

03 Linear Modeling Exercise: Power Posing

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Power posing: Background

The claim is that adopting a high power pose for two minutes will increase your testosterone, improving your performance in, e.g., job interviews. We are going to evaluate this claim based on Cuddy's data. The data were released by Cuddy via Nathan Fosse:

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/FMEGS6>

Incidentally, the first author of the Cuddy paper has disavowed the paper: see here.

Carney, D. R., Cuddy, A. J., & Yap, A. J. (2010). Power posing: Brief nonverbal displays affect neuroendocrine levels and risk tolerance. *Psychological science*, 21(10), 1363-1368.

Preparation for the exercise

Load the data, basic checks

```
## cleaned data
datc<-read.csv("data/ccy-clean-data.csv",
              header=TRUE)

## sanity check: one subject, one row
dim(datc)

## [1] 47 41
length(unique(datc$id))

## [1] 47
#drop ineligible and something else as in stata code:
datc<-subset(datc,inelig!="Ineligible (drop)" & anyoutv1!="Selected")
```

A fairly typical characteristic of data is the sheer messiness of it.

```
head(datc)

##   id          inelig ccydrop cortm1v2 cortm2v2 cdiffv2 testm1v2
## 2 29 Analytic sample (keep)      0    0.003    0.025    0.022    38.72
## 3 30 Analytic sample (keep)      0    0.086    0.167    0.081    32.77
## 4 31 Analytic sample (keep)      0    0.047    0.059    0.012    32.32
## 5 32 Analytic sample (keep)      0    0.106    0.112    0.006    17.99
## 7 34 Analytic sample (keep)      1      NA    0.171      NA    73.58
## 8 35 Analytic sample (keep)      0    0.153    0.183    0.030    80.69
##   testm2v2 tdiffv2   testoutv1   cortoutv1   anyoutv1   testoutv2
## 2    62.37   23.65 Not selected Not selected Not selected Not selected
## 3    29.23   -3.54 Not selected Not selected Not selected Not selected
## 4    27.51   -4.81 Not selected Not selected Not selected Not selected
```

```
## 5    28.66    10.67 Not selected Not selected Not selected Not selected
## 7    44.67   -28.91 Not selected Not selected Not selected Not selected
## 8   105.48    24.79 Not selected Not selected Not selected Not selected
##      cortoutv2      anyoutv2 poseirate pose2rate poseratem  saldiff
## 2 Not selected Not selected         6         6         6.0 24.30556
## 3 Not selected Not selected         7         6         6.5 20.83333
## 4 Not selected Not selected         6         5         5.5 29.16667
## 5 Not selected Not selected         6         7         6.5 18.75000
## 7      Selected      Selected         7         7         7.0 23.61111
## 8 Not selected Not selected         7         7         7.0 34.02778
##      sal2manip hptreat female age cort1a1 cort1a2 cort2a1 cort2a2 cortm1
## 2 19.80556      High   Male  19   0.004   0.001   0.027   0.023 0.0025
## 3 16.33333      Low  Female  20   0.085   0.086   0.174   0.161 0.0855
## 4 24.66667      High  Female  20   0.049   0.045   0.056   0.062 0.0470
## 5 14.25000      Low  Female  18   0.107   0.105   0.111   0.113 0.1060
## 7 19.11111      Low  Female  21   0.486   0.482   0.175   0.166 0.4840
## 8 29.52778      High  Female  20   0.159   0.147   0.179   0.188 0.1530
##      cortm2      cdiff test1a1 test1a2 test2a1 test2a2 testm1 testm2
## 2 0.0250 0.022500001  39.87  37.58  64.22  60.53 38.725 62.375
## 3 0.1675 0.082000002  33.22  32.32  29.43  29.04 32.770 29.235
## 4 0.0590 0.012000002  32.52  32.12  27.98  27.04 32.320 27.510
## 5 0.1120 0.006000005  19.74  16.25  28.17  29.14 17.995 28.655
## 7 0.1705 -0.313499990  78.85  68.31  46.14  43.20 73.580 44.670
## 8 0.1835 0.030500010  83.51  77.88 105.92 105.05 80.695 105.485
##      tdiff  feelpower  incharge powm diceroll
## 2 23.650002          3          2 2.5      Yes
## 3 -3.535000 Not at all          2 1.5      No
## 4 -4.809999          2 Not at all 1.5      Yes
## 5 10.660000          3  Very much 3.5      Yes
## 7 -28.910004          2          2 2      No
## 8 24.790001          3          3 3      Yes
```

