PART-2: Training a model to classify an ECG with AF

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Null Values Handling

The data is checked for any Null values and if found are replaced by the mean of the respective feature/column as shown below.

Null value report:

FEATURE	NULL VALUE COUNT
bpm	23
ibi	23
sdnn	23
sdsd	106
rmssd	106
pnn20	106
pnn50	106
hr_mad	23
sd1	106
sd2	106
s	106
sd1/sd2	161
breathingrate	115

The null values are replaced with median using the below code:

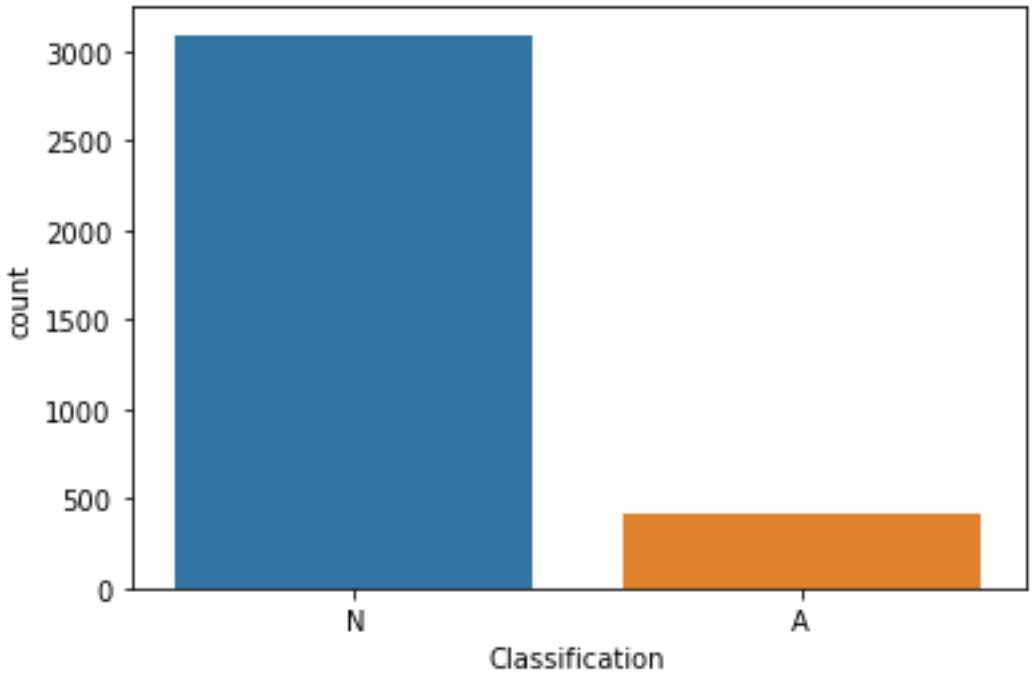
```
# Function to remove null values
def clear_nan(xx_noise):
    xx_noise = pd.DataFrame(xx_noise).replace('--',float('Nan'))
    # Imputer object using the mean strategy and
    # missing_values type for imputation
    imputer = SimpleImputer(missing_values = np.nan,
                            strategy ='mean')

    imputer = imputer.fit(xx_noise.iloc[:,:-1])

    # Imputing the data
    xx_noise.iloc[:,:-1] = imputer.transform(xx_noise.iloc[:,:-1])

    return xx_noise

xx_noise = clear_nan(xx_noise)
xx_noise
```

Data Analysing & Outlier Detection

The data is analysed to check the skewness and detect outliers.

Count Plot for the Output/Predicted variable with two possible outputs that are:

- Normal (N)
- AF episode (AF)



The count plot shows that the data having normal reading is a lot higher than the data dealing with AF episode.

The skewness of data is checked as below:

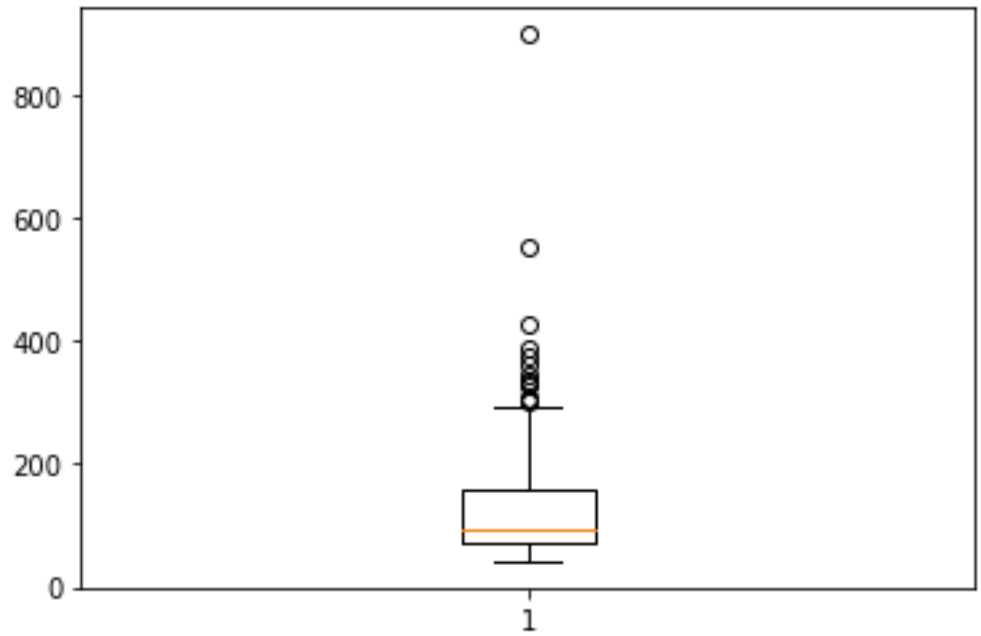
```
# Checking Skewness of features

for column in xx_noise.columns[:-1]:
    print(column,'skewness:',xx_noise[column].skew())
```

```
bpm skewness: 1.7225403355998257
ibi skewness: 0.18061994491252278
sdnn skewness: 0.14470856318984826
sdsd skewness: 0.5673517267619748
rmssd skewness: 0.4729273752227066
pnn20 skewness: -0.48056216436576576
pnn50 skewness: 0.006890443533169791
hr_mad skewness: 0.9123081957165963
sd1 skewness: 0.5134504333916752
sd2 skewness: 0.6805479653622352
s skewness: 0.8826475613133172
sd1/sd2 skewness: 15.283806168391749
breathingrate skewness: 3.6419024221751273
```

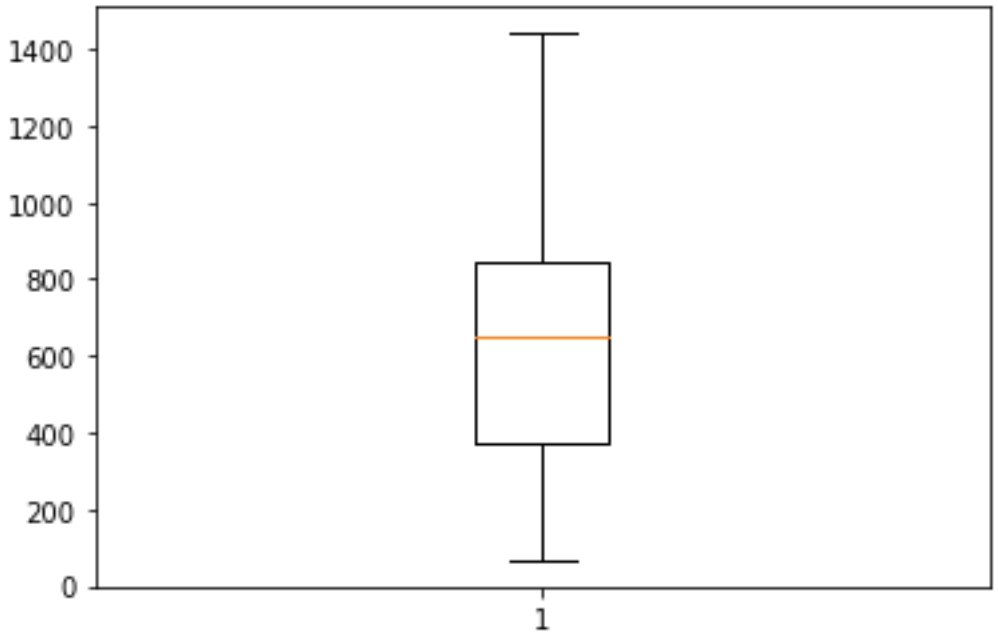
This skewness is a lot higher for ‘ sd1/sd2 ‘ feature.

Checking outliers using the box plot graph as shown below.

