LabTask4

September 15, 2019

1 Lab Task 4

Done by 16BIS0072 - Sangeeth Kumar V

1.1 Upload files

[32]:
```
from google.colab import files

uploaded = files.upload()

for fn in uploaded.keys():
  print('User uploaded file "{name}" with length {length} bytes'.format(
      name=fn, length=len(uploaded[fn])))
```

```
<IPython.core.display.HTML object>


Saving indian_liver_patient.csv to indian_liver_patient (1).csv
User uploaded file "indian_liver_patient.csv" with length 23347 bytes
```

1.2 Import necessary

[0]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.linear_model import LogisticRegression
```

1.3 Data Analysis

[34]:
```
liver_df = pd.read_csv('indian_liver_patient.csv')
liver_df.head()
```

[34]:
```
   Age  Gender  Total_Bilirubin  ...  Albumin  Albumin_and_Globulin_Ratio
Dataset
0   65  Female              0.7  ...      3.3                        0.90
1
1   62    Male             10.9  ...      3.2                        0.74
1
2   62    Male              7.3  ...      3.3                        0.89
1
3   58    Male              1.0  ...      3.4                        1.00
1
4   72    Male              3.9  ...      2.4                        0.40
1

[5 rows x 11 columns]
```

This data set contains 416 liver patient records and 167 non liver patient records collected from North East of Andhra Pradesh, India. The "Dataset" column is a class label used to divide groups into liver patient (liver disease) or not (no disease).

```
**Features available in the dataset are as follows**
```

[62]:
```
liver_df.columns
```

[62]:
```
Index(['Age', 'Gender', 'Total_Bilirubin', 'Direct_Bilirubin',
       'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
       'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
       'Albumin_and_Globulin_Ratio', 'Dataset', 'Gender_Female',
       'Gender_Male'],
      dtype='object')
```

[35]:
```
# Check for null values
liver_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 583 entries, 0 to 582
Data columns (total 11 columns):
Age                           583 non-null int64
Gender                        583 non-null object
Total_Bilirubin               583 non-null float64
Direct_Bilirubin              583 non-null float64
Alkaline_Phosphotase          583 non-null int64
Alamine_Aminotransferase      583 non-null int64
Aspartate_Aminotransferase    583 non-null int64
Total_Protiens                583 non-null float64
```

```
Albumin                        583 non-null float64
Albumin_and_Globulin_Ratio     579 non-null float64
Dataset                        583 non-null int64
dtypes: float64(5), int64(5), object(1)
memory usage: 50.2+ KB
```

Here is the observation from the dataset:

1. Only gender is non-numeric veriable. All others are numeric.
2. There are 10 features and 1 output - dataset. Value 1 indicates that the patient has liver disease and 0 indicates the patient does not have liver disease.

[36]:
```
liver_df.describe(include='all')
```

[36]:
```
               Age Gender  ...  Albumin_and_Globulin_Ratio     Dataset
count   583.000000    583  ...                  579.000000  583.000000
unique         NaN      2  ...                         NaN         NaN
top            NaN   Male  ...                         NaN         NaN
freq           NaN    441  ...                         NaN         NaN
mean     44.746141    NaN  ...                    0.947064    1.286449
std      16.189833    NaN  ...                    0.319592    0.452490
min       4.000000    NaN  ...                    0.300000    1.000000
25%      33.000000    NaN  ...                    0.700000    1.000000
50%      45.000000    NaN  ...                    0.930000    1.000000
75%      58.000000    NaN  ...                    1.100000    2.000000
max      90.000000    NaN  ...                    2.800000    2.000000

[11 rows x 11 columns]
```

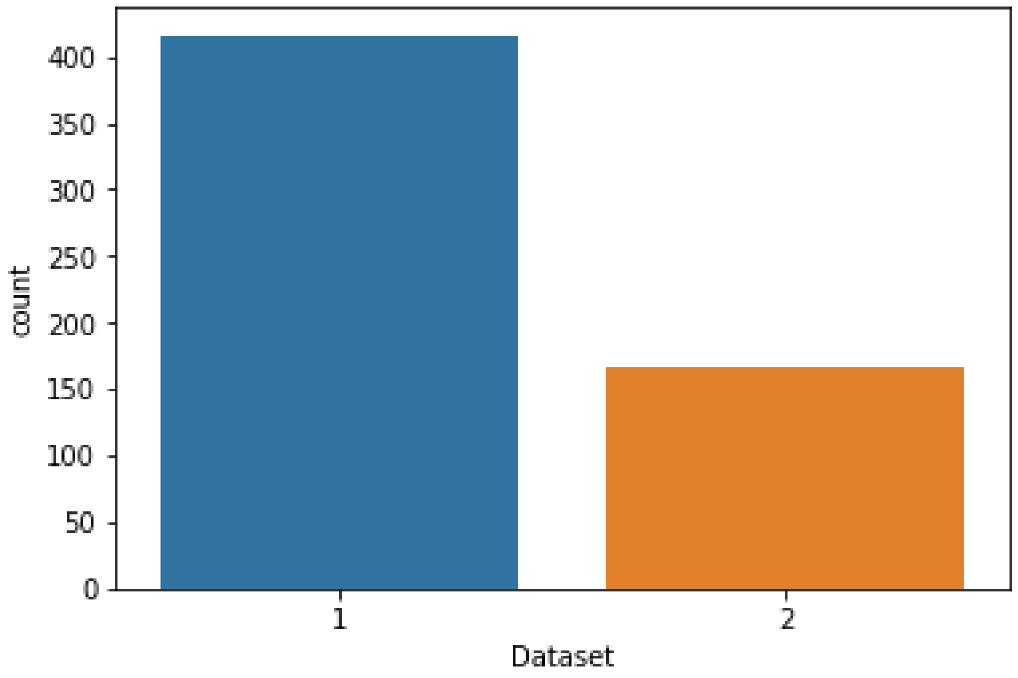
[37]:
```
liver_df.isnull().sum()
```

[37]:
```
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
dtype: int64
```

1.4 Data Visualization

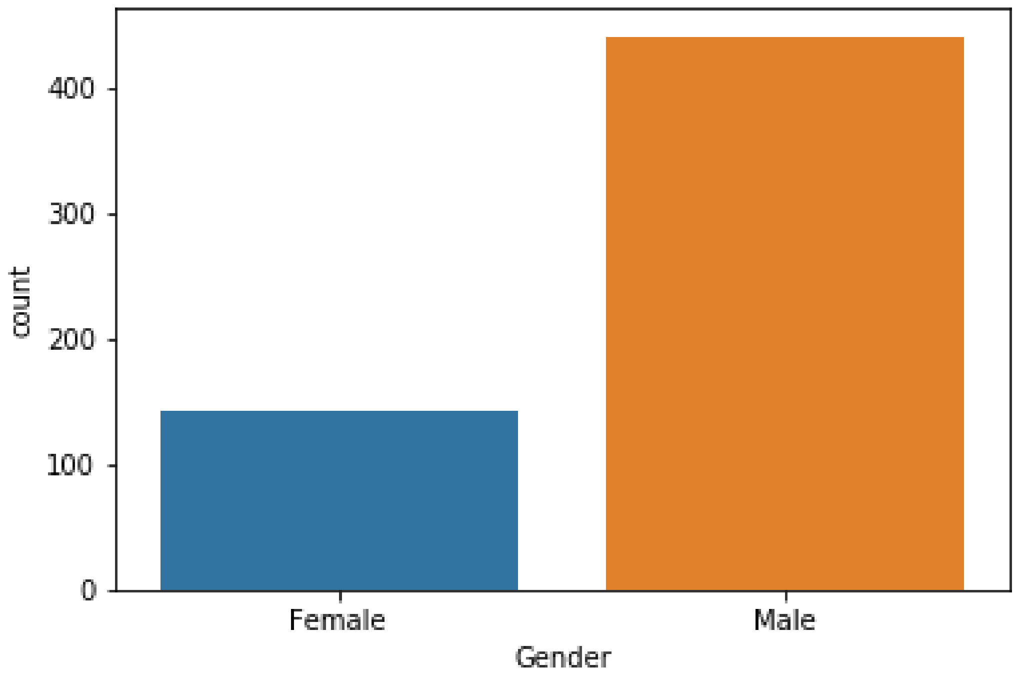
[38]:
```
sns.countplot(data=liver_df, x='Dataset', label='Count')
LD, NLD = liver_df['Dataset'].value_counts()
print('Number of patients diagnosed with liver disease: ', LD)
print('Number of patients not diagnosed with liver disease: ', NLD)
```

