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