Week6_5_Bagging_randomForest_classifier

May 13, 2021

Bagging and Random Forest

Bagging

Import Libraries

*Bootstrap Aggregation (Bagging)

*An ensemble method is a technique that combines the predictions from multiple machine learning algorithms together to make more accurate predictions than any individual model.

*Bagging constructs n classification trees using bootstrap sampling of the training data and then combines their predictions to produce a final meta-prediction.

*Reduces variance of individual model in the ensemble

[1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn import preprocessing
from scipy.stats import pearsonr

import warnings
warnings.filterwarnings('ignore')
```

Import dataset

[2]:
```
# data = pd.read_csv('/home/jayanthikishore/Downloads/ML_classwork/
↪DT_RF_Ensemble/indian_liver_patient.csv')
data = pd.read_csv('/Users/preethamvignesh/Downloads/ML_classwork/
↪DT_RF_Ensemble/indian_liver_patient.csv')

data.head()
```

[2]:
```
   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
```

Features in dataset

[3]:
```
data.columns
```

[3]:
```
Index(['Age', 'Gender', 'Total_Bilirubin', 'Direct_Bilirubin',
       'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
       'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
       'Albumin_and_Globulin_Ratio', 'Dataset'],
      dtype='object')
```

Data type

[4]:
```
data.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
```

Checking the NaN values

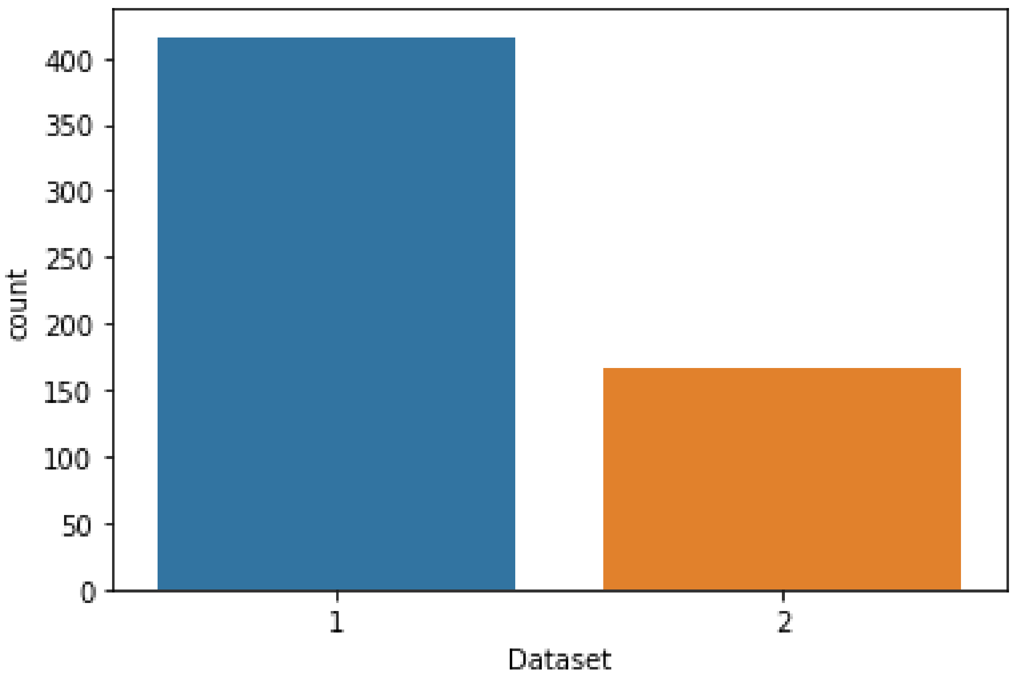
```
[5]: data.isnull().sum()
```