Critical variables:

- id (numerical, should be factor): subject id
- testm1 (numerical): pre-treatment testosterone
- testm2 (numerical): post-treatment testosterone
- cortm1 (numerical): pre-treatment cortisone
- cortm2 (numerical): post-treatment cortisone
- female (factor): Female, Male
- hptreat (factor): High, Low (power pose)

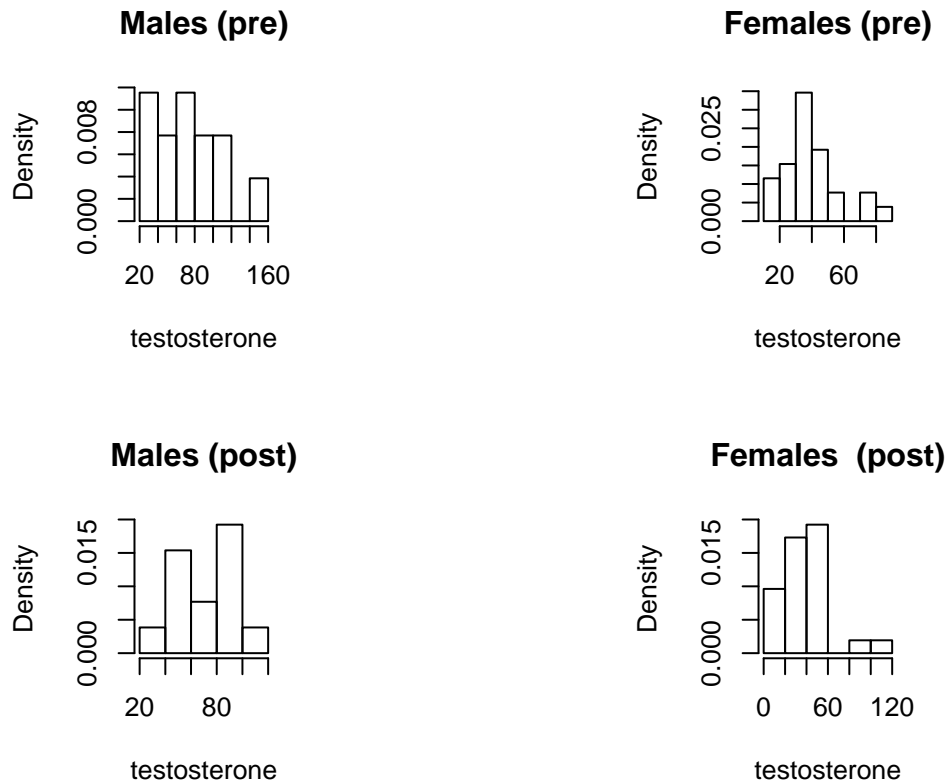
So, isolate relevant columns:

```
dat<-datc[,c(1,21,22,28,29,35,36)]
head(dat)
```

```
##   id hptreat female cortm1 cortm2 testm1 testm2
## 2 29   High   Male 0.0025 0.0250 38.725 62.375
## 3 30   Low  Female 0.0855 0.1675 32.770 29.235
## 4 31   High  Female 0.0470 0.0590 32.320 27.510
## 5 32   Low  Female 0.1060 0.1120 17.995 28.655
## 7 34   Low  Female 0.4840 0.1705 73.580 44.670
## 8 35   High  Female 0.1530 0.1835 80.695 105.485
```

Exercise 1:

Plot the distributions of male vs female testosterone levels before and after treatment:



##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	30.99	47.81	60.56	70.47	90.37	143.57
##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	11.65	27.98	36.57	39.53	48.56	80.69
##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	34.78	58.69	65.15	72.38	91.31	111.61
##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	2.145	23.704	38.775	38.818	48.265	105.485

Exercise 2

Calculate mean post-treatment testosterone by gender and by hptreatment (high or low power pose).

##		High	Low
##	Female	45	33
##	Male	65	82

Exercise 3

Calculate mean post-treatment testosterone ignoring gender, by hptreatment (high or low power pose).

