Statistics

June 7, 2020

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

1 Load the datasets

let's see how they look's like

[2]:
```
diagnosis_df = pd.read_excel('patients_diagnosis.xlsx')
auscultation_df = pd.read_excel('auscultation_features.xlsx')

diagnosis_df = diagnosis_df.set_index(['patient_ID'])
auscultation_df = auscultation_df.set_index(['patient_ID'])

features = auscultation_df.columns.values
features = list(features[11:])
```

[3]:
```
print(diagnosis_df.head())
```

```
           Diagnosis    age sex    IMC  weight  height
patient_ID
101             URTI   3.00   F    NaN    19.0    99.0
102          Healthy   0.75   F    NaN     9.8    73.0
103           Asthma  70.00   F  33.00     NaN     NaN
104             COPD  70.00   F  28.47     NaN     NaN
105             URTI   7.00   F    NaN    32.0   135.0
```

[4]:
```
print(auscultation_df.head())
```

```
           Diagnosis  age sex  IMC  weight  height          adq_format  start  \
patient_ID
101             URTI  3.0   F  NaN    19.0    99.0  1b1_Al_sc_Meditron  0.036
101             URTI  3.0   F  NaN    19.0    99.0  1b1_Al_sc_Meditron  0.579
101             URTI  3.0   F  NaN    19.0    99.0  1b1_Al_sc_Meditron  2.450
101             URTI  3.0   F  NaN    19.0    99.0  1b1_Al_sc_Meditron  3.893
101             URTI  3.0   F  NaN    19.0    99.0  1b1_Al_sc_Meditron  5.793

              end  crackles  wheezes  state       Var     Range  Coarse_Av  \
patient_ID
101         0.579          0         0       0  0.000048  0.113594   0.000446
101         2.450          0         0       0  0.000066  0.159031   0.012435
101         3.893          0         0       0  0.000044  0.115345  -0.101963
101         5.793          0         0       0  0.000074  0.187316  -0.113660
101         7.521          0         0       0  0.000036  0.117565  -0.017593

             Fine_Av   Spectrum Av
patient_ID
101         0.000599  2.537207e-08
101        -0.001276  3.532798e-08
101        -0.000701  2.213387e-08
101        -0.000223  3.485673e-08
101        -0.001040  1.806783e-08
```

```
[5]: print("Features to analyze")
     print(features)
```

```
Features to analyze
['state', 'Var', 'Range', 'Coarse_Av', 'Fine_Av', 'Spectrum Av']
```

2 Statistics

2.0.1 Which and how many diagnostics of each one, are in the dataset

```
[6]: diagnosis_df['Diagnosis'].value_counts()
```

```
[6]: COPD              64
     Healthy           26
     URTI              14
     Bronchiectasis     7
     Bronchiolitis      6
     Pneumonia          6
     LRTI               2
     Asthma             1
     Name: Diagnosis, dtype: int64
```

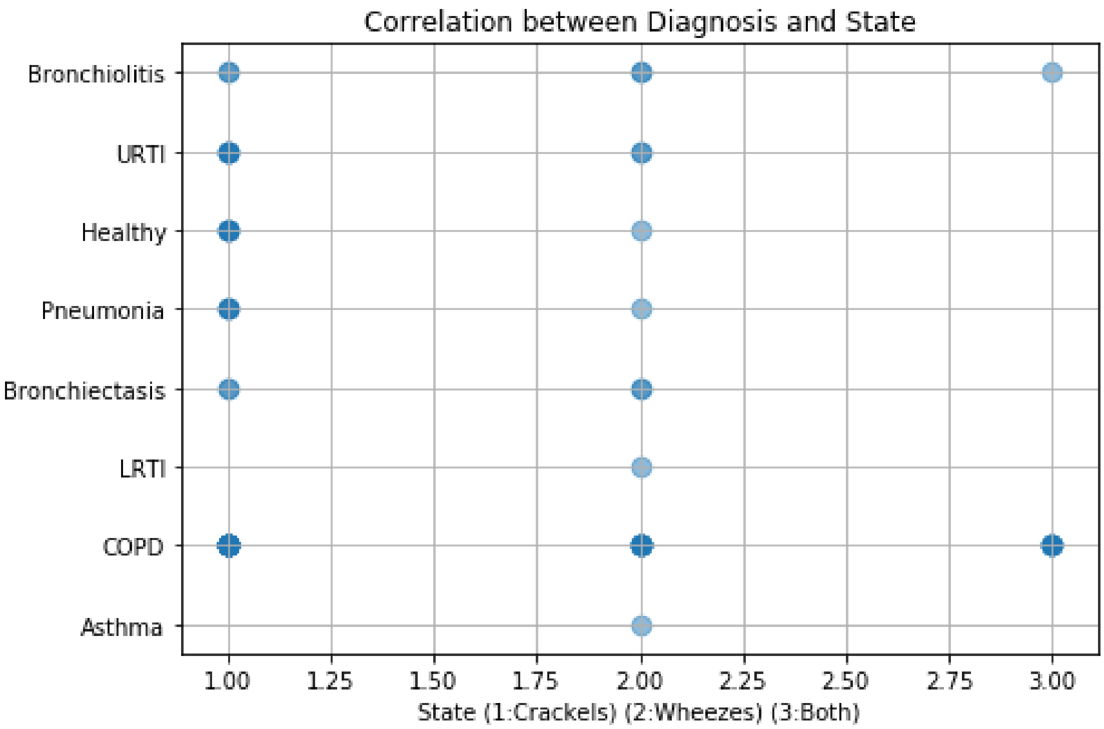
2.0.2 Number of people with Crackles and/or Wheezes in at least one of their auscultation audios

```
[7]: number_c_w = auscultation_df.loc[auscultation_df['state'] >␣
      ↪0,['Diagnosis','age','sex','state']]
     # remove repeated rows
     number_c_w = number_c_w.drop_duplicates(subset=['Diagnosis','age','sex'],␣
      ↪keep='first')
     print(number_c_w)
     print('\n'+str(len(number_c_w))+' of 126 patients with any of this conditions')
     print('\nDistributed like this: Only Crackles (Index 1), Only Wheezes (Index␣
      ↪2), Both (Index 3)')
     print(number_c_w['state'].value_counts())
```

```
                Diagnosis   age  sex  state
patient_ID
103                Asthma  70.0    F      2
104                  COPD  70.0    F      2
106                  COPD  73.0    F      1
107                  COPD  75.0    F      1
109                  COPD  84.0    F      1
…                     …   …    …    …
216         Bronchiolitis   1.0    M      1
219             Pneumonia  81.0    M      1
221                  COPD  74.0    F      2
223                  COPD   NaN  NaN      2
226             Pneumonia   4.0    M      1

[66 rows x 4 columns]

66 of 126 patients with any of this conditions

Distributed like this: Only Crackles (Index 1), Only Wheezes (Index 2), Both
(Index 3)
1    38
2    20
3     8
Name: state, dtype: int64
```

[8]:

```
# Esta relacionado el diagnóstico con tener C, W o ambas?
plt.axes([0.025, 0.025, 0.95, 0.95])
plt.scatter(number_c_w['state'],number_c_w['Diagnosis'], s=75, alpha=.5)

plt.title('Correlation between Diagnosis and State')
plt.xlabel('State (1:Crackels) (2:Wheezes) (3:Both)')
plt.grid(True)

# Sí, y podemos notar como los puntos con tonos mas oscuros son aquellos que
# se relacionan fuertemente, y los claros no. Por ejemplos las personas que
# padecen COPD, tienen en su mayoria ambos (C & W), la mayoria de diagnósticos,␣
 ↪en la mayoria
# de los casos presentan C y algunos otros W, sin embargo solo para Bronch y␣
 ↪COPD
# presentan ambos.
```



