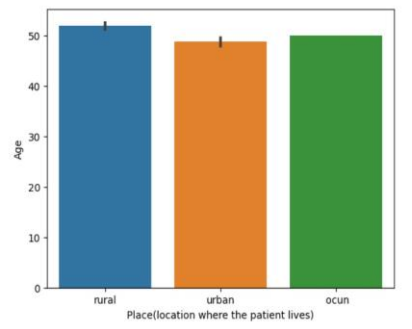
<table>
<tr><th></th><th>S.NO</th><th>Age</th><th>Duration of alcohol consumption(years)</th><th>Quantity of alcohol consumption (quarters/day)</th><th>TCH</th><th>HDL</th><th>Hemoglobin (g/dl)</th><th>PCV (%)</th><th>RBC (million cells/microliter)</th><th>MCV (femtoliters/cell)</th><th>...</th><th>Basophils (%)</th><th>Platelet Count (lakhs/mm)</th><th>Direct (mg/dl)</th><th>Indirect (mg/dl)</th></tr>
<tr><td>count</td><td>950.000000</td><td>950.000000</td><td>950.000000</td><td>950.000000</td><td>591.000000</td><td>582.000000</td><td>950.000000</td><td>920.000000</td><td>398.000000</td><td>941.000000</td><td>...</td><td>901.000000</td><td>950.000000</td><td>950.000000</td><td>895.000000</td></tr>
<tr><td>mean</td><td>475.500000</td><td>50.632632</td><td>20.606316</td><td>5.158947</td><td>197.544839</td><td>35.486254</td><td>10.263979</td><td>33.810000</td><td>3.390704</td><td>87.651435</td><td>...</td><td>0.498557</td><td>475.130042</td><td>4.040737</td><td>2.457542</td></tr>
<tr><td>std</td><td>274.385677</td><td>8.808272</td><td>7.980664</td><td>22.908785</td><td>26.694968</td><td>7.982057</td><td>1.942300</td><td>5.751592</td><td>0.937089</td><td>13.844181</td><td>...</td><td>0.712546</td><td>6515.406159</td><td>2.757443</td><td>1.093691</td></tr>
<tr><td>min</td><td>1.000000</td><td>32.000000</td><td>4.000000</td><td>1.000000</td><td>100.000000</td><td>25.000000</td><td>4.000000</td><td>12.000000</td><td>1.000000</td><td>60.000000</td><td>...</td><td>0.000000</td><td>0.520000</td><td>0.800000</td><td>0.200000</td></tr>
<tr><td>25%</td><td>238.250000</td><td>44.000000</td><td>15.000000</td><td>2.000000</td><td>180.000000</td><td>30.000000</td><td>9.000000</td><td>30.000000</td><td>2.825000</td><td>78.000000</td><td>...</td><td>0.000000</td><td>1.200000</td><td>2.700000</td><td>2.000000</td></tr>
<tr><td>50%</td><td>475.500000</td><td>50.000000</td><td>20.000000</td><td>2.000000</td><td>194.000000</td><td>35.000000</td><td>10.000000</td><td>35.000000</td><td>3.500000</td><td>87.000000</td><td>...</td><td>0.000000</td><td>1.420000</td><td>3.700000</td><td>2.300000</td></tr>
<tr><td>75%</td><td>712.750000</td><td>57.000000</td><td>26.000000</td><td>3.000000</td><td>210.000000</td><td>38.000000</td><td>11.500000</td><td>38.000000</td><td>4.000000</td><td>94.000000</td><td>...</td><td>1.000000</td><td>1.700000</td><td>4.200000</td><td>3.000000</td></tr>
<tr><td>max</td><td>950.000000</td><td>80.000000</td><td>45.000000</td><td>180.000000</td><td>296.000000</td><td>81.000000</td><td>15.900000</td><td>48.000000</td><td>5.700000</td><td>126.000000</td><td>...</td><td>4.000000</td><td>90000.000000</td><td>25.000000</td><td>6.600000</td></tr>
</table>
</td></tr>
<tr><td>Univariate Analysis</td><td>

```
sns.countplot(data=df,x='Place(location where the patient lives)')
plt.title("Location",color='y',size=20,loc='left')
plt.show()
```