```
[5]: 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
```

Exploratory data Analysis (EDA)

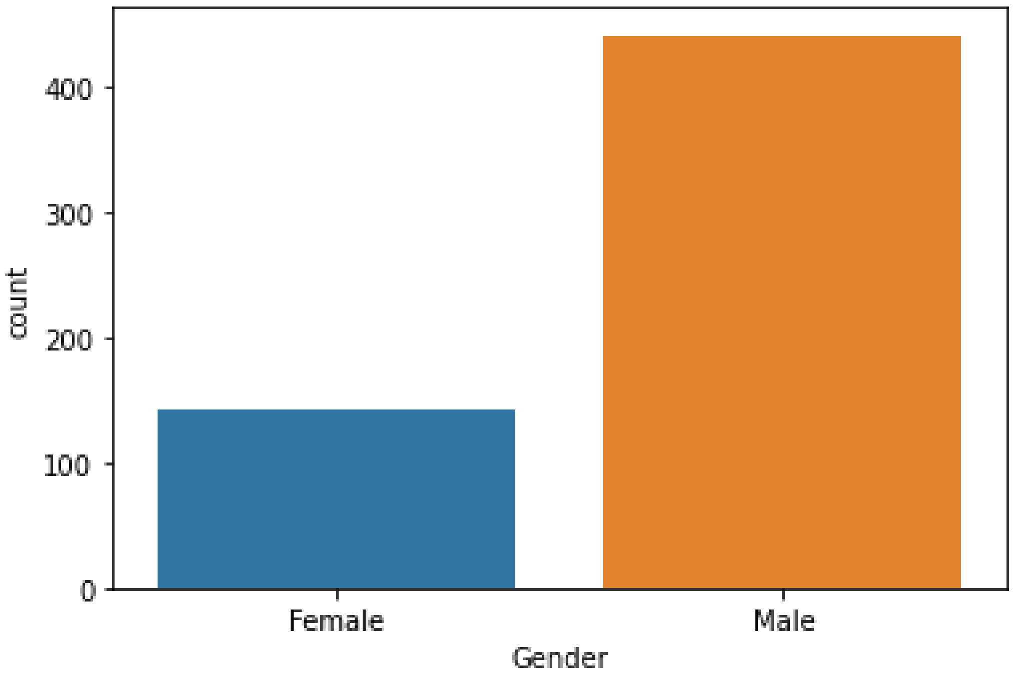
```
[6]: sns.countplot(data = data, x = "Dataset", label = "Count")
```

```
[6]: <AxesSubplot:xlabel='Dataset', ylabel='count'>
```



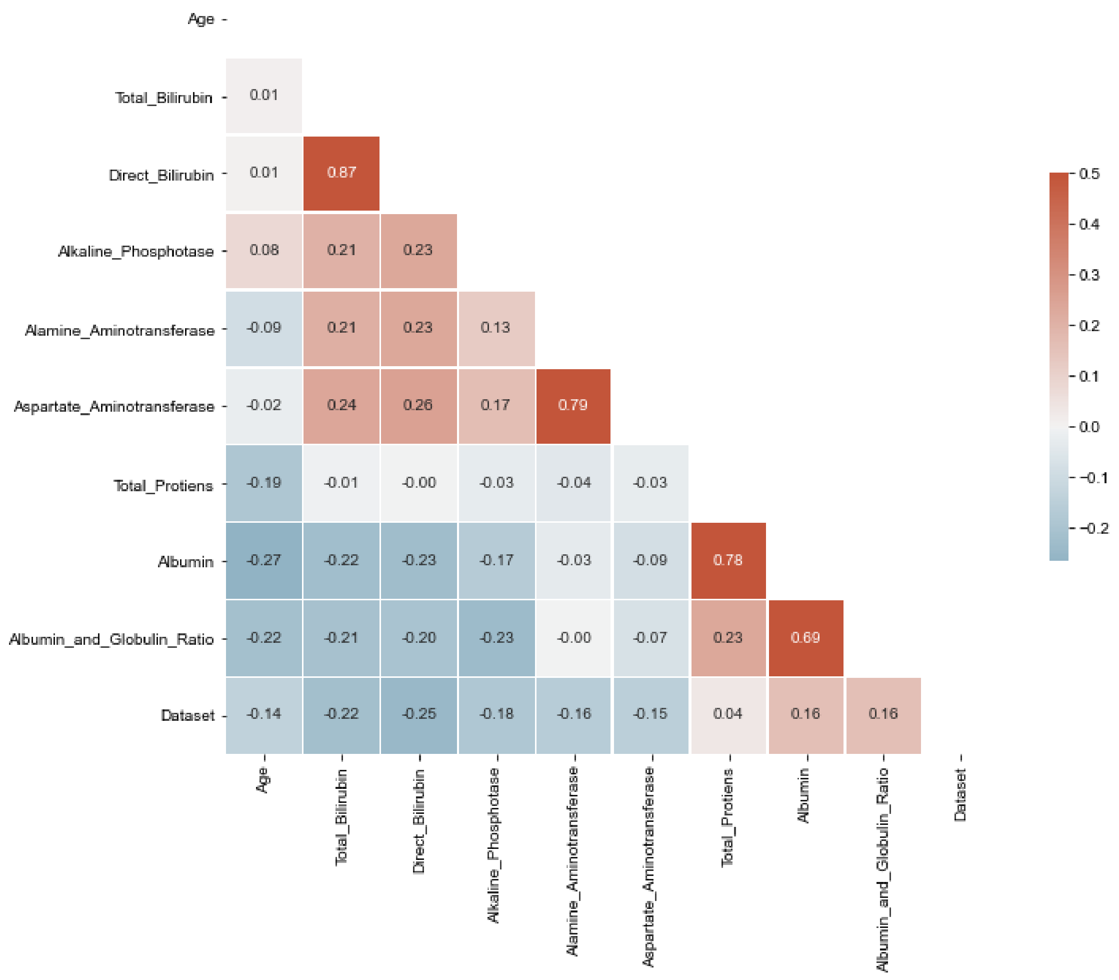
```
[7]: sns.countplot(data = data, x = "Gender", label = "Count")
```

