indian-liver-patient

February 28, 2024

0.1 Importing necessary libraries

[1]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn import metrics
from sklearn.neighbors import KNeighborsClassifier as KNN
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
```

[2]:
```
#Loading dataset
data = pd.read_csv("indian_liver_patient.csv")

df=data_raw.describe()
df.to_csv('cardio.csv')
df = pd.DataFrame(data)
```

[3]:
```
df.head()
```

[3]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	\
0	65	Female	0.7	0.1	187	
1	62	Male	10.9	5.5	699	
2	62	Male	7.3	4.1	490	
3	58	Male	1.0	0.4	182	
4	72	Male	3.9	2.0	195	

	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	\
0	16	18	6.8	
1	64	100	7.5	
2	60	68	7.0	
3	14	20	6.8	
4	27	59	7.3	

	Albumin	Albumin_and_Globulin_Ratio	Dataset

```
0      3.3                         0.90        1
1      3.2                         0.74        1
2      3.3                         0.89        1
3      3.4                         1.00        1
4      2.4                         0.40        1
```

[4]:
```
df.shape
```

[4]:
```
(583, 11)
```

[5]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 583 entries, 0 to 582
Data columns (total 11 columns):
 #   Column                      Non-Null Count  Dtype
---  ------                      --------------  -----
 0   Age                         583 non-null    int64
 1   Gender                      583 non-null    object
 2   Total_Bilirubin             583 non-null    float64
 3   Direct_Bilirubin            583 non-null    float64
 4   Alkaline_Phosphotase        583 non-null    int64
 5   Alamine_Aminotransferase    583 non-null    int64
 6   Aspartate_Aminotransferase  583 non-null    int64
 7   Total_Protiens              583 non-null    float64
 8   Albumin                     583 non-null    float64
 9   Albumin_and_Globulin_Ratio  579 non-null    float64
 10  Dataset                     583 non-null    int64
dtypes: float64(5), int64(5), object(1)
memory usage: 50.2+ KB
```

0.1.1 Null Values

[6]:
```
#Showing column wise %ge of NaN values they contains
null_col = []
for i in df.columns:
    print(i, df[i].isna().mean()*100)
    if df[i].isna().mean()*100 > 0:
        null_col.append(i)
```

```
Age 0.0
Gender 0.0
Total_Bilirubin 0.0
Direct_Bilirubin 0.0
Alkaline_Phosphotase 0.0
Alamine_Aminotransferase 0.0
Aspartate_Aminotransferase 0.0
Total_Protiens 0.0
```

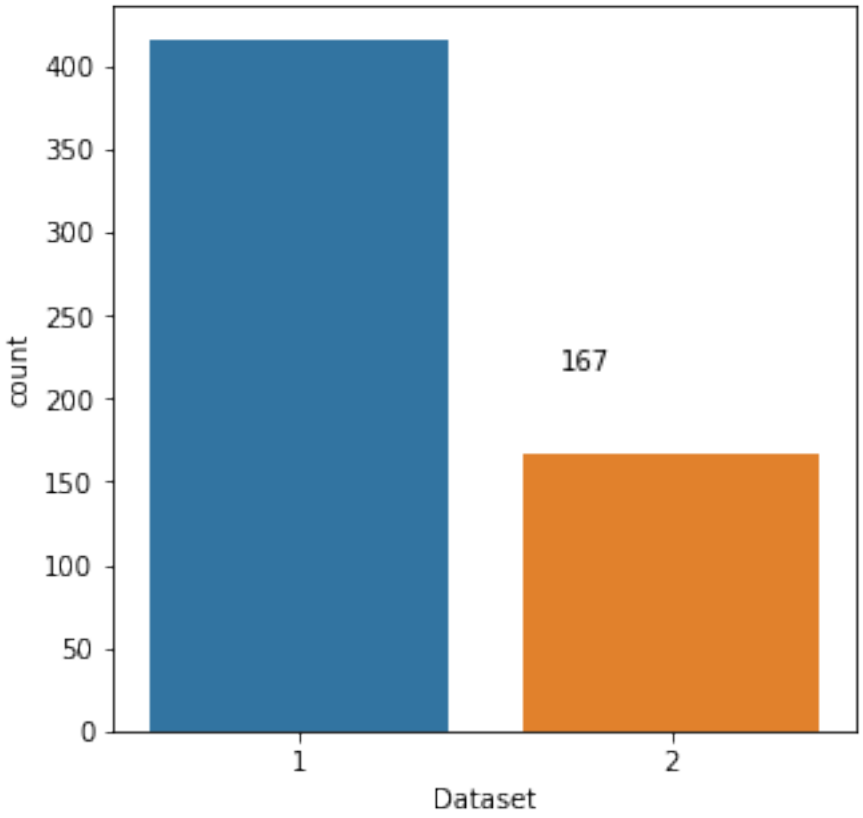
```
Albumin 0.0
Albumin_and_Globulin_Ratio 0.6861063464837049
Dataset 0.0
```

