ASSIGNMENTDATE	**22SEPTEMBER2022**
STUDENTNAME	**NASINA BALA CHAITHANYA**
STUDENT ROLLNO	**110719104034**
MAXIMUMMARKS	**2 MARKS**

ASSIGNMENT:2

DataVisualizationandPre-processing

```
liver_data_train['HasDisease'].value_counts()
```

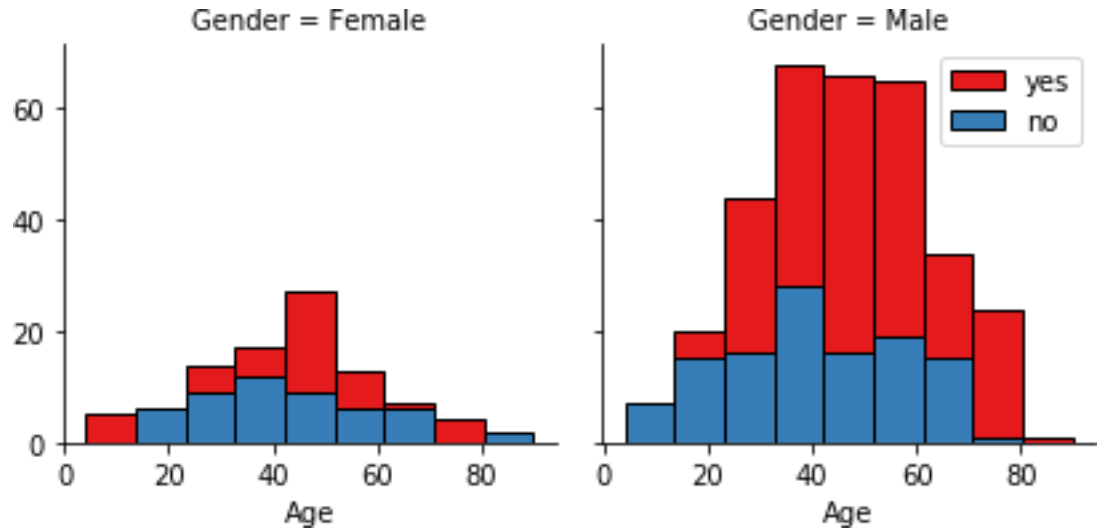
```
yes    416
no     167
Name:HasDisease,dtype:int64
```

Plottingsomecolumnstogaininsightsfromthedata

```
!condainstall-canacondaseaborn-y
```

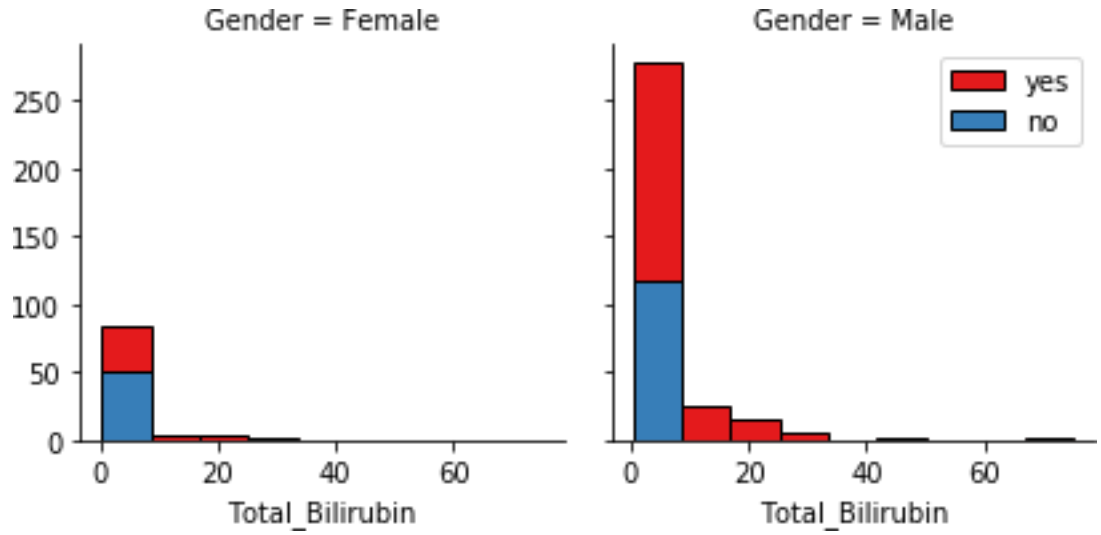
First,therelationshipbetweengenderandage

```
import seaborn as sns
bins = np.linspace(liver_data_train.Age.min(),
liver_data_train.Age.max(),10)grids = sns.FacetGrid(liver_data_train,
col="Gender", hue="HasDisease",palette="Set1",col_wrap=2)
grids.map(plt.hist,'Age',bins=bins,ec="k")

grids.axes[-
1].legend()plt.show()
```