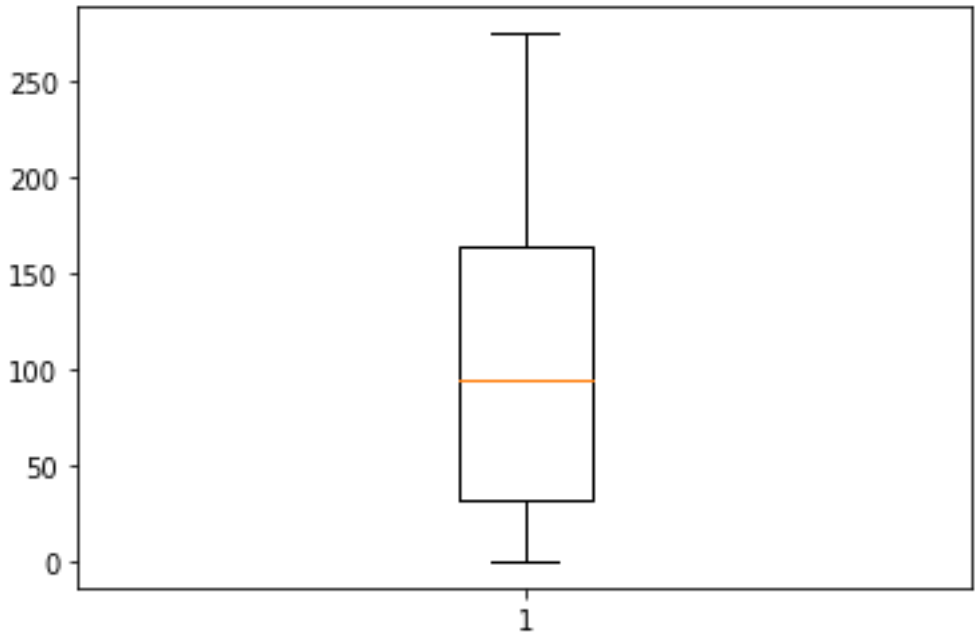
BOX PLOT for bpm



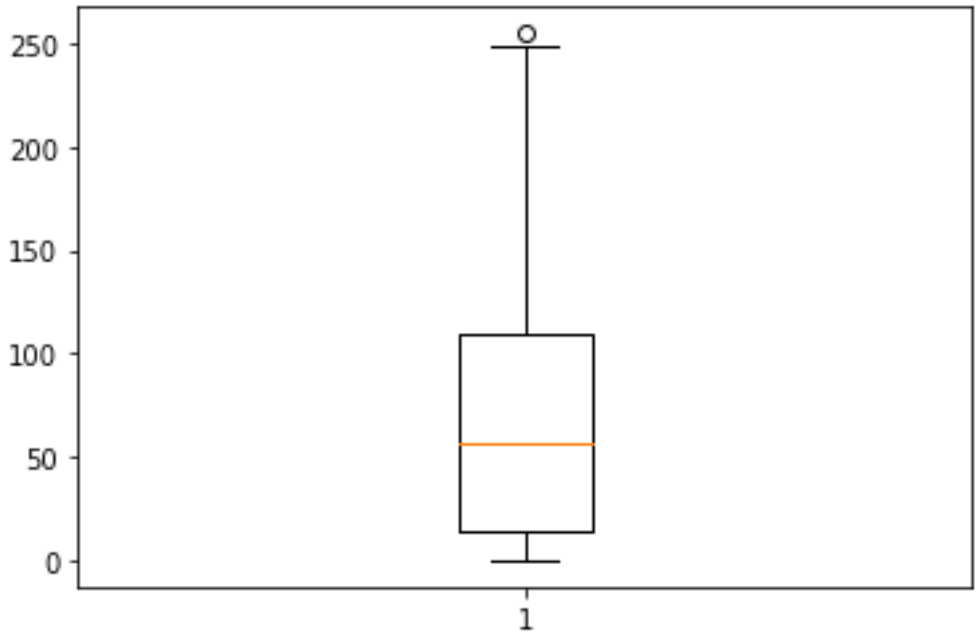
BOX PLOT for ibi



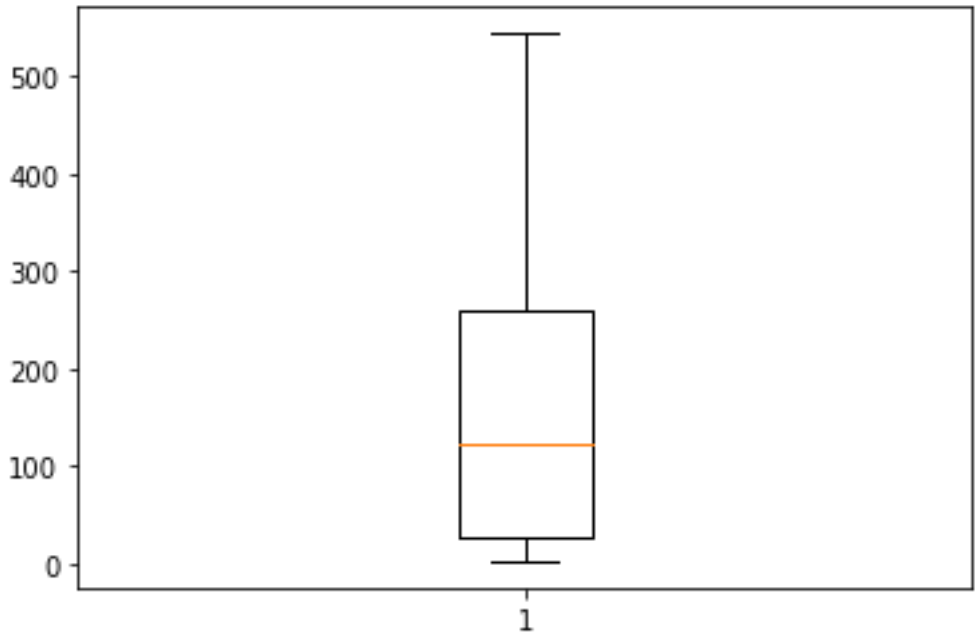
BOX PLOT for sdnn



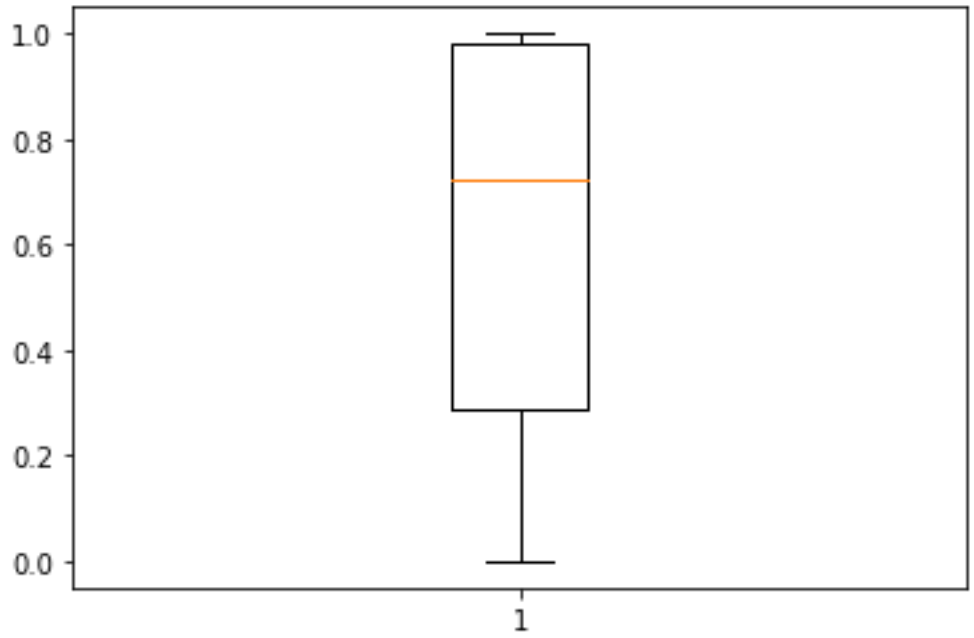
BOX PLOT for sdsd



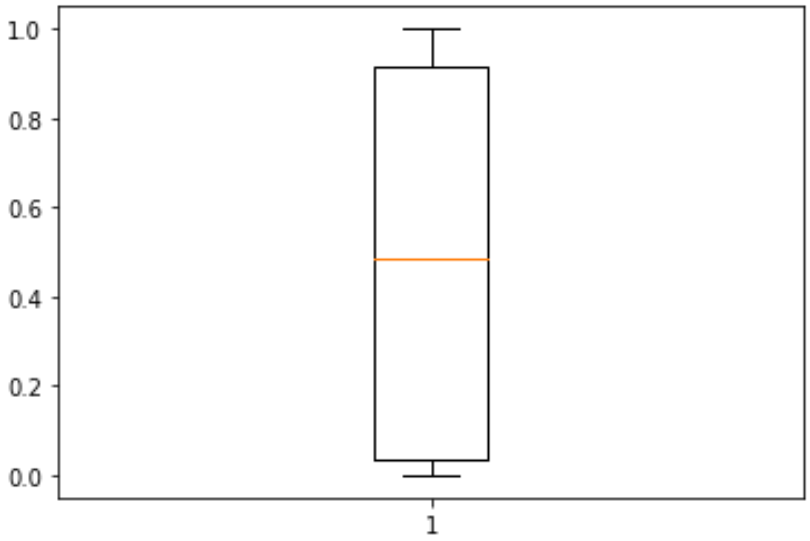
BOX PLOT for rmssd



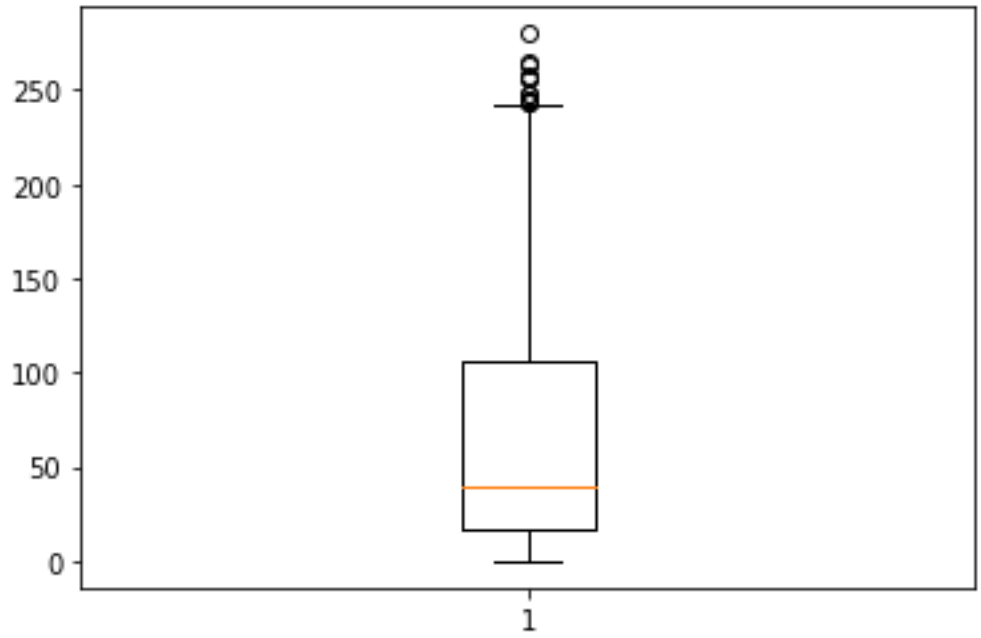
BOX PLOT for pnn20



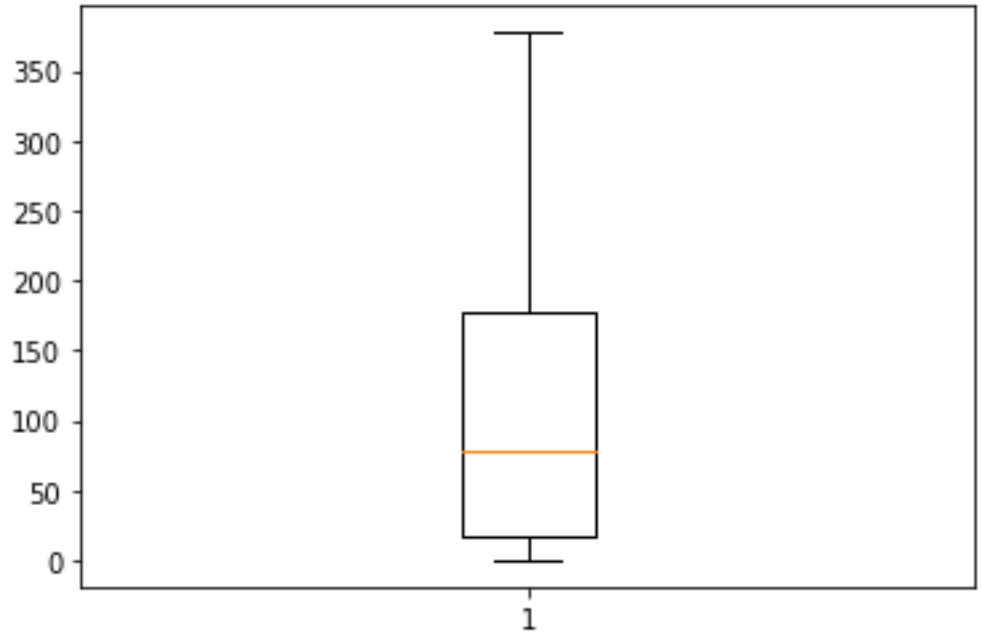
BOX PLOT for pnn50



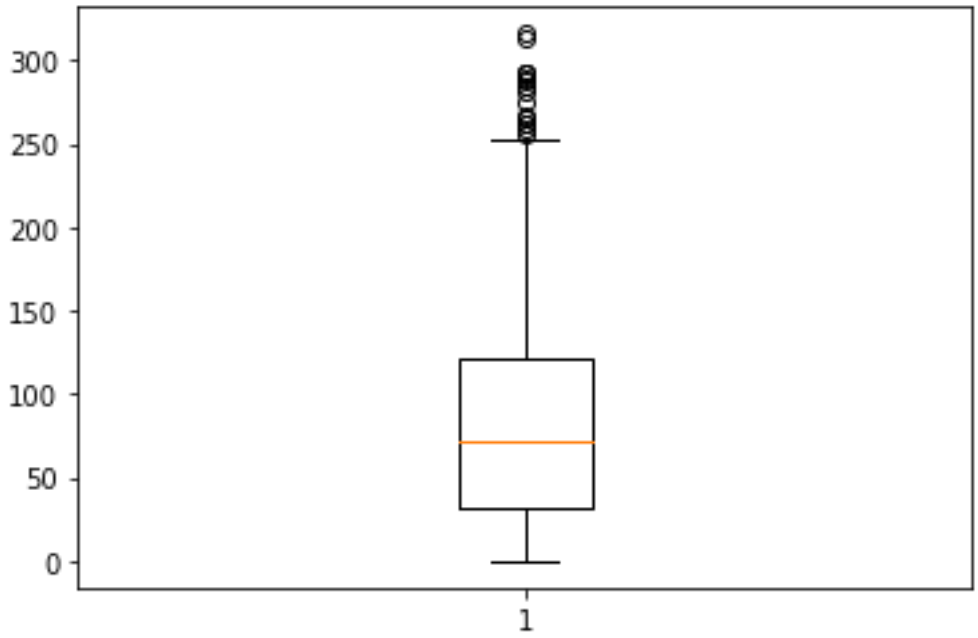
BOX PLOT for hr_mad



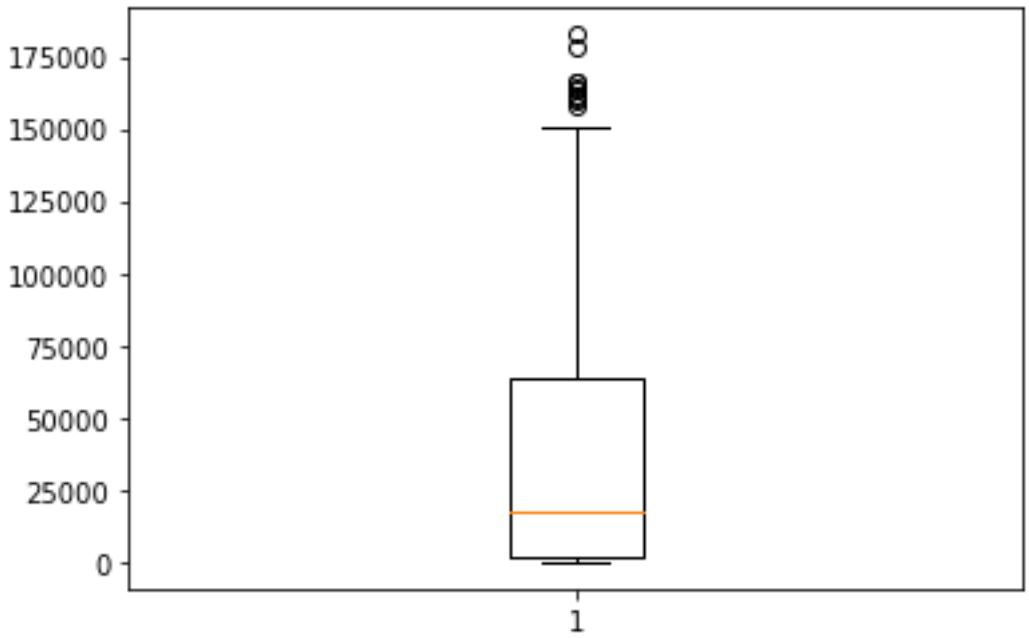
BOX PLOT for sd1