Filling null values of column *Albumin_and_Globulin_Ratio* with mean of column (as it is only column with few Nan values)

[7]:
```
for i in null_col:
    df[i] = df[i].fillna(df[i].mean())

# lets check for null values again
for i in df.columns:
    print(i, df[i].isna().mean()*100)
```

```
Age 0.0
Gender 0.0
Total_Bilirubin 0.0
Direct_Bilirubin 0.0
Alkaline_Phosphotase 0.0
Alamine_Aminotransferase 0.0
Aspartate_Aminotransferase 0.0
Total_Protiens 0.0
Albumin 0.0
Albumin_and_Globulin_Ratio 0.0
Dataset 0.0
```

[8]:
```
# Checking dataset balance or not

plt.figure(figsize=(5,5))
ax = sns.countplot(x='Dataset', data=df)

for p in ax.patches:
        ax.annotate('{}'.format(p.get_height()), (p.get_x()+0.1, p.
 ↪get_height()+50))
```



The bar graph easily shows how data is imbalanced. Less than 30% data is in class . So, first, we have to balance the data in to get more precise predictions.

For that I am using Over sampling it may have over fitting but under sampling result in low accurate.

0.1.2 Over sampling

[9]:
```
from imblearn.over_sampling import RandomOverSampler

oversample = RandomOverSampler()
x, y = oversample.fit_resample(df.drop(['Dataset'], axis=1), df['Dataset'])

new_df = pd.DataFrame(x, columns=df.drop(['Dataset'], axis=1).columns)
new_df['Dataset'] = y

new_df.head()
```

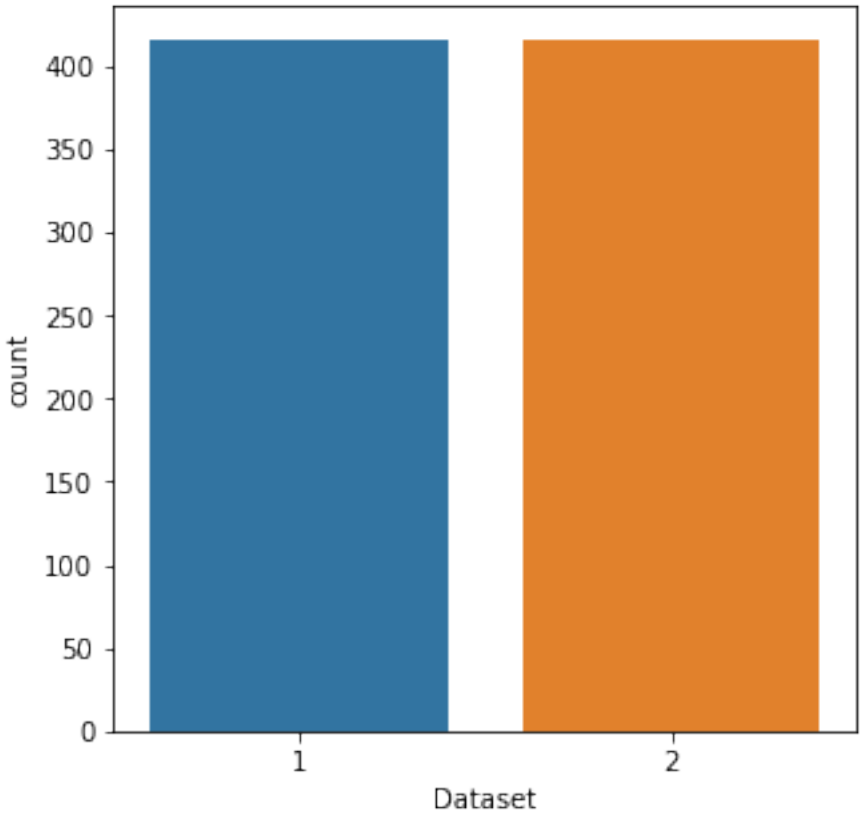
[9]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	\
0	65	Female	0.7	0.1	187	
1	62	Male	10.9	5.5	699	
2	62	Male	7.3	4.1	490	
3	58	Male	1.0	0.4	182	
4	72	Male	3.9	2.0	195	