```
[7]: <AxesSubplot:xlabel='Gender', ylabel='count'>
```



Correlation Analysis

```
[8]: from string import ascii_letters
corr = data.corr()
# Generate a mask for the upper triangle
mask = np.triu(np.ones_like(corr, dtype=bool))

# Set up the matplotlib figure
f, ax = plt.subplots(figsize=(11, 9))

# Generate a custom diverging colormap
cmap = sns.diverging_palette(230, 20, as_cmap=True)

# Draw the heatmap with the mask and correct aspect ratio
sns.heatmap(corr, mask=mask, cmap=cmap, vmax=.5, center=0,
            square=True, linewidths=.5, cbar_kws={"shrink": .5},␣
 ↪annot=True,fmt='.2f')
sns.set(font_scale=1.1)
```



*Two category columns: Age and Dataset(y value). In the Dataset 1 mean ill and 2 means healty. Albumin_and_Globulin_Ratio has missing values.

[9]:
```
#Convert the Dataset colums into strings.
data['Dataset'].replace({1:'ill',2:'healthy'}, inplace=True)
# converts all string columns into catergory
data["Dataset"] = data["Dataset"].astype("category")
data["Gender"] = data["Gender"].astype("category")
data.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    category
 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    category
dtypes: category(2), float64(5), int64(4)
memory usage: 42.4 KB
```

Label encoder

[10]:
```
#label encoder
le = preprocessing.LabelEncoder()
le.fit(data['Gender'])
data['Gender_Encoded'] = le.transform(data['Gender'])
```

[11]:
```
data.tail()
```

[11]:
```
     Age Gender  Total_Bilirubin  Direct_Bilirubin  Alkaline_Phosphotase  \
578   60   Male              0.5               0.1                   500
579   40   Male              0.6               0.1                    98
580   52   Male              0.8               0.2                   245
581   31   Male              1.3               0.5                   184
582   38   Male              1.0               0.3                   216

     Alamine_Aminotransferase  Aspartate_Aminotransferase  Total_Protiens  \
578                        20                          34             5.9
579                        35                          31             6.0
580                        48                          49             6.4
581                        29                          32             6.8
582                        21                          24             7.3