2.0.3 Features of auscultation cycles without Crackles or Wheezes

```
[9]: any_c_w = auscultation_df.loc[auscultation_df['state'] == 0, features]
     any_c_w = any_c_w.describe()
     any_c_w
```

```
[9]:         state           Var        Range    Coarse_Av      Fine_Av  \
     count  3642.0  3.642000e+03  3642.000000  3642.000000  3642.000000
     mean      0.0  1.193481e-03     0.388487    -0.001282    -0.000120
     std       0.0  2.839762e-03     0.460638     0.093403     0.022191
     min       0.0  9.642802e-08     0.002815    -1.152474    -0.310829
     25%       0.0  2.840777e-05     0.077589    -0.010511    -0.003023
     50%       0.0  1.765182e-04     0.205141    -0.000288    -0.000027
     75%       0.0  9.826176e-04     0.521051     0.008255     0.002794
     max       0.0  4.033774e-02     2.936117     1.354314     0.365529

              Spectrum_Av
     count  3.642000e+03
     mean   6.007755e-07
     std    1.427217e-06
     min    4.153491e-11
     25%    1.438862e-08
     50%    8.902104e-08
```

```
75%    4.978222e-07
max    2.066292e-05
```

2.0.4 Features of auscultation cycles with Only Crackles

[10]:

```
only_crackles = auscultation_df.loc[auscultation_df['state'] == 1, features]
only_crackles = only_crackles.describe()
only_crackles
```

[10]:

```
        state           Var        Range    Coarse_Av      Fine_Av  \
count  1864.0  1.864000e+03  1864.000000  1864.000000  1864.000000
mean      1.0  1.445824e-03     0.542236    -0.002947    -0.001165
std       0.0  2.839023e-03     0.485124     0.098594     0.034198
min       1.0  9.701599e-08     0.003967    -0.758343    -0.294916
25%       1.0  1.085176e-04     0.184965    -0.015374    -0.006992
50%       1.0  4.720408e-04     0.387087    -0.000290    -0.000112
75%       1.0  1.634318e-03     0.745689     0.014746     0.006101
max       1.0  4.527466e-02     2.848768     1.625250     0.350306

        Spectrum Av
count  1.864000e+03
mean   7.257461e-07
std    1.425981e-06
min    4.852559e-11
25%    5.333458e-08
50%    2.368138e-07
75%    8.141661e-07
max    2.253853e-05
```

2.0.5 Features of auscultation cycles with Only Wheezes

[11]:

```
only_wheezes = auscultation_df.loc[auscultation_df['state'] == 2, features]
only_wheezes = only_wheezes.describe()
only_wheezes
```

[11]:

```
       state           Var       Range   Coarse_Av     Fine_Av   Spectrum Av
count  886.0  8.860000e+02  886.000000  886.000000  886.000000  8.860000e+02
mean     2.0  3.043243e-03    0.559886   -0.010843    0.002533  1.543631e-06
std      0.0  7.072023e-03    0.591344    0.163561    0.037337  3.599746e-06
min      2.0  3.104253e-07    0.006402   -2.047764   -0.186309  1.580335e-10
25%      2.0  9.493528e-05    0.147722   -0.014935   -0.004085  4.846846e-08
50%      2.0  5.878429e-04    0.342562   -0.000152    0.000207  2.982085e-07
75%      2.0  2.382902e-03    0.740389    0.013695    0.004738  1.215346e-06
max      2.0  7.292195e-02    3.421153    1.893362    0.433157  3.685974e-05
```

2.0.6 Features of auscultation cycles with Crackles and Wheezes

[12]:
```
both_c_w = auscultation_df.loc[auscultation_df['state'] == 3, features]
both_c_w = both_c_w.describe()
both_c_w
```

[12]:
```
       state           Var       Range   Coarse_Av     Fine_Av   Spectrum Av
count  506.0  5.060000e+02  506.000000  506.000000  506.000000  5.060000e+02
mean     3.0  2.271708e-03    0.590130    0.004311   -0.001196  1.147357e-06
std      0.0  4.581759e-03    0.541853    0.173277    0.028778  2.347203e-06
min      3.0  3.268198e-07    0.006327   -2.424723   -0.431638  1.630643e-10
25%      3.0  1.215953e-04    0.180335   -0.010403   -0.006209  6.146923e-08
50%      3.0  5.549011e-04    0.386970    0.000395    0.000123  2.829200e-07
75%      3.0  2.360277e-03    0.907443    0.016116    0.005407  1.197696e-06
max      3.0  5.431369e-02    2.894315    1.777617    0.087551  2.808853e-05
```

3 Comparison between features of each condition

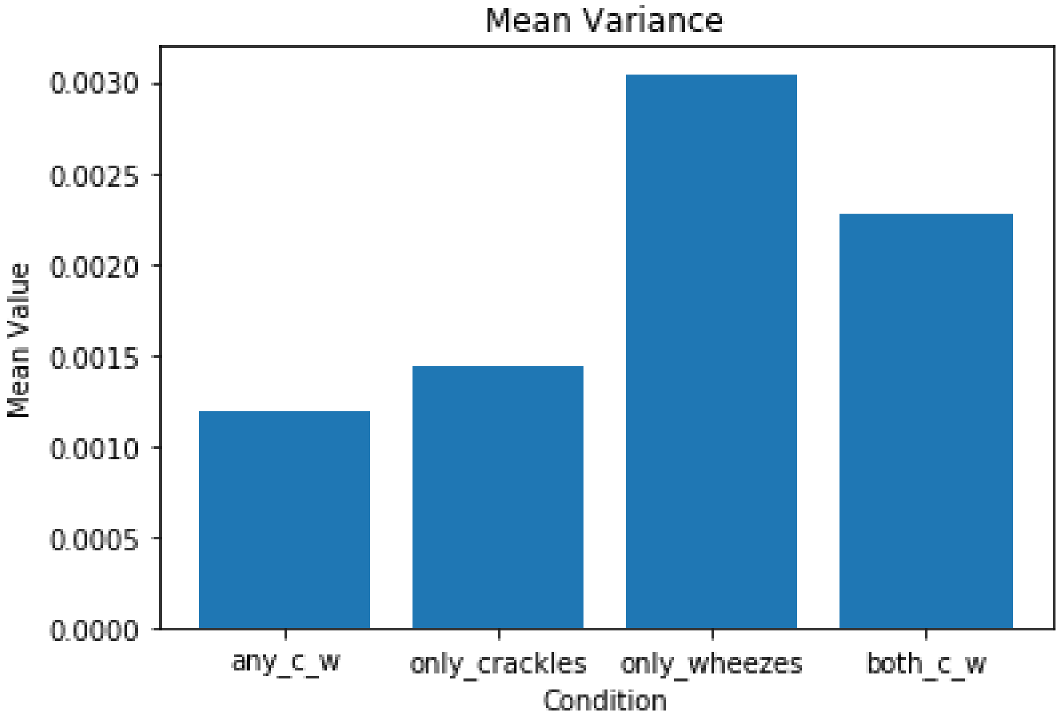
[13]:
```
conditions = ['any_c_w','only_crackles','only_wheezes','both_c_w']
feature_colection = [any_c_w,only_crackles,only_wheezes,both_c_w]
```

Comparison between Averages for each feature of the auscultation signal

[14]:
```
Variance = []
Range = []
Coarse_Av = []
Fine_Av = []
Spectrum_Av = []

for i in feature_colection:
    Variance.append(i['Var'][1])
    Range.append(i['Range'][1])
    Coarse_Av.append(i['Coarse_Av'][1])
    Fine_Av.append(i['Fine_Av'][1])
    Spectrum_Av.append(i['Spectrum Av'][1])
```

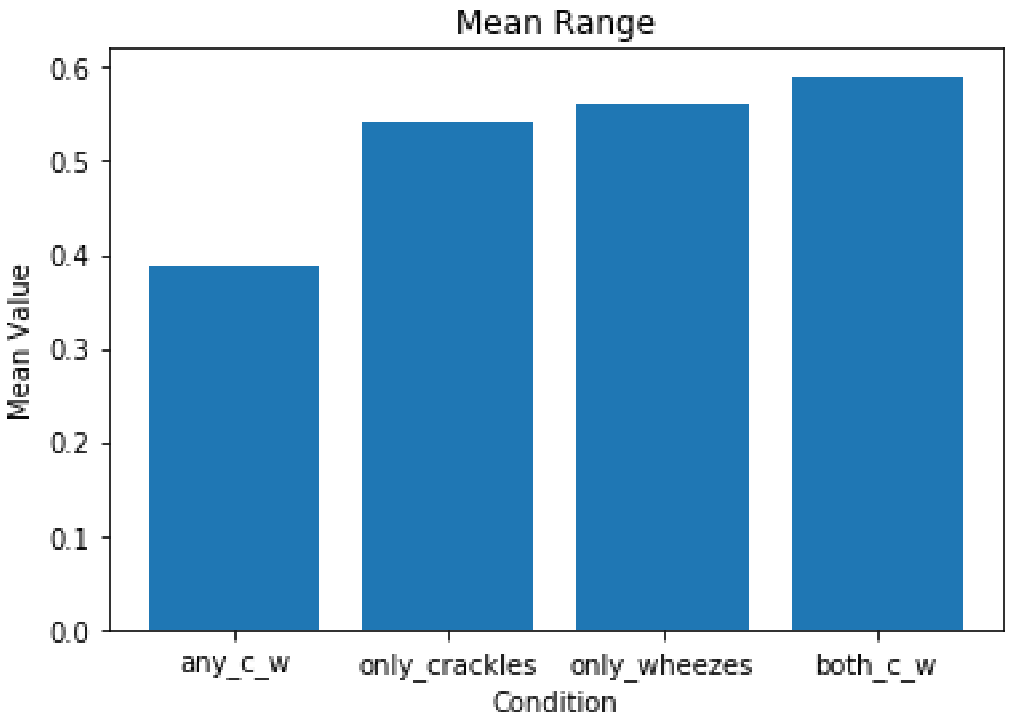
[15]:
```
plt.figure()
plt.bar(conditions,Variance)
plt.title('Mean Variance')
plt.ylabel('Mean Value')
plt.xlabel('Condition')
```

[15]:
```
Text(0.5, 0, 'Condition')
```



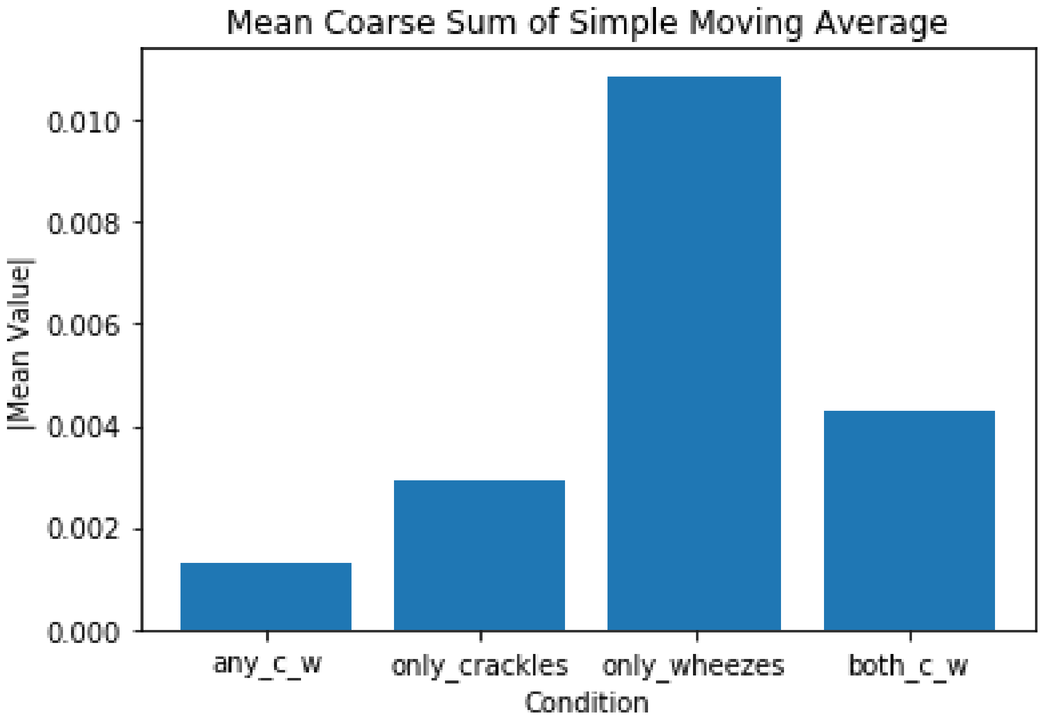
```
[16]: plt.figure()
      plt.bar(conditions,Range)
      plt.title('Mean Range')
      plt.ylabel('Mean Value')
      plt.xlabel('Condition')
```

```
[16]: Text(0.5, 0, 'Condition')
```



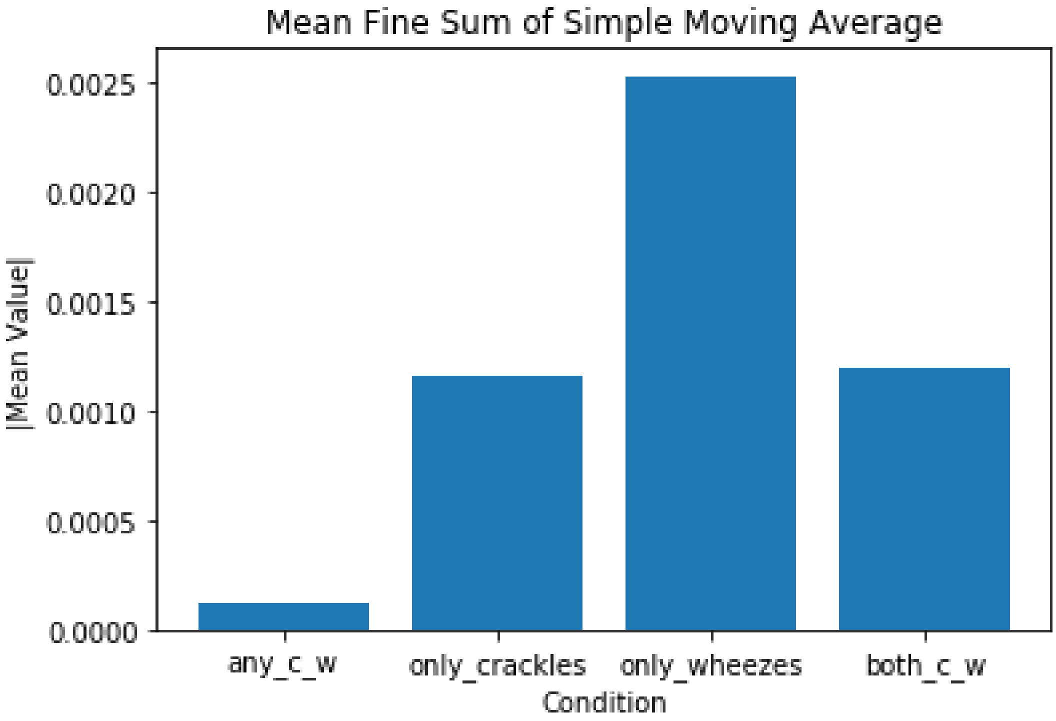
```
[17]: plt.figure()
      plt.bar(conditions,np.abs(Coarse_Av))
      plt.title('Mean Coarse Sum of Simple Moving Average')
      plt.ylabel('|Mean Value|')
      plt.xlabel('Condition')
```

```
[17]: Text(0.5, 0, 'Condition')
```



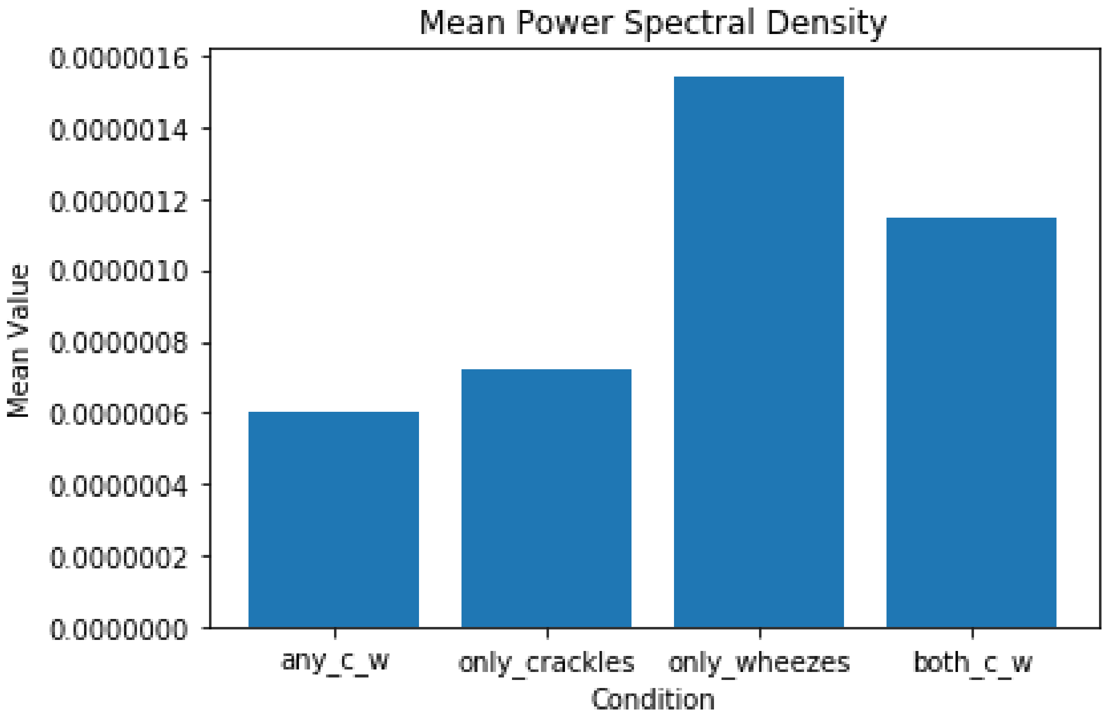
```
[18]: plt.figure()
      plt.bar(conditions,np.abs(Fine_Av))
      plt.title('Mean Fine Sum of Simple Moving Average')
      plt.ylabel('|Mean Value|')
      plt.xlabel('Condition')
```

```
[18]: Text(0.5, 0, 'Condition')
```



```
[19]: plt.figure()
      plt.bar(conditions,Spectrum_Av)
      plt.title('Mean Power Spectral Density')
      plt.ylabel('Mean Value')
      plt.xlabel('Condition')
```

```
[19]: Text(0.5, 0, 'Condition')
```



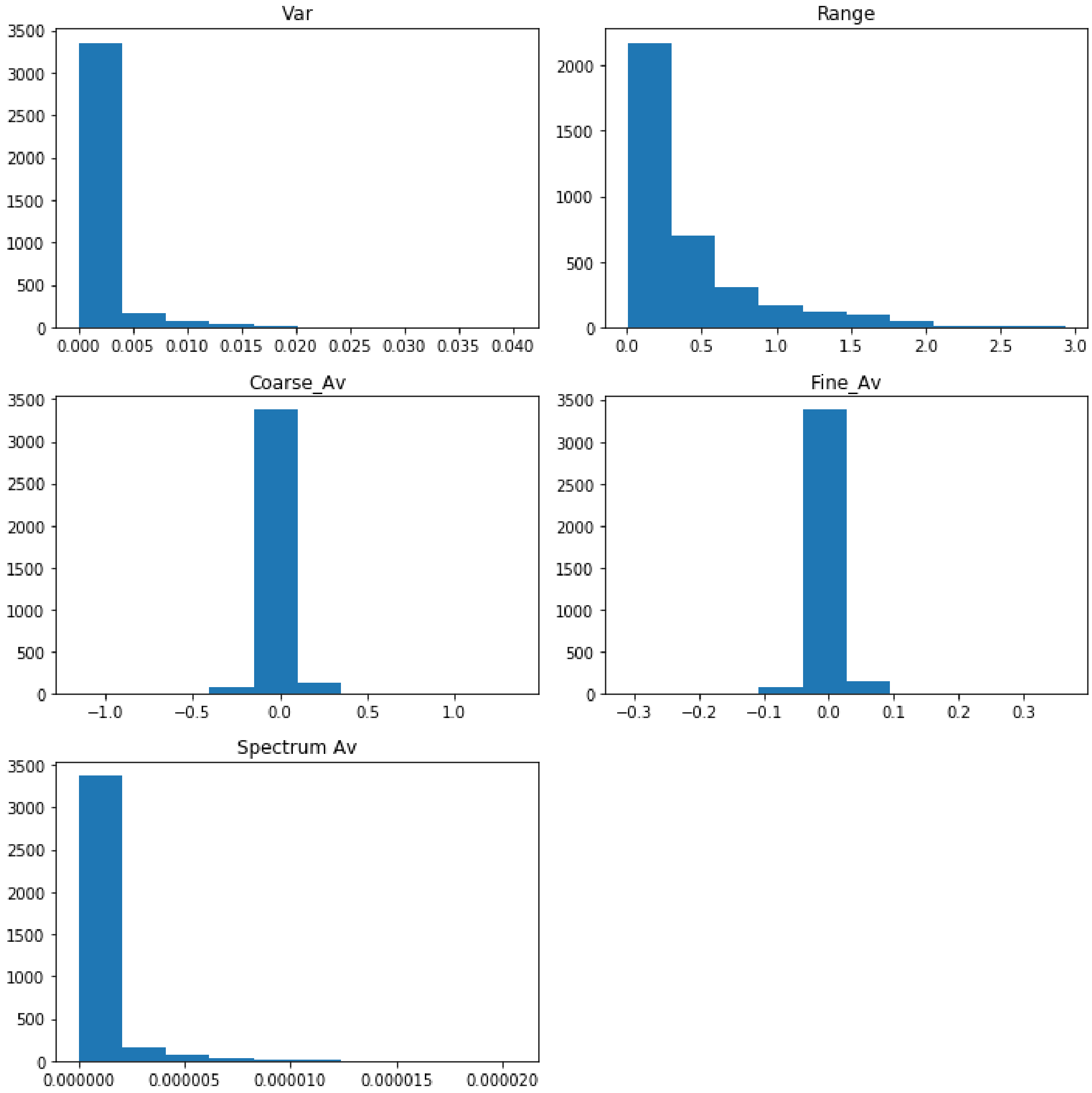
3.1 Let's see the distribution of the data

[20]:
```
features = ['Var', 'Range', 'Coarse_Av', 'Fine_Av', 'Spectrum Av']
any_c_w = auscultation_df.loc[auscultation_df['state'] == 0, features]
only_crackles = auscultation_df.loc[auscultation_df['state'] == 1, features]
only_wheezes = auscultation_df.loc[auscultation_df['state'] == 2, features]
both_c_w = auscultation_df.loc[auscultation_df['state'] == 3, features]
features
```