Amountofbilirubinbasedongender

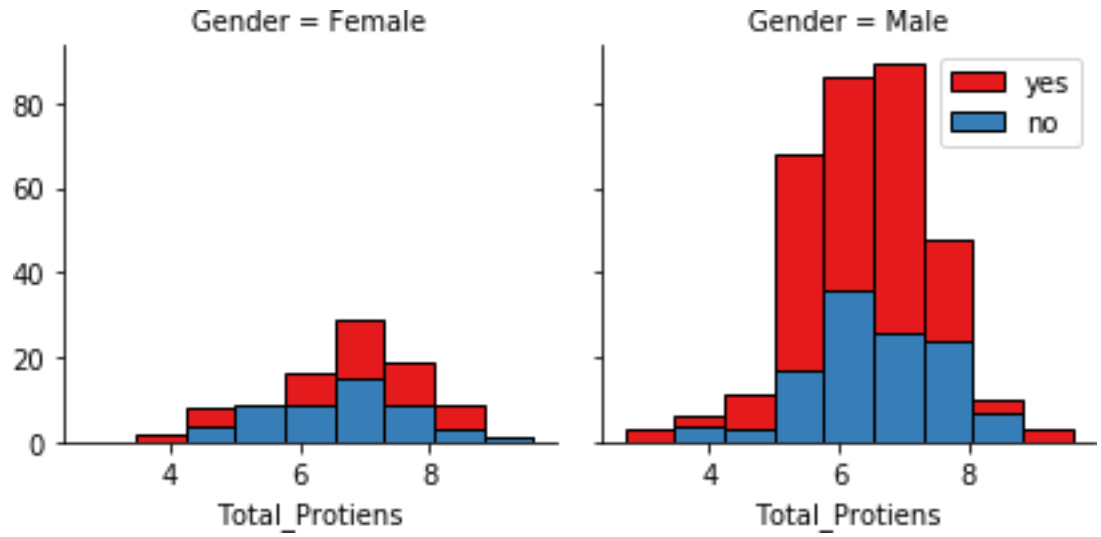
```
bins =
np.linspace(liver_data_train.Total_Bilirubin.min(),liver_
data_train.Total_Bilirubin.max(),10)
grids = sns.FacetGrid(liver_data_train, col="Gender",
hue="HasDisease",palette="Set1",col_wrap=2)
grids.map(plt.hist,'Total_Bilirubin',bins=bins,ec="k")

grids.axes[-
1].legend()plt.show()
```



Totalprotiensplayamajorroleinliverdisease.So plottingitgenderwise

```
bins =
np.linspace(liver_data_train.Total_Protiens.min(),liver_
data_train.Total_Protiens.max(),10)
grids = sns.FacetGrid(liver_data_train, col="Gender",
hue="HasDisease",palette="Set1",col_wrap=2)
grids.map(plt.hist,'Total_Protiens',bins=bins,ec="k")
```

grids.axes[-
1].legend()plt.show()



convertmales andfemales to0and1

liver_data_train['Gender'].replace(to_replace=['Male','Female'],value=[0,1],inplace=**True**)

Checkifanycolumnhas null valuesandreplacewithmean

liver_data_train.isna().sum()

Age 0
Gender 0
Total_Bilirubin 0
Direct_Bilirubin 0
Alkaline_Phosphotase 0
Alamine_Aminotransferase 0
Aspartate_Aminotransferase 0
Total_Protiens 0
Albumin 0
Albumin_and_Globulin_Ratio 4
Dataset 0
HasDisease 0
dtype:
int64liver_data_train['Albumin_and_Globulin_Ratio'].fillna((liver_data_train['Albumin_and_Globulin_Ratio'].mean()),inplace=**True**)