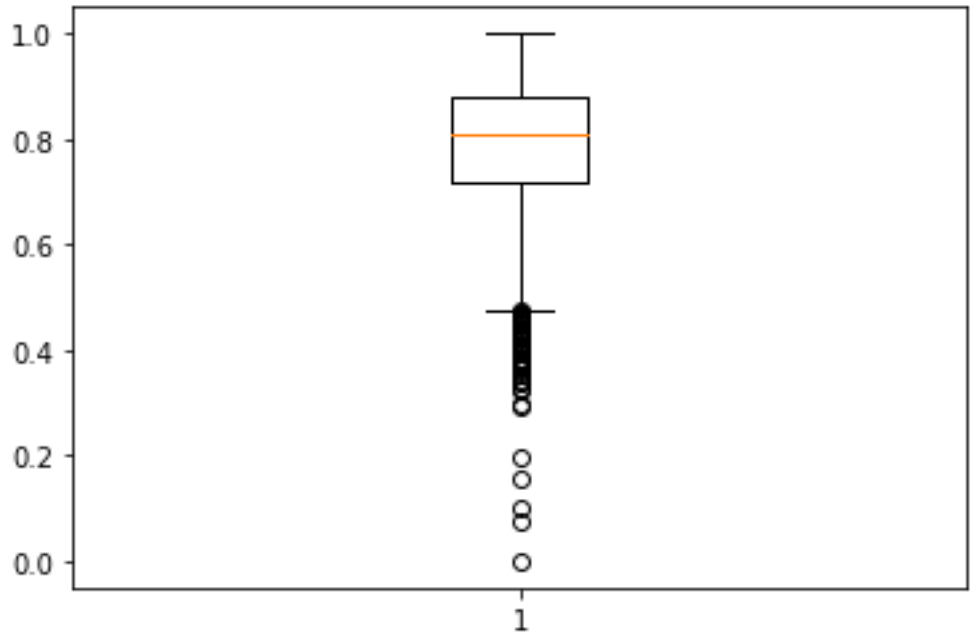
BOX PLOT for sd2



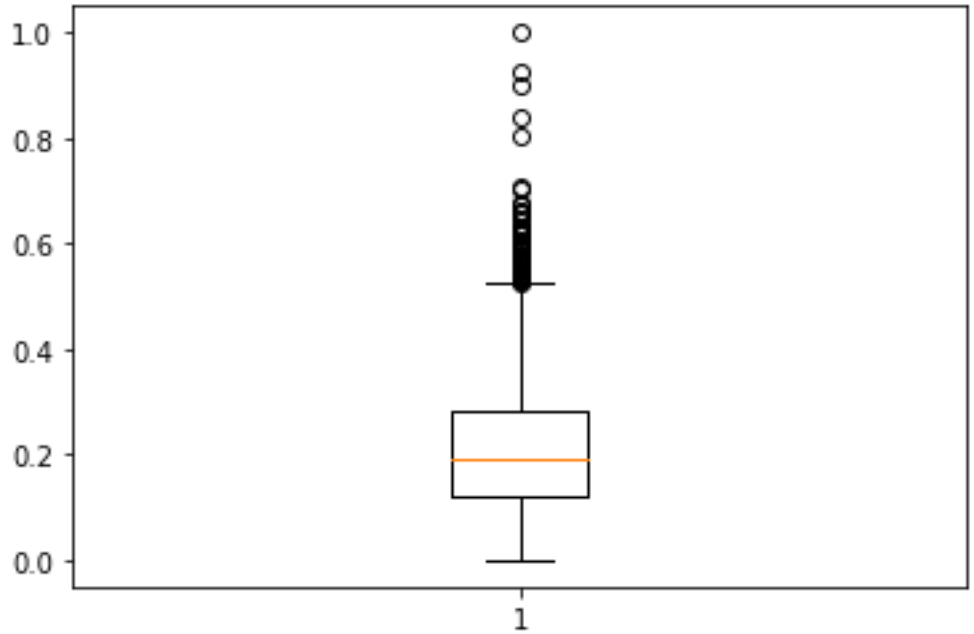
BOX PLOT for s



BOX PLOT for sd1/sd2



BOX PLOT for breathingrate



Data Transformation

As observed from the analysis the data is skewed and has outliers. We can perform log transformation to reduce the skewness and data normalisation using L1 regularization (Lasso regression) with a penalty function to transform the data in a range of 0 to 1.

```
from sklearn.preprocessing import Normalizer
Data_normalizer = Normalizer(norm='l1').fit(xx_noise.iloc[:,:13])