[20]:
```
['Var', 'Range', 'Coarse_Av', 'Fine_Av', 'Spectrum Av']
```

3.2 For Healthy Cycles

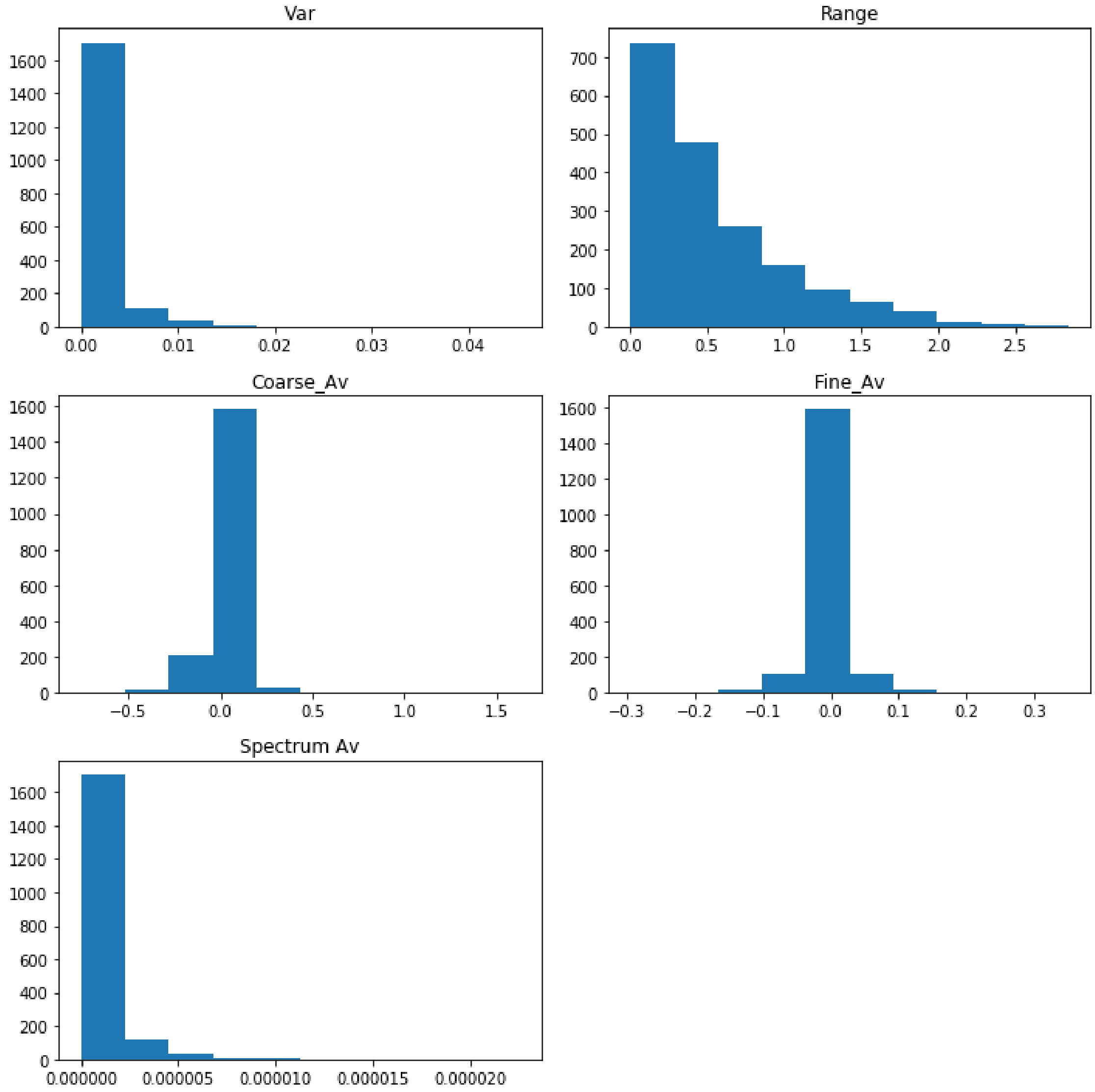
[21]:
```
position = 1
plt.figure(figsize=(10,10))
for i in any_c_w:
    plt.subplot(3,2,position)
    plt.hist(any_c_w[i].values)
    plt.title(i)
    position += 1
plt.tight_layout()
```



3.3 For Cycles with Only Crackles

[22]:

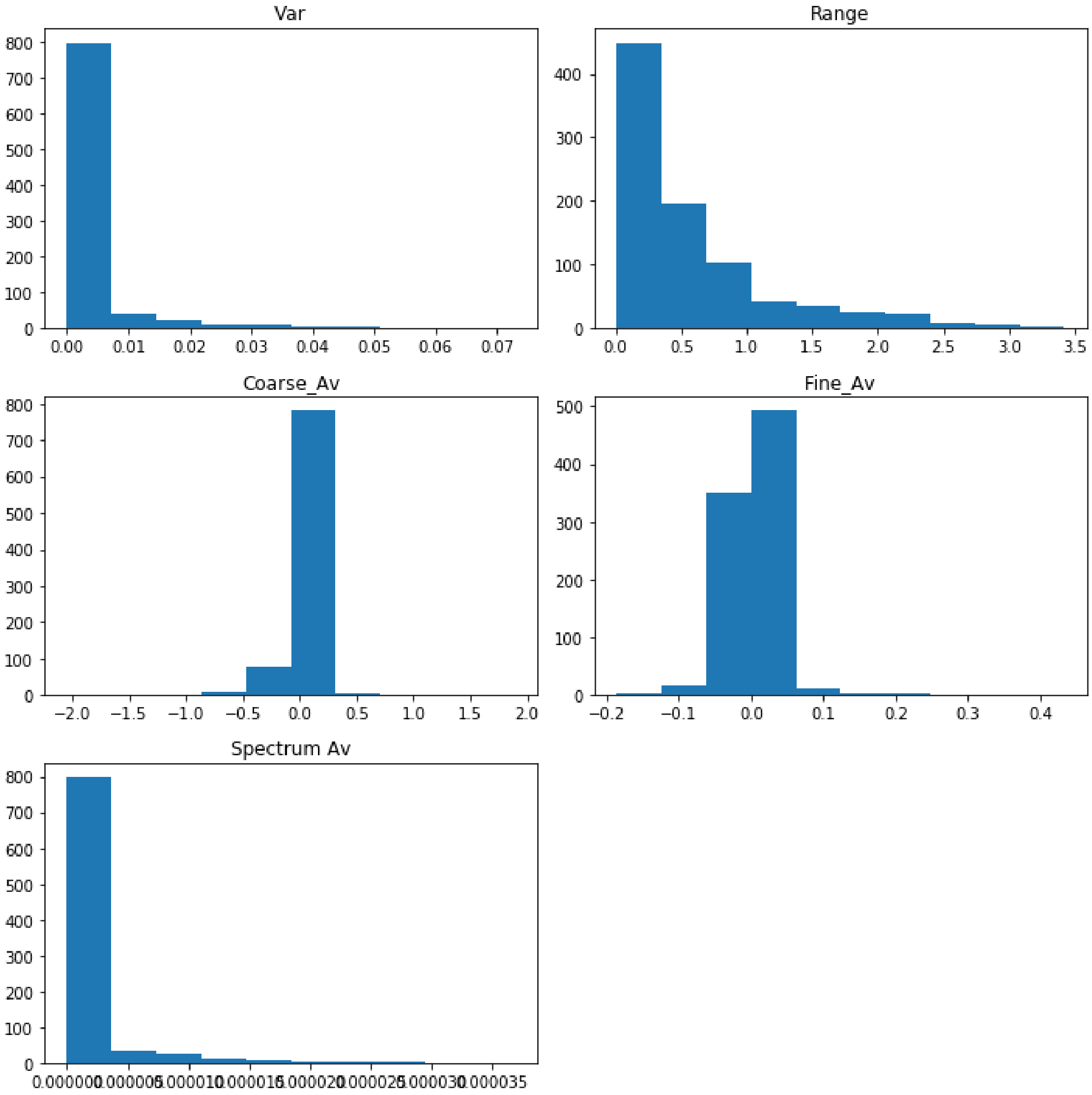
```
position = 1
plt.figure(figsize=(10,10))
for i in any_c_w:
    plt.subplot(3,2,position)
    plt.hist(only_crackles[i].values)
    plt.title(i)
    position += 1
plt.tight_layout()
```



3.4 For Cycles with Only Wheezes

[23]:

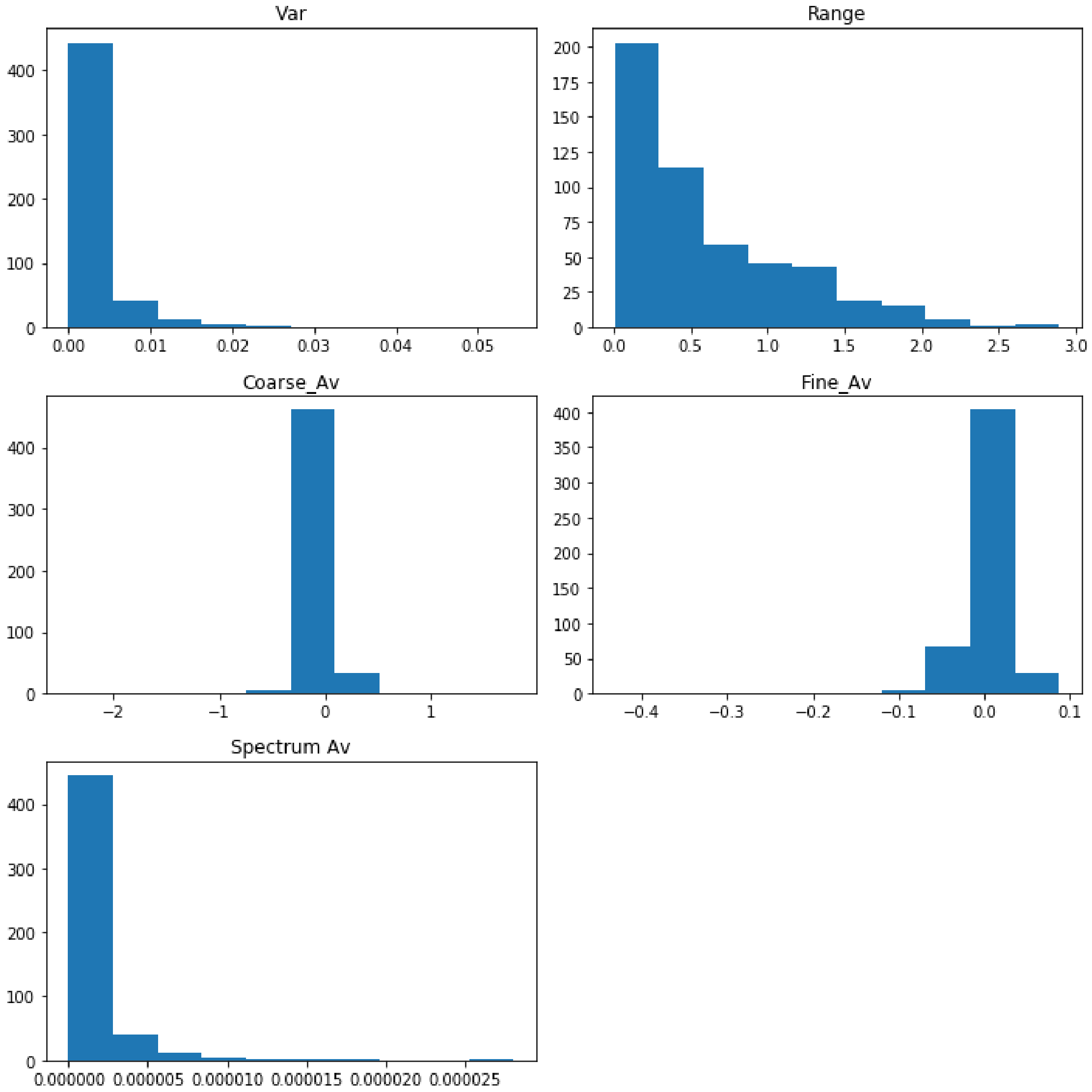
```
position = 1
plt.figure(figsize=(10,10))
for i in any_c_w:
    plt.subplot(3,2,position)
    plt.hist(only_wheezes[i].values)
    plt.title(i)
    position += 1
plt.tight_layout()
```



3.5 For Cycles with Crackles and Wheezes

[24]:

```
position = 1
plt.figure(figsize=(10,10))
for i in any_c_w:
    plt.subplot(3,2,position)
    plt.hist(both_c_w[i].values)
    plt.title(i)
    position += 1
plt.tight_layout()
```



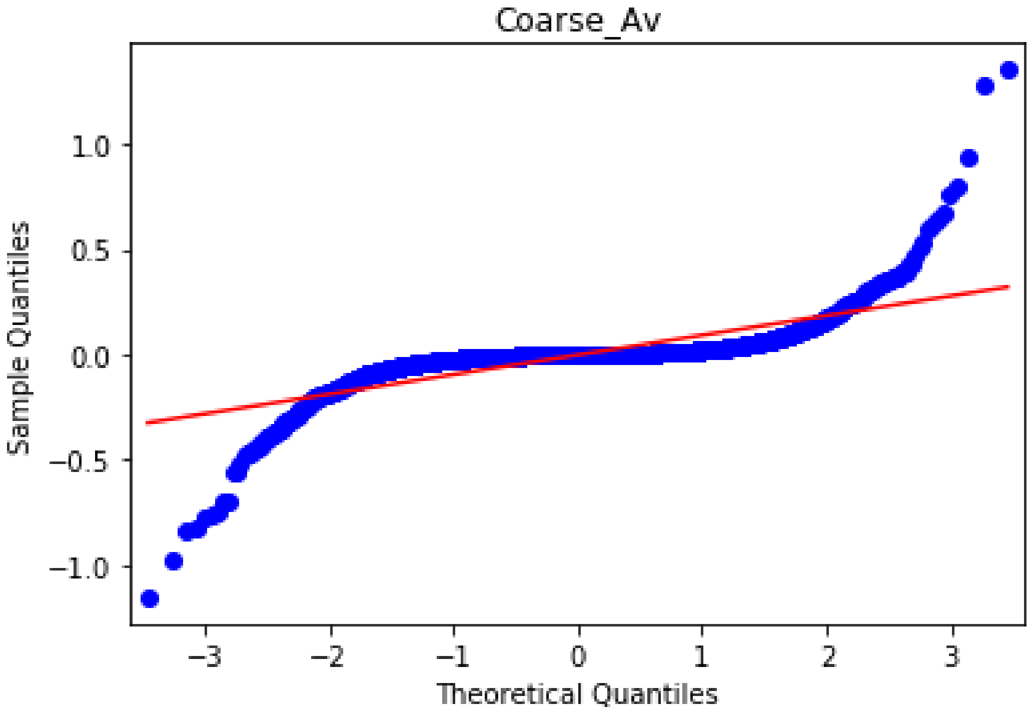
4 Let's verify distributions of Short Moving Averages and Spectrum__Av of any of those above

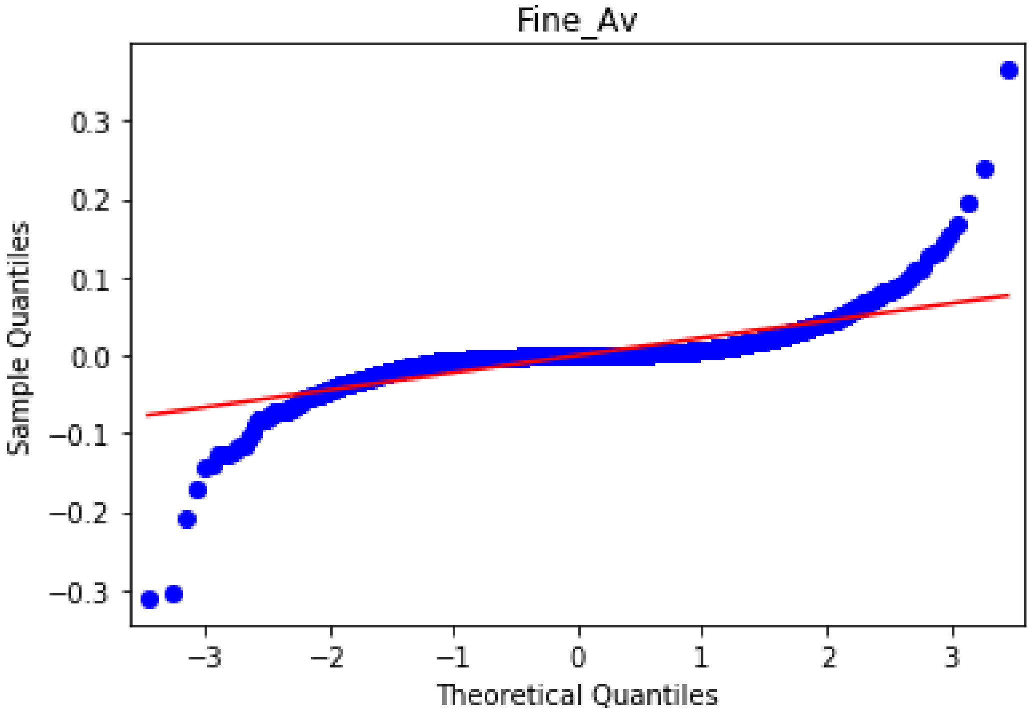
[25]:

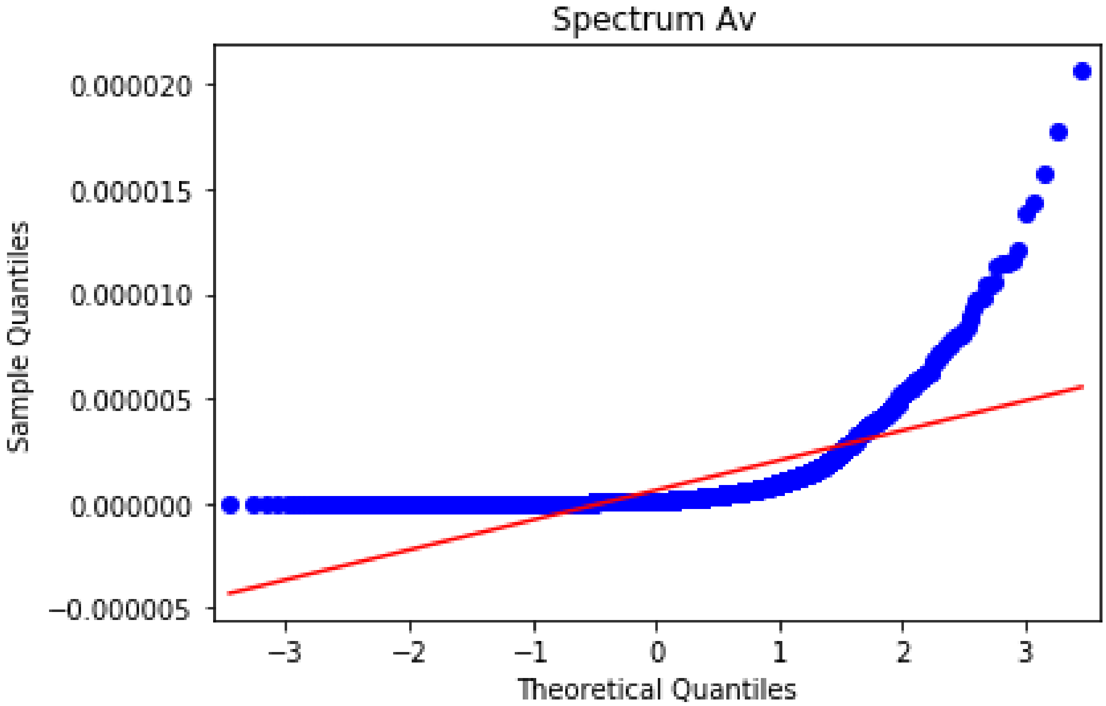
```
from statsmodels.graphics.gofplots import qqplot
```

[26]:

```
# For Healthy Cycles
qqplot(any_c_w['Coarse_Av'].values, line='s')
plt.title('Coarse_Av')
plt.show()
qqplot(any_c_w['Fine_Av'].values, line='s')
plt.title('Fine_Av')
plt.show()
qqplot(any_c_w['Spectrum Av'].values, line='s')
plt.title('Spectrum Av')
plt.show()
```

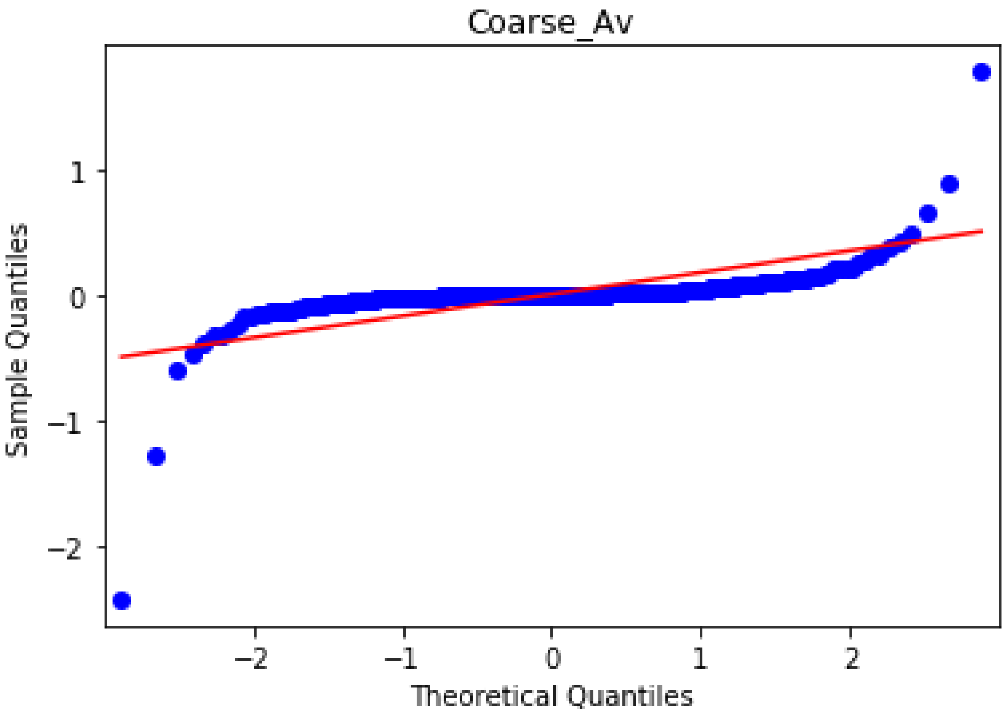


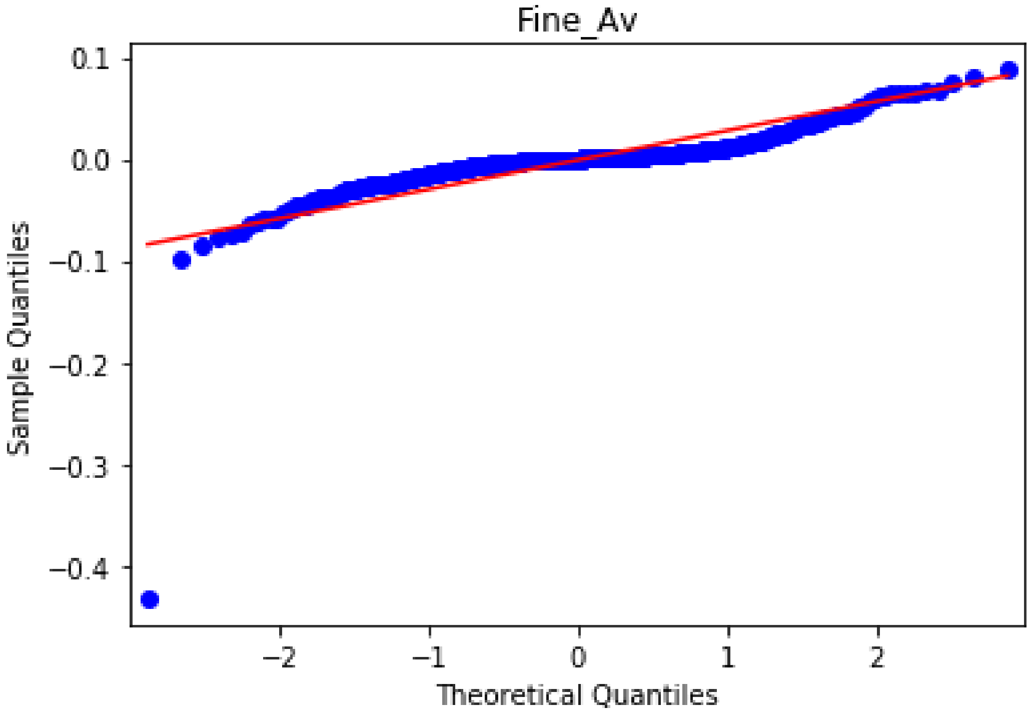

Fine_Av
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
Sample Quantiles
−3
−2
−1
0
1
2
3
Theoretical Quantiles

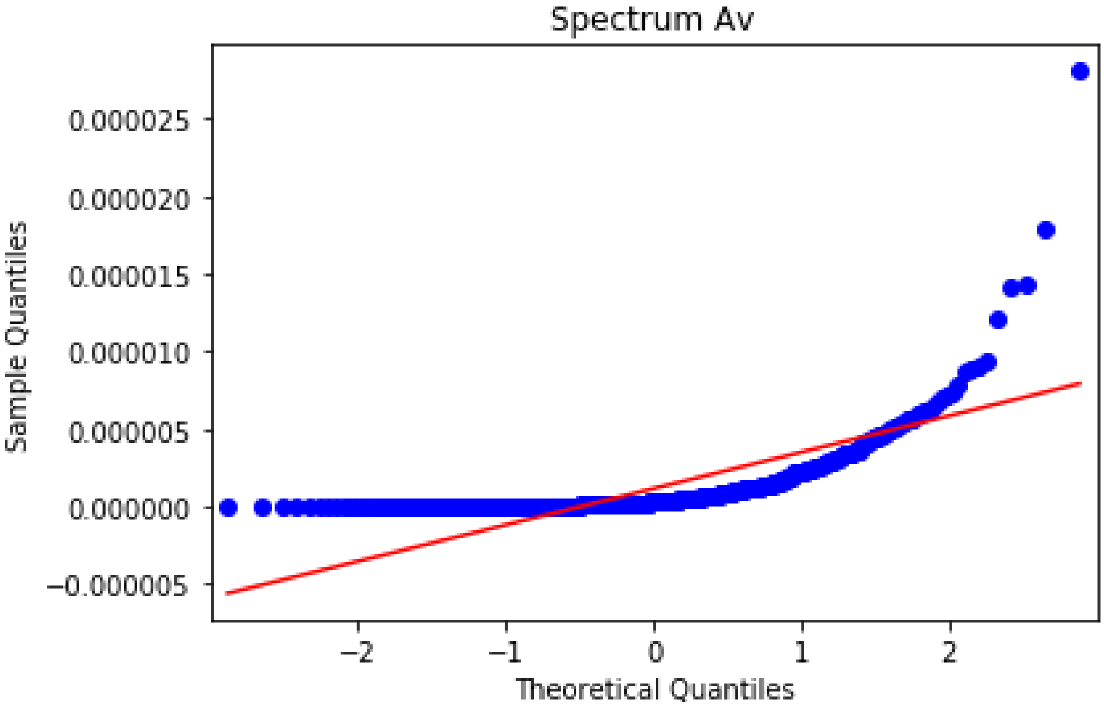

Spectrum Av
0.000020
0.000015
0.000010
0.000005
0.000000
−0.000005
Sample Quantiles
−3
−2
−1
0
1
2
3
Theoretical Quantiles

[27]:

```
# For Cycles with Crackles and Wheezes
qqplot(both_c_w['Coarse_Av'].values, line='s')
plt.title('Coarse_Av')
plt.show()
qqplot(both_c_w['Fine_Av'].values, line='s')
plt.title('Fine_Av')
plt.show()
qqplot(both_c_w['Spectrum Av'].values, line='s')
plt.title('Spectrum Av')
plt.show()
```




Fine_Av
0.1
0.0
−0.1
−0.2
−0.3
−0.4
Sample Quantiles
−2
−1
0
1
2
Theoretical Quantiles


Spectrum Av
0.000025
0.000020
0.000015
0.000010
0.000005
0.000000
−0.000005
Sample Quantiles
−2
−1
0
1
2
Theoretical Quantiles

4.1 Let’s do a hypothetical test for Fine__Av and Spectrum__Av, for which first “apparently has normal distribution”, and second does not.

5 1) Null and Alternative Hypothesis Tests

Null: Healthy **cycles** has **similar Fine__Av** to those who have Crackles and Wheezes.

Alternative: Healthy **cycles** has **different Fine__Av** to those who have Crackles and Wheezes.

6 Parametric Analysis

[28]:

```
from scipy.stats import ttest_ind, mannwhitneyu, pearsonr, spearmanr, wilcoxon,␣
 ↪mannwhitneyu
```

6.1 Pearson’s Correlation

[29]:

```
pearsonr(any_c_w['Fine_Av'][:430].values,both_c_w['Fine_Av'][:430].values)
```

[29]:

```
(0.027213911831310836, 0.5735838393591834)
```

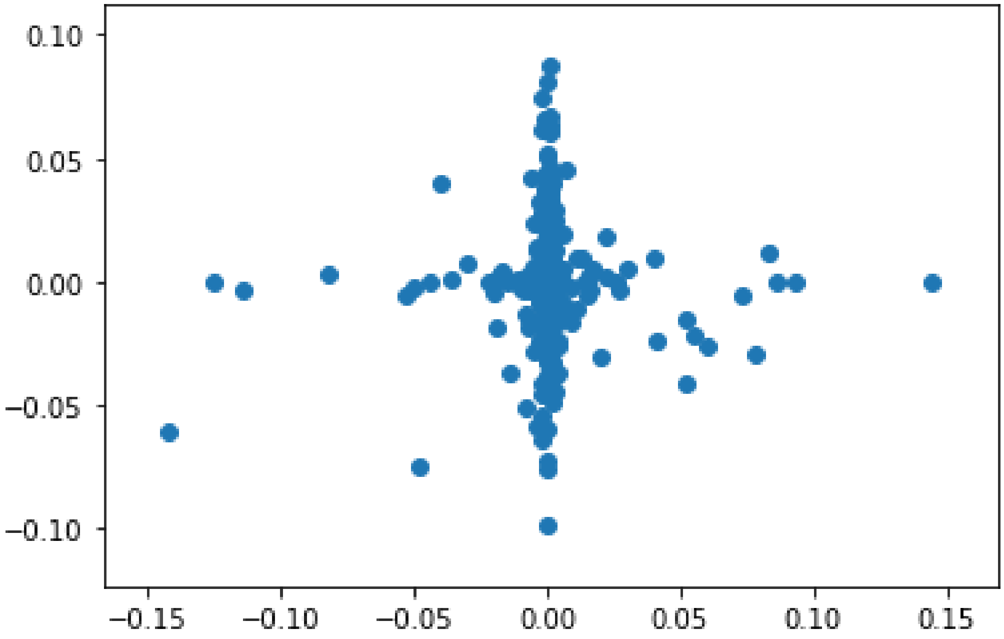
This result shows that there is a positive, linear and weak relationship between healthy patients and those with Crackles and Wheezes. The relationship is about the 2%, but there exist a probability about 50% of get an extreme value of the distribution assuming that the null hypothesis is true, so **we can’t reject the null hypothesis**

[30]:

```
plt.scatter(any_c_w['Fine_Av'][:430].values,both_c_w['Fine_Av'][:430].values)
```

[30]:

```
<matplotlib.collections.PathCollection at 0x2e3b11a8788>
```



6.2 In the correlation, the different outliers break the normal distribution, so they must be studied under a non-parametric analysis

6.3 Two Sample T-Test

```
[31]: ttest_ind(any_c_w['Fine_Av'][:430].values, both_c_w['Fine_Av'][:430].values)
```

```
[31]: Ttest_indResult(statistic=0.38536778364947677, pvalue=0.70006046524553)
```

However, in 31% of cases I cannot identify without the subject being healthy or having Crackles and Wheezes. **This is because parametric analysis is probably not the right study***

7 Non-Parametric Analysis

```
[32]: spearmanr(any_c_w['Fine_Av'][:430].values, both_c_w['Fine_Av'][:430].values)
```

```
[32]: SpearmanrResult(correlation=0.051782663998711044, pvalue=0.2839979597004261)
```

```
[33]: mannwhitneyu(any_c_w['Fine_Av'][:430].values, both_c_w['Fine_Av'][:430].values)
```

```
[33]: MannwhitneyuResult(statistic=90933.0, pvalue=0.33857539885051546)
```

7.0.1 Even if the data are not very closely related, there is a high probability that mixed results will be obtained because of the random. So the Alternative Hyphotesis can't be considered

8 2) Null and Alternative Hypothesis Tests

Null: Healthy **cycles** has **similar Spectrum Av** to those who have Crackles and Wheezes.

Alternative: Healthy **cycles** has **different Spectrum Av** to those who have Crackles and Wheezes.

9 Non-Parametric Analysis

```
[34]: spearmanr(any_c_w['Spectrum Av'][:430].values, both_c_w['Spectrum Av'][:430].
       ↪values)
```

```
[34]: SpearmanrResult(correlation=-0.09939593671315464, pvalue=0.039377264045743904)
```

```
[35]: mannwhitneyu(any_c_w['Spectrum Av'][:430].values, both_c_w['Spectrum Av'][:430].
       ↪values)
```

```
[35]: MannwhitneyuResult(statistic=62830.0, pvalue=2.1110159275072014e-16)
```

9.1 In this case, it becomes evident that the spectral power of healthy cycles is totally different from those that have Crackles and Wheezes