     Albumin  Albumin_and_Globulin_Ratio  Dataset  Gender_Encoded
578      1.6                        0.37  healthy               1
579      3.2                        1.10      ill               1
580      3.2                        1.00      ill               1
581      3.4                        1.00      ill               1
582      4.4                        1.50  healthy               1
```

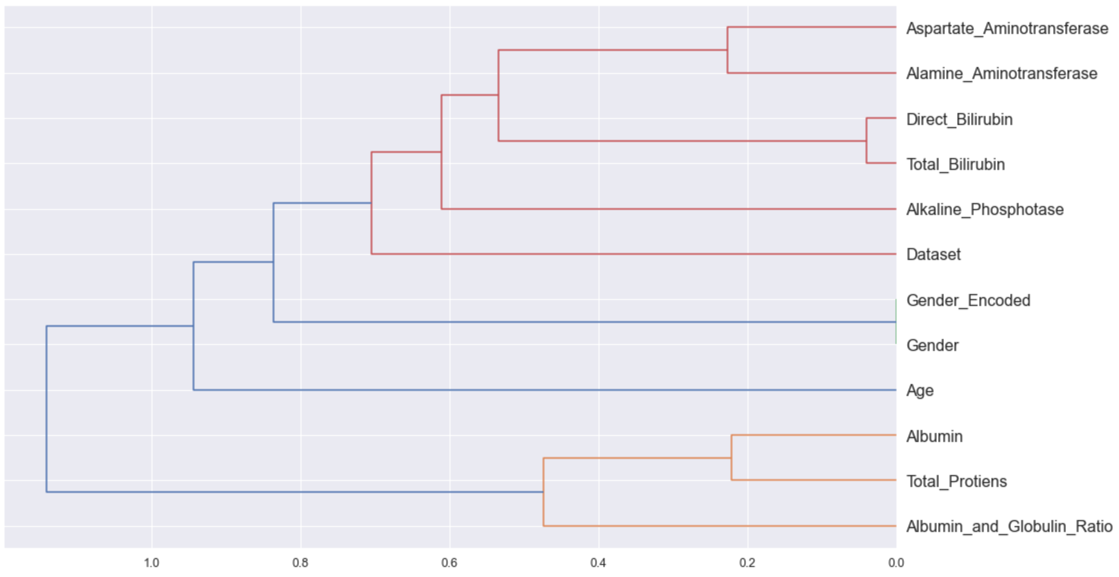
Liver disease patients information

[12]:
```
# Counting the number of patients
LD, NLD = data['Dataset'].value_counts()
print('Number of patients diagnosed with liver disease: ',LD)
print('Number of patients not diagnosed with liver disease: ',NLD)
print(f'Ill patients in the dataset are {LD/(NLD+LD)*100} percent of the total')
```

```
Number of patients diagnosed with liver disease:  416
Number of patients not diagnosed with liver disease:  167
Ill patients in the dataset are 71.35506003430532 percent of the total
```

Dendogram diagram