```
Number of patients diagnosed with liver disease:  416
Number of patients not diagnosed with liver disease:  167
```



[39]:
```
sns.countplot(data=liver_df, x='Gender', label='Count')
M, F = liver_df['Gender'].value_counts()
print('Number of patients that are male: ', M)
print('Number of patients that are female: ', F)
```

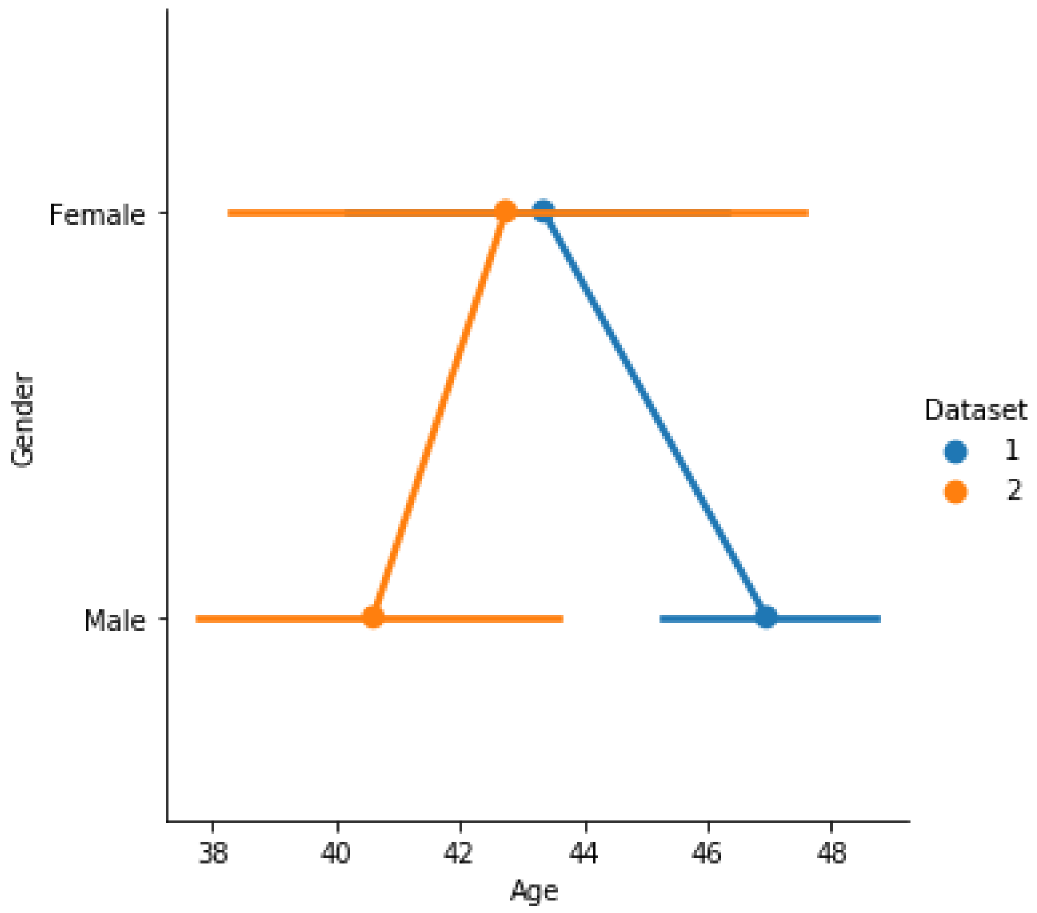
```
Number of patients that are male:  441
Number of patients that are female:  142
```



[40]:
```
sns.factorplot(x="Age", y="Gender", hue="Dataset", data=liver_df)
```

