Analysis of power pose data

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1 October 2016

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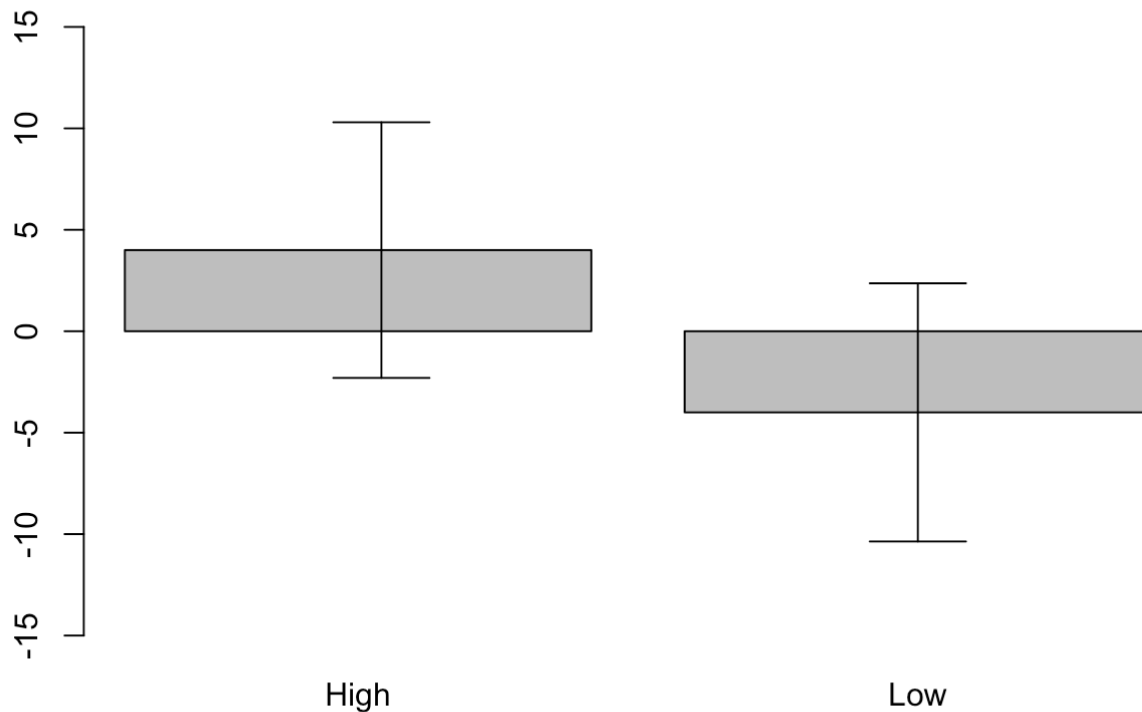
```
##     High      Low
## 20.07414 20.27339
```

```
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)
```
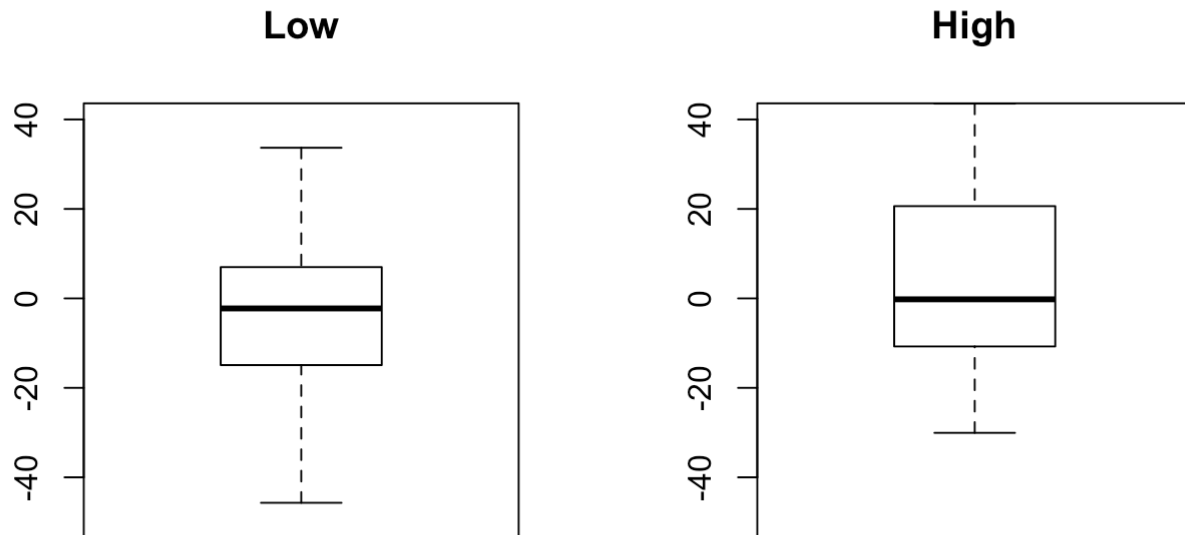

One could do a two-sample t-test like this:

```
diff<-datc$testm2-datc$testm1
treatment<-datc$hptreat
diff_df<-data.frame(diff=diff,treatment=treatment)
lowdiff<-subset(diff_df,treatment=="Low")
highdiff<-subset(diff_df,treatment=="High")
op<-par(mfrow=c(1,2),pty="s")
boxplot(lowdiff$diff,main="Low",ylim=c(-50,40))
boxplot(highdiff$diff,main="High",ylim=c(-50,40))
```

```
t.test(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 cortisone (?) 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
```

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 question.

```
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, in fact, both the t-test and the likelihood ratio test show that there is *no* evidence in the Cuddy data for power posing raising testosterone. Her Ted talk was based on a fictional claim.