Statistical Methods In Research

Nafisa Jassani -1543203
Mohit G Kaduskar -1544187

6 May, 2017

Contents

List of Figures

1 Introduction

The dataset is acquired by carrying out a controlled experiment on a driving simulator where n=68 volunteers drove under four different conditions: No distraction, cognitive distraction, emotional distraction, and sensorimotor distraction. Different response variables were recorded including speed, acceleration, brake force, steering, and lane position signals, and different explanatory variables including perinasal EDA, palm EDA, heart rate, breathing rate, and facial expression signals; biographical and psychometric covariates were also obtained.

The dataset is organized into various folders T001, T002 and so on which indicate the different volunteers on which the experiment was carried. Each of those folders include sub-folders (Sessions) like, BL for the Baseline, PD for the Practice Drive, RD for the Relaxing Drive, ND for the Normal Drive, CD for the Cognitive Drive, ED for the Emotional Drive, MD for the Sensorimotor Drive, and FDL or FDN for the Failure Drive. Each of the subfolder includes various data channels like Heart Rate(HR), Breathing Rate (BR), Perinasal Perspiration (pp), Performance Response (res) and Palm EDA(peda) signal, FACS Signals, thermal data, stm, facial (avi), ROI and OT.

The fundamental assumption of the experiment that produced the dataset is that the distracting stressors used, did indeed create stress. If this is not the case, then the experiment is invalid, as it failed to generate what its design purported. Stress is assessed through a number of peripheral physiological measures in such cases. In this simulation, the physiological measures recorded for this purpose include: perinasal perspiration, palm EDA, breathing rate, and heart rate.

The purpose of the project is to ensure the validity of the dataset. Using statistical tests we need to determine which of these measures signify significant elevation of stress and which are not, and comment on the results.

2 Methodology

2.1 Data Cleaning And Division into Phases

1. We read the updated index created in Homework 1, which assigns a value 1 to the data cell corresponding to a given subject, session and data channel if the data is within the valid range. If the file is not present the value is 0 and is -1 if the data is not valid.

2. The below process is repeated for each data channel and session:

   - Filter out the values 1 for that particular session and data channel.
   - Using the data found in the above step, we find the datapath containing the files.
   - For each subject in the session and data channel if the file for that session (CD, MD or ED) and the corresponding ND file is present, we read the stm file. This stm file contains the start and end times for 2 time slices.
   - Using this time slice, the data for each is divided into 5 phases - 1. Before the start time 1, 2. Between start time 1 and end time 1, 3. Between end time 1 and start time 2, 4. Between start time 2 and end time 2, 5. After end time 2. We then calculate the mean for that subject.
   - We repeat the above step for ND file. And we subtract this mean from that in the above step.
   - The mean for each subject is concatenated with the corresponding phase means of other subjects of that data channel and session.
   - The naming convention used is:
     - (datachannel).(Session).(Phase) eg. HR.ED.Ph1 -
       This is for the vector of the means of data channel, session and phase.
     - (datachannel.(Session).ND.(Phase) eg. HR.CD.ND.Ph1-
       This is for the vector corresponding to mean of the session - mean of session ND.
   - We also combine the means for all phases which can be used for plotting the same using boxplots.

2.2 Testing the validity of dataset

1. After finding the difference of means of the particular session with the Normal Drive, we perform t-test on these differences.

2. T-test is used to check whether there is a signicant dierence in the means of the sessions when compared with the means of Normal Drive for each phase.

3. Inorder to perform the t-test, the data needs to be normal. We test the normality of data using Shapiro test, Kolmogorov–Smirnov test and QQPlot.

4. If the p value calculated through the Shapiro test or Kolmogorov–Smirnov test is greater than alpha , we can say that the data follows a normal distribution.

5. If p value calculated using the Wilcoxon signed rank test is less than alpha we reject the null hypothesis and say that the data is normal.

6. If the data is found to be normal for any of the above tests, we say that the data is normal.

7. If the data is not normal that is both the normality tests fail, we perform necessary transformations to normalize the data and then perform the t-test on them.

8. The Bonferroni correction is applied since there are several statistical tests are being performed simultaneously. The alpha value needs to be lowered to account for the number of comparisons being performed. And so we set the alpha value to alpha/n where n is the number of drives applied

   The simplest and most conservative approach is the Bonferroni correction, which sets the alpha value for the entire set of n comparisons equal to alpha by taking the alpha value for each comparison equal to alpha/n

2.3 Data Plotting

We plot the combined data for means of all phases using boxplot. The observed value vs the phase data is plotted. We plot the data of means of

CD-ND, ED-ND and MD-ND on different rows using mfrow.
The combined view of the different sessions of a particular data channel is used to easily visualize the data.
The star notation denotes the significance of stress created.

- No star - p value of t-test is greater than 0.05
- * - p value of t-test is between 0.01 and 0.05
- ** - p value of t-test is between 0.001 and 0.01
- *** - p value of t-test is less than 0.001

3 Assumptions

1. If data is in valid range for both the particular Session (CD, ED or MD) as well as for ND for a particular subject, only then we calculate the mean of that subject.
2. If the data for stm file for a particular subject is not present we ignore that subject.

4 Results and Observations

- Data Channel: BR
  - Session: CD
    - ∗ Test for BR-CD-Phase1
      Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

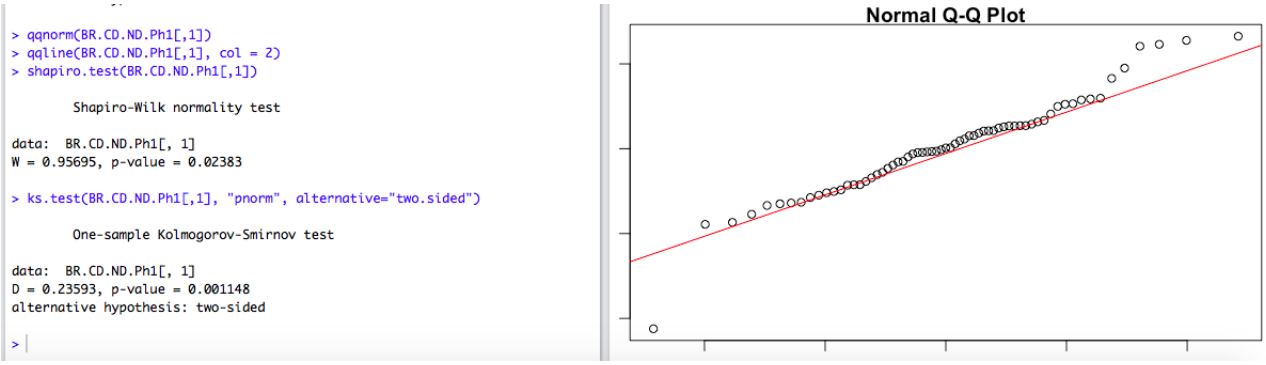

Figure 1: Normality tests for BR-CD-Phase1

Normality test for the difference between means of breath rate signals for CD and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
        One Sample t-test

data:  BR.CD.ND.Ph1[, 1]
t = 0.19568, df = 64, p-value = 0.8455
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.6515216  0.7930140
sample estimates:
 mean of x
0.07074618
```

Figure 2: Paired t test tests for BR-CD-Phase1

$$p = 0.8455$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-CD-Phase2
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

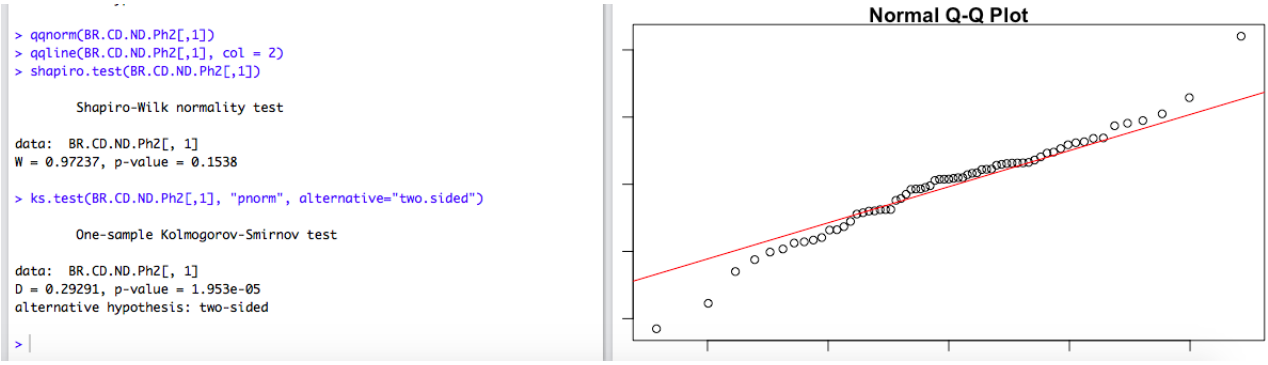

Figure 3: Normality tests for BR-CD-Phase2

Normality test for the difference between means of breath rate signals for CD and ND for phase 2.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for CD and ND for phase 2 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.CD.ND.Ph2[,1])

        One Sample t-test

data:  BR.CD.ND.Ph2[, 1]
t = -0.22514, df = 64, p-value = 0.8226
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.9819189  0.7830172
sample estimates:
  mean of x
-0.09945083
```

Figure 4: Paired t test tests for BR-CD-Phase2

$$p = 0.8226$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-CD-Phase3
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

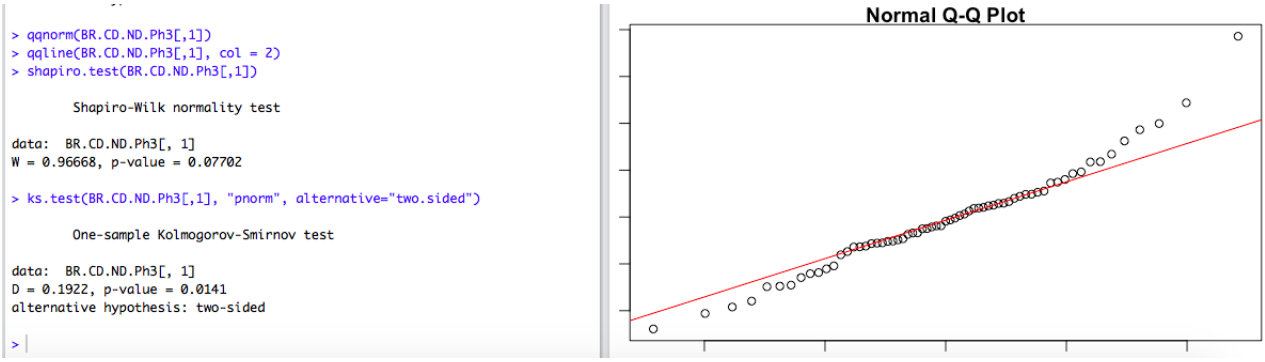

Figure 5: Normality tests for BR-CD-Phase3

Normality test for the difference between means of breath rate signals for CD and ND for phase 3.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for CD and ND for phase 3 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.CD.ND.Ph3[,1])

        One Sample t-test

data:  BR.CD.ND.Ph3[, 1]
t = -0.35102, df = 64, p-value = 0.7267
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.6348052  0.4450641
sample estimates:
  mean of x
-0.09487057
```

Figure 6: Paired t test tests for BR-CD-Phase3

$$p = 0.7267$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-CD-Phase4
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

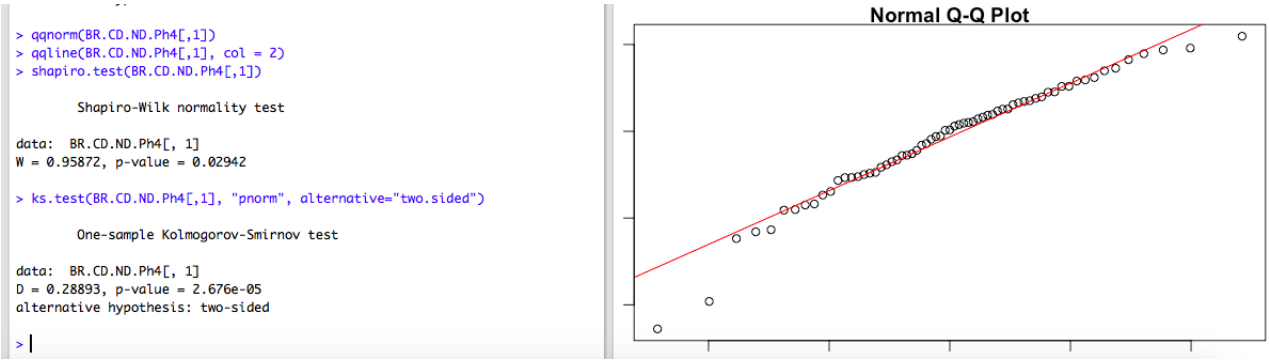

Figure 7: Normality tests for BR-CD-Phase4

Normality test for the difference between means of breath rate signals for CD and ND for phase 4.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(BR.CD.ND.Ph4[,1])

        One Sample t-test

data:  BR.CD.ND.Ph4[, 1]
t = -1.0207, df = 64, p-value = 0.3112
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -1.2418783  0.4019625
sample estimates:
 mean of x
-0.4199579
```

Figure 8: Paired t test tests for BR-CD-Phase4

$$p = 0.3112$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-CD-Phase5
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

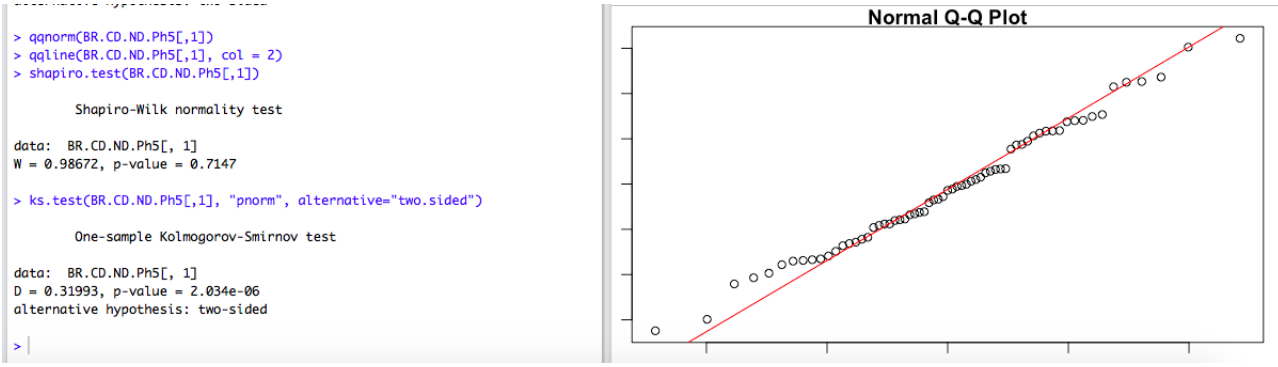

Figure 9: Normality tests for BR-CD-Phase5

Normality test for the difference between means of breath rate signals for CD and ND for phase 5.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.
- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for CD and ND for phase 5 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.CD.ND.Ph5[,1])

        One Sample t-test

data:  BR.CD.ND.Ph5[, 1]
t = -0.63621, df = 64, p-value = 0.5269
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.9193803  0.4752420
sample estimates:
 mean of x
-0.2220692
```

Figure 10: Paired t test tests for BR-CD-Phase5

$$p = 0.5269$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: ED

∗ Test for BR-ED-Phase1
Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

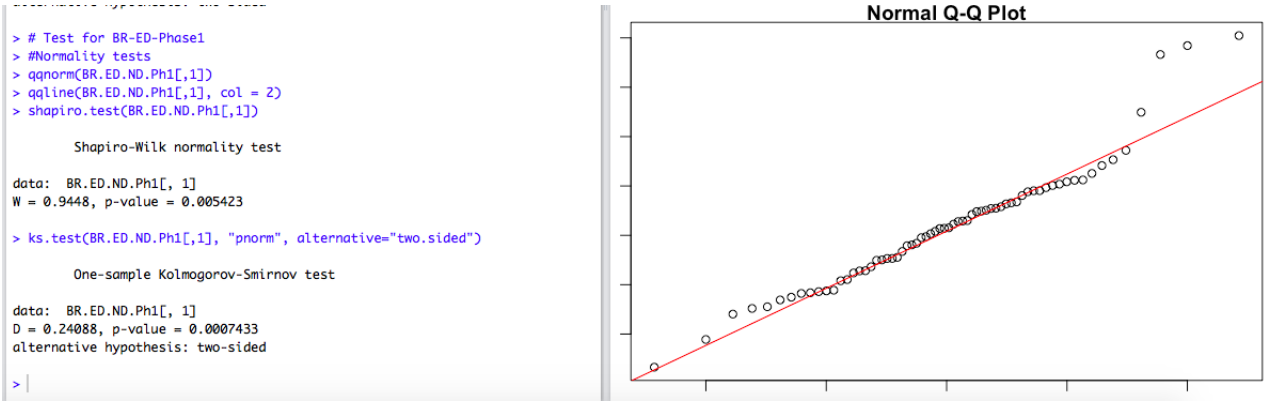

Figure 11: Normality tests for BR-ED-Phase1

Normality test for the difference between means of breath rate signals for ED and ND for phase 1.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.
- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for ED and ND for phase 1 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.ED.ND.Ph1[,1])

        One Sample t-test

data:  BR.ED.ND.Ph1[, 1]
t = 1.1069, df = 65, p-value = 0.2724
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.2775537  0.9677400
sample estimates:
mean of x
0.3450931
```

Figure 12: Paired t test tests for BR-ED-Phase1

$$p = 0.2724$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-ED-Phase2
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

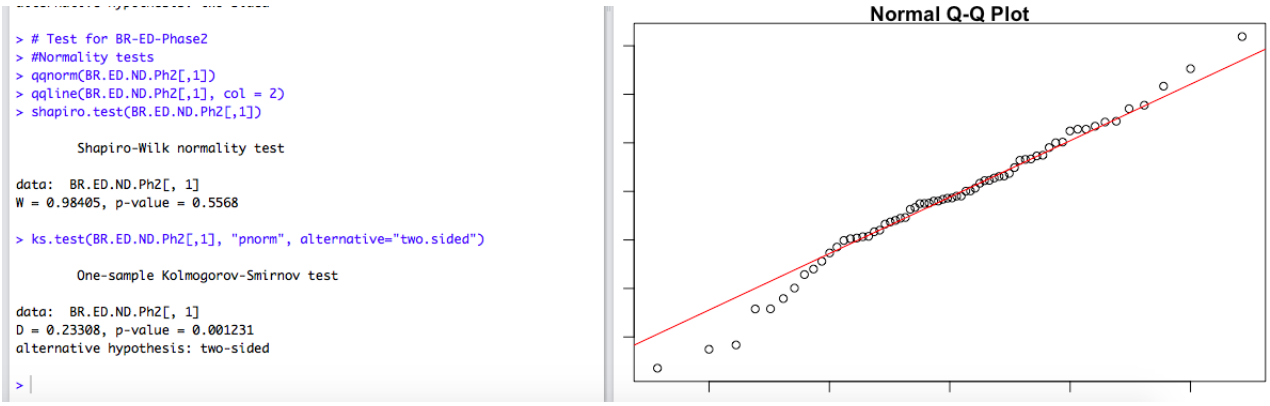

Figure 13: Normality tests for BR-ED-Phase2

Normality test for the difference between means of breath rate signals for ED and ND for phase 2.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for ED and ND for phase 2 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.ED.ND.Ph2[,1])

        One Sample t-test

data:  BR.ED.ND.Ph2[, 1]
t = -0.9208, df = 65, p-value = 0.3606
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.9591087  0.3537867
sample estimates:
mean of x
-0.302661
```

Figure 14: Paired t test tests for BR-ED-Phase2

$$p = 0.3606$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-ED-Phase3
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

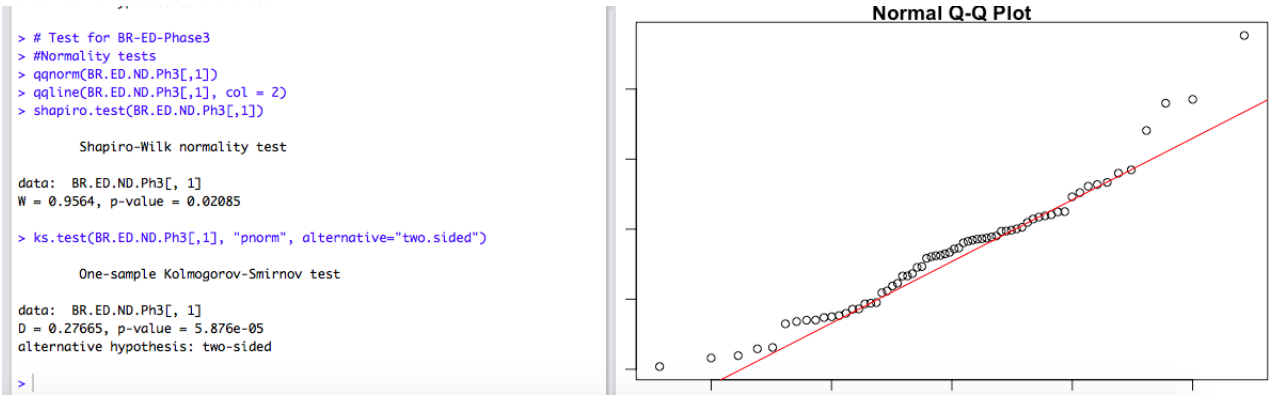

Figure 15: Normality tests for BR-ED-Phase3

Normality test for the difference between means of breath rate signals for ED and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(BR.ED.ND.Ph3[,1])

        One Sample t-test

data:  BR.ED.ND.Ph3[, 1]
t = -2.8919, df = 65, p-value = 0.005203
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -1.095743 -0.200541
sample estimates:
 mean of x
-0.6481422
```

Figure 16: Paired t test tests for BR-ED-Phase3

$$p = 0.005203\ **$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for BR-ED-Phase4
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

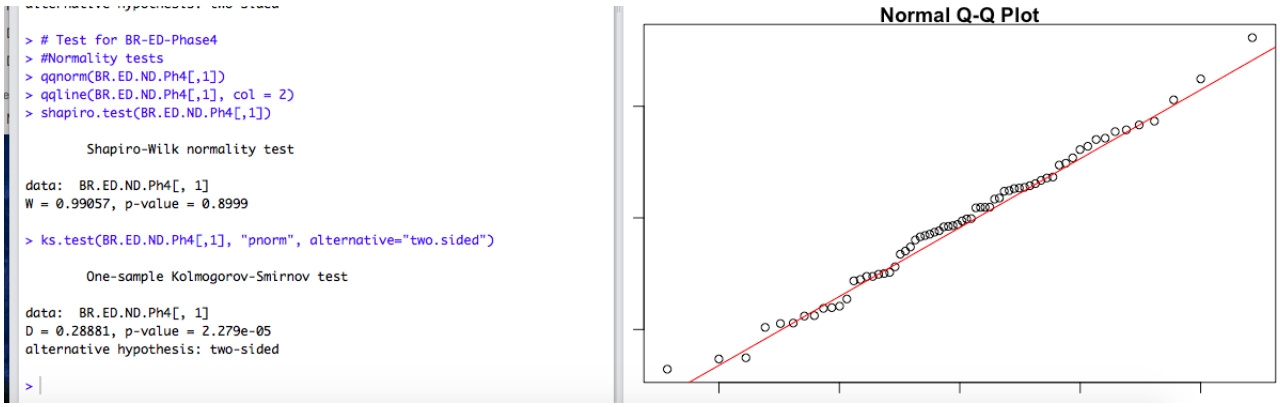

Figure 17: Normality tests for BR-ED-Phase4

Normality test for the difference between means of breath rate signals for ED and ND for phase 4.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for ED and ND for phase 4 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.ED.ND.Ph4[,1])