##	High	Low
##	52	48

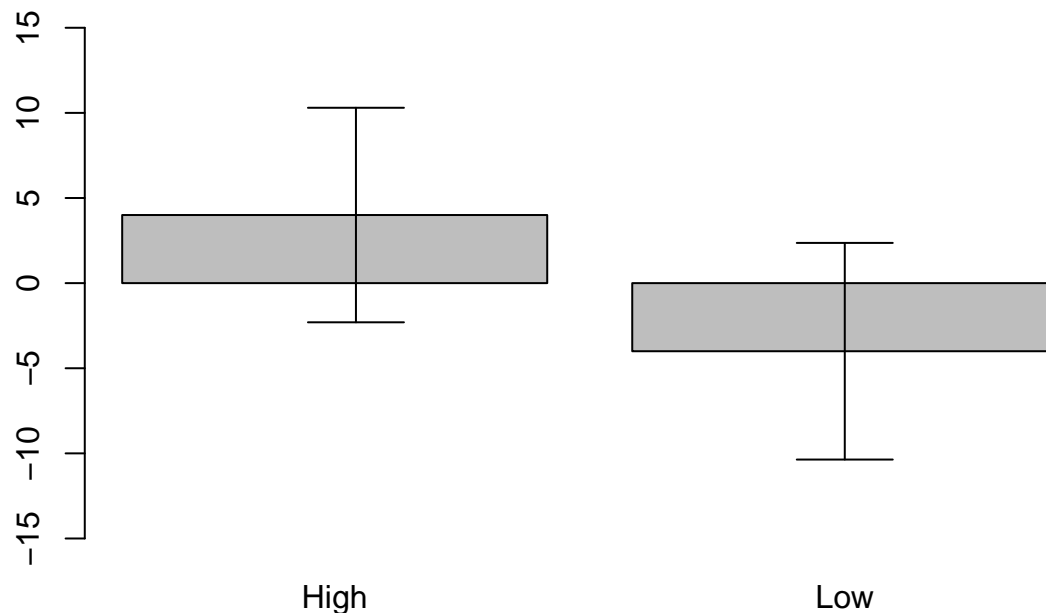


Figure 1: Recreation of Figure 3 in the Cuddy power posing study.

Exercise 4

By how much did testosterone increase after treatment (testm2-testm1 tells you the increase in testosterone), taking gender and hptreat (treatment: high vs low power pose) into account?

```
##           High Low
## Female      1  -2
## Male      12 -10
```

Exercise 4

By how much did testosterone increase after treatment (testm2-testm1 tells you the increase in testosterone), ignoring gender but taking hptreat (treatment: high vs low power pose) into account?

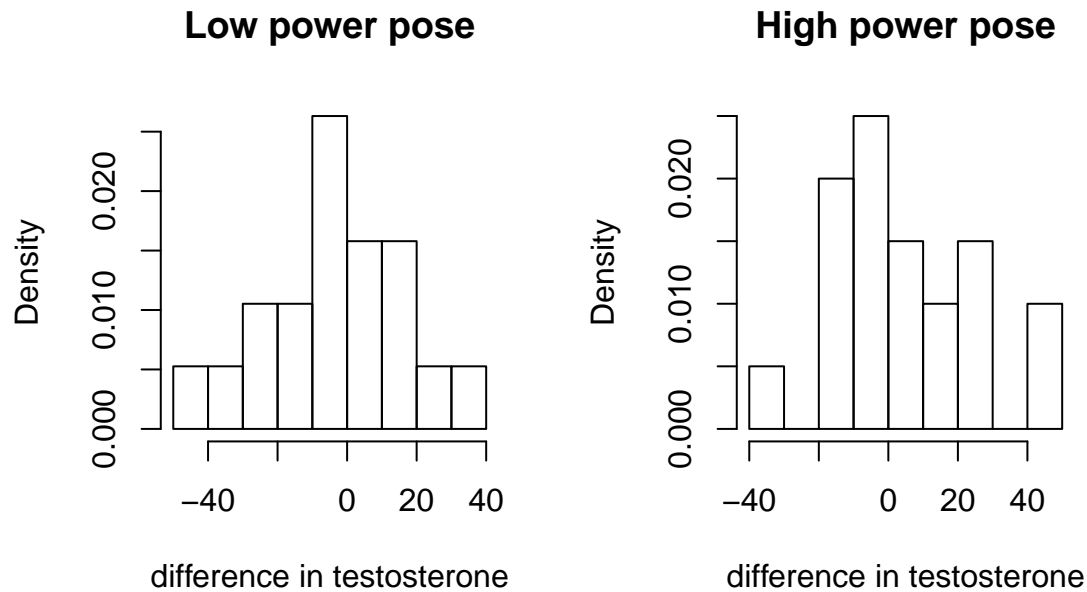
You should be able to reproduce Figure 1 here. This is the rough and ready version of fig 3 of the paper.

