

# No evidence for associations between men's salivary testosterone and responses on the Intrasexual Competitiveness Scale

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```
library(tidyverse)

## Warning: package 'tidyverse' was built under R version 3.3.2
## Warning: package 'tibble' was built under R version 3.3.2
## Warning: package 'dplyr' was built under R version 3.3.2

library(lmerTest)
library(psych)
sessionInfo()

## R version 3.3.1 (2016-06-21)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.11.6 (El Capitan)
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] psych_1.7.8      lmerTest_2.0-32 lme4_1.1-12      Matrix_1.2-6
## [5] dplyr_0.7.3      purrr_0.2.2      readr_1.0.0      tidyr_0.6.0
## [9] tibble_1.3.4     ggplot2_2.1.0    tidyverse_1.1.1
##
## loaded via a namespace (and not attached):
## [1] reshape2_1.4.2      splines_3.3.1      haven_1.0.0
## [4] lattice_0.20-33     colorspace_1.2-7   htmltools_0.3.5
## [7] yaml_2.1.13         chron_2.3-47       survival_2.40-1
## [10] rlang_0.1.2         nloptr_1.0.4       foreign_0.8-66
## [13] glue_1.1.1          RColorBrewer_1.1-2 modelr_0.1.0
## [16] readxl_0.1.1        bindrcpp_0.2       bindr_0.1
## [19] plyr_1.8.4          stringr_1.3.0      munsell_0.4.3
## [22] gtable_0.2.0        rvest_0.3.2        evaluate_0.10
## [25] latticeExtra_0.6-28 knitr_1.20          forcats_0.2.0
## [28] parallel_3.3.1     htmlTable_1.7      broom_0.4.2
## [31] Rcpp_0.12.12       acepack_1.4.1      scales_0.4.0
```

```
## [34] backports_1.1.2      Hmisc_4.0-0      jsonlite_1.1
## [37] gridExtra_2.2.1      mnormt_1.5-5     hms_0.2
## [40] digest_0.6.10        stringi_1.1.7    grid_3.3.1
## [43] rprojroot_1.3-2      tools_3.3.1      magrittr_1.5
## [46] cluster_2.0.4        Formula_1.2-1    pkgconfig_2.0.1
## [49] MASS_7.3-45          data.table_1.9.6 xml2_1.1.1
## [52] lubridate_1.6.0      assertthat_0.2.0 minqa_1.2.4
## [55] rmarkdown_1.9        httr_1.2.1       rpart_4.1-10
## [58] R6_2.2.2             nnet_7.3-12     nlme_3.1-128
```

## Load Data

```
data_hormones <- read_csv("hm_intrasexual_comp_anon.csv")
```

## Descriptives

The number of sessions completed per man

```
data_hormones %>%
  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     4
## 5         5    47
```

Mean age for the sample

```
data_hormones %>%
  group_by(hm_id, date, age) %>%
  summarise(n = n()) %>%
  ungroup() %>%
  group_by() %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    sd_age = sd(age, na.rm = TRUE),
    se_age = se(age, na.rm = TRUE)
  ) %>%
  mutate_all(round, 4)
```

```
## Warning: package 'bindrcpp' was built under R version 3.3.2
## # A tibble: 1 x 3
##   mean_age sd_age se_age
##   <dbl> <dbl> <dbl>
## 1 21.9679 3.1446 0.1932
```

## Data Processing

### Exclude hormone outliers

```
# calculate means and SDs
test_mean <- mean(data_hormones$test)
test_sd <- sd(data_hormones$test)
cort_mean <- mean(data_hormones$cort)
cort_sd <- sd(data_hormones$cort)

# set values > 3SD from the mean to NA
data_final <- data_hormones %>%
  mutate (
    test = ifelse (test > test_mean + 3*test_sd |
                  test < test_mean - 3*test_sd, NA, test),
    cort = ifelse (cort > cort_mean + 3*cort_sd |
                  cort < cort_mean - 3*cort_sd, NA, cort)
  )

# determine how many values were excluded
data_final %>%
  group_by(hm_id, date) %>%
  summarise(
    t = is.na(mean(test)),
    c = is.na(mean(cort))
  ) %>%
  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 264 1
## 2 t 261 4
```

### Calculate average hormones for each participant