```
[13]: import scipy
      from scipy.cluster import hierarchy as hc
      # Redundant Features
      corr = np.round(scipy.stats.spearmanr(data).correlation, 4)
      corr_condensed = hc.distance.squareform(1-corr)
      z = hc.linkage(corr_condensed, method='average')
      fig = plt.figure(figsize=(16,10))
      dendrogram = hc.dendrogram(z, labels=data.columns, orientation='left',␣
       ↪leaf_font_size=16)
      plt.show()
```



Filling missing values

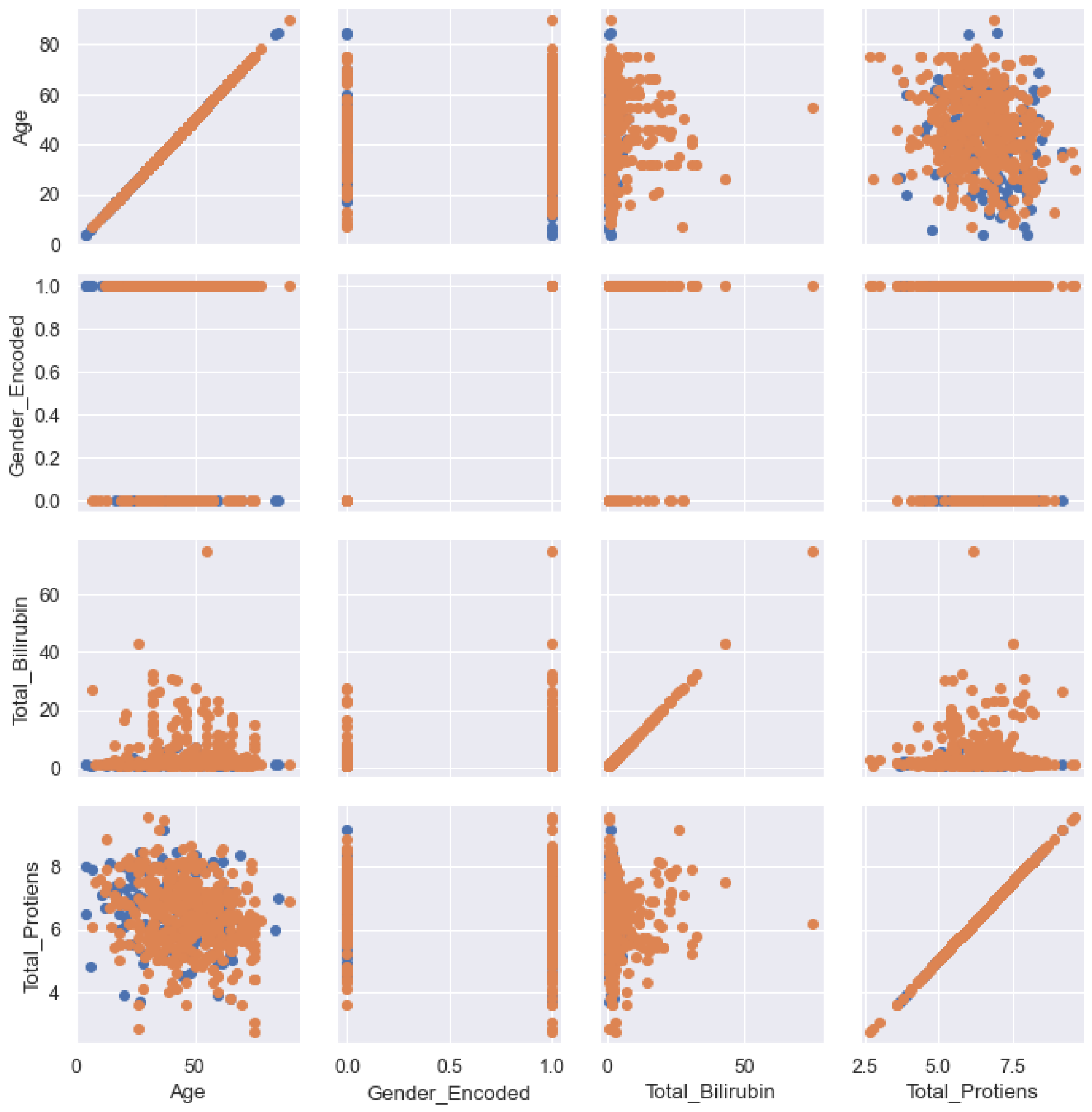
```
[14]: data['Albumin_and_Globulin_Ratio'].fillna(data['Albumin_and_Globulin_Ratio'].
       ↪median(), inplace=True)
```

```
[15]: data
```

```
[15]:     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
..   …     …               …               …                  …
578   60    Male              0.5               0.1                500
579   40    Male              0.6               0.1                 98
580   52    Male              0.8               0.2                245
581   31    Male              1.3               0.5                184
582   38    Male              1.0               0.3                216

     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
..                        …                         …             …
578                        20                          34             5.9
579                        35                          31             6.0
580                        48                          49             6.4
581                        29                          32             6.8
582                        21                          24             7.3

