

Analysis of power pose data

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Load and prepare data

```
## cleaned data
datc<-read.csv("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")
```

Examine male and female testosterone levels

```
## subset males and females
males<-subset(datc,female=="Male")
females<-subset(datc,female=="Female")

## initial testosterone:
summary(males$testm1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  30.99   47.81   60.56   70.47   90.37  143.60
```

```
summary(females$testm1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  11.65   27.98   36.57   39.53   48.56   80.69
```

```
## after treatment:
summary(males$testm2)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  34.78   58.69   65.15   72.38   91.32  111.60
```

```
summary(females$testm2)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   2.145   23.700   38.780   38.820   48.270  105.500
```

Calculate mean post-treatment testosterone by gender

```
round(with(datc,tapply(testm2,IND=list(female,hptreat),mean)))
```

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

```
round(with(datc,tapply(testm2,IND=list(hptreat),mean)))
```

```
## High  Low
##   52   48
```

By how much did testosterone increase after treatment? Means by gender.

```
## difference scores:
round(with(datc,tapply(testm2-testm1,IND=list(female,hptreat),mean)))
```

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

Means ignoring gender: here 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 the statistician's cleaning up of the data.

```
(means<-round(with(datc,tapply(testm2-testm1,IND=hptreat,mean))))
```

```
## High  Low
##    4   -4
```

```
(sds<-with(datc,tapply(testm2-testm1,IND=hptreat,sd)))
```

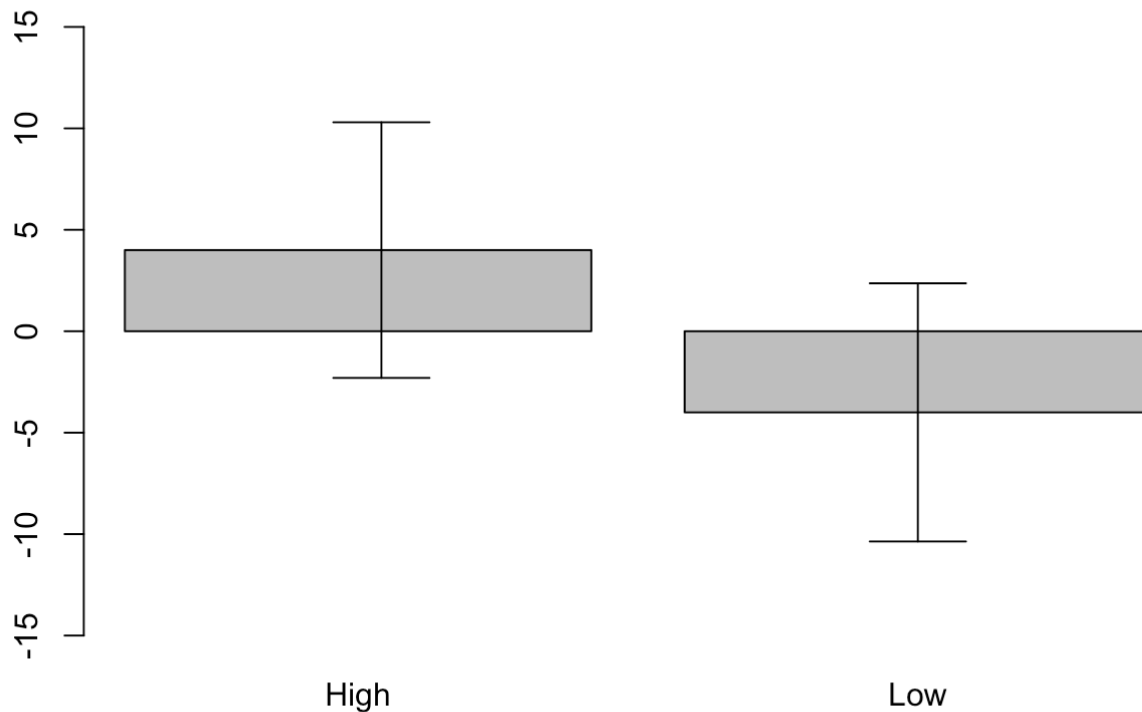
```
##           High      Low
## 20.07414 20.27339
```

```

n<-length(datc$testm2)
ses<-sds/sqrt(n)

barplot(means,ylim=c(-15,15))
arrows(x0=.75,x1=.75,y0=means[1]-1.96*ses[1],y1=means[1]+1.96*ses[1],angle=90,code=3)
arrows(x0=1.9,x1=1.9,y0=means[2]-1.96*ses[2],y1=means[2]+1.96*ses[2],angle=90,code=3)