```

data_avg <- data_final %>%
  group_by(hm_id) %>%
  summarise(
    avg_test = mean(test, na.rm = TRUE),
    avg_cort = mean(cort, na.rm = TRUE)
  ) %>%
  group_by() %>%
  # divide by constants to make range approx -.5 to +.5 for lmer
  mutate(
    avg_test.s = (avg_test - mean(avg_test, na.rm=TRUE)) / 180,
    avg_cort.s = (avg_cort - mean(avg_cort, na.rm=TRUE)) / 0.5
  )

```

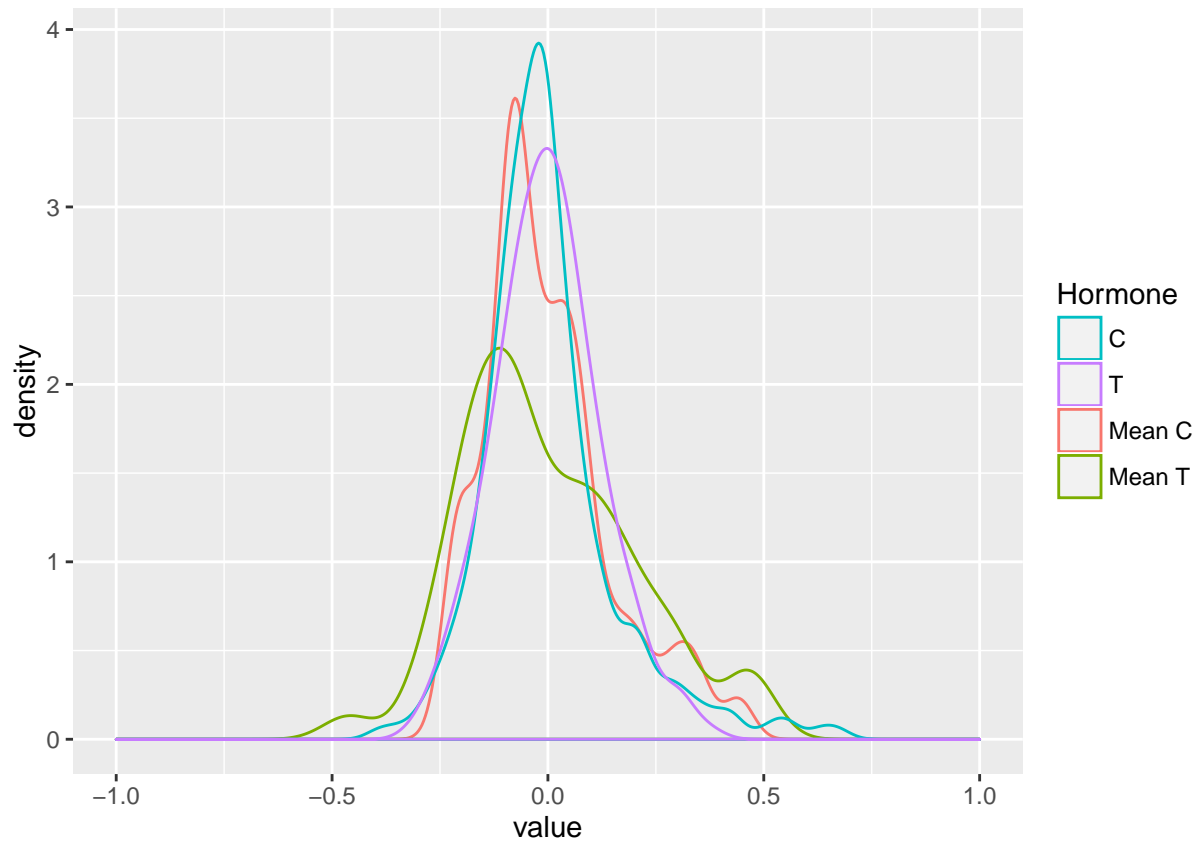
## Centre and scale hormones

Centre hormones on subject-specific means, and bring values between -0.5 and 0.5

```

# 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(
    test.s = (test - mean(test, na.rm=TRUE)) / 180,
    cort.s = (cort - mean(cort, na.rm=TRUE)) / 0.5
  ) %>%
  ungroup() %>%
  left_join(data_avg, by="hm_id")

```



### Mean hormone levels

```
data_scaled %>%
  group_by(hm_id, date, age, test, cort) %>%
  summarise(n = n()) %>%
  ungroup() %>%
  group_by() %>%
  summarise(
    mean_test = mean(test, na.rm = TRUE),
    sd_test = sd(test, na.rm = TRUE),
    se_test = se(test, na.rm = TRUE),
    mean_cort = mean(cort, na.rm = TRUE),
    sd_cort = sd(cort, na.rm = TRUE),
    se_cort = se(cort, 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   cort    0.1877 0.1075 0.0066
## 2   test 177.5396 42.1505 2.6090
```

## Intrasexual Competitiveness Analyses

### Descriptives

```
data_scaled %>%
  summarise(
    mean = mean(intr_cmpt, na.rm = TRUE),
    sd = sd(intr_cmpt, na.rm = TRUE),
    se = se(intr_cmpt, na.rm = TRUE)
  ) %>%
  mutate_all(round, 4)
```

```
## # A tibble: 1 x 3
##   mean    sd    se
##   <dbl> <dbl> <dbl>
## 1 2.9534 0.9847 0.0607
```

### Cronbach's Alpha

