Feedback\_Analysis\_-\_BMJSubmission.R

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#Description of code: this code processes the PUFQs looking at summary of these data,  
#within-participant comparison of PUFQ data ("before/after"), and between-participants  
#comparison of PUFQ data (bulk test for differences btw all treatment nights vs all  
#sham nights)  
  
#Summary/Status:  
#08APR: No difference on within-participant or between-participant comparisons (treatment   
#vs. sham) for all variables.  
  
#setting the workspace directory  
setwd("/Users/Allan/Desktop/HPTStats/08APR2017")  
  
#importing the PrenaBelt User Feedback (PBUF) Data  
PBUFdata=read.csv("PUFD Data Halifax - 08APR2017.csv")  
  
#Loading the functions (ad.test, etc.) into your workspace  
library(nortest)  
  
#Exclude drop outs  
#How many drop outs?  
summary(PBUFdata$drop.out)

## N Y   
## 40 6

#6 dropout nights = 3 participants  
#Remove the drop outs ("Y")  
PBUFdata <- PBUFdata[!(PBUFdata$drop.out=="Y"),]  
nrow(PBUFdata)

## [1] 40

#Separate into sham and treat group for within-participant comparisons  
PBUF\_sham <- subset(PBUFdata, Intervention == "sham")  
PBUF\_treat <- subset(PBUFdata, Intervention == "treatment")  
  
#############################SR POSITION ADOPTED#############################  
#summary data  
summary(PBUFdata$SR.position.adopted)

## left left and right left and supine   
## 0 27 5 1   
## right supine   
## 5 2

length(PBUFdata$SR.position.adopted)

## [1] 40

#between participants (grouped) comparison  
xtabs(~SR.position.adopted + Intervention, data = PBUFdata)

## Intervention  
## SR.position.adopted sham treatment  
## 0 0  
## left 13 14  
## left and right 2 3  
## left and supine 1 0  
## right 3 2  
## supine 1 1

#build 2-row table for fisher test: sham vs treatment  
SR.position.adopted\_table <- matrix(c(16,17,5,5,2,1),  
 nrow = 2)  
colnames(SR.position.adopted\_table) <- c("left","right","supine")  
rownames(SR.position.adopted\_table) <- c("Sham",  
 "Treatment")  
SR.position.adopted\_table

## left right supine  
## Sham 16 5 2  
## Treatment 17 5 1

t(SR.position.adopted\_table)

## Sham Treatment  
## left 16 17  
## right 5 5  
## supine 2 1

#Perform Fisher's Exact Tests  
  
temp\_table <- t(SR.position.adopted\_table)  
j=nrow(temp\_table)  
ControlCsum=colSums(temp\_table)[1]  
TreatmentCsum=colSums(temp\_table)[2]  
for(i in 1:j) {  
 a=temp\_table[i,1]  
 b=temp\_table[i,2]  
 c=ControlCsum-a  
 d=TreatmentCsum-b  
 ORtable <- matrix(c(a,c,b,d),nrow = 2)  
 colnames(ORtable) <- c("Sham","Treatment")  
 rownames(ORtable) <- c(row.names(temp\_table)[i],"Other")  
 print(row.names(temp\_table)[i])  
 print(ORtable)  
 print(fisher.test(ORtable))  
}

## [1] "left"  
## Sham Treatment  
## left 16 17  
## Other 7 6  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.181121 3.522335  
## sample estimates:  
## odds ratio   
## 0.810505   
##   
## [1] "right"  
## Sham Treatment  
## right 5 5  
## Other 18 18  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1927805 5.1872475  
## sample estimates:  
## odds ratio   
## 1   
##   
## [1] "supine"  
## Sham Treatment  
## supine 2 1  
## Other 21 22  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1003416 129.0322645  
## sample estimates:  
## odds ratio   
## 2.062812

#############################SR POSITION FELL ASLEEP#############################  
#summary data  
summary(PBUFdata$SR.position.fell.asleep)

## left left and right   
## 0 27 5   
## left, right and back right supine   
## 1 5 2

length(PBUFdata$SR.position.fell.asleep)

## [1] 40

#between participants (grouped) comparison  
xtabs(~SR.position.fell.asleep + Intervention, data = PBUFdata)

## Intervention  
## SR.position.fell.asleep sham treatment  
## 0 0  
## left 13 14  
## left and right 2 3  
## left, right and back 1 0  
## right 3 2  
## supine 1 1

#build 2-row table for fisher test: sham vs treatment  
SR.position.fell.asleep\_table <- matrix(c(16,17,6,5,2,1),  
 nrow = 2)  
colnames(SR.position.fell.asleep\_table) <- c("left","right","supine")  
rownames(SR.position.fell.asleep\_table) <- c("Sham",  
 "Treatment")  
t(SR.position.fell.asleep\_table)

## Sham Treatment  
## left 16 17  
## right 6 5  
## supine 2 1

#Perform Fisher's Exact Tests  
  
temp\_table <- t(SR.position.fell.asleep\_table)  
j=nrow(temp\_table)  
ControlCsum=colSums(temp\_table)[1]  
TreatmentCsum=colSums(temp\_table)[2]  
for(i in 1:j) {  
 a=temp\_table[i,1]  
 b=temp\_table[i,2]  
 c=ControlCsum-a  
 d=TreatmentCsum-b  
 ORtable <- matrix(c(a,c,b,d),nrow = 2)  
 colnames(ORtable) <- c("Sham","Treatment")  
 rownames(ORtable) <- c(row.names(temp\_table)[i],"Other")  
 print(row.names(temp\_table)[i])  
 print(ORtable)  
 print(fisher.test(ORtable))  
}

## [1] "left"  
## Sham Treatment  
## left 16 17  
## Other 8 6  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 0.7516  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1630989 2.9521011  
## sample estimates:  
## odds ratio   
## 0.7111464   
##   
## [1] "right"  
## Sham Treatment  
## right 6 5  
## Other 18 18  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.2513307 5.9379379  
## sample estimates:  
## odds ratio   
## 1.195355   
##   
## [1] "supine"  
## Sham Treatment  
## supine 2 1  
## Other 22 22  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.09605226 123.17436447  
## sample estimates:  
## odds ratio   
## 1.971677

#############################SR SNORING#############################  
#summary data  
summary(PBUFdata$SR.snored.last.night)

## don't know no yes   
## 3 26 8 3

length(PBUFdata$SR.snored.last.night)

## [1] 40

#between participants (grouped) comparison  
xtabs(~SR.snored.last.night + Intervention, data = PBUFdata)[-1,]

## Intervention  
## SR.snored.last.night sham treatment  
## don't know 13 13  
## no 4 4  
## yes 1 2

#Perform Fisher's Exact Tests  
temp\_table <- xtabs(~SR.snored.last.night + Intervention, data = PBUFdata)[-1,]  
j=nrow(temp\_table)  
ControlCsum=colSums(temp\_table)[1]  
TreatmentCsum=colSums(temp\_table)[2]  
for(i in 1:j) {  
 a=temp\_table[i,1]  
 b=temp\_table[i,2]  
 c=ControlCsum-a  
 d=TreatmentCsum-b  
 ORtable <- matrix(c(a,c,b,d),nrow = 2)  
 colnames(ORtable) <- c("Sham","Treatment")  
 rownames(ORtable) <- c(row.names(temp\_table)[i],"Other")  
 print(row.names(temp\_table)[i])  
 print(ORtable)  
 print(fisher.test(ORtable))  
}

## [1] "don't know"  
## Sham Treatment  
## don't know 13 13  
## Other 5 6  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.2341604 6.3402606  
## sample estimates:  
## odds ratio   
## 1.1941   
##   
## [1] "no"  
## Sham Treatment  
## no 4 4  
## Other 14 15  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1643428 6.9643241  
## sample estimates:  
## odds ratio   
## 1.06941   
##   
## [1] "yes"  
## Sham Treatment  
## yes 1 2  
## Other 17 17  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.008017856 10.654170427  
## sample estimates:  
## odds ratio   
## 0.509154

#############################SR LEGS TWITCH/JERK#############################  
#summary data  
summary(PBUFdata$SR.legs.twitch.jerk)

## don't know no yes   
## 3 19 14 4

length(PBUFdata$SR.legs.twitch.jerk)

## [1] 40

#between participants (grouped) comparison  
xtabs(~SR.legs.twitch.jerk + Intervention, data = PBUFdata)[-1,]

## Intervention  
## SR.legs.twitch.jerk sham treatment  
## don't know 9 10  
## no 8 6  
## yes 2 2

#Perform Fisher's Exact Tests  
temp\_table <- xtabs(~SR.legs.twitch.jerk + Intervention, data = PBUFdata)[-1,]  
j=nrow(temp\_table)  
ControlCsum=colSums(temp\_table)[1]  
TreatmentCsum=colSums(temp\_table)[2]  
for(i in 1:j) {  
 a=temp\_table[i,1]  
 b=temp\_table[i,2]  
 c=ControlCsum-a  
 d=TreatmentCsum-b  
 ORtable <- matrix(c(a,c,b,d),nrow = 2)  
 colnames(ORtable) <- c("Sham","Treatment")  
 rownames(ORtable) <- c(row.names(temp\_table)[i],"Other")  
 print(row.names(temp\_table)[i])  
 print(ORtable)  
 print(fisher.test(ORtable))  
}

## [1] "don't know"  
## Sham Treatment  
## don't know 9 10  
## Other 10 8  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 0.7459  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1631369 3.1478545  
## sample estimates:  
## odds ratio   
## 0.7264619   
##   
## [1] "no"  
## Sham Treatment  
## no 8 6  
## Other 11 12  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 0.7374  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.3156971 6.8777204  
## sample estimates:  
## odds ratio   
## 1.439815   
##   
## [1] "yes"  
## Sham Treatment  
## yes 2 2  
## Other 17 16  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.06145761 14.45806216  
## sample estimates:  
## odds ratio   
## 0.9426919

#############################SR WAKE POSITION#############################  
#summary data  
summary(PBUFdata$SR.position.woke.up)

## left right   
## 0 28 12

length(PBUFdata$SR.position.woke.up)

## [1] 40

#between participants (grouped) comparison  
xtabs(~SR.position.woke.up + Intervention, data = PBUFdata)[-1,]

## Intervention  
## SR.position.woke.up sham treatment  
## left 13 15  
## right 7 5

fisher.test(xtabs(~SR.position.woke.up + Intervention, data = PBUFdata)[-1,])

##   
## Fisher's Exact Test for Count Data  
##   
## data:   
## p-value = 0.7311  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.1235598 2.9574108  
## sample estimates:  
## odds ratio   
## 0.6265621

#############################SR - did you change positions?#############################  
#summary data  
summary(PBUFdata$SR.position.changed)

## don\xcdt know no yes   
## 1 1 3 35

length(PBUFdata$SR.position.changed)

## [1] 40

#between participants (grouped) comparison  
xtabs(~SR.position.changed + Intervention, data = PBUFdata)[-1,]

## Intervention  
## SR.position.changed sham treatment  
## don\xcdt know 1 0  
## no 1 2  
## yes 18 17

#Perform Fisher's Exact Tests  
temp\_table <- xtabs(~SR.position.changed + Intervention, data = PBUFdata)[-1,]  
j=nrow(temp\_table)  
ControlCsum=colSums(temp\_table)[1]  
TreatmentCsum=colSums(temp\_table)[2]  
for(i in 1:j) {  
 a=temp\_table[i,1]  
 b=temp\_table[i,2]  
 c=ControlCsum-a  
 d=TreatmentCsum-b  
 ORtable <- matrix(c(a,c,b,d),nrow = 2)  
 colnames(ORtable) <- c("Sham","Treatment")  
 rownames(ORtable) <- c(row.names(temp\_table)[i],"Other")  
 print(row.names(temp\_table)[i])  
 print(ORtable)  
 print(fisher.test(ORtable))  
}

## [1] "don\xcdt know"  
## Sham Treatment  
## don\xcdt know 1 0  
## Other 19 19  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.02435859 Inf  
## sample estimates:  
## odds ratio   
## Inf   
##   
## [1] "no"  
## Sham Treatment  
## no 1 2  
## Other 19 17  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 0.605  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.007216433 9.507277143  
## sample estimates:  
## odds ratio   
## 0.456456   
##   
## [1] "yes"  
## Sham Treatment  
## yes 18 17  
## Other 2 2  
##   
## Fisher's Exact Test for Count Data  
##   
## data: ORtable  
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.0693477 16.1216542  
## sample estimates:  
## odds ratio   
## 1.057301

#Take out the pts that we don't have complete data on (these participants' studies were   
#before the PUFQ was revised to ask about the participant's estimate of how much time  
#she spent in each position)  
PBUF\_shamSRpos <- PBUF\_sham[-c(1,2,3),]  
PBUF\_treatSRpos <- PBUF\_treat[-c(1,2,3),]  
  
#############################SR PROPORTION OF TIME ON LEFT#############################  
#summary data  
summary(PBUFdata$SR.Ptime.left)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 0.00 41.50 66.00 59.91 84.00 100.00 5

sd(PBUFdata$SR.Ptime.left, na.rm = TRUE)

## [1] 28.14915

length(na.omit(PBUFdata$SR.Ptime.left))

## [1] 35

#within-participants (paired) comparison  
#Paired t-test  
t.test(PBUF\_shamSRpos$SR.Ptime.left, PBUF\_treatSRpos$SR.Ptime.left, paired = TRUE)

##   
## Paired t-test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.left and PBUF\_treatSRpos$SR.Ptime.left  
## t = 0.38979, df = 16, p-value = 0.7018  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -6.266297 9.089826  
## sample estimates:  
## mean of the differences   
## 1.411765

#between participants (grouped) comparison  
summary(PBUF\_treatSRpos$SR.Ptime.left)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 10.00 36.00 60.00 58.76 85.00 95.00

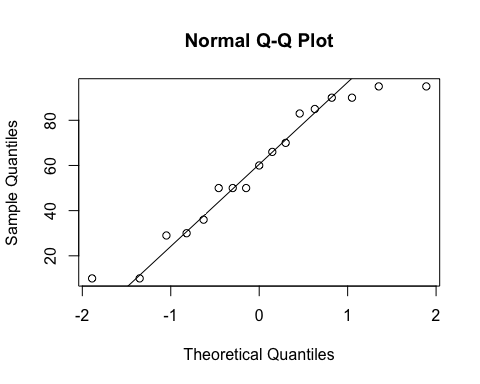
sd(PBUF\_treatSRpos$SR.Ptime.left)

## [1] 28.77831

length(PBUF\_treatSRpos$SR.Ptime.left)

## [1] 17

qqnorm(PBUF\_treatSRpos$SR.Ptime.left)  
qqline(PBUF\_treatSRpos$SR.Ptime.left)



ad.test(PBUF\_treatSRpos$SR.Ptime.left)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treatSRpos$SR.Ptime.left  
## A = 0.40809, p-value = 0.3093

#normal  
  
summary(PBUF\_shamSRpos$SR.Ptime.left)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.00 43.00 70.00 60.18 80.00 100.00

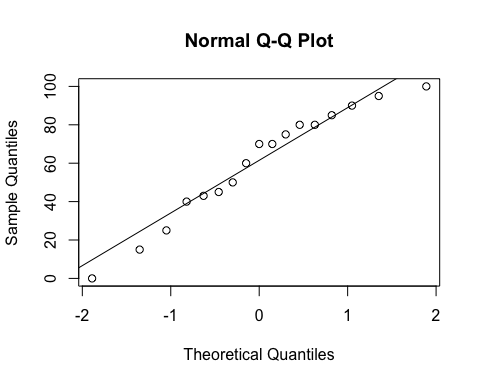
sd(PBUF\_shamSRpos$SR.Ptime.left)

## [1] 28.9811

length(PBUF\_shamSRpos$SR.Ptime.left)

## [1] 17

qqnorm(PBUF\_shamSRpos$SR.Ptime.left)  
qqline(PBUF\_shamSRpos$SR.Ptime.left)



ad.test(PBUF\_shamSRpos$SR.Ptime.left)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.left  
## A = 0.31945, p-value = 0.506

#normal  
  
#Perform 2-sample t-test (Welch's t-test)  
t.test(PBUF\_shamSRpos$SR.Ptime.left, PBUF\_treatSRpos$SR.Ptime.left)

##   
## Welch Two Sample t-test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.left and PBUF\_treatSRpos$SR.Ptime.left  
## t = 0.14252, df = 31.998, p-value = 0.8876  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -18.76556 21.58909  
## sample estimates:  
## mean of x mean of y   
## 60.17647 58.76471

#############################SR PROPORTION OF TIME ON RIGHT#############################  
#summary data  
summary(PBUFdata$SR.Ptime.right)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 0.00 2.50 30.00 31.29 50.00 90.00 5

sd(PBUFdata$SR.Ptime.right, na.rm = TRUE)

## [1] 27.30177

length(na.omit(PBUFdata$SR.Ptime.right))

## [1] 35

#within-participants (paired) comparison  
#Paired t-test  
t.test(PBUF\_shamSRpos$SR.Ptime.right, PBUF\_treatSRpos$SR.Ptime.right, paired = TRUE)

##   
## Paired t-test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.right and PBUF\_treatSRpos$SR.Ptime.right  
## t = -0.10277, df = 16, p-value = 0.9194  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -7.633106 6.927224  
## sample estimates:  
## mean of the differences   
## -0.3529412

#between participants (grouped) comparison  
summary(PBUF\_treatSRpos$SR.Ptime.right)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.00 0.00 34.00 31.65 50.00 88.00

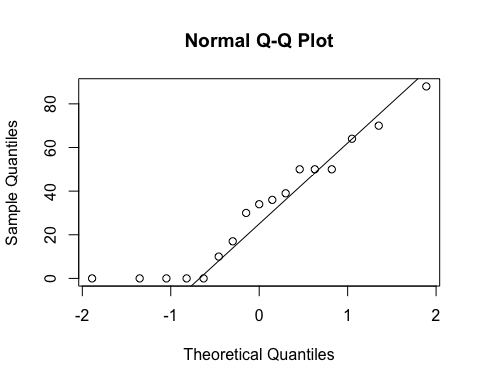
sd(PBUF\_treatSRpos$SR.Ptime.right)

## [1] 27.92387

length(PBUF\_treatSRpos$SR.Ptime.right)

## [1] 17

qqnorm(PBUF\_treatSRpos$SR.Ptime.right)  
qqline(PBUF\_treatSRpos$SR.Ptime.right)



ad.test(PBUF\_treatSRpos$SR.Ptime.right)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treatSRpos$SR.Ptime.right  
## A = 0.51449, p-value = 0.1649

#normal  
  
summary(PBUF\_shamSRpos$SR.Ptime.right)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.00 5.00 30.00 31.29 50.00 90.00

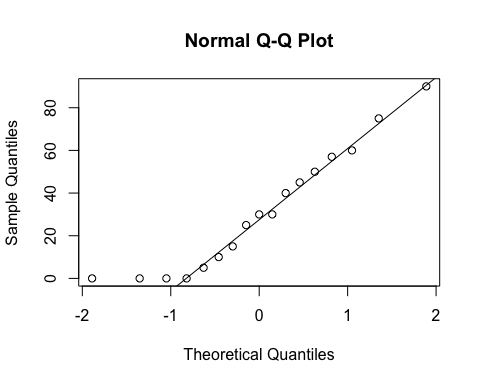
sd(PBUF\_shamSRpos$SR.Ptime.right)

## [1] 28.31246

length(PBUF\_shamSRpos$SR.Ptime.right)

## [1] 17

qqnorm(PBUF\_shamSRpos$SR.Ptime.right)  
qqline(PBUF\_shamSRpos$SR.Ptime.right)



ad.test(PBUF\_shamSRpos$SR.Ptime.right)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.right  
## A = 0.43793, p-value = 0.2602

#normal  
  
#Perform 2-sample t-test (Welch's t-test)  
t.test(PBUF\_shamSRpos$SR.Ptime.right, PBUF\_treatSRpos$SR.Ptime.right)

##   
## Welch Two Sample t-test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.right and PBUF\_treatSRpos$SR.Ptime.right  
## t = -0.036594, df = 31.994, p-value = 0.971  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -19.99866 19.29278  
## sample estimates:  
## mean of x mean of y   
## 31.29412 31.64706

#############################SR PROPORTION OF TIME ON BACK#############################  
#summary data  
summary(PBUFdata$SR.Ptime.back)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 0.0 0.0 0.0 7.8 5.0 90.0 5

sd(PBUFdata$SR.Ptime.back, na.rm = TRUE)

## [1] 19.98205

length(na.omit(PBUFdata$SR.Ptime.back))

## [1] 35

#within-participants (paired) comparison - non-normal, use parametric test (Wilcoxon)  
wilcox.test(PBUF\_shamSRpos$SR.Ptime.back, PBUF\_treatSRpos$SR.Ptime.back,  
 paired = TRUE, conf.int = TRUE)

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.back,  
## PBUF\_treatSRpos$SR.Ptime.back, : cannot compute exact p-value with ties

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.back,  
## PBUF\_treatSRpos$SR.Ptime.back, : cannot compute exact confidence interval  
## with ties

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.back,  
## PBUF\_treatSRpos$SR.Ptime.back, : cannot compute exact p-value with zeroes

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.back,  
## PBUF\_treatSRpos$SR.Ptime.back, : cannot compute exact confidence interval  
## with zeroes

##   
## Wilcoxon signed rank test with continuity correction  
##   
## data: PBUF\_shamSRpos$SR.Ptime.back and PBUF\_treatSRpos$SR.Ptime.back  
## V = 18.5, p-value = 0.4951  
## alternative hypothesis: true location shift is not equal to 0  
## 95 percent confidence interval:  
## -7.499958 8.999966  
## sample estimates:  
## (pseudo)median   
## 4.090518

#between participants (grouped) comparison  
summary(PBUF\_treatSRpos$SR.Ptime.back)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.000 0.000 0.000 7.529 5.000 90.000

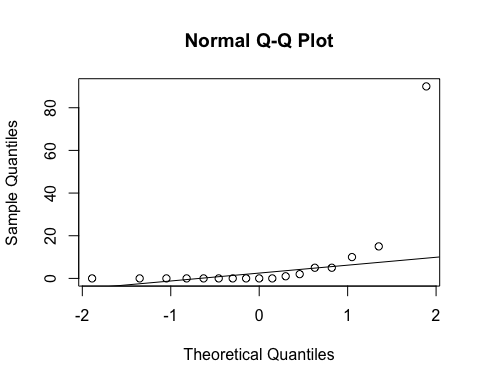
sd(PBUF\_treatSRpos$SR.Ptime.back)

## [1] 21.67406

length(PBUF\_treatSRpos$SR.Ptime.back)

## [1] 17

qqnorm(PBUF\_treatSRpos$SR.Ptime.back)  
qqline(PBUF\_treatSRpos$SR.Ptime.back)



ad.test(PBUF\_treatSRpos$SR.Ptime.back)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treatSRpos$SR.Ptime.back  
## A = 4.2859, p-value = 3.533e-11

#non-normal  
  
summary(PBUF\_shamSRpos$SR.Ptime.back)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.000 0.000 0.000 8.529 5.000 80.000

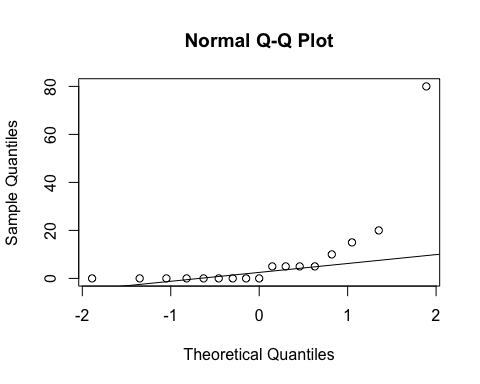
sd(PBUF\_shamSRpos$SR.Ptime.back)

## [1] 19.34592

length(PBUF\_shamSRpos$SR.Ptime.back)

## [1] 17

qqnorm(PBUF\_shamSRpos$SR.Ptime.back)  
qqline(PBUF\_shamSRpos$SR.Ptime.back)



ad.test(PBUF\_shamSRpos$SR.Ptime.back)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_shamSRpos$SR.Ptime.back  
## A = 3.3048, p-value = 1.097e-08

#non-normal  
  
#Perform non-parametric test (Wilcoxon)  
wilcox.test(PBUF\_shamSRpos$SR.Ptime.back, PBUF\_treatSRpos$SR.Ptime.back, conf.int = TRUE)

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.back,  
## PBUF\_treatSRpos$SR.Ptime.back, : cannot compute exact p-value with ties

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.back,  
## PBUF\_treatSRpos$SR.Ptime.back, : cannot compute exact confidence intervals  
## with ties

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: PBUF\_shamSRpos$SR.Ptime.back and PBUF\_treatSRpos$SR.Ptime.back  
## W = 159, p-value = 0.5944  
## alternative hypothesis: true location shift is not equal to 0  
## 95 percent confidence interval:  
## -3.745025e-05 4.999982e+00  
## sample estimates:  
## difference in location   
## 3.7504e-05

#############################SR PROPORTION OF TIME ON STOMACH#############################  
#summary data  
summary(PBUFdata$SR.Ptime.stomach)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 0.0000 0.0000 0.0000 0.7143 0.0000 18.0000 5

sd(PBUFdata$SR.Ptime.stomach, na.rm = TRUE)

## [1] 3.231931

length(na.omit(PBUFdata$SR.Ptime.stomach))

## [1] 35

#within-participants (paired) comparison - non-normal, use parametric test (Wilcoxon)  
wilcox.test(PBUF\_shamSRpos$SR.Ptime.stomach, PBUF\_treatSRpos$SR.Ptime.stomach,   
 paired = TRUE)

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.stomach,  
## PBUF\_treatSRpos$SR.Ptime.stomach, : cannot compute exact p-value with  
## zeroes

##   
## Wilcoxon signed rank test with continuity correction  
##   
## data: PBUF\_shamSRpos$SR.Ptime.stomach and PBUF\_treatSRpos$SR.Ptime.stomach  
## V = 0, p-value = 0.3711  
## alternative hypothesis: true location shift is not equal to 0

#between participants (grouped) comparison  
summary(PBUF\_treatSRpos$SR.Ptime.stomach)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.000 0.000 0.000 1.471 0.000 18.000

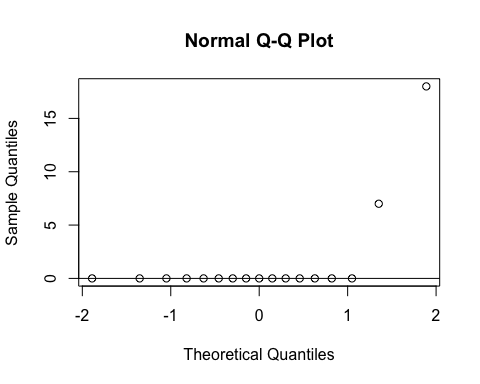
sd(PBUF\_treatSRpos$SR.Ptime.stomach)

## [1] 4.58418

length(PBUF\_treatSRpos$SR.Ptime.stomach)

## [1] 17

qqnorm(PBUF\_treatSRpos$SR.Ptime.stomach)  
qqline(PBUF\_treatSRpos$SR.Ptime.stomach)



ad.test(PBUF\_treatSRpos$SR.Ptime.stomach)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treatSRpos$SR.Ptime.stomach  
## A = 4.9879, p-value = 5.961e-13

#non-normal  
  
summary(PBUF\_shamSRpos$SR.Ptime.stomach)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0 0 0 0 0 0

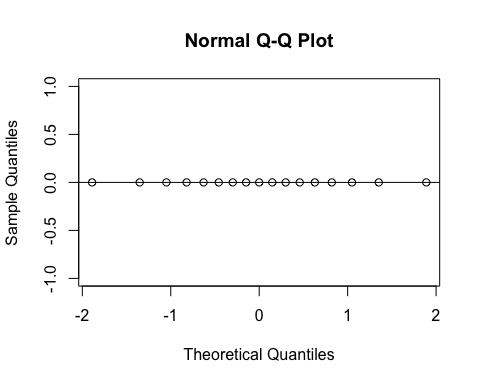
sd(PBUF\_shamSRpos$SR.Ptime.stomach)

## [1] 0

length(PBUF\_shamSRpos$SR.Ptime.stomach)

## [1] 17

qqnorm(PBUF\_shamSRpos$SR.Ptime.stomach)  
qqline(PBUF\_shamSRpos$SR.Ptime.stomach)



#ad.test(PBUF\_shamSRpos$SR.Ptime.stomach)  
#distribution is entirely zeroes  
  
#Perform non-parametric test (Wilcoxon)  
wilcox.test(PBUF\_shamSRpos$SR.Ptime.stomach, PBUF\_treatSRpos$SR.Ptime.stomach, conf.int = TRUE)

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.stomach,  
## PBUF\_treatSRpos$SR.Ptime.stomach, : cannot compute exact p-value with ties

## Warning in wilcox.test.default(PBUF\_shamSRpos$SR.Ptime.stomach,  
## PBUF\_treatSRpos$SR.Ptime.stomach, : cannot compute exact confidence  
## intervals with ties

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: PBUF\_shamSRpos$SR.Ptime.stomach and PBUF\_treatSRpos$SR.Ptime.stomach  
## W = 127.5, p-value = 0.1635  
## alternative hypothesis: true location shift is not equal to 0  
## 95 percent confidence interval:  
## -7.272004e-05 0.000000e+00  
## sample estimates:  
## difference in location   
## 0

#############################REMEMBER CHANGING POSITIONS#############################  
#summary data  
summary(PBUFdata$remember.changing.positions)

## no yes   
## 0 7 33

length(PBUFdata$remember.changing.positions)

## [1] 40

#between participants (grouped) comparison  
xtabs(~remember.changing.positions + Intervention, data = PBUFdata)[-1,]

## Intervention  
## remember.changing.positions sham treatment  
## no 4 3  
## yes 16 17

fisher.test(xtabs(~remember.changing.positions + Intervention, data = PBUFdata)[-1,])

##   
## Fisher's Exact Test for Count Data  
##   
## data:   
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.2020801 11.1277720  
## sample estimates:  
## odds ratio   
## 1.404393

#Remove rows with missing data or with participants who did not change position or did  
#not remember changing positions  
PBUF\_shamSRchangepos <- PBUF\_sham[-c(1,5,6,7,14,19),]  
PBUF\_treatSRchangepos <- PBUF\_treat[-c(1,5,6,7,14,19),]  
  
#############################SR NUMBER OF TIMES CHANGED POSITION###########################  
#summary data  
summary(PBUFdata$SR.how.many.times.changed.positions)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 0.000 2.000 3.000 3.194 4.000 7.000 9

sd(PBUFdata$SR.how.many.times.changed.positions, na.rm = TRUE)

## [1] 1.740103

length(na.omit(PBUFdata$SR.how.many.times.changed.positions))

## [1] 31

#within-participants (paired) comparison  
#Paired t-test  
t.test(PBUF\_shamSRchangepos$SR.how.many.times.changed.positions,   
 PBUF\_treatSRchangepos$SR.how.many.times.changed.positions,   
 paired = TRUE)

##   
## Paired t-test  
##   
## data: PBUF\_shamSRchangepos$SR.how.many.times.changed.positions and PBUF\_treatSRchangepos$SR.how.many.times.changed.positions  
## t = 0.31382, df = 13, p-value = 0.7586  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.8405766 1.1262909  
## sample estimates:  
## mean of the differences   
## 0.1428571

#between participants (grouped) comparison  
summary(PBUF\_treat$SR.how.many.times.changed.positions)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 1.000 2.000 3.000 3.125 4.000 7.000 4

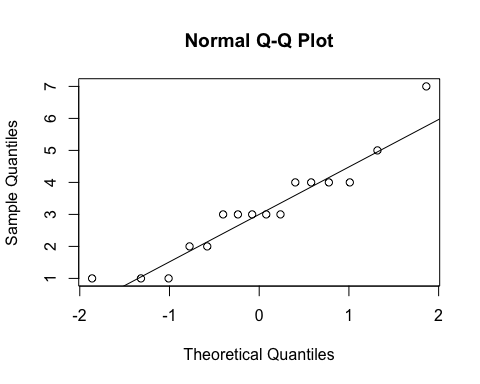
sd(PBUF\_treat$SR.how.many.times.changed.positions, na.rm = TRUE)

## [1] 1.586401

length(na.omit(PBUF\_treat$SR.how.many.times.changed.positions))

## [1] 16

qqnorm(PBUF\_treat$SR.how.many.times.changed.positions)  
qqline(PBUF\_treat$SR.how.many.times.changed.positions)



ad.test(PBUF\_treat$SR.how.many.times.changed.positions)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treat$SR.how.many.times.changed.positions  
## A = 0.51178, p-value = 0.1658

#normal  
  
summary(PBUF\_sham$SR.how.many.times.changed.positions)

## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's   
## 0.000 1.500 4.000 3.267 4.500 7.000 5

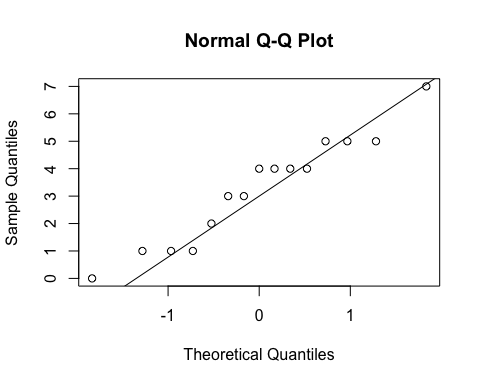
sd(PBUF\_sham$SR.how.many.times.changed.positions, na.rm = TRUE)

## [1] 1.944467

length(na.omit(PBUF\_sham$SR.how.many.times.changed.positions))

## [1] 15

qqnorm(PBUF\_sham$SR.how.many.times.changed.positions)  
qqline(PBUF\_sham$SR.how.many.times.changed.positions)



ad.test(PBUF\_sham$SR.how.many.times.changed.positions)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_sham$SR.how.many.times.changed.positions  
## A = 0.41783, p-value = 0.287

#normal  
  
#Perform 2-sample t-test (Welch's t-test)  
t.test(PBUF\_sham$SR.how.many.times.changed.positions,   
 PBUF\_treat$SR.how.many.times.changed.positions)

##   
## Welch Two Sample t-test  
##   
## data: PBUF\_sham$SR.how.many.times.changed.positions and PBUF\_treat$SR.how.many.times.changed.positions  
## t = 0.22142, df = 27.082, p-value = 0.8264  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -1.170927 1.454261  
## sample estimates:  
## mean of x mean of y   
## 3.266667 3.125000

#############################SATISFACTION LEVEL#############################  
#summary data  
summary(PBUFdata$satisfaction.level)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.000 6.000 7.500 7.338 9.000 10.000

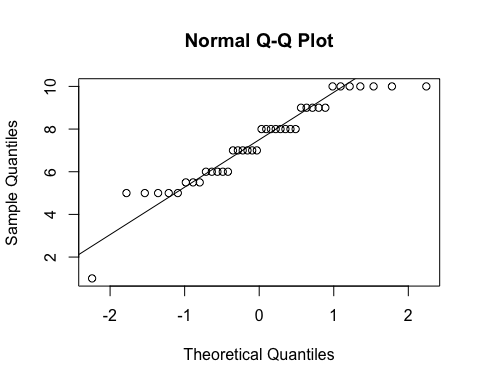
sd(PBUFdata$satisfaction.level)

## [1] 1.988388

length(PBUFdata$satisfaction.level)

## [1] 40

qqnorm(PBUFdata$satisfaction.level)  
qqline(PBUFdata$satisfaction.level)



ad.test(PBUFdata$satisfaction.level)

##   
## Anderson-Darling normality test  
##   
## data: PBUFdata$satisfaction.level  
## A = 0.79381, p-value = 0.03625

#within-participants (paired) comparison  
#t-test (individual distributions are normal)  
t.test(PBUF\_sham$satisfaction.level,PBUF\_treat$satisfaction.level, paired = TRUE)

##   
## Paired t-test  
##   
## data: PBUF\_sham$satisfaction.level and PBUF\_treat$satisfaction.level  
## t = 0.74891, df = 19, p-value = 0.4631  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.4935575 1.0435575  
## sample estimates:  
## mean of the differences   
## 0.275

#between participants (grouped) comparison  
summary(PBUF\_treat$satisfaction.level)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.00 6.00 7.50 7.20 8.25 10.00

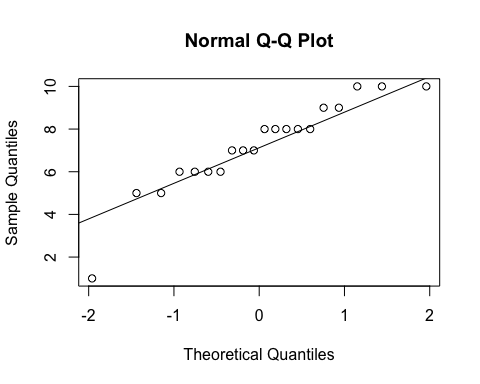
sd(PBUF\_treat$satisfaction.level, na.rm = TRUE)

## [1] 2.142306

length(na.omit(PBUF\_treat$satisfaction.level))

## [1] 20

qqnorm(PBUF\_treat$satisfaction.level)  
qqline(PBUF\_treat$satisfaction.level)



ad.test(PBUF\_treat$satisfaction.level)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treat$satisfaction.level  
## A = 0.54062, p-value = 0.1445

#normal  
  
summary(PBUF\_sham$satisfaction.level)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 5.000 5.500 7.500 7.475 9.000 10.000

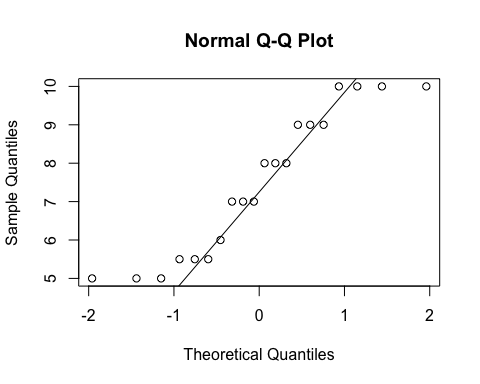
sd(PBUF\_sham$satisfaction.level, na.rm = TRUE)

## [1] 1.867133

length(na.omit(PBUF\_sham$satisfaction.level))

## [1] 20

qqnorm(PBUF\_sham$satisfaction.level)  
qqline(PBUF\_sham$satisfaction.level)



ad.test(PBUF\_sham$satisfaction.level)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_sham$satisfaction.level  
## A = 0.69241, p-value = 0.0596

#normal  
  
#Perform 2-sample t-test (Welch's t-test)  
t.test(PBUF\_sham$satisfaction.level,   
 PBUF\_treat$satisfaction.level)

##   
## Welch Two Sample t-test  
##   
## data: PBUF\_sham$satisfaction.level and PBUF\_treat$satisfaction.level  
## t = 0.43277, df = 37.304, p-value = 0.6677  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -1.012168 1.562168  
## sample estimates:  
## mean of x mean of y   
## 7.475 7.200

#############################COMFORT LEVEL#############################  
#summary data  
summary(PBUFdata$comfort.level)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.000 7.000 9.000 8.175 10.000 10.000

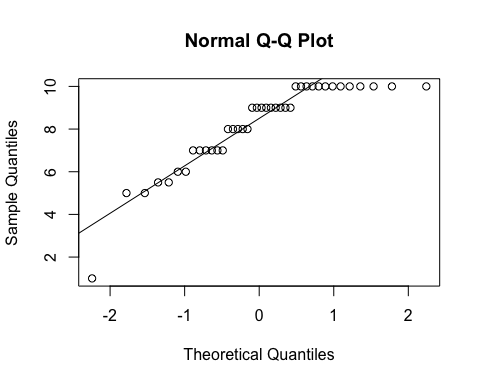
sd(PBUFdata$comfort.level)

## [1] 1.982455

length(PBUFdata$comfort.level)

## [1] 40

qqnorm(PBUFdata$comfort.level)  
qqline(PBUFdata$comfort.level)



ad.test(PBUFdata$comfort.level)

##   
## Anderson-Darling normality test  
##   
## data: PBUFdata$comfort.level  
## A = 1.8563, p-value = 7.865e-05

#within-participants (paired) comparison  
#non-normal - perform Wilcoxon  
wilcox.test(PBUF\_sham$comfort.level,PBUF\_treat$comfort.level,   
 paired = TRUE, conf.int = TRUE)

## Warning in wilcox.test.default(PBUF\_sham$comfort.level, PBUF\_treat  
## $comfort.level, : cannot compute exact p-value with ties

## Warning in wilcox.test.default(PBUF\_sham$comfort.level, PBUF\_treat  
## $comfort.level, : cannot compute exact confidence interval with ties

## Warning in wilcox.test.default(PBUF\_sham$comfort.level, PBUF\_treat  
## $comfort.level, : cannot compute exact p-value with zeroes

## Warning in wilcox.test.default(PBUF\_sham$comfort.level, PBUF\_treat  
## $comfort.level, : cannot compute exact confidence interval with zeroes

##   
## Wilcoxon signed rank test with continuity correction  
##   
## data: PBUF\_sham$comfort.level and PBUF\_treat$comfort.level  
## V = 54.5, p-value = 0.0574  
## alternative hypothesis: true location shift is not equal to 0  
## 95 percent confidence interval:  
## -0.0000318032 2.7499508366  
## sample estimates:  
## (pseudo)median   
## 1.000052

#between participants (grouped) comparison  
summary(PBUF\_treat$comfort.level)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.00 6.75 9.00 7.80 9.25 10.00

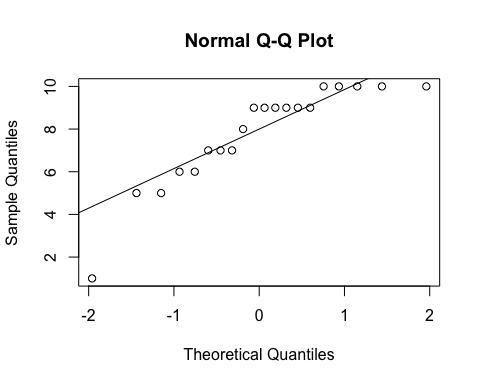
sd(PBUF\_treat$comfort.level, na.rm = TRUE)

## [1] 2.330575

length(na.omit(PBUF\_treat$comfort.level))

## [1] 20

qqnorm(PBUF\_treat$comfort.level)  
qqline(PBUF\_treat$comfort.level)



ad.test(PBUF\_treat$comfort.level)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treat$comfort.level  
## A = 1.0308, p-value = 0.008039

#non-normal  
  
summary(PBUF\_sham$comfort.level)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 5.50 7.75 9.00 8.55 10.00 10.00

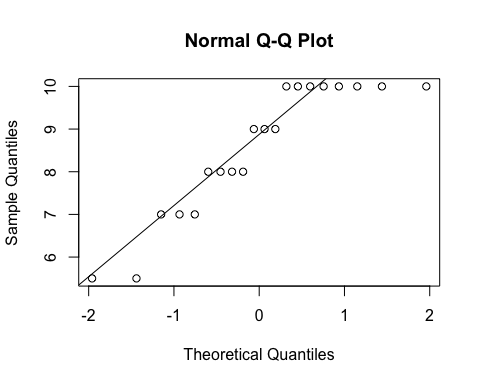
sd(PBUF\_sham$comfort.level, na.rm = TRUE)

## [1] 1.529534

length(na.omit(PBUF\_sham$comfort.level))

## [1] 20

qqnorm(PBUF\_sham$comfort.level)  
qqline(PBUF\_sham$comfort.level)



ad.test(PBUF\_sham$comfort.level)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_sham$comfort.level  
## A = 1.1179, p-value = 0.004803

#non-normal  
  
#Perform non-parametric test (Wilcoxon)  
wilcox.test(PBUF\_sham$comfort.level, PBUF\_treat$comfort.level, conf.int = TRUE)

## Warning in wilcox.test.default(PBUF\_sham$comfort.level, PBUF\_treat  
## $comfort.level, : cannot compute exact p-value with ties

## Warning in wilcox.test.default(PBUF\_sham$comfort.level, PBUF\_treat  
## $comfort.level, : cannot compute exact confidence intervals with ties

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: PBUF\_sham$comfort.level and PBUF\_treat$comfort.level  
## W = 235.5, p-value = 0.3312  
## alternative hypothesis: true location shift is not equal to 0  
## 95 percent confidence interval:  
## -0.4999358 1.0000188  
## sample estimates:  
## difference in location   
## 0.3425784

#################INTENTION TO USE IN FUTURE PREGNANCY LEVEL######################  
#summary data  
summary(PBUFdata$intention.to.use)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.00 6.00 7.50 7.05 8.25 10.00

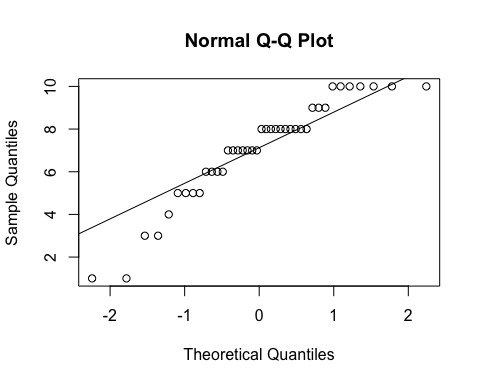
sd(PBUFdata$intention.to.use)

## [1] 2.363722

length(PBUFdata$intention.to.use)

## [1] 40

qqnorm(PBUFdata$intention.to.use)  
qqline(PBUFdata$intention.to.use)



ad.test(PBUFdata$intention.to.use)

##   
## Anderson-Darling normality test  
##   
## data: PBUFdata$intention.to.use  
## A = 1.0575, p-value = 0.00788

#within-participants (paired) comparison  
#t-test (individual distributions are normal)  
t.test(PBUF\_sham$intention.to.use,PBUF\_treat$intention.to.use, paired = TRUE)

##   
## Paired t-test  
##   
## data: PBUF\_sham$intention.to.use and PBUF\_treat$intention.to.use  
## t = 0.24031, df = 19, p-value = 0.8127  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.7709543 0.9709543  
## sample estimates:  
## mean of the differences   
## 0.1

#between participants (grouped) comparison  
summary(PBUF\_treat$intention.to.use)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.00 5.75 8.00 7.00 8.00 10.00

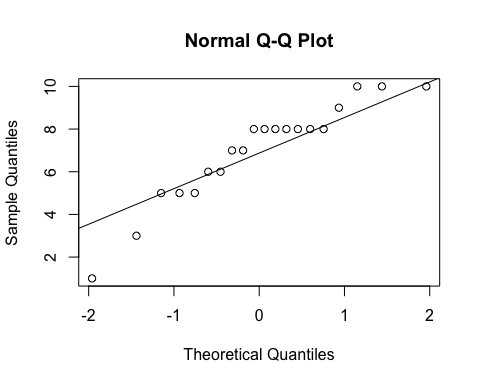
sd(PBUF\_treat$intention.to.use, na.rm = TRUE)

## [1] 2.339591

length(na.omit(PBUF\_treat$intention.to.use))

## [1] 20

qqnorm(PBUF\_treat$intention.to.use)  
qqline(PBUF\_treat$intention.to.use)



ad.test(PBUF\_treat$intention.to.use)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_treat$intention.to.use  
## A = 0.70743, p-value = 0.05453

#normal  
  
summary(PBUF\_sham$intention.to.use)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1.0 6.0 7.0 7.1 9.0 10.0

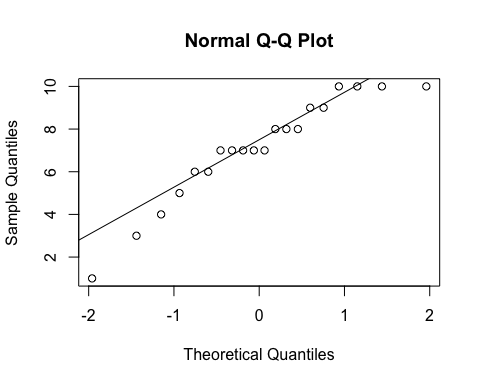
sd(PBUF\_sham$intention.to.use, na.rm = TRUE)

## [1] 2.44734

length(na.omit(PBUF\_sham$intention.to.use))

## [1] 20

qqnorm(PBUF\_sham$intention.to.use)  
qqline(PBUF\_sham$intention.to.use)



ad.test(PBUF\_sham$intention.to.use)

##   
## Anderson-Darling normality test  
##   
## data: PBUF\_sham$intention.to.use  
## A = 0.54305, p-value = 0.1424

#normal  
  
#Perform 2-sample t-test (Welch's t-test)  
t.test(PBUF\_sham$intention.to.use,   
 PBUF\_treat$intention.to.use)

##   
## Welch Two Sample t-test  
##   
## data: PBUF\_sham$intention.to.use and PBUF\_treat$intention.to.use  
## t = 0.13209, df = 37.923, p-value = 0.8956  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -1.432714 1.632714  
## sample estimates:  
## mean of x mean of y   
## 7.1 7.0

#################WOULD MAKE CHANGES######################  
#summary data  
summary(PBUFdata$would.make.changes)

## no yes   
## 2 31 7

length(PBUFdata$would.make.changes)

## [1] 40

#7 nights, but only 6 participants of 20 (30%)  
  
#between participants (grouped) comparison  
xtabs(~would.make.changes + Intervention, data = PBUFdata)[-1,]

## Intervention  
## would.make.changes sham treatment  
## no 16 15  
## yes 3 4

fisher.test(xtabs(~would.make.changes + Intervention, data = PBUFdata)[-1,])

##   
## Fisher's Exact Test for Count Data  
##   
## data:   
## p-value = 1  
## alternative hypothesis: true odds ratio is not equal to 1  
## 95 percent confidence interval:  
## 0.2007118 11.2700012  
## sample estimates:  
## odds ratio   
## 1.409106

#END