        One Sample t-test

data:  BR.ED.ND.Ph4[, 1]
t = -0.55818, df = 65, p-value = 0.5786
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.9875462  0.5561115
sample estimates:
 mean of x
-0.2157173
```

Figure 18: Paired t test tests for BR-ED-Phase4

$$p = 0.5786$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-ED-Phase5
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

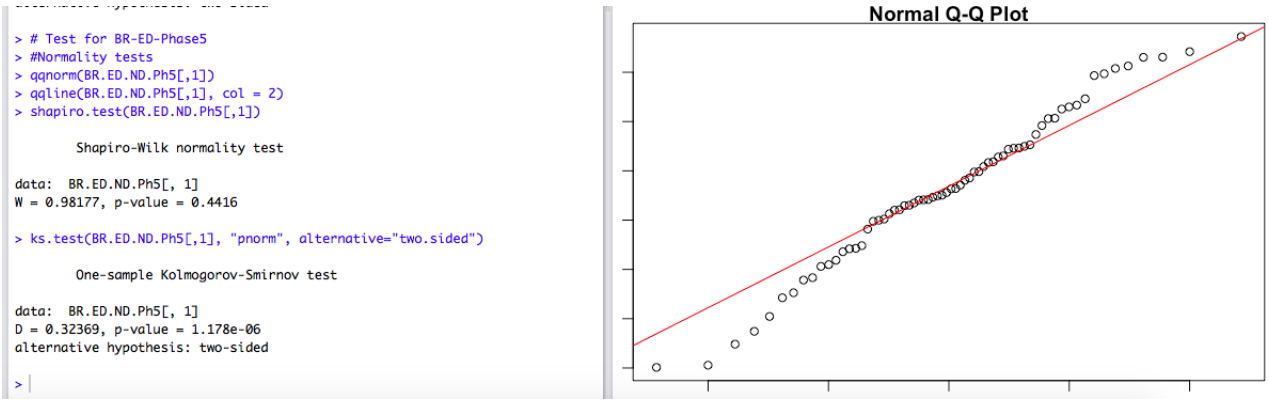

Figure 19: Normality tests for BR-ED-Phase5

Normality test for the difference between means of breath rate signals for ED and ND for phase 5.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for ED and ND for phase 5 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.ED.ND.Ph5[,1])

        One Sample t-test

data:  BR.ED.ND.Ph5[, 1]
t = -1.7582, df = 65, p-value = 0.08342
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -1.45630024  0.09265464
sample estimates:
 mean of x
-0.6818228
```

Figure 20: Paired t test tests for BR-ED-Phase5

$$p = 0.08342$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: MD

* Test for BR-MD-Phase1
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

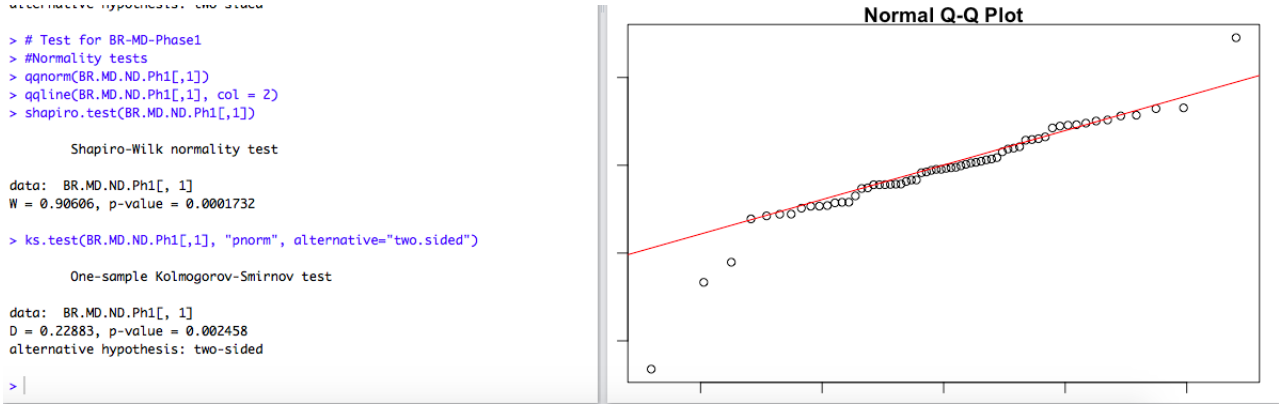

Figure 21: Normality tests for BR-MD-Phase1

Normality test for the difference between means of breath rate signals for MD and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(BR.MD.ND.Ph1[,1])

        One Sample t-test

data:  BR.MD.ND.Ph1[, 1]
t = -0.92151, df = 61, p-value = 0.3604
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.9857906  0.3638294
sample estimates:
 mean of x
-0.3109806
```

Figure 22: Paired t test tests for BR-MD-Phase1

$$p = 0.3604$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-MD-Phase2
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

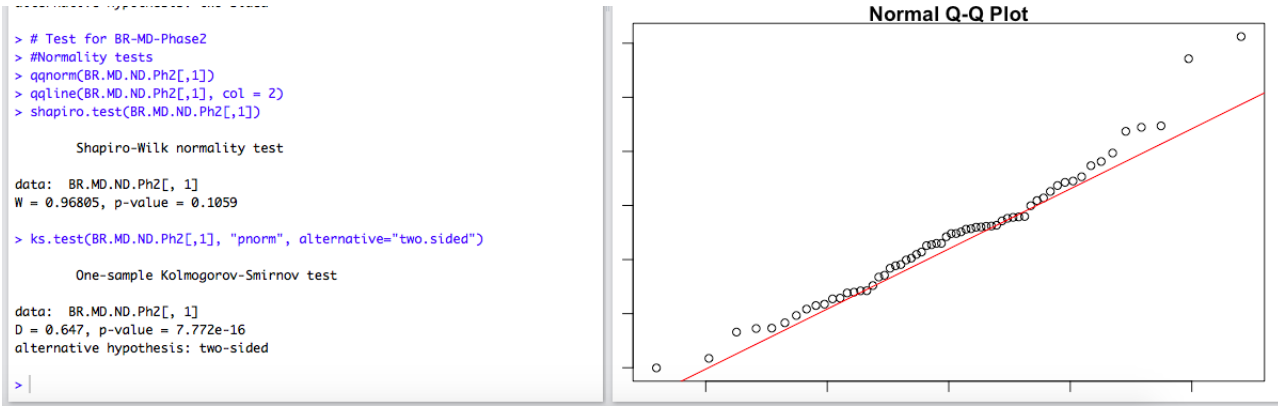

Figure 23: Normality tests for BR-MD-Phase2

Normality test for the difference between means of breath rate signals for MD and ND for phase 2.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for MD and ND for phase 2 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.MD.ND.Ph2[,1])

        One Sample t-test

data:  BR.MD.ND.Ph2[, 1]
t = 9.0807, df = 61, p-value = 6.24e-13
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 2.174606 3.402782
sample estimates:
mean of x
 2.788694
```

Figure 24: Paired t test tests for BR-MD-Phase2

$$p = 6.24e - 13 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for BR-MD-Phase3
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

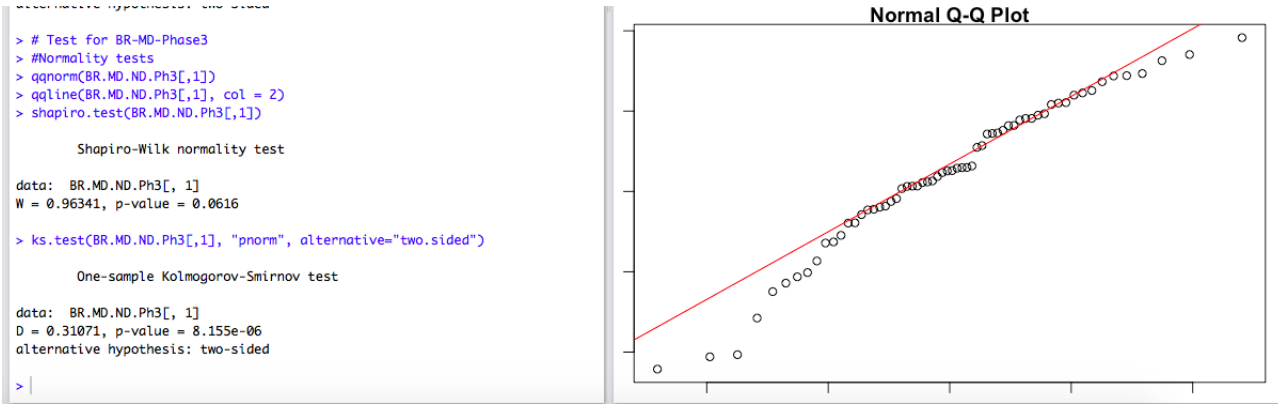

Figure 25: Normality tests for BR-MD-Phase3

Normality test for the difference between means of breath rate signals for MD and ND for phase 3.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for MD and ND for phase 3 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.MD.ND.Ph3[,1])

        One Sample t-test

data:  BR.MD.ND.Ph3[, 1]
t = 1.8539, df = 61, p-value = 0.06859
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.03502995  0.92648122
sample estimates:
mean of x
0.4457256
```

Figure 26: Paired t test tests for BR-MD-Phase3

$$p = 0.06859$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for BR-MD-Phase4
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

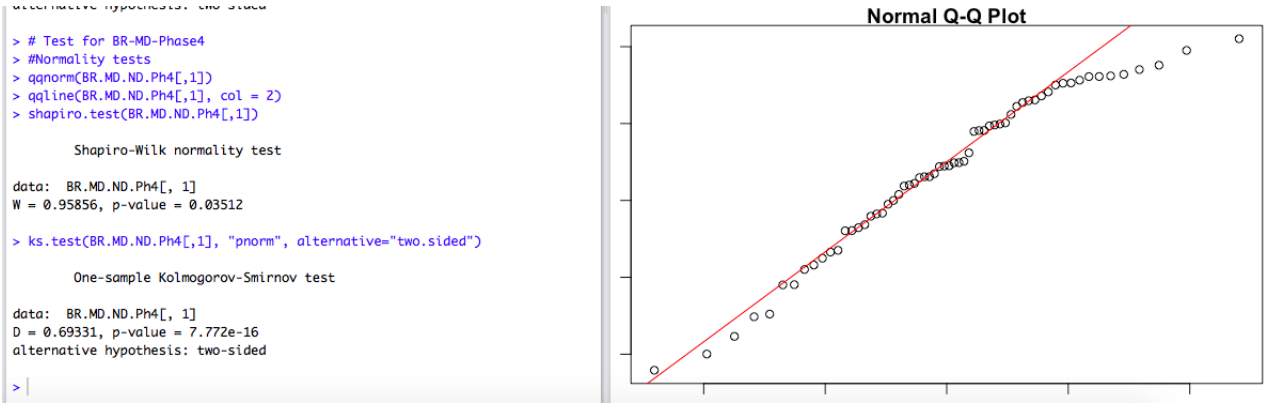

Figure 27: Normality tests for BR-MD-Phase4

Normality test for the difference between means of breath rate signals for MD and ND for phase 4.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(BR.MD.ND.Ph4[,1])

        One Sample t-test

data:  BR.MD.ND.Ph4[, 1]
t = 10.411, df = 61, p-value = 3.729e-15
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 2.245370 3.312902
sample estimates:
mean of x
 2.779136
```

Figure 28: Paired t test tests for BR-MD-Phase4

$$p = 3.729e - 15 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for BR-MD-Phase5
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

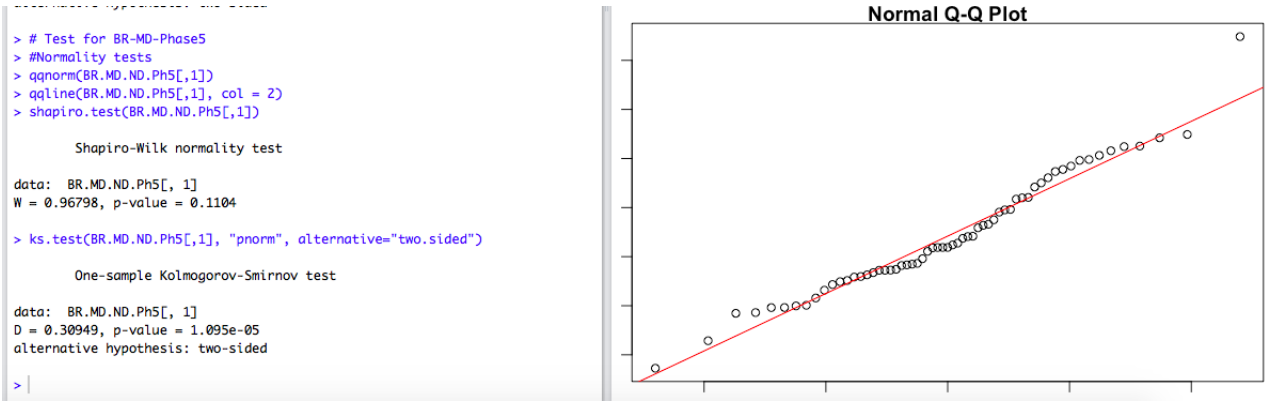

Figure 29: Normality tests for BR-MD-Phase5

Normality test for the difference between means of breath rate signals for MD and ND for phase 5.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of breath rate signals for MD and ND for phase 5 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(BR.MD.ND.Ph5[,1])

        One Sample t-test

data:  BR.MD.ND.Ph5[, 1]
t = 2.7894, df = 60, p-value = 0.007066
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.248714 1.509572
sample estimates:
mean of x
0.8791429
```

Figure 30: Paired t test tests for BR-MD-Phase5

$$p = 0.007066\ **$$

Since p $< \alpha$ we reject the null hypothesis.

- Data Channel: HR
  - Session: CD
    - Test for HR-CD-Phase1
      Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

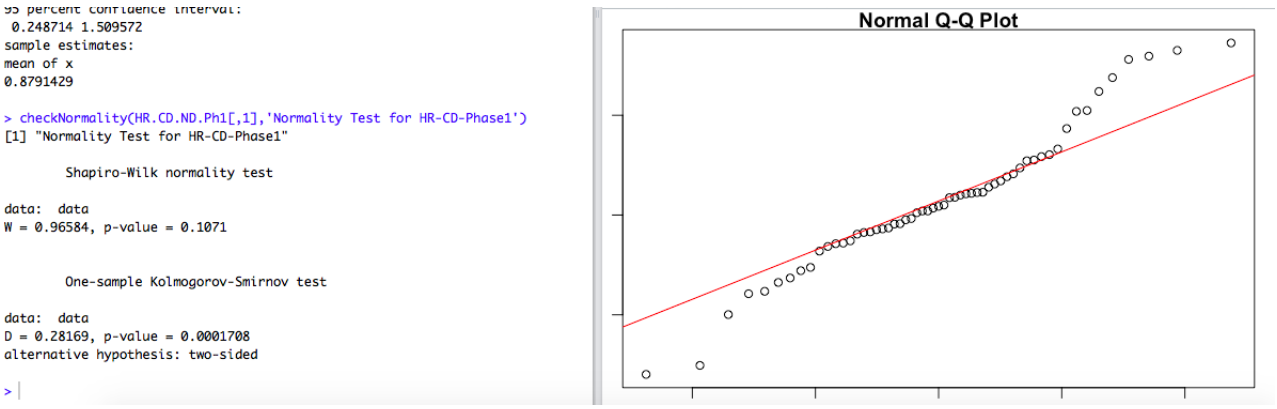

Figure 31: Normality tests for HR-CD-Phase1

Normality test for the difference between means of heart rate signals for CD and ND for phase 1.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.
- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for CD and ND for phase 1 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.CD.ND.Ph1[,1])

        One Sample t-test

data:  HR.CD.ND.Ph1[, 1]
t = 1.5553, df = 56, p-value = 0.1255
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.2090947  1.6610657
sample estimates:
mean of x
0.7259855
```

Figure 32: Paired t test tests for HR-CD-Phase1

$$p = 0.1255$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for HR-CD-Phase2
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

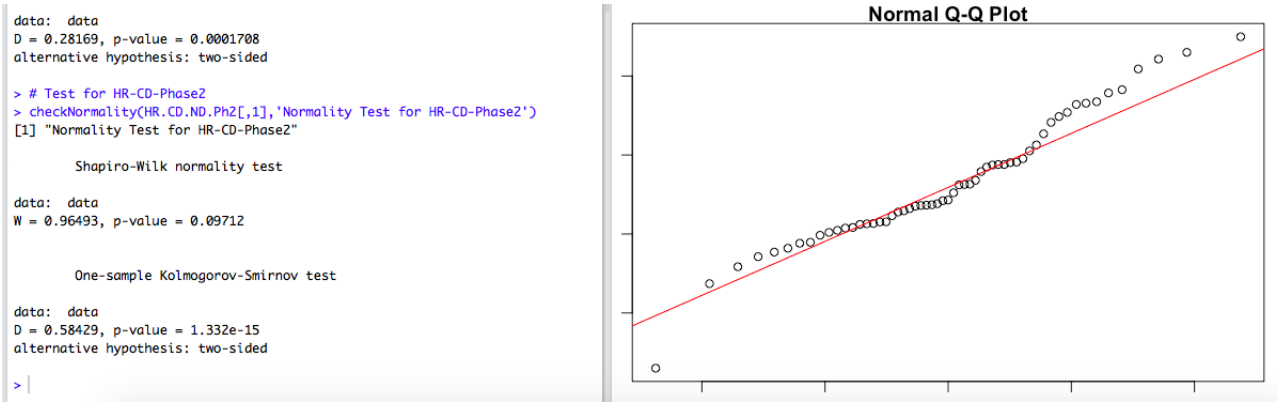

Figure 33: Normality tests for HR-CD-Phase2

Normality test for the difference between means of heart rate signals for CD and ND for phase 2.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for CD and ND for phase 2 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.CD.ND.Ph2[,1])

        One Sample t-test

data:  HR.CD.ND.Ph2[, 1]
t = 6.0947, df = 56, p-value = 1.066e-07
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 2.162855 4.280773
sample estimates:
mean of x
 3.221814
```

Figure 34: Paired t test tests for HR-CD-Phase2

$$p = 1.066e - 07 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for HR-CD-Phase3
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

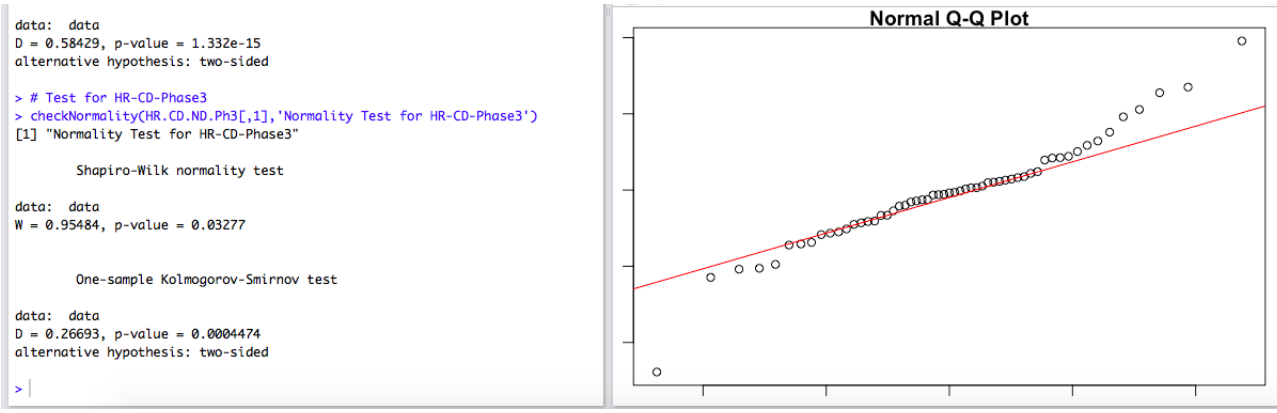

Figure 35: Normality tests for HR-CD-Phase3

Normality test for the difference between means of breath rate signals for CD and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(HR.CD.ND.Ph3[,1])

        One Sample t-test

data:  HR.CD.ND.Ph3[, 1]
t = -0.48356, df = 56, p-value = 0.6306
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -1.1170061  0.6826008
sample estimates:
 mean of x
-0.2172027
```

Figure 36: Paired t test tests for HR-CD-Phase3

$$p = 0.6306$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for HR-CD-Phase4
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

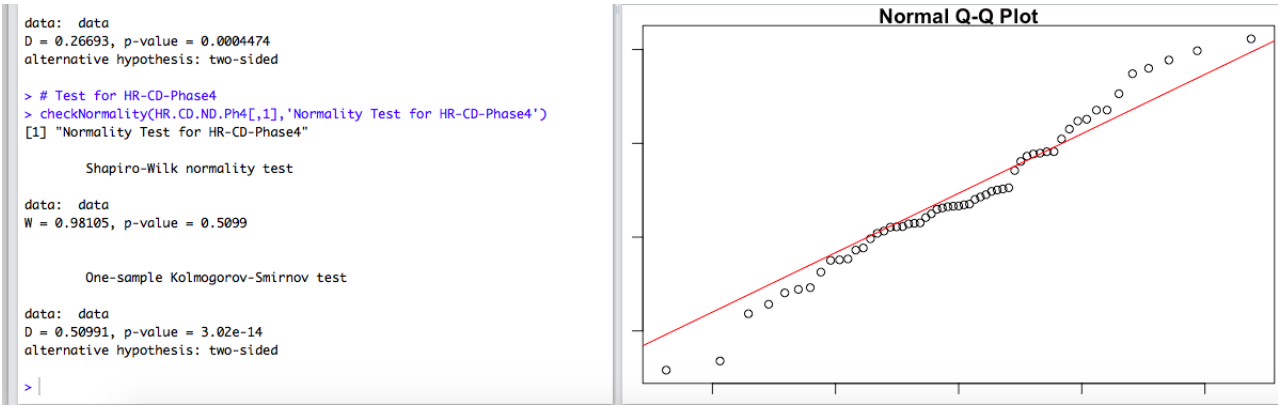

Figure 37: Normality tests for HR-CD-Phase4

Normality test for the difference between means of heart rate signals for CD and ND for phase 4.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for CD and ND for phase 4 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.CD.ND.Ph4[,1])

        One Sample t-test

data:  HR.CD.ND.Ph4[, 1]
t = 4.114, df = 56, p-value = 0.0001288
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 1.082390 3.136909
sample estimates:
mean of x
  2.10965
```

Figure 38: Paired t test tests for HR-CD-Phase4

$$p = 0.0001288 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for HR-CD-Phase5
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

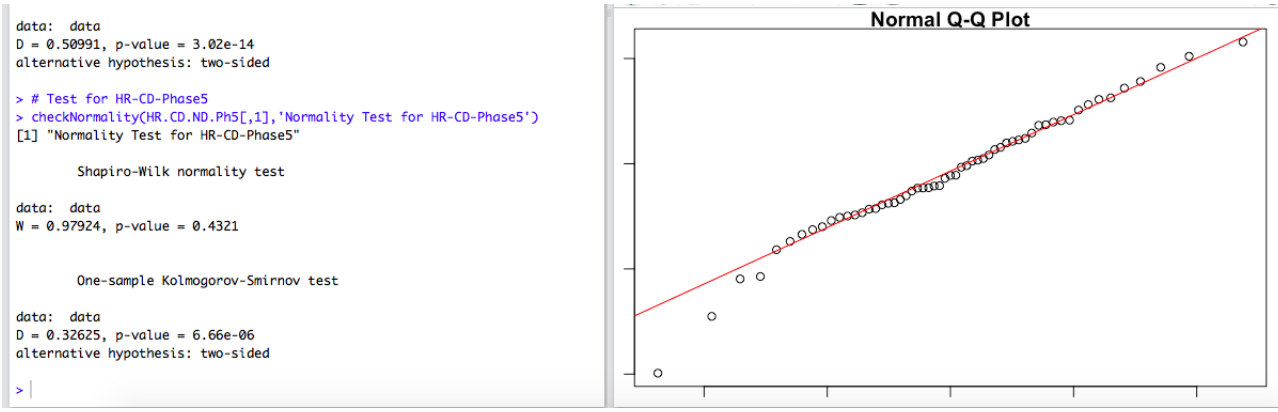

Figure 39: Normality tests for HR-CD-Phase5

Normality test for the difference between means of heart rate signals for CD and ND for phase 5.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for CD and ND for phase 5 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.CD.ND.Ph5[,1])

        One Sample t-test

data:  HR.CD.ND.Ph5[, 1]
t = -1.2249, df = 56, p-value = 0.2258
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -1.2684941  0.3058611
sample estimates:
 mean of x
-0.4813165
```