```
horm_alphas <- data_hormones %>%
  select(ICS1:ICS12) %>%
  alpha()
```

```
horm_alphas$total$raw_alpha
```

```
## [1] 0.8634041
```

### LMEM Analysis

```
model.IC.TbyC <- lmer(intr_cmpt ~ 1 + test.s * cort.s +
  avg_test.s * avg_cort.s +
  (test.s * cort.s || hm_id),
  data = data_scaled, REML = FALSE)
summary(model.IC.TbyC)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [lmerMod]
## Formula:
## intr_cmpt ~ 1 + test.s * cort.s + avg_test.s * avg_cort.s + ((1 |
##   hm_id) + (0 + test.s | hm_id) + (0 + cort.s | hm_id) + (0 +
##   test.s:cort.s | hm_id))
## Data: data_scaled
##
##      AIC      BIC   logLik deviance df.resid
##  459.9   502.5  -217.9   435.9     246
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.74196 -0.51653 -0.01937  0.50550  2.56552
##
## Random effects:
## Groups   Name                Variance Std.Dev.
```

```

## hm_id (Intercept) 7.217e-01 8.495e-01
## hm_id.1 test.s 3.064e-01 5.536e-01
## hm_id.2 cort.s 3.949e-01 6.284e-01
## hm_id.3 test.s:cort.s 1.533e-11 3.916e-06
## Residual 1.468e-01 3.831e-01
## Number of obs: 258, groups: hm_id, 59
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 3.03493 0.12320 59.39000 24.634 <2e-16 ***
## test.s 0.05333 0.22668 38.28000 0.235 0.815
## cort.s 0.09377 0.21610 34.62000 0.434 0.667
## avg_test.s 0.38921 0.64713 60.29000 0.601 0.550
## avg_cort.s -0.22143 0.86546 61.43000 -0.256 0.799
## test.s:cort.s 2.56471 1.56636 162.41000 1.637 0.103
## avg_test.s:avg_cort.s -4.42082 3.02851 59.54000 -1.460 0.150
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) test.s cort.s avg_t. avg_c. tst...
## test.s -0.004
## cort.s 0.025 -0.209
## avg_test.s 0.054 -0.003 0.002
## avg_cort.s 0.085 -0.002 0.016 -0.443
## tst.s:crt.s -0.069 0.017 -0.198 -0.013 -0.029
## avg_tst.:_ -0.380 0.002 -0.012 -0.142 -0.211 0.021

```

## State Anxiety Analyses

### Descriptives

```

data_scaled %>%
  group_by() %>%
  summarise(
    mean = mean(st_anx, na.rm = TRUE),
    sd = sd(st_anx, na.rm = TRUE),
    se = se(st_anx, na.rm = TRUE)
  ) %>%
  mutate_all(round, 4)

```

```

## # A tibble: 1 x 3
##   mean    sd    se
##   <dbl> <dbl> <dbl>
## 1 36.1217 8.8062 0.543

```

### LMEM Analysis

```

model.SA.TbyC <- lmer(st_anx ~ 1 + test.s * cort.s +
  avg_test.s * avg_cort.s +
  (test.s * cort.s || hm_id),

```

```

data = data_scaled, REML = FALSE)
summary(model.SA.TbyC)

```

```

## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [lmerMod]
## Formula: st_anx ~ 1 + test.s * cort.s + avg_test.s * avg_cort.s + ((1 |
## hm_id) + (0 + test.s | hm_id) + (0 + cort.s | hm_id) + (0 +
## test.s:cort.s | hm_id))
## Data: data_scaled
##
##      AIC      BIC   logLik deviance df.resid
## 1797.6  1840.2  -886.8  1773.6     246
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.73890 -0.54520 -0.08963  0.40247  2.98275
##
## Random effects:
## Groups Name          Variance Std.Dev.
## hm_id (Intercept)    32.25    5.679
## hm_id.1 test.s       91.40    9.560
## hm_id.2 cort.s        0.00    0.000
## hm_id.3 test.s:cort.s 1237.24 35.174
## Residual              38.55    6.209
## Number of obs: 258, groups: hm_id, 59
##
## Fixed effects:
##              Estimate Std. Error   df t value Pr(>|t|)
## (Intercept)    36.5557    0.9238 55.5000  39.569 <2e-16 ***
## test.s         2.9672    3.6544 45.5900   0.812  0.421
## cort.s         7.0999    2.8540 146.3300   2.488  0.014 *
## avg_test.s     5.6698    4.9084 57.7900   1.155  0.253
## avg_cort.s    -6.1653    6.6422 60.2500  -0.928  0.357
## test.s:cort.s  1.0943   24.5607 18.1800   0.045  0.965
## avg_test.s:avg_cort.s -26.5258  22.8242 56.5500  -1.162  0.250
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) test.s cort.s avg_t. avg_c. tst.:.
## test.s          0.002
## cort.s          0.051 -0.220
## avg_test.s      0.061  0.001 -0.002
## avg_cort.s      0.094 -0.005  0.033 -0.446
## tst.s:crt.s    -0.127 -0.005 -0.229 -0.015 -0.060
## avg_tst.:.    -0.382  0.004 -0.028 -0.167 -0.204  0.042

```