The effects are a bit smaller in this data-set than the published result, probably because of Fosse (the statistician) cleaning up of the publicly released data.

Exercise 5

Carry out a two-sample t-test on the differences in testosterone pre- vs. post-test. What do you conclude from this test?

It will help to visualize the distributions:



```
##
## Welch Two Sample t-test
##
## data: highdiff$diff and lowdiff$diff
## t = 1.3668, df = 36.856, p-value = 0.18
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -4.264045 21.933205
## sample estimates:
## mean of x mean of y
## 4.46800 -4.36658
```

Exercise 6

Now, refit the model using various predictors:

- the initial testosterone value
- the initial and final cortisone levels
- the gender of the subject.

The question we ask here is, is post-treatment testosterone higher for subjects exposed to high vs low power, controlling for the above variables?

First, center all predictors:

```
## center all predictors
datc$ctestm1<-scale(datc$testm1,scale=FALSE)
datc$hptreat<-ifelse(datc$hptreat=="High",1,-1)
datc$cortm1<-scale(datc$cortm1,scale=FALSE)
datc$cortm2<-scale(datc$cortm2,scale=FALSE)
datc$female<-ifelse(datc$female=="Female",1,-1)
```

Exercise 6.1

Fit the Bayesian version of model m0 below, using brms Here is the frequentist linear model:

This is the result that Fosse, Cuddy's statistician, found:

```
m0<-lm(testm2~ctestm1+chptreat+female,datc)
summary(m0)

##
## Call:
## lm(formula = testm2 ~ ctestm1 + chptreat + female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -31.827 -11.543   0.141   7.732  40.626
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  52.4155     3.1752  16.508 < 2e-16 ***
## ctestm1       0.5946     0.1279   4.649 4.61e-05 ***
## chptreat      3.0443     2.9561   1.030  0.3101
## female       -7.4637     3.6887  -2.023  0.0507 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.25 on 35 degrees of freedom
## Multiple R-squared:  0.5932, Adjusted R-squared:  0.5584
## F-statistic: 17.02 on 3 and 35 DF,  p-value: 5.508e-07
```

Because we are starting with a state of no knowledge (and we have no expert opinions), we will use vague Cauchy(0,1) priors on all parameters. You could also use Cauchy(0,2.5).

```
library(brms)

## Loading required package: Rcpp
## Loading required package: ggplot2

## Loading 'brms' package (version 2.5.0). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').
## Run theme_set(theme_default()) to use the default bayesplot theme.

priors_cauchy <- c(set_prior("cauchy(0, 1)",
                           class = "Intercept"),
                  set_prior("cauchy(0,1)",
                           class = "b"),
                  set_prior("cauchy(0,1)",
                           class = "sigma"))

priors_cauchy25 <- c(set_prior("cauchy(0, 2.5)",
                           class = "Intercept"),
                   set_prior("cauchy(0,2.5)",
                           class = "b"),
                   set_prior("cauchy(0,2.5)",
                           class = "sigma"))
```

Then visualize the result using shinystan (I assume the model in brms is called m0brms):

```
library(shiny)
library(shinytan)
launch_shinytan(m0brms)
```