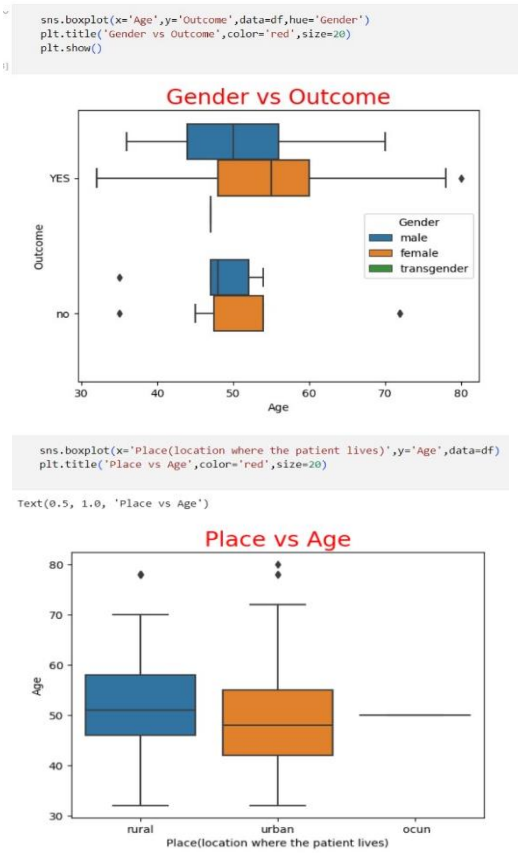



```
sns.barplot(x=df['Place(location where the patient lives)'],y=df['Age'])
```

```
<AxesSubplot:xlabel='Place(location where the patient lives)', ylabel='Age'>
```



</td></tr>
</table>

Bivariate Analysis	
Multivariate Analysis	

Outliers and Anomalies	
Data Preprocessing Code Screenshots	
Loading Data	``` # Loading the Dataset df = pd.read_excel('C:\SI project\Codes\Data\HealthCareData.xlsx') df.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	Blood pressure (mmhg)	Obesity	Family history of cirrhosis/ hereditary	TCH	TG	LDL	HDL	Hemoglobin (g/dl)	PCV (%)
0	1	55	male	rural	12	2	branded liquor	negative	negative	YES	138/90	yes	no	205.0	115	120	35.0	12.0	40.0
1	2	55	male	rural	12	2	branded liquor	negative	negative	YES	138/90	yes	no	205.0	115	120	35.0	9.2	40.0
2	3	55	male	rural	12	2	branded liquor	negative	negative	YES	138/90	no	no	205.0	115	120	35.0	10.2	40.0
3	4	55	male	rural	12	2	branded liquor	negative	negative	NO	138/90	no	no	NaN	NaN	NaN	NaN	7.2	40.0
4	5	55	female	rural	12	2	branded liquor	negative	negative	YES	138/90	no	no	205.0	115	120	35.0	10.2	40.0

Handling Missing Data

```
df['TCH']=df['TCH'].fillna(df['TCH'].mean())
df['HDL']=df['HDL'].fillna(df['HDL'].mean())
df['PCV  (%)']=df['PCV  (%)'].fillna(df['PCV  (%)'].mean())
df['RBC  (million cells/microliter)']=df['RBC  (million cells/microliter)'].fillna(df['RBC  (million cells/microliter)'].mean())
df['MCV  (femtoliters/cell)']=df['MCV  (femtoliters/cell)'].fillna(df['MCV  (femtoliters/cell)'].mean())
df['MCH  (picograms/cell)']=df['MCH  (picograms/cell)'].fillna(df['MCH  (picograms/cell)'].mean())
df['MCHC  (grams/deciliter)']=df['MCHC  (grams/deciliter)'].fillna(df['MCHC  (grams/deciliter)'].mean())
df['Total Count']=df['Total Count'].fillna(df['Total Count'].mean())
df['Monocytes  (%)']=df['Monocytes  (%)'].fillna(df['Monocytes  (%)'].mean())
df['Eosinophils  (%)']=df['Eosinophils  (%)'].fillna(df['Eosinophils  (%)'].mean())
df['Basophils  (%)']=df['Basophils  (%)'].fillna(df['Basophils  (%)'].mean())
df['Indirect  (mg/dl)']=df['Indirect  (mg/dl)'].fillna(df['Indirect  (mg/dl)'].mean())
df['Total Protein  (g/dl)']=df['Total Protein  (g/dl)'].fillna(df['Total Protein  (g/dl)'].mean())
df['Albumin  (g/dl)']=df['Albumin  (g/dl)'].fillna(df['Albumin  (g/dl)'].mean())
df['Globulin  (g/dl)']=df['Globulin  (g/dl)'].fillna(df['Globulin  (g/dl)'].mean())
df['AL.Phosphatase  (U/L)']=df['AL.Phosphatase  (U/L)'].fillna(df['AL.Phosphatase  (U/L)'].mean())
df['Place(location where the patient lives)']=df['Place(location where the patient lives)'].fillna(df['Place(location where the patient lives)'].mode(
df['TG']=df['TG'].fillna(df['TG'].mode()[0])
df['LDL']=df['LDL'].fillna(df['LDL'].mode()[0])
df['Outcome']=df['Outcome'].fillna(df['Outcome'].mode()[0])
df['Total Bilirubin  (mg/dl)']=df['Total Bilirubin  (mg/dl)'].fillna(df['Total Bilirubin  (mg/dl)'].mode()[0])
```

```
df['A/G Ratio']=df['A/G Ratio'].fillna(df['A/G Ratio'].mode()[0])
```