```
/usr/local/lib/python3.6/dist-packages/seaborn/categorical.py:3666: UserWarning:
The `factorplot` function has been renamed to `catplot`. The original name will
be removed in a future release. Please update your code. Note that the default
`kind` in `factorplot` (`'point'`) has changed `'strip'` in `catplot`.
  warnings.warn(msg)
```

[40]:
```
<seaborn.axisgrid.FacetGrid at 0x7f3303f34b00>
```



Age seems to be a factor for liver disease for both male and female genders

[41]:
```
liver_df[['Gender', 'Dataset', 'Age']]\
    .groupby(['Dataset', 'Gender'], as_index=False)\
    .count()\
    .sort_values(by='Dataset', ascending=False)
```

[41]:
```
   Dataset  Gender  Age
2        2  Female   50
3        2    Male  117
0        1  Female   92
1        1    Male  324
```

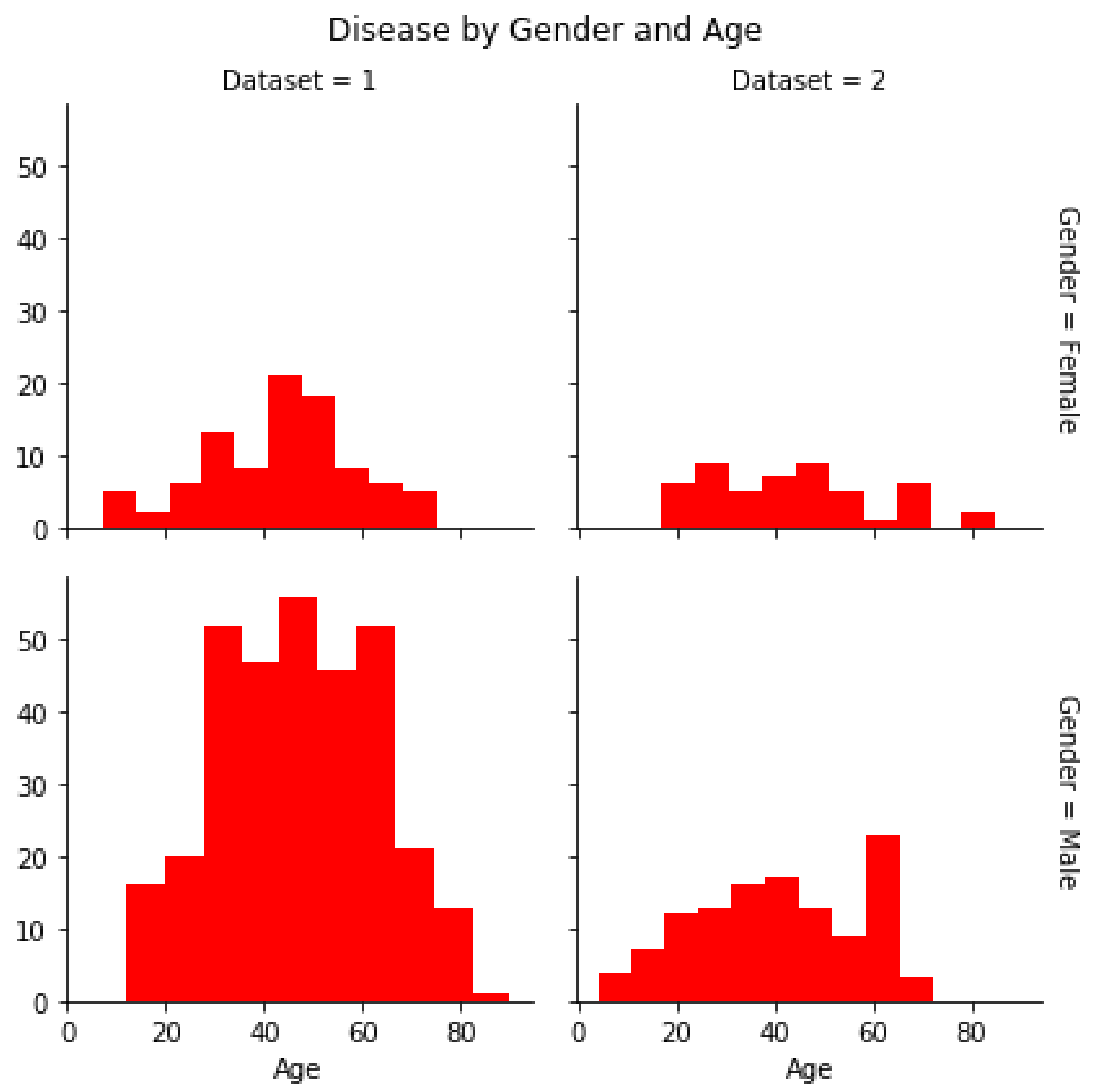
[42]:
```
liver_df[['Gender', 'Dataset', 'Age']]\
    .groupby(['Dataset', 'Gender'], as_index=False)\
    .mean()\
    .sort_values(by='Dataset', ascending=False)
```

[42]:
```
   Dataset  Gender        Age
2        2  Female  42.740000
3        2    Male  40.598291
```

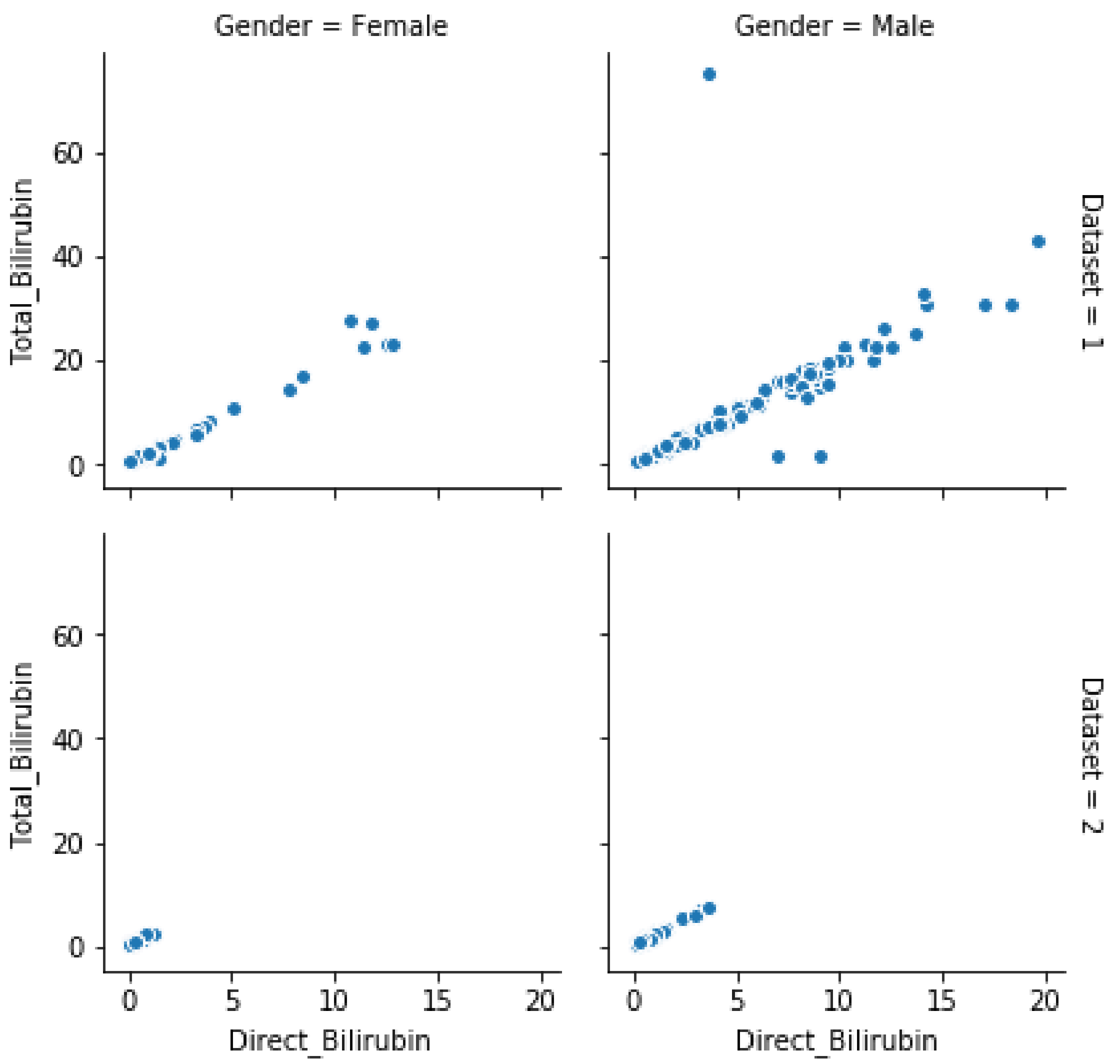
```
0         1  Female  43.347826
1         1    Male  46.950617
```

[43]:
```
g = sns.FacetGrid(liver_df, col="Dataset", row="Gender", margin_titles=True)
g.map(plt.hist, "Age", color="red")
plt.subplots_adjust(top=0.9)