Figure 40: Paired t test tests for HR-CD-Phase5

$$p = 0.2258$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: ED

* Test for HR-ED-Phase1
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

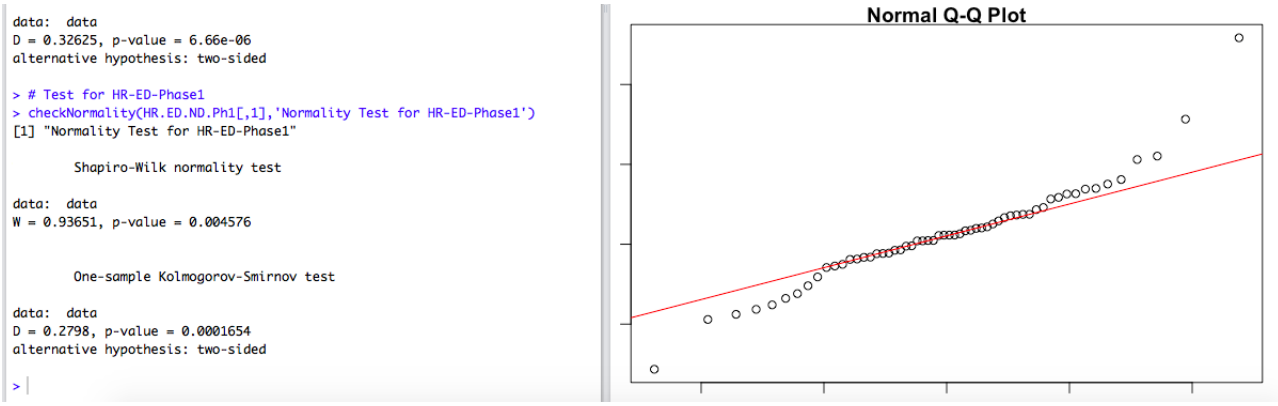

Figure 41: Normality tests for HR-ED-Phase1

Normality test for the difference between means of breath rate signals for ED and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(HR.ED.ND.Ph1[,1])

        One Sample t-test

data:  HR.ED.ND.Ph1[, 1]
t = 1.5445, df = 57, p-value = 0.128
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.1895777  1.4683166
sample estimates:
mean of x
0.6393695
```

Figure 42: Paired t test tests for HR-ED-Phase1

$$p = 0.128$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for HR-ED-Phase2
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

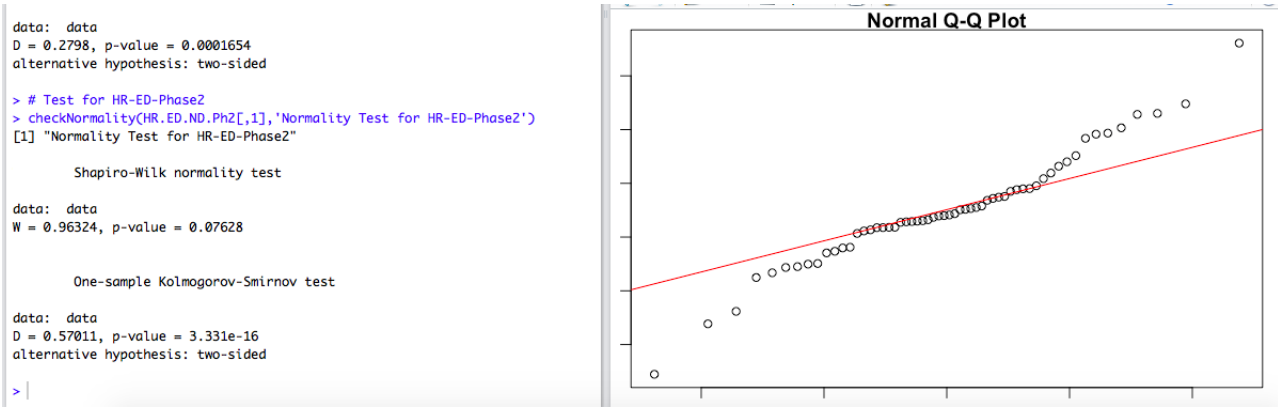

Figure 43: Normality tests for HR-ED-Phase2

Normality test for the difference between means of heart rate signals for ED and ND for phase 2.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for ED and ND for phase 2 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.ED.ND.Ph2[,1])

        One Sample t-test

data:  HR.ED.ND.Ph2[, 1]
t = 3.795, df = 57, p-value = 0.0003597
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 1.211400 3.917952
sample estimates:
mean of x
 2.564676
```

Figure 44: Paired t test tests for HR-ED-Phase2

$$p = 0.0003597 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for HR-ED-Phase3
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

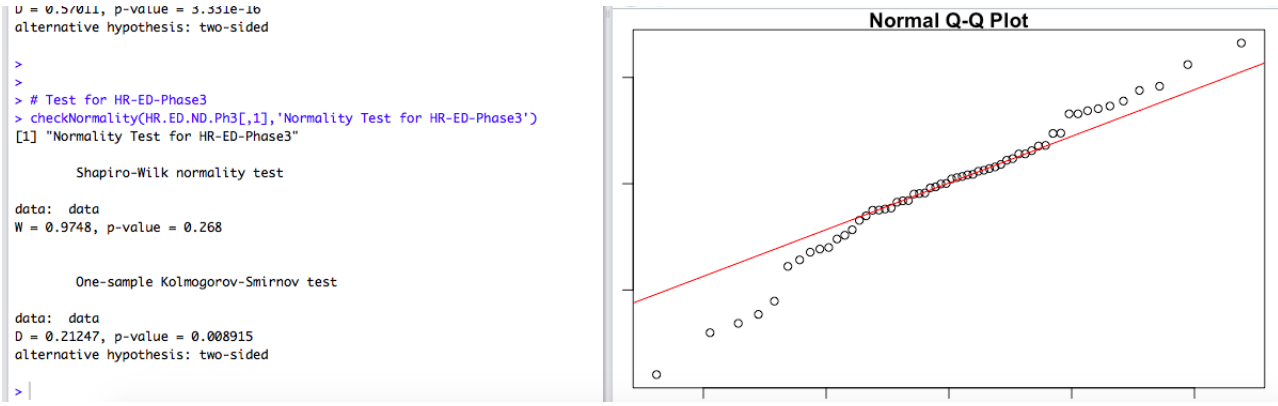

Figure 45: Normality tests for HR-ED-Phase3

Normality test for the difference between means of heart rate signals for ED and ND for phase 3.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for ED and ND for phase 3 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.ED.ND.Ph3[,1])

        One Sample t-test

data:  HR.ED.ND.Ph3[, 1]
t = -0.33297, df = 57, p-value = 0.7404
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.9506187  0.6795547
sample estimates:
mean of x
-0.135532
```

Figure 46: Paired t test tests for HR-ED-Phase3

$$p = 0.7404$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for HR-ED-Phase4
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

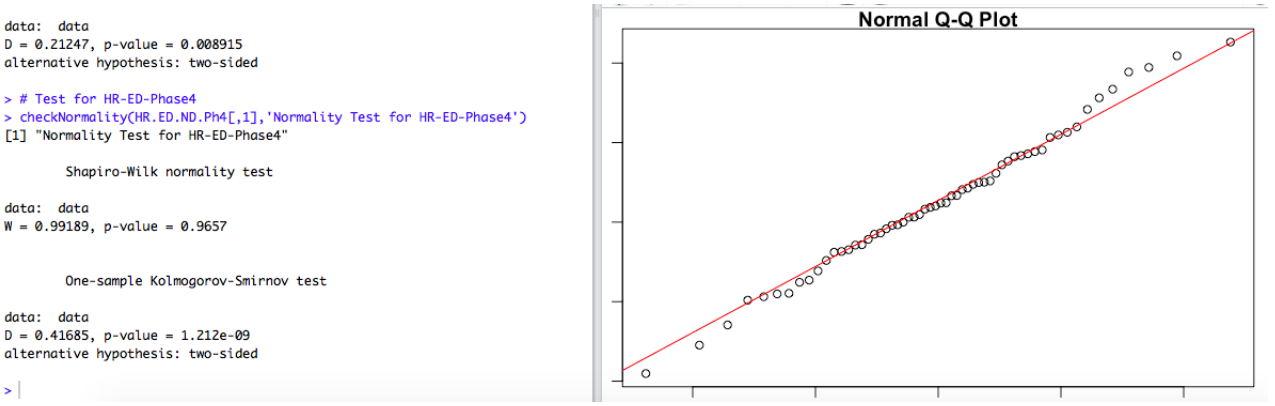

Figure 47: Normality tests for HR-ED-Phase4

Normality test for the difference between means of heart rate signals for ED and ND for phase 4.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for ED and ND for phase 4 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.ED.ND.Ph4[,1])

        One Sample t-test

data:  HR.ED.ND.Ph4[, 1]
t = 2.2167, df = 57, p-value = 0.03065
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.1259534 2.4809508
sample estimates:
mean of x
 1.303452
```

Figure 48: Paired t test tests for HR-ED-Phase4

$$p = 0.03065\ *$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for HR-ED-Phase5
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

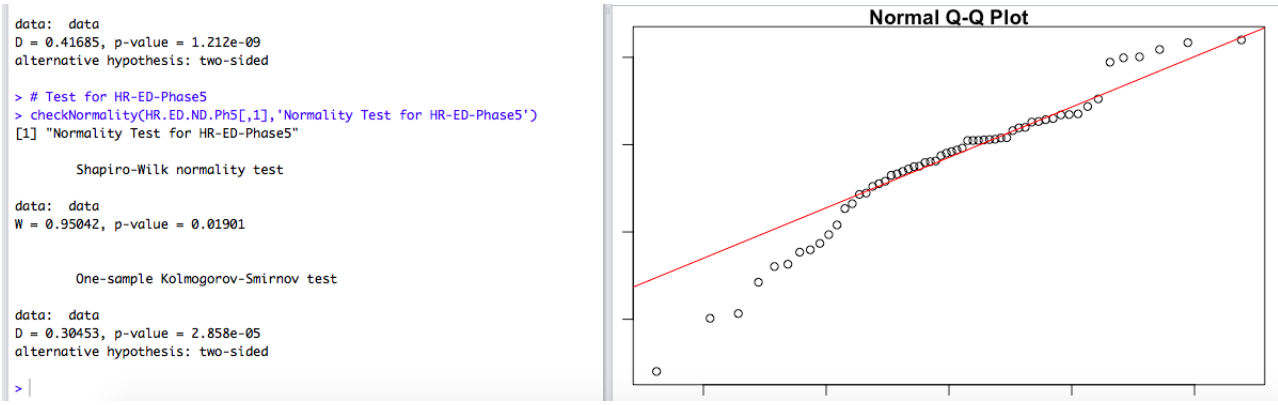

Figure 49: Normality tests for HR-ED-Phase5

Normality test for the difference between means of breath rate signals for ED and ND for phase 5.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests

```
> t.test(HR.ED.ND.Ph5[,1])

        One Sample t-test

data:  HR.ED.ND.Ph5[, 1]
t = -2.0841, df = 57, p-value = 0.04165
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -2.11062025 -0.04214455
sample estimates:
mean of x
-1.076382
```

Figure 50: Paired t test tests for HR-ED-Phase5

$$p = 0.04165\ *$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: MD

∗ Test for HR-MD-Phase1
Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

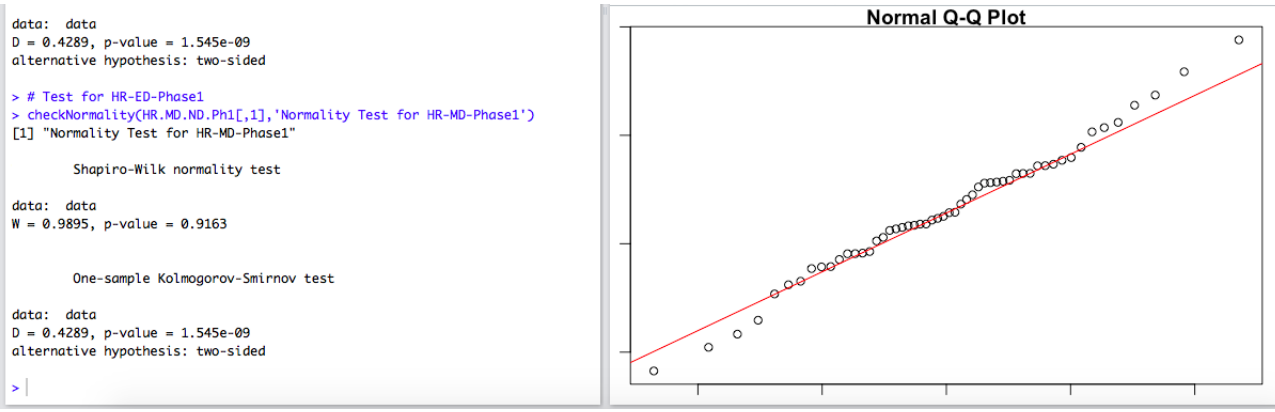

Figure 51: Normality tests for HR-MD-Phase1

Normality test for the difference between means of heart rate signals for MD and ND for phase 1.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.
- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for MD and ND for phase 1 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.MD.ND.Ph1[,1])

        One Sample t-test

data:  HR.MD.ND.Ph1[, 1]
t = 3.7992, df = 53, p-value = 0.000376
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.7421204 2.4020804
sample estimates:
mean of x
   1.5721
```

Figure 52: Paired t test tests for HR-MD-Phase1

$$p = 0.000376 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for HR-MD-Phase2
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
data:  data
D = 0.4289, p-value = 1.545e-09
alternative hypothesis: two-sided

> # Test for HR-ED-Phase1
> checkNormality(HR.MD.ND.Ph2[,1],'Normality Test for HR-MD-Phase2')
[1] "Normality Test for HR-MD-Phase2"

        Shapiro-Wilk normality test

data:  data
W = 0.96948, p-value = 0.1829


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.72906, p-value = 6.661e-16
alternative hypothesis: two-sided

>
```

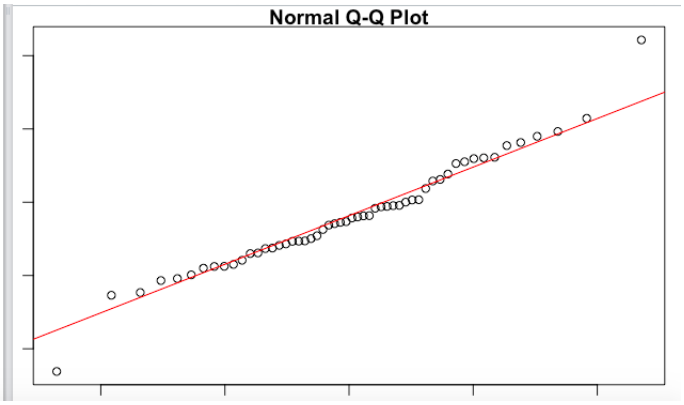

Figure 53: Normality tests for HR-MD-Phase2

Normality test for the difference between means of heart rate signals for MD and ND for phase 2.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.
- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for MD and ND for phase 2 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.MD.ND.Ph2[,1])

        One Sample t-test

data:  HR.MD.ND.Ph2[, 1]
t = 8.045, df = 53, p-value = 9.484e-11
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 3.043384 5.064914
sample estimates:
mean of x
 4.054149
```

Figure 54: Paired t test tests for HR-MD-Phase2

$$p = 0.9.48e - 11\ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for HR-MD-Phase3
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

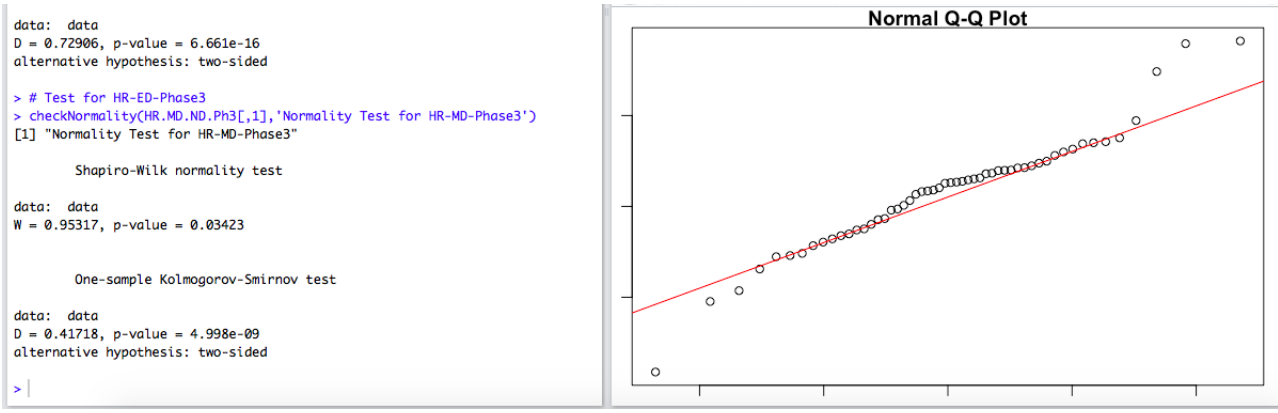

Figure 55: Normality tests for HR-MD-Phase3

Normality test for the difference between means of breath rate signals for MD and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we are performing paired t tests.

```
> t.test(HR.MD.ND.Ph3[,1])

        One Sample t-test

data:  HR.MD.ND.Ph3[, 1]
t = 1.8923, df = 53, p-value = 0.06392
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0488986  1.6800647
sample estimates:
mean of x
0.8155831
```

Figure 56: Paired t test tests for HR-MD-Phase3

$$p = 0.06392$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for HR-MD-Phase4
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

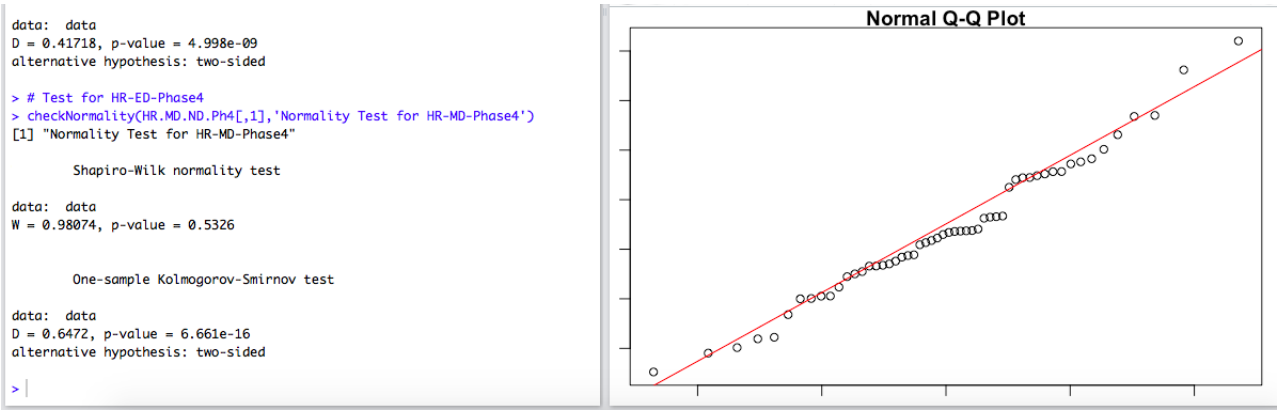

Figure 57: Normality tests for HR-MD-Phase4

Normality test for the difference between means of heart rate signals for MD and ND for phase 4.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.

- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for MD and ND for phase 4 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.MD.ND.Ph4[,1])

        One Sample t-test

data:  HR.MD.ND.Ph4[, 1]
t = 7.2509, df = 53, p-value = 1.78e-09
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 2.001760 3.532705
sample estimates:
mean of x
 2.767232
```

Figure 58: Paired t test tests for HR-MD-Phase4

$$p = 1.78e - 09 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for HR-MD-Phase5
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
data:  data
D = 0.6472, p-value = 6.661e-16
alternative hypothesis: two-sided

> # Test for HR-ED-Phase5
> checkNormality(HR.MD.ND.Ph5[,1],'Normality Test for HR-MD-Phase5')
[1] "Normality Test for HR-MD-Phase5"

        Shapiro-Wilk normality test

data:  data
W = 0.97276, p-value = 0.2648


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.22866, p-value = 0.006433
alternative hypothesis: two-sided

>
```

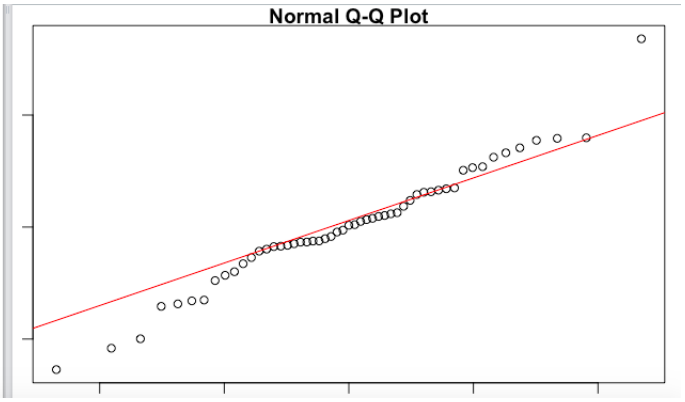

Figure 59: Normality tests for HR-MD-Phase5

Normality test for the difference between means of heart rate signals for MD and ND for phase 5.

- Analysis of Q-Q Plot: We can observe that apart from the points at edges majority of points are clustering well around the line. Hence, we can conclude that the data is normal.
- Shapiro test: Since p is greater than .05, there is no significant difference between the input distribution i.e. the difference between means of heart rate signals for MD and ND for phase 5 and the normal distribution.

Hence, we are performing paired t tests

```
> t.test(HR.MD.ND.Ph5[,1])

        One Sample t-test

data:  HR.MD.ND.Ph5[, 1]
t = 0.22022, df = 52, p-value = 0.8266
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.6425933  0.8010237
sample estimates:
mean of x
0.0792152
```

Figure 60: Paired t test tests for HR-MD-Phase5

$$p = 0.8266$$

Since p $> \alpha$ we fail to reject the null hypothesis.

- Data Channel: peda

  - Session: CD

    * Test for peda-CD-Phase1
      Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

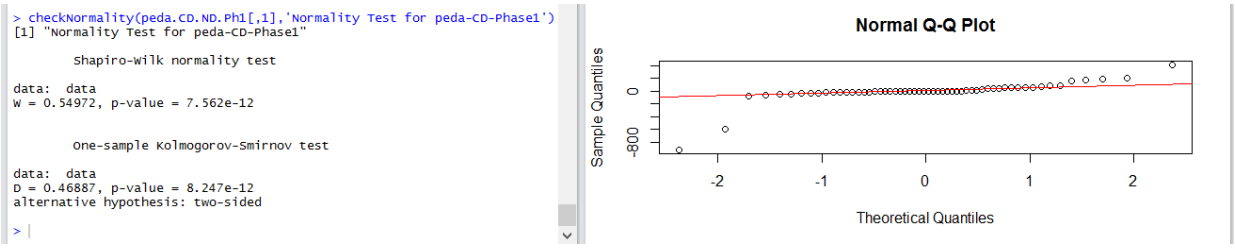

Figure 61: Normality tests for peda-CD-Phase1

Normality test for the difference between means of breath rate signals for CD and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(peda.CD.ND.Ph1[,1])

        One Sample t-test

data:  peda.CD.ND.Ph1[, 1]
t = -0.17742, df = 55, p-value = 0.8598
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -48.88444  40.93263
sample estimates:
mean of x
-3.975907
```

Figure 62: Paired t test tests for peda-CD-Phase1

$$p = 0.8598$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-CD-Phase2
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

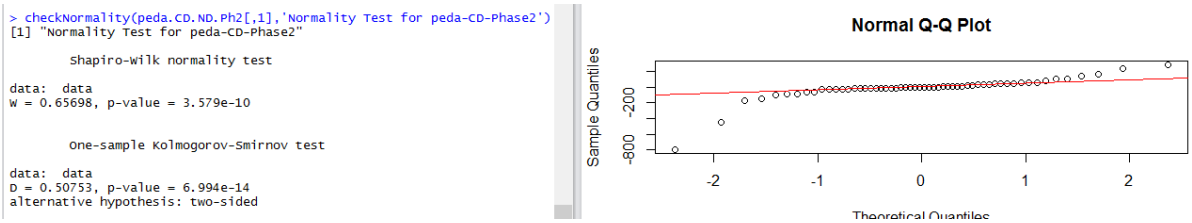

Figure 63: Normality tests for peda-CD-Phase2

Normality test for the difference between means of breath rate signals for CD and ND for phase 2.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around

the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(peda.CD.ND.Ph2[,1])

        One Sample t-test

data:  peda.CD.ND.Ph2[, 1]
t = -0.53979, df = 55, p-value = 0.5915
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -49.30316  28.37928
sample estimates:
mean of x
-10.46194
```

Figure 64: Paired t test tests for peda-CD-Phase2

$$p = 0.5915$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-CD-Phase3
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(peda.CD.ND.Ph3[,1],'Normality Test for peda-CD-Phase3')
[1] "Normality Test for peda-CD-Phase3"

        Shapiro-Wilk normality test

data:  data
W = 0.75104, p-value = 2.193e-08


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.58546, p-value = 7.772e-16
alternative hypothesis: two-sided
```