	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	\
0	16	18	6.8	
1	64	100	7.5	
2	60	68	7.0	
3	14	20	6.8	
4	27	59	7.3	

	Albumin	Albumin_and_Globulin_Ratio	Dataset
0	3.3	0.90	1
1	3.2	0.74	1
2	3.3	0.89	1
3	3.4	1.00	1
4	2.4	0.40	1

[10]:
```
plt.figure(figsize=(5,5))
ax = sns.countplot(x='Dataset', data=new_df)

for p in ax.patches:
        ax.annotate('{}'.format(p.get_height()), (p.get_x()+0.1, p.
 ↪get_height()+50))
```



Here we can see that all the classes are balanced.

0.1.3 Lebel Encoding Gender

[11]:
```
from sklearn.preprocessing import LabelEncoder

enc = LabelEncoder()
new_df['Gender'] = enc.fit_transform(new_df['Gender'].astype('str'))
```

[12]:
```
new_df.head()
```

[12]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	\
0	65	0	0.7	0.1	187	
1	62	1	10.9	5.5	699	
2	62	1	7.3	4.1	490	
3	58	1	1.0	0.4	182	
4	72	1	3.9	2.0	195	

	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	\

```
0                          16                          18              6.8
1                          64                         100              7.5
2                          60                          68              7.0
3                          14                          20              6.8
4                          27                          59              7.3

   Albumin  Albumin_and_Globulin_Ratio  Dataset
0      3.3                        0.90        1
1      3.2                        0.74        1
2      3.3                        0.89        1
3      3.4                        1.00        1
4      2.4                        0.40        1
```

[13]:
```
new_df.shape
```

[13]:
```
(832, 11)
```

[14]:
```
new_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 832 entries, 0 to 831
Data columns (total 11 columns):
 #   Column                      Non-Null Count  Dtype
---  ------                      --------------  -----
 0   Age                         832 non-null    int64
 1   Gender                      832 non-null    int32
 2   Total_Bilirubin             832 non-null    float64
 3   Direct_Bilirubin            832 non-null    float64
 4   Alkaline_Phosphotase        832 non-null    int64
 5   Alamine_Aminotransferase    832 non-null    int64
 6   Aspartate_Aminotransferase  832 non-null    int64
 7   Total_Protiens              832 non-null    float64
 8   Albumin                     832 non-null    float64
 9   Albumin_and_Globulin_Ratio  832 non-null    float64
 10  Dataset                     832 non-null    int64
dtypes: float64(5), int32(1), int64(5)
memory usage: 68.4 KB
```