```



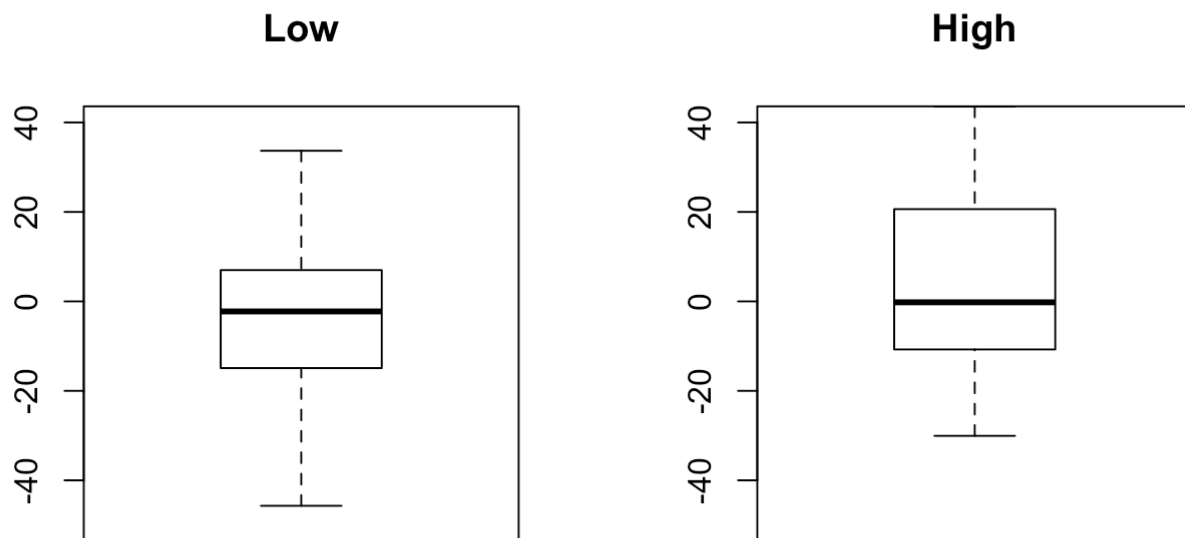
One could do a two-sample t-test as shown below. Note the high variability in the change in testosterone in low and high pose subjects. There were many cases where testosterone went down post high-power power.

```

## calculate difference
diff<-datc$testm2-datc$testm1
## make data frame with differences as DV:
treatment<-datc$hptreat
diff_df<-data.frame(diff=diff,treatment=treatment)
## subset low and high pose subjects' data:
lowdiff<-subset(diff_df,treatment=="Low")
highdiff<-subset(diff_df,treatment=="High")

## graphical summary of distributions:
op<-par(mfrow=c(1,2),pty="s")
boxplot(lowdiff$diff,main="Low",ylim=c(-50,40))
boxplot(highdiff$diff,main="High",ylim=c(-50,40))

```



```
## t-test, two sample:
t.test(lowdiff$diff,highdiff$diff)
```

```
##
## Welch Two Sample t-test
##
## data: lowdiff$diff and highdiff$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:
## -21.933205 4.264045
## sample estimates:
## mean of x mean of y
## -4.36658 4.46800
```

The bummer here is that there is actually no evidence of power posing. Cuddy's Ted talk was based on a lie about the data.

Analyze testosterone using linear models

Now, we will refit the model using various predictors: the initial testosterone value, the initial and final cortisolone (?) levels, and 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 these variables?