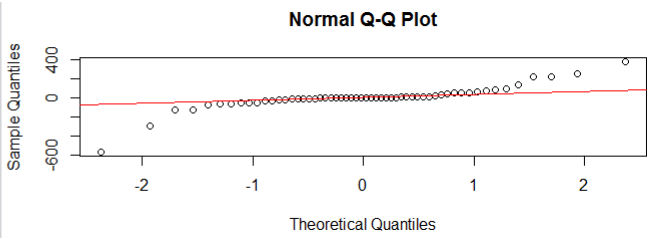

Figure 65: Normality tests for peda-CD-Phase3

Normality test for the difference between means of breath rate signals for CD and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(log(peda.CD.ND.Ph3.pos),mu=log(-min(peda.CD.ND.Ph3[,1])+1))

        One Sample t-test

data:  log(peda.CD.ND.Ph3.pos)
t = -0.83989, df = 55, p-value = 0.4046
alternative hypothesis: true mean is not equal to 6.336679
95 percent confidence interval:
 6.007913 6.471258
sample estimates:
mean of x
 6.239586
```

Figure 66: Paired t test tests for peda-CD-Phase3

$$p = 0.4046$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-CD-Phase4
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

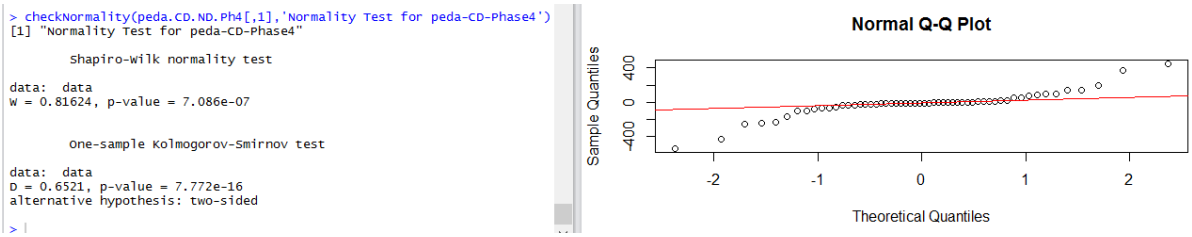

Figure 67: Normality tests for peda-CD-Phase4

Normality test for the difference between means of breath rate signals for CD and ND for phase 4.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for CD and ND for phase 1, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for CD and ND for phase 4, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

```
> checkNormality(log(peda.CD.ND.Ph4.pos),'Normality test after log for peda-
CD-Phase4')
[1] "Normality test after log for peda-CD-Phase4"

        Shapiro-Wilk normality test

data:  data
W = 0.32863, p-value = 1.433e-14


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.98214, p-value = 7.772e-16
alternative hypothesis: two-sided

>
```

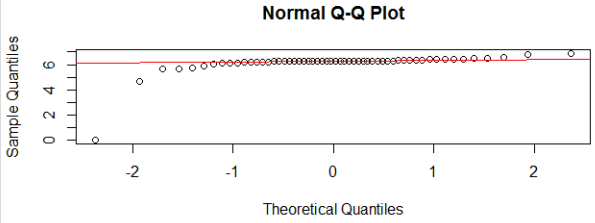

Figure 68: Normality tests after log transformation of peda-CD-Phase4

```
> t.test(log(peda.CD.ND.Ph4.pos),mu=log(-min(peda.CD.ND.Ph4[,1])+1))

        One Sample t-test

data:  log(peda.CD.ND.Ph4.pos)
t = -1.3251, df = 55, p-value = 0.1906
alternative hypothesis: true mean is not equal to 6.289999
95 percent confidence interval:
 5.896222 6.370300
sample estimates:
mean of x
 6.133261
```

Figure 69: Paired t test tests for log transformation of peda-CD-Phase4

$$p = 0.1906$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-CD-Phase5
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

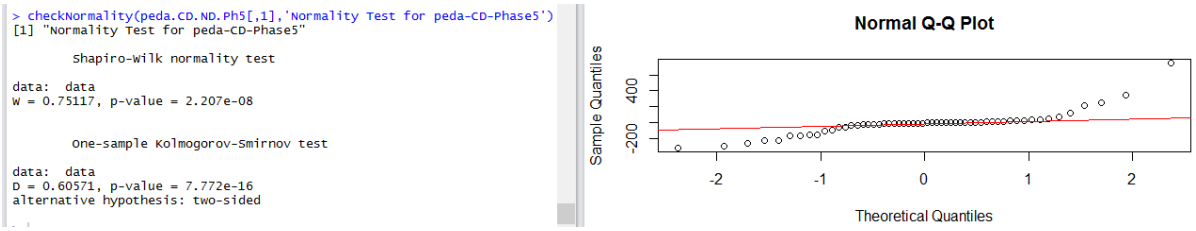

Figure 70: Normality tests for peda-CD-Phase5

Normality test for the difference between means of breath rate signals for CD and ND for phase 5.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for CD and ND for phase 1, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for CD and ND for phase 5, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform Inverse of Square-root transformation.
On analyzing the QQPlot after Inverse of Square-root transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

```
> checkNormality(1/sqrt(peda.CD.ND.Ph5.pos),'Normality test after Inverse of
square root of positive numbers of peda-CD-Phase5')
[1] "Normality test after Inverse of square root of positive numbers of peda-
CD-Phase5"

        Shapiro-Wilk normality test

data:  data
W = 0.21113, p-value = 9.288e-16


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.51214, p-value = 3.786e-14
alternative hypothesis: two-sided
```

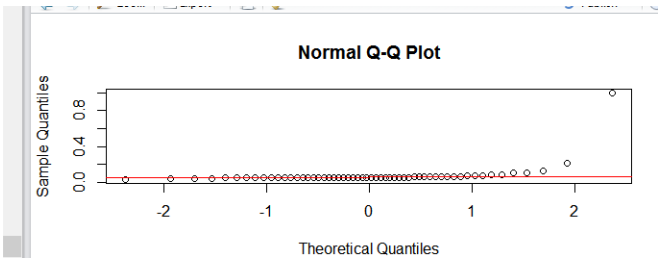

Figure 71: Normality tests after Inverse of Square-root transformation of peda-CD-Phase5

```
> t.test(1/sqrt(peda.CD.ND.Ph5.pos),mu=1/sqrt(-min(peda.CD.ND.Ph5[,1])+1))

        One Sample t-test

data:  1/sqrt(peda.CD.ND.Ph5.pos)
t = 1.3793, df = 55, p-value = 0.1734
alternative hypothesis: true mean is not equal to 0.05546197
95 percent confidence interval:
 0.04479292 0.11324432
sample estimates:
 mean of x
0.07901862
```

Figure 72: Paired t test tests for Inverse of Square-root of peda-CD-Phase5

$$p \ = 0.1734$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: ED

∗ Test for peda-ED-Phase1
Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

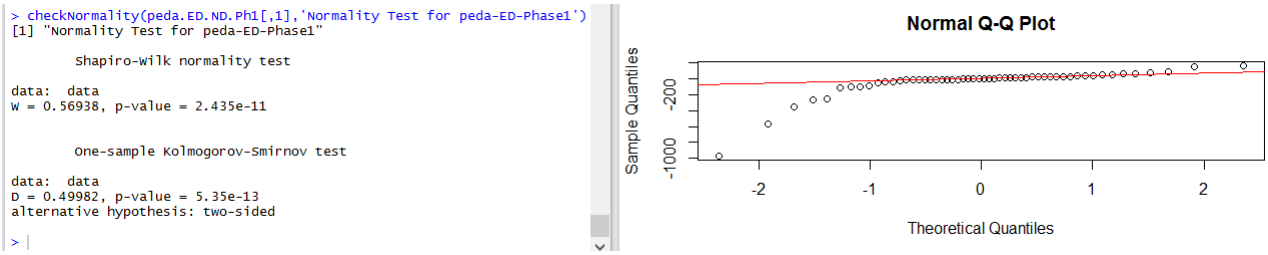

Figure 73: Normality tests for peda-ED-Phase1

Normality test for the difference between means of breath rate signals for ED and ND for phase 1.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for ED and ND for phase 1, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for ED and ND for phase 1, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points

are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

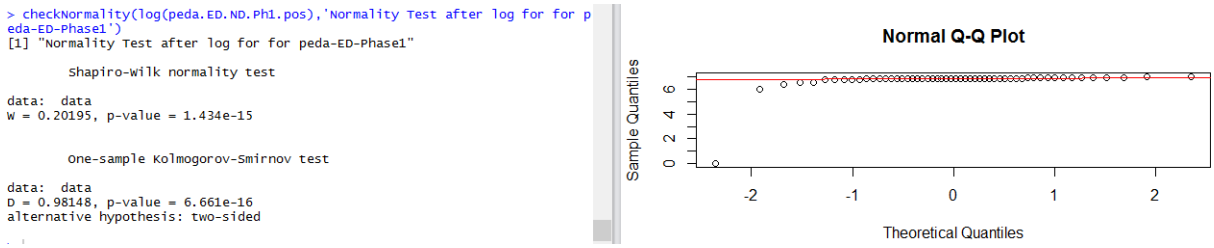

Figure 74: Normality tests after log transformation of peda-ED-Phase1

```
> t.test(log(peda.ED.ND.Ph1.pos),mu=log(-min(peda.ED.ND.Ph1[,1])+1))

        One Sample t-test

data:  log(peda.ED.ND.Ph1.pos)
t = -1.2156, df = 53, p-value = 0.2295
alternative hypothesis: true mean is not equal to 6.880337
95 percent confidence interval:
 6.466113 6.981937
sample estimates:
mean of x
 6.724025
```

Figure 75: Paired t test tests for log transformation of peda-ED-Phase1

$$p = 0.2295$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-ED-Phase2
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

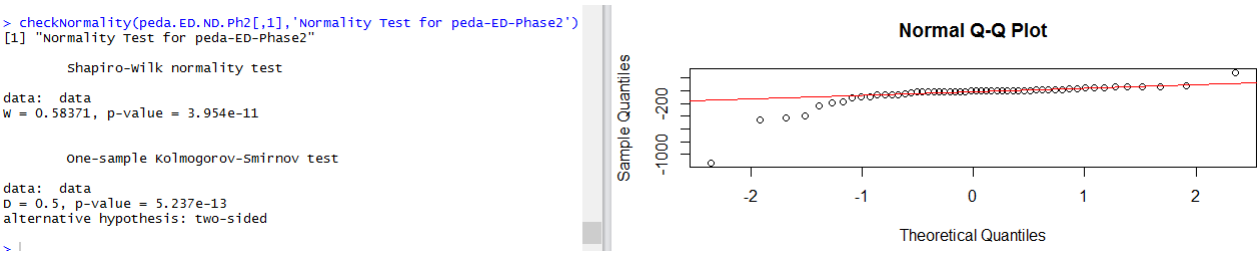

Figure 76: Normality tests for peda-ED-Phase2

Normality test for the difference between means of breath rate signals for ED and ND for phase 2.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for ED and ND for phase 2, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for ED and ND for phase 2, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

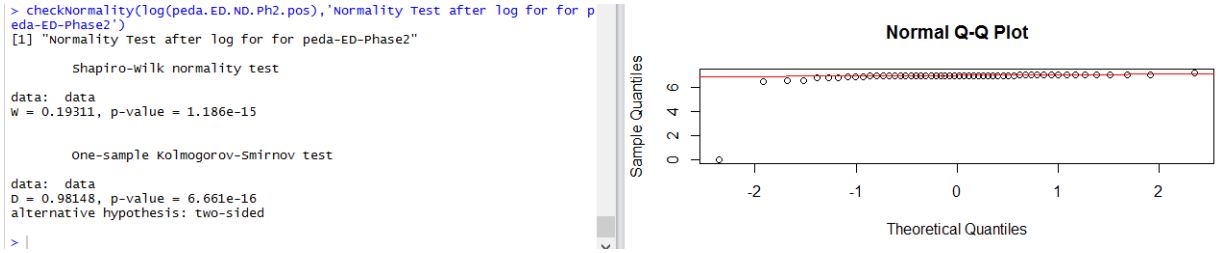

Figure 77: Normality tests after log transformation of peda-ED-Phase2

```
> t.test(log(peda.ED.ND.Ph2.pos),mu=log(-min(peda.ED.ND.Ph2[,1])+1))

        One Sample t-test

data:  log(peda.ED.ND.Ph2.pos)
t = -1.2615, df = 53, p-value = 0.2127
alternative hypothesis: true mean is not equal to 7.034664
95 percent confidence interval:
 6.607490 7.131971
sample estimates:
mean of x
 6.869731
```

Figure 78: Paired t test tests for log transformation of peda-ED-Phase2

$$p \ = 0.2127$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-ED-Phase3
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

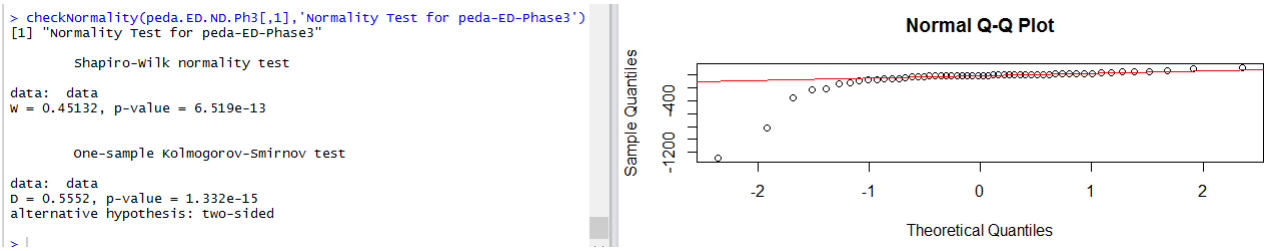

Figure 79: Normality tests for peda-ED-Phase3

Normality test for the difference between means of breath rate signals for ED and ND for phase 3.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for ED and ND for phase 3, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for ED and ND for phase 3, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

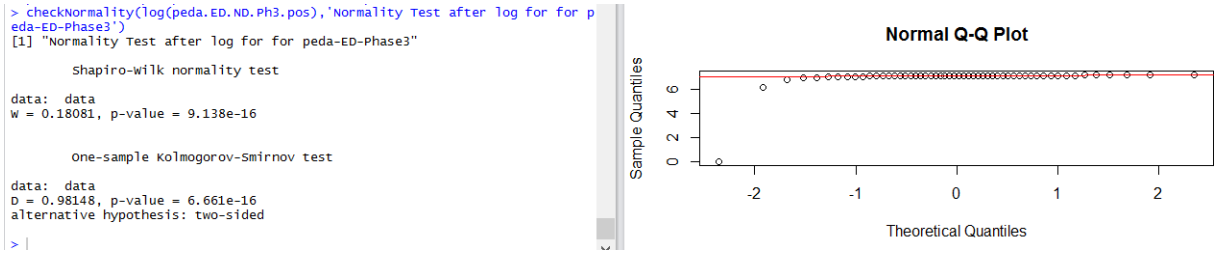

Figure 80: Normality tests after log transformation of peda-ED-Phase3

```
> t.test(log(peda.ED.ND.Ph3.pos),mu=log(-min(peda.ED.ND.Ph3[,1])+1))

        One Sample t-test

data:  log(peda.ED.ND.Ph3.pos)
t = -1.264, df = 53, p-value = 0.2118
alternative hypothesis: true mean is not equal to 7.162042
95 percent confidence interval:
 6.725518 7.261073
sample estimates:
mean of x
 6.993296
```

Figure 81: Paired t test tests for log transformation of peda-ED-Phase3

$$p \ = 0.2118$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-ED-Phase4
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

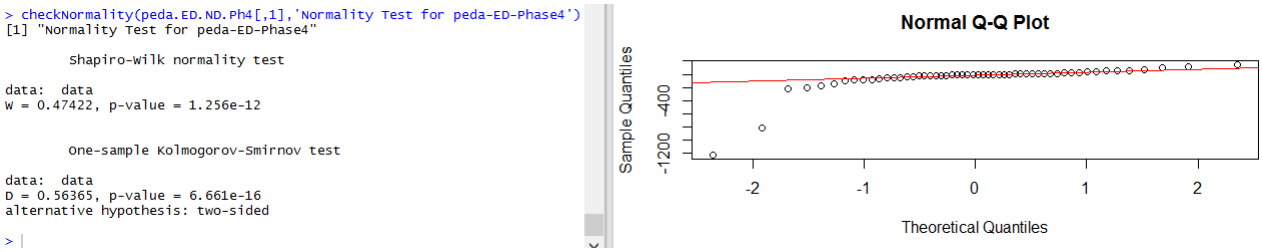

Figure 82: Normality tests for peda-ED-Phase4

Normality test for the difference between means of breath rate signals for ED and ND for phase 4.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for ED and ND for phase 4, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for ED and ND for phase 4, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

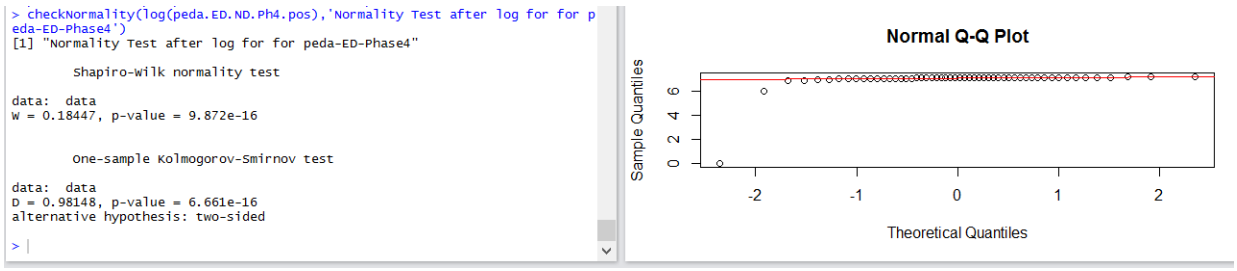

Figure 83: Normality tests after log transformation of peda-ED-Phase4

```
> t.test(log(peda.ED.ND.Ph4.pos),mu=log(-min(peda.ED.ND.Ph4[,1])+1))

        One Sample t-test

data:  log(peda.ED.ND.Ph4.pos)
t = -1.2457, df = 53, p-value = 0.2183
alternative hypothesis: true mean is not equal to 7.111434
95 percent confidence interval:
 6.679659 7.212357
sample estimates:
mean of x
 6.946008
```

Figure 84: Paired t test tests for log transformation of peda-ED-Phase4

$$p \ = 0.2183$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-ED-Phase5
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

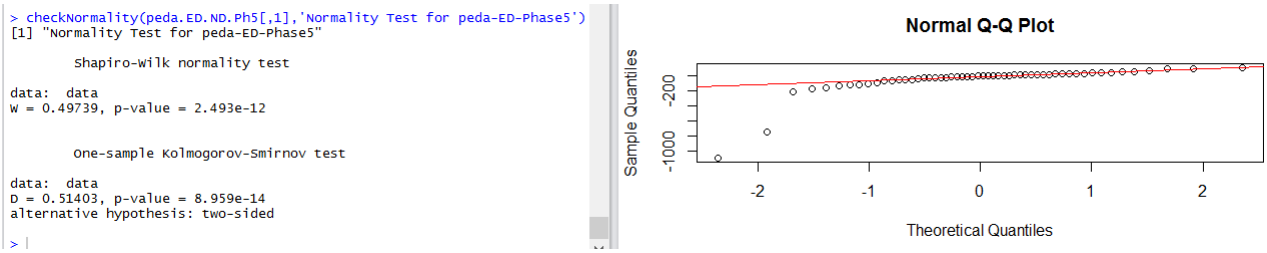

Figure 85: Normality tests for peda-ED-Phase5

Normality test for the difference between means of breath rate signals for ED and ND for phase 5.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for ED and ND for phase 5, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for ED and ND for phase 5, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

```
> checkNormality(log(peda.ED.ND.Ph5.pos),'Normality Test after log for for p
eda-ED-Phase5')
[1] "Normality Test after log for for peda-ED-Phase5"

        Shapiro-Wilk normality test

data:  data
W = 0.19133, p-value = 1.142e-15


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.98148, p-value = 6.661e-16
alternative hypothesis: two-sided
```

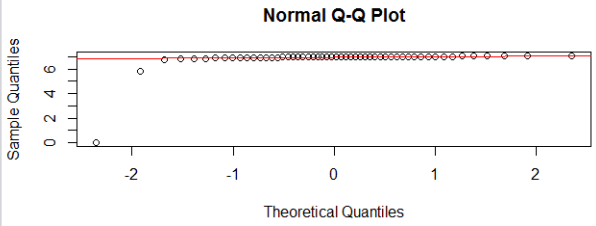

Figure 86: Normality tests after log transformation of peda-ED-Phase5

```
> t.test(log(peda.ED.ND.Ph5.pos),mu=log(-min(peda.ED.ND.Ph5[,1])+1))

        One Sample t-test

data:  log(peda.ED.ND.Ph5.pos)
t = -1.2755, df = 53, p-value = 0.2077
alternative hypothesis: true mean is not equal to 6.993757
95 percent confidence interval:
 6.564500 7.089294
sample estimates:
mean of x
 6.826897
```

Figure 87: Paired t test tests for log transformation of peda-ED-Phase5

$$p \ = 0.2077$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: MD

∗ Test for peda-MD-Phase1
Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

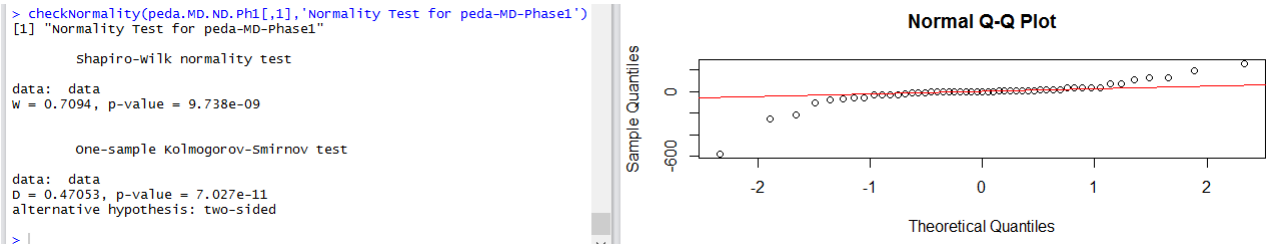

Figure 88: Normality tests for peda-MD-Phase1

Normality test for the difference between means of breath rate signals for MD and ND for phase 1.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for MD and ND for phase 1, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for MD and ND for phase 1, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points

are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

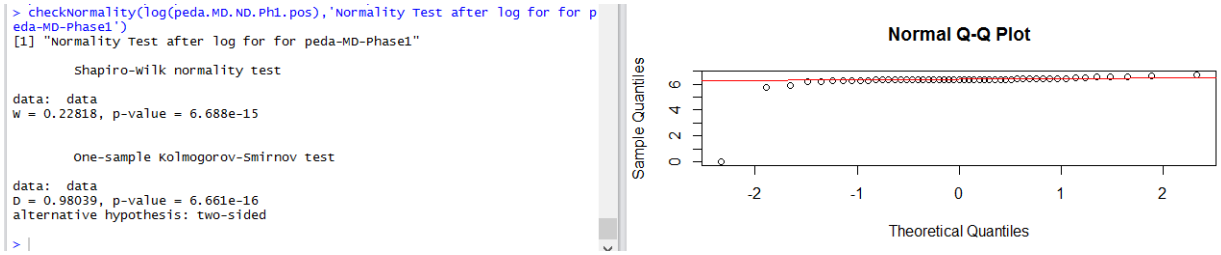

Figure 89: Normality tests after log transformation of peda-MD-Phase1

```
> t.test(log(peda.MD.ND.Ph1.pos),mu=log(-min(peda.MD.ND.Ph1[,1])+1))