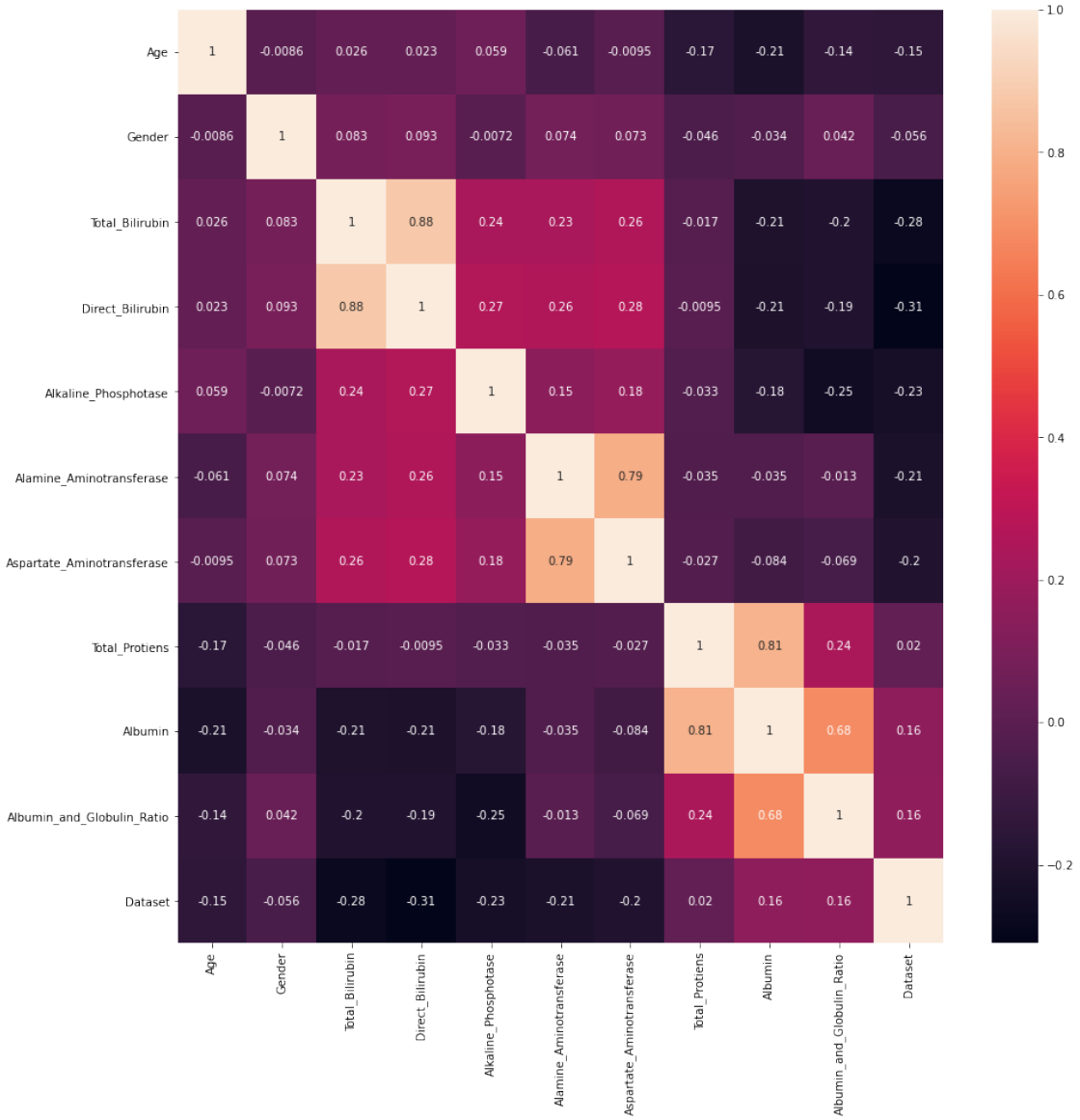
Since due to over sampling some of columns get converted in *objec* type, lets convert them back in numericals