     Albumin  Albumin_and_Globulin_Ratio  Dataset  Gender_Encoded
0        3.3                        0.90      ill               0
1        3.2                        0.74      ill               1
2        3.3                        0.89      ill               1
3        3.4                        1.00      ill               1
4        2.4                        0.40      ill               1
..       …                         …      …             …
578      1.6                        0.37  healthy               1
579      3.2                        1.10      ill               1
580      3.2                        1.00      ill               1
581      3.4                        1.00      ill               1
582      4.4                        1.50  healthy               1

[583 rows x 12 columns]
```

[16]:
```
g = sns.PairGrid(data, hue = "Dataset",␣
↪vars=['Age','Gender_Encoded','Total_Bilirubin','Total_Protiens'])
g.map(plt.scatter)
plt.show()
```



Split trian and test datasets

```
[17]: # machine learning  - supervised
      from sklearn.model_selection import train_test_split
      from sklearn.ensemble import RandomForestClassifier
      from sklearn.metrics import classification_report,confusion_matrix
      from sklearn.metrics import accuracy_score
```

```
[18]: X = data[['Age', 'Total_Bilirubin', 'Direct_Bilirubin', 'Alkaline_Phosphotase',
              'Alamine_Aminotransferase', 'Aspartate_Aminotransferase',␣
       ↪'Total_Protiens',
              'Albumin', 'Albumin_and_Globulin_Ratio','Gender_Encoded']]
      y = data[['Dataset']]
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,␣
↪stratify=y)
print(X_train.shape,X_test.shape)
```

```
(408, 10) (175, 10)
```

Random Forest Classifier

[19]:
```
#Random Forest
rf = RandomForestClassifier(n_estimators=25, random_state=0)
rf.fit(X_train, y_train)
rf_predicted = rf.predict(X_test)

random_forest_score      = round(rf.score(X_train, y_train) * 100, 2)
random_forest_score_test = round(rf.score(X_test, y_test) * 100, 2)

print('Random Forest Score: ', random_forest_score)
print('Random Forest Test Score: ', random_forest_score_test)
print('Accuracy: ', (accuracy_score(y_test,rf_predicted)) *100,4)