        One Sample t-test

data:  log(peda.MD.ND.Ph1.pos)
t = -1.008, df = 50, p-value = 0.3183
alternative hypothesis: true mean is not equal to 6.363545
95 percent confidence interval:
 5.982371 6.489974
sample estimates:
mean of x
 6.236173
```

Figure 90: Paired t test tests for log transformation of peda-MD-Phase1

$$p \ = 0.3183$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-MD-Phase2
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

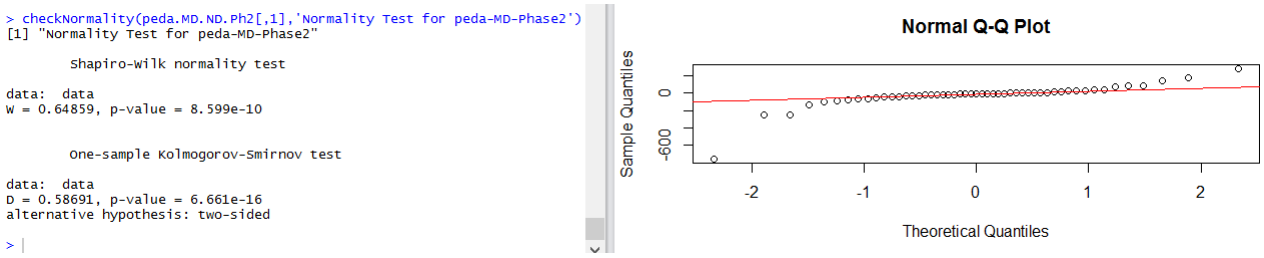

Figure 91: Normality tests for peda-MD-Phase2

Normality test for the difference between means of breath rate signals for MD and ND for phase 2.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for MD and ND for phase 2, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for MD and ND for phase 2, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

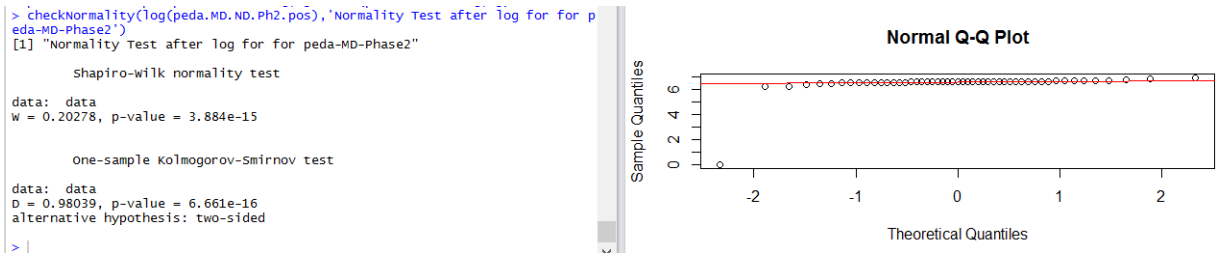

Figure 92: Normality tests after log transformation of peda-MD-Phase2

```
> t.test(log(peda.MD.ND.Ph2.pos),mu=log(-min(peda.MD.ND.Ph2[,1])+1))

        One Sample t-test

data:  log(peda.MD.ND.Ph2.pos)
t = -1.1121, df = 50, p-value = 0.2714
alternative hypothesis: true mean is not equal to 6.630995
95 percent confidence interval:
 6.223253 6.748122
sample estimates:
mean of x
 6.485688
```

Figure 93: Paired t test tests for log transformation of peda-MD-Phase2

$$p \ = 0.2714$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-MD-Phase3
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

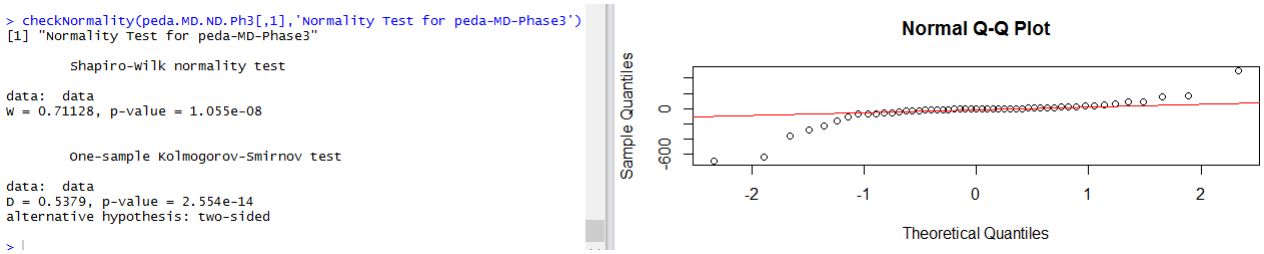

Figure 94: Normality tests for peda-MD-Phase3

Normality test for the difference between means of breath rate signals for MD and ND for phase 3.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for MD and ND for phase 3, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for MD and ND for phase 3, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

```
> checkNormality(log(peda.MD.ND.Ph3.pos),'Normality Test after log for for p
eda-MD-Phase3')
[1] "Normality Test after log for for peda-MD-Phase3"

        Shapiro-Wilk normality test

data:  data
W = 0.30617, p-value = 3.868e-14


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.98036, p-value = 6.661e-16
alternative hypothesis: two-sided

>
```

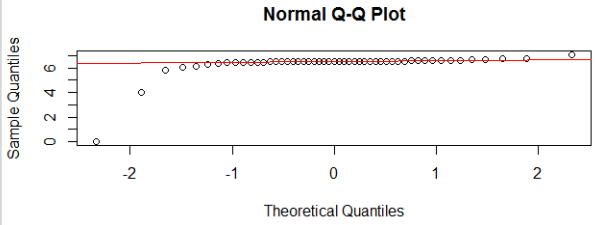

Figure 95: Normality tests after log transformation of peda-MD-Phase3

```
> t.test(log(peda.MD.ND.Ph3.pos),mu=log(-min(peda.MD.ND.Ph3[,1])+1))

        One Sample t-test

data:  log(peda.MD.ND.Ph3.pos)
t = -1.4772, df = 50, p-value = 0.1459
alternative hypothesis: true mean is not equal to 6.532651
95 percent confidence interval:
 6.051706 6.605968
sample estimates:
mean of x
 6.328837
```

Figure 96: Paired t test tests for log transformation of peda-MD-Phase3

$$p \ = 0.1459$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-MD-Phase4
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

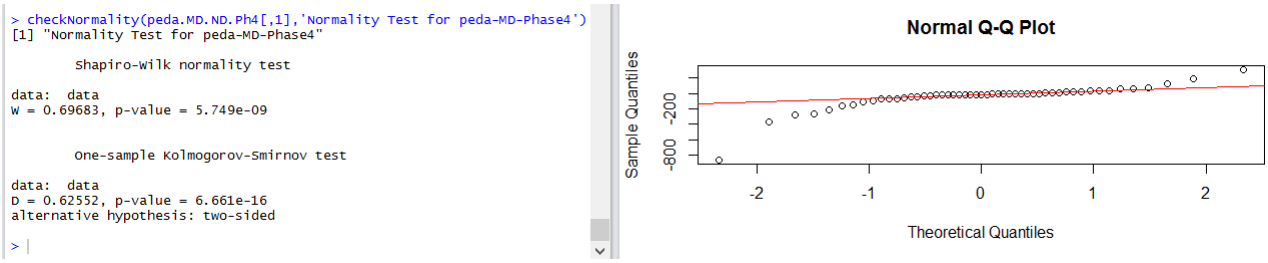

Figure 97: Normality tests for peda-MD-Phase4

Normality test for the difference between means of breath rate signals for MD and ND for phase 4.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for MD and ND for phase 4, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for MD and ND for phase 4, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

```
> checkNormality(log(peda.MD.ND.Ph4.pos),'Normality Test after log for for p
eda-MD-Phase4')
[1] "Normality Test after log for for peda-MD-Phase4"

        Shapiro-Wilk normality test

data:  data
W = 0.21812, p-value = 5.385e-15


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.98039, p-value = 6.661e-16
alternative hypothesis: two-sided
```

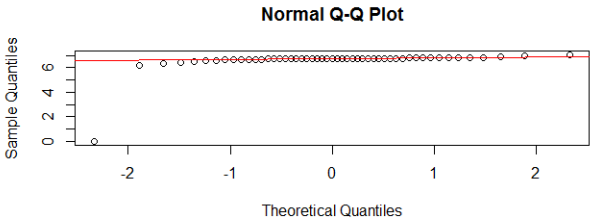

Figure 98: Normality tests after log transformation of peda-MD-Phase4

```
> t.test(log(peda.MD.ND.Ph4.pos),mu=log(-min(peda.MD.ND.Ph4[,1])+1))

        One Sample t-test

data:  log(peda.MD.ND.Ph4.pos)
t = -1.277, df = 50, p-value = 0.2075
alternative hypothesis: true mean is not equal to 6.760433
95 percent confidence interval:
 6.322780 6.857875
sample estimates:
mean of x
 6.590328
```

Figure 99: Paired t test tests for log transformation of peda-MD-Phase4

$$p = 0.2075$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for peda-MD-Phase5
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

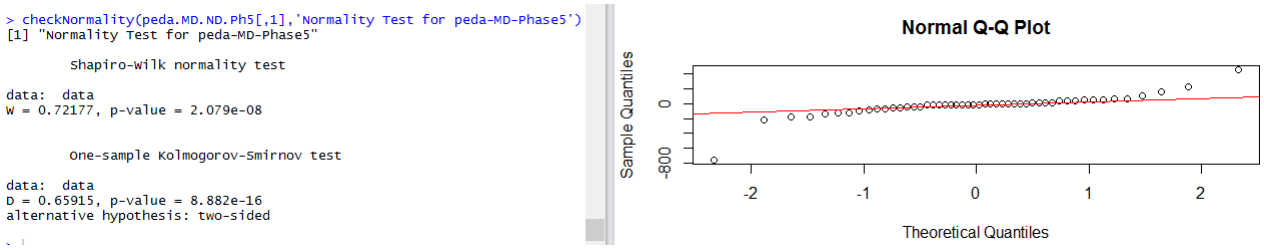

Figure 100: Normality tests for peda-MD-Phase5

Normality test for the difference between means of breath rate signals for MD and ND for phase 5.
Shapiro test: Since p <0.05, there is significant difference between the input distribution i.e. the there is a difference between means of peda signals for MD and ND for phase 5, thus data is not normal.
Kolmogorov–Smirnov test: Since p <0.05, there is significant difference between the input distribution i.e. there is significant difference between means of peda rate signals for MD and ND for phase 5, thus data is not normal.
Analysis of Q-Q Plot: We can observe that there are many data points deviating from the qqline.
Since all tests for normality fail we decide to perform transformations.
We perform log transformation.
On analyzing the QQPlot after log transformation: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data after log transformation is normal.

```
> checkNormality(log(peda.MD.ND.Ph5.pos),'Normality Test after log for for p
eda-MD-Phase5')
[1] "Normality Test after log for for peda-MD-Phase5"

        Shapiro-Wilk normality test

data:  data
W = 0.51433, p-value = 3.464e-10


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.97419, p-value = 7.772e-16
alternative hypothesis: two-sided

> |
```

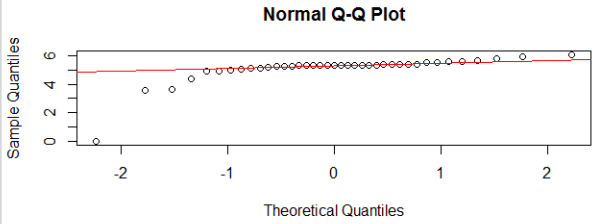

Figure 101: Normality tests after log transformation of peda-MD-Phase5

```
> t.test(log(peda.MD.ND.Ph5.pos),mu=log(-min(peda.MD.ND.Ph5[,1])+1))

        One Sample t-test

data:  log(peda.MD.ND.Ph5.pos)
t = -1.7373, df = 38, p-value = 0.09044
alternative hypothesis: true mean is not equal to 5.377668
95 percent confidence interval:
 4.796203 5.422049
sample estimates:
mean of x
 5.109126
```

Figure 102: Paired t test tests for log transformation of peda-MD-Phase5

$$p = 0.09044$$

Since p $> \alpha$ we fail to reject the null hypothesis.

- Data Channel: pp

  - Session: CD

    * Test for pp-CD-Phase1
      Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

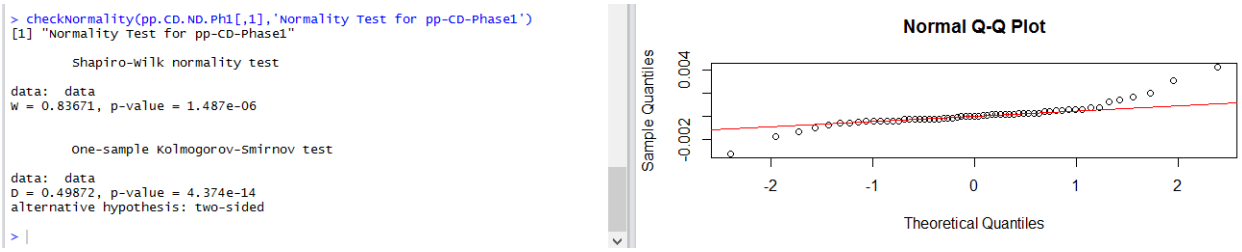

Figure 103: Normality tests for pp-CD-Phase1

Normality test for the difference between means of breath rate signals for CD and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.CD.ND.Ph1[,1])

        One Sample t-test

data:  pp.CD.ND.Ph1[, 1]
t = 0.9658, df = 58, p-value = 0.3382
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0001369473  0.0003923031
sample estimates:
   mean of x
0.0001276779
```

Figure 104: Paired t test tests for peda-CD-Phase1

$$p = 0.3382$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for pp-CD-Phase2
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.CD.ND.Ph2[,1],'Normality Test for pp-CD-Phase2')
[1] "Normality Test for pp-CD-Phase2"

        Shapiro-Wilk normality test

data:  data
W = 0.82905, p-value = 9.15e-07


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49967, p-value = 3.919e-14
alternative hypothesis: two-sided

>
```

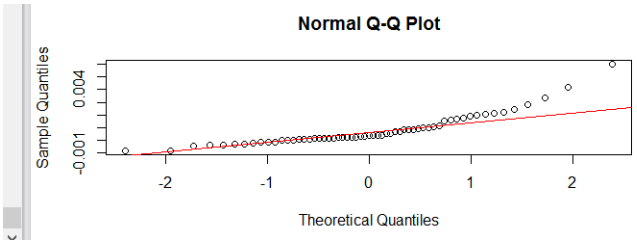

Figure 105: Normality tests for pp-CD-Phase2

Normality test for the difference between means of breath rate signals for CD and ND for phase 2.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around

the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.CD.ND.Ph2[,1])

        One Sample t-test

data:  pp.CD.ND.Ph2[, 1]
t = 4.959, df = 58, p-value = 6.515e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.0004707661 0.0011080572
sample estimates:
   mean of x
0.0007894117
```

Figure 106: Paired t test tests for peda-CD-Phase2

$$p = 6.515e - 06\ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for pp-CD-Phase3
Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.CD.ND.Ph3[,1],'Normality Test for pp-CD-Phase3')
[1] "Normality Test for pp-CD-Phase3"

        Shapiro-Wilk normality test

data:  data
W = 0.87623, p-value = 2.291e-05


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49949, p-value = 3.919e-14
alternative hypothesis: two-sided

>
```

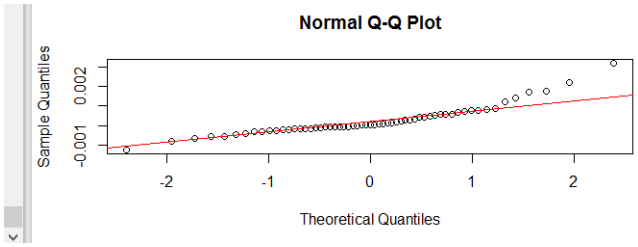

Figure 107: Normality tests for pp-CD-Phase3

Normality test for the difference between means of breath rate signals for CD and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.CD.ND.Ph3[,1])

        One Sample t-test

data:  pp.CD.ND.Ph3[, 1]
t = 2.4182, df = 58, p-value = 0.01876
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 4.028722e-05 4.275825e-04
sample estimates:
   mean of x
0.0002339348
```

Figure 108: Paired t test tests for peda-CD-Phase3

$$p = 0.01876\ *$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for pp-CD-Phase4
Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.CD.ND.Ph4[,1],'Normality Test for pp-CD-Phase4')
[1] "Normality Test for pp-CD-Phase4"

        Shapiro-Wilk normality test

data:  data
W = 0.81359, p-value = 3.567e-07


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49947, p-value = 3.919e-14
alternative hypothesis: two-sided
```

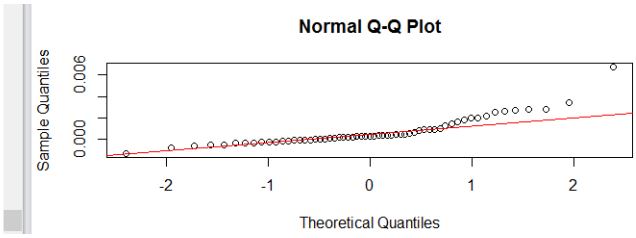

Figure 109: Normality tests for pp-CD-Phase4

Normality test for the difference between means of breath rate signals for CD and ND for phase 4.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.CD.ND.Ph4[,1])

        One Sample t-test

data:  pp.CD.ND.Ph4[, 1]
t = 4.0899, df = 58, p-value = 0.0001348
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.0003544401 0.0010339598
sample estimates:
mean of x
0.0006942
```

Figure 110: Paired t test tests for peda-CD-Phase4

$$p = 0.0001348\ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for pp-CD-Phase5
  Hypothesis:

$$H_0 : \mu_{CD} - \mu_{ND} = 0$$

$$H_1 : \mu_{CD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

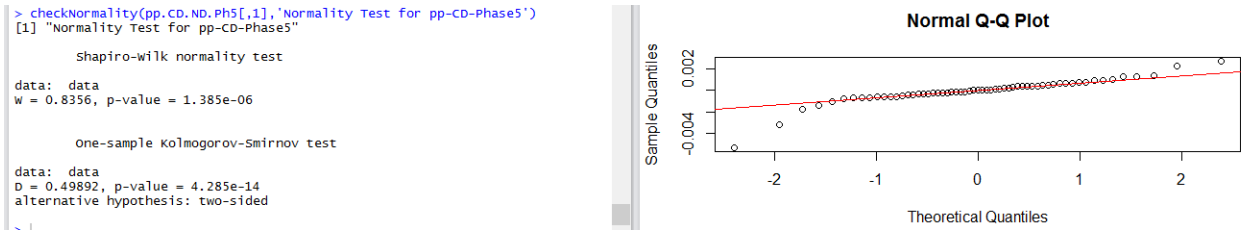

Figure 111: Normality tests for pp-CD-Phase5

Normality test for the difference between means of breath rate signals for CD and ND for phase 5.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.CD.ND.Ph5[,1])

        One Sample t-test

data:  pp.CD.ND.Ph5[, 1]
t = -0.26313, df = 58, p-value = 0.7934
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0003317421  0.0002546589
sample estimates:
    mean of x
-3.854157e-05
```

Figure 112: Paired t test tests for peda-CD-Phase5

$$p = 0.7934$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: ED

∗ Test for pp-ED-Phase1
Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$
$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$
$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

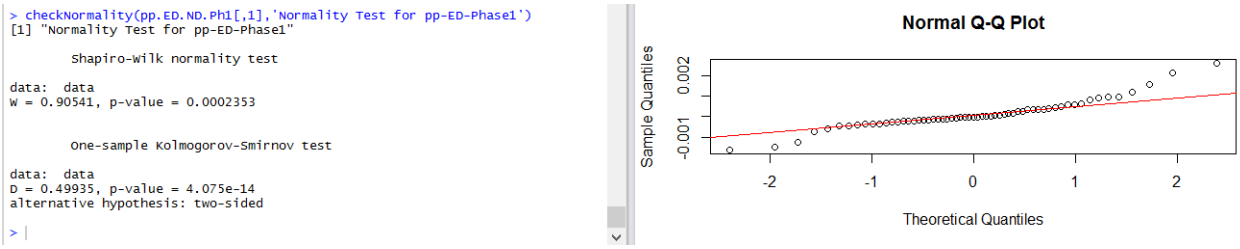

Figure 113: Normality tests for pp-ED-Phase1

Normality test for the difference between means of breath rate signals for ED and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.ED.ND.Ph1[,1])

        One Sample t-test

data:  pp.ED.ND.Ph1[, 1]
t = 1.0453, df = 58, p-value = 0.3002
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -8.761579e-05  2.791404e-04
sample estimates:
   mean of x
9.576229e-05
```

Figure 114: Paired t test tests for peda-ED-Phase1

$$p = 0.3002$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for pp-ED-Phase2
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferroni correction)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

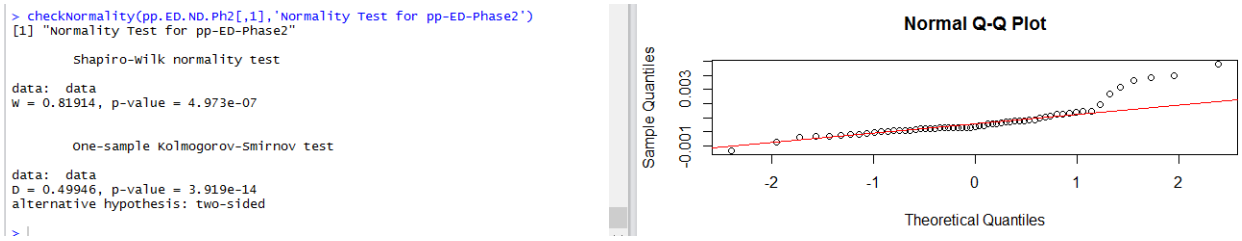

Figure 115: Normality tests for pp-ED-Phase2

Normality test for the difference between means of breath rate signals for ED and ND for phase 2.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.ED.ND.Ph2[,1])

        One Sample t-test

data:  pp.ED.ND.Ph2[, 1]
t = 4.8966, df = 58, p-value = 8.158e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.0004416802 0.0010524914
sample estimates:
   mean of x
0.0007470858
```

Figure 116: Paired t test tests for peda-ED-Phase2

$$p = 8.15e - 06 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for pp-ED-Phase3
  Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.ED.ND.Ph3[,1],'Normality Test for pp-ED-Phase3')
[1] "Normality Test for pp-ED-Phase3"

        Shapiro-Wilk normality test

data:  data
W = 0.71893, p-value = 2.578e-09


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49903, p-value = 4.285e-14
alternative hypothesis: two-sided

>
```

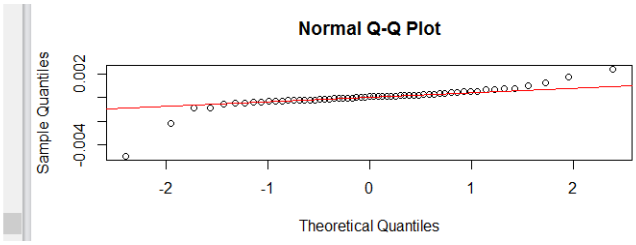

Figure 117: Normality tests for pp-ED-Phase3

Normality test for the difference between means of breath rate signals for ED and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the

points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.ED.ND.Ph3[,1])

        One Sample t-test

data:  pp.ED.ND.Ph3[, 1]
t = 0.24749, df = 58, p-value = 0.8054
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0002093464  0.0002684156
sample estimates:
   mean of x
2.953458e-05
```

Figure 118: Paired t test tests for peda-ED-Phase3

$$p = 0.8054$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for pp-ED-Phase4
Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.ED.ND.Ph4[,1],'Normality Test for pp-ED-Phase4')
[1] "Normality Test for pp-ED-Phase4"

        Shapiro-Wilk normality test

data:  data
W = 0.84527, p-value = 2.599e-06


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49925, p-value = 4.13e-14
alternative hypothesis: two-sided
```

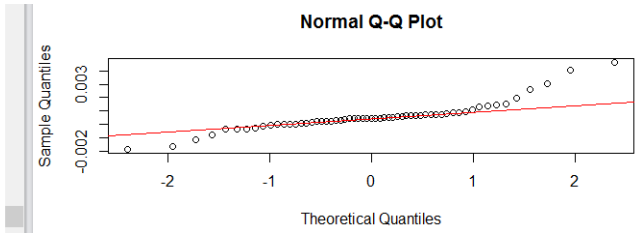

Figure 119: Normality tests for pp-ED-Phase4

Normality test for the difference between means of breath rate signals for ED and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.ED.ND.Ph4[,1])

        One Sample t-test

data:  pp.ED.ND.Ph4[, 1]
t = 3.968, df = 58, p-value = 0.0002019
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.0002755841 0.0008366767
sample estimates:
   mean of x
0.0005561304
```

Figure 120: Paired t test tests for peda-ED-Phase4

$$p = 0.0002019 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for pp-ED-Phase5
Hypothesis:

$$H_0 : \mu_{ED} - \mu_{ND} = 0$$

$$H_1 : \mu_{ED} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

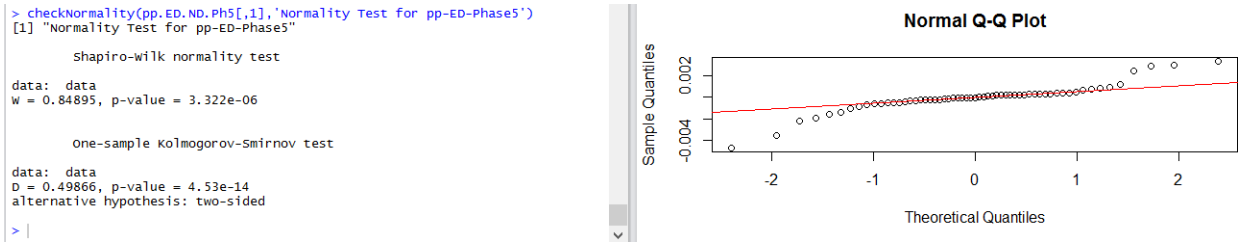

Figure 121: Normality tests for pp-ED-Phase5

Normality test for the difference between means of breath rate signals for ED and ND for phase 5.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.ED.ND.Ph5[,1])

        One Sample t-test

data:  pp.ED.ND.Ph5[, 1]
t = -0.25836, df = 58, p-value = 0.797
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0003696501  0.0002851368
sample estimates:
    mean of x
-4.225664e-05
```

Figure 122: Paired t test tests for peda-ED-Phase5

$$p = 0.797$$

Since p $> \alpha$ we fail to reject the null hypothesis.

– Session: MD

∗ Test for pp-MD-Phase1
Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$
$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$
$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

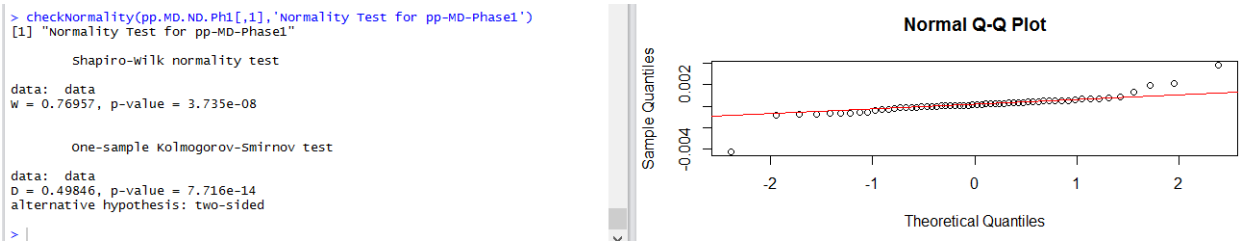

Figure 123: Normality tests for pp-MD-Phase1

Normality test for the difference between means of breath rate signals for MD and ND for phase 1.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.MD.ND.Ph1[,1])

        One Sample t-test

data:  pp.MD.ND.Ph1[, 1]
t = 1.3371, df = 57, p-value = 0.1865
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -8.297987e-05  4.164562e-04
sample estimates:
   mean of x
0.0001667382
```

Figure 124: Paired t test tests for peda-MD-Phase1

$$p = 0.1865$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for pp-MD-Phase2
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

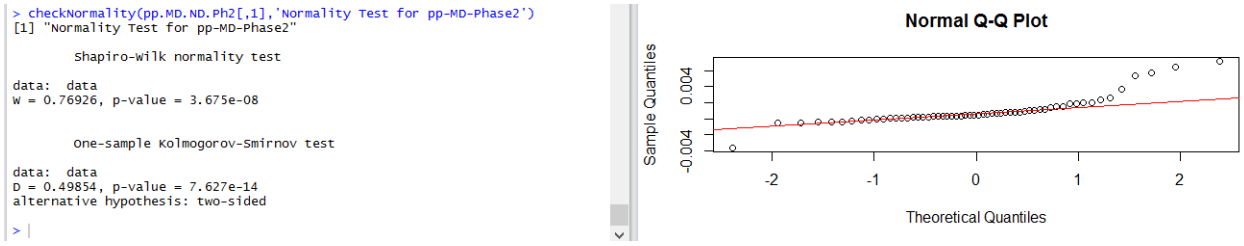

Figure 125: Normality tests for pp-MD-Phase2

Normality test for the difference between means of breath rate signals for MD and ND for phase 2.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.MD.ND.Ph2[,1])

        One Sample t-test

data:  pp.MD.ND.Ph2[, 1]
t = 4.1375, df = 57, p-value = 0.000117
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.0004951072 0.0014238546
sample estimates:
   mean of x
0.0009594809
```

Figure 126: Paired t test tests for peda-MD-Phase2

$$p = 0.000117 \ ***$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for pp-MD-Phase3
  Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.MD.ND.Ph3[,1],'Normality Test for pp-MD-Phase3')
[1] "Normality Test for pp-MD-Phase3"

        Shapiro-Wilk normality test

data:  data
W = 0.81664, p-value = 5.094e-07


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49873, p-value = 7.35e-14
alternative hypothesis: two-sided

>
```

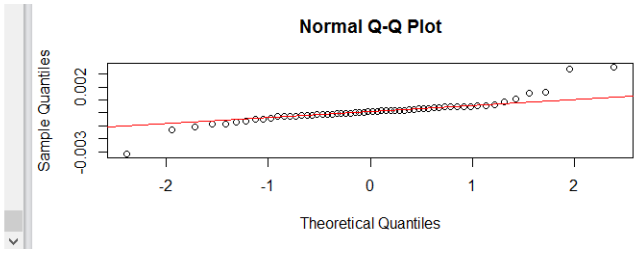

Figure 127: Normality tests for pp-MD-Phase3

Normality test for the difference between means of breath rate signals for MD and ND for phase 3.
Analysis of Q-Q Plot: We can observe that apart from the

points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.MD.ND.Ph3[,1])

        One Sample t-test

data:  pp.MD.ND.Ph3[, 1]
t = 1.083, df = 57, p-value = 0.2834
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0001133740  0.0003804316
sample estimates:
   mean of x
0.0001335288
```

Figure 128: Paired t test tests for peda-MD-Phase3

$$p = 0.2834$$

Since p $> \alpha$ we fail to reject the null hypothesis.

* Test for pp-MD-Phase4
Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

```
> checkNormality(pp.MD.ND.Ph4[,1],'Normality Test for pp-MD-Phase4')
[1] "Normality Test for pp-MD-Phase4"

        Shapiro-Wilk normality test

data:  data
W = 0.70322, p-value = 1.572e-09


        One-sample Kolmogorov-Smirnov test

data:  data
D = 0.49907, p-value = 7.072e-14
alternative hypothesis: two-sided

>
```

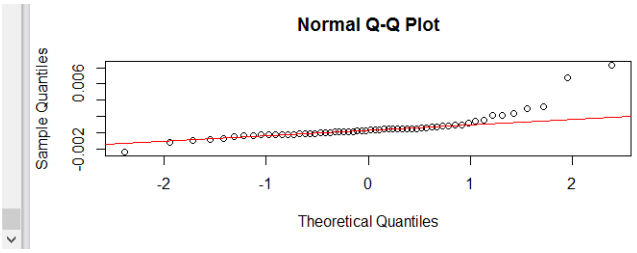

Figure 129: Normality tests for pp-MD-Phase4

Normality test for the difference between means of breath rate signals for MD and ND for phase 4.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.MD.ND.Ph4[,1])

        One Sample t-test

data:  pp.MD.ND.Ph4[, 1]
t = 3.0166, df = 57, p-value = 0.003815
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.0002155921 0.0010670146
sample estimates:
   mean of x
0.0006413033
```

Figure 130: Paired t test tests for peda-MD-Phase4

$$p = 0.003815\ **$$

Since p $< \alpha$ we reject the null hypothesis.

* Test for pp-MD-Phase5
Hypothesis:

$$H_0 : \mu_{MD} - \mu_{ND} = 0$$

$$H_1 : \mu_{MD} - \mu_{ND} \neq 0$$

$$\alpha = 0.0125(Bonferronicorrection)$$

Test: Paired t Test
Assumption for Paired t test is Normality test which is satisfied.

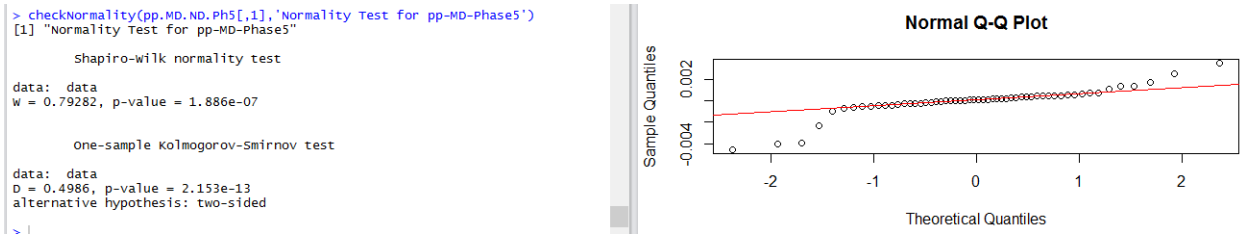

Figure 131: Normality tests for pp-MD-Phase5

Normality test for the difference between means of breath rate signals for MD and ND for phase 5.
Analysis of Q-Q Plot: We can observe that apart from the points at edges, majority of points are clustering well around the line. It is quite clear that just couple of points at edges deviate from the qqline which may be noise.
Hence, we can conclude that the data is normal.

```
> t.test(pp.MD.ND.Ph5[,1])

        One Sample t-test

data:  pp.MD.ND.Ph5[, 1]
t = -0.11735, df = 55, p-value = 0.907
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.0003667601  0.0003261835
sample estimates:
    mean of x
-2.028831e-05
```

Figure 132: Paired t test tests for peda-MD-Phase5

$$p = 0.907$$

Since p $> \alpha$ we fail to reject the null hypothesis.

5 Conclusion

In the results and observation we have seen a complete step by step analysis of all the tests performed in the expirement. Below is the conclusion for each data channel stating observations for all significant phases.
Here All the three types of stresses are applied and in Phase 2 and Phase 4. We are trying to analyse whether they really made impact on BR, HR, PP and PEDA.

- Breathing rate

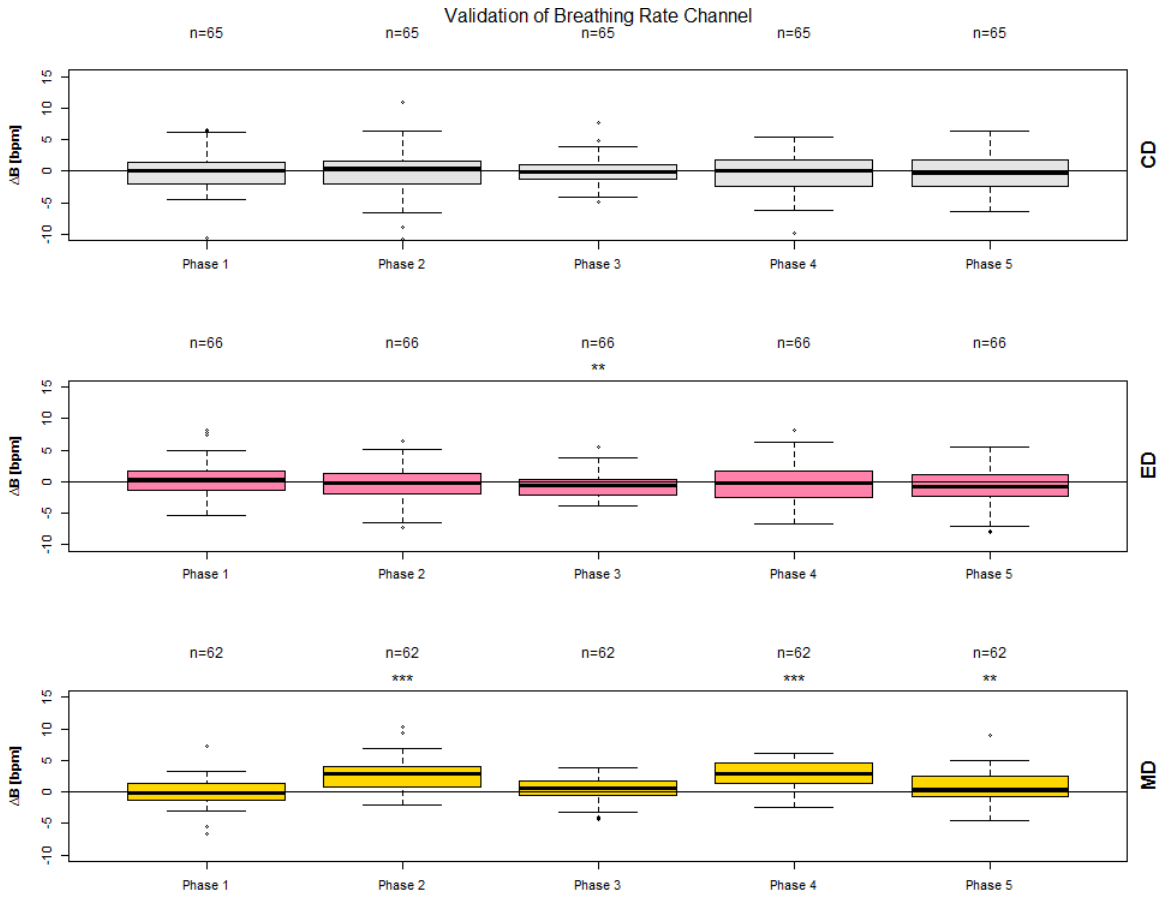

Figure 133: BR Boxplot Results

Following are the conclusions:

- We can say that there was no impact of cognitive distractors on the breathing rate when stress was applied in phase 2 and 4.
- We can observe that there was some impact observed in phase 3 due to emotional distractors, which may be due to the late impact of the stress applied in phase 2. However, phase 5 did
- We can say that there was a significant impact of mixed distractors on the breathing rate when stress was applied in phase 2 and 4 as expected.

- Heart rate

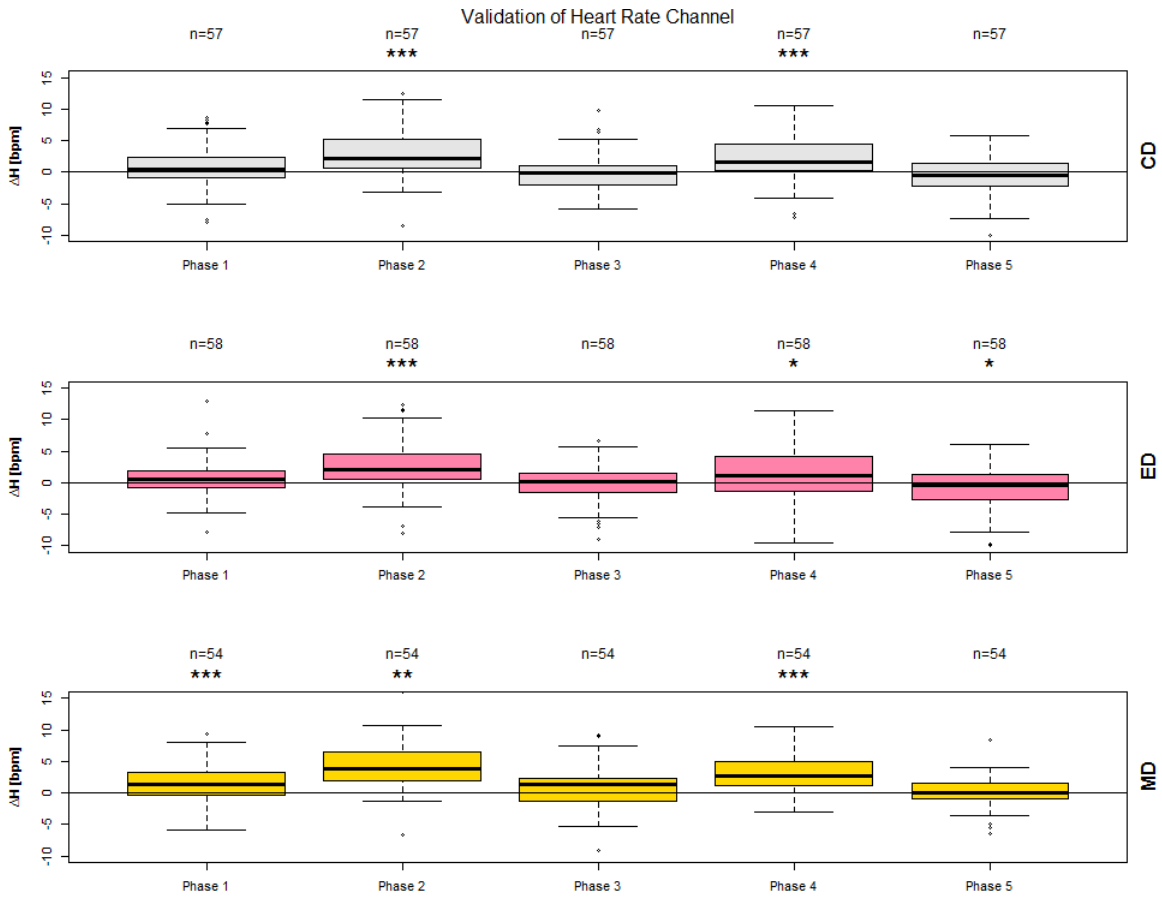

Figure 134: HR Boxplot Results

Following are the conclusions:

- We can say that there was a significant impact of cognitive distractors on the heart rate when stress was applied in phase 2 and 4 as expected.
- We can say that there was a significant impact of emotional distractors on the heart rate. When stress was applied in phase 2 and 4 we can see that it was significant but in phase 4 it was not

as significant as phase 2. Even phase 5 has stress, this may be because of a carry forward effect of stress in phase 4.

– We can say that there was a significant impact of mixed distractors on the heart rate when stress was applied in phase 2 and 4 as expected. Moreover we can also observe stress in Phase 1 probable reason being some initial stress.

- Perinasal Perspiration

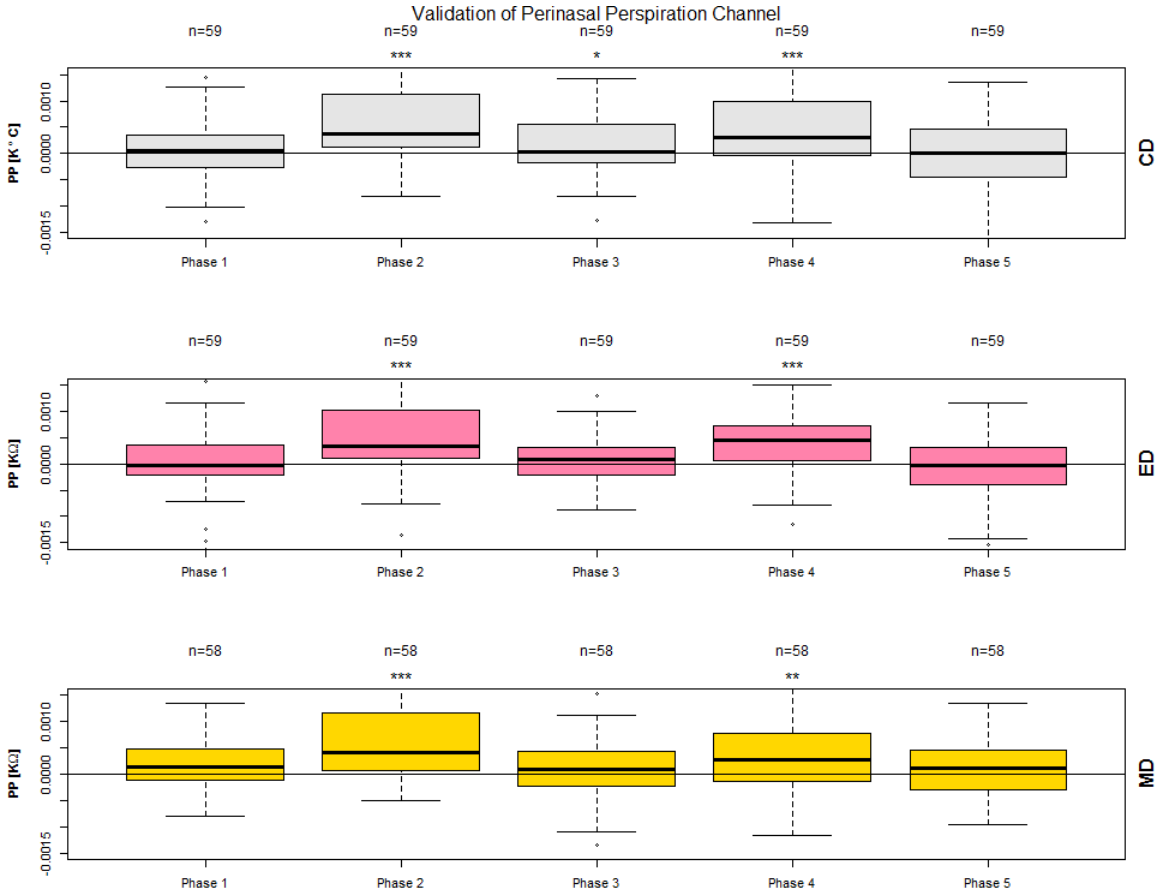

Figure 135: PP Boxplot Results

Following are the conclusions:

- We can say that there was a significant impact of cognitive distractors on the perinasal perspiration when stress was applied in phase 2 and 4 as expected.
- We can say that there was a significant impact of emotional distractors on the perinasal perspiration when stress was applied in phase 2 and 4 as expected.
- We can say that there was a significant impact of mixed distractors on the perinasal perspiration when stress was applied in phase 2 and 4 as expected.

- Palm electrodermal

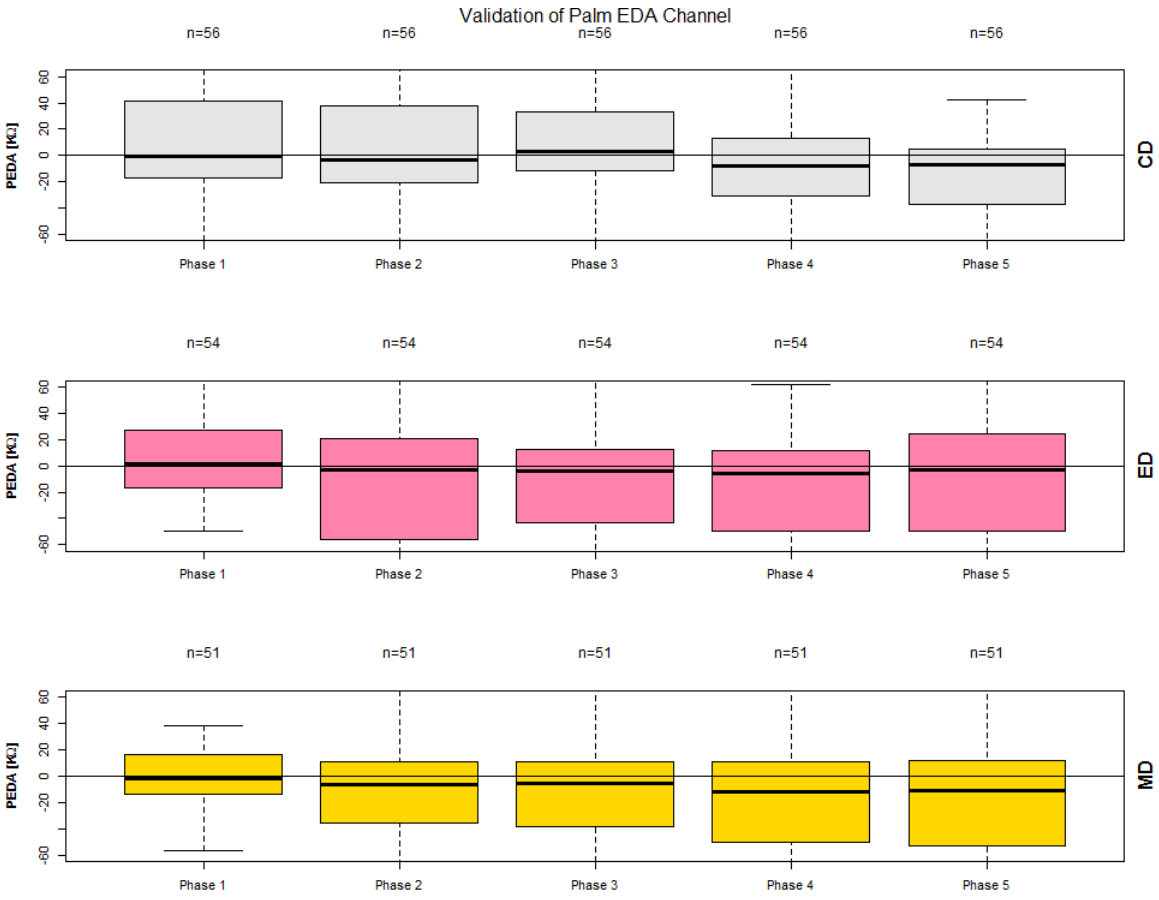

Figure 136: PEDA Boxplot Results

We can see that none of the phases have even a small impact of stress applied in phase 2 and 4 probable reason being that palmar electrodermal activity sensor was placed on palm in such a way that it sensed stress even when distractors where not applied externally.

6 Appendix

```
library(gdata)

### function to check Normality of data

checkNormality <- function(data,printstmt){
  print(printstmt)
  qqnorm(data)
  qqline(data, col = 2)
  print(shapiro.test(data))
  ks.test(data, "pnorm", alternative="two.sided")
}

## the path where data is stored
dataPath="C:/Users/nafis/Desktop/data"

workingDir="C:/Users/nafis/Desktop/Project"
setwd(workingDir)
dataChannels=c("BR","HR","peda","pp")
#dataChannels=c("BR")

### read the updated index file - the values in updated file are 1 if the data

metaDataSet=read.xls("C:/Users/nafis/Desktop/Project/output2/output/UpdatedInd
str=dataPath
folderNames = c("CD" ,  "ED" , "MD")
setwd(dataPath)

cnt=0
### for each data channel say HR
for(chan in 1:length(dataChannels))
{
  ### for each folder say CD

  for(folder in folderNames)
  {
    if(!is.na(folder) & !folder=="")
```

```
{

  ### metaDataSetrelVal2 will contain all cells where values are ==1 , metaData
  if(!dataChannels[chan]=="res"){
     metaDataSetrelVal2=metaDataSet[is.na(metaDataSet[dataChannels[chan]])==FAL
    metaDataSetrelVal=metaDataSetrelVal2[grep(as.character(folder),metaDataSetr

  }else{
    metaDataSetrelVal2=metaDataSet[is.na(metaDataSet["performance..res."])==FAL
    metaDataSetrelVal=metaDataSetrelVal2[grep(as.character(folder),metaDataSetr

  }

  ### the number of rows for which the subject, folder combination was 1 -- num
  numOfRows=length(unique(metaDataSetrelVal$Subject))
  if(!nrow(metaDataSetrelVal)==0)
  {
    ### construct the path of the folder containing the file -- in drawPath var
    drawPath=cbind(rep(str,each=nrow(metaDataSetrelVal)),'/',metaDataSetrelVal[
    colnames(drawPath) <- c("ParentDir","FstSlash","Subject","SecSlash")
    drawPath=paste(drawPath$ParentDir,drawPath$FstSlash,drawPath$Subject,drawPa

    ### for each path of the file
    for(i in 1:length(drawPath))
    {
      #i=1
      print(drawPath[i])
      setwd(drawPath[i])
      tempArr = strsplit(drawPath[i], "/")
      folderT = lapply(tempArr, tail, 1)

      ### if the value for that particular subject and ND combination exists in
      if(nrow(metaDataSetrelVal2[metaDataSetrelVal2$Subject==folderT & metaData
        cnt=cnt+1
        print("in if")
        if(folderT == list.files())
          setwd(as.character(folderT))
```

```
### find the final folder containing the file CD
FinalFolder=list.files(pattern = paste(as.character(folder)))
setwd(as.character(FinalFolder))

### find final file name
FinalfileName=list.files(pattern = paste(dataChannels[chan]))

### find file with .stm extension
FinalfileNameStm = list.files(pattern = paste(".stm"))

print(FinalfileName)
print(FinalfileNameStm)


### if there exists a .stm file in the folder find the start and
if(!length(FinalfileNameStm)==0)
{
  FinalfileDataStm=read.xls(FinalfileNameStm, stringsAsFactors=F
  st1=FinalfileDataStm$X[9]
  st1=sapply(st1, as.numeric)
  en1=FinalfileDataStm$X.1[9]
  en1=sapply(en1, as.numeric)

  st2=FinalfileDataStm$X[10]
  st2=sapply(st2, as.numeric)
  en2=FinalfileDataStm$X.1[10]
  en2=sapply(en2, as.numeric)
}


if(!length(FinalfileName)==0)
{
  ### read the final file using appropriate format -- the res fi
  if(!dataChannels[chan]=="res")
    FinalfileData=read.xls(FinalfileName, stringsAsFactors=FALSE
  else
    FinalfileData=read.csv(FinalfileName, stringsAsFactors=FALSE
```

```
### reset datapath to fetch ND files
setwd(dataPath)
setwd(drawPath[i])

### find final folder for ND files
FinalFolder2=list.files(pattern = paste(as.character("ND")))
setwd(as.character(FinalFolder2))


### find final filename for ND file and read in FinalfileDataND
FinalfileNameND=list.files(pattern = paste(dataChannels[chan]))

if(!dataChannels[chan]=="res")
  FinalfileDataND=read.xls(FinalfileNameND, stringsAsFactors=FALSE)
else
  FinalfileDataND=read.csv(FinalfileNameND, stringsAsFactors=FALSE)


### convert both files of the particular session ( folder ) eg CD and
FinalfileData = sapply(FinalfileData, as.numeric)
FinalfileData = data.frame(FinalfileData)
FinalfileDataND = sapply(FinalfileDataND, as.numeric)
FinalfileDataND = data.frame(FinalfileDataND)
FinalfileDataND=FinalfileDataND[colSums(!is.na(FinalfileDataND)) > 0]
FinalfileData=FinalfileData[colSums(!is.na(FinalfileData)) > 0]

### this block eliminates the issue caused by multiple columns in pp
if(as.character(dataChannels[chan])=="pp"){
  FinalfileData=FinalfileData[, 1:4]
  colnames(FinalfileData) <- c("Perinasal.Perspiration","X","X.1","X.
  FinalfileDataND=FinalfileDataND[, 1:4]
  colnames(FinalfileDataND) <- c("Perinasal.Perspiration","X","X.1","


}

### omit NA files in both files (CD and ND)
FinalfileData=data.frame(na.omit(FinalfileData))
```

```
FinalfileDataND=data.frame(na.omit(FinalfileDataND))

### divide the file data into phases based on time slice value
FinalfileDataPH1= FinalfileData[FinalfileData$X<st1,]
FinalfileDataPH2= FinalfileData[FinalfileData$X>=st1 & Finalfi
FinalfileDataPH3= FinalfileData[FinalfileData$X>=en1 & Finalfi
FinalfileDataPH4= FinalfileData[FinalfileData$X>=st2 & Finalfi
FinalfileDataPH5= FinalfileData[FinalfileData$X>=en2,]



### divide the ND file data into phases based on time slice va
FinalfileDataNDPH1= FinalfileDataND[FinalfileDataND$X<st1,]
FinalfileDataNDPH2= FinalfileDataND[FinalfileDataND$X>=st1 & F
FinalfileDataNDPH3= FinalfileDataND[FinalfileDataND$X>=en1 & F
FinalfileDataNDPH4= FinalfileDataND[FinalfileDataND$X>=st2 & F
FinalfileDataNDPH5= FinalfileDataND[FinalfileDataND$X>=en2,]

### eliminate the channel if the data in any phase has 0 rows
if(nrow(FinalfileDataPH1)==0 || nrow(FinalfileDataPH2)==0 || n
  break

### assign or append the means to vectors combinedDataPh1, com
if(i==1)
{
  combinedDataPh1=mean(sapply(FinalfileDataPH1$X.1, as.numeric
  combinedDataPh2=mean(sapply(FinalfileDataPH2$X.1, as.numeric
  combinedDataPh3=mean(sapply(FinalfileDataPH3$X.1, as.numeric
  combinedDataPh4=mean(sapply(FinalfileDataPH4$X.1, as.numeric
  combinedDataPh5=mean(sapply(FinalfileDataPH5$X.1, as.numeric

  combinedDataNDPh1=mean(sapply(FinalfileDataNDPH1$X.1, as.num
  combinedDataNDPh2=mean(sapply(FinalfileDataNDPH2$X.1, as.num
  combinedDataNDPh3=mean(sapply(FinalfileDataNDPH3$X.1, as.num
  combinedDataNDPh4=mean(sapply(FinalfileDataNDPH4$X.1, as.num
  combinedDataNDPh5=mean(sapply(FinalfileDataNDPH5$X.1, as.num

}
```

```
      if(i!=1)
      {
        combinedDataPh1 = rbind(combinedDataPh1,mean(sapply(FinalfileDataPH
        combinedDataPh2 = rbind(combinedDataPh2,mean(sapply(FinalfileDataPH
        combinedDataPh3 = rbind(combinedDataPh3,mean(sapply(FinalfileDataPH
        combinedDataPh4 = rbind(combinedDataPh4,mean(sapply(FinalfileDataPH
        combinedDataPh5 = rbind(combinedDataPh5,mean(sapply(FinalfileDataPH


        combinedDataNDPh1 = rbind(combinedDataNDPh1,mean(sapply(FinalfileDa
        combinedDataNDPh2 = rbind(combinedDataNDPh2,mean(sapply(FinalfileDa
        combinedDataNDPh3 = rbind(combinedDataNDPh3,mean(sapply(FinalfileDa
        combinedDataNDPh4 = rbind(combinedDataNDPh4,mean(sapply(FinalfileDa
        combinedDataNDPh5 = rbind(combinedDataNDPh5,mean(sapply(FinalfileDa

      }
    }
  }



}



### convert all values to numerica data frame
#combinedData = sapply(combinedData, as.numeric)
#combinedData = data.frame(combinedData)
combinedDataPh1 = sapply(combinedDataPh1, as.numeric)
combinedDataPh1 = data.frame(combinedDataPh1)
combinedDataPh2 = sapply(combinedDataPh2, as.numeric)
combinedDataPh2 = data.frame(combinedDataPh2)
combinedDataPh3 = sapply(combinedDataPh3, as.numeric)
combinedDataPh3 = data.frame(combinedDataPh3)
combinedDataPh4 = sapply(combinedDataPh4, as.numeric)
combinedDataPh4 = data.frame(combinedDataPh4)
combinedDataPh5 = sapply(combinedDataPh5, as.numeric)
combinedDataPh5 = data.frame(combinedDataPh5)
```

```
      #combinedDataND = sapply(combinedDataND, as.numeric)
      #combinedDataND = data.frame(combinedDataND)
      combinedDataNDPh1 = sapply(combinedDataNDPh1, as.numeric)
      combinedDataNDPh1 = data.frame(combinedDataNDPh1)
      combinedDataNDPh2 = sapply(combinedDataNDPh2, as.numeric)
      combinedDataNDPh2 = data.frame(combinedDataNDPh2)
      combinedDataNDPh3 = sapply(combinedDataNDPh3, as.numeric)
      combinedDataNDPh3 = data.frame(combinedDataNDPh3)
      combinedDataNDPh4 = sapply(combinedDataNDPh4, as.numeric)
      combinedDataNDPh4 = data.frame(combinedDataNDPh4)
      combinedDataNDPh5 = sapply(combinedDataNDPh5, as.numeric)
      combinedDataNDPh5 = data.frame(combinedDataNDPh5)


    }

  }

### assign the mean values to appropriate vectors

### naming convention used : <datachannel eg HR>.<Session eg CD>.<Phase eg
### and for vectors containing difference of the session from ND (eg CD-ND
### <datachannel eg HR>.<Session eg CD>.ND.<Phase eg Ph1>

if(as.character(dataChannels[chan])=="HR"){
  HR.ND.Ph1=combinedDataNDPh1
  HR.ND.Ph2=combinedDataNDPh2
  HR.ND.Ph3=combinedDataNDPh3
  HR.ND.Ph4=combinedDataNDPh4
  HR.ND.Ph5=combinedDataNDPh5



  if(folder=="CD"){
    HR.CD.Ph1=combinedDataPh1
    HR.CD.Ph2=combinedDataPh2
    HR.CD.Ph3=combinedDataPh3
```

```
  HR.CD.Ph4=combinedDataPh4
  HR.CD.Ph5=combinedDataPh5


  HR.CD.ND.Ph1=HR.CD.Ph1-HR.ND.Ph1
  HR.CD.ND.Ph2=HR.CD.Ph2-HR.ND.Ph2
  HR.CD.ND.Ph3=HR.CD.Ph3-HR.ND.Ph3
  HR.CD.ND.Ph4=HR.CD.Ph4-HR.ND.Ph4
  HR.CD.ND.Ph5=HR.CD.Ph5-HR.ND.Ph5


  HR.CD=cbind(HR.CD.ND.Ph1,"Phase 1")
  colnames(HR.CD) <- c("Rate","Phase" )
  temp=cbind(HR.CD.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  HR.CD=rbind(HR.CD,temp)
  temp=cbind(HR.CD.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  HR.CD=rbind(HR.CD,temp)
  temp=cbind(HR.CD.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  HR.CD=rbind(HR.CD,temp)
  temp=cbind(HR.CD.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  HR.CD=rbind(HR.CD,temp)

}



if(folder=="ED"){
  HR.ED.Ph1=combinedDataPh1
  HR.ED.Ph2=combinedDataPh2
  HR.ED.Ph3=combinedDataPh3
  HR.ED.Ph4=combinedDataPh4
  HR.ED.Ph5=combinedDataPh5
```

```
  HR.ED.ND.Ph1=HR.ED.Ph1-HR.ND.Ph1
  HR.ED.ND.Ph2=HR.ED.Ph2-HR.ND.Ph2
  HR.ED.ND.Ph3=HR.ED.Ph3-HR.ND.Ph3
  HR.ED.ND.Ph4=HR.ED.Ph4-HR.ND.Ph4
  HR.ED.ND.Ph5=HR.ED.Ph5-HR.ND.Ph5

  HR.ED=cbind(HR.ED.ND.Ph1,"Phase 1")
  colnames(HR.ED) <- c("Rate","Phase" )
  temp=cbind(HR.ED.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  HR.ED=rbind(HR.ED,temp)
  temp=cbind(HR.ED.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  HR.ED=rbind(HR.ED,temp)
  temp=cbind(HR.ED.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  HR.ED=rbind(HR.ED,temp)
  temp=cbind(HR.ED.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  HR.ED=rbind(HR.ED,temp)


}

if(folder=="MD"){
  HR.MD.Ph1=combinedDataPh1
  HR.MD.Ph2=combinedDataPh2
  HR.MD.Ph3=combinedDataPh3
  HR.MD.Ph4=combinedDataPh4
  HR.MD.Ph5=combinedDataPh5

  HR.MD.ND.Ph1=HR.MD.Ph1-HR.ND.Ph1
  HR.MD.ND.Ph2=HR.MD.Ph2-HR.ND.Ph2
  HR.MD.ND.Ph3=HR.MD.Ph3-HR.ND.Ph3
  HR.MD.ND.Ph4=HR.MD.Ph4-HR.ND.Ph4
  HR.MD.ND.Ph5=HR.MD.Ph5-HR.ND.Ph5

  HR.MD=cbind(HR.MD.ND.Ph1,"Phase 1")
```

```
    colnames(HR.MD) <- c("Rate","Phase" )
    temp=cbind(HR.MD.ND.Ph2,"Phase 2")
    colnames(temp) <- c("Rate","Phase" )
    HR.MD=rbind(HR.MD,temp)
    temp=cbind(HR.MD.ND.Ph3,"Phase 3")
    colnames(temp) <- c("Rate","Phase" )
    HR.MD=rbind(HR.MD,temp)
    temp=cbind(HR.MD.ND.Ph4,"Phase 4")
    colnames(temp) <- c("Rate","Phase" )
    HR.MD=rbind(HR.MD,temp)
    temp=cbind(HR.MD.ND.Ph5,"Phase 5")
    colnames(temp) <- c("Rate","Phase" )
    HR.MD=rbind(HR.MD,temp)

  }



}

if(as.character(dataChannels[chan])=="BR"){
 BR.ND.Ph1=combinedDataNDPh1
  BR.ND.Ph2=combinedDataNDPh2
  BR.ND.Ph3=combinedDataNDPh3
  BR.ND.Ph4=combinedDataNDPh4
  BR.ND.Ph5=combinedDataNDPh5



  if(folder=="CD"){
    BR.CD.Ph1=combinedDataPh1
    BR.CD.Ph2=combinedDataPh2
    BR.CD.Ph3=combinedDataPh3
    BR.CD.Ph4=combinedDataPh4
    BR.CD.Ph5=combinedDataPh5

    BR.CD.ND.Ph1=BR.CD.Ph1-BR.ND.Ph1
    BR.CD.ND.Ph2=BR.CD.Ph2-BR.ND.Ph2
```

```
  BR.CD.ND.Ph3=BR.CD.Ph3-BR.ND.Ph3
  BR.CD.ND.Ph4=BR.CD.Ph4-BR.ND.Ph4
  BR.CD.ND.Ph5=BR.CD.Ph5-BR.ND.Ph5

  BR.CD=cbind(BR.CD.ND.Ph1,"Phase 1")
  colnames(BR.CD) <- c("Rate","Phase" )
  temp=cbind(BR.CD.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  BR.CD=rbind(BR.CD,temp)
  temp=cbind(BR.CD.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  BR.CD=rbind(BR.CD,temp)
  temp=cbind(BR.CD.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  BR.CD=rbind(BR.CD,temp)
  temp=cbind(BR.CD.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  BR.CD=rbind(BR.CD,temp)

}



if(folder=="ED"){
  BR.ED.Ph1=combinedDataPh1
  BR.ED.Ph2=combinedDataPh2
  BR.ED.Ph3=combinedDataPh3
  BR.ED.Ph4=combinedDataPh4
  BR.ED.Ph5=combinedDataPh5

  BR.ED.ND.Ph1=BR.ED.Ph1-BR.ND.Ph1
  BR.ED.ND.Ph2=BR.ED.Ph2-BR.ND.Ph2
  BR.ED.ND.Ph3=BR.ED.Ph3-BR.ND.Ph3
  BR.ED.ND.Ph4=BR.ED.Ph4-BR.ND.Ph4
  BR.ED.ND.Ph5=BR.ED.Ph5-BR.ND.Ph5

  BR.ED=cbind(BR.ED.ND.Ph1,"Phase 1")
  colnames(BR.CD) <- c("Rate","Phase" )
```

```
  temp=cbind(BR.ED.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  colnames(BR.ED) <- c("Rate","Phase" )
  BR.ED=rbind(BR.ED,temp)
  temp=cbind(BR.ED.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  BR.ED=rbind(BR.ED,temp)
  temp=cbind(BR.ED.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  BR.ED=rbind(BR.ED,temp)
  temp=cbind(BR.ED.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  BR.ED=rbind(BR.ED,temp)

}

if(folder=="MD"){
  BR.MD.Ph1=combinedDataPh1
  BR.MD.Ph2=combinedDataPh2
  BR.MD.Ph3=combinedDataPh3
  BR.MD.Ph4=combinedDataPh4
  BR.MD.Ph5=combinedDataPh5

  BR.MD.ND.Ph1=BR.MD.Ph1-BR.ND.Ph1
  BR.MD.ND.Ph2=BR.MD.Ph2-BR.ND.Ph2
  BR.MD.ND.Ph3=BR.MD.Ph3-BR.ND.Ph3
  BR.MD.ND.Ph4=BR.MD.Ph4-BR.ND.Ph4
  BR.MD.ND.Ph5=BR.MD.Ph5-BR.ND.Ph5

  BR.MD=cbind(BR.MD.ND.Ph1,"Phase 1")
  colnames(BR.MD) <- c("Rate","Phase" )
  temp=cbind(BR.MD.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  BR.MD=rbind(BR.MD,temp)
  temp=cbind(BR.MD.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  BR.MD=rbind(BR.MD,temp)
  temp=cbind(BR.MD.ND.Ph4,"Phase 4")
```

```
    colnames(temp) <- c("Rate","Phase" )
    BR.MD=rbind(BR.MD,temp)
    temp=cbind(BR.MD.ND.Ph5,"Phase 5")
    colnames(temp) <- c("Rate","Phase" )
    BR.MD=rbind(BR.MD,temp)

  }


}

if(as.character(dataChannels[chan])=="peda"){
   peda.ND.Ph1=combinedDataNDPh1
  peda.ND.Ph2=combinedDataNDPh2
  peda.ND.Ph3=combinedDataNDPh3
  peda.ND.Ph4=combinedDataNDPh4
  peda.ND.Ph5=combinedDataNDPh5



  if(folder=="CD"){
    peda.CD.Ph1=combinedDataPh1
    peda.CD.Ph2=combinedDataPh2
    peda.CD.Ph3=combinedDataPh3
    peda.CD.Ph4=combinedDataPh4
    peda.CD.Ph5=combinedDataPh5


    peda.CD.ND.Ph1=peda.CD.Ph1-peda.ND.Ph1
    peda.CD.ND.Ph2=peda.CD.Ph2-peda.ND.Ph2
    peda.CD.ND.Ph3=peda.CD.Ph3-peda.ND.Ph3
    peda.CD.ND.Ph4=peda.CD.Ph4-peda.ND.Ph4
    peda.CD.ND.Ph5=peda.CD.Ph5-peda.ND.Ph5

    peda.CD=cbind(peda.CD.ND.Ph1,"Phase 1")
    colnames(peda.CD) <- c("Rate","Phase" )
    temp=cbind(peda.CD.ND.Ph2,"Phase 2")
    colnames(temp) <- c("Rate","Phase" )
```

```
  peda.CD=rbind(peda.CD,temp)
  temp=cbind(peda.CD.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  peda.CD=rbind(peda.CD,temp)
  temp=cbind(peda.CD.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  peda.CD=rbind(peda.CD,temp)
  temp=cbind(peda.CD.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  peda.CD=rbind(peda.CD,temp)
}



if(folder=="ED"){
  peda.ED.Ph1=combinedDataPh1
  peda.ED.Ph2=combinedDataPh2
  peda.ED.Ph3=combinedDataPh3
  peda.ED.Ph4=combinedDataPh4
  peda.ED.Ph5=combinedDataPh5


  peda.ED.ND.Ph1=peda.ED.Ph1-peda.ND.Ph1
  peda.ED.ND.Ph2=peda.ED.Ph2-peda.ND.Ph2
  peda.ED.ND.Ph3=peda.ED.Ph3-peda.ND.Ph3
  peda.ED.ND.Ph4=peda.ED.Ph4-peda.ND.Ph4
  peda.ED.ND.Ph5=peda.ED.Ph5-peda.ND.Ph5

  peda.ED=cbind(peda.ED.ND.Ph1,"Phase 1")
  colnames(peda.ED) <- c("Rate","Phase" )
  temp=cbind(peda.ED.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  peda.ED=rbind(peda.ED,temp)
  temp=cbind(peda.ED.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  peda.ED=rbind(peda.ED,temp)
  temp=cbind(peda.ED.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
```

```
  peda.ED=rbind(peda.ED,temp)
  temp=cbind(peda.ED.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  peda.ED=rbind(peda.ED,temp)


}

if(folder=="MD"){
  peda.MD.Ph1=combinedDataPh1
  peda.MD.Ph2=combinedDataPh2
  peda.MD.Ph3=combinedDataPh3
  peda.MD.Ph4=combinedDataPh4
  peda.MD.Ph5=combinedDataPh5

  peda.MD.ND.Ph1=peda.MD.Ph1-peda.ND.Ph1
  peda.MD.ND.Ph2=peda.MD.Ph2-peda.ND.Ph2
  peda.MD.ND.Ph3=peda.MD.Ph3-peda.ND.Ph3
  peda.MD.ND.Ph4=peda.MD.Ph4-peda.ND.Ph4
  peda.MD.ND.Ph5=peda.MD.Ph5-peda.ND.Ph5

  peda.MD=cbind(peda.MD.ND.Ph1,"Phase 1")
  colnames(peda.MD) <- c("Rate","Phase" )
  temp=cbind(peda.MD.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  peda.MD=rbind(peda.MD,temp)
  temp=cbind(peda.MD.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  peda.MD=rbind(peda.MD,temp)
  temp=cbind(peda.MD.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  peda.MD=rbind(peda.MD,temp)
  temp=cbind(peda.MD.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  peda.MD=rbind(peda.MD,temp)

