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, and ignoring 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)))
```
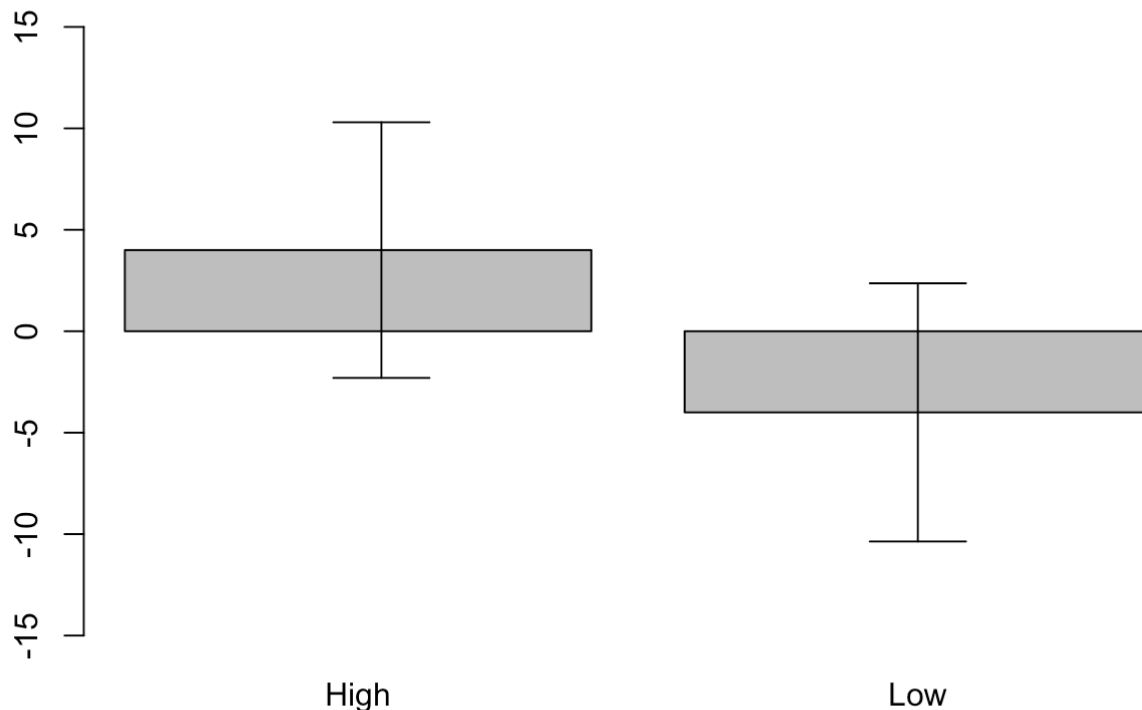
```
##      High      Low
## 20.07414 20.27339
```

```
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(subj=1:length(treatment),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(2,2),pty="s")
boxplot(lowdiff$diff,main="Low",ylim=c(-50,50),ylab="change in testosterone")
boxplot(highdiff$diff,main="High",ylim=c(-50,50),ylab="change in testosterone")
barplot(lowdiff$diff,main="Low",ylim=c(-50,