g.fig.suptitle('Disease by Gender and Age')
```

[43]:
```
Text(0.5, 0.98, 'Disease by Gender and Age')
```



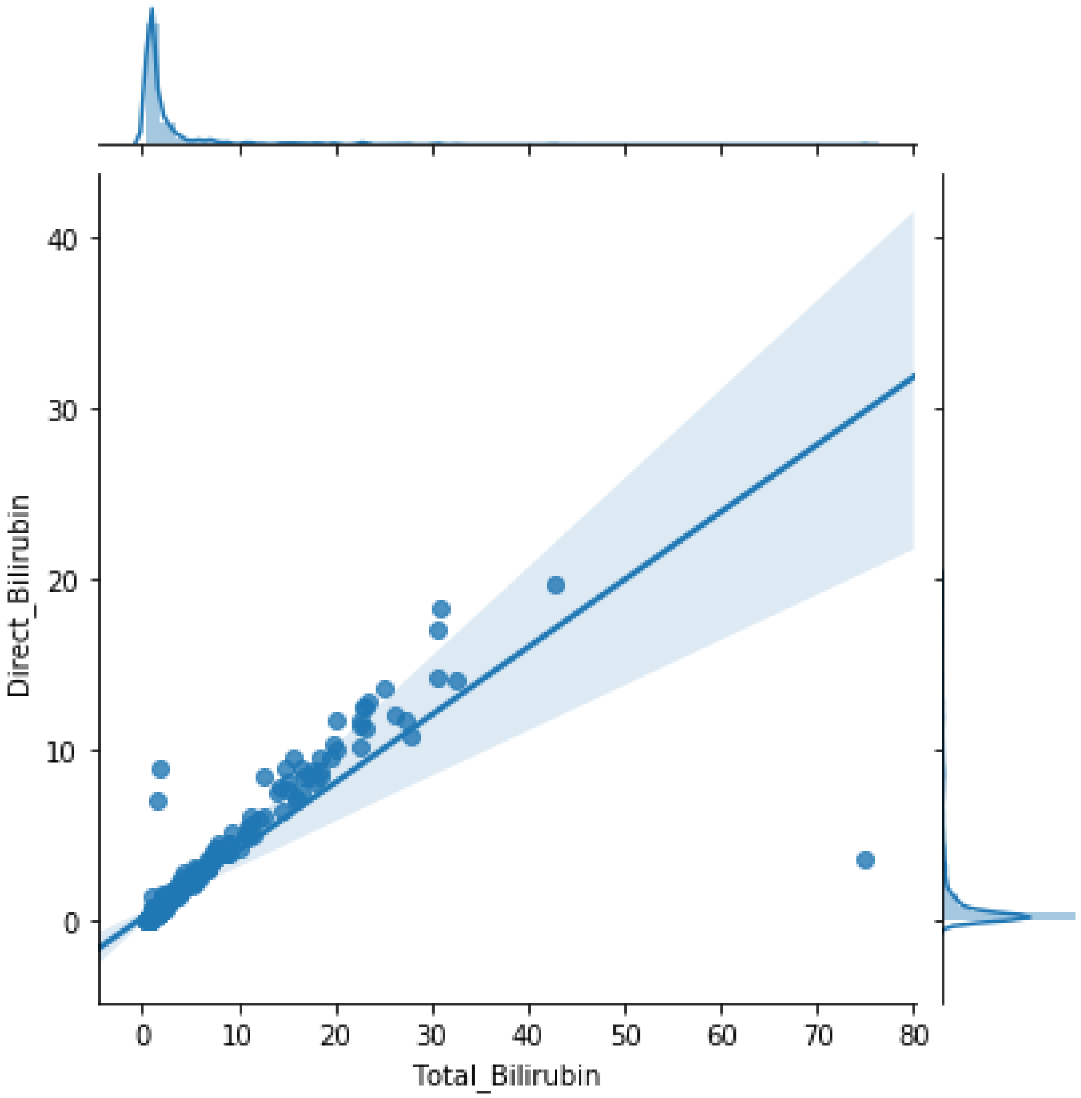
[44]:
```
g = sns.FacetGrid(liver_df, col="Gender", row="Dataset", margin_titles=True)
g.map(plt.scatter, "Direct_Bilirubin", "Total_Bilirubin", edgecolor="w")
plt.subplots_adjust(top=0.9)
```



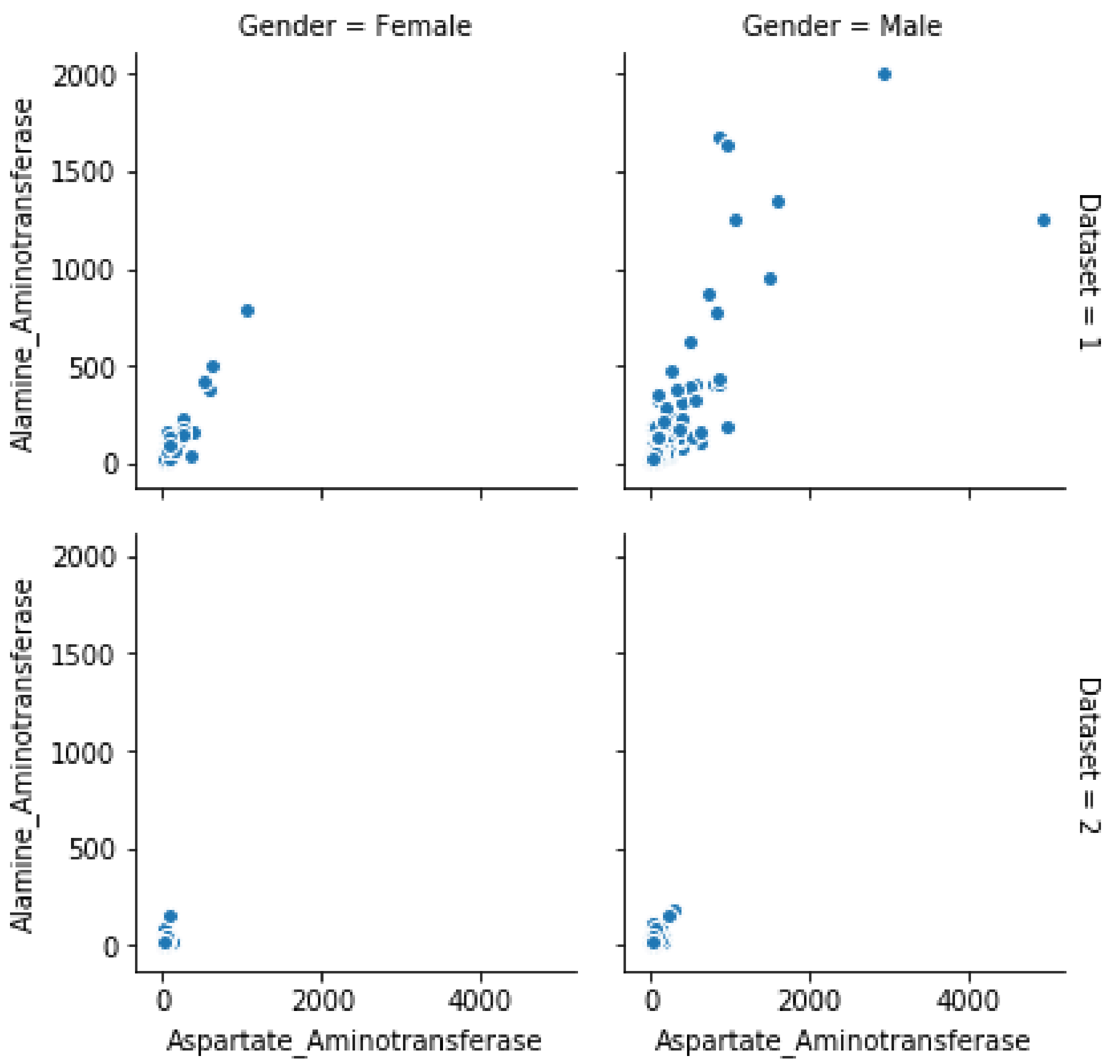
There seems to be direct relationship between Total_Bilirubin and Direct_Bilirubin. We have the possibility of removing one of this feature.

[45]:
```
sns.jointplot("Total_Bilirubin", "Direct_Bilirubin", data=liver_df, kind="reg")
```

[45]:
```
<seaborn.axisgrid.JointGrid at 0x7f3304123518>
```



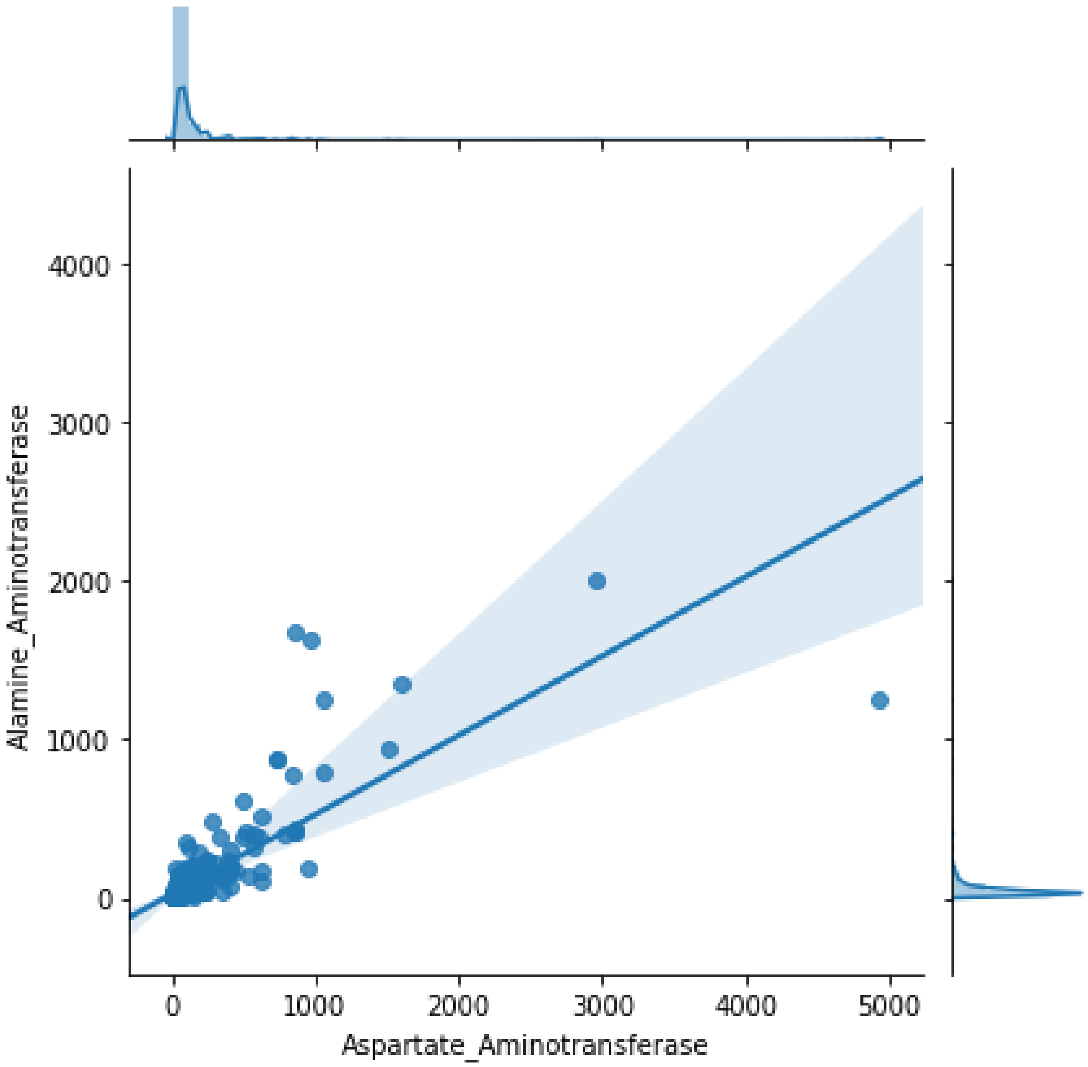
[46]:
```
g = sns.FacetGrid(liver_df, col="Gender", row="Dataset", margin_titles=True)
g.map(plt.scatter, "Aspartate_Aminotransferase", "Alamine_Aminotransferase",
      edgecolor="w")
plt.subplots_adjust(top=0.9)
```



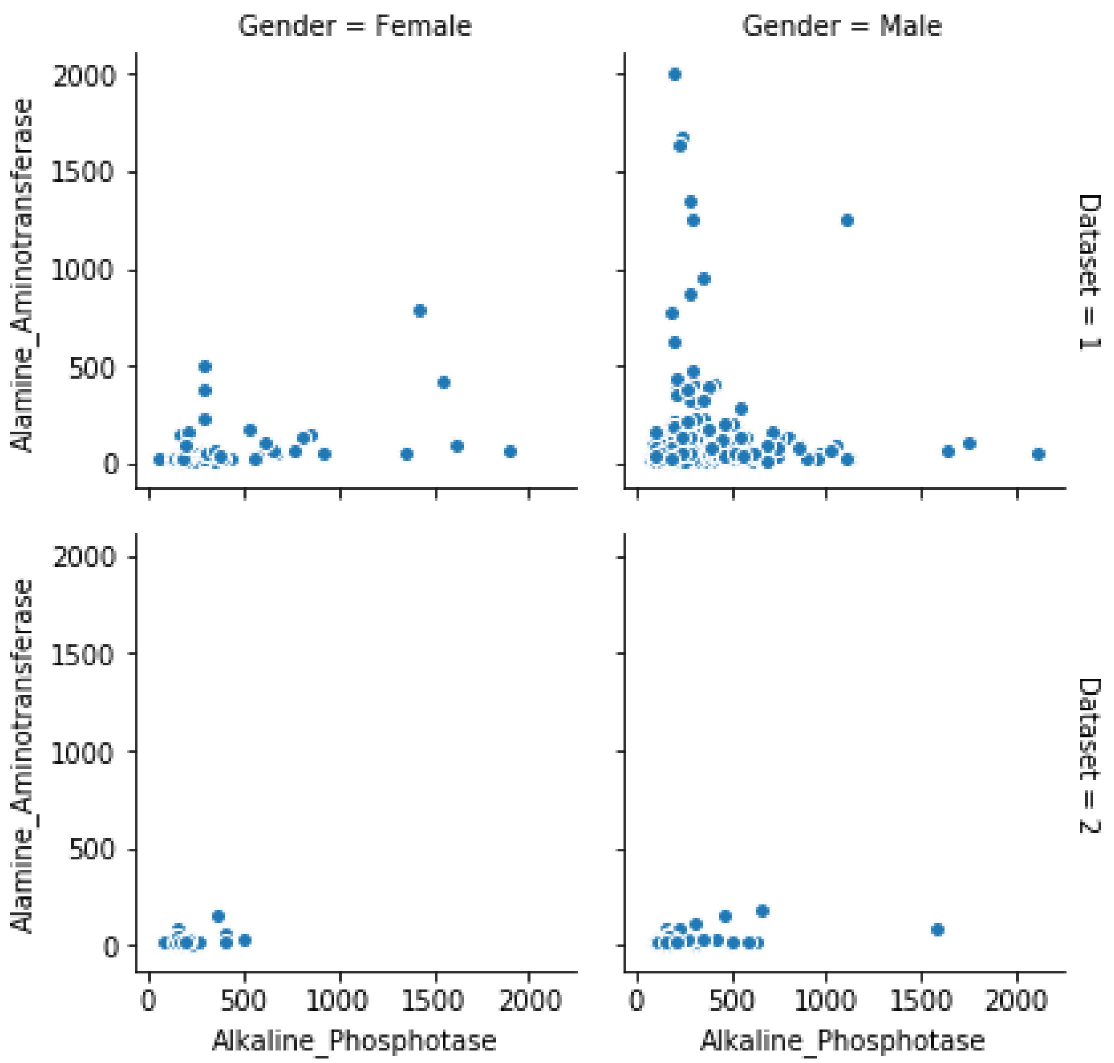
There is linear relationship between Aspartate_Aminotransferase and Alamine_Aminotransferase and the gender. We have the possibility of removing one of this feature.

[47]:
```
sns.jointplot("Aspartate_Aminotransferase", "Alamine_Aminotransferase",
                data=liver_df, kind="reg")
```

[47]:
```
<seaborn.axisgrid.JointGrid at 0x7f3303505160>
```

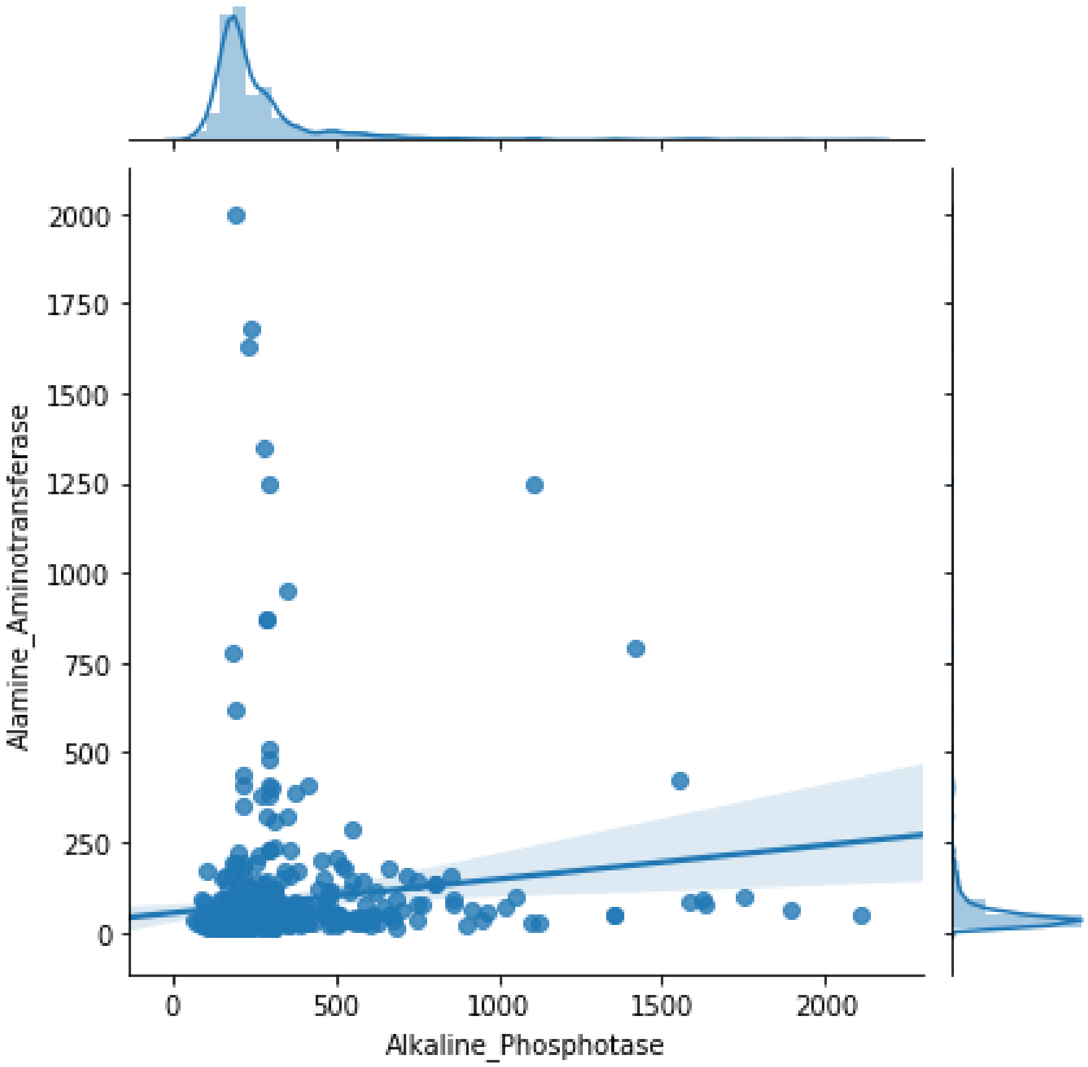


[48]:
```