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

## This is the result that Fosse, Cuddy's statistician, found:
summary(m0<-lm(testm2~ctestm1+chptreat+cortm1+cortm2+female,datc))
```

```
##
## 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
```

```
summary(m0a<-lm(testm2~ctestm1+cortm1+cortm2+female,datc))
```

```
##
## Call:
## lm(formula = testm2 ~ ctestm1 + cortm1 + cortm2 + female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -29.177 -12.229  -1.509   8.982  40.730
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  53.7430     2.9688  18.102 < 2e-16 ***
## ctestm1       0.4471     0.1291   3.464  0.00146 **
## cortm1      -4.6595    28.6987  -0.162  0.87198
## cortm2     117.2815    43.4694   2.698  0.01078 *
## female     -11.2122     3.7216  -3.013  0.00486 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.84 on 34 degrees of freedom
## Multiple R-squared:  0.6636, Adjusted R-squared:  0.624
## F-statistic: 16.76 on 4 and 34 DF,  p-value: 1.114e-07
```

```
## effect on testosterone of power posing:
anova(m0,m0a)
```

```
## Analysis of Variance Table
##
## Model 1: testm2 ~ ctestm1 + chptreat + cortm1 + cortm2 + female
## Model 2: testm2 ~ ctestm1 + cortm1 + cortm2 + female
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      33 8463.3
## 2      34 9646.8 -1   -1183.5 4.6147 0.03913 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##
## 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
```

```
summary(m1a<-lm(testm2~ctestm1 +cortm1+cortm2+female+chptreat:female,datc))
```

```
##
## Call:
## lm(formula = testm2 ~ ctestm1 + cortm1 + cortm2 + female + chptreat:female,
##      data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -29.246  -9.904  -1.481   8.345  39.439
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    54.6520     2.9633  18.443 < 2e-16 ***
## ctestm1         0.3309     0.1464   2.261  0.03051 *
## cortm1         1.3209    28.3515   0.047  0.96312
## cortm2       134.5826    43.9535   3.062  0.00435 **
## female       -13.5656     3.9384  -3.444  0.00158 **
## female:chptreat  4.8545     3.0854   1.573  0.12517
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.49 on 33 degrees of freedom
## Multiple R-squared:  0.687, Adjusted R-squared:  0.6396
## F-statistic: 14.49 on 5 and 33 DF,  p-value: 1.578e-07
```

```
anova(m1,m1a)
```

```
## Analysis of Variance Table
##
## Model 1: testm2 ~ ctestm1 + chptreat + cortm1 + cortm2 + female + chptreat:female
## Model 2: testm2 ~ ctestm1 + cortm1 + cortm2 + female + chptreat:female
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      32 8271.2
## 2      33 8973.6 -1    -702.4 2.7175 0.109
```

There seems to be no evidence here either that power posing increases testosterone.

Analyzing the data using change 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

summary(m2<-lm(change~chptreat+cortm1+cortm2+female,datc))
```

```
##
## Call:
## lm(formula = change ~ chptreat + cortm1 + cortm2 + female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -44.519  -8.528  -2.533   11.695   40.565
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.5055     3.3976   0.149  0.8826
## chptreat        6.1655     3.3737   1.828  0.0764 .
## cortm1       -32.6931    33.0813  -0.988  0.3300
## cortm2       100.6842    52.1607   1.930  0.0619 .
## female        -1.4990     3.4730  -0.432  0.6688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 19.94 on 34 degrees of freedom
## Multiple R-squared:  0.1449, Adjusted R-squared:  0.04425
## F-statistic:  1.44 on 4 and 34 DF,  p-value: 0.2421
```

```
summary(m2a<-lm(change~cortm1+cortm2+female,datc))
```



```
##
## Call:
## lm(formula = change ~ cortm1 + cortm2 + female, data = datc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -44.840 -10.938  -2.482  13.464  46.153
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.6302     3.5086   0.180   0.858
## cortm1       -32.7490    34.1692  -0.958   0.344
## cortm2        73.8304    51.6941   1.428   0.162
## female        -1.3987     3.5867  -0.390   0.699
##
## Residual standard error: 20.6 on 35 degrees of freedom
## Multiple R-squared:  0.06086,    Adjusted R-squared:  -0.01964
## F-statistic: 0.756 on 3 and 35 DF,  p-value: 0.5264
```

```
anova(m2,m2a) ## no effect
```

```
## Analysis of Variance Table
##
## Model 1: change ~ chptreat + cortm1 + cortm2 + female
## Model 2: change ~ cortm1 + cortm2 + female
##   Res.Df  RSS Df Sum of Sq    F Pr(>F)
## 1      34 13524
## 2      35 14853 -1    -1328.5 3.3399 0.07641 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So, the linear model also shows no effect of power posing on change in testosterone.

Summary

Both the t-test and the likelihood ratio test show that there is *no* evidence in the Cuddy data for power posing raising testosterone. Cuddy's Ted talk was based on a fictional claim.