Data_normalized = Data_normalizer.transform(xx_noise.iloc[:,:13])
```

The above piece of code is used to normalize the data using L1 regularization technique. Now that the data is transformed we have to split it into test and train variables using below code.

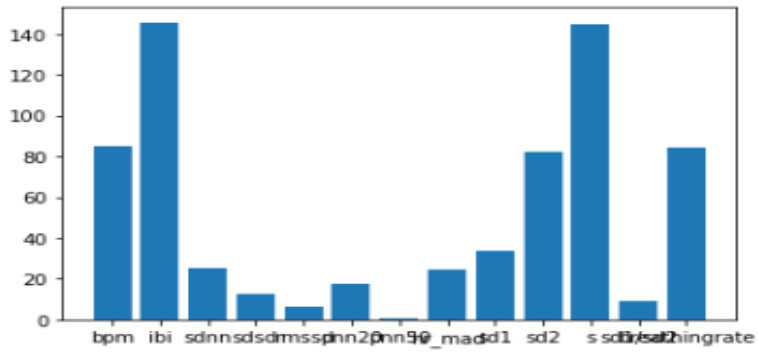
```
# Data splitting into train and test with 80:20 split
x_train,x_test,y_train,y_test=train_test_split(Data_normalized,y,test_size=0.2)
```

Now we can perform feature selection method using **ANOVA (Analysis of Variance)** to check the relation between features and understand