[15]:
```
for i in new_df.select_dtypes(include=['object']).columns:
    new_df[i] = new_df[i].astype(str).astype(float)
```

0.1.4 Correlation Matrix

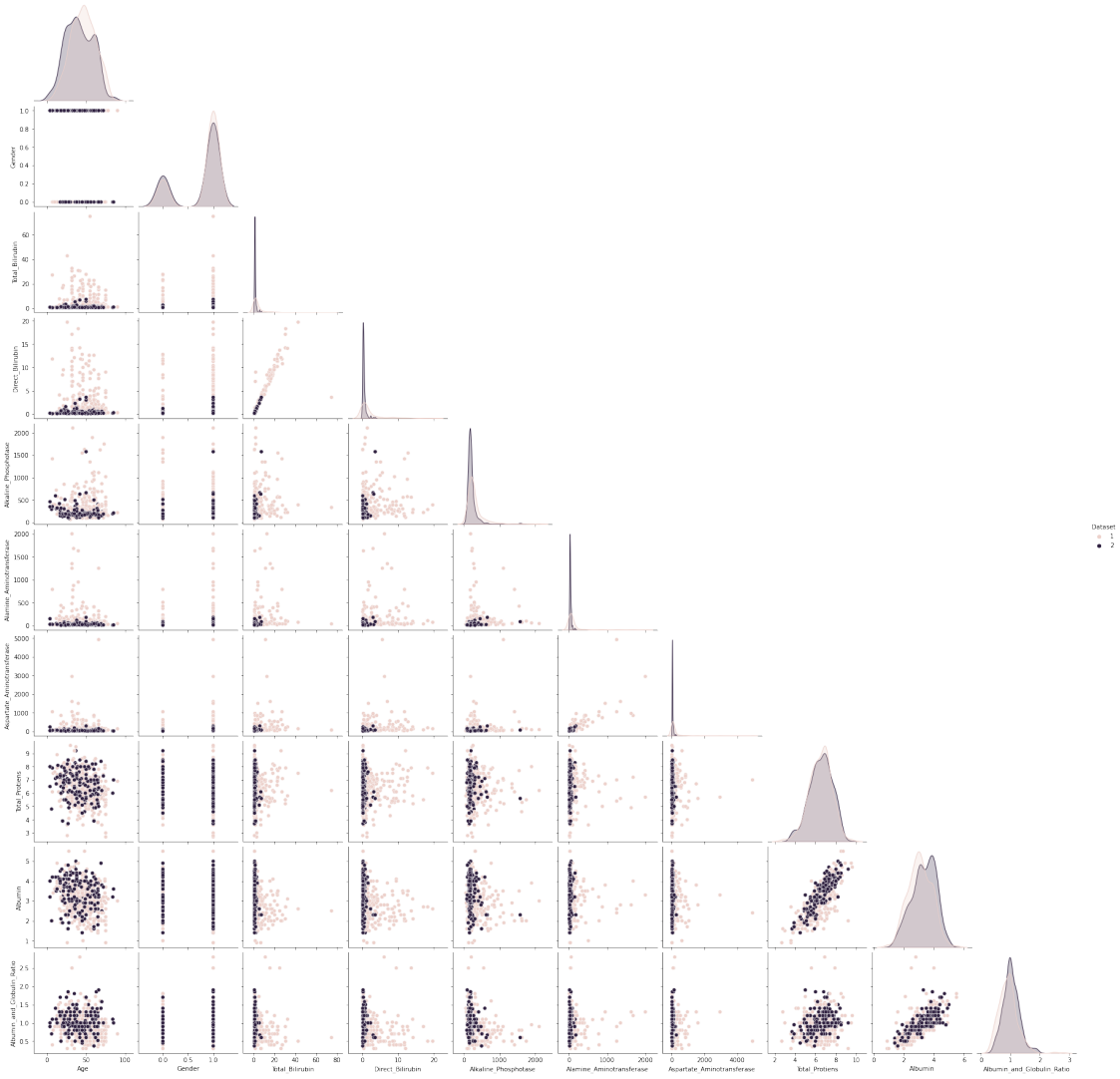
[16]:
```
cormap = new_df.corr()
fig, ax = plt.subplots(figsize=(15,15))
sns.heatmap(cormap, annot = True)
```

