

Theory of mind analysis

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Introduction

This document presents inferential statistical analysis of participants' application of theory of mind to virtual characters as reported in the paper:

Creating windows to the soul: How eye gaze behaviour can make virtual characters more believable, more socially present and have mental states attributed to them

The OSF form belonging to this paper can be found here: <https://osf.io/8u2kf>

Authored by Zilla Garama, Ding Ding, and Willem-Paul Brinkman.

For this measure, participants were asked to think aloud during the experiment. This was recorded. Two coders then scored all moments in which the participant either ascribed reasoning or thinking, or attributed feelings to the virtual characters in 10 second intervals. All scores were then summed up per virtual character and separated per phase. The first two columns called "ToM_1_vague_difference" and "ToM_2_noticed_gaze_following" were explorative and are not used in this analysis. The columns that were used in this analysis are:

- ToM_3_total_reasoning_phase_1: The total number of times the participant wondered about or assumed some kind of reasoning or thinking by the virtual character during phase 1.
- ToM_4_total_feeling_phase_1: The total number of times the participant attributed a feeling to the virtual character during phase 1.

- ToM_5_total_reasoning_phase_2: The total number of times the participant wondered about or assumed some kind of reasoning or thinking by the virtual character during phase 2.
- ToM_6_total_feeling_phase_2: The total number of times the participant attributed a feeling to the virtual character during phase 2.

Abbreviations: * virtual character (VC) * Control virtual character (CVC) * Gaze aware virtual character (GAVC)

Libraries used:

```
library(ggplot2)      # plotting & data
library(psych)        # reliability function
library(pastecs)      # plotting & data
library(lsr)          # effect size
```

Read in the Theory of Mind data:

```
ToM_data <- read.csv("ToM_data.csv", header = TRUE, stringsAsFactors = FALSE,
                    fileEncoding="UTF-8-BOM")

#Gaze behaviour data is needed for information about the roles of the virtual characters
GB_data <- read.csv("GB_data.csv", header = TRUE, stringsAsFactors = FALSE,
                  fileEncoding="UTF-8-BOM")
GB_data<-GB_data[-c(25:28),]
```

Data preparation

The coders filled this form in for both virtual characters separately. In the raw data this is represented by A and B for the physical position (left or right) of the virtual characters in the virtual environment during the experiment. However, the roles of the virtual characters (CVC or GAVC) have been randomized so A and B don't directly correspond to the roles of the virtual characters. Before further analysis can be done, information about the roles need to be added to a data table:

```
#calculate the roles per virtual character:
CVC_position = ifelse(GB_data$GB_1_CVC %in% c("UMA_2", "UMA_3S", "UMA_4", "UMA_5S"),
                     "A", "B")
GAVC_position = ifelse(CVC_position %in% c("A"), "B", "A")

#Put the roles in a table to get a clearer overview:
GB_roles <- data.frame(Participant_number = GB_data$Participant_number,
                      CVC = GB_data$GB_1_CVC, GAVC = GB_data$GB_2_GAVC,
                      CVC_role = CVC_position, GAVC_role = GAVC_position)

print(GB_roles)
```

##	Participant_number	CVC	GAVC	CVC_role	GAVC_role
## 1	180	UMA_4	UMA_5	A	B
## 2	122	UMA_5S	UMA_4S	A	B
## 3	198	UMA_4	UMA_5	A	B
## 4	182	UMA_5	UMA_4	B	A
## 5	132	UMA_4S	UMA_5S	B	A
## 6	107	UMA_2	UMA_3	A	B
## 7	184	UMA_3	UMA_2	B	A
## 8	137	UMA_4S	UMA_5S	B	A
## 9	103	UMA_3	UMA_2	B	A

## 10	136	UMA_3	UMA_2	B	A
## 11	128	UMA_4	UMA_5	A	B
## 12	185	UMA_3S	UMA_2S	A	B
## 13	163	UMA_2S	UMA_3S	B	A
## 14	112	UMA_3	UMA_2	B	A
## 15	149	UMA_5S	UMA_4S	A	B
## 16	173	UMA_3	UMA_2	B	A
## 17	195	UMA_2	UMA_3	A	B
## 18	115	UMA_4	UMA_5	A	B
## 19	169	UMA_4S	UMA_5S	B	A
## 20	120	UMA_5S	UMA_4S	A	B
## 21	146	UMA_5S	UMA_4S	A	B
## 22	178	UMA_2S	UMA_3S	B	A
## 23	119	UMA_3S	UMA_2S	A	B
## 24	157	UMA_2S	UMA_3S	B	A

Using the mapping of roles with A/B calculated in the believability questionnaire section we can create a new table for each of the avatar roles that contains only the answers given by the participants for those avatars. Thus the data table of the think aloud measurement for the CVC avatar:

Using the above mapping of roles with A/B we can separate the ToM data entries per role. Thus the data table of the ToM measurement for the CVC is:

```

ToM_CVC <- data.frame(ToM_3_total_reasoning_phase_1=rep(NA,24),
                      ToM_4_total_feeling_phase_1=rep(NA, 24),
                      ToM_5_total_reasoning_phase_2=rep(NA, 24),
                      ToM_6_total_feeling_phase_2=rep(NA, 24),
                      stringsAsFactors = FALSE)

for(i in 1:24){
  if(CVC_position[i] == "A"){
    ToM_CVC[i,] <- ToM_data[i, 4:7]
  }
  else{
    ToM_CVC[i,] <- ToM_data[i, 8:11]
  }
}

print(ToM_CVC)

```

##	ToM_3_total_reasoning_phase_1	ToM_4_total_feeling_phase_1
## 1	2	1
## 2	0	0
## 3	0	2
## 4	0	0
## 5	0	1
## 6	0	1
## 7	0	0
## 8	1	1
## 9	0	1
## 10	1	2
## 11	1	1
## 12	0	0
## 13	0	0
## 14	0	2
## 15	0	0

## 16	0	1
## 17	0	1
## 18	0	0
## 19	0	3
## 20	1	1
## 21	0	1
## 22	0	0
## 23	0	0
## 24	0	0
## ToM_5_total_reasoning_phase_2	ToM_6_total_feeling_phase_2	
## 1	1	1
## 2	0	0
## 3	0	0
## 4	0	0
## 5	0	0
## 6	0	0
## 7	0	0
## 8	1	0
## 9	0	0
## 10	1	0
## 11	0	0
## 12	1	1
## 13	0	0
## 14	1	0
## 15	0	0
## 16	0	0
## 17	0	0
## 18	0	1
## 19	1	0
## 20	0	0
## 21	0	0
## 22	0	0
## 23	0	0
## 24	0	0

And for the GAVC:

```

ToM_GAVC <- data.frame(ToM_3_total_reasoning_phase_1=rep(NA,24),
                      ToM_4_total_feeling_phase_1=rep(NA, 24),
                      ToM_5_total_reasoning_phase_2=rep(NA, 24),
                      ToM_6_total_feeling_phase_2=rep(NA, 24),
                      stringsAsFactors = FALSE)

for(i in 1:24){
  if(GAVC_position[i] == "A"){
    ToM_GAVC[i,] <- ToM_data[i, 4:7]
  }
  else{
    ToM_GAVC[i,] <- ToM_data[i, 8:11]
  }
}

print(ToM_GAVC)

```

```
## ToM_3_total_reasoning_phase_1 ToM_4_total_feeling_phase_1
```

## 1	2	1
## 2	0	0
## 3	0	0
## 4	0	0
## 5	0	1
## 6	0	1
## 7	0	0
## 8	0	0
## 9	0	1
## 10	1	1
## 11	0	0
## 12	0	0
## 13	0	0
## 14	0	1
## 15	1	0
## 16	0	2
## 17	1	2
## 18	0	0
## 19	0	1
## 20	1	1
## 21	0	1
## 22	0	0
## 23	0	1
## 24	0	0
## ToM_5_total_reasoning_phase_2	ToM_6_total_feeling_phase_2	
## 1	1	1
## 2	0	0
## 3	0	0
## 4	0	0
## 5	0	0
## 6	0	0
## 7	0	0
## 8	0	0
## 9	0	0
## 10	1	0
## 11	1	0
## 12	1	0
## 13	0	0
## 14	1	0
## 15	0	0
## 16	0	0
## 17	0	0
## 18	0	1
## 19	2	0
## 20	0	0
## 21	0	0
## 22	0	0
## 23	0	0
## 24	0	0

Assumption checking: normal distribution

Phase 1: total reasoning

The analysis method depends on the normality of the data distribution. This is usually done visually:

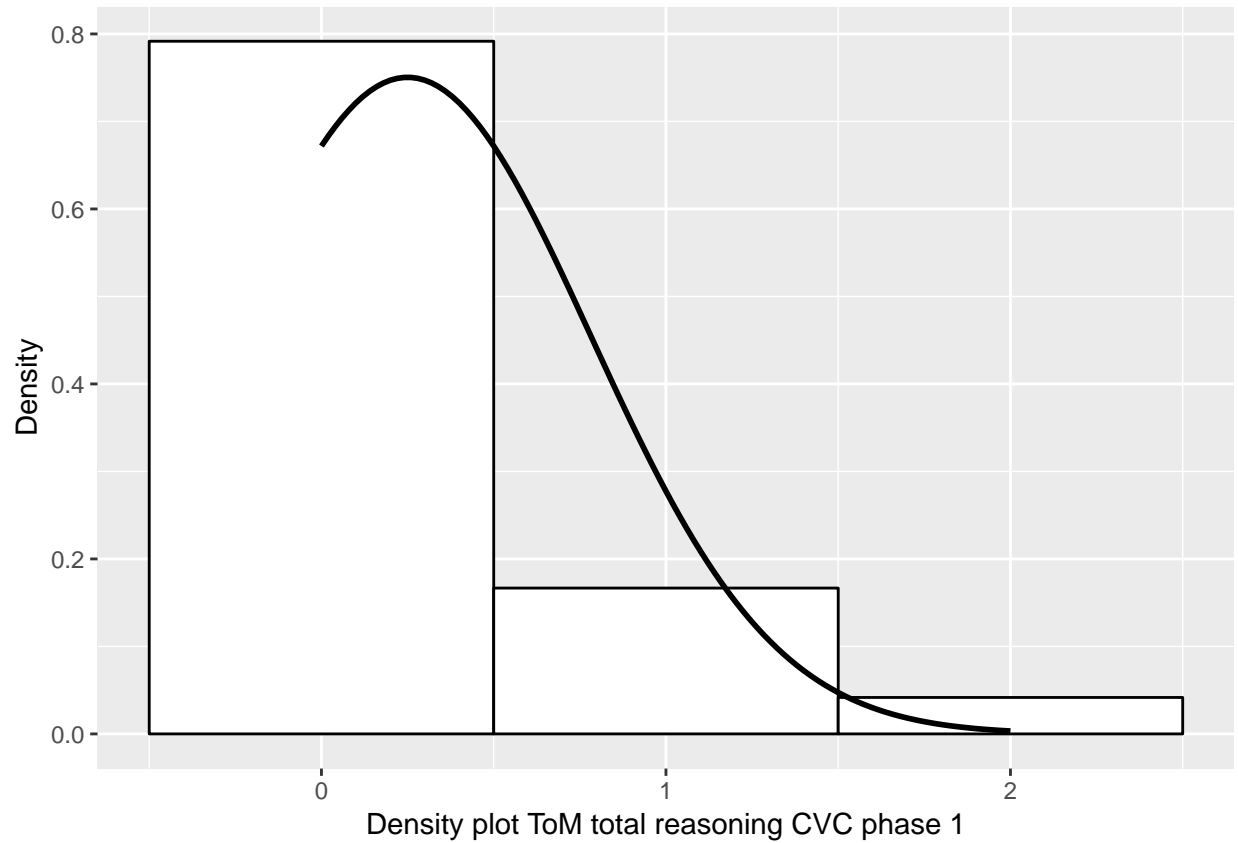
```
stem(ToM_CVC$ToM_3_total_reasoning_phase_1)
```

```
##
##  The decimal point is at the |
##
##  0 | 00000000000000000000
##  0 |
##  1 | 0000
##  1 |
##  2 | 0
```