g = sns.FacetGrid(liver_df, col="Gender", row="Dataset", margin_titles=True)
g.map(plt.scatter, "Alkaline_Phosphotase", "Alamine_Aminotransferase",
      edgecolor="w")
plt.subplots_adjust(top=0.9)
```



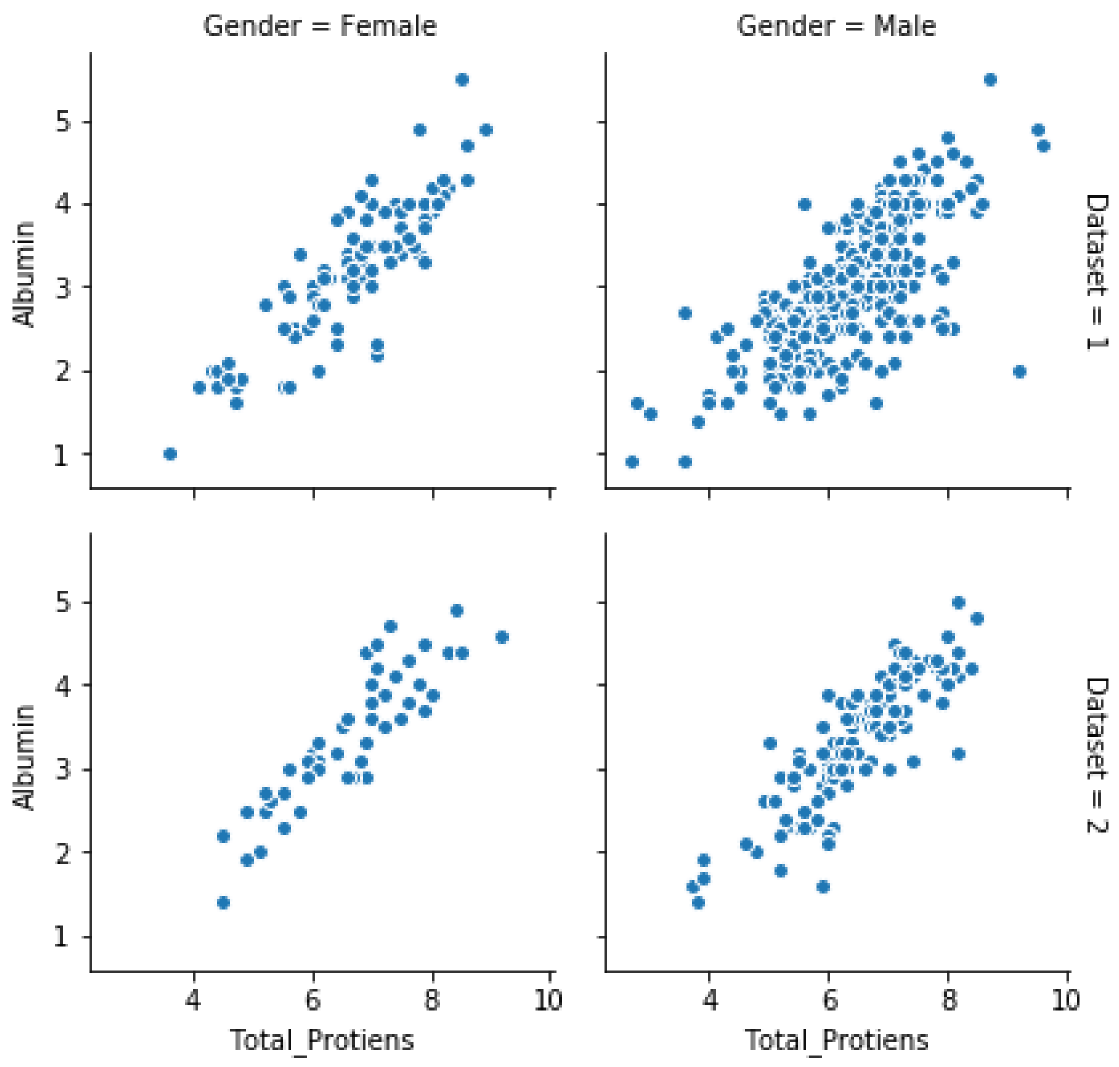
[49]:
```
sns.jointplot("Alkaline_Phosphotase", "Alamine_Aminotransferase",
              data=liver_df, kind="reg")
```

[49]:
```
<seaborn.axisgrid.JointGrid at 0x7f3303cfbbe0>
```



No linear correlation between Alkaline_Phosphotase and Alamine_Aminotransferase

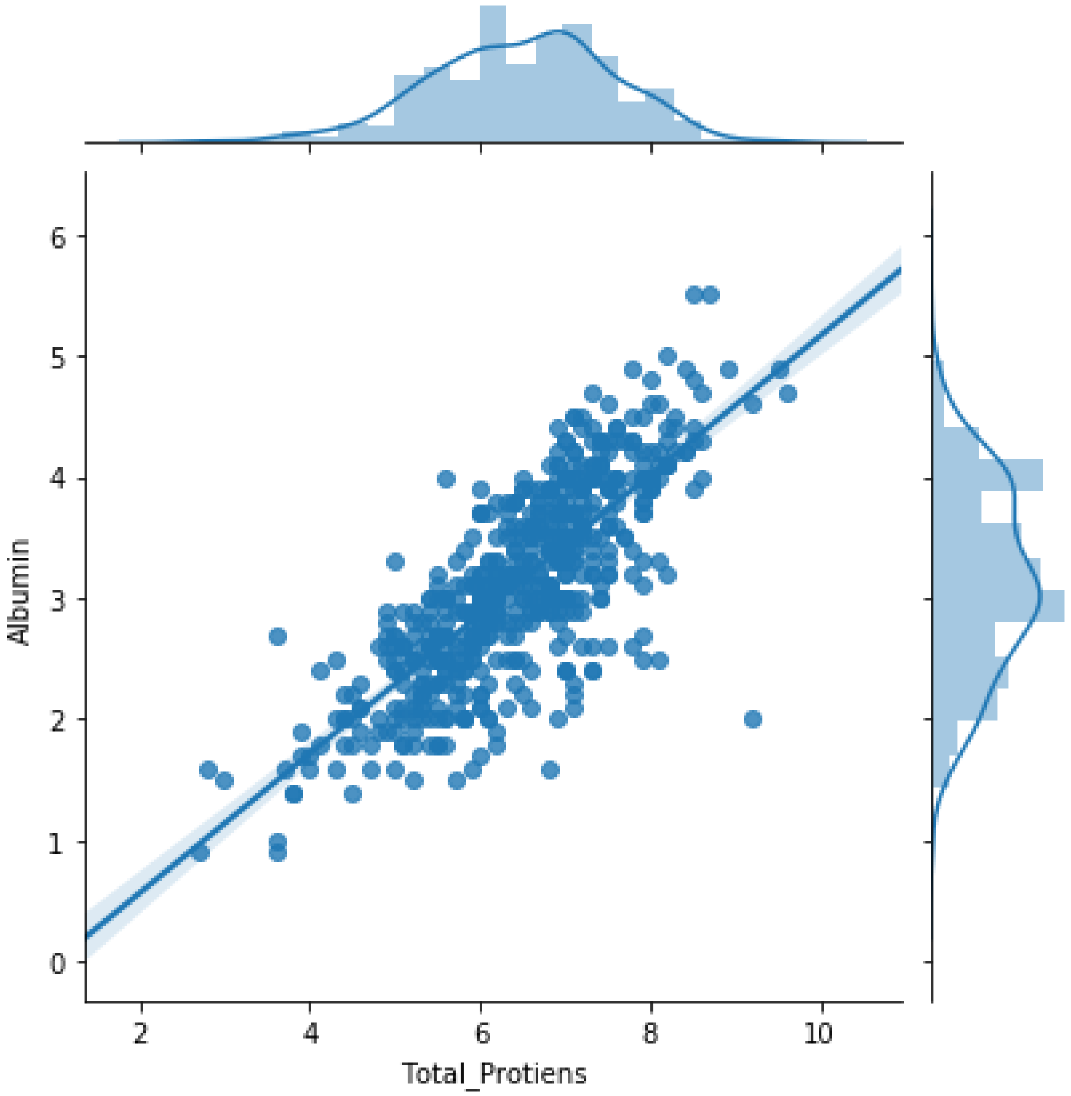
[50]:
```
g = sns.FacetGrid(liver_df, col="Gender", row="Dataset", margin_titles=True)
g.map(plt.scatter, "Total_Protiens", "Albumin", edgecolor="w")
plt.subplots_adjust(top=0.9)
```



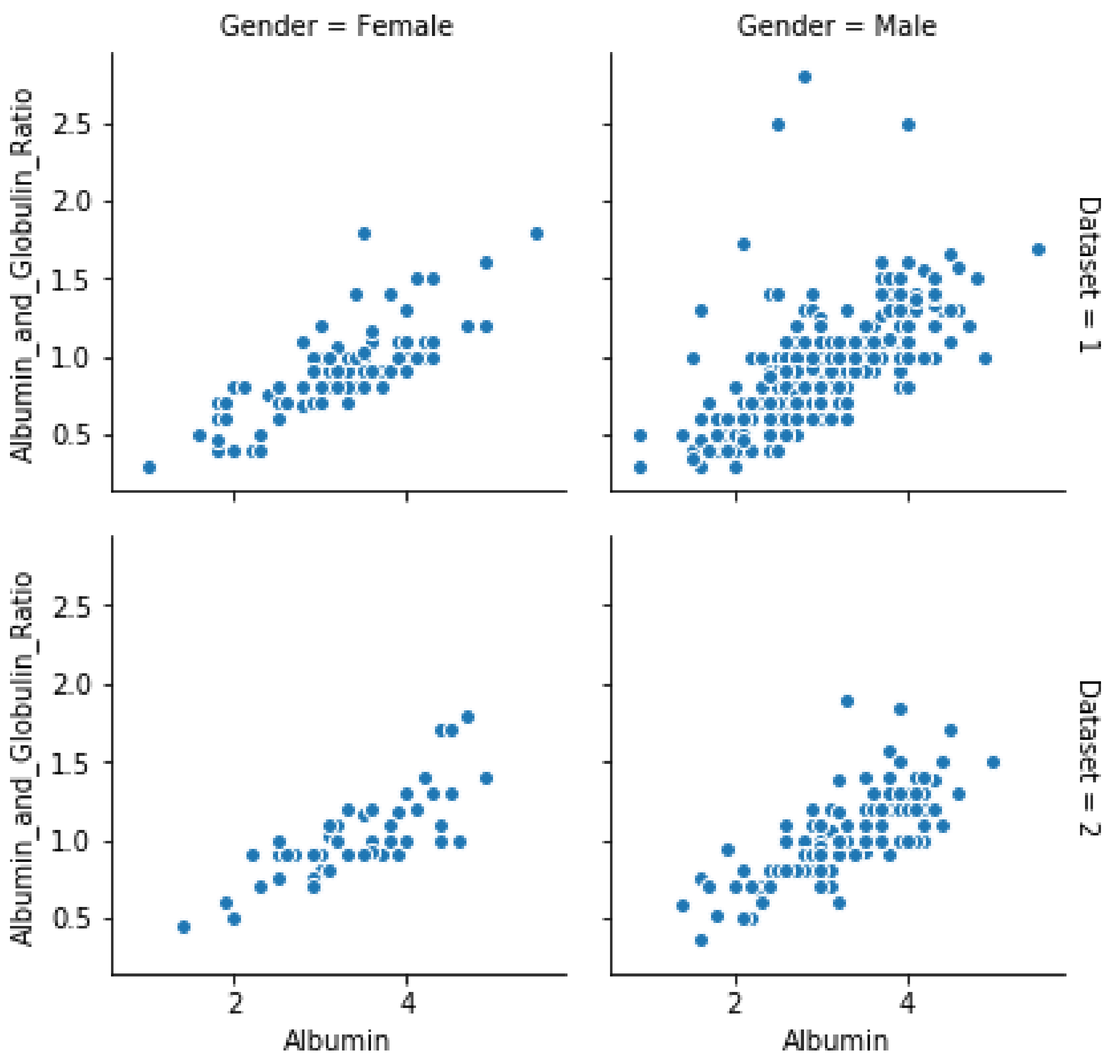
There is linear relationship between Total_Protiens and Albumin and the gender. We have the possibility of removing one of this feature.

[51]:
```
sns.jointplot("Total_Protiens", "Albumin", data=liver_df, kind="reg")
```

[51]:
```
<seaborn.axisgrid.JointGrid at 0x7f33031af860>
```



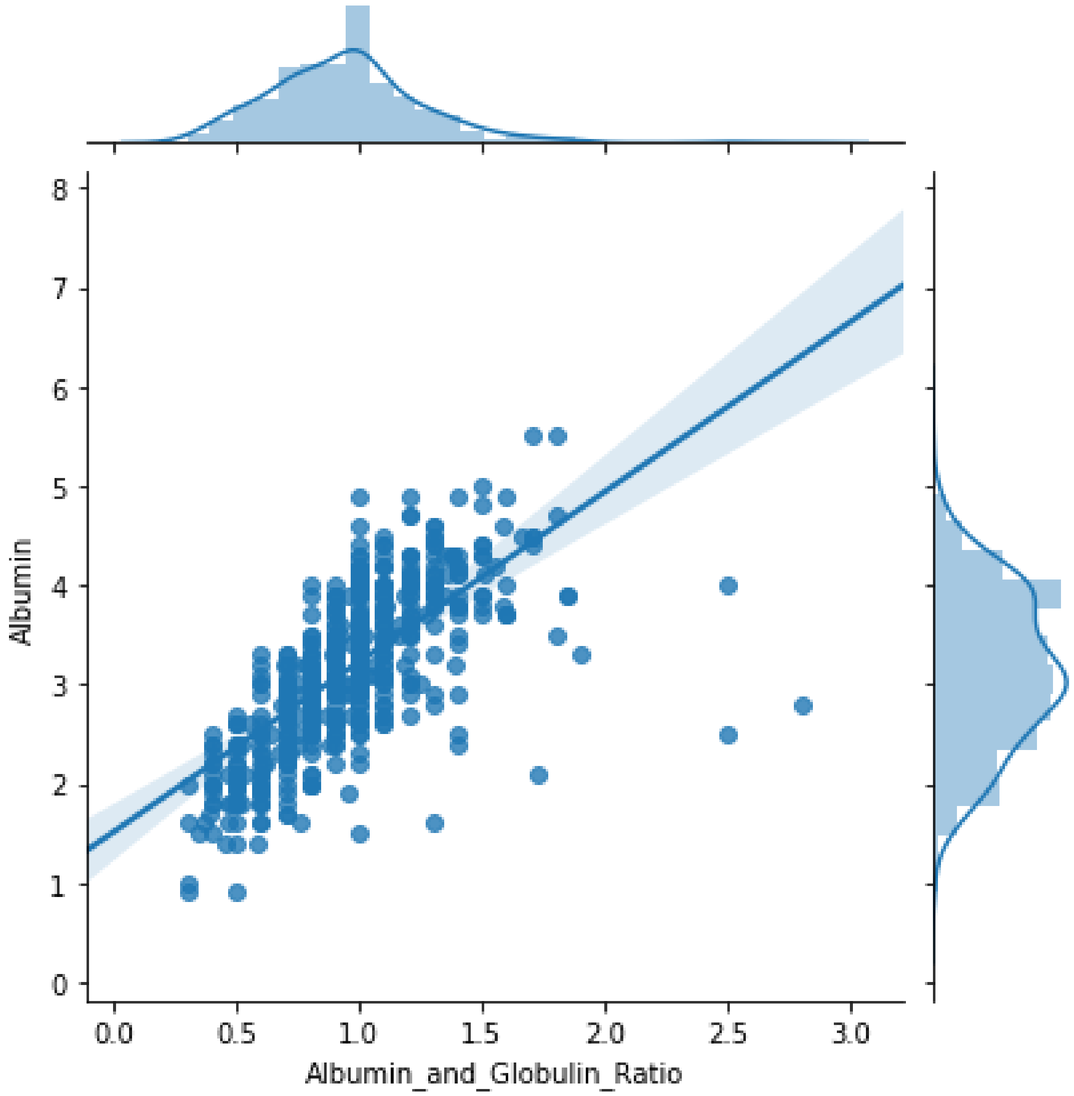
[52]:
```
g = sns.FacetGrid(liver_df, col="Gender", row="Dataset", margin_titles=True)
g.map(plt.scatter, "Albumin", "Albumin_and_Globulin_Ratio", edgecolor="w")
plt.subplots_adjust(top=0.9)
```



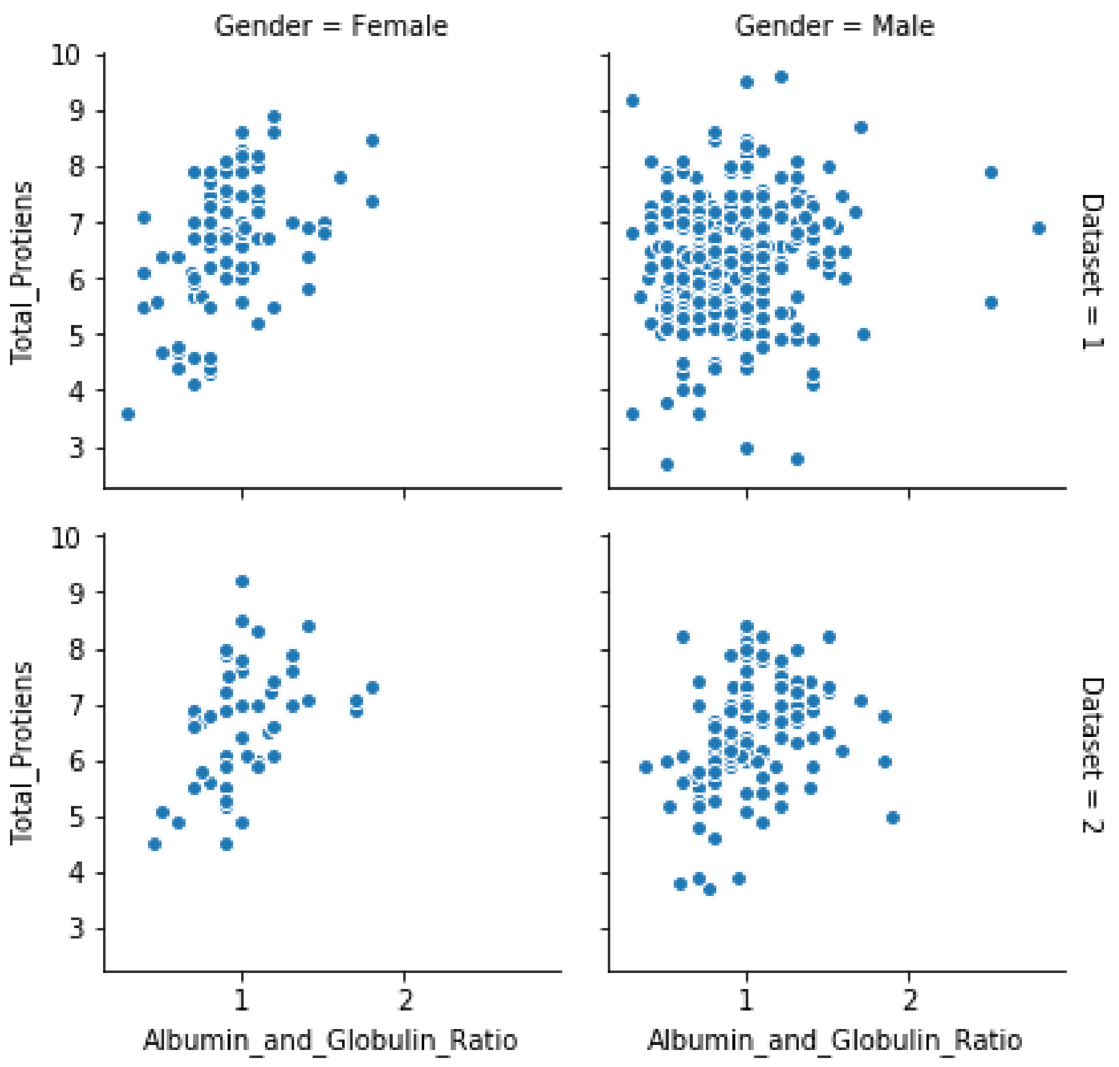
There is linear relationship between Albumin_and_Globulin_Ratio and Albumin. We have the possibility of removing one of this feature.

[53]:
```
sns.jointplot("Albumin_and_Globulin_Ratio", "Albumin",
                  data=liver_df, kind="reg")
```

[53]:
```
<seaborn.axisgrid.JointGrid at 0x7f3302e56710>
```



[54]:
```
g = sns.FacetGrid(liver_df, col="Gender", row="Dataset", margin_titles=True)
g.map(plt.scatter, "Albumin_and_Globulin_Ratio", "Total_Protiens",
      edgecolor="w")
plt.subplots_adjust(top=0.9)
```



1.5 Observation

Therefore from the analysis we can come to conclusion that the following features are important for analysis which should be taken into consideration.

Features:

1. Total_Bilirubin
2. Alamine_Aminotransferase
3. Total_Protiens
4. Albumin_and_Globulin_Ratio
5. Albumin
6. Age
7. Gender
8. Dataset

[55]:
```
liver_df = pd.concat([liver_df, pd.get_dummies(
        liver_df['Gender'], prefix='Gender')], axis=1)
liver_df.head()
```

[55]:
```
   Age  Gender  Total_Bilirubin  ...  Dataset  Gender_Female  Gender_Male
0   65  Female              0.7  ...        1              1            0
1   62    Male             10.9  ...        1              0            1
2   62    Male              7.3  ...        1              0            1
3   58    Male              1.0  ...        1              0            1
4   72    Male              3.9  ...        1              0            1

[5 rows x 13 columns]
```

[56]:
```
liver_df[liver_df['Albumin_and_Globulin_Ratio'].isnull()]
# the columns having null values
```

[56]:
```
     Age  Gender  Total_Bilirubin  ...  Dataset  Gender_Female  Gender_Male
209   45  Female              0.9  ...        1              1            0
241   51    Male              0.8  ...        1              0            1
253   35  Female              0.6  ...        2              1            0
312   27    Male              1.3  ...        2              0            1

[4 rows x 13 columns]
```

[0]:
```
liver_df["Albumin_and_Globulin_Ratio"] = liver_df\
    .Albumin_and_Globulin_Ratio\
    .fillna(liver_df['Albumin_and_Globulin_Ratio'].mean())
```

1.6 Training a model

[0]:
```
# Building ML MODEL
Droop_gender = liver_df.drop(labels=['Gender'], axis=1)
X = Droop_gender
y = liver_df['Dataset']
```

[0]:
```
# split data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,
                                                    random_state=101)
```

1.7 Random Forest

[60]:
```
random_forest = RandomForestClassifier(n_estimators=100)
random_forest.fit(X_train, y_train)
# Predicting Output
rf_predicted = random_forest.predict(X_test)
random_forest_score = round(random_forest.score(X_train, y_train) * 100, 2)
random_forest_score_test = round(random_forest.score(X_test, y_test) * 100, 2)

print('Random Forest Score: \n', random_forest_score)
print('Random Forest Test Score: \n', random_forest_score_test)
print('Accuracy: \n', accuracy_score(y_test, rf_predicted))
print(confusion_matrix(y_test, rf_predicted))
print(classification_report(y_test, rf_predicted))
```

```
Random Forest Score:
 100.0
Random Forest Test Score:
 100.0
Accuracy:
 1.0
[[124   0]
 [  0  51]]
              precision    recall  f1-score   support

           1       1.00      1.00      1.00       124
           2       1.00      1.00      1.00        51

    accuracy                           1.00       175
   macro avg       1.00      1.00      1.00       175
weighted avg       1.00      1.00      1.00       175
```

1.8 Logistic Regression

[61]:
```
logreg = LogisticRegression()
# Train the model using the training sets and check score
logreg.fit(X_train, y_train)
# Predict Output
log_predicted = logreg.predict(X_test)

logreg_score = round(logreg.score(X_train, y_train) * 100, 2)
logreg_score_test = round(logreg.score(X_test, y_test) * 100, 2)
# Equation coefficient and Intercept
print('Logistic Regression Training Score: \n', logreg_score)
print('Logistic Regression Test Score: \n', logreg_score_test)
print('Coefficient: \n', logreg.coef_)
print('Intercept: \n', logreg.intercept_)
print('Accuracy: \n', accuracy_score(y_test, log_predicted))
print('Confusion Matrix: \n', confusion_matrix(y_test, log_predicted))
print('Classification Report: \n',
      classification_report(y_test, log_predicted))
```

```
Logistic Regression Training Score:
 100.0
Logistic Regression Test Score:
 98.86
```

```
Coefficient:
 [[-3.61842884e-02 -2.35758572e-01 -5.50833198e-03 -5.36935885e-04
  -6.02768391e-03 -7.33968459e-03 -8.97245204e-01  4.75630916e-01
  -4.95118468e-01  6.02857390e+00 -4.73341804e-01 -7.39013220e-01]]
Intercept:
 [-1.21235502]
Accuracy:
 0.9885714285714285
Confusion Matrix:
 [[123   1]
 [  1  50]]
Classification Report:
               precision    recall  f1-score   support

           1       0.99      0.99      0.99       124
           2       0.98      0.98      0.98        51

    accuracy                           0.99       175
   macro avg       0.99      0.99      0.99       175
weighted avg       0.99      0.99      0.99       175


/usr/local/lib/python3.6/dist-packages/sklearn/linear_model/logistic.py:432:
FutureWarning: Default solver will be changed to 'lbfgs' in 0.22. Specify a
solver to silence this warning.
  FutureWarning)
```

1.9 Model Test Scores

[0]:
```
models = pd.DataFrame({
    'Model': ['Logistic Regression', 'Random Forest'],
    'Score': [logreg_score, random_forest_score],
    'Test Score': [logreg_score_test, random_forest_score_test]})
models.sort_values(by='Test Score', ascending=False)
```

[0]:
```
                 Model  Score  Test Score
1        Random Forest  100.0      100.00
0  Logistic Regression  100.0       98.86
```

[0]: