

Social presence questionnaire analysis

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September 2019

Contents

Introduction	1
Social presence questionnaire	2
Data preparation	2
Combining into a single score	5
Assumption checking: normal distribution	6
Paired difference test	11
Effect size	11

Introduction

This document presents inferential statistical analyses of participants' perception of the social presence of 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>

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This questionnaire on the perception of the social presence of the virtual characters is from J. N. Bailenson, J. Blascovich, A. C. Beall, and J. M. Loomis titled "Equilibrium theory revisited: Mutual gaze and personal space in virtual environments". It was published in *Presence: Teleoperators & Virtual Environments*, pages 583-598, 2001.

Participants evaluated to what extent each of the sentences matched with the virtual character (VC), using a seven-point Likert scale (1: "Totally disagree", 7: "Totally agree") for each item. The virtual characters have been given a randomised name, as they differ, a placeholder has been used here:

- I perceive that *Name of the VC* is another person in the room with me.
Totally disagree 1 2 3 4 5 6 7 Totally agree
- I feel that *Name of the VC* is watching me and is aware of my presence.
Totally disagree 1 2 3 4 5 6 7 Totally agree
- The thought that *Name of the VC* is not a real person crosses my mind often.
Totally disagree 1 2 3 4 5 6 7 Totally agree
- *Name of the VC* appears to be sentient (conscious and alive) to me.
Totally disagree 1 2 3 4 5 6 7 Totally agree
- I perceive *Name of the VC* as being only a computerized image, not as a real person.
Totally disagree 1 2 3 4 5 6 7 Totally agree

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 questionnaire data:

```
SPQ_data <- read.csv("SPQ_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),]
```

Social presence questionnaire

Data preparation

The participants were asked to fill this questionnaire 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 above mapping of roles with A/B we can separate the questionnaire answers per role. Thus the data table of the social presence questionnaire for the CVC is:

```
SPQ_CVC <- data.frame(SPQ_1_room=rep(NA,24), SPQ_2_presence_aware=rep(NA, 24),
  SPQ_3_real_person=rep(NA, 24), SPQ_4_sentience=rep(NA, 24),
  SPQ_5_computerized_image=rep(NA, 24), stringsAsFactors = FALSE)

for(i in 1:24){
  if(CVC_position[i] == "A"){
    SPQ_CVC[i,] <- SPQ_data[i, 2:6]
  }
  else{
    SPQ_CVC[i,] <- SPQ_data[i, 7:11]
  }
}

print(SPQ_CVC)
```

##	SPQ_1_room	SPQ_2_presence_aware	SPQ_3_real_person	SPQ_4_sentience
## 1	5	7	7	1
## 2	6	6	3	5
## 3	5	7	7	2
## 4	4	5	4	4
## 5	6	4	7	5
## 6	5	4	3	2
## 7	4	1	7	2
## 8	3	1	2	3
## 9	6	2	2	6
## 10	6	2	2	4
## 11	1	1	6	5
## 12	6	5	5	3
## 13	1	5	7	1
## 14	3	4	4	5
## 15	7	7	1	5
## 16	2	1	4	3
## 17	6	3	2	5
## 18	3	2	3	2
## 19	4	5	6	1
## 20	5	5	7	6
## 21	5	6	2	3
## 22	4	3	5	2
## 23	1	1	1	3
## 24	3	4	3	4

##	SPQ_5_computerized_image
## 1	7
## 2	7

```
## 3          7
## 4          5
## 5          3
## 6          6
## 7          7
## 8          7
## 9          4
## 10         3
## 11         6
## 12         4
## 13         7
## 14         3
## 15         4
## 16         6
## 17         3
## 18         4
## 19         7
## 20         3
## 21         3
## 22         7
## 23         5
## 24         5
```

And the GAVC:

```
SPQ_GAVC <- data.frame(SPQ_1_room=rep(NA,24), SPQ_2_presence_aware=rep(NA, 24),
                      SPQ_3_real_person=rep(NA, 24), SPQ_4_sentience=rep(NA, 24),
                      SPQ_5_computerized_image=rep(NA, 24), stringsAsFactors = FALSE)

for(i in 1:24){
  if(GAVC_position[i] == "A"){
    SPQ_GAVC[i,] <- SPQ_data[i, 2:6]
  }
  else{
    SPQ_GAVC[i,] <- SPQ_data[i, 7:11]
  }
}

print(SPQ_GAVC)
```

```
##      SPQ_1_room SPQ_2_presence_aware SPQ_3_real_person SPQ_4_sentience
## 1           5           7           7           1
## 2           6           7           3           7
## 3           5           7           6           2
## 4           6           7           3           6
## 5           6           4           7           5
## 6           4           3           3           2
## 7           6           5           3           4
## 8           5           7           2           5
## 9           5           5           2           4
## 10          6           6           2           4
## 11          5           5           6           5
## 12          3           3           5           3
## 13          6           6           7           1
## 14          3           1           4           5
```

```
## 15      3      3      5      3
## 16      2      3      4      3
## 17      6      6      2      5
## 18      5      6      3      6
## 19      6      6      5      1
## 20      5      5      7      6
## 21      5      7      2      4
## 22      6      4      5      3
## 23      1      1      1      3
## 24      7      6      3      5
##      SPQ_5_computerized_image
## 1      7
## 2      7
## 3      7
## 4      4
## 5      3
## 6      6
## 7      5
## 8      6
## 9      5
## 10     3
## 11     4
## 12     5
## 13     7
## 14     3
## 15     4
## 16     6
## 17     3
## 18     3
## 19     7
## 20     3
## 21     3
## 22     7
## 23     5
## 24     4
```

Combining into a single score

According to the analysis from the source paper (referenced at the top of this document), the individual items need to be combined into a single score:

```
SPQ_simple_sum_CVC <- SPQ_CVC
SPQ_simple_sum_CVC[, c(3,5)] <- -SPQ_simple_sum_CVC[,c(3,5)]
SPQ_simple_sum_CVC <- rowSums(SPQ_simple_sum_CVC)

SPQ_simple_sum_GAVC <- SPQ_GAVC
SPQ_simple_sum_GAVC[, c(3,5)] <- -SPQ_simple_sum_GAVC[,c(3,5)]
SPQ_simple_sum_GAVC <- rowSums(SPQ_simple_sum_GAVC)

print(SPQ_simple_sum_CVC)
```

```
## [1] -1  7  0  4  5  2 -7 -2  8  7 -5  5 -7  5 14 -4  9  0 -3  6  9 -3 -1
## [24]  3
```

```
print(SPQ_simple_sum_GAVC)

## [1] -1 10 1 12 5 0 7 9 7 11 5 -1 -1 2 0 -2 12 11 1 6 11 1 -1
## [24] 11

SPQ_simple_sum <- data.frame(CVC = SPQ_simple_sum_CVC, GAVC = SPQ_simple_sum_GAVC)
```

Assumption checking: normal distribution

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

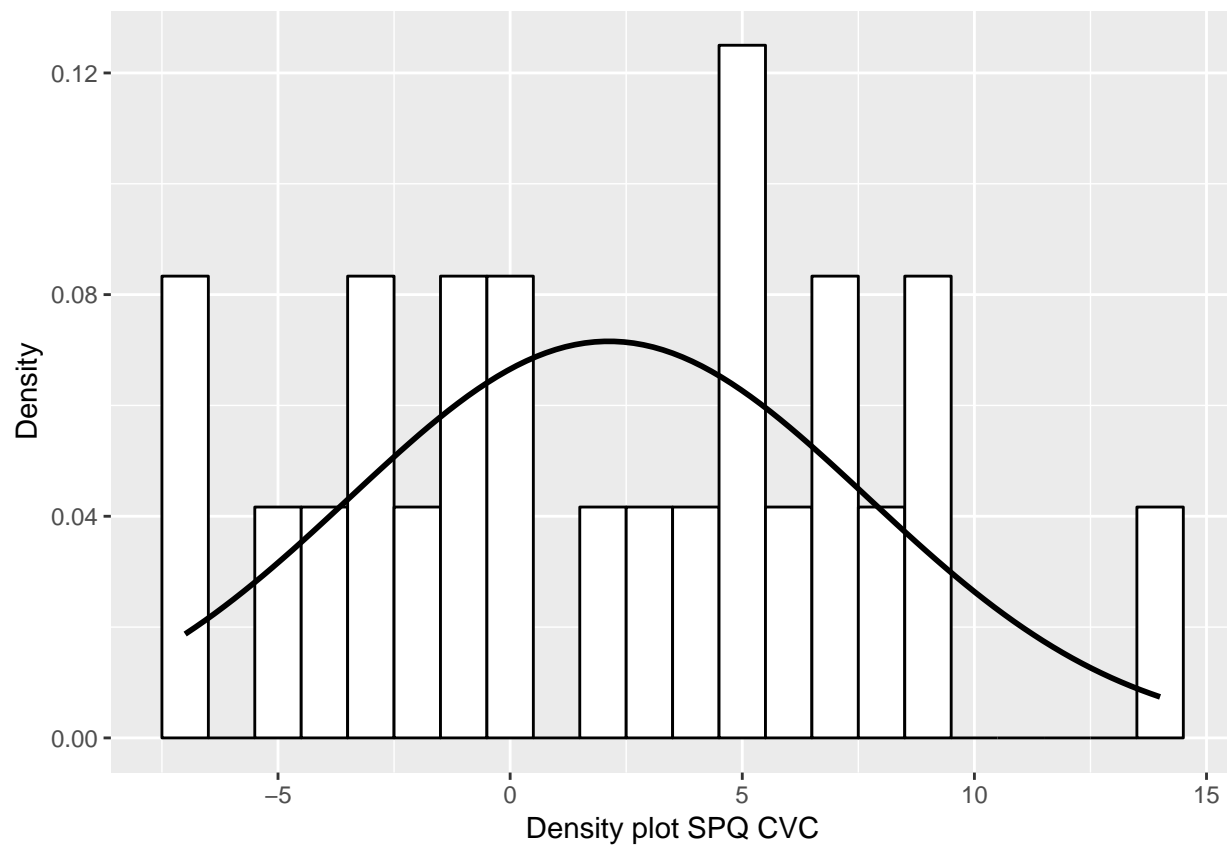
```
stem(SPQ_simple_sum$CVC)

##
## The decimal point is 1 digit(s) to the right of the |
##
## -0 | 775
## -0 | 433211
## 0 | 00234
## 0 | 555677899
## 1 | 4

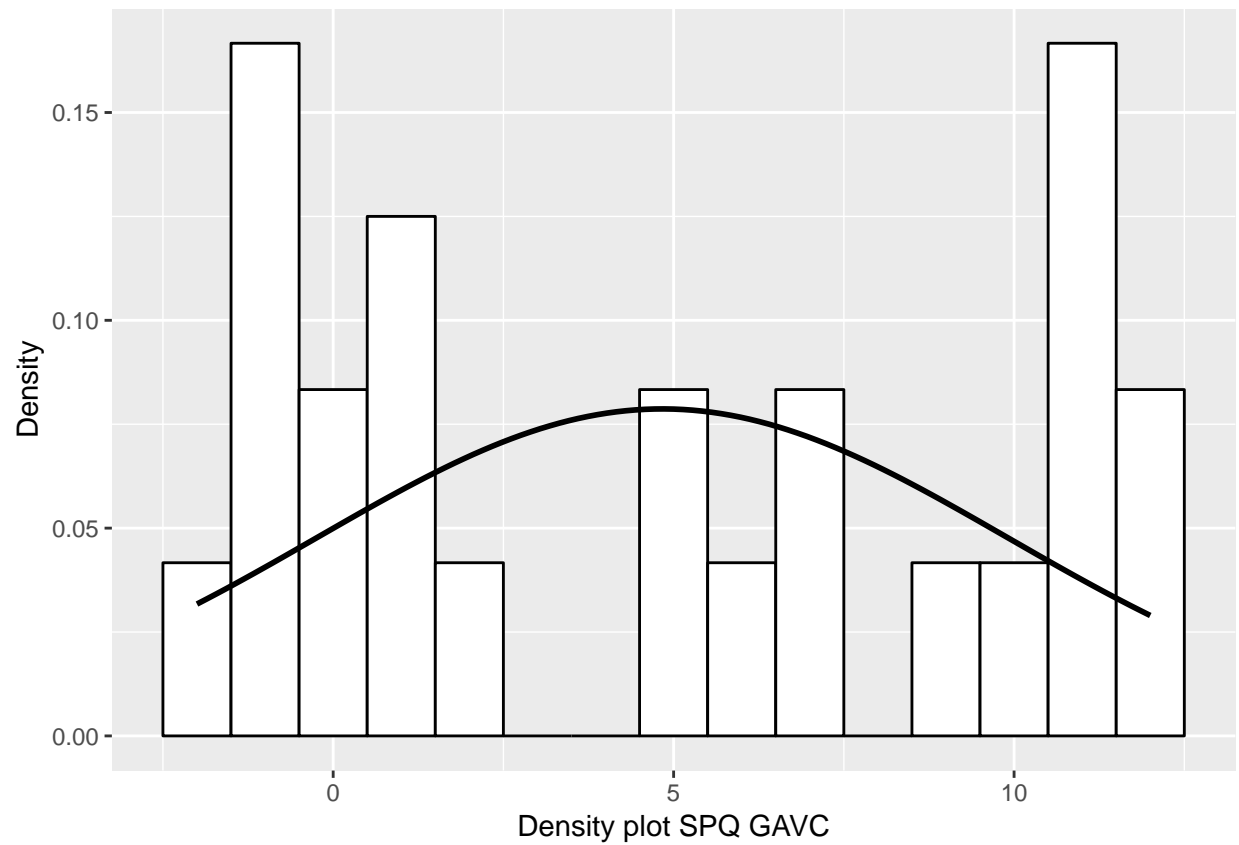
stem(SPQ_simple_sum$GAVC)

##
## The decimal point is 1 digit(s) to the right of the |
##
## -0 | 21111
## 0 | 001112
## 0 | 556779
## 1 | 0111122

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

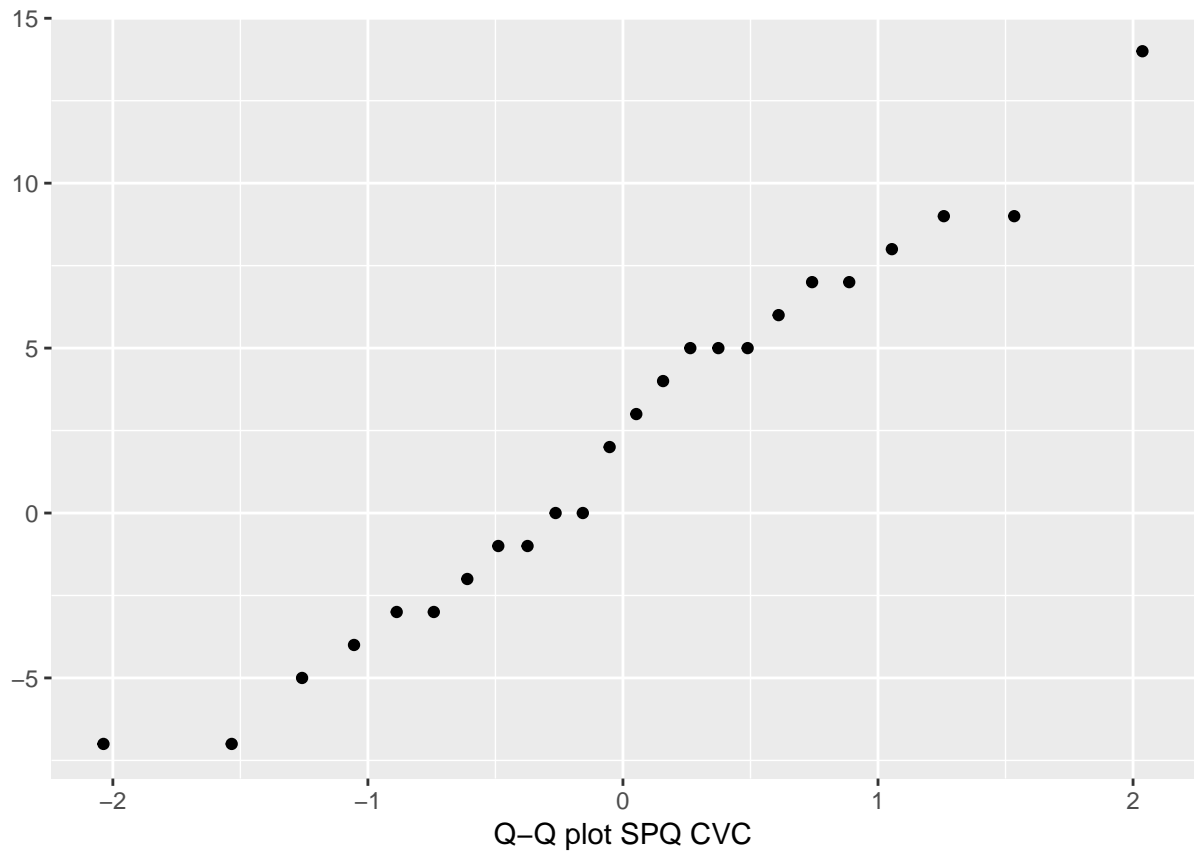


```
ggplot(SPQ_simple_sum,
  aes(GAVC)) + geom_histogram(aes(y=..density..), binwidth = 1,
  colour="black", fill="white") + labs(x="Density plot SPQ GAVC",
  y="Density") + stat_function(fun=dnorm,
  args=list(mean=mean(SPQ_simple_sum$GAVC, na.rm=TRUE),
  sd=sd(SPQ_simple_sum$GAVC, na.rm=TRUE)), colour="black",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



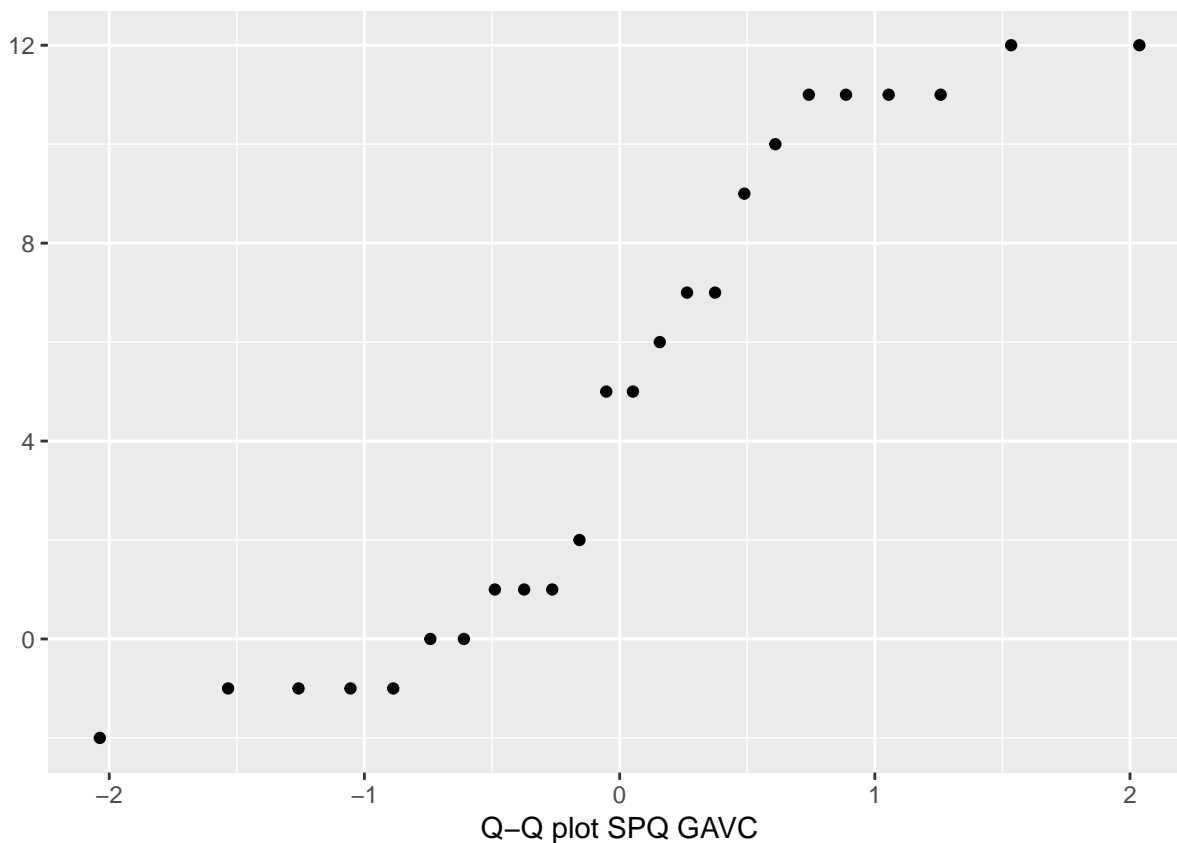
```
qplot(sample=SPQ_simple_sum$CVC, stat="qq") + labs(x="Q-Q plot SPQ CVC")
```

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

```
qplot(sample=SPQ_simple_sum$GAVC, stat="qq") + labs(x="Q-Q plot SPQ GAVC")
```

```
## 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(SPQ_simple_sum[,c("CVC", "GAVC")], basic = FALSE, norm = TRUE), digits = 3)
```

##	CVC	GAVC
## median	2.500	5.000
## mean	2.125	4.833
## SE.mean	1.138	1.035
## CI.mean.0.95	2.354	2.141
## var	31.071	25.710
## std.dev	5.574	5.071
## coef.var	2.623	1.049
## skewness	0.088	0.120
## skew.2SE	0.093	0.127
## kurtosis	-0.977	-1.693
## kurt.2SE	-0.532	-0.922
## normtest.W	0.970	0.875
## normtest.p	0.664	0.007

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 show that the CVC is normally distributed. The GAVC, however, has a p-value < 0.05 and thus deviates from normality.

Paired difference test

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 <- wilcox.test(SPQ_simple_sum$CVC, SPQ_simple_sum$GAVC, paired = TRUE, exact = TRUE, cor
```

```
## Warning in wilcox.test.default(SPQ_simple_sum$CVC, SPQ_simple_sum$GAVC, :  
## cannot compute exact p-value with ties  
  
## Warning in wilcox.test.default(SPQ_simple_sum$CVC, SPQ_simple_sum$GAVC, :  
## cannot compute exact p-value with zeroes  
  
wilcox_result
```

```
##  
## Wilcoxon signed rank test  
##  
## data: SPQ_simple_sum$CVC and SPQ_simple_sum$GAVC  
## V = 44.5, p-value = 0.0237  
## alternative hypothesis: true location shift is not equal to 0
```

The p-value is 0.02 which is < 0.05 which means that we can reject the null hypothesis and the result is statistically significant.

```
Zstat <- qnorm(wilcox_result$p.value/2)  
Zstat
```

```
## [1] -2.261979
```

The Z-value is -2.26, which will be used to calculate the effect size.

Effect size

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

```
abs(Zstat)/sqrt(24)
```

```
## [1] 0.4617245
```

The effect size r is 0.46.