}
```

```
}

if(as.character(dataChannels[chan])=="pp"){
  pp.ND.Ph1=combinedDataNDPh1
  pp.ND.Ph2=combinedDataNDPh2
  pp.ND.Ph3=combinedDataNDPh3
  pp.ND.Ph4=combinedDataNDPh4
  pp.ND.Ph5=combinedDataNDPh5



  if(folder=="CD"){
    pp.CD.Ph1=combinedDataPh1
    pp.CD.Ph2=combinedDataPh2
    pp.CD.Ph3=combinedDataPh3
    pp.CD.Ph4=combinedDataPh4
    pp.CD.Ph5=combinedDataPh5

    pp.CD.ND.Ph1=pp.CD.Ph1-pp.ND.Ph1
    pp.CD.ND.Ph2=pp.CD.Ph2-pp.ND.Ph2
    pp.CD.ND.Ph3=pp.CD.Ph3-pp.ND.Ph3
    pp.CD.ND.Ph4=pp.CD.Ph4-pp.ND.Ph4
    pp.CD.ND.Ph5=pp.CD.Ph5-pp.ND.Ph5

    pp.CD=cbind(pp.CD.ND.Ph1,"Phase 1")
    colnames(pp.CD) <- c("Rate","Phase" )
    temp=cbind(pp.CD.ND.Ph2,"Phase 2")
    colnames(temp) <- c("Rate","Phase" )
    pp.CD=rbind(pp.CD,temp)
    temp=cbind(pp.CD.ND.Ph3,"Phase 3")
    colnames(temp) <- c("Rate","Phase" )
    pp.CD=rbind(pp.CD,temp)
    temp=cbind(pp.CD.ND.Ph4,"Phase 4")
    colnames(temp) <- c("Rate","Phase" )
    pp.CD=rbind(pp.CD,temp)
    temp=cbind(pp.CD.ND.Ph5,"Phase 5")
    colnames(temp) <- c("Rate","Phase" )
```

```
  pp.CD=rbind(pp.CD,temp)


}



if(folder=="ED"){
   pp.ED.Ph1=combinedDataPh1
  pp.ED.Ph2=combinedDataPh2
  pp.ED.Ph3=combinedDataPh3
  pp.ED.Ph4=combinedDataPh4
  pp.ED.Ph5=combinedDataPh5

  pp.ED.ND.Ph1=pp.ED.Ph1-pp.ND.Ph1
  pp.ED.ND.Ph2=pp.ED.Ph2-pp.ND.Ph2
  pp.ED.ND.Ph3=pp.ED.Ph3-pp.ND.Ph3
  pp.ED.ND.Ph4=pp.ED.Ph4-pp.ND.Ph4
  pp.ED.ND.Ph5=pp.ED.Ph5-pp.ND.Ph5

  pp.ED=cbind(pp.ED.ND.Ph1,"Phase 1")
  colnames(pp.ED) <- c("Rate","Phase" )
  temp=cbind(pp.ED.ND.Ph2,"Phase 2")
  colnames(temp) <- c("Rate","Phase" )
  pp.ED=rbind(pp.ED,temp)
  temp=cbind(pp.ED.ND.Ph3,"Phase 3")
  colnames(temp) <- c("Rate","Phase" )
  pp.ED=rbind(pp.ED,temp)
  temp=cbind(pp.ED.ND.Ph4,"Phase 4")
  colnames(temp) <- c("Rate","Phase" )
  pp.ED=rbind(pp.ED,temp)
  temp=cbind(pp.ED.ND.Ph5,"Phase 5")
  colnames(temp) <- c("Rate","Phase" )
  pp.ED=rbind(pp.ED,temp)


}
```

```
      if(folder=="MD"){
        pp.MD.Ph1=combinedDataPh1
        pp.MD.Ph2=combinedDataPh2
        pp.MD.Ph3=combinedDataPh3
        pp.MD.Ph4=combinedDataPh4
        pp.MD.Ph5=combinedDataPh5

        pp.MD.ND.Ph1=pp.MD.Ph1-pp.ND.Ph1
        pp.MD.ND.Ph2=pp.MD.Ph2-pp.ND.Ph2
        pp.MD.ND.Ph3=pp.MD.Ph3-pp.ND.Ph3
        pp.MD.ND.Ph4=pp.MD.Ph4-pp.ND.Ph4
        pp.MD.ND.Ph5=pp.MD.Ph5-pp.ND.Ph5

        pp.MD=cbind(pp.MD.ND.Ph1,"Phase 1")
        colnames(pp.MD) <- c("Rate","Phase" )
        temp=cbind(pp.MD.ND.Ph2,"Phase 2")
        colnames(temp) <- c("Rate","Phase" )
        pp.MD=rbind(pp.MD,temp)
        temp=cbind(pp.MD.ND.Ph3,"Phase 3")
        colnames(temp) <- c("Rate","Phase" )
        pp.MD=rbind(pp.MD,temp)
        temp=cbind(pp.MD.ND.Ph4,"Phase 4")
        colnames(temp) <- c("Rate","Phase" )
        pp.MD=rbind(pp.MD,temp)
        temp=cbind(pp.MD.ND.Ph5,"Phase 5")
        colnames(temp) <- c("Rate","Phase" )
        pp.MD=rbind(pp.MD,temp)
      }


    }


  }

}

# Test for BR-CD-Phase1
```

```
#Normality tests
checkNormality(BR.CD.ND.Ph1[,1],'Normality Test for BR-CD-Phase1')

t.test(BR.CD.ND.Ph1[,1])

# Test for BR-CD-Phase2
#Normality tests

checkNormality(BR.CD.ND.Ph2[,1],'Normality Test for BR-CD-Phase2')

t.test(BR.CD.ND.Ph2[,1])



# Test for BR-CD-Phase3
#Normality tests
checkNormality(BR.CD.ND.Ph3[,1],'Normality Test for BR-CD-Phase3')

t.test(BR.CD.ND.Ph3[,1])




# Test for BR-CD-Phase4
#Normality tests
checkNormality(BR.CD.ND.Ph4[,1],'Normality Test for BR-CD-Phase4')
t.test(BR.CD.ND.Ph4[,1])


# Test for BR-CD-Phase5
#Normality tests
checkNormality(BR.CD.ND.Ph5[,1],'Normality Test for BR-CD-Phase5')

t.test(BR.CD.ND.Ph5[,1])


# Test for BR-ED-Phase1
#Normality tests
```

```
checkNormality(BR.ED.ND.Ph1[,1],'Normality Test for BR-ED-Phase1')
t.test(BR.ED.ND.Ph1[,1])
# Test for BR-ED-Phase2
#Normality tests
checkNormality(BR.ED.ND.Ph2[,1],'Normality Test for BR-ED-Phase2')
t.test(BR.ED.ND.Ph2[,1])

# Test for BR-ED-Phase3
#Normality tests
checkNormality(BR.ED.ND.Ph3[,1],'Normality Test for BR-ED-Phase3')
t.test(BR.ED.ND.Ph3[,1])


# Test for BR-ED-Phase4
#Normality tests
checkNormality(BR.ED.ND.Ph4[,1],'Normality Test for BR-ED-Phase4')

t.test(BR.ED.ND.Ph4[,1])
# Test for BR-ED-Phase5
#Normality tests
checkNormality(BR.ED.ND.Ph5[,1],'Normality Test for BR-ED-Phase5')
t.test(BR.ED.ND.Ph5[,1])
# Test for BR-MD-Phase1
#Normality tests
checkNormality(BR.MD.ND.Ph1[,1],'Normality Test for BR-MD-Phase1')
t.test(BR.MD.ND.Ph1[,1])

# Test for BR-MD-Phase2
#Normality tests

checkNormality(BR.MD.ND.Ph2[,1],'Normality Test for BR-MD-Phase2')

t.test(BR.MD.ND.Ph2[,1])
# Test for BR-MD-Phase3
#Normality tests

checkNormality(BR.MD.ND.Ph3[,1],'Normality Test for BR-MD-Phase3')
t.test(BR.MD.ND.Ph3[,1])
```

```
# Test for BR-MD-Phase4
#Normality tests
checkNormality(BR.MD.ND.Ph4[,1],'Normality Test for BR-MD-Phase4')
t.test(BR.MD.ND.Ph4[,1])


# Test for BR-MD-Phase5
#Normality tests
checkNormality(BR.MD.ND.Ph5[,1],'Normality Test for BR-MD-Phase5')

t.test(BR.MD.ND.Ph5[,1])


# Test for HR-CD-Phase1
checkNormality(HR.CD.ND.Ph1[,1],'Normality Test for HR-CD-Phase1')
t.test(HR.CD.ND.Ph1[,1])

# Test for HR-CD-Phase2
checkNormality(HR.CD.ND.Ph2[,1],'Normality Test for HR-CD-Phase2')
t.test(HR.CD.ND.Ph2[,1])



# Test for HR-CD-Phase3
checkNormality(HR.CD.ND.Ph3[,1],'Normality Test for HR-CD-Phase3')
t.test(HR.CD.ND.Ph3[,1])

# Test for HR-CD-Phase4
checkNormality(HR.CD.ND.Ph4[,1],'Normality Test for HR-CD-Phase4')
t.test(HR.CD.ND.Ph4[,1])
# Test for HR-CD-Phase5
checkNormality(HR.CD.ND.Ph5[,1],'Normality Test for HR-CD-Phase5')
t.test(HR.CD.ND.Ph5[,1])

# Test for HR-ED-Phase1
checkNormality(HR.ED.ND.Ph1[,1],'Normality Test for HR-ED-Phase1')

t.test(HR.ED.ND.Ph1[,1])
```

```
# Test for HR-ED-Phase2
checkNormality(HR.ED.ND.Ph2[,1],'Normality Test for HR-ED-Phase2')
t.test(HR.ED.ND.Ph2[,1])

# Test for HR-ED-Phase3
checkNormality(HR.ED.ND.Ph3[,1],'Normality Test for HR-ED-Phase3')
t.test(HR.ED.ND.Ph3[,1])

# Test for HR-ED-Phase4
checkNormality(HR.ED.ND.Ph4[,1],'Normality Test for HR-ED-Phase4')
t.test(HR.ED.ND.Ph4[,1])
# Test for HR-ED-Phase5
checkNormality(HR.ED.ND.Ph5[,1],'Normality Test for HR-ED-Phase5')
t.test(HR.ED.ND.Ph5[,1])



# Test for HR-MD-Phase1
checkNormality(HR.MD.ND.Ph1[,1],'Normality Test for HR-MD-Phase1')
t.test(HR.MD.ND.Ph1[,1])

# Test for HR-MD-Phase2
checkNormality(HR.MD.ND.Ph2[,1],'Normality Test for HR-MD-Phase2')
t.test(HR.MD.ND.Ph2[,1])

# Test for HR-MD-Phase3
checkNormality(HR.MD.ND.Ph3[,1],'Normality Test for HR-MD-Phase3')
t.test(HR.MD.ND.Ph3[,1])

# Test for HR-MD-Phase4
checkNormality(HR.MD.ND.Ph4[,1],'Normality Test for HR-MD-Phase4')
t.test(HR.MD.ND.Ph4[,1])


# Test for HR-MD-Phase5
checkNormality(HR.MD.ND.Ph5[,1],'Normality Test for HR-MD-Phase5')
t.test(HR.MD.ND.Ph5[,1])
```

```
### Code to test Normality of Peda and Apply T-Test

checkNormality(peda.CD.ND.Ph1[,1],'Normality Test for peda-CD-Phase1')
t.test(peda.CD.ND.Ph1[,1])

checkNormality(peda.CD.ND.Ph2[,1],'Normality Test for peda-CD-Phase2')
t.test(peda.CD.ND.Ph2[,1])

checkNormality(peda.CD.ND.Ph3[,1],'Normality Test for peda-CD-Phase3')
peda.CD.ND.Ph3.pos=peda.CD.ND.Ph3[,1]+1-min(peda.CD.ND.Ph3[,1])
checkNormality(log(peda.CD.ND.Ph3.pos),'Normality test after log for peda-CD-P
t.test(log(peda.CD.ND.Ph3.pos),mu=log(-min(peda.CD.ND.Ph3[,1])+1))


checkNormality(peda.CD.ND.Ph4[,1],'Normality Test for peda-CD-Phase4')
peda.CD.ND.Ph4.pos=peda.CD.ND.Ph4[,1]+1-min(peda.CD.ND.Ph4[,1])
hist(log(peda.CD.ND.Ph4.pos))
checkNormality(log(peda.CD.ND.Ph4.pos),'Normality test after log for peda-CD-P
t.test(log(peda.CD.ND.Ph4.pos),mu=log(-min(peda.CD.ND.Ph4[,1])+1))

checkNormality(peda.CD.ND.Ph5[,1],'Normality Test for peda-CD-Phase5')
peda.CD.ND.Ph5.pos=peda.CD.ND.Ph5[,1]+1-min(peda.CD.ND.Ph5[,1])
checkNormality(1/sqrt(peda.CD.ND.Ph5.pos),'Normality test after Inverse of squ
t.test(1/sqrt(peda.CD.ND.Ph5.pos),mu=1/sqrt(-min(peda.CD.ND.Ph5[,1])+1))


checkNormality(peda.ED.ND.Ph1[,1],'Normality Test for peda-ED-Phase1')
peda.ED.ND.Ph1.pos=peda.ED.ND.Ph1[,1]+1-min(peda.ED.ND.Ph1[,1])
checkNormality(log(peda.ED.ND.Ph1.pos),'Normality Test after log for for peda-
t.test(log(peda.ED.ND.Ph1.pos),mu=log(-min(peda.ED.ND.Ph1[,1])+1))


checkNormality(peda.ED.ND.Ph2[,1],'Normality Test for peda-ED-Phase2')
peda.ED.ND.Ph2.pos=peda.ED.ND.Ph2[,1]+1-min(peda.ED.ND.Ph2[,1])
checkNormality(log(peda.ED.ND.Ph2.pos),'Normality Test after log for for peda-
t.test(log(peda.ED.ND.Ph2.pos),mu=log(-min(peda.ED.ND.Ph2[,1])+1))
```

```
checkNormality(peda.ED.ND.Ph3[,1],'Normality Test for peda-ED-Phase3')
peda.ED.ND.Ph3.pos=peda.ED.ND.Ph3[,1]+1-min(peda.ED.ND.Ph3[,1])
checkNormality(log(peda.ED.ND.Ph3.pos),'Normality Test after log for for peda-ED-Phas
t.test(log(peda.ED.ND.Ph3.pos),mu=log(-min(peda.ED.ND.Ph3[,1])+1))



checkNormality(peda.ED.ND.Ph4[,1],'Normality Test for peda-ED-Phase4')
peda.ED.ND.Ph4.pos=peda.ED.ND.Ph4[,1]+1-min(peda.ED.ND.Ph4[,1])
checkNormality(log(peda.ED.ND.Ph4.pos),'Normality Test after log for for peda-ED-Phas
t.test(log(peda.ED.ND.Ph4.pos),mu=log(-min(peda.ED.ND.Ph4[,1])+1))



checkNormality(peda.ED.ND.Ph5[,1],'Normality Test for peda-ED-Phase5')
peda.ED.ND.Ph5.pos=peda.ED.ND.Ph5[,1]+1-min(peda.ED.ND.Ph5[,1])
checkNormality(log(peda.ED.ND.Ph5.pos),'Normality Test after log for for peda-ED-Phas
t.test(log(peda.ED.ND.Ph5.pos),mu=log(-min(peda.ED.ND.Ph5[,1])+1))



checkNormality(peda.MD.ND.Ph1[,1],'Normality Test for peda-MD-Phase1')
peda.MD.ND.Ph1.pos=peda.MD.ND.Ph1[,1]+1-min(peda.MD.ND.Ph1[,1])
checkNormality(log(peda.MD.ND.Ph1.pos),'Normality Test after log for for peda-MD-Phas
t.test(log(peda.MD.ND.Ph1.pos),mu=log(-min(peda.MD.ND.Ph1[,1])+1))



checkNormality(peda.MD.ND.Ph2[,1],'Normality Test for peda-MD-Phase2')
peda.MD.ND.Ph2.pos=peda.MD.ND.Ph2[,1]+1-min(peda.MD.ND.Ph2[,1])
checkNormality(log(peda.MD.ND.Ph2.pos),'Normality Test after log for for peda-MD-Phas
t.test(log(peda.MD.ND.Ph2.pos),mu=log(-min(peda.MD.ND.Ph2[,1])+1))



checkNormality(peda.MD.ND.Ph3[,1],'Normality Test for peda-MD-Phase3')
peda.MD.ND.Ph3.pos=peda.MD.ND.Ph3[,1]+1-min(peda.MD.ND.Ph3[,1])
checkNormality(log(peda.MD.ND.Ph3.pos),'Normality Test after log for for peda-MD-Phas
t.test(log(peda.MD.ND.Ph3.pos),mu=log(-min(peda.MD.ND.Ph3[,1])+1))
```

```
checkNormality(peda.MD.ND.Ph4[,1],'Normality Test for peda-MD-Phase4')
peda.MD.ND.Ph4.pos=peda.MD.ND.Ph4[,1]+1-min(peda.MD.ND.Ph4[,1])
checkNormality(log(peda.MD.ND.Ph4.pos),'Normality Test after log for for peda-
t.test(log(peda.MD.ND.Ph4.pos),mu=log(-min(peda.MD.ND.Ph4[,1])+1))

checkNormality(peda.MD.ND.Ph5[,1],'Normality Test for peda-MD-Phase5')
peda.MD.ND.Ph5.pos=peda.MD.ND.Ph5[,1]+1-min(peda.MD.ND.Ph5[,1])
checkNormality(log(peda.MD.ND.Ph5.pos),'Normality Test after log for for peda-
t.test(log(peda.MD.ND.Ph5.pos),mu=log(-min(peda.MD.ND.Ph5[,1])+1))


### Code to test Normality of PP and Apply T-Test

checkNormality(pp.CD.ND.Ph1[,1],'Normality Test for pp-CD-Phase1')
t.test(pp.CD.ND.Ph1[,1])


checkNormality(pp.CD.ND.Ph2[,1],'Normality Test for pp-CD-Phase2')
t.test(pp.CD.ND.Ph2[,1])

checkNormality(pp.CD.ND.Ph3[,1],'Normality Test for pp-CD-Phase3')
t.test(pp.CD.ND.Ph3[,1])


checkNormality(pp.CD.ND.Ph4[,1],'Normality Test for pp-CD-Phase4')
t.test(pp.CD.ND.Ph4[,1])

checkNormality(pp.CD.ND.Ph5[,1],'Normality Test for pp-CD-Phase5')
t.test(pp.CD.ND.Ph5[,1])

checkNormality(pp.ED.ND.Ph1[,1],'Normality Test for pp-ED-Phase1')
t.test(pp.ED.ND.Ph1[,1])

checkNormality(pp.ED.ND.Ph2[,1],'Normality Test for pp-ED-Phase2')
t.test(pp.ED.ND.Ph2[,1])

checkNormality(pp.ED.ND.Ph3[,1],'Normality Test for pp-ED-Phase3')
```

```
t.test(pp.ED.ND.Ph3[,1])


checkNormality(pp.ED.ND.Ph4[,1],'Normality Test for pp-ED-Phase4')
t.test(pp.ED.ND.Ph4[,1])



checkNormality(pp.ED.ND.Ph5[,1],'Normality Test for pp-ED-Phase5')
t.test(pp.ED.ND.Ph5[,1])

checkNormality(pp.MD.ND.Ph1[,1],'Normality Test for pp-MD-Phase1')
t.test(pp.MD.ND.Ph1[,1])

checkNormality(pp.MD.ND.Ph2[,1],'Normality Test for pp-MD-Phase2')
t.test(pp.MD.ND.Ph2[,1])


checkNormality(pp.MD.ND.Ph3[,1],'Normality Test for pp-MD-Phase3')
t.test(pp.MD.ND.Ph3[,1])


checkNormality(pp.MD.ND.Ph4[,1],'Normality Test for pp-MD-Phase4')
t.test(pp.MD.ND.Ph4[,1])


checkNormality(pp.MD.ND.Ph5[,1],'Normality Test for pp-MD-Phase5')
t.test(pp.MD.ND.Ph5[,1])




### boxplot for HR

par(mfrow=c(3,1))

boxplot(data=HR.CD, Rate~Phase, col="grey90", ylab=expression(bold(paste(Delta, "H [b
mtext(side=4, line=1, expression(bold("CD")))
```

```
abline(0,0)
mtext(c("","***","","***",""), side = 3,0, at=1:5,cex=1.5)
mtext(c(paste("n=",c(nrow(HR.CD.ND.Ph1)),sep=""),paste("n=",c(nrow(HR.CD.ND.Ph
mtext("Validation of Heart Rate Channel", side = 3,3)


boxplot(data=HR.ED, Rate~Phase, col="palevioletred1" , ylab=expression(bold(pa
mtext(side=4, line=1, expression(bold("ED")))
abline(0,0)
mtext(c("","***","","*","*"), side = 3,0, at=1:5,cex=1.5)
mtext(c(paste("n=",c(nrow(HR.ED.ND.Ph1)),sep=""),paste("n=",c(nrow(HR.ED.ND.Ph



boxplot(data=HR.MD, Rate~Phase, col="gold" , ylab=expression(bold(paste(Delta,
mtext(side=4, line=1, expression(bold("MD")))
abline(0,0)
mtext(c("***","**","","***",""), side = 3,0, at=1:5,cex=1.5)
mtext(c(paste("n=",c(nrow(HR.MD.ND.Ph1)),sep=""),paste("n=",c(nrow(HR.MD.ND.Ph



### boxplot for BR

par(mfrow=c(3,1))

boxplot(data=BR.CD, Rate~Phase, col="grey90", ylab=expression(bold(paste(Delta
mtext(side=4, line=1, expression(bold("CD")))
abline(0,0)
#mtext(c("","***","","***",""), side = 3,0, at=1:5)
mtext(c(paste("n=",c(nrow(BR.CD.ND.Ph1)),sep=""),paste("n=",c(nrow(BR.CD.ND.Ph
mtext("Validation of Breathing Rate Channel", side = 3,3)



boxplot(data=BR.ED, Rate~Phase, col="palevioletred1" , ylab=expression(bold(pa
mtext(side=4, line=1, expression(bold("ED")))
```

```
abline(0,0)
mtext(c("","","**","",""), side = 3,0, at=1:5)
mtext(c(paste("n=",c(nrow(BR.ED.ND.Ph1)),sep=""),paste("n=",c(nrow(BR.ED.ND.Ph2)),sep


boxplot(data=BR.MD, Rate~Phase, col="gold" , ylab=expression(bold(paste(Delta, "B [bp
mtext(side=4, line=1, expression(bold("MD")))
abline(0,0)
mtext(c("","***","","***","**"), side = 3,0, at=1:5)
mtext(c(paste("n=",c(nrow(BR.MD.ND.Ph1)),sep=""),paste("n=",c(nrow(BR.MD.ND.Ph2)),sep



### boxplot for Peda
par(mfrow=c(3,1))

boxplot(data=peda.CD, Rate~Phase, col="grey90", ylab=expression(bold(paste("PEDA [K",(
mtext(side=4, line=1, expression(bold("CD")))
abline(0,0)
mtext(c(paste("n=",c(nrow(peda.CD.ND.Ph1)),sep=""),paste("n=",c(nrow(peda.CD.ND.Ph2))
mtext("Validation of Palm EDA Channel", side = 3,3)



boxplot(data=peda.ED, Rate~Phase, col="palevioletred1" , ylab=expression(bold(paste("
mtext(side=4, line=1, expression(bold("ED")))
abline(0,0)
mtext(c(paste("n=",c(nrow(peda.ED.ND.Ph1)),sep=""),paste("n=",c(nrow(peda.ED.ND.Ph2))


boxplot(data=peda.MD, Rate~Phase, col="gold" , ylab=expression(bold(paste("PEDA [K",O
mtext(side=4, line=1, expression(bold("MD")))
abline(0,0)
mtext(c(paste("n=",c(nrow(peda.MD.ND.Ph1)),sep=""),paste("n=",c(nrow(peda.MD.ND.Ph2))
```

```
### Boxplot for PP
par(mfrow=c(3,1))

boxplot(data=pp.CD, Rate~Phase, col="grey90", ylab=expression(bold(paste("PP [
mtext(side=4, line=1, expression(bold("CD")))
abline(0,0)
mtext(c("","***","","***",""), side = 3,0, at=1:5)
mtext(c(paste("n=",c(nrow(pp.CD.ND.Ph1)),sep=""),paste("n=",c(nrow(pp.CD.ND.Ph
mtext("Validation of Perinasal Perspiration Channel", side = 3,3)


boxplot(data=pp.ED, Rate~Phase, col="palevioletred1" , ylab=expression(bold(pa
mtext(side=4, line=1, expression(bold("ED")))
abline(0,0)
mtext(c("","***","","***",""), side = 3,0, at=1:5)
mtext(c(paste("n=",c(nrow(pp.ED.ND.Ph1)),sep=""),paste("n=",c(nrow(pp.ED.ND.Ph


boxplot(data=pp.MD, Rate~Phase, col="gold" , ylab=expression(bold(paste("PP [K
mtext(side=4, line=1, expression(bold("MD")))
abline(0,0)
mtext(c("","***","","**",""), side = 3,0, at=1:5)
mtext(c(paste("n=",c(nrow(pp.MD.ND.Ph1)),sep=""),paste("n=",c(nrow(pp.MD.ND.Ph
```