Data Transformation

```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
x_train = sc.fit_transform(x_train)
#x_test = sc.transform(x_test)
```

```
x_train
```

```
array([[ 2.44060333, -1.84159498,  1.29329571, ...,  1.08599342,
         4.92950302,  6.81450659],
       [ 0.15458485,  0.50365769,  1.29329571, ..., -0.83331467,
        -0.20286021, -0.14674577],
       [-1.44562809,  0.50365769,  1.29329571, ...,  0.49543709,
        -0.20286021, -0.14674577],
       ...,
       [ 0.72608947,  0.50365769, -0.76458992, ...,  0.27397846,
        -0.20286021, -0.14674577],
       [ 0.49748762, -1.84159498, -0.76458992, ...,  2.61774893,
        -0.20286021, -0.14674577],
       [ 0.15458485,  0.50365769, -0.76458992, ...,  0.20015892,
        -0.20286021, -0.14674577]])
```

```
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
```

```
for column in df.columns:
    # Check if the column has categorical data
    if df[column].dtype == 'object':
        # Perform label encoding
        df[column] = le.fit_transform(df[column])
```

Feature Engineering

```
categorical_features = df.select_dtypes(include=[np.object])
categorical_features.columns
```

```
Index(['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)', 'Outcome'],
      dtype='object')
```

```
numeric_features = df.select_dtypes(include=[np.number])
numeric_features.columns
```

```
Index(['S.NO', 'Age', 'Duration of alcohol consumption(years)',
       'Quantity of alcohol consumption (quarters/day)', 'TCH', 'HDL',
       'Hemoglobin  (g/dl)', 'PCV  (%)', 'RBC  (million cells/microliter)',
       'MCV   (femtoliters/cell)', 'MCH  (picograms/cell)',
       'MCHC  (grams/deciliter)', 'Total Count', 'Polymorphs  (%) ',
       'Lymphocytes  (%)', 'Monocytes   (%)', 'Eosinophils   (%)',
       'Basophils  (%)', 'Platelet Count  (lakhs/mm)', 'Direct    (mg/dl)',
       'Indirect     (mg/dl)', 'Total Protein     (g/dl)', 'Albumin   (g/dl)',
       'Globulin  (g/dl)', 'AL.Phosphatase      (U/L)', 'SGOT/AST      (U/L)',
       'SGPT/ALT (U/L)'],
      dtype='object')
```

Save Processed Data

```
# Save the cleaned and processed DataFrame to a CSV file
df.to_csv('cleaned_data.csv', index=False)
df.head()
```

✓ 0.0s

	Age	Gender	Place(location where the patient lives)	Duration of alcohol consumption(years)	Quantity of alcohol consumption (quarters/day)	Type of alcohol consumed	Diabetes Result	Blood pressure (mmhg)	Obesity
0	55.0	1	1	12.0	2.0	2	1	32	1
1	55.0	1	1	12.0	2.0	2	1	32	1
2	55.0	1	1	12.0	2.0	2	1	32	0
3	55.0	1	1	12.0	2.0	2	0	32	0
4	55.0	0	1	12.0	2.0	2	1	32	0