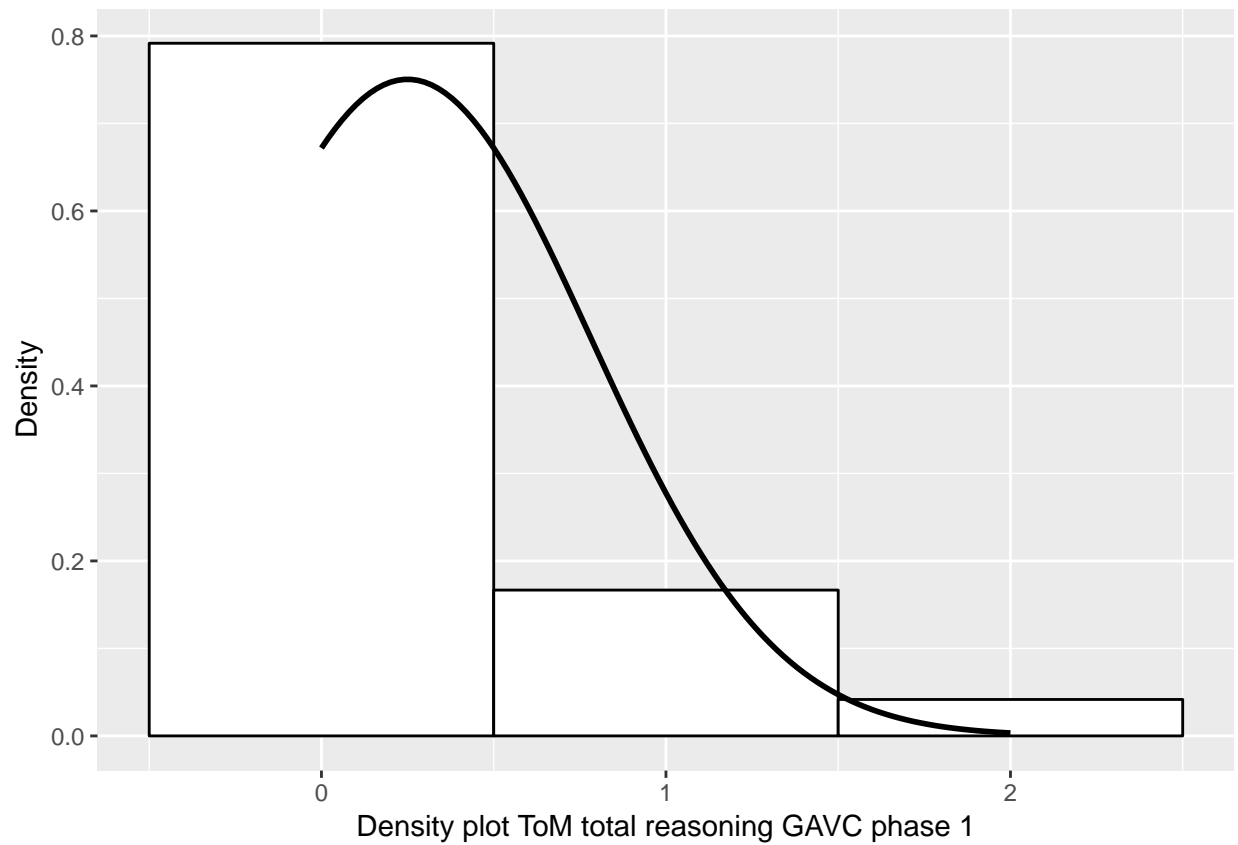
```
stem(ToM_GAVC$ToM_3_total_reasoning_phase_1)
```

```
##
##  The decimal point is at the |
##
##  0 | 00000000000000000000
##  0 |
##  1 | 0000
##  1 |
##  2 | 0
```

```
ggplot(ToM_CVC,
  aes(ToM_3_total_reasoning_phase_1)) + geom_histogram(aes(y=..density..),
  binwidth = 1, colour="black",
  fill="white") + labs(x="Density plot ToM total reasoning CVC phase 1",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_CVC$ToM_3_total_reasoning_phase_1, na.rm=TRUE),
  sd=sd(ToM_CVC$ToM_3_total_reasoning_phase_1, na.rm=TRUE)), colour="black", size=1)
```

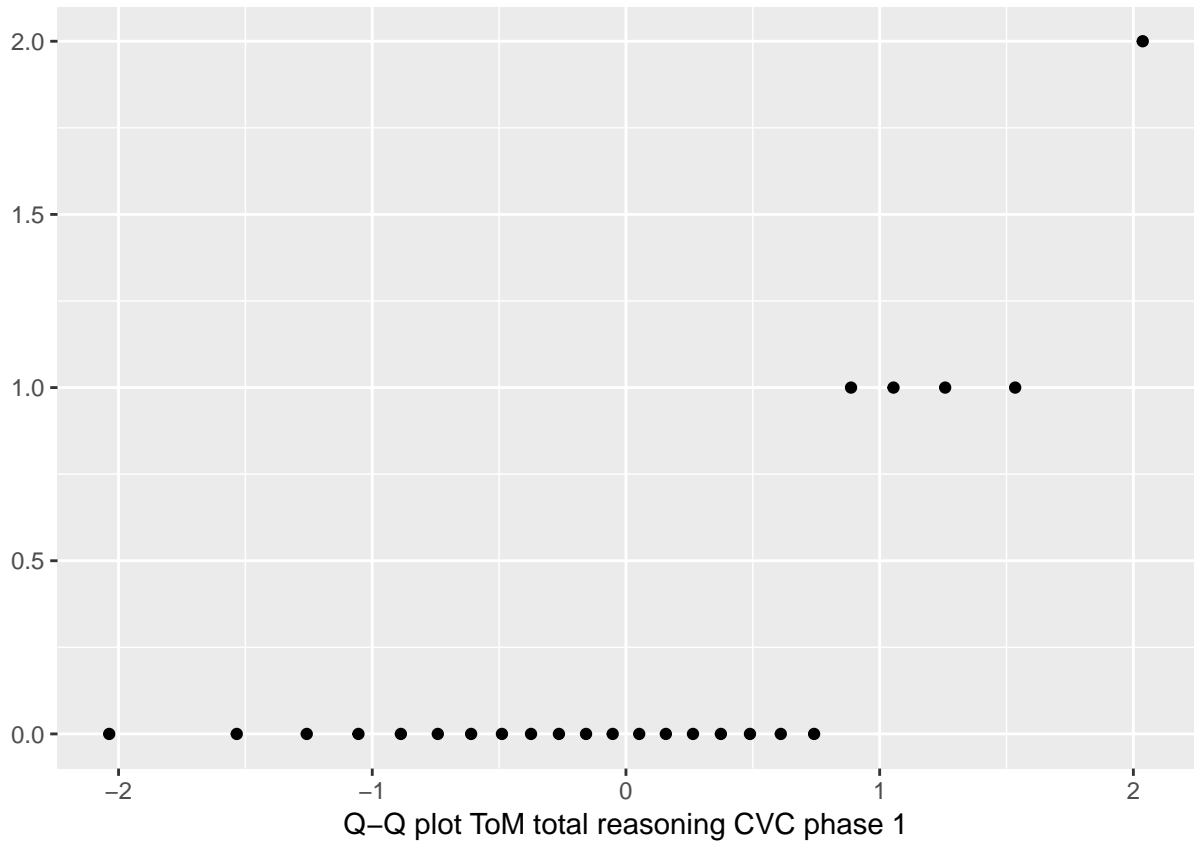


```
ggplot(ToM_GAVC,
  aes(ToM_3_total_reasoning_phase_1)) + geom_histogram(aes(y=..density..),
    binwidth = 1, colour="black",
    fill="white") + labs(x="Density plot ToM total reasoning GAVC phase 1",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_GAVC$ToM_3_total_reasoning_phase_1, na.rm=TRUE),
  sd=sd(ToM_GAVC$ToM_3_total_reasoning_phase_1, na.rm=TRUE)), colour="black", size=1)
```



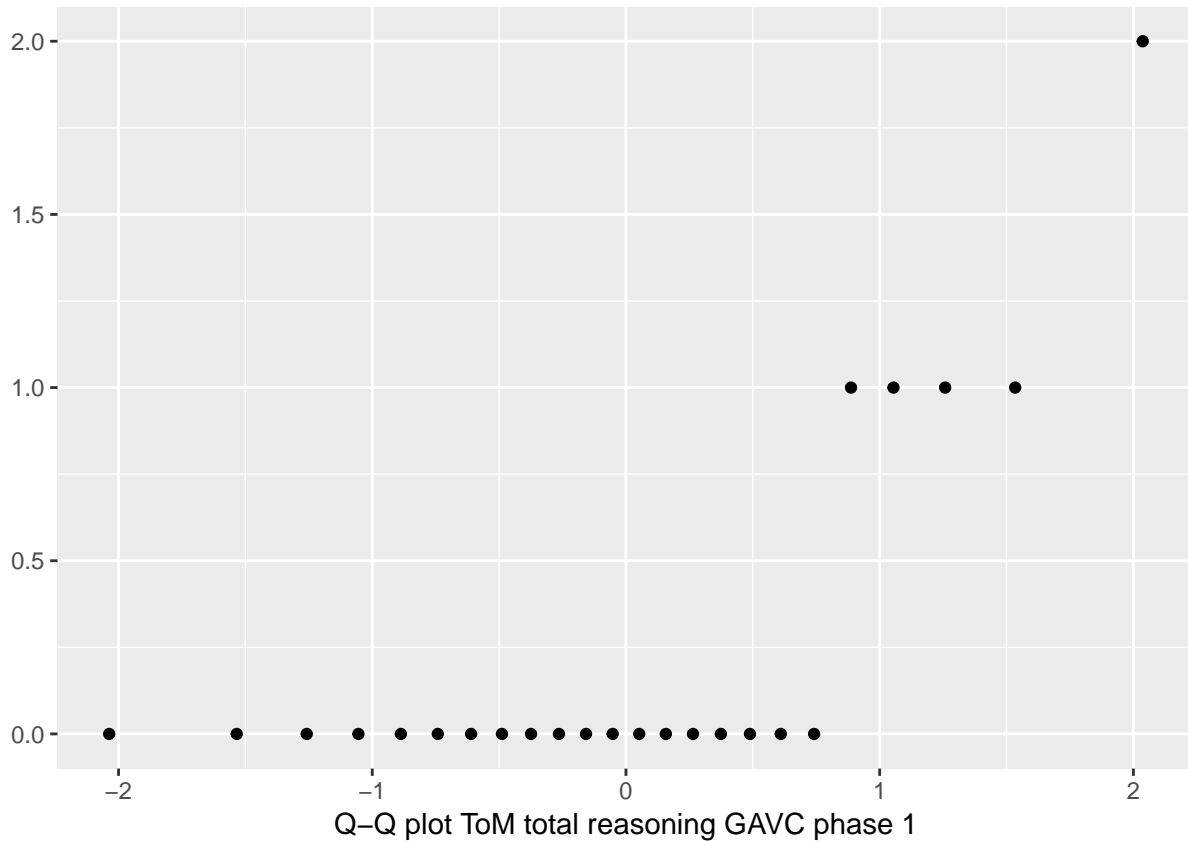
```
qplot(sample=ToM_CVC$ToM_3_total_reasoning_phase_1,  
      stat="qq") + labs(x="Q-Q plot ToM total reasoning CVC phase 1")
```

```
## Warning: `stat` is deprecated
```

```
qplot(sample=ToM_GAVC$ToM_3_total_reasoning_phase_1,
      stat="qq") + labs(x="Q-Q plot ToM total reasoning GAVC phase 1")
```

```
## Warning: `stat` is deprecated
```



By visually inspecting the histogram and qqplot it seems that the data is not normally distributed. However, the sample size is rather small ($n < 30$) so it is better to quantify the shape of the distribution:

```
round(stat.desc(data.frame(ToM_CVC$ToM_3_total_reasoning_phase_1,
                           ToM_GAVC$ToM_3_total_reasoning_phase_1),
      basic = FALSE, norm = TRUE), digits = 3)
```

```
##           ToM_CVC.ToM_3_total_reasoning_phase_1
## median                                0.000
## mean                                  0.250
## SE.mean                              0.109
## CI.mean.0.95                         0.224
## var                                  0.283
## std.dev                              0.532
## coef.var                             2.126
## skewness                             1.872
## skew.2SE                             1.982
## kurtosis                             2.592
## kurt.2SE                             1.412
## normtest.W                           0.531
## normtest.p                           0.000
##           ToM_GAVC.ToM_3_total_reasoning_phase_1
## median                                0.000
## mean                                  0.250
## SE.mean                              0.109
## CI.mean.0.95                         0.224
## var                                  0.283
```

```
## std.dev                0.532
## coef.var               2.126
## skewness               1.872
## skew.2SE              1.982
## kurtosis               2.592
## kurt.2SE              1.412
## normtest.W             0.531
## normtest.p             0.000
```

The skew.2SE and kurt.2SE are higher than 0.98 (ignoring the plus or minus sign), which means the skew and kurtosis are significant (at $p < 0.05$). The p-values (indicated by normtest.p) obtained by the Shapiro-Wilk test are not >0.05 and thus both the CVC and GAVC are not normally distributed.

Phase 1: total feeling

The analysis method depends on the normality of the data distribution. This is usually done visually:

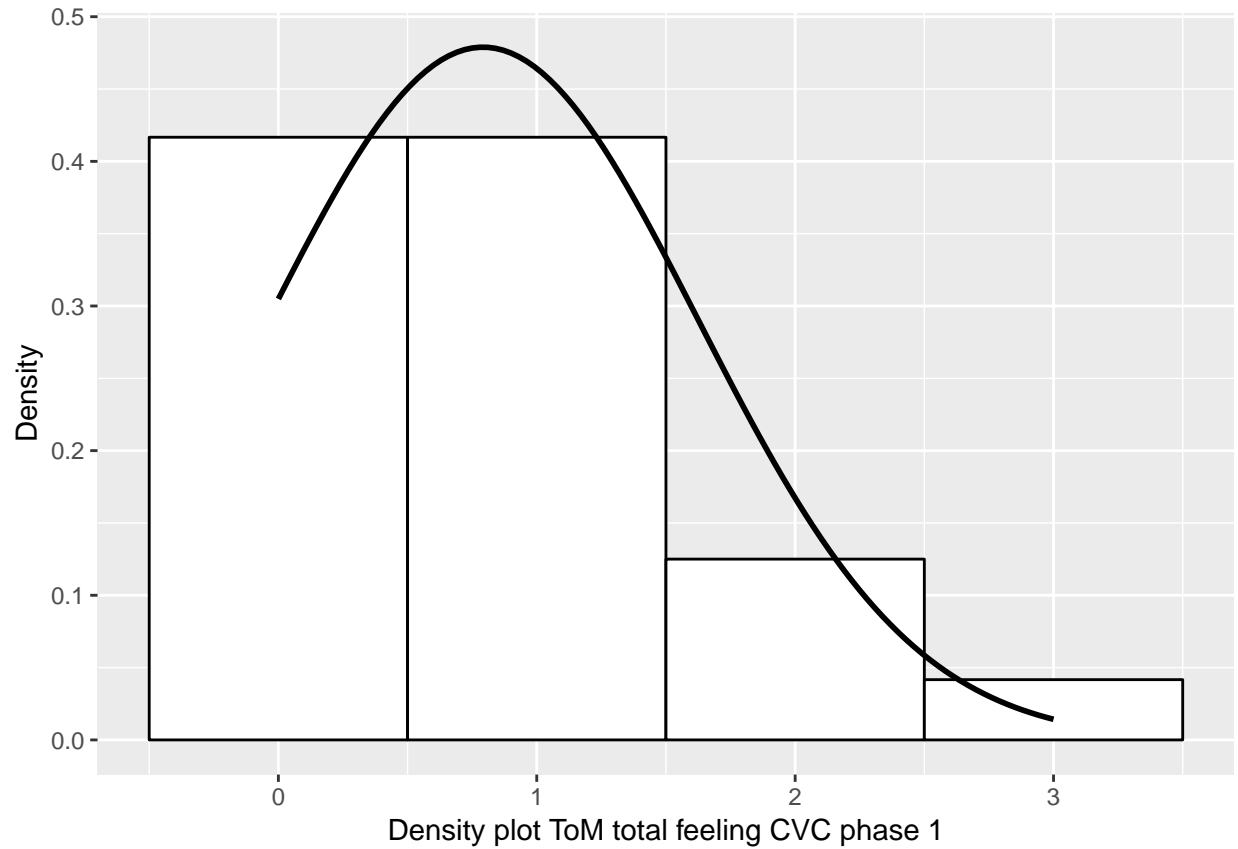
```
stem(ToM_CVC$ToM_4_total_feeling_phase_1)
```

```
##
##   The decimal point is at the |
##
##  0 | 0000000000
##  1 | 0000000000
##  2 | 000
##  3 | 0
```

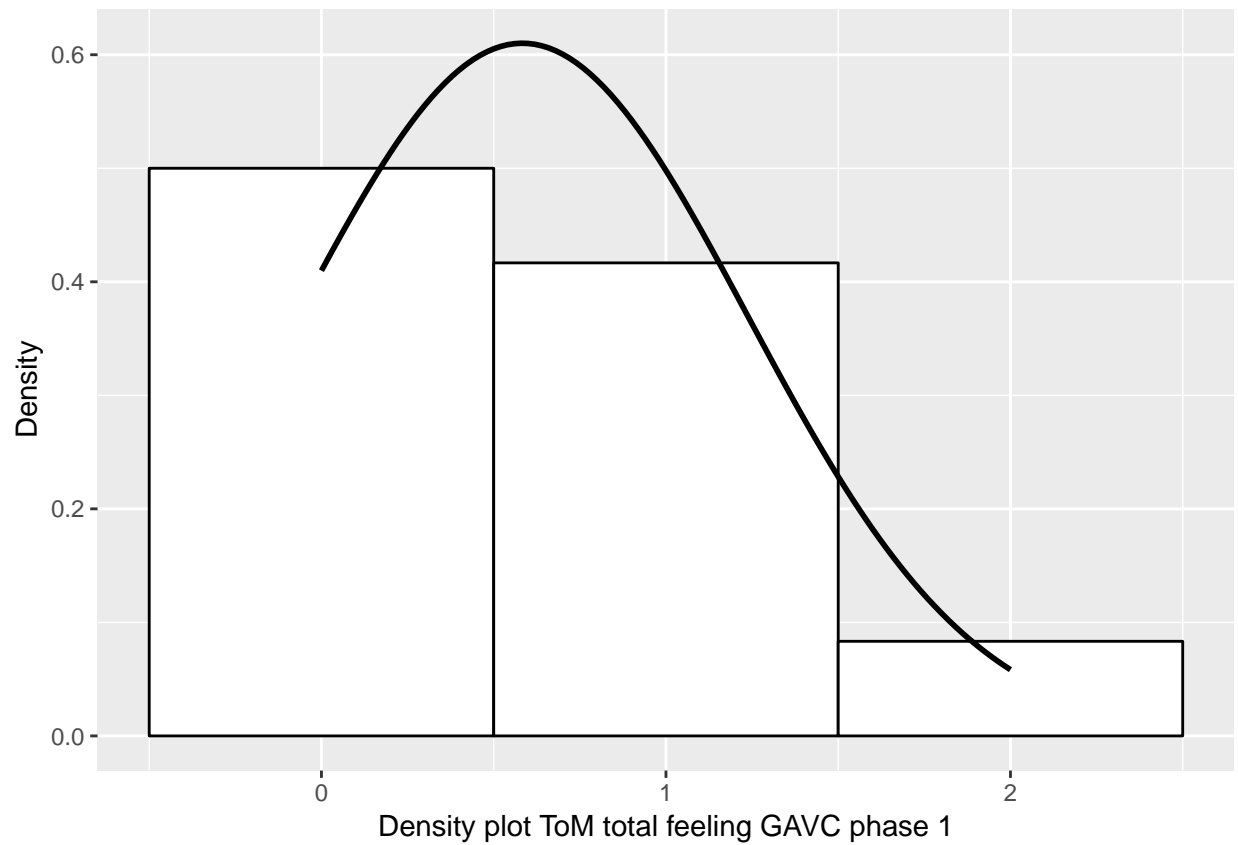
```
stem(ToM_GAVC$ToM_4_total_feeling_phase_1)
```

```
##
##   The decimal point is at the |
##
##  0 | 000000000000
##  0 |
##  1 | 0000000000
##  1 |
##  2 | 00
```

```
ggplot(ToM_CVC,
  aes(ToM_4_total_feeling_phase_1)) + geom_histogram(aes(y=..density..),
  binwidth = 1, colour="black",
  fill="white") + labs(x="Density plot ToM total feeling CVC phase 1",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_CVC$ToM_4_total_feeling_phase_1, na.rm=TRUE),
  sd=sd(ToM_CVC$ToM_4_total_feeling_phase_1, na.rm=TRUE)), colour="black", size=1)
```

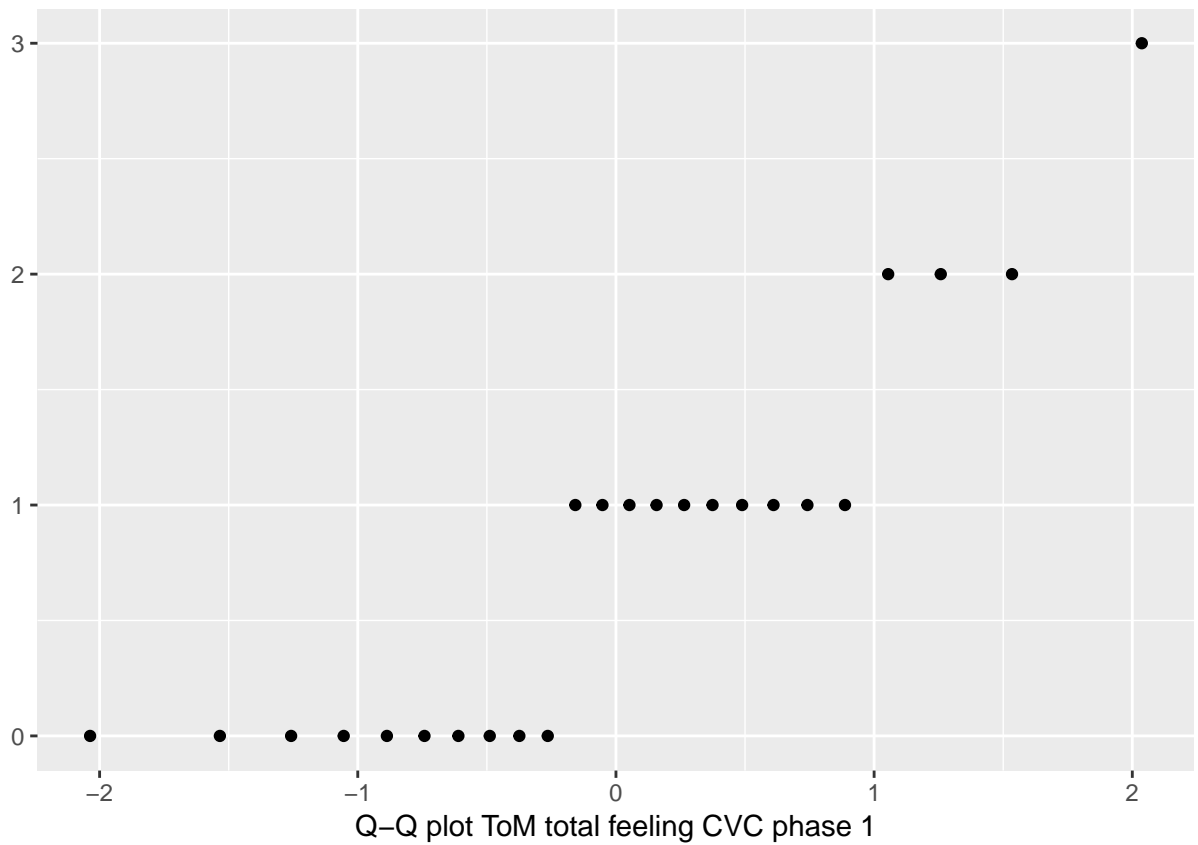


```
ggplot(ToM_GAVC,
  aes(ToM_4_total_feeling_phase_1)) + geom_histogram(aes(y=..density..),
  binwidth = 1, colour="black",
  fill="white") + labs(x="Density plot ToM total feeling GAVC phase 1",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_GAVC$ToM_4_total_feeling_phase_1, na.rm=TRUE),
  sd=sd(ToM_GAVC$ToM_4_total_feeling_phase_1, na.rm=TRUE)), colour="black", size=1)
```



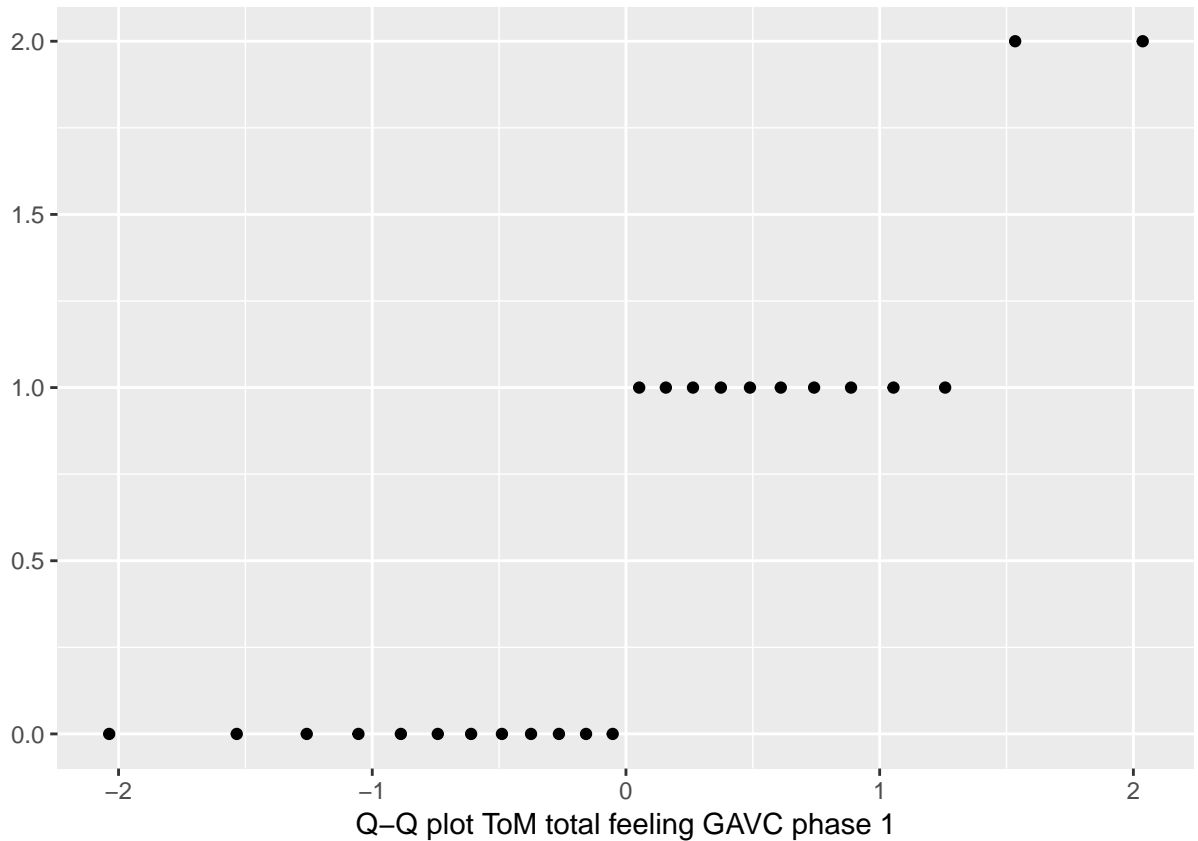
```
qplot(sample=ToM_CVC$ToM_4_total_feeling_phase_1,  
      stat="qq") + labs(x="Q-Q plot ToM total feeling CVC phase 1")
```

```
## Warning: `stat` is deprecated
```



```
qplot(sample=ToM_GAVC$ToM_4_total_feeling_phase_1,
      stat="qq") + labs(x="Q-Q plot ToM total feeling GAVC phase 1")
```

```
## Warning: `stat` is deprecated
```



By visually inspecting the histogram and qqplot it seems that the data is not normally distributed. However, the sample size is rather small ($n < 30$) so it is better to quantify the shape of the distribution:

```
round(stat.desc(data.frame(ToM_CVC$ToM_4_total_feeling_phase_1,
                           ToM_GAVC$ToM_4_total_feeling_phase_1),
      basic = FALSE, norm = TRUE), digits = 3)
```

```
##          ToM_CVC.ToM_4_total_feeling_phase_1
## median                                1.000
## mean                                 0.792
## SE.mean                             0.170
## CI.mean.0.95                        0.352
## var                                 0.694
## std.dev                             0.833
## coef.var                             1.052
## skewness                             0.807
## skew.2SE                             0.854
## kurtosis                             -0.046
## kurt.2SE                             -0.025
## normtest.W                           0.809
## normtest.p                           0.000
##          ToM_GAVC.ToM_4_total_feeling_phase_1
## median                                0.500
## mean                                 0.583
## SE.mean                             0.133
## CI.mean.0.95                        0.276
## var                                 0.428
```

```
## std.dev                0.654
## coef.var               1.121
## skewness               0.600
## skew.2SE              0.636
## kurtosis              -0.778
## kurt.2SE              -0.424
## normtest.W             0.752
## normtest.p             0.000
```

The skew.2SE and kurt.2SE are smaller than 0.98 (ignoring the plus or minus sign), which means the skew and kurtosis are not significant (at $p < 0.05$). The p-values (indicated by normtest.p) obtained by the Shapiro-Wilk test are not >0.05 and thus both the CVC and GAVC are not normally distributed.

Phase 2: total reasoning

The analysis method depends on the normality of the data distribution. This is usually done visually:

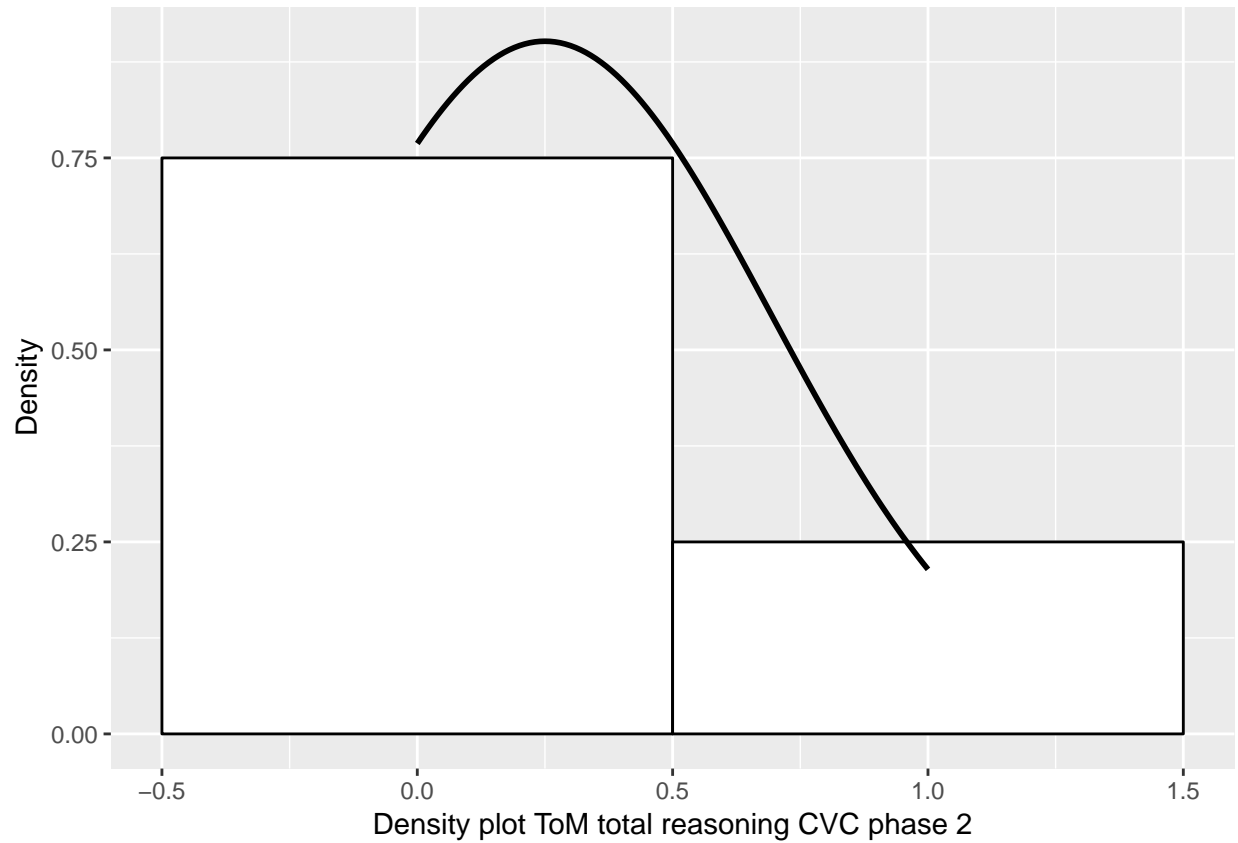
```
stem(ToM_CVC$ToM_5_total_reasoning_phase_2)
```

```
##
## The decimal point is at the |
##
## 0 | 0000000000000000000
## 0 |
## 1 | 000000
```

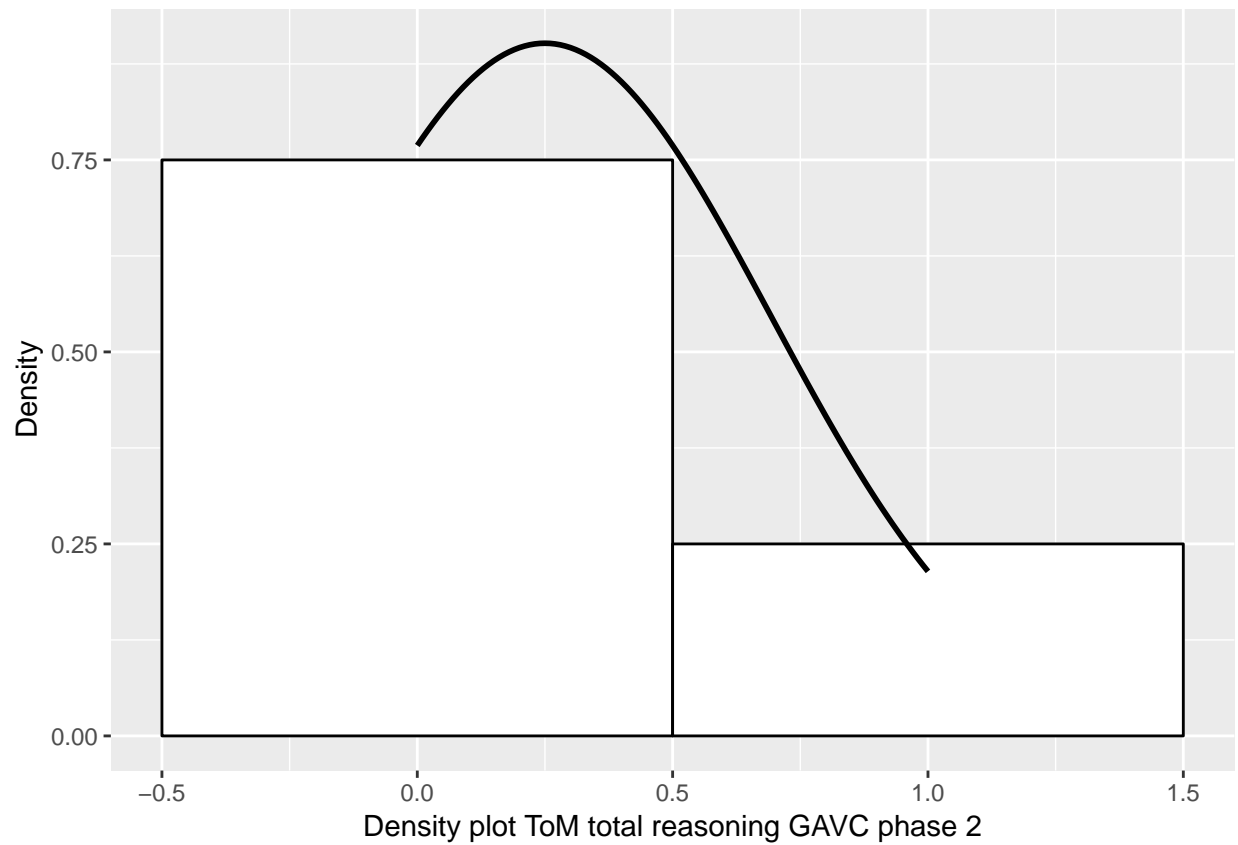
```
stem(ToM_GAVC$ToM_5_total_reasoning_phase_2)
```

```
##
## The decimal point is at the |
##
## 0 | 0000000000000000000
## 0 |
## 1 | 00000
## 1 |
## 2 | 0
```

```
ggplot(ToM_CVC,
  aes(ToM_5_total_reasoning_phase_2)) + geom_histogram(aes(y=..density..),
  binwidth = 1, colour="black",
  fill="white") + labs(x="Density plot ToM total reasoning CVC phase 2",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_CVC$ToM_5_total_reasoning_phase_2, na.rm=TRUE),
  sd=sd(ToM_CVC$ToM_5_total_reasoning_phase_2, na.rm=TRUE)), colour="black", size=1)
```

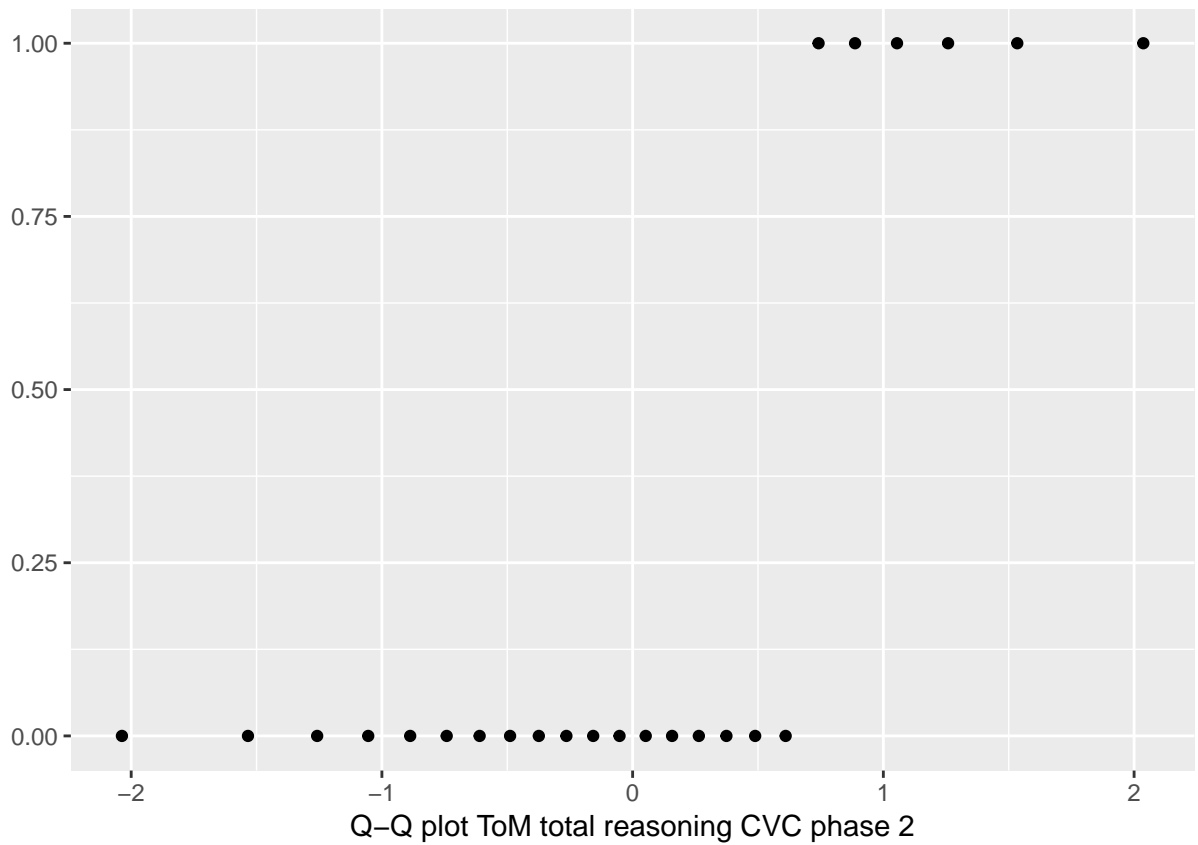



```
ggplot(ToM_CVC,
  aes(ToM_5_total_reasoning_phase_2)) + geom_histogram(aes(y=..density..),
    binwidth = 1, colour="black",
    fill="white") + labs(x="Density plot ToM total reasoning GAVC phase 2",
    y="Density") + stat_function(fun=dnorm,
    args=list(mean=mean(ToM_CVC$ToM_5_total_reasoning_phase_2, na.rm=TRUE),
    sd=sd(ToM_CVC$ToM_5_total_reasoning_phase_2, na.rm=TRUE)), colour="black", size=1)
```



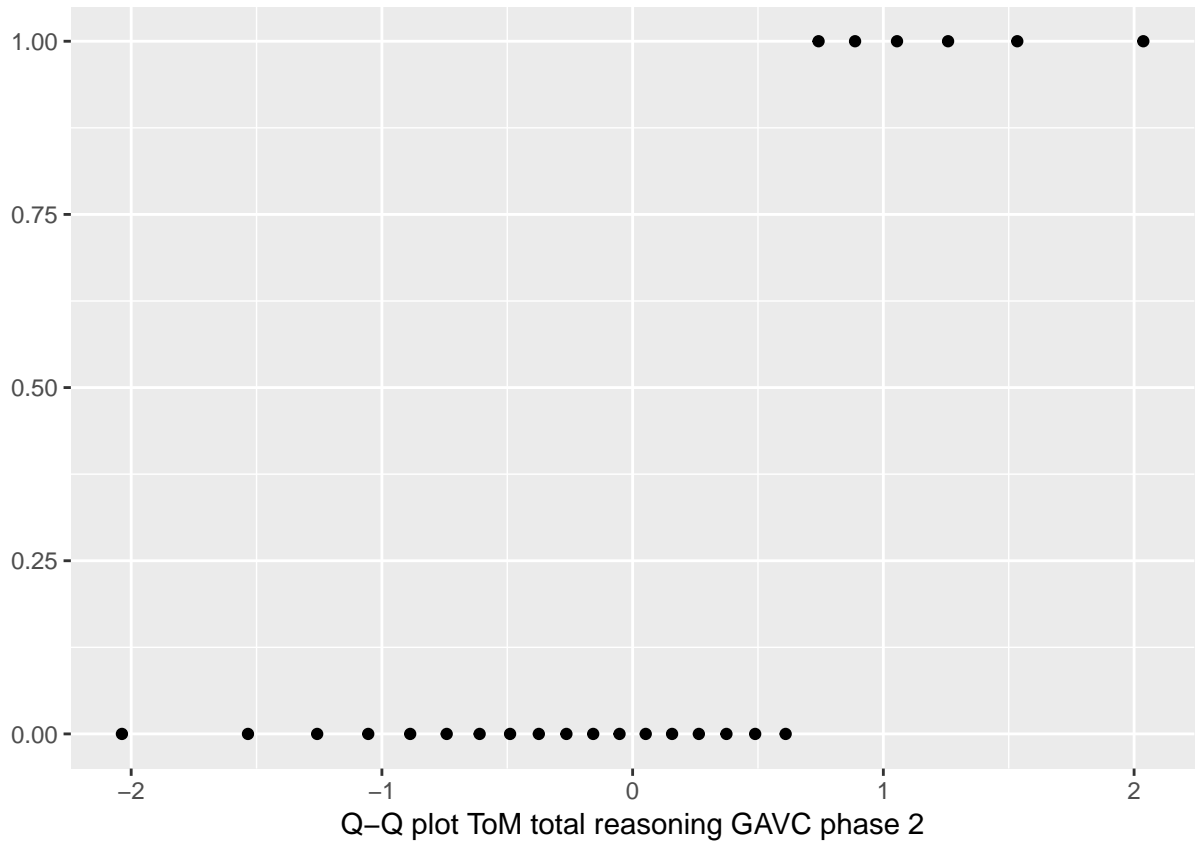
```
qplot(sample=ToM_CVC$ToM_5_total_reasoning_phase_2,
      stat="qq") + labs(x="Q-Q plot ToM total reasoning CVC phase 2")
```

Warning: `stat` is deprecated



```
qplot(sample=ToM_CVC$ToM_5_total_reasoning_phase_2,
      stat="qq") + labs(x="Q-Q plot ToM total reasoning GAVC phase 2")
```

```
## Warning: `stat` is deprecated
```



By visually inspecting the histogram and qqplot it seems that the data is not normally distributed. However, the sample size is rather small ($n < 30$) so it is better to quantify the shape of the distribution:

```
round(stat.desc(data.frame(ToM_CVC$ToM_5_total_reasoning_phase_2,
                          ToM_GAVC$ToM_5_total_reasoning_phase_2),
      basic = FALSE, norm = TRUE), digits = 3)
```

```
##          ToM_CVC.ToM_5_total_reasoning_phase_2
## median                                0.000
## mean                                  0.250
## SE.mean                              0.090
## CI.mean.0.95                         0.187
## var                                  0.196
## std.dev                              0.442
## coef.var                             1.769
## skewness                             1.083
## skew.2SE                             1.147
## kurtosis                             -0.857
## kurt.2SE                             -0.467
## normtest.W                           0.542
## normtest.p                           0.000
##          ToM_GAVC.ToM_5_total_reasoning_phase_2
## median                                0.000
## mean                                  0.292
## SE.mean                              0.112
## CI.mean.0.95                         0.232
## var                                  0.303
```

```
## std.dev                0.550
## coef.var               1.886
## skewness               1.581
## skew.2SE              1.674
## kurtosis               1.510
## kurt.2SE               0.822
## normtest.W             0.580
## normtest.p             0.000
```

The skew.2SE is higher than 0.98 (ignoring the plus or minus sign), which means that the skew is significant (at $p < 0.05$). The kurt.2SE is smaller than 0.98 (ignoring the plus or minus sign), which means that the skew is not significant (at $p < 0.05$). The p-value (indicated by normtest.p) obtained by the Shapiro-Wilk test for the CVC is >0.05 and thus the CVC is normally distributed. However, the p-value (indicated by normtest.p) obtained by the Shapiro-Wilk test for the GAVC is not >0.05 and thus the GAVC is not normally distributed.

Phase 2: total feeling

The analysis method depends on the normality of the data distribution. This is usually done visually:

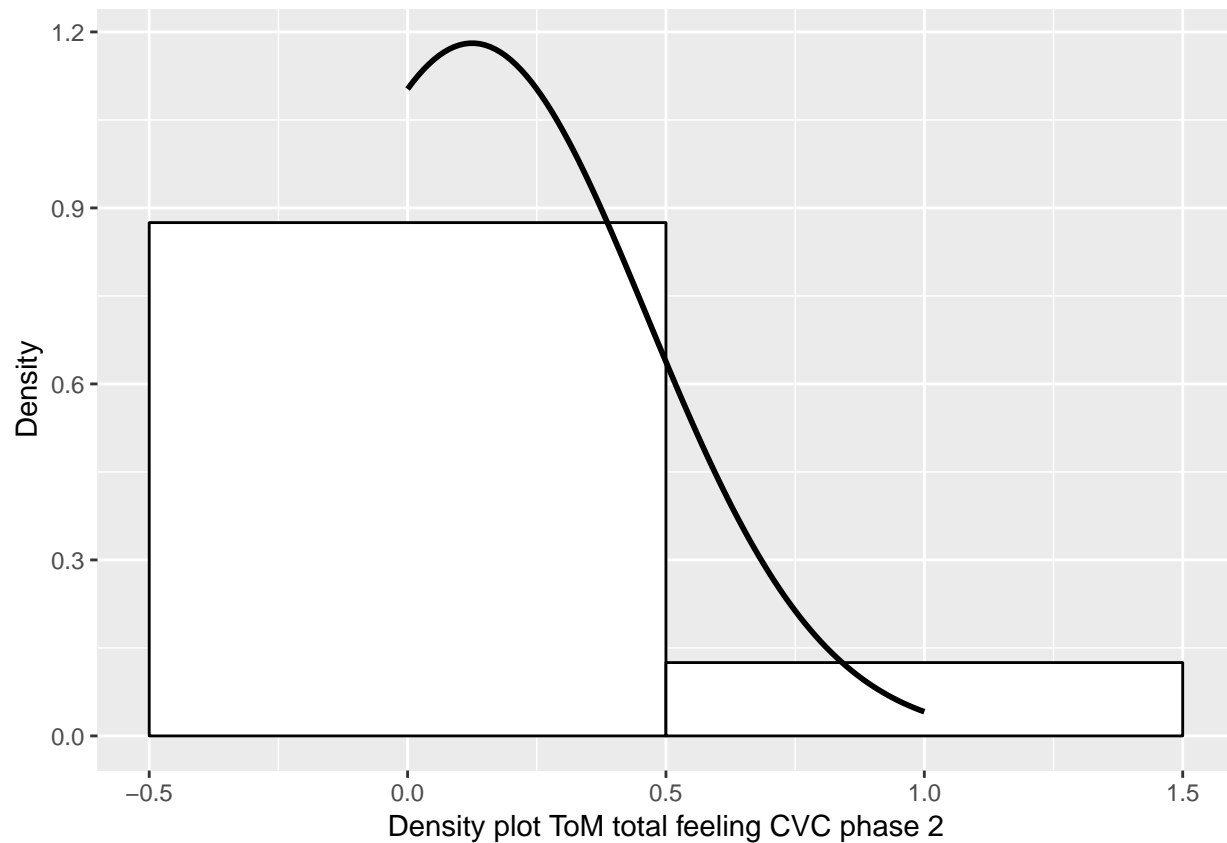
```
stem(ToM_CVC$ToM_6_total_feeling_phase_2)
```

```
##
##   The decimal point is at the |
##
##  0 | 0000000000000000000000
##  0 |
##  1 | 000
```

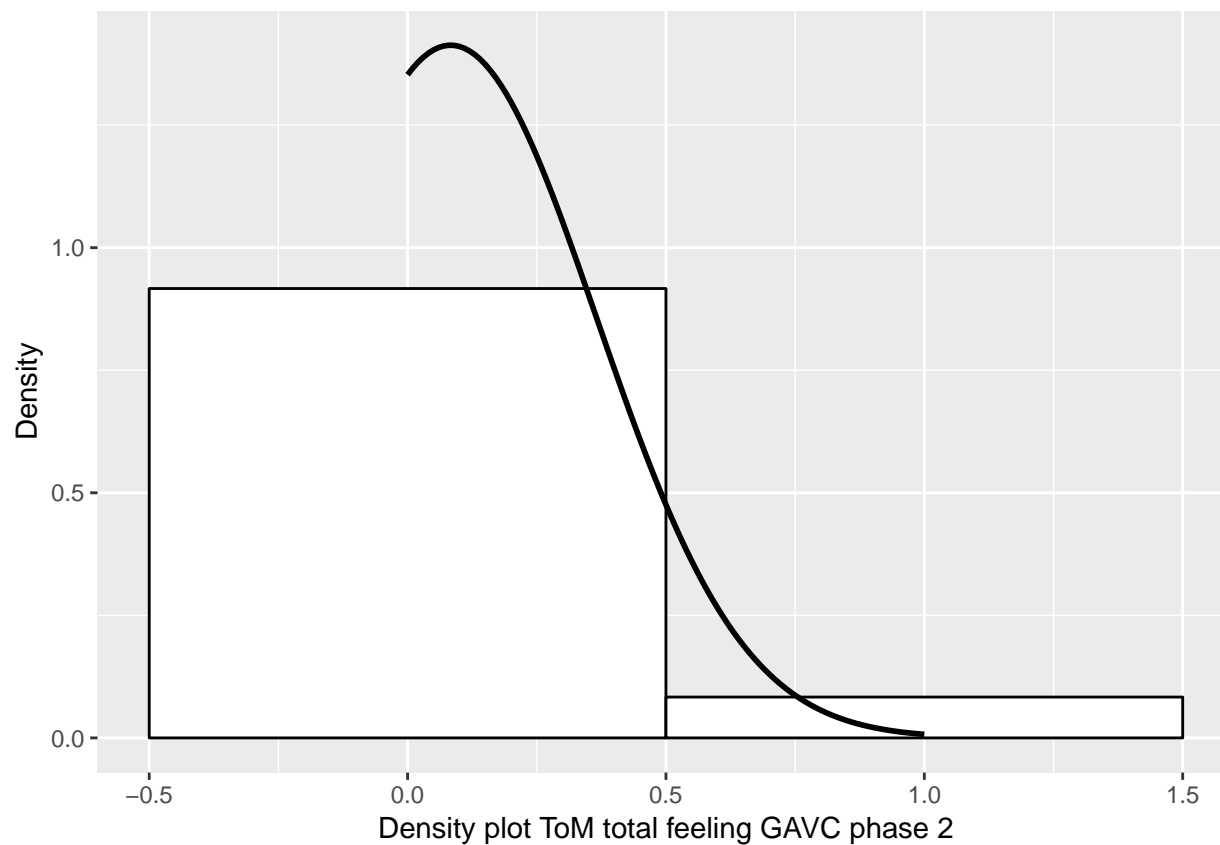
```
stem(ToM_GAVC$ToM_6_total_feeling_phase_2)
```

```
##
##   The decimal point is at the |
##
##  0 | 0000000000000000000000
##  0 |
##  1 | 00
```

```
ggplot(ToM_CVC,
  aes(ToM_6_total_feeling_phase_2)) + geom_histogram(aes(y=..density..),
  binwidth = 1, colour="black",
  fill="white") + labs(x="Density plot ToM total feeling CVC phase 2",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_CVC$ToM_6_total_feeling_phase_2, na.rm=TRUE),
  sd=sd(ToM_CVC$ToM_6_total_feeling_phase_2, na.rm=TRUE)), colour="black", size=1)
```

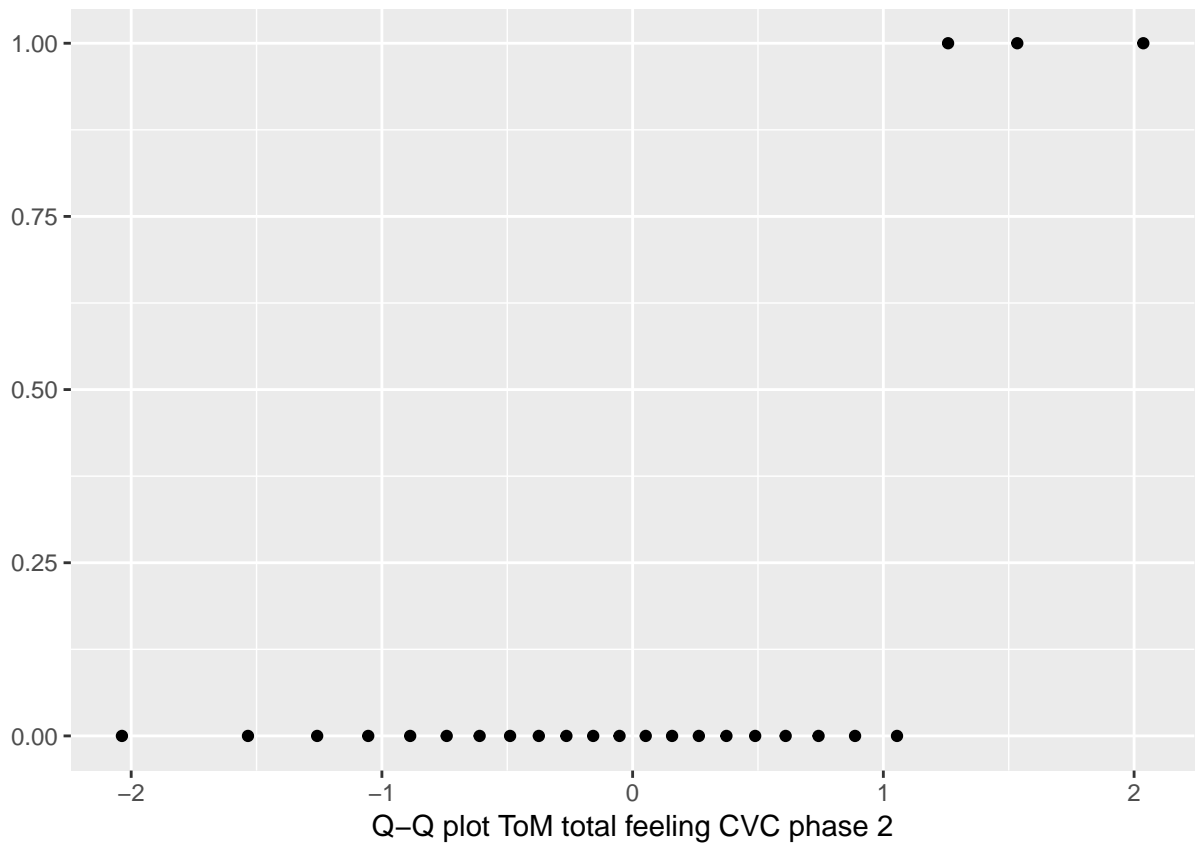


```
ggplot(ToM_GAVC,
  aes(ToM_6_total_feeling_phase_2)) + geom_histogram(aes(y=..density..),
  binwidth = 1, colour="black",
  fill="white") + labs(x="Density plot ToM total feeling GAVC phase 2",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(ToM_GAVC$ToM_6_total_feeling_phase_2, na.rm=TRUE),
  sd=sd(ToM_GAVC$ToM_6_total_feeling_phase_2, na.rm=TRUE)), colour="black", size=1)
```



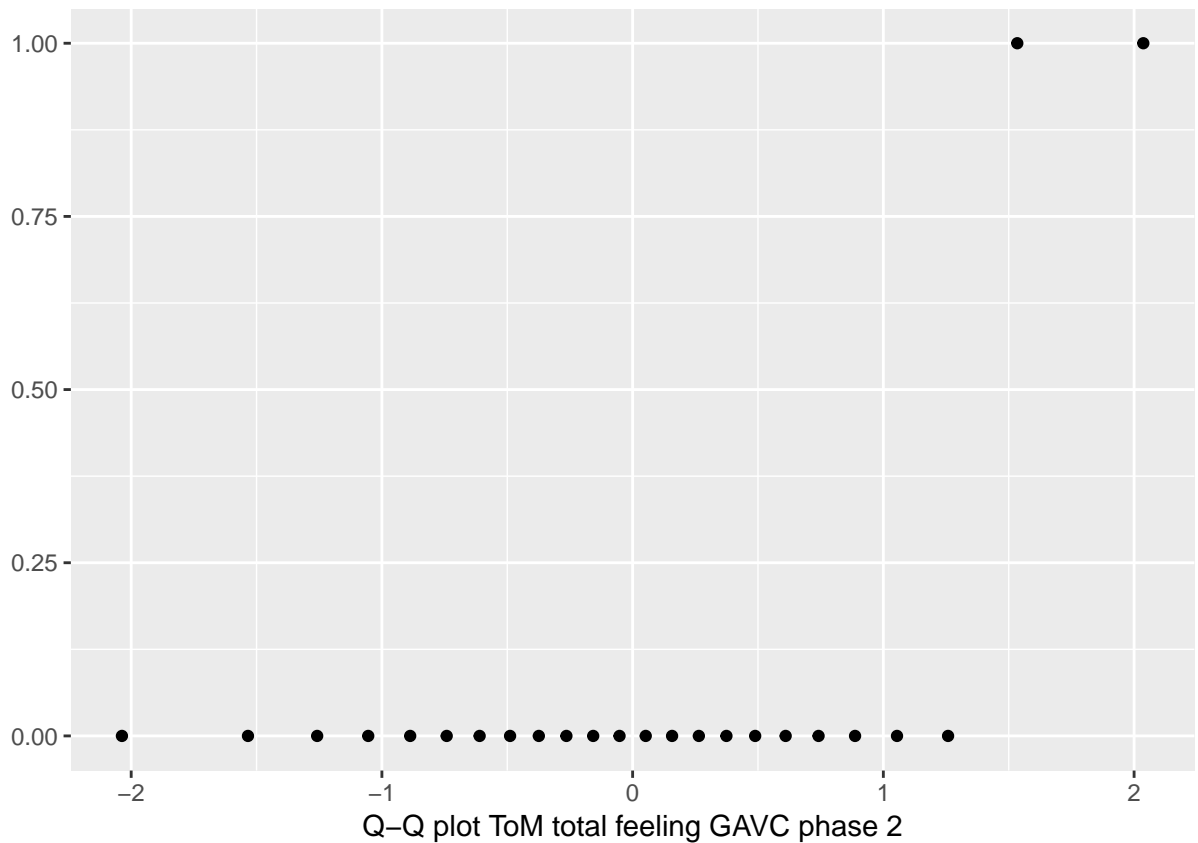
```
qplot(sample=ToM_CVC$ToM_6_total_feeling_phase_2,  
      stat="qq") + labs(x="Q-Q plot ToM total feeling CVC phase 2")
```

```
## Warning: `stat` is deprecated
```



```
qplot(sample=ToM_GAVC$ToM_6_total_feeling_phase_2,
      stat="qq") + labs(x="Q-Q plot ToM total feeling GAVC phase 2")
```

```
## Warning: `stat` is deprecated
```

By visually inspecting the histogram and qqplot it seems that the data is not normally distributed. However, the sample size is rather small ($n < 30$) so it is better to quantify the shape of the distribution:

```
round(stat.desc(data.frame(ToM_CVC$ToM_6_total_feeling_phase_2,
                           ToM_GAVC$ToM_6_total_feeling_phase_2),
      basic = FALSE, norm = TRUE), digits = 3)
```

```
##          ToM_CVC.ToM_6_total_feeling_phase_2
## median                                0.000
## mean                                  0.125
## SE.mean                              0.069
## CI.mean.0.95                         0.143
## var                                  0.114
## std.dev                              0.338
## coef.var                             2.703
## skewness                             2.128
## skew.2SE                             2.253
## kurtosis                             2.642
## kurt.2SE                             1.439
## normtest.W                           0.393
## normtest.p                           0.000
##          ToM_GAVC.ToM_6_total_feeling_phase_2
## median                                0.000
## mean                                  0.083
## SE.mean                              0.058
## CI.mean.0.95                         0.119
## var                                  0.080
```

```
## std.dev                0.282
## coef.var               3.388
## skewness               2.829
## skew.2SE              2.995
## kurtosis               6.268
## kurt.2SE              3.415
## normtest.W             0.316
## normtest.p             0.000
```

The skew.2SE and kurt.2SE are higher than 0.98 (ignoring the plus or minus sign), which means the skew and kurtosis are significant (at $p < 0.05$). The p-values (indicated by normtest.p) obtained by the Shapiro-Wilk test are not >0.05 and thus both the CVC and GAVC are not normally distributed.

Paired difference test

Phase 1: total reasoning

The results were analysed using either a parametric or non-parametric paired difference test depending on the normality of the distribution. In this case the GAVC data is not normally distributed and thus a Wilcoxon signed-rank test was used:

```
wilcox_result_total_reasoning_phase_1 <- wilcox.test(ToM_CVC$ToM_3_total_reasoning_phase_1, ToM_GAVC$ToM_3_total_reasoning_phase_1,
  paired = TRUE, exact = TRUE, correct = FALSE)
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_3_total_reasoning_phase_1,
## ToM_GAVC$ToM_3_total_reasoning_phase_1, : cannot compute exact p-value with
## ties
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_3_total_reasoning_phase_1,
## ToM_GAVC$ToM_3_total_reasoning_phase_1, : cannot compute exact p-value with
## zeroes
```

```
wilcox_result_total_reasoning_phase_1
```

```
##
## Wilcoxon signed rank test
##
## data: ToM_CVC$ToM_3_total_reasoning_phase_1 and ToM_GAVC$ToM_3_total_reasoning_phase_1
## V = 5, p-value = 1
## alternative hypothesis: true location shift is not equal to 0
```

The p-value is 1 which is higher than 0.05, so we can't reject the null hypothesis.

```
Zstat_total_reasoning_phase_1 <- qnorm(wilcox_result_total_reasoning_phase_1$p.value/2)
Zstat_total_reasoning_phase_1
```

```
## [1] 0
```

The Z-value is 0, which will be used to calculate the effect size.

Phase 1: total feeling

The results were analysed using either a parametric or non-parametric paired difference test depending on the normality of the distribution. In this case the GAVC data is not normally distributed and thus a Wilcoxon signed-rank test was used:

```
wilcox_result_total_feeling_phase_1 <- wilcox.test(ToM_CVC$ToM_4_total_feeling_phase_1, ToM_GAVC$ToM_4_total_feeling_phase_1,
  paired = TRUE, exact = TRUE, correct = FALSE)
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_4_total_feeling_phase_1,
## ToM_GAVC$ToM_4_total_feeling_phase_1, : cannot compute exact p-value with
## ties
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_4_total_feeling_phase_1,
## ToM_GAVC$ToM_4_total_feeling_phase_1, : cannot compute exact p-value with
## zeroes
```

```
wilcox_result_total_feeling_phase_1
```

```
##
## Wilcoxon signed rank test
##
## data: ToM_CVC$ToM_4_total_feeling_phase_1 and ToM_GAVC$ToM_4_total_feeling_phase_1
## V = 33, p-value = 0.1898
## alternative hypothesis: true location shift is not equal to 0
```

The p-value is 0.19 which is higher than 0.05, so we can't reject the null hypothesis.

```
Zstat_total_feeling_phase_1 <- qnorm(wilcox_result_total_feeling_phase_1$p.value/2)
Zstat_total_feeling_phase_1
```

```
## [1] -1.31122
```

The Z-value is -1.31, which will be used to calculate the effect size.

Phase 2: total reasoning

The results were analysed using either a parametric or non-parametric paired difference test depending on the normality of the distribution. In this case the GAVC data is not normally distributed and thus a Wilcoxon signed-rank test was used:

```
wilcox_result_total_reasoning_phase_2 <- wilcox.test(ToM_CVC$ToM_5_total_reasoning_phase_2, ToM_GAVC$ToM_5_total_reasoning_phase_2,
paired = TRUE, exact = TRUE, correct = FALSE)
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_5_total_reasoning_phase_2,
## ToM_GAVC$ToM_5_total_reasoning_phase_2, : cannot compute exact p-value with
## ties
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_5_total_reasoning_phase_2,
## ToM_GAVC$ToM_5_total_reasoning_phase_2, : cannot compute exact p-value with
## zeroes
```

```
wilcox_result_total_reasoning_phase_2
```

```
##
## Wilcoxon signed rank test
##
## data: ToM_CVC$ToM_5_total_reasoning_phase_2 and ToM_GAVC$ToM_5_total_reasoning_phase_2
## V = 2, p-value = 0.5637
## alternative hypothesis: true location shift is not equal to 0
```

The p-value is 0.56 which is higher than 0.05, so we can't reject the null hypothesis.

```
Zstat_total_reasoning_phase_2 <- qnorm(wilcox_result_total_reasoning_phase_2$p.value/2)
Zstat_total_reasoning_phase_2
```

```
## [1] -0.5773503
```

The Z-value is -0.58, which will be used to calculate the effect size.

Phase 2: total feeling

The results were analysed using either a parametric or non-parametric paired difference test depending on the normality of the distribution. In this case the GAVC data is not normally distributed and thus a Wilcoxon signed-rank test was used:

```
wilcox_result_total_feeling_phase_2 <- wilcox.test(ToM_CVC$ToM_6_total_feeling_phase_2, ToM_GAVC$ToM_6_
  paired = TRUE, exact = TRUE, correct = FALSE)
```

```
## Warning in wilcox.test.default(ToM_CVC$ToM_6_total_feeling_phase_2,
## ToM_GAVC$ToM_6_total_feeling_phase_2, : cannot compute exact p-value with
## zeroes
```

```
wilcox_result_total_feeling_phase_2
```

```
##
## Wilcoxon signed rank test
##
## data: ToM_CVC$ToM_6_total_feeling_phase_2 and ToM_GAVC$ToM_6_total_feeling_phase_2
## V = 1, p-value = 0.3173
## alternative hypothesis: true location shift is not equal to 0
```

The p-value is 0.32 which is higher than 0.05, so we can't reject the null hypothesis.

```
Zstat_total_feeling_phase_2 <- qnorm(wilcox_result_total_feeling_phase_2$p.value/2)
Zstat_total_feeling_phase_2
```

```
## [1] -1
```

The Z-value is -1, which will be used to calculate the effect size.

Effect size

Phase 1: total reasoning

The effect size is calculated using Pearson's r for a non-parametric test:

```
abs(Zstat_total_reasoning_phase_1)/sqrt(24)
```

```
## [1] 0
```

The effect size r is 0.

Phase 1: total feeling

The effect size is calculated using Pearson's r for a non-parametric test:

```
abs(Zstat_total_feeling_phase_1)/sqrt(24)
```

```
## [1] 0.2676517
```

The effect size r is 0.27.

Phase 2: total reasoning

The effect size is calculated using Pearson's r for a non-parametric test:

```
abs(Zstat_total_reasoning_phase_2)/sqrt(24)
```

```
## [1] 0.1178511
```

The effect size r is 0.12.

Phase 2: total feeling

The effect size is calculated using Pearson's r for a non-parametric test:

```
abs(Zstat_total_feeling_phase_2)/sqrt(24)
```

```
## [1] 0.2041241
```

The effect size r is 0.20.