[16]: <AxesSubplot:>



[17]:
```
# Pair plot
sns.pairplot(data=new_df, hue='Dataset', corner=True)
```

[17]: <seaborn.axisgrid.PairGrid at 0x1882db6e280>



0.2 KNN

[18]:
```
X = new_df.drop(['Dataset'], axis=1)
y = new_df['Dataset']
```

[20]:
```
X.describe()
```

[20]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	\
count	832.000000	832.000000	832.000000	832.000000	
mean	43.640625	0.754808	2.677764	1.173197	
std	16.589964	0.430460	5.316799	2.417902	
min	4.000000	0.000000	0.400000	0.100000	
25%	32.000000	1.000000	0.700000	0.200000	
50%	43.500000	1.000000	0.900000	0.300000	

```
75%     57.000000    1.000000         1.900000          0.900000
max     90.000000    1.000000        75.000000         19.700000

       Alkaline_Phosphotase  Alamine_Aminotransferase  \
count            832.000000                832.000000
mean             267.673077                 66.506010
std              221.886971                154.914269
min               63.000000                 10.000000
25%              168.000000                 22.000000
50%              196.000000                 31.000000
75%              282.000000                 54.000000
max             2110.000000               2000.000000

       Aspartate_Aminotransferase  Total_Protiens     Albumin  \
count                  832.000000      832.000000  832.000000
mean                    89.758413        6.481010    3.186178
std                    244.626252        1.096203    0.797145
min                     10.000000        2.700000    0.900000
25%                     24.000000        5.800000    2.600000
50%                     38.000000        6.600000    3.200000
75%                     71.000000        7.200000    3.800000
max                   4929.000000        9.600000    5.500000

       Albumin_and_Globulin_Ratio
count                  832.000000
mean                     0.963730
std                      0.304998
min                      0.300000
25%                      0.800000
50%                      1.000000
75%                      1.100000
max                      2.800000
```

[19]:
```
print("\nInfo\n")
print(X.info())
print("\nMaximum\n")
print(X.max())
print("\nMinimum\n")
print(X.min())
```

```
Info

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 832 entries, 0 to 831
Data columns (total 10 columns):
 #   Column                      Non-Null Count  Dtype
```

```
---  ------                       --------------  -----
 0   Age                          832 non-null    int64
 1   Gender                       832 non-null    int32
 2   Total_Bilirubin              832 non-null    float64
 3   Direct_Bilirubin             832 non-null    float64
 4   Alkaline_Phosphotase         832 non-null    int64
 5   Alamine_Aminotransferase     832 non-null    int64
 6   Aspartate_Aminotransferase   832 non-null    int64
 7   Total_Protiens               832 non-null    float64
 8   Albumin                      832 non-null    float64
 9   Albumin_and_Globulin_Ratio   832 non-null    float64
dtypes: float64(5), int32(1), int64(4)
memory usage: 61.9 KB
None

Maximum

Age                             90.0
Gender                           1.0
Total_Bilirubin                 75.0
Direct_Bilirubin                19.7
Alkaline_Phosphotase          2110.0
Alamine_Aminotransferase      2000.0
Aspartate_Aminotransferase    4929.0
Total_Protiens                   9.6
Albumin                          5.5
Albumin_and_Globulin_Ratio       2.8
dtype: float64

Minimum

Age                              4.0
Gender                           0.0
Total_Bilirubin                  0.4
Direct_Bilirubin                 0.1
Alkaline_Phosphotase            63.0
Alamine_Aminotransferase        10.0
Aspartate_Aminotransferase      10.0
Total_Protiens                   2.7
Albumin                          0.9
Albumin_and_Globulin_Ratio       0.3
dtype: float64
```