it. Then with the understanding of the data ANOVA can transform the data to give more accuracy as shown below.

```
# configure to select all features
fs = SelectKBest(score_func=f_classif, k='all')
# learn relationship from training data
fs.fit(x_train, y_train)
# transform train input data
X_train_fs = fs.transform(x_train)
# transform test input data
X_test_fs = fs.transform(x_test)
```

```
1
2  # what are scores for the features
3  for i in range(len(fs.scores_)):
4      print('Feature %s: %f' % (fields[i], fs.scores_[i]))
5  # plot the scores
6  plt.bar([fields[i] for i in range(len(fs.scores_))], fs.scores_)
7  plt.show()
```

```
Feature bpm: 85.122236
Feature ibi: 145.617810
Feature sdnn: 25.540149
Feature sdsd: 12.373494
Feature rmssd: 6.131819
Feature pnn20: 17.541750
Feature pnn50: 0.482023
Feature hr_mad: 24.648128
Feature sd1: 33.849232
Feature sd2: 81.964857
Feature s: 144.879213
Feature sd1/sd2: 9.334291
Feature breathingrate: 84.039136
```



The Scores of the features can be observed above.

The target variable/ predicted variable is label encoded by replacing values of ‘N’ with ‘0’ and values of ‘A’ with ‘1’.