Exercise 6.2

How does gender affect the conclusions?

```
## with interaction with gender, the effect disappears:
## with interaction:
m1<-lm(testm2~ctestm1+chptreat+cortm1+cortm2+female+chptreat:female,datc)
summary(m1)
```

```
##
## Call:
## lm(formula = testm2 ~ ctestm1 + chptreat + cortm1 + cortm2 +
##     female + chptreat:female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.095  -9.512  -2.588   9.337  33.538
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    54.1331     2.9062  18.627 < 2e-16 ***
## ctestm1         0.3862     0.1466   2.634  0.01288 *
## chptreat        4.8527     2.9437   1.648  0.10904
## cortm1        -1.4782    27.6935  -0.053  0.95776
## cortm2       147.9227    43.6099   3.392  0.00186 **
## female       -12.5397     3.8899  -3.224  0.00291 **
## chptreat:female  2.8056     3.2548   0.862  0.39511
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.08 on 32 degrees of freedom
## Multiple R-squared:  0.7115, Adjusted R-squared:  0.6574
## F-statistic: 13.15 on 6 and 32 DF,  p-value: 1.868e-07
## without interaction:
m1a<-lm(testm2~ctestm1+chptreat+cortm1+cortm2+female,datc)
summary(m1a)
```

```
##
## Call:
## lm(formula = testm2 ~ ctestm1 + chptreat + cortm1 + cortm2 +
##     female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.631  -9.163  -3.286   8.468  32.997
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    53.5807     2.8236  18.976 < 2e-16 ***
```

```
## ctestm1      0.4546      0.1228      3.703 0.000775 ***
## chptreat     5.8217      2.7100      2.148 0.039133 *
## cortm1      -4.9894     27.2854     -0.183 0.856028
## cortm2     142.0457     42.9056      3.311 0.002261 **
## female     -11.1731      3.5383     -3.158 0.003389 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.01 on 33 degrees of freedom
## Multiple R-squared:  0.7048, Adjusted R-squared:  0.6601
## F-statistic: 15.76 on 5 and 33 DF,  p-value: 6.221e-08
```

Fit the above model m1 using brms, and compare the Bayesian posteriors of the effect of treatment to the model m0 above.

Exercise 6.3

An alternative analysis using difference in testosterone

We could also have as dependent measure the **change** in testosterone in low vs high power subjects. This corresponds to the Fig 3 plot in the paper.

```
datc$change<-datc$testm2-datc$testm1
m2a<-lm(change~chptreat,datc)
summary(m2a) ## same t-value as in two-sample t-test
```

```
##
## Call:
## lm(formula = change ~ chptreat, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -41.328 -14.896  -0.673  15.112  39.082
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.05071    3.23106   0.016   0.988
## chptreat     4.41729    3.23106   1.367   0.180
##
## Residual standard error: 20.17 on 37 degrees of freedom
## Multiple R-squared:  0.04809,    Adjusted R-squared:  0.02236
## F-statistic: 1.869 on 1 and 37 DF,  p-value: 0.1798
```

Fit the above model 2a in brms.

Exercise 6.4

Now take gender into account and check if gender has an effect

```
## taking gender into account
m3a<-lm(change~chptreat+female,datc)
summary(m3a)
```

```
##
## Call:
```



```
## lm(formula = change ~ chptreat + female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -42.888 -14.922  -0.803  14.731  39.880
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.4317     3.4703   0.124   0.902
## chptreat       4.3783     3.2729   1.338   0.189
## female        -1.1400     3.4703  -0.328   0.744
##
## Residual standard error: 20.42 on 36 degrees of freedom
## Multiple R-squared:  0.05093,    Adjusted R-squared:  -0.001795
## F-statistic: 0.966 on 2 and 36 DF,  p-value: 0.3903
```

Fit m3a in brms.

Exercise 6.5

Take the interaction between treatment and gender into account

```
## taking interaction between treatment and gender into account
m4a<-lm(change~chptreat*female,datc)
summary(m4a)
```

```
##
## Call:
## lm(formula = change ~ chptreat * female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -36.166 -12.357  -0.261   9.945  42.983
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.1916     3.4345   0.056   0.9558
## chptreat       5.9481     3.4345   1.732   0.0921 .
## female        -0.8999     3.4345  -0.262   0.7948
## chptreat:female -4.6725     3.4345  -1.360   0.1824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 20.18 on 35 degrees of freedom
## Multiple R-squared:  0.0986, Adjusted R-squared:  0.02134
## F-statistic: 1.276 on 3 and 35 DF,  p-value: 0.2977
```

This is an exciting result!!!! ... Well, almost. Sadly, the p-value for treatment *just* misses significance.

Fit model 4a using brms.

Exercise 6.6

Interpretation: What can we conclude from this data? Does power posing change testosterone levels?

Exercise 6.7

Fit model m4a using RStan