[19]:
```
# Scale the data to be between -1 and 1
scaler = StandardScaler()
X = pd.DataFrame(scaler.fit_transform(X), columns=X.columns)
X.head()
```

[19]:
```
        Age    Gender  Total_Bilirubin  Direct_Bilirubin  \
0  1.285741 -1.743225        -0.362680         -0.432877
1  1.106555  0.573649         1.558454          1.803330
2  1.106555  0.573649         0.880407          1.223573
3  0.867642  0.573649        -0.306176         -0.308643
4  1.703840  0.573649         0.240029          0.353937

   Alkaline_Phosphotase  Alamine_Aminotransferase  Aspartate_Aminotransferase  \
0             -0.376569                 -0.325199                   -0.292878
1              2.049838                 -0.014999                    0.042570
2              1.059371                 -0.040849                   -0.088336
3             -0.400264                 -0.338124                   -0.284696
4             -0.338656                 -0.254112                   -0.125154

   Total_Protiens   Albumin  Albumin_and_Globulin_Ratio
0        0.268194  0.098981                   -0.252136
1        0.917387 -0.025606                   -0.762470
2        0.453677  0.098981                   -0.284032
3        0.268194  0.223567                    0.066822
4        0.731903 -1.022300                   -1.846929
```

0.2.1 Spliting Dataset into train and test set

[20]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.1)
```

0.2.2 Model Training

[21]:
```
model= KNN()
model.fit(X_train, y_train)
```

[21]:
```
KNeighborsClassifier()
```

[22]:
```
model.get_params()
```

[22]:
```
{'algorithm': 'auto',
 'leaf_size': 30,
 'metric': 'minkowski',
 'metric_params': None,
 'n_jobs': None,
 'n_neighbors': 5,
 'p': 2,
 'weights': 'uniform'}
```

0.2.3 Hyper parameter tunning

[23]:
```
from sklearn.model_selection import GridSearchCV
n_neighbors = [x for x in range(5, 86, 2)]
algorithm = ['auto', 'ball_tree', 'kd_tree', 'brute']
weights = ['uniform', 'distance']

grid = {'n_neighbors': n_neighbors,
        'algorithm': algorithm,
        'weights': weights}
```

[24]:
```
new_model = KNN()

knn_grid = GridSearchCV(estimator = new_model, param_grid = grid, cv = 7,␣
 ↪verbose=0)
knn_grid.fit(X_train, y_train)
```

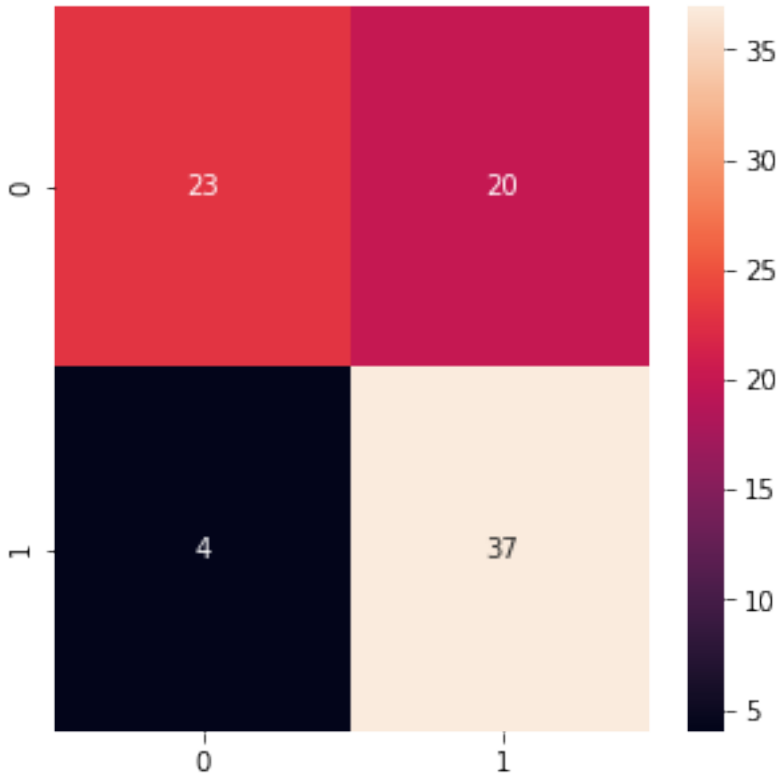
[24]:
```
GridSearchCV(cv=7, estimator=KNeighborsClassifier(),
             param_grid={'algorithm': ['auto', 'ball_tree', 'kd_tree', 'brute'],
                         'n_neighbors': [5, 7, 9, 11, 13, 15, 17, 19, 21, 23,
                                         25, 27, 29, 31, 33, 35, 37, 39, 41, 43,
                                         45, 47, 49, 51, 53, 55, 57, 59, 61, 63,
…],
                         'weights': ['uniform', 'distance']})
```

[25]:
```
knn_grid.best_params_
```

[25]:
```
{'algorithm': 'auto', 'n_neighbors': 17, 'weights': 'distance'}
```

[26]:
```
y_pred = knn_grid.best_estimator_.predict(X_test)
mat = confusion_matrix(y_test, y_pred)
fig, ax = plt.subplots(figsize=(5,5))
sns.heatmap(mat, annot = True)
```

[26]:
```
<AxesSubplot:>
```



[27]:
```
print("Accuracy Score {}".format(accuracy_score(y_test,y_pred)))
print("Classification report: {}".format(classification_report(y_test,y_pred)))
```

