

# testosterone and sexual desire in men

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```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
##   filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(tidyverse)
```

```
## -- Attaching packages -----  
- tidyverse 1.2.1 --
```

```
## v ggplot2 3.2.1    v readr    1.3.1  
## v tibble  2.1.3    v purrr   0.3.2  
## v tidyr   1.0.0    v stringr 1.4.0  
## v ggplot2 3.2.1    v forcats 0.4.0
```

```
## -- Conflicts ----- tidy  
verse_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()
```

```
library(lmerTest)
```

```
## Loading required package: lme4
```

```
## Loading required package: Matrix
```

```
##  
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':  
##  
##     expand, pack, unpack
```

```
##  
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':  
##  
##     lmer
```

```
## The following object is masked from 'package:stats':  
##  
##     step
```

```
library(psych)
```

```
##  
## Attaching package: 'psych'
```

```
## The following objects are masked from 'package:ggplot2':  
##  
##     %+%, alpha
```

```
library(ggplot2)  
library(reshape2)
```

```
## Warning: package 'reshape2' was built under R version 3.6.3
```

```
##  
## Attaching package: 'reshape2'
```

```
## The following object is masked from 'package:tidyr':  
##  
##     smiths
```

```
library(sjPlot)
```

```
## Warning: package 'sjPlot' was built under R version 3.6.3
```

```
## Learn more about sjPlot with 'browseVignettes("sjPlot")'.
```

```
library(sjmisc)
```

```
## Learn more about sjmisc with 'browseVignettes("sjmisc")'.
```

```
##  
## Attaching package: 'sjmisc'
```

```
## The following object is masked from 'package:purrr':  
##  
##   is_empty
```

```
## The following object is masked from 'package:tidyr':  
##  
##   replace_na
```

```
## The following object is masked from 'package:tibble':  
##  
##   add_case
```

Descriptive statistics and full output for all analyses. This document also includes analyses of reported anxiety levels that are not reported in the main text.

```

# Load Data
setwd("C:/Users/jjuenge/Desktop/data")
data <- read.csv2("C:/Users/jjuenge/Desktop/data/testosterone_cortisol_desire_relationship.csv")

###numbers as numeric, categories as factor variables
for(i in c(3,8:10,12:36)){
  data[,i] <- as.numeric(as.character(data[,i]))
}

for(i in c(1,2)){
  data[,i] <- as.factor(data[,i])
}

#exclude participants who reported using hormonal supplements (n = 7)

data <- data[- grep("1001", data$hm_id),]
data <- data[- grep("1006", data$hm_id),]
data <- data[- grep("1023", data$hm_id),]
data <- data[- grep("1026", data$hm_id),]
data <- data[- grep("1029", data$hm_id),]
data <- data[- grep("1031", data$hm_id),]
data <- data[- grep("1054", data$hm_id),]

```

## Basic Descriptive Information for Sample

The number of sessions completed per man

```

data %>%
  group_by(hm_id) %>%
  summarise(
    sessions = n_distinct(date)
  ) %>%
  group_by(sessions) %>%
  summarise(
    n = n()
  )

```

```

## # A tibble: 5 x 2
##   sessions      n
##   <int> <int>
## 1         1     4
## 2         2     2
## 3         3     2
## 4         4     3
## 5         5    50

```

## Mean age for the sample

```
data %>%
  group_by(hm_id) %>%
  summarise(age = mean(age, na.rm = T)) %>%
  ungroup() %>%
  group_by() %>%
  summarise(
    n = n(),
    mean_age = mean(age, na.rm = TRUE),
    sd_age = sd(age, na.rm = TRUE),
    se_age = se(age, na.rm = TRUE)
  ) %>%
  mutate_all(round, 2)
```

```
## # A tibble: 1 x 4
##       n mean_age sd_age se_age
##   <dbl>   <dbl> <dbl> <dbl>
## 1    61    22.2   3.32  0.43
```

# Data Processing

## Exclude hormone outliers

```
# calculate means and SDs
testosterone_mean <- mean(data$testosterone)
testosterone_sd <- sd(data$testosterone)
cortisol_mean <- mean(data$cortisol)
cortisol_sd <- sd(data$cortisol)

# set values > 3SD from the mean to NA
data_final <- data %>%
  mutate (
    testosterone = ifelse (testosterone > testosterone_mean + 3*testosterone_sd |
                          testosterone < testosterone_mean - 3*testosterone_sd, NA, testosterone),
    cortisol = ifelse (cortisol > cortisol_mean + 3*cortisol_sd |
                      cortisol < cortisol_mean - 3*cortisol_sd, NA, cortisol)
  )

# determine how many values were excluded
data_final %>%
  group_by(hm_id, date) %>%
  summarise(
    t = is.na(mean(testosterone)),
    c = is.na(mean(cortisol))
  ) %>%
  ungroup() %>%
  select(t:c) %>%
  gather('hormone', 'na', t:c) %>%
  group_by(hormone) %>%
  summarise(
    'valid' = n() - sum(na),
    'excluded' = sum(na)
  ) %>%
  arrange(hormone)
```

```
## # A tibble: 2 x 3
##   hormone valid excluded
##   <chr>    <int>    <int>
## 1 c      275      1
## 2 t      272      4
```

```

# Calculate average hormones for each participant
data_avg <- data_final %>%
  group_by(hm_id) %>%
  summarise(
    avg_testosterone = mean(testosterone, na.rm = TRUE),
    avg_cortisol = mean(cortisol, na.rm = TRUE)
  ) %>%
  group_by() %>%
  # divide by constants to make range approx -.5 to +.5 for lmer
  mutate(
    avg_testosterone.s = (avg_testosterone - mean(avg_testosterone, na.rm=TRUE)) /
180,
    avg_cortisol.s = (avg_cortisol-mean(avg_cortisol, na.rm=TRUE)) / 0.5
  )

```

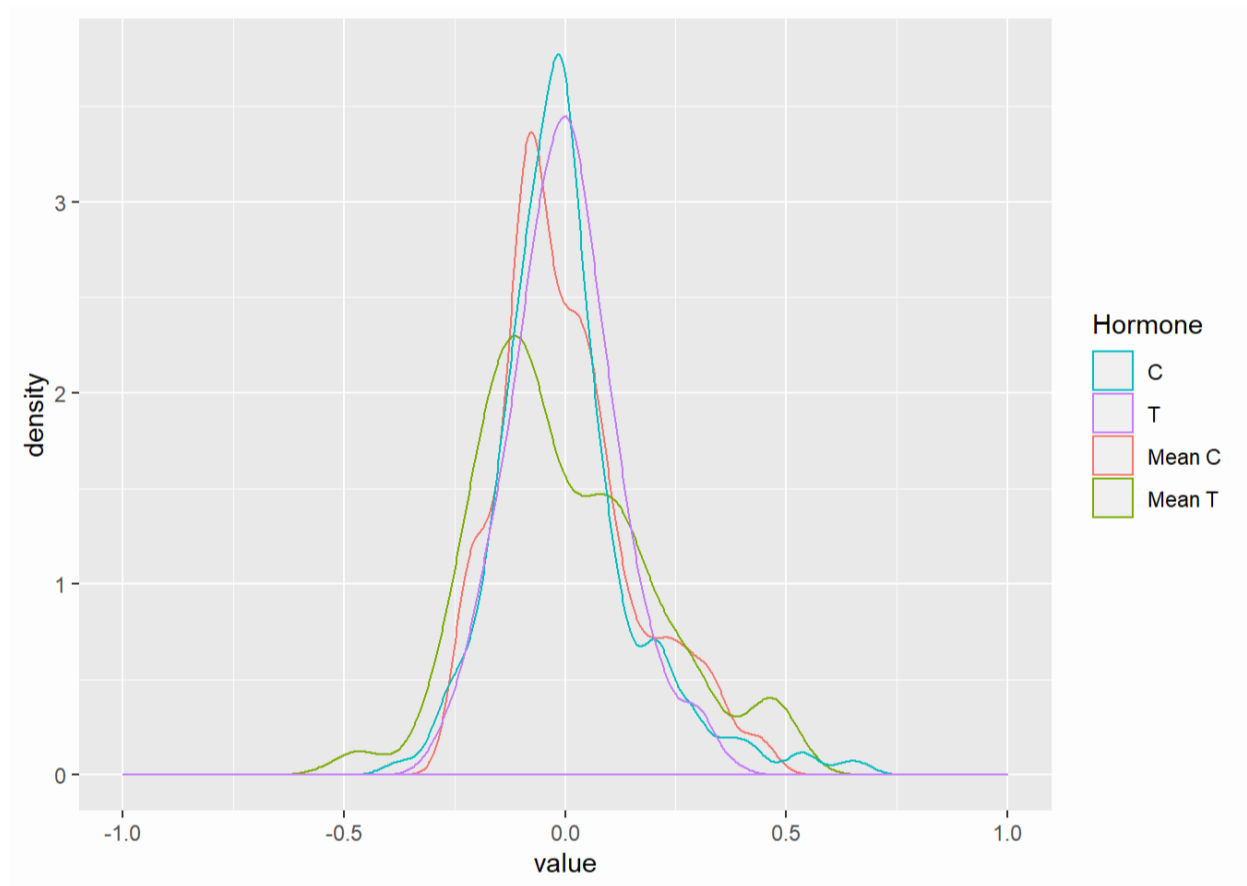
## Centre and scale hormones

Centre hormones on subject-specific means, and bring values between -0.5 and 0.5 to facilitate calculations in linear mixed effects models. This graph illustrates that testosterone and cortisol values are not skewed.

```

# centre hormones within-subject
# divide by same constants above to make range approx -.5 to +.5 for lmer
data_scaled <- data_final %>%
  group_by(hm_id) %>%
  mutate(
    testosterone.s = (testosterone-mean(testosterone, na.rm=TRUE)) / 180,
    cortisol.s = (cortisol-mean(cortisol, na.rm=TRUE)) / 0.5
  ) %>%
  ungroup() %>%
  left_join(data_avg, by="hm_id")

```



## Mean hormone levels

```
data_scaled %>%
  group_by(hm_id, date, age, testosterone, cortisol) %>%
  summarise(n = n()) %>%
  ungroup() %>%
  group_by() %>%
  summarise(
    mean_testosterone = mean(testosterone, na.rm = TRUE),
    sd_testosterone = sd(testosterone, na.rm = TRUE),
    se_testosterone = se(testosterone, na.rm = TRUE),
    mean_cortisol = mean(cortisol, na.rm = TRUE),
    sd_cortisol = sd(cortisol, na.rm = TRUE),
    se_cortisol = se(cortisol, na.rm = TRUE)
  ) %>% gather("stat", "value", 1:length(.)) %>%
  mutate(value = round(value, 4)) %>%
  separate(stat, c("stat", "hormone")) %>%
  spread(stat, value)
```

```
## # A tibble: 2 x 4
##   hormone      mean    sd    se
##   <chr>      <dbl> <dbl> <dbl>
## 1 cortisol    0.190  0.107 0.0064
## 2 testosterone 178.   41.4  2.50
```

# Sexual desire Analyses

Notes:

SOI already reverse scored.

Average items to get subscale values for each facet

Then average all items for the SOI-R full scale score

```
data_scaled$SOIR_behavior <- rowMeans(data_scaled[,c(12:14)])  
data_scaled$SOIR_attitude <- rowMeans(data_scaled[,c(15:17)])  
data_scaled$SOIR_desire <- rowMeans(data_scaled[,c(18:20)])  
data_scaled$SOIR_full <- rowMeans(data_scaled[,c(12:20)])
```

Notes SDI: SDI equations below (some need 1 subtracted)

Items 10-12 = solitary desire, (Item10) + Item11-1 + (Item12-1) as solitary\_SDI,

Items 1-8 = dyadic desire Item1 + Item2 + (Item3-1) + (Item4-1) + (Item5-1) + (Item6-1) + (Item7-1) + (Item8-1) as dyadic\_SDI,

All items summed = (again those with 9-point scales -1, which are Items 3-9, 11-14) as total\_SDI

```
data_scaled$SDI_solitary <- data_scaled$SDI10 + (data_scaled$SDI11-1) + (data_scaled$SDI12 -1)
```

```
data_scaled$SDI_dyadic <- data_scaled$SDI1 + data_scaled$SDI2 + (data_scaled$SDI3 -1) + (data_scaled$SDI4 -1) + (data_scaled$SDI5 -1) + (data_scaled$SDI6 -1) + (data_scaled$SDI7 -1) + (data_scaled$SDI8 -1)
```

```
data_scaled$SDI_full <- data_scaled$SDI1 + data_scaled$SDI2 + (data_scaled$SDI3 -1) + (data_scaled$SDI4 -1) + (data_scaled$SDI5 -1) + (data_scaled$SDI6 -1) + (data_scaled$SDI7 -1) + (data_scaled$SDI8 -1) + (data_scaled$SDI9 -1) + data_scaled$SDI10 + (data_scaled$SDI11 -1) + (data_scaled$SDI12 -1) + (data_scaled$SDI13 -1) + (data_scaled$SDI14 -1)
```

```
###descriptives
```

```
psych::describe(data_scaled)
```

| ##                    | vars  | n     | mean     | sd    | median | trimmed | mad   | min   | max    |
|-----------------------|-------|-------|----------|-------|--------|---------|-------|-------|--------|
| ## hm_id*             | 1     | 283   | 34.59    | 19.53 | 35.00  | 34.63   | 25.20 | 1.00  | 68.00  |
| ## relationship*      | 2     | 283   | 1.49     | 0.50  | 1.00   | 1.48    | 0.00  | 1.00  | 2.00   |
| ## age                | 3     | 283   | 22.11    | 3.15  | 21.50  | 21.69   | 2.82  | 18.20 | 31.50  |
| ## date*              | 4     | 283   | 20.33    | 10.71 | 21.00  | 20.50   | 13.34 | 1.00  | 39.00  |
| ## sex*               | 5     | 283   | 1.00     | 0.00  | 1.00   | 1.00    | 0.00  | 1.00  | 1.00   |
| ## ethnicity*         | 6     | 283   | 4.81     | 0.72  | 5.00   | 5.00    | 0.00  | 1.00  | 5.00   |
| ## sexpref*           | 7     | 283   | 3.88     | 0.52  | 4.00   | 4.00    | 0.00  | 1.00  | 4.00   |
| ## session            | 8     | 283   | 2.95     | 1.45  | 3.00   | 2.93    | 1.48  | 1.00  | 6.00   |
| ## testosterone       | 9     | 279   | 178.26   | 41.97 | 169.66 | 175.41  | 37.97 | 60.70 | 314.95 |
| ## cortisol           | 10    | 282   | 0.19     | 0.11  | 0.16   | 0.18    | 0.07  | 0.04  | 0.62   |
| ## labnotes*          | 11    | 283   | 1.00     | 0.06  | 1.00   | 1.00    | 0.00  | 1.00  | 2.00   |
| ## behavior1          | 12    | 257   | 2.27     | 0.91  | 2.00   | 2.21    | 1.48  | 1.00  | 4.00   |
| ## behavior2          | 13    | 262   | 2.09     | 0.95  | 2.00   | 1.99    | 1.48  | 1.00  | 5.00   |
| ## behavior3          | 14    | 262   | 2.24     | 1.15  | 2.00   | 2.11    | 1.48  | 1.00  | 5.00   |
| ## attitude1          | 15    | 274   | 3.72     | 1.30  | 4.00   | 3.90    | 1.48  | 1.00  | 5.00   |
| ## attitude2          | 16    | 273   | 3.18     | 1.33  | 3.00   | 3.23    | 1.48  | 1.00  | 5.00   |
| ## attitude3          | 17    | 270   | 3.63     | 1.29  | 4.00   | 3.79    | 1.48  | 1.00  | 5.00   |
| ## desire1            | 18    | 269   | 3.53     | 1.08  | 4.00   | 3.54    | 1.48  | 1.00  | 5.00   |
| ## desire2            | 19    | 270   | 3.05     | 1.01  | 3.00   | 3.06    | 1.48  | 1.00  | 5.00   |
| ## desire3            | 20    | 270   | 3.16     | 1.18  | 3.00   | 3.14    | 1.48  | 1.00  | 5.00   |
| ## trait_sexdrive     | 21    | 275   | 4.72     | 1.38  | 5.00   | 4.80    | 1.48  | 1.00  | 7.00   |
| ## state_sexdrive     | 22    | 274   | 4.29     | 1.57  | 4.00   | 4.35    | 1.48  | 1.00  | 7.00   |
| ## SDI1               | 23    | 270   | 4.00     | 1.79  | 4.00   | 4.13    | 1.48  | 0.00  | 7.00   |
| ## SDI2               | 24    | 269   | 4.17     | 1.74  | 4.00   | 4.25    | 1.48  | 0.00  | 7.00   |
| ## SDI3               | 25    | 274   | 6.36     | 1.80  | 7.00   | 6.49    | 1.48  | 1.00  | 9.00   |
| ## SDI4               | 26    | 275   | 5.37     | 1.80  | 6.00   | 5.44    | 1.48  | 1.00  | 9.00   |
| ## SDI5               | 27    | 275   | 5.75     | 1.83  | 6.00   | 5.89    | 1.48  | 1.00  | 9.00   |
| ## SDI6               | 28    | 274   | 6.11     | 1.84  | 6.00   | 6.23    | 1.48  | 1.00  | 9.00   |
| ## SDI7               | 29    | 274   | 6.64     | 1.64  | 7.00   | 6.79    | 1.48  | 1.00  | 9.00   |
| ## SDI8               | 30    | 274   | 6.09     | 2.10  | 7.00   | 6.24    | 1.48  | 1.00  | 9.00   |
| ## SDI9               | 31    | 272   | 5.39     | 1.80  | 5.00   | 5.50    | 1.48  | 1.00  | 9.00   |
| ## SDI10              | 32    | 268   | 3.51     | 1.73  | 4.00   | 3.62    | 1.48  | 0.00  | 7.00   |
| ## SDI11              | 33    | 271   | 4.82     | 1.93  | 5.00   | 4.81    | 1.48  | 1.00  | 9.00   |
| ## SDI12              | 34    | 271   | 4.31     | 2.27  | 4.00   | 4.27    | 2.97  | 1.00  | 9.00   |
| ## SDI13              | 35    | 272   | 4.58     | 1.84  | 5.00   | 4.56    | 1.48  | 1.00  | 9.00   |
| ## SDI14              | 36    | 273   | 3.70     | 1.58  | 4.00   | 3.70    | 1.48  | 1.00  | 8.00   |
| ## testosterone.s     | 37    | 279   | 0.00     | 0.12  | 0.00   | 0.00    | 0.11  | -0.31 | 0.38   |
| ## cortisol.s         | 38    | 282   | 0.00     | 0.16  | -0.02  | -0.01   | 0.11  | -0.39 | 0.67   |
| ## avg_testosterone   | 39    | 283   | 179.11   | 36.28 | 169.30 | 176.69  | 37.23 | 94.81 | 265.10 |
| ## avg_cortisol       | 40    | 283   | 0.19     | 0.08  | 0.18   | 0.19    | 0.06  | 0.07  | 0.41   |
| ## avg_testosterone.s | 41    | 283   | 0.00     | 0.20  | -0.06  | -0.01   | 0.21  | -0.47 | 0.48   |
| ## avg_cortisol.s     | 42    | 283   | 0.00     | 0.15  | -0.01  | -0.01   | 0.12  | -0.25 | 0.44   |
| ## SOIR_behavior      | 43    | 257   | 2.17     | 0.81  | 2.00   | 2.12    | 0.99  | 1.00  | 4.67   |
| ## SOIR_attitude      | 44    | 270   | 3.52     | 1.15  | 3.67   | 3.63    | 0.99  | 1.00  | 5.00   |
| ## SOIR_desire        | 45    | 269   | 3.25     | 0.95  | 3.33   | 3.25    | 0.99  | 1.33  | 5.00   |
| ## SOIR_full          | 46    | 255   | 2.98     | 0.75  | 3.11   | 3.02    | 0.66  | 1.11  | 4.33   |
| ## SDI_solitary       | 47    | 268   | 10.63    | 5.11  | 11.00  | 10.70   | 5.93  | 0.00  | 23.00  |
| ## SDI_dyadic         | 48    | 267   | 38.55    | 10.04 | 40.00  | 39.33   | 8.90  | 1.00  | 59.00  |
| ## SDI_full           | 49    | 264   | 60.11    | 16.33 | 60.00  | 60.41   | 14.83 | 11.00 | 96.00  |
| ##                    | range | skew  | kurtosis | se    |        |         |       |       |        |
| ## hm_id*             | 67.00 | -0.02 | -1.24    | 1.16  |        |         |       |       |        |

|                       |        |       |        |      |
|-----------------------|--------|-------|--------|------|
| ## relationship*      | 1.00   | 0.05  | -2.00  | 0.03 |
| ## age                | 13.30  | 1.11  | 0.80   | 0.19 |
| ## date*              | 38.00  | -0.15 | -1.16  | 0.64 |
| ## sex*               | 0.00   | NaN   | NaN    | 0.00 |
| ## ethnicity*         | 4.00   | -4.01 | 15.72  | 0.04 |
| ## sexpref*           | 3.00   | -4.63 | 20.92  | 0.03 |
| ## session            | 5.00   | 0.09  | -1.29  | 0.09 |
| ## testosterone       | 254.25 | 0.54  | 0.15   | 2.51 |
| ## cortisol           | 0.58   | 1.52  | 2.48   | 0.01 |
| ## labnotes*          | 1.00   | 16.64 | 276.02 | 0.00 |
| ## behavior1          | 3.00   | 0.28  | -0.72  | 0.06 |
| ## behavior2          | 4.00   | 0.99  | 1.14   | 0.06 |
| ## behavior3          | 4.00   | 0.62  | -0.46  | 0.07 |
| ## attitude1          | 4.00   | -0.85 | -0.31  | 0.08 |
| ## attitude2          | 4.00   | -0.23 | -1.12  | 0.08 |
| ## attitude3          | 4.00   | -0.91 | -0.23  | 0.08 |
| ## desire1            | 4.00   | -0.23 | -1.20  | 0.07 |
| ## desire2            | 4.00   | -0.06 | -1.01  | 0.06 |
| ## desire3            | 4.00   | -0.01 | -1.19  | 0.07 |
| ## trait_sexdrive     | 6.00   | -0.49 | 0.03   | 0.08 |
| ## state_sexdrive     | 6.00   | -0.27 | -0.63  | 0.09 |
| ## SDI1               | 7.00   | -0.62 | -0.12  | 0.11 |
| ## SDI2               | 7.00   | -0.37 | -0.74  | 0.11 |
| ## SDI3               | 8.00   | -0.62 | -0.08  | 0.11 |
| ## SDI4               | 8.00   | -0.41 | -0.78  | 0.11 |
| ## SDI5               | 8.00   | -0.60 | -0.44  | 0.11 |
| ## SDI6               | 8.00   | -0.56 | -0.28  | 0.11 |
| ## SDI7               | 8.00   | -0.88 | 0.92   | 0.10 |
| ## SDI8               | 8.00   | -0.61 | -0.38  | 0.13 |
| ## SDI9               | 8.00   | -0.44 | -0.10  | 0.11 |
| ## SDI10              | 7.00   | -0.53 | -0.27  | 0.11 |
| ## SDI11              | 8.00   | 0.05  | -0.61  | 0.12 |
| ## SDI12              | 8.00   | 0.14  | -1.13  | 0.14 |
| ## SDI13              | 8.00   | 0.12  | -0.29  | 0.11 |
| ## SDI14              | 7.00   | 0.11  | -0.77  | 0.10 |
| ## testosterone.s     | 0.69   | 0.29  | 0.19   | 0.01 |
| ## cortisol.s         | 1.06   | 1.18  | 2.82   | 0.01 |
| ## avg_testosterone   | 170.30 | 0.52  | -0.01  | 2.16 |
| ## avg_cortisol       | 0.34   | 0.79  | 0.21   | 0.00 |
| ## avg_testosterone.s | 0.95   | 0.52  | -0.01  | 0.01 |
| ## avg_cortisol.s     | 0.68   | 0.79  | 0.21   | 0.01 |
| ## SOIR_behavior      | 3.67   | 0.44  | -0.38  | 0.05 |
| ## SOIR_attitude      | 4.00   | -0.69 | -0.28  | 0.07 |
| ## SOIR_desire        | 3.67   | -0.17 | -1.09  | 0.06 |
| ## SOIR_full          | 3.22   | -0.53 | -0.60  | 0.05 |
| ## SDI_solitary       | 23.00  | -0.10 | -0.71  | 0.31 |
| ## SDI_dyadic         | 58.00  | -0.93 | 1.29   | 0.61 |
| ## SDI_full           | 85.00  | -0.27 | 0.24   | 1.01 |

## Exclude non-straight men (n=4) to see if that changes any results

```
# set values > 3SD from the mean to NA
data_scaled2 <- data_scaled

data_scaled2 <- data_scaled2[(data_scaled2$sexpref=="women"),]
```

### ANALYSES

## Results for LMEM Analysis for SDI

```
##full scale sdi
SDI_full_model <- lmer(SDI_full ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SDI_full_model <- summary(SDI_full_model)
```

```
summary.SDI_full_model$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##              Effect Estimate Std. Error    df t value
## 1              (Intercept)   61.916      2.166  58.796  28.591
## 2            testosterone.s    1.285      2.787   30.489   0.461
## 3              cortisol.s   -2.068      2.236   11.103  -0.925
## 4          avg_testosterone.s    2.089     11.812   59.179   0.177
## 5            avg_cortisol.s  -17.122     14.742   60.012  -1.161
## 6      testosterone.s:cortisol.s   27.039     17.940   59.409   1.507
## 7 avg_testosterone.s:avg_cortisol.s -74.805     52.565   58.647  -1.423
##           p
## 1 0.000
## 2 0.648
## 3 0.375
## 4 0.860
## 5 0.250
## 6 0.137
## 7 0.160
```

```
#sdi solitary
SDI_solitary_model <- lmer(SDI_solitary ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SDI_solitary_model <- summary(SDI_solitary_model)

summary.SDI_solitary_model$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##              Effect Estimate Std. Error    df t value
## 1      (Intercept)   11.324      0.651  60.158  17.398
## 2      testosterone.s   -1.647      0.928  202.934  -1.776
## 3          cortisol.s    0.409      0.772  204.013   0.530
## 4    avg_testosterone.s    3.689      3.550   60.532   1.039
## 5      avg_cortisol.s   -4.056      4.441   61.884  -0.913
## 6 testosterone.s:cortisol.s    2.245      6.267  207.805   0.358
## 7 avg_testosterone.s:avg_cortisol.s -28.445     15.801   60.045  -1.800
##      p
## 1 0.000
## 2 0.077
## 3 0.597
## 4 0.303
## 5 0.365
## 6 0.720
## 7 0.077
```

```
#sdi dyadic
SDI_dyadic_model <- lmer(SDI_dyadic ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SDI_dyadic_model <- summary(SDI_dyadic_model)

summary.SDI_dyadic_model$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##              Effect Estimate Std. Error      df t value
## 1      (Intercept)   39.280      1.322   58.594   29.710
## 2      testosterone.s    3.961      2.351   30.147    1.685
## 3      cortisol.s    -1.182      1.673  190.276   -0.706
## 4      avg_testosterone.s -0.754      7.269   59.111   -0.104
## 5      avg_cortisol.s  -10.168      9.083   60.291   -1.119
## 6      testosterone.s:cortisol.s  22.269     13.633  201.732    1.633
## 7      avg_testosterone.s:avg_cortisol.s -38.649     32.345   58.347   -1.195
##           p
## 1 0.000
## 2 0.102
## 3 0.481
## 4 0.918
## 5 0.267
## 6 0.104
## 7 0.237
```

## Results for LMEM Analysis for SOI\_R

```
#SOIR full scale
SOIR_full_model <- lmer(SOIR_full ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge: degenerate Hessian with 1
## negative eigenvalues
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -3.2e-02
```

```
summary.SOIR_full_model <- summary(SOIR_full_model)
```

```
summary.SOIR_full_model$coefficients %>%  
  as.data.frame() %>%  
  rownames_to_column(var = "Effect") %>%  
  mutate_if(is.numeric, round, 3) %>%  
  rename(p = `Pr(>|t|)`)
```

```
##              Effect Estimate Std. Error      df t value  
## 1      (Intercept)    3.108      0.096  57.056  32.461  
## 2      testosterone.s -0.050      0.131  37.534  -0.384  
## 3      cortisol.s    -0.126      0.119  28.839  -1.061  
## 4      avg_testosterone.s  0.912      0.509  57.403   1.791  
## 5      avg_cortisol.s   -0.201      0.641  58.431  -0.314  
## 6      testosterone.s:cortisol.s  0.473      0.874 154.809   0.542  
## 7      avg_testosterone.s:avg_cortisol.s -6.174      2.269  56.976  -2.721  
##           p  
## 1 0.000  
## 2 0.703  
## 3 0.297  
## 4 0.079  
## 5 0.755  
## 6 0.589  
## 7 0.009
```

```
#SOIR behavior
```

```
SOIR_behavior_model <- lmer(SOIR_behavior ~ 1 + testosterone.s * cortisol.s +  
  avg_testosterone.s * avg_cortisol.s +  
  (testosterone.s * cortisol.s || hm_id),  
  data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SOIR_behavior_model <- summary(SOIR_behavior_model)
```

```
summary.SOIR_behavior_model$coefficients %>%  
  as.data.frame() %>%  
  rownames_to_column(var = "Effect") %>%  
  mutate_if(is.numeric, round, 3) %>%  
  rename(p = `Pr(>|t|)`)
```

```
##
##           Effect Estimate Std. Error    df t value
## 1      (Intercept)    2.208      0.114  57.101  19.422
## 2      testosterone.s -0.139      0.139 192.790  -1.000
## 3      cortisol.s    -0.043      0.116 144.071  -0.366
## 4      avg_testosterone.s  0.756      0.610  57.327   1.239
## 5      avg_cortisol.s    0.291      0.767  58.387   0.380
## 6      testosterone.s:cortisol.s  1.703      0.999  14.449   1.706
## 7      avg_testosterone.s:avg_cortisol.s -0.324      2.717  56.984  -0.119
##      p
## 1 0.000
## 2 0.318
## 3 0.715
## 4 0.220
## 5 0.705
## 6 0.109
## 7 0.906
```

```
#SOIR attitude
SOIR_attitude_model <- lmer(SOIR_attitude ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge: degenerate Hessian with 1
## negative eigenvalues
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -2.0e-03
```

```
summary.SOIR_attitude_model <- summary(SOIR_attitude_model)

summary.SOIR_attitude_model$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 3.761    | 0.136      | 60.653  | 27.697  |
| ## 2 | testosterone.s                    | 0.116    | 0.256      | 36.505  | 0.452   |
| ## 3 | cortisol.s                        | 0.094    | 0.215      | 23.516  | 0.437   |
| ## 4 | avg_testosterone.s                | 1.236    | 0.740      | 61.020  | 1.671   |
| ## 5 | avg_cortisol.s                    | -0.293   | 0.927      | 62.556  | -0.317  |
| ## 6 | testosterone.s:cortisol.s         | -1.504   | 1.537      | 148.323 | -0.979  |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -11.834  | 3.296      | 60.509  | -3.590  |

## p

## 1 0.000

## 2 0.654

## 3 0.666

## 4 0.100

## 5 0.753

## 6 0.329

## 7 0.001

```
#SOIR desire
SOIR_desire_model <- lmer(SOIR_desire ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge: degenerate Hessian with 1
## negative eigenvalues
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -3.8e-02
```

```
summary.SOIR_desire_model <- summary(SOIR_desire_model)

summary.SOIR_desire_model$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 3.374    | 0.116      | 60.286  | 29.174  |
| ## 2 | testosterone.s                    | -0.003   | 0.207      | 200.316 | -0.013  |
| ## 3 | cortisol.s                        | -0.473   | 0.237      | 44.869  | -1.995  |
| ## 4 | avg_testosterone.s                | 0.892    | 0.631      | 60.940  | 1.414   |
| ## 5 | avg_cortisol.s                    | -0.716   | 0.792      | 62.679  | -0.904  |
| ## 6 | testosterone.s:cortisol.s         | 1.425    | 1.527      | 200.029 | 0.933   |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -6.425   | 2.806      | 60.044  | -2.290  |

|      | p     |
|------|-------|
| ## 1 | 0.000 |
| ## 2 | 0.989 |
| ## 3 | 0.052 |
| ## 4 | 0.163 |
| ## 5 | 0.369 |
| ## 6 | 0.352 |
| ## 7 | 0.026 |

## ANALYSES PART 2

# Do all analyses again for straight people only

## Results for LMEM Analysis for SDI

```
##full scale sdi
SDI_full_model2 <- lmer(SDI_full ~ 1 + testosterone.s * cortisol.s +
                        avg_testosterone.s * avg_cortisol.s +
                        (testosterone.s * cortisol.s || hm_id),
                        data = data_scaled2, REML = FALSE)

summary.SDI_full_model2 <- summary(SDI_full_model2)

summary.SDI_full_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df     | t value |
|------|-----------------------------------|----------|------------|--------|---------|
| ## 1 | (Intercept)                       | 62.776   | 2.124      | 55.925 | 29.563  |
| ## 2 | testosterone.s                    | 1.678    | 2.876      | 29.906 | 0.584   |
| ## 3 | cortisol.s                        | -2.449   | 2.291      | 9.979  | -1.069  |
| ## 4 | avg_testosterone.s                | 0.263    | 11.297     | 56.460 | 0.023   |
| ## 5 | avg_cortisol.s                    | -14.751  | 14.430     | 57.077 | -1.022  |
| ## 6 | testosterone.s:cortisol.s         | 25.871   | 18.636     | 58.717 | 1.388   |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -84.068  | 50.115     | 55.945 | -1.677  |

## p

## 1 0.000

## 2 0.564

## 3 0.310

## 4 0.982

## 5 0.311

## 6 0.170

## 7 0.099

```
#sdi solitary
SDI_solitary_model2 <- lmer(SDI_solitary ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled2, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SDI_solitary_model2 <- summary(SDI_solitary_model2)

summary.SDI_solitary_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 11.335   | 0.684      | 56.175  | 16.566  |
| ## 2 | testosterone.s                    | -1.418   | 0.939      | 194.816 | -1.510  |
| ## 3 | cortisol.s                        | 0.583    | 0.792      | 195.899 | 0.736   |
| ## 4 | avg_testosterone.s                | 3.293    | 3.640      | 56.697  | 0.905   |
| ## 5 | avg_cortisol.s                    | -3.408   | 4.656      | 57.629  | -0.732  |
| ## 6 | testosterone.s:cortisol.s         | 1.221    | 6.507      | 199.586 | 0.188   |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -29.426  | 16.155     | 56.297  | -1.821  |

## p

## 1 0.000

## 2 0.133

## 3 0.462

## 4 0.369

## 5 0.467

## 6 0.851

## 7 0.074

```
#sdi dyadic
SDI_dyadic_model2 <- lmer(SDI_dyadic ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled2, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SDI_dyadic_model2 <- summary(SDI_dyadic_model2)

summary.SDI_dyadic_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 39.907   | 1.266      | 56.804  | 31.512  |
| ## 2 | testosterone.s                    | 4.006    | 2.365      | 28.512  | 1.694   |
| ## 3 | cortisol.s                        | -1.747   | 1.721      | 188.755 | -1.015  |
| ## 4 | avg_testosterone.s                | -2.159   | 6.799      | 57.568  | -0.318  |
| ## 5 | avg_cortisol.s                    | -8.194   | 8.692      | 58.477  | -0.943  |
| ## 6 | testosterone.s:cortisol.s         | 23.292   | 14.175     | 198.260 | 1.643   |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -45.025  | 30.154     | 56.784  | -1.493  |

|      | p     |
|------|-------|
| ## 1 | 0.000 |
| ## 2 | 0.101 |
| ## 3 | 0.311 |
| ## 4 | 0.752 |
| ## 5 | 0.350 |
| ## 6 | 0.102 |
| ## 7 | 0.141 |

## Results for LMEM Analysis for SOI\_R

```
#SOIR full scale
SOIR_full_model2 <- lmer(SOIR_full ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled2, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00252753
## (tol = 0.002, component 1)
```

```
summary.SOIR_full_model2 <- summary(SOIR_full_model2)

summary.SOIR_full_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df     | t value |
|------|-----------------------------------|----------|------------|--------|---------|
| ## 1 | (Intercept)                       | 3.099    | 0.098      | 54.948 | 31.487  |
| ## 2 | testosterone.s                    | -0.061   | 0.132      | 36.574 | -0.464  |
| ## 3 | cortisol.s                        | -0.132   | 0.120      | 27.724 | -1.104  |
| ## 4 | avg_testosterone.s                | 0.917    | 0.520      | 55.401 | 1.765   |
| ## 5 | avg_cortisol.s                    | -0.148   | 0.664      | 56.120 | -0.222  |
| ## 6 | testosterone.s:cortisol.s         | 0.674    | 0.945      | 20.104 | 0.714   |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -6.195   | 2.304      | 54.983 | -2.688  |

## p

## 1 0.000

## 2 0.646

## 3 0.279

## 4 0.083

## 5 0.825

## 6 0.484

## 7 0.009

*#SOIR behavior*

```
SOIR_behavior_model2 <- lmer(SOIR_behavior ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled2, REML = FALSE)
```

## boundary (singular) fit: see ?isSingular

```
summary.SOIR_behavior_model2 <- summary(SOIR_behavior_model2)
```

```
summary.SOIR_behavior_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 2.195    | 0.112      | 53.964  | 19.545  |
| ## 2 | testosterone.s                    | -0.143   | 0.141      | 188.610 | -1.017  |
| ## 3 | cortisol.s                        | -0.041   | 0.118      | 141.171 | -0.351  |
| ## 4 | avg_testosterone.s                | 0.767    | 0.593      | 54.406  | 1.294   |
| ## 5 | avg_cortisol.s                    | 0.553    | 0.758      | 55.248  | 0.729   |
| ## 6 | testosterone.s:cortisol.s         | 1.683    | 1.004      | 14.226  | 1.677   |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -0.778   | 2.630      | 54.067  | -0.296  |

## p

## 1 0.000

## 2 0.310

## 3 0.726

## 4 0.201

## 5 0.469

## 6 0.115

## 7 0.768

*#SOIR attitude*

```
SOIR_attitude_model2 <- lmer(SOIR_attitude ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled2, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.0174095
## (tol = 0.002, component 1)
```

```
summary.SOIR_attitude_model2 <- summary(SOIR_attitude_model2)
```

```
summary.SOIR_attitude_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##
```

|      | Effect                            | Estimate | Std. Error | df     | t value |
|------|-----------------------------------|----------|------------|--------|---------|
| ## 1 | (Intercept)                       | 3.738    | 0.141      | 57.762 | 26.516  |
| ## 2 | testosterone.s                    | 0.095    | 0.265      | 35.385 | 0.358   |
| ## 3 | cortisol.s                        | 0.104    | 0.227      | 24.313 | 0.457   |
| ## 4 | avg_testosterone.s                | 1.197    | 0.756      | 58.146 | 1.584   |
| ## 5 | avg_cortisol.s                    | -0.135   | 0.967      | 59.302 | -0.140  |
| ## 6 | testosterone.s:cortisol.s         | -1.577   | 1.668      | 16.481 | -0.946  |
| ## 7 | avg_testosterone.s:avg_cortisol.s | -11.895  | 3.356      | 57.697 | -3.544  |

```
## p
## 1 0.000
## 2 0.722
## 3 0.652
## 4 0.119
## 5 0.889
## 6 0.358
## 7 0.001
```

```
#SOIR desire
```

```
SOIR_desire_model2 <- lmer(SOIR_desire ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s +
  (testosterone.s * cortisol.s || hm_id),
  data = data_scaled2, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SOIR_desire_model2 <- summary(SOIR_desire_model2)
```

```
summary.SOIR_desire_model2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##
##          Effect Estimate Std. Error      df t value
## 1      (Intercept)    3.391      0.118  57.218  28.817
## 2      testosterone.s -0.075      0.215 194.366  -0.351
## 3      cortisol.s    -0.505      0.248  45.424  -2.040
## 4      avg_testosterone.s  0.889      0.632  58.024   1.407
## 5      avg_cortisol.s   -1.010      0.809  59.220  -1.248
## 6      testosterone.s:cortisol.s  2.085      1.838  18.539   1.135
## 7      avg_testosterone.s:avg_cortisol.s -6.100      2.800  57.097  -2.178
##          p
## 1 0.000
## 2 0.726
## 3 0.047
## 4 0.165
## 5 0.217
## 6 0.271
## 7 0.034
```

## Additional analyses as requested in the review process

```
#Cronbachs alpha for the scales

#first SOI-R
data_soibehavior <- data[,c(12:14)]
data_soiaattitude <- data[,c(15:17)]
data_soidesire <- data[,c(18:20)]
data_soifull <- data[,c(12:20)]

psych::alpha(data_soidesire)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = data_soidesire)
##
##   raw_alpha std.alpha G6(smc) average_r S/N   ase mean   sd median_r
##      0.84      0.84    0.78      0.64 5.3 0.016  3.2 0.95      0.61
##
## lower alpha upper      95% confidence boundaries
## 0.81 0.84 0.87
##
## Reliability if an item is dropped:
##      raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## desire1      0.75      0.75    0.61      0.61 3.1   0.029   NA  0.61
## desire2      0.82      0.82    0.70      0.70 4.7   0.021   NA  0.70
## desire3      0.75      0.75    0.60      0.60 3.1   0.029   NA  0.60
##
## Item statistics
##      n raw.r std.r r.cor r.drop mean  sd
## desire1 269 0.88 0.88 0.80  0.73 3.5 1.1
## desire2 270 0.83 0.85 0.71  0.66 3.1 1.0
## desire3 270 0.89 0.88 0.80  0.73 3.2 1.2
##
## Non missing response frequency for each item
##      1    2    3    4    5 miss
## desire1 0.00 0.25 0.16 0.38 0.20 0.05
## desire2 0.04 0.31 0.24 0.35 0.05 0.05
## desire3 0.06 0.33 0.16 0.32 0.14 0.05
```

```
psych::alpha(data_soiattitude)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = data_soiattitude)
##
##   raw_alpha std.alpha G6(smc) average_r S/N   ase mean  sd median_r
##      0.85      0.85    0.79      0.65 5.5 0.016  3.5 1.1      0.64
##
## lower alpha upper      95% confidence boundaries
## 0.82 0.85 0.88
##
## Reliability if an item is dropped:
##           raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## attitude1      0.78      0.78    0.64      0.64 3.5   0.026   NA  0.64
## attitude2      0.76      0.76    0.61      0.61 3.2   0.028   NA  0.61
## attitude3      0.82      0.82    0.69      0.69 4.4   0.022   NA  0.69
##
## Item statistics
##           n raw.r std.r r.cor r.drop mean  sd
## attitude1 274  0.88  0.88  0.79  0.72  3.7 1.3
## attitude2 273  0.89  0.89  0.81  0.74  3.2 1.3
## attitude3 270  0.85  0.86  0.74  0.68  3.6 1.3
##
## Non missing response frequency for each item
##           1    2    3    4    5 miss
## attitude1 0.12 0.04 0.20 0.28 0.35 0.03
## attitude2 0.15 0.17 0.22 0.27 0.19 0.04
## attitude3 0.13 0.05 0.14 0.41 0.27 0.05
```

```
psych::alpha(data_soibehavior)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = data_soibehavior)
##
##   raw_alpha std.alpha G6(smc) average_r S/N   ase mean   sd median_r
##      0.77      0.77      0.71      0.53 3.4 0.023  2.2 0.86      0.51
##
## lower alpha upper      95% confidence boundaries
## 0.73 0.77 0.82
##
## Reliability if an item is dropped:
##           raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## behavior1      0.78      0.79      0.65      0.65 3.7   0.026   NA  0.65
## behavior2      0.66      0.67      0.51      0.51 2.0   0.039   NA  0.51
## behavior3      0.61      0.61      0.44      0.44 1.5   0.047   NA  0.44
##
## Item statistics
##           n raw.r std.r r.cor r.drop mean   sd
## behavior1 257  0.78  0.78  0.58  0.52  2.3 0.91
## behavior2 262  0.85  0.84  0.73  0.64  2.1 0.95
## behavior3 262  0.88  0.87  0.78  0.68  2.2 1.15
##
## Non missing response frequency for each item
##           1    2    3    4    5 miss
## behavior1 0.21 0.42 0.27 0.11 0.00 0.09
## behavior2 0.28 0.45 0.20 0.03 0.03 0.07
## behavior3 0.34 0.27 0.26 0.09 0.05 0.07
```

```
psych::alpha(data_soifull)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = data_soifull)
##
##   raw_alpha std.alpha G6(smc) average_r S/N   ase mean   sd median_r
##      0.83      0.83      0.87      0.35 4.9 0.015    3 0.76      0.3
##
##   lower alpha upper      95% confidence boundaries
## 0.8 0.83 0.86
##
## Reliability if an item is dropped:
##           raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## behavior1      0.83      0.83      0.87      0.38 4.9   0.015 0.029 0.33
## behavior2      0.82      0.81      0.85      0.35 4.3   0.016 0.034 0.28
## behavior3      0.82      0.82      0.85      0.36 4.4   0.016 0.033 0.31
## attitude1      0.81      0.81      0.85      0.35 4.3   0.017 0.030 0.31
## attitude2      0.80      0.81      0.85      0.34 4.1   0.018 0.030 0.29
## attitude3      0.80      0.80      0.85      0.33 4.0   0.018 0.033 0.27
## desire1        0.80      0.80      0.84      0.34 4.1   0.017 0.029 0.28
## desire2        0.82      0.82      0.86      0.36 4.5   0.016 0.031 0.33
## desire3        0.82      0.82      0.85      0.36 4.5   0.016 0.026 0.31
##
## Item statistics
##           n raw.r std.r r.cor r.drop mean   sd
## behavior1 257 0.49 0.52 0.43 0.38 2.3 0.91
## behavior2 262 0.63 0.66 0.61 0.53 2.1 0.95
## behavior3 262 0.61 0.63 0.58 0.49 2.2 1.15
## attitude1 274 0.69 0.67 0.64 0.58 3.7 1.30
## attitude2 273 0.72 0.70 0.67 0.62 3.2 1.33
## attitude3 270 0.76 0.74 0.70 0.66 3.6 1.29
## desire1   269 0.73 0.73 0.71 0.63 3.5 1.08
## desire2   270 0.60 0.61 0.55 0.48 3.1 1.01
## desire3   270 0.60 0.61 0.57 0.48 3.2 1.18
##
## Non missing response frequency for each item
##           1    2    3    4    5 miss
## behavior1 0.21 0.42 0.27 0.11 0.00 0.09
## behavior2 0.28 0.45 0.20 0.03 0.03 0.07
## behavior3 0.34 0.27 0.26 0.09 0.05 0.07
## attitude1 0.12 0.04 0.20 0.28 0.35 0.03
## attitude2 0.15 0.17 0.22 0.27 0.19 0.04
## attitude3 0.13 0.05 0.14 0.41 0.27 0.05
## desire1   0.00 0.25 0.16 0.38 0.20 0.05
## desire2   0.04 0.31 0.24 0.35 0.05 0.05
## desire3   0.06 0.33 0.16 0.32 0.14 0.05
```

```
#then SDI-2
SDI_solitary <- data[,c(32,33,34)]
SDI_dyadic <- data[,c(23:30)]
SDI_full <- data[,c(23:36)]

psych::alpha(SDI_solitary)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = SDI_solitary)
##
##   raw_alpha std.alpha G6(smc) average_r S/N   ase mean  sd median_r
##      0.82      0.82    0.76      0.6 4.6 0.018  4.2 1.7    0.57
##
##   lower alpha upper      95% confidence boundaries
## 0.78 0.82 0.85
##
## Reliability if an item is dropped:
##      raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## SDI10      0.81      0.81    0.69      0.69 4.4   0.022  NA  0.69
## SDI11      0.71      0.73    0.57      0.57 2.6   0.033  NA  0.57
## SDI12      0.71      0.71    0.55      0.55 2.5   0.034  NA  0.55
##
## Item statistics
##      n raw.r std.r r.cor r.drop mean  sd
## SDI10 268  0.80  0.82  0.67  0.61  3.5 1.7
## SDI11 271  0.87  0.87  0.78  0.71  4.8 1.9
## SDI12 271  0.90  0.88  0.79  0.72  4.3 2.3
```

```
psych::alpha(SDI_dyadic)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = SDI_dyadic)
##
##   raw_alpha std.alpha G6(smc) average_r S/N   ase mean  sd median_r
##      0.84      0.84      0.88      0.4 5.3 0.015  5.6 1.2      0.36
##
## lower alpha upper      95% confidence boundaries
## 0.81 0.84 0.87
##
## Reliability if an item is dropped:
##   raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## SDI1      0.81      0.81      0.85      0.39 4.4   0.017 0.033 0.36
## SDI2      0.83      0.84      0.87      0.42 5.1   0.016 0.030 0.42
## SDI3      0.80      0.81      0.85      0.37 4.1   0.018 0.034 0.32
## SDI4      0.82      0.83      0.84      0.41 4.8   0.016 0.032 0.37
## SDI5      0.84      0.84      0.86      0.44 5.4   0.014 0.025 0.45
## SDI6      0.83      0.83      0.87      0.42 5.1   0.016 0.035 0.42
## SDI7      0.79      0.79      0.83      0.35 3.8   0.019 0.027 0.32
## SDI8      0.82      0.82      0.87      0.40 4.6   0.017 0.036 0.37
##
## Item statistics
##      n raw.r std.r r.cor r.drop mean  sd
## SDI1 270 0.73 0.74 0.71 0.64 4.0 1.8
## SDI2 269 0.59 0.61 0.54 0.47 4.2 1.7
## SDI3 274 0.79 0.79 0.77 0.71 6.4 1.8
## SDI4 275 0.66 0.65 0.62 0.53 5.4 1.8
## SDI5 275 0.55 0.55 0.50 0.40 5.7 1.8
## SDI6 274 0.60 0.61 0.53 0.47 6.1 1.8
## SDI7 274 0.86 0.86 0.87 0.80 6.6 1.6
## SDI8 274 0.71 0.70 0.64 0.58 6.1 2.1
```

```
psych::alpha(SDI_full)
```

```
##
## Reliability analysis
## Call: psych::alpha(x = SDI_full)
##
##   raw_alpha std.alpha G6(smc) average_r S/N ase mean sd median_r
##      0.88      0.88      0.93      0.35 7.7 0.01  5.1 1.2      0.32
##
## lower alpha upper      95% confidence boundaries
## 0.86 0.88 0.9
##
## Reliability if an item is dropped:
##      raw_alpha std.alpha G6(smc) average_r S/N alpha se var.r med.r
## SDI1      0.87      0.87      0.92      0.34 6.8   0.011 0.030 0.32
## SDI2      0.88      0.88      0.92      0.36 7.3   0.011 0.031 0.33
## SDI3      0.87      0.87      0.92      0.35 6.9   0.011 0.029 0.32
## SDI4      0.88      0.88      0.91      0.36 7.3   0.011 0.031 0.34
## SDI5      0.88      0.89      0.92      0.37 7.7   0.010 0.028 0.35
## SDI6      0.88      0.88      0.93      0.37 7.6   0.010 0.029 0.35
## SDI7      0.87      0.87      0.91      0.34 6.6   0.012 0.027 0.32
## SDI8      0.88      0.88      0.92      0.35 7.1   0.011 0.031 0.33
## SDI9      0.87      0.88      0.92      0.35 7.1   0.011 0.029 0.32
## SDI10     0.88      0.89      0.93      0.38 7.8   0.010 0.025 0.35
## SDI11     0.87      0.87      0.92      0.35 7.0   0.011 0.029 0.32
## SDI12     0.88      0.88      0.92      0.35 7.1   0.011 0.030 0.32
## SDI13     0.87      0.87      0.92      0.34 6.8   0.011 0.030 0.32
## SDI14     0.88      0.88      0.92      0.35 7.1   0.011 0.032 0.32
##
## Item statistics
##      n raw.r std.r r.cor r.drop mean sd
## SDI1 270 0.71 0.72 0.71 0.66 4.0 1.8
## SDI2 269 0.59 0.60 0.57 0.51 4.2 1.7
## SDI3 274 0.71 0.72 0.70 0.65 6.4 1.8
## SDI4 275 0.60 0.60 0.59 0.52 5.4 1.8
## SDI5 275 0.47 0.47 0.44 0.38 5.7 1.8
## SDI6 274 0.50 0.50 0.45 0.40 6.1 1.8
## SDI7 274 0.80 0.80 0.80 0.75 6.6 1.6
## SDI8 274 0.65 0.64 0.62 0.57 6.1 2.1
## SDI9 272 0.65 0.66 0.64 0.58 5.4 1.8
## SDI10 268 0.46 0.45 0.41 0.36 3.5 1.7
## SDI11 271 0.69 0.67 0.66 0.61 4.8 1.9
## SDI12 271 0.67 0.65 0.63 0.58 4.3 2.3
## SDI13 272 0.74 0.74 0.73 0.69 4.6 1.8
## SDI14 273 0.62 0.64 0.60 0.56 3.7 1.6
```

```
#Correlation matrix for all relevant variables

#scale all variables first to bring them to the same scale

data_scaled_cor <- data_scaled
data_scaled_cor$SOIR_behavior.s <- scale(data_scaled_cor$SOIR_behavior)
data_scaled_cor$SOIR_attitude.s <- scale(data_scaled_cor$SOIR_attitude)
data_scaled_cor$SOIR_desire.s <- scale(data_scaled_cor$SOIR_desire)
data_scaled_cor$SOIR_full.s <- scale(data_scaled_cor$SOIR_full)
data_scaled_cor$SDI_solitary.s <- scale(data_scaled_cor$SDI_solitary)
data_scaled_cor$SDI_dyadic.s <- scale(data_scaled_cor$SDI_dyadic)
data_scaled_cor$SDI_full.s <- scale(data_scaled_cor$SDI_full)

#names(data_scaled_cor)

cor_data <- data_scaled_cor[,c(37,38,41,42,50:56)]

cor(cor_data, use = "pairwise.complete.obs")
```

```

##          testosterone.s      cortisol.s avg_testosterone.s
## testosterone.s      1.000000e+00  2.578466e-01      -6.169168e-17
## cortisol.s          2.578466e-01  1.000000e+00      -1.407057e-17
## avg_testosterone.s  -6.169168e-17 -1.407057e-17      1.000000e+00
## avg_cortisol.s      -1.450170e-16 -7.790847e-18      5.370004e-01
## SOIR_behavior.s     -2.275679e-02 -1.323380e-02      2.571439e-01
## SOIR_attitude.s     8.176030e-03  7.372913e-03      7.528622e-03
## SOIR_desire.s       -2.434361e-02 -7.457555e-02      2.419963e-02
## SOIR_full.s         -2.228729e-02 -3.191351e-02      1.129076e-01
## SDI_solitary.s      -3.998329e-02 -5.273162e-03      -1.559370e-02
## SDI_dyadic.s        4.554488e-02 -1.898856e-03      -1.681698e-01
## SDI_full.s          8.200642e-03 -1.973151e-02      -1.557184e-01
##          avg_cortisol.s SOIR_behavior.s SOIR_attitude.s
## testosterone.s      -1.450170e-16      -0.02275679      0.008176030
## cortisol.s          -7.790847e-18      -0.01323380      0.007372913
## avg_testosterone.s  5.370004e-01      0.25714394      0.007528622
## avg_cortisol.s      1.000000e+00      0.15976094      -0.136189891
## SOIR_behavior.s     1.597609e-01      1.00000000      0.406564026
## SOIR_attitude.s     -1.361899e-01      0.40656403      1.000000000
## SOIR_desire.s       -1.146684e-01      0.25869555      0.409897761
## SOIR_full.s         -6.090962e-02      0.68098169      0.845557429
## SDI_solitary.s      -1.337217e-01      0.10585670      0.324664945
## SDI_dyadic.s        -3.049896e-01      0.38233735      0.453113328
## SDI_full.s          -2.840101e-01      0.34821981      0.479378984
##          SOIR_desire.s SOIR_full.s SDI_solitary.s SDI_dyadic.s
## testosterone.s      -0.02434361 -0.02228729      -0.039983288  0.045544882
## cortisol.s          -0.07457555 -0.03191351      -0.005273162 -0.001898856
## avg_testosterone.s  0.02419963  0.11290763      -0.015593699 -0.168169810
## avg_cortisol.s      -0.11466842 -0.06090962      -0.133721698 -0.304989587
## SOIR_behavior.s     0.25869555  0.68098169      0.105856696  0.382337354
## SOIR_attitude.s     0.40989776  0.84555743      0.324664945  0.453113328
## SOIR_desire.s       1.00000000  0.74341877      0.257381621  0.383806796
## SOIR_full.s         0.74341877  1.00000000      0.320323589  0.537031914
## SDI_solitary.s      0.25738162  0.32032359      1.000000000  0.423063989
## SDI_dyadic.s        0.38380680  0.53703191      0.423063989  1.000000000
## SDI_full.s          0.38713756  0.53964411      0.717170502  0.915848137
##          SDI_full.s
## testosterone.s      0.008200642
## cortisol.s          -0.019731512
## avg_testosterone.s  -0.155718439
## avg_cortisol.s      -0.284010139
## SOIR_behavior.s     0.348219811
## SOIR_attitude.s     0.479378984
## SOIR_desire.s       0.387137558
## SOIR_full.s         0.539644109
## SDI_solitary.s      0.717170502
## SDI_dyadic.s        0.915848137
## SDI_full.s          1.000000000

```

```
#single correlations to get p-values and 95% CIs (results identical when computing correlation matrix with all variables at once)  
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$cortisol.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$testosterone.s and data_scaled_cor$cortisol.s  
## t = 4.4336, df = 276, p-value = 1.339e-05  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.1445896 0.3644349  
## sample estimates:  
## cor  
## 0.2578466
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$avg_testosterone.s, na.rm  
= TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$testosterone.s and data_scaled_cor$avg_testosterone.s  
## t = -1.0268e-15, df = 277, p-value = 1  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1174317 0.1174317  
## sample estimates:  
## cor  
## -6.169544e-17
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$avg_cortisol.s, na.rm = TR  
UE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$testosterone.s and data_scaled_cor$avg_cortisol.s  
## t = -2.4135e-15, df = 277, p-value = 1  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1174317 0.1174317  
## sample estimates:  
## cor  
## -1.45014e-16
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SOIR_behavior.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SOIR_behavior.s  
## t = -0.36063, df = 251, p-value = 0.7187  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1456759 0.1008542  
## sample estimates:  
## cor  
## -0.02275679
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SOIR_attitude.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SOIR_attitude.s  
## t = 0.13285, df = 264, p-value = 0.8944  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1122059 0.1283214  
## sample estimates:  
## cor  
## 0.00817603
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SOIR_desire.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SOIR_desire.s  
## t = -0.3949, df = 263, p-value = 0.6932  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.14441861 0.09643792  
## sample estimates:  
## cor  
## -0.02434361
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SOIR_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SOIR_full.s
## t = -0.35177, df = 249, p-value = 0.7253
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1457044 0.1018129
## sample estimates:
## cor
## -0.02228729
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SDI_solitary.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SDI_solitary.s
## t = -0.6477, df = 262, p-value = 0.5177
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.15993827 0.08113537
## sample estimates:
## cor
## -0.03998329
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SDI_dyadic.s
## t = 0.73656, df = 261, p-value = 0.462
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.07582955 0.16558934
## sample estimates:
## cor
## 0.04554488
```

```
cor.test(data_scaled_cor$testosterone.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$testosterone.s and data_scaled_cor$SDI_full.s
## t = 0.13173, df = 258, p-value = 0.8953
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1135663 0.1297249
## sample estimates:
## cor
## 0.008200642
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$avg_testosterone.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$cortisol.s and data_scaled_cor$avg_testosterone.s
## t = -2.3533e-16, df = 280, p-value = 1
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1168044 0.1168044
## sample estimates:
## cor
## -1.406379e-17
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$avg_cortisol.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$cortisol.s and data_scaled_cor$avg_cortisol.s
## t = -1.3019e-16, df = 280, p-value = 1
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1168044 0.1168044
## sample estimates:
## cor
## -7.780155e-18
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$SOIR_behavior.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$cortisol.s and data_scaled_cor$SOIR_behavior.s  
## t = -0.21093, df = 254, p-value = 0.8331  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1356158 0.1095459  
## sample estimates:  
## cor  
## -0.0132338
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$SOIR_attitude.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$cortisol.s and data_scaled_cor$SOIR_attitude.s  
## t = 0.12048, df = 267, p-value = 0.9042  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1123241 0.1268590  
## sample estimates:  
## cor  
## 0.007372913
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$SOIR_desire.s, na.rm = TRUE)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: data_scaled_cor$cortisol.s and data_scaled_cor$SOIR_desire.s  
## t = -1.2197, df = 266, p-value = 0.2237  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.19267507 0.04565361  
## sample estimates:  
## cor  
## -0.07457555
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$SOIR_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$cortisol.s and data_scaled_cor$$OIR_full.s
## t = -0.50687, df = 252, p-value = 0.6127
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.15439160 0.09153057
## sample estimates:
## cor
## -0.03191351
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$$SDI_solitary.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$cortisol.s and data_scaled_cor$$SDI_solitary.s
## t = -0.085842, df = 265, p-value = 0.9317
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1252396 0.1148453
## sample estimates:
## cor
## -0.005273162
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$cortisol.s and data_scaled_cor$$SDI_dyadic.s
## t = -0.030853, df = 264, p-value = 0.9754
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1221425 0.1183997
## sample estimates:
## cor
## -0.001898856
```

```
cor.test(data_scaled_cor$cortisol.s, data_scaled_cor$$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$cortisol.s and data_scaled_cor$SDI_full.s
## t = -0.31883, df = 261, p-value = 0.7501
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1403532 0.1014673
## sample estimates:
## cor
## -0.01973151
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$avg_cortisol.s, na.rm
= TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$avg_cortisol.s
## t = 10.671, df = 281, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.4484837 0.6150856
## sample estimates:
## cor
## 0.5370004
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SOIR_behavior.s, na.rm
= TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SOIR_behavior.s
## t = 4.2491, df = 255, p-value = 3.011e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1391598 0.3679299
## sample estimates:
## cor
## 0.2571439
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SOIR_attitude.s, na.rm
= TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SOIR_attitude.s
## t = 0.12325, df = 268, p-value = 0.902
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1119479 0.1267906
## sample estimates:
## cor
## 0.007528622
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SOIR_desire.s, na.rm =
TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SOIR_desire.s
## t = 0.39554, df = 267, p-value = 0.6928
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.0956752 0.1433826
## sample estimates:
## cor
## 0.02419963
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SOIR_full.s, na.rm = T
RUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SOIR_full.s
## t = 1.8075, df = 253, p-value = 0.07188
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.01007466 0.23252510
## sample estimates:
## cor
## 0.1129076
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SDI_solitary.s, na.rm
= TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SDI_solitary.s
## t = -0.25436, df = 266, p-value = 0.7994
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1351624 0.1044226
## sample estimates:
## cor
## -0.0155937
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SDI_dyadic.s, na.rm =
TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SDI_dyadic.s
## t = -2.7772, df = 265, p-value = 0.005875
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.28251218 -0.04911561
## sample estimates:
## cor
## -0.1681698
```

```
cor.test(data_scaled_cor$avg_testosterone.s, data_scaled_cor$SDI_full.s, na.rm = TR
UE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_testosterone.s and data_scaled_cor$SDI_full.s
## t = -2.5516, df = 262, p-value = 0.01129
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.27134433 -0.03566185
## sample estimates:
## cor
## -0.1557184
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SOIR_behavior.s, na.rm = T
RUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SOIR_behavior.s
## t = 2.5844, df = 255, p-value = 0.01031
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.03814377 0.27671434
## sample estimates:
## cor
## 0.1597609
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SOIR_attitude.s, na.rm = T
RUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SOIR_attitude.s
## t = -2.2505, df = 268, p-value = 0.02523
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.25147732 -0.01709188
## sample estimates:
## cor
## -0.1361899
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SOIR_desire.s, na.rm = TRU
E)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SOIR_desire.s
## t = -1.8861, df = 267, p-value = 0.06036
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.231097055 0.004998057
## sample estimates:
## cor
## -0.1146684
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SOIR_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SOIR_full.s
## t = -0.97063, df = 253, p-value = 0.3327
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.18238750 0.06239984
## sample estimates:
## cor
## -0.06090962
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SDI_solitary.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SDI_solitary.s
## t = -2.2007, df = 266, p-value = 0.02862
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.24954453 -0.01412684
## sample estimates:
## cor
## -0.1337217
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SDI_dyadic.s
## t = -5.2133, df = 265, p-value = 3.739e-07
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.4100233 -0.1919725
## sample estimates:
## cor
## -0.3049896
```

```
cor.test(data_scaled_cor$avg_cortisol.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$avg_cortisol.s and data_scaled_cor$SDI_full.s
## t = -4.7945, df = 262, p-value = 2.737e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3913197 -0.1690805
## sample estimates:
## cor
## -0.2840101
```

```
cor.test(data_scaled_cor$SOIR_behavior.s, data_scaled_cor$SOIR_attitude.s, na.rm =
TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_behavior.s and data_scaled_cor$SOIR_attitude.s
## t = 7.0922, df = 254, p-value = 1.308e-11
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2988588 0.5040418
## sample estimates:
## cor
## 0.406564
```

```
cor.test(data_scaled_cor$SOIR_behavior.s, data_scaled_cor$SOIR_desire.s, na.rm = TR
UE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_behavior.s and data_scaled_cor$SOIR_desire.s
## t = 4.2598, df = 253, p-value = 2.888e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1403119 0.3697867
## sample estimates:
## cor
## 0.2586955
```

```
cor.test(data_scaled_cor$SOIR_behavior.s, data_scaled_cor$SOIR_full.s, na.rm = TRU
E)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_behavior.s and data_scaled_cor$SOIR_full.s
## t = 14.791, df = 253, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.6090918 0.7417724
## sample estimates:
## cor
## 0.6809817
```

```
cor.test(data_scaled_cor$SOIR_behavior.s, data_scaled_cor$SDI_solitary.s, na.rm = T
RUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_behavior.s and data_scaled_cor$SDI_solitary.s
## t = 1.6933, df = 253, p-value = 0.09164
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.01720965 0.22576349
## sample estimates:
## cor
## 0.1058567
```

```
cor.test(data_scaled_cor$SOIR_behavior.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRU
E)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_behavior.s and data_scaled_cor$SDI_dyadic.s
## t = 6.5424, df = 250, p-value = 3.398e-10
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2715965 0.4830861
## sample estimates:
## cor
## 0.3823374
```

```
cor.test(data_scaled_cor$SOIR_behavior.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_behavior.s and data_scaled_cor$SDI_full.s
## t = 5.8617, df = 249, p-value = 1.447e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2345119 0.4525277
## sample estimates:
## cor
## 0.3482198
```

```
cor.test(data_scaled_cor$SOIR_attitude.s, data_scaled_cor$SOIR_desire.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_attitude.s and data_scaled_cor$SOIR_desire.s
## t = 7.343, df = 267, p-value = 2.531e-12
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.3052648 0.5047513
## sample estimates:
## cor
## 0.4098978
```

```
cor.test(data_scaled_cor$SOIR_attitude.s, data_scaled_cor$SOIR_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_attitude.s and data_scaled_cor$SOIR_full.s
## t = 25.192, df = 253, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.8064848 0.8772769
## sample estimates:
## cor
## 0.8455574
```

```
cor.test(data_scaled_cor$SOIR_attitude.s, data_scaled_cor$SDI_solitary.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_attitude.s and data_scaled_cor$SDI_solitary.s
## t = 5.5879, df = 265, p-value = 5.701e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2129176 0.4280284
## sample estimates:
## cor
## 0.3246649
```

```
cor.test(data_scaled_cor$SOIR_attitude.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_attitude.s and data_scaled_cor$SDI_dyadic.s
## t = 8.2273, df = 262, p-value = 9.032e-15
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.3516211 0.5440776
## sample estimates:
## cor
## 0.4531133
```

```
cor.test(data_scaled_cor$SOIR_attitude.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_attitude.s and data_scaled_cor$SDI_full.s
## t = 8.8247, df = 261, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.3804843 0.5674336
## sample estimates:
## cor
## 0.479379
```

```
cor.test(data_scaled_cor$SOIR_desire.s, data_scaled_cor$SOIR_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_desire.s and data_scaled_cor$SOIR_full.s
## t = 17.68, df = 253, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.6829451 0.7937714
## sample estimates:
## cor
## 0.7434188
```

```
cor.test(data_scaled_cor$SOIR_desire.s, data_scaled_cor$SDI_solitary.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_desire.s and data_scaled_cor$SDI_solitary.s
## t = 4.3278, df = 264, p-value = 2.139e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1414900 0.3663137
## sample estimates:
## cor
## 0.2573816
```

```
cor.test(data_scaled_cor$SOIR_desire.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_desire.s and data_scaled_cor$SDI_dyadic.s
## t = 6.7277, df = 262, p-value = 1.079e-10
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2758621 0.4821911
## sample estimates:
## cor
## 0.3838068
```

```
cor.test(data_scaled_cor$SOIR_desire.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_desire.s and data_scaled_cor$SDI_full.s
## t = 6.7834, df = 261, p-value = 7.832e-11
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2792576 0.4853661
## sample estimates:
## cor
## 0.3871376
```

```
cor.test(data_scaled_cor$SOIR_full.s, data_scaled_cor$SDI_solitary.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_full.s and data_scaled_cor$SDI_solitary.s
## t = 5.3572, df = 251, p-value = 1.912e-07
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2050980 0.4267912
## sample estimates:
## cor
## 0.3203236
```

```
cor.test(data_scaled_cor$SOIR_full.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_full.s and data_scaled_cor$SDI_dyadic.s
## t = 10.046, df = 249, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.4426464 0.6196477
## sample estimates:
## cor
## 0.5370319
```

```
cor.test(data_scaled_cor$SOIR_full.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SOIR_full.s and data_scaled_cor$SDI_full.s
## t = 10.094, df = 248, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.4453974 0.6220628
## sample estimates:
## cor
## 0.5396441
```

```
cor.test(data_scaled_cor$SDI_solitary.s, data_scaled_cor$SDI_dyadic.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SDI_solitary.s and data_scaled_cor$SDI_dyadic.s
## t = 7.5575, df = 262, p-value = 6.9e-13
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.3186101 0.5173664
## sample estimates:
## cor
## 0.423064
```

```
cor.test(data_scaled_cor$SDI_solitary.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SDI_solitary.s and data_scaled_cor$SDI_full.s
## t = 16.657, df = 262, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.6529797 0.7711315
## sample estimates:
## cor
## 0.7171705
```

```
cor.test(data_scaled_cor$SDI_dyadic.s, data_scaled_cor$SDI_full.s, na.rm = TRUE)
```

```
##
## Pearson's product-moment correlation
##
## data: data_scaled_cor$SDI_dyadic.s and data_scaled_cor$SDI_full.s
## t = 36.92, df = 262, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.8939647 0.9333742
## sample estimates:
## cor
## 0.9158481
```

*###Repeating analyses from Puts et al., 2015*

*#First: Cross sectional*

```
Putsdata = data_scaled %>%
  filter(session == "1")
```

```
Putsdata$sociosexpsych <- rowMeans(Putsdata[,c(15:20)])
```

```
Putsmodel1 <- lm(testosterone.s ~ sociosexpsych + behavior1, data = Putsdata)
summary.Putsmodel1 <- summary(Putsmodel1)
```

```
summary.Putsmodel1$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

| ##   |               | Effect | Estimate | Std. Error | t value | p |
|------|---------------|--------|----------|------------|---------|---|
| ## 1 | (Intercept)   | 0.123  | 0.081    | 1.530      | 0.132   |   |
| ## 2 | sociosexpsych | -0.022 | 0.023    | -0.931     | 0.356   |   |
| ## 3 | behavior1     | -0.023 | 0.023    | -0.985     | 0.329   |   |

*#Second: Longitudinal*

```
data_scaled$sociosexpsych <- rowMeans(data_scaled[,c(15:20)])
```

```
Putsmodel2 <- lmer(testosterone.s ~ 1 + sociosexpsych + behavior1 +
  (sociosexpsych + behavior1 || hm_id), data = data_scaled, R
EML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.Putsmodel2 <- summary(Putsmodel2)

summary.Putsmodel2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##           Effect Estimate Std. Error  df t value    p
## 1  (Intercept)    0.009      0.033 251   0.284 0.777
## 2 sociosexpsych  -0.002      0.009 251  -0.169 0.866
## 3   behavior1   -0.002      0.009 251  -0.207 0.836
```

```
#analyses for men's relationship status
```

```
#contrast code relationship status (-1 = single, 1 = partnered)
library(car)
```

```
## Loading required package: carData
```

```
## Registered S3 methods overwritten by 'car':
##   method                      from
##   influence.merMod             lme4
##   cooks.distance.influence.merMod lme4
##   dfbeta.influence.merMod      lme4
##   dfbetas.influence.merMod     lme4
```

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:psych':
##
##   logit
```

```
## The following object is masked from 'package:purrr':
##
##   some
```

```
## The following object is masked from 'package:dplyr':
##
##   recode
```

```
data_scaled$relationship <- car::recode(data_scaled$relationship, "0 = -1")

#Following Edelstein et al., 2011: Investigating associations between testosterone
and SOI-R subscales interacting with relationship status

#first between-subjects
Edelsteinmodel1 <- lm(avg_testosterone.s ~ SOIR_desire * relationship + SOIR_behavior * relationship + SOIR_attitude * relationship, data = Putsdata)
summary.Edelsteinmodel1 <- summary(Edelsteinmodel1)

summary.Edelsteinmodel1$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

| ##   | Effect                      | Estimate | Std. Error | t value | p     |
|------|-----------------------------|----------|------------|---------|-------|
| ## 1 | (Intercept)                 | 0.053    | 0.149      | 0.355   | 0.724 |
| ## 2 | SOIR_desire                 | 0.000    | 0.043      | 0.006   | 0.995 |
| ## 3 | relationship1               | -0.480   | 0.220      | -2.184  | 0.034 |
| ## 4 | SOIR_behavior               | 0.054    | 0.065      | 0.836   | 0.407 |
| ## 5 | SOIR_attitude               | -0.034   | 0.041      | -0.836  | 0.407 |
| ## 6 | SOIR_desire:relationship1   | 0.029    | 0.063      | 0.451   | 0.654 |
| ## 7 | relationship1:SOIR_behavior | 0.052    | 0.077      | 0.680   | 0.500 |
| ## 8 | relationship1:SOIR_attitude | 0.048    | 0.056      | 0.846   | 0.402 |

```
#second within-subjects
Edelsteinmodel2 <- lmer(testosterone.s ~ 1 + SOIR_desire * relationship + SOIR_behavior * relationship + SOIR_attitude * relationship +
  (SOIR_desire + SOIR_behavior + SOIR_attitude + relationship
  || hm_id), data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.Edelsteinmodel2 <- summary(Edelsteinmodel2)

summary.Edelsteinmodel2$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                      | Estimate | Std. Error | df  | t value | p     |
|------|-----------------------------|----------|------------|-----|---------|-------|
| ## 1 | (Intercept)                 | 0.023    | 0.044      | 251 | 0.522   | 0.602 |
| ## 2 | SOIR_desire                 | -0.004   | 0.013      | 251 | -0.322  | 0.748 |
| ## 3 | relationship1               | -0.017   | 0.065      | 251 | -0.266  | 0.790 |
| ## 4 | SOIR_behavior               | 0.006    | 0.019      | 251 | 0.298   | 0.766 |
| ## 5 | SOIR_attitude               | -0.006   | 0.012      | 251 | -0.468  | 0.640 |
| ## 6 | SOIR_desire:relationship1   | -0.003   | 0.019      | 251 | -0.139  | 0.890 |
| ## 7 | relationship1:SOIR_behavior | -0.014   | 0.024      | 251 | -0.582  | 0.561 |
| ## 8 | relationship1:SOIR_attitude | 0.015    | 0.016      | 251 | 0.907   | 0.365 |

As requested in the review process: Repeat all main models including relationship status as a covariate (exploratory analyses part 3)

```
##full scale sdi
SDI_full_model_rel <- lmer(SDI_full ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s + relationship+
  (testosterone.s * cortisol.s + relationship || hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge: degenerate Hessian with 2
## negative eigenvalues
```

```
## Warning: Model failed to converge with 2 negative eigenvalues: -3.5e-03
## -4.4e-03
```

```
summary.SDI_full_model_rel <- summary(SDI_full_model_rel)

summary.SDI_full_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df     | t value |
|------|-----------------------------------|----------|------------|--------|---------|
| ## 1 | (Intercept)                       | 56.009   | 3.440      | 28.938 | 16.281  |
| ## 2 | testosterone.s                    | 1.250    | 2.786      | 30.606 | 0.449   |
| ## 3 | cortisol.s                        | -2.002   | 2.246      | 11.273 | -0.891  |
| ## 4 | avg_testosterone.s                | 13.492   | 10.193     | 53.598 | 1.324   |
| ## 5 | avg_cortisol.s                    | -12.420  | 12.856     | 59.056 | -0.966  |
| ## 6 | relationship1                     | 11.610   | 3.971      | 46.598 | 2.924   |
| ## 7 | testosterone.s:cortisol.s         | 26.189   | 17.904     | 61.893 | 1.463   |
| ## 8 | avg_testosterone.s:avg_cortisol.s | -80.897  | 45.777     | 56.917 | -1.767  |

|      | p     |
|------|-------|
| ## 1 | 0.000 |
| ## 2 | 0.657 |
| ## 3 | 0.392 |
| ## 4 | 0.191 |
| ## 5 | 0.338 |
| ## 6 | 0.005 |
| ## 7 | 0.149 |
| ## 8 | 0.083 |

```
#sdi solitary
SDI_solitary_model_rel <- lmer(SDI_solitary ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s + relationship+
  (testosterone.s * cortisol.s + relationship|| hm_id),
  data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary.SDI_solitary_model_rel <- summary(SDI_solitary_model_rel)

summary.SDI_solitary_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 10.807   | 0.855      | 28.107  | 12.643  |
| ## 2 | testosterone.s                    | -1.646   | 0.928      | 202.486 | -1.774  |
| ## 3 | cortisol.s                        | 0.403    | 0.772      | 203.583 | 0.522   |
| ## 4 | avg_testosterone.s                | 4.526    | 3.614      | 58.626  | 1.252   |
| ## 5 | avg_cortisol.s                    | -4.174   | 4.362      | 55.651  | -0.957  |
| ## 6 | relationship1                     | 0.990    | 1.242      | 59.527  | 0.797   |
| ## 7 | testosterone.s:cortisol.s         | 2.214    | 6.271      | 207.306 | 0.353   |
| ## 8 | avg_testosterone.s:avg_cortisol.s | -28.136  | 15.625     | 55.031  | -1.801  |

## p

## 1 0.000

## 2 0.078

## 3 0.602

## 4 0.215

## 5 0.343

## 6 0.428

## 7 0.724

## 8 0.077

```
#sdi dyadic
SDI_dyadic_model_rel <- lmer(SDI_dyadic ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s + relationship+
  (testosterone.s * cortisol.s + relationship|| hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00657013
## (tol = 0.002, component 1)
```

```
summary.SDI_dyadic_model_rel <- summary(SDI_dyadic_model_rel)
```

```
summary.SDI_dyadic_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 35.282   | 2.195      | 28.450  | 16.074  |
| ## 2 | testosterone.s                    | 3.954    | 2.339      | 30.475  | 1.690   |
| ## 3 | cortisol.s                        | -1.113   | 1.669      | 190.173 | -0.667  |
| ## 4 | avg_testosterone.s                | 6.891    | 5.688      | 49.269  | 1.212   |
| ## 5 | avg_cortisol.s                    | -5.888   | 7.282      | 56.106  | -0.809  |
| ## 6 | relationship1                     | 7.324    | 2.431      | 41.448  | 3.013   |
| ## 7 | testosterone.s:cortisol.s         | 20.042   | 13.499     | 208.447 | 1.485   |
| ## 8 | avg_testosterone.s:avg_cortisol.s | -21.968  | 25.765     | 52.606  | -0.853  |

|      | p     |
|------|-------|
| ## 1 | 0.000 |
| ## 2 | 0.101 |
| ## 3 | 0.506 |
| ## 4 | 0.231 |
| ## 5 | 0.422 |
| ## 6 | 0.004 |
| ## 7 | 0.139 |
| ## 8 | 0.398 |

## Results for LMEM Analysis for SOI\_R

```
#SOIR full scale
SOIR_full_model_rel <- lmer(SOIR_full ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s + relationship+
  (testosterone.s * cortisol.s + relationship|| hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00951461
## (tol = 0.002, component 1)
```

```
summary.SOIR_full_model_rel <- summary(SOIR_full_model_rel)

summary.SOIR_full_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

```
##
##           Effect Estimate Std. Error    df t value
## 1      (Intercept)    3.059      0.147 25.217  20.824
## 2      testosterone.s -0.050      0.131 37.999  -0.380
## 3      cortisol.s    -0.131      0.119 28.408  -1.097
## 4      avg_testosterone.s  1.120      0.521 56.981   2.150
## 5      avg_cortisol.s   -0.176      0.644 58.997  -0.273
## 6      relationship1    0.080      0.188 52.542   0.425
## 7      testosterone.s:cortisol.s  0.663      0.938 19.932   0.707
## 8 avg_testosterone.s:avg_cortisol.s -5.732      2.282 57.717  -2.512
##           p
## 1 0.000
## 2 0.706
## 3 0.282
## 4 0.036
## 5 0.786
## 6 0.672
## 7 0.488
## 8 0.015
```

```
#SOIR behavior
```

```
SOIR_behavior_model_rel <- lmer(SOIR_behavior ~ 1 + testosterone.s * cortisol.s +
                                avg_testosterone.s * avg_cortisol.s + relationship+
                                (testosterone.s * cortisol.s+ relationship || hm_id),
                                data = data_scaled, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -8.5e-03
```

```
summary.SOIR_behavior_model_rel <- summary(SOIR_behavior_model_rel)
```

```
summary.SOIR_behavior_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df      | t value |
|------|-----------------------------------|----------|------------|---------|---------|
| ## 1 | (Intercept)                       | 1.945    | 0.165      | 22.814  | 11.821  |
| ## 2 | testosterone.s                    | -0.144   | 0.139      | 192.970 | -1.041  |
| ## 3 | cortisol.s                        | -0.054   | 0.115      | 193.999 | -0.465  |
| ## 4 | avg_testosterone.s                | 1.242    | 0.599      | 56.517  | 2.074   |
| ## 5 | avg_cortisol.s                    | 0.354    | 0.740      | 59.053  | 0.478   |
| ## 6 | relationship1                     | 0.493    | 0.213      | 53.547  | 2.311   |
| ## 7 | testosterone.s:cortisol.s         | 1.644    | 0.954      | 197.284 | 1.723   |
| ## 8 | avg_testosterone.s:avg_cortisol.s | 0.157    | 2.626      | 57.677  | 0.060   |

## p

## 1 0.000

## 2 0.299

## 3 0.642

## 4 0.043

## 5 0.634

## 6 0.025

## 7 0.086

## 8 0.953

```
#SOIR attitude
```

```
SOIR_attitude_model_rel <- lmer(SOIR_attitude ~ 1 + testosterone.s * cortisol.s +
                                avg_testosterone.s * avg_cortisol.s + relationship+
                                (testosterone.s * cortisol.s + relationship|| hm_id),
                                data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge: degenerate Hessian with 2
## negative eigenvalues
```

```
## Warning: Model failed to converge with 2 negative eigenvalues: -4.5e-04
## -1.1e-03
```

```
summary.SOIR_attitude_model_rel <- summary(SOIR_attitude_model_rel)

summary.SOIR_attitude_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

|      | Effect                            | Estimate | Std. Error | df     | t value |
|------|-----------------------------------|----------|------------|--------|---------|
| ## 1 | (Intercept)                       | 3.706    | 0.190      | 28.676 | 19.516  |
| ## 2 | testosterone.s                    | 0.115    | 0.255      | 35.800 | 0.449   |
| ## 3 | cortisol.s                        | 0.094    | 0.215      | 23.139 | 0.439   |
| ## 4 | avg_testosterone.s                | 1.336    | 0.764      | 61.254 | 1.749   |
| ## 5 | avg_cortisol.s                    | -0.277   | 0.928      | 60.276 | -0.299  |
| ## 6 | relationship1                     | 0.110    | 0.262      | 59.804 | 0.419   |
| ## 7 | testosterone.s:cortisol.s         | -1.501   | 1.541      | 10.016 | -0.974  |
| ## 8 | avg_testosterone.s:avg_cortisol.s | -11.928  | 3.317      | 58.994 | -3.596  |

## p

## 1 0.000

## 2 0.656

## 3 0.665

## 4 0.085

## 5 0.766

## 6 0.677

## 7 0.353

## 8 0.001

```
#SOIR desire
SOIR_desire_model_rel <- lmer(SOIR_desire ~ 1 + testosterone.s * cortisol.s +
  avg_testosterone.s * avg_cortisol.s + relationship+
  (testosterone.s * cortisol.s + relationship|| hm_id),
  data = data_scaled, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00722477
## (tol = 0.002, component 1)
```

```
summary.SOIR_desire_model_rel <- summary(SOIR_desire_model_rel)

summary.SOIR_desire_model_rel$coefficients %>%
  as.data.frame() %>%
  rownames_to_column(var = "Effect") %>%
  mutate_if(is.numeric, round, 3) %>%
  rename(p = `Pr(>|t|)`)
```

| ##   |       | Effect                            | Estimate | Std. Error | df      | t value |
|------|-------|-----------------------------------|----------|------------|---------|---------|
| ## 1 |       | (Intercept)                       | 3.551    | 0.157      | 29.109  | 22.595  |
| ## 2 |       | testosterone.s                    | -0.002   | 0.207      | 202.291 | -0.010  |
| ## 3 |       | cortisol.s                        | -0.489   | 0.237      | 45.462  | -2.066  |
| ## 4 |       | avg_testosterone.s                | 0.647    | 0.640      | 61.451  | 1.011   |
| ## 5 |       | avg_cortisol.s                    | -0.756   | 0.776      | 60.193  | -0.974  |
| ## 6 |       | relationship1                     | -0.361   | 0.218      | 59.709  | -1.656  |
| ## 7 |       | testosterone.s:cortisol.s         | 1.839    | 1.682      | 18.469  | 1.093   |
| ## 8 |       | avg_testosterone.s:avg_cortisol.s | -5.887   | 2.767      | 58.271  | -2.128  |
| ##   | p     |                                   |          |            |         |         |
| ## 1 | 0.000 |                                   |          |            |         |         |
| ## 2 | 0.992 |                                   |          |            |         |         |
| ## 3 | 0.045 |                                   |          |            |         |         |
| ## 4 | 0.316 |                                   |          |            |         |         |
| ## 5 | 0.334 |                                   |          |            |         |         |
| ## 6 | 0.103 |                                   |          |            |         |         |
| ## 7 | 0.288 |                                   |          |            |         |         |
| ## 8 | 0.038 |                                   |          |            |         |         |