R code copy pasted from R script

#Not all code here provided was used in data analysis but it can be used in similar research.

#R packages that need to be installed and loaded

```
citation("npmv") # for citation
library(npmv)
library(tidyr) #for short to long data form
library("MPsychoR")
library("psych")
library("reshape2")
library(sjPlot)
library(PerformanceAnalytics)
library(corrplot)
library(MVN)
library(lavaan)
library(semPlot)
library(semTools)
library(tidyverse)
library(ggpubr)
library(rstatix)
library(DescTools)
library(coin)
library(ggplot2)
library(mvnormtest)
library(pwr)
library(effectsize)
```

#import data in R environment in a TXT file.

I have to copy and paste all the variables from "Excel" - without column name, just #numbers. R studio is automatically naming it with letter V and ordinal numbers: V1,V2,V3...

It is important to know the names for renaming variables in R studio

R studio - import dataset- from Text ...

Dealing with QoR-40 questioner:

"Natural" order of items and dimensions from QoR-40 survey

#Emotional state: 2,9,12,28,36,37,38,39,40

#Physical comfort: 1,5,10,11,19,20,21,24,25,26,27,34

#Psychological support: 13,14,15,16,17,18,35

#Physical independence: 3,4,6,7,8

#Pain: 22,23,29,30,31,32,33

in our excel items are rearranged to follow the dimensions, not the natural order from QoR-40 questioner

To create dimensions sum score we need to sum score of the items.

bubrezi.vizualizacija <- read.delim("C:/Users/38591/OneDrive/Desktop/bubrezi vizualizacija.txt", header=FALSE)   #import txt file

q= bubrezi.vizualizacija

#make summary dimensional score

q$Comfort = as.numeric(apply(q[,1:12], 1, sum))

q$Emotions = as.numeric(apply(q[,13:21], 1, sum))

q$Independence= as.numeric(apply(q[,22:26], 1, sum))

q$PschyologicalSupport= as.numeric(apply(q[,27:33], 1, sum))

q$Pain= as.numeric(apply(q[,34:40], 1, sum))

#The sum of QoR score = global QoR score

Creating the global score sum and name. First 40 columns are QoR-40 items, next 15 are QoR-15 items

q$QoR40= as.numeric(apply(q[,1:40], 1, sum))

q$QoR15= as.numeric(apply(q[,41:55], 1, sum))

#naming other variables

        q$QoRVAS <- q$V56

        q$Nausea <- q$V57

        q$PainR<- q$V58

        q$PainA<- q$V59

        q$Anxiety<- q$V60

        #q$Epidural <- factor(q$V61)

        q$Epidural[q$V61 == '0'] <- 'Control group' # changing name of binary variable outcome

        q$Epidural[q$V61 == '1'] <- 'Epidural group'

        q$subject<- factor(q$V62)

```r
q$Age<- q$V63

q$ASA<- as.integer(q$V64) # ASA is ordinal variable.

q$Timeanest<- as.integer(q$V65)

q$Timesurgery<- as.integer(q$V66)

q$fentanyl<- (q$V67)

q$vecuronium<- as.integer(q$V68)

q$Analgesia[q$V69 == '0'] <- 'Control  group'   #renaming


q$Analgesia[q$V69 == '1'] <- 'Class I'

q$Analgesia[q$V69 == '2'] <- 'Class II'

q$Analgesia[q$V69 == '3'] <- 'Class III'

q$cristaloid<- q$V70

q$RBC<- (q$V71)

q$atropin<- (q$V72)

q$efedrin<- (q$V73)
```

```r
#data visualisation with boxplot
boxplot(QoR40 ~ Epidural, data = q,
    xlab = " ",
    ylab = "QoR-40 ",
    notch = FALSE,
    varwidth = TRUE,
    col = c("orange"," violet"),
    names = c("Control group","Epidural group")
)
boxplot(QoR15 ~ Epidural, data = q,
    xlab = " ",
    ylab = "QoR-15 ",
    notch = FALSE,
    varwidth = TRUE,
    col = c("orange"," violet"),
    names = c("Control group","Epidural group")
)
```

```r
boxplot(QoRVAS ~ Epidural, data = q,

    xlab = " ",

    ylab = "QoR-VAS ",

    notch = FALSE,

    varwidth = TRUE,

    col = c("orange"," violet"),

    names = c("Control group","Epidural group")

)


boxplot(Anxiety ~ Epidural, data = q,

    xlab = " ",

    ylab = "VAS anxiety ",

    notch = FALSE,

    varwidth = TRUE,

    col = c("orange"," violet"),

    names = c("Control group","Epidural group")

)


boxplot(PainR ~ Epidural, data = q,

    xlab = " ",

    ylab = "VAS pain at rest ",

    notch = FALSE,

    varwidth = TRUE,

    col = c("orange"," violet"),

    names = c("Control group","Epidural group")

)

boxplot(PainA ~ Epidural, data = q,

    xlab = " ",

    ylab = "VAS pain at activity",

    notch = FALSE,

    varwidth = TRUE,

    col = c("orange"," violet"),

    names = c("Control group","Epidural group")

)


boxplot(Nausea~ Epidural, data = q,

    xlab = " ",

    ylab = "VAS Nausea",
```

```r
            notch = FALSE,

            varwidth = TRUE,

            col = c("orange"," violet"),

            names = c("Control group","Epidural group")

    )
```

<mark>#Normality analyisis</mark>

```r
describe(q[72:92])
```

the problem with mvn test is that category variable needs to be excluded from analysis or test will
#not work. MVN test calculate univariate Shapiro-Wilk test, and descriptives.

```r
        m1<- mvn(data = q[72:83], mvnTest = c("mardia"), showOutliers = TRUE,
univariateTest="SW")

        r1 <- mvn(data = q[72:83],univariatePlot = "qqplot")

        r2<- mvn(data = q[72:83], univariatePlot = "histogram")


        m1<- mvn(data = q[86:89], mvnTest = c("mardia"), showOutliers = TRUE,
univariateTest="SW")

        r1 <- mvn(data = q[, c(86:89)],univariatePlot = "qqplot")

        r2<- mvn(data = q[, c(86:89)], univariatePlot = "histogram")


        #-qq plot analysis, shorted for all other variables

        ggqqplot(q, x = "QoR40", facet.by = "Epidural")

        ggqqplot(q, x = "QoR40
```

<mark>#reliability calculation</mark>

```r
        QoR40= q[,1:40]

        QoR15= q[,41:55]

        tab_itemscale(QoR40,show.shapiro = TRUE, show.kurtosis = TRUE,use.viewer= TRUE)
#Cronbach's =0.882

        psych::alpha(QoR40)

        tab_itemscale(QoR15,show.shapiro = TRUE, show.kurtosis = TRUE,use.viewer= TRUE)
#Cronbach's =0.727

        psych::alpha(QoR15)
```

```
mardia<- mvn(data = q[79:85], mvnTest = c("mardia"), showOutliers = TRUE,
univariateTest="SW")

        chart.Correlation(q[, c(79:85)], method= "spearman", histogram=TRUE, pch=19)

        chart.Correlation(q[, c(79:83)], method= "spearman", histogram=TRUE, pch=19)

        chart.Correlation(q[, c(83:85)], method= "spearman", histogram=TRUE, pch=19)

        chart.Correlation(q[, c(74:79)], method= "spearman", histogram=TRUE, pch=19)
```

(demographic variables)

```
summary(q)

 describe(QoR40 ~ Epidural,IQR=TRUE, data=q)

 describe(QoR15 ~ Epidural,IQR=TRUE, data=q)

 describe(QoRVAS ~ Epidural,IQR=TRUE, data=q)

 describe(Nausea ~ Epidural,IQR=TRUE, data=q)

 describe(PainA ~ Epidural,IQR=TRUE, data=q)

 describe( Anxiety ~ Epidural,IQR=TRUE, data=q)

 describe(q$Age,IQR=TRUE)

 describe(q$Timeanest,IQR=TRUE)

 describe(q$Timesurgery,IQR=TRUE)

 describe(Age ~ Epidural,IQR=TRUE, data=q)

 wilcox.test(Age ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 table(q$ASA,q$Epidural)

 wilcox.test(ASA ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 shapiro.test(q$Timesurgery)

 shapiro.test(q$Timeanest)

 describe(Timesurgery~ Epidural,IQR=TRUE, data=q)

 describe( Timeanest~ Epidural,IQR=TRUE, data=q)

 wilcox.test(Timesurgery ~ Epiduraldata=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 wilcox.test(Timeanest ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 contingency_table <- table(q$RBC,q$Epidural)

  contingency_table
```

```r
fisher.test(contingency_table)

describe( cristaloid ~ Epidural,IQR=TRUE, data=q)

wilcox.test(cristaloid ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

describe( efedrin ~ Epidural,IQR=TRUE, data=q)

shapiro.test(q$cristaloid)

atropin <- read.delim2("C:/Users/38591/OneDrive/Desktop/atropin.txt", header=FALSE,
comment.char="#")  #there was some error with variable atropine, so the column was copy paste in
other txt file together with epidural group.

describe( V2 ~ V1,IQR=TRUE, data=atropin)

shapiro.test(atropin$V2)

wilcox.test(V2 ~ V1, data=atropin,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

shapiro.test(q$vecuronium)

summary(q$atropin)

shapiro.test(q$vecuronium)

describe(vecuronium ~ Epidural,IQR=TRUE, data=q)

wilcox.test(vecuronium ~ Epidural,
data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

describe(fentanyl ~ Epidural,IQR=TRUE, data=q)

summary (q$fentanyl)

table(q$fentanyl,q$Epidural)

table(q$Analgesia, q$Epidural)


# Primary outcome

wilcox.test( QoR40 ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)


# Wilcoxon rank sum test with continuity correctin     #data:  QoR40 by Epidural

# W = 403.5, p-value = 0.0001374    # alternative hypothesis: true location shift is not equal to 0

# 95 percent confidence interval:    # -14.000036  -5.000017

#sample estimates:    # difference in location    # -9.999982


describe(QoR40 ~ Epidural,IQR=TRUE, data=q)

q %>% wilcox_effsize(QoR40 ~ Epidural)
```

```
wilcox.test( Comfort ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 q %>% wilcox_effsize(Comfort ~ Epidural)

describe(Comfort ~ Epidural,IQR=TRUE, data=q)


 q %>% wilcox_effsize( Emotions~ Epidural)

wilcox.test( Emotions ~ Epidural, data=q,conf.lev=0.95

,conf.int=TRUE,exact=F,correct=T)

describe(Emotions ~ Epidural,IQR=TRUE, data=q)


 q %>% wilcox_effsize(PschyologicalSupport ~ Epidural)

 wilcox.test( PschyologicalSupport ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

describe(PschyologicalSupport ~ Epidural,IQR=TRUE, data=q)


 q %>% wilcox_effsize( Independence~ Epidural)

 wilcox.test( Independence ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 describe(Independence ~ Epidural,IQR=TRUE, data=q)


 q %>% wilcox_effsize( Pain ~ Epidural)

 wilcox.test( Pain~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

 describe(Pain ~ Epidural,IQR=TRUE, data=q)
```

```
        q$Epidural=  as.factor(q$Epidural)

        independence_test( QoR15 + QoRVAS ~ Epidural, data= q, distribution =
approximate(nresample = 100000))

        # maxT 3.9337, p-value = 3e-05

        independence_test(PainR +PainA + Anxiety +  Nausea ~ Epidural, data= q, distribution =
approximate(nresample = 100000))

        #maxT = 3.5935, p-value = 0.00078
```

```
wilcox.test( Nausea ~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

wilcox.test( QoRVAS~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

wilcox.test( PainR~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

wilcox.test( PainA~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

wilcox.test( QoR15~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

wilcox.test( Anxiety~ Epidural, data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

q %>% wilcox_effsize( QoRVAS ~ Epidural)

q %>% wilcox_effsize( PainR ~ Epidural)

q %>% wilcox_effsize( PainA ~ Epidural)

q %>% wilcox_effsize( Nausea ~ Epidural)

q %>% wilcox_effsize( QoR15 ~ Epidural)

q %>% wilcox_effsize( Anxiety ~ Epidural)

describe(PainR ~ Epidural,IQR=TRUE, data=q)

describe(PainA ~ Epidural,IQR=TRUE, data=q)
```

```
#VAS analysis with predetermined cut off points

x= q$PainA

wilcox.test( x, y = NULL, mu = 40,alternative = "less" ,data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

x= q$PainR

wilcox.test( x, y = NULL, mu = 30, alternative ="higher", data=q,conf.lev=0.95,conf.int=TRUE,exact=F,correct=T)

q %>% wilcox_effsize( Anxiety ~ Epidural)
```