```
Accuracy Score 0.7142857142857143
Classification report:               precision    recall  f1-score   support

           1       0.85      0.53      0.66        43
           2       0.65      0.90      0.76        41

    accuracy                           0.71        84
   macro avg       0.75      0.72      0.71        84
weighted avg       0.75      0.71      0.70        84
```

0.2.4 Saving Model

[28]:
```
import pickle
pickle.dump(knn_grid.best_estimator_, open("Liver_disease.sav", 'wb'))
```

0.2.5 Loading Model

[29]:
```
import joblib
loaded_model = joblib.load("Liver_disease.sav")
```

[30]:
```
X.columns
```

[30]:
```
Index(['Age', 'Gender', 'Total_Bilirubin', 'Direct_Bilirubin',
       'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
       'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
       'Albumin_and_Globulin_Ratio'],
      dtype='object')
```

[31]:
```
df=pd.read_csv("indian_liver_patient.csv",usecols=['Age', 'Gender',␣
 ↪'Total_Bilirubin', 'Direct_Bilirubin',
       'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
       'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
       'Albumin_and_Globulin_Ratio',"Dataset"])

df.tail(2)
```

[31]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	\
581	31	Male	1.3	0.5	184	
582	38	Male	1.0	0.3	216	

	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	\
581	29	32	6.8	
582	21	24	7.3	

	Albumin	Albumin_and_Globulin_Ratio	Dataset
581	3.4	1.0	1
582	4.4	1.5	2

[32]:
```
df=pd.read_csv("indian_liver_patient.csv",usecols=['Age', 'Gender',␣
 ↪'Total_Bilirubin', 'Direct_Bilirubin',
       'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
       'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
       'Albumin_and_Globulin_Ratio'])
df["Gender"]=1
df["Gender"]=1
X1=[df.iloc[581].values]
X2=[df.iloc[582].values]
```

[33]:
```
print("X1 if person who is having liver problem:\n",X1)
print("\nX1 prediction is: ",loaded_model.predict(X1))
```

```
X1 if person who is having liver problem:
 [array([ 31. ,   1. ,   1.3,   0.5, 184. ,  29. ,  32. ,   6.8,   3.4,
```

```
          1. ])]
```

```
X1 prediction is:  [1]
```

X1 prediction is 1 means person having liver disease