Model Building

Now that the data is transformed, we are going to train the K nearest neighbour classifier model. This can be observed below.

```
from sklearn.neighbors import KNeighborsClassifier

knn = KNeighborsClassifier()
knn.fit(x_train, y_train)
# evaluate the model
yhat = knn.predict(x_test)
# evaluate predictions
accuracy = accuracy_score(y_test, yhat)
print('Accuracy: %.2f' % (accuracy*100))
y_pred=knn.predict(x_test)
print('MSE:',np.sqrt(mean_squared_error(y_test,y_pred)))
print('f1_score:',f1_score(y_test,y_pred))
```

```
Accuracy: 92.29
MSE: 0.27774602993176545
f1_score: 0.6301369863013698
```

As we can see the model’s accuracy is 92.29% but it varies when trained at different times. The highest accuracy achieved was 93% and the f1_score ranged from 0.6 to 0.64. The Mean squared error is 0.277

Model Analysis

```
--->CLASSIFICATION REPORT=>

              precision    recall  f1-score   support

           0       0.95      0.97      0.96       620
           1       0.70      0.57      0.63        80

    accuracy                           0.92       700
   macro avg       0.82      0.77      0.79       700
weighted avg       0.92      0.92      0.92       700

--->CONFUSION MATRIX=>

 [[600  20]
 [ 34  46]]
```

In the classification report the class values ‘0’ and ‘1’ stand for ‘N’ normal reading and ‘A’ AF episode respectively. Due to imbalance of the data we can observe low ‘ f1_score ‘ for class ‘A’ i.e., AF episode.

Saving the KNN Model, L1 Normalizer, ANOVA Transformer

The KNN Model, L1 Normalizer, ANOVA Transformer models can be saved using pickle module as shown.

```
import pickle as pkl
pkl.dump(knn,open('knn_model.pkl','wb'))
pkl.dump(Data_normalizer,open('normalizer.pkl','wb'))
pkl.dump(fs,open('ANOVA.pkl','wb'))
```

Evaluation Script

The following script can be used to evaluate the model using three pre-trained model files which are:

- **KNN model** saved as Pickle file
- **L1 normaliser** saved as Pickle file
- **ANOVA transformer** saved as Pickle file

The code for the evaluation can be observed below.

```
import pickle

import pandas as pd

from sklearn.metrics import accuracy_score,f1_score

import heartpy as hp

import warnings

warnings.filterwarnings("ignore")

from sklearn.impute import SimpleImputer


# Function to remove null values

def clear_nan(xx_noise):

    xx_noise = pd.DataFrame(xx_noise).replace('--',float('Nan'))

    # Imputer object using the mean strategy and

    # missing_values type for imputation

    imputer = SimpleImputer(missing_values = np.nan,

                            strategy ='mean')
```

```
    imputer = imputer.fit(xx_noise.iloc[:,:-1])

    # Imputing the data
    xx_noise.iloc[:,:-1] = imputer.transform(xx_noise.iloc[:,:-1])

    return xx_noise

sample_rate = 300

# Function to filter signals
def filter_and_visualise(data, sample_rate):
    '''
    function that filters using remove_baseline_wander
    and visualises result
    '''

    filtered = hp.remove_baseline_wander(data, sample_rate)
    return filtered



# loading model and normalizer
model = pickle.load(open('knn_model.pkl','rb'))
normalizer = pickle.load(open('normalizer.pkl','rb'))
fs = pickle.load(open('ANOVA.pkl','rb'))

# loading dataset
try:
    df = pd.read_csv('ECG_testing.csv')
```

```
except:
    print('Check File/ path')

features=[]          # list to store extracted features as 2D list

for i in range(len(df)):

    # Save each reading as csv file
    np.savetxt("GFG.csv",
           list(df['ECG'][i].split(',')),
           delimiter =", ",
           fmt ='% s')

    # Load the saved file using HeartPy
    data = hp.get_data('GFG.csv')

    #run analysis
    try:
        wd, m = hp.process(data, sample_rate)
        # Data stored in wd, m as dictionary



        #Append computed measures to features

        temp = list(m.values())
        temp.append(df['Classification'][i])
        features.append(temp)

    except Exception as e:
```

```
        filtered = filter_and_visualise(hp.get_data('GFG.csv'), sample_rate)
        wd, m = hp.process(hp.scale_data(filtered), sample_rate)

        temp = list(m.values())
        temp.append(df['Classification'][index])
        noisy_l.append(temp)



# Replace Nan values with median
x = clear_nan(features)
y = x.iloc[:,-1:]

# Label encoding
y = y.replace('N',0)
y = y.replace('A',1)

# Data Normalization
normalized_data = normalizer.transform(x.iloc[:,:-1])

# ANOVA Transformation
anova_data = fs.transform(normalized_data)

# Predicting values
y_pred = model.predict(anova_data)

# checking scores
print('F1_score is :',f1_score(y.values,y_pred))
print('accuracy is:',accuracy_score(y.values,y_pred)*100)
```

Output is the f1_score of the model with test_data and the accuracy_score. For example, when evaluated on Train data the results are,

```
F1_score is : 0.6666666666666667
accuracy is: 93.19161160586037
```