# g = sns.heatmap(confusion_matrix(y_test,rf_predicted), annot=True, fmt="d")
```

```
Random Forest Score:  99.75
Random Forest Test Score:  72.0
Accuracy:  72.0 4
```

[20]:
```
print('\nClassification report: \n', classification_report(y_test,rf_predicted))
```

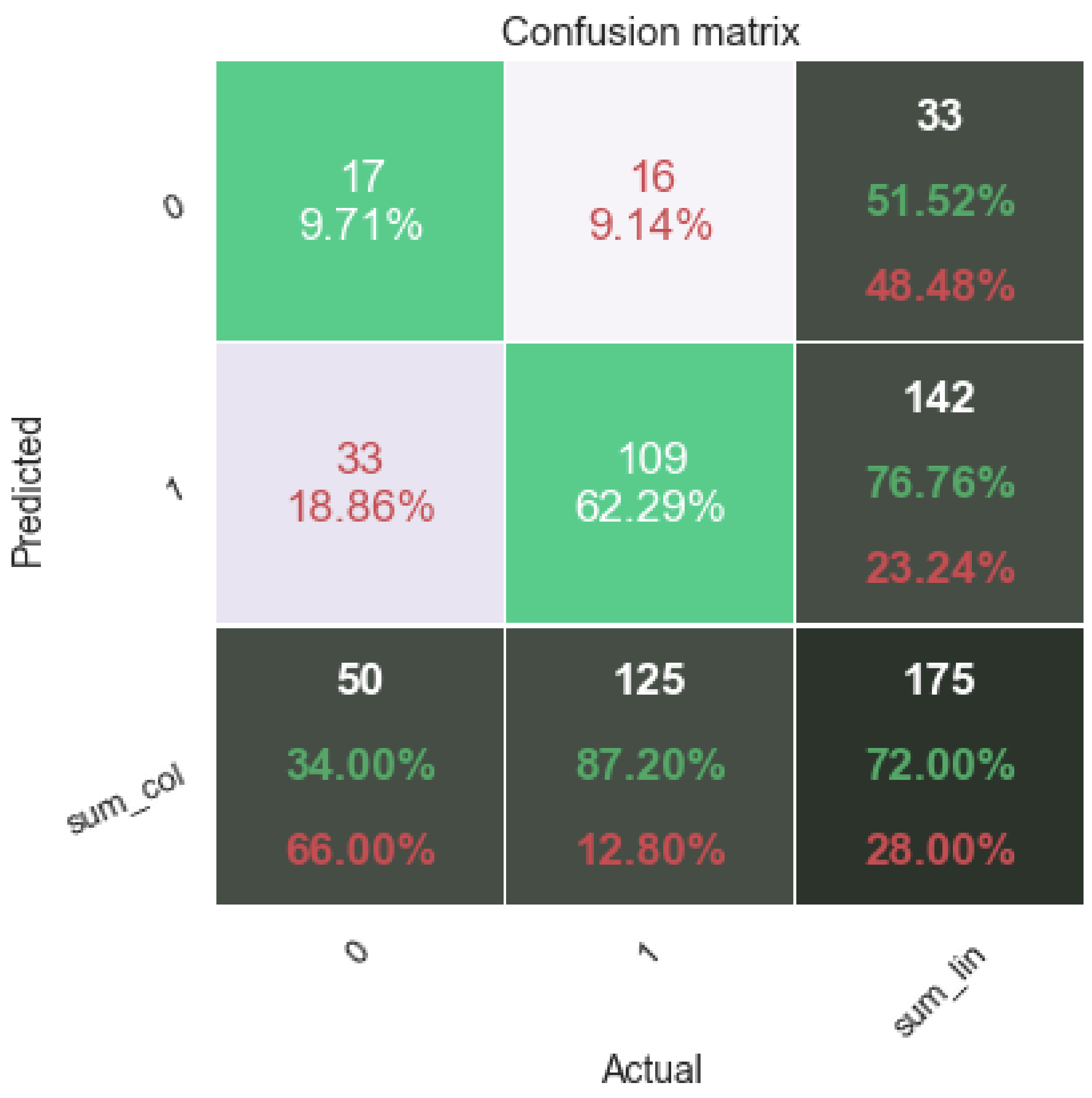
```
Classification report:
               precision    recall  f1-score   support

     healthy       0.52      0.34      0.41        50
         ill       0.77      0.87      0.82       125

    accuracy                           0.72       175
   macro avg       0.64      0.61      0.61       175
weighted avg       0.70      0.72      0.70       175
```

[21]:
```
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix, accuracy_score

y_pred = rf.predict(X_test)
con_res = confusion_matrix(y_test,rf_predicted)
# con_res = metrics.confusion_matrix(y_test,y_pred, labels=[0, 1])
```

```
print("Confusion matrix:")
print(confusion_matrix(y_test,y_pred))
print("Accuracy: {:.2f}%".format(accuracy_score(y_test, y_pred)*100))
```

```
Confusion matrix:
[[ 17  33]
 [ 16 109]]
Accuracy: 72.00%
```

[22]:
```
# %run -i '/home/jayanthikishore/Desktop/Analysis/Work/ML_EIT/
 ↪confusion_matrix_different_ways1.py'
%run -i '/Users/preethamvignesh/Desktop/Work/ML_EIT/
 ↪confusion_matrix_different_ways1.py'

df_confmatrx = pd.DataFrame(con_res, range(2),range(2))
df_confmatrx
cmap = 'PuRd'
confusion_matrix_dfrntway(df_confmatrx, cmap=cmap,fz=17)
```



Confusion matrix
Predicted
Actual
0
1
sum_col
0
1
sum_lin
17
9.71%
16
9.14%
33
51.52%
48.48%
33
18.86%
109
62.29%
142
76.76%
23.24%
50
34.00%
66.00%
125
87.20%
12.80%
175
72.00%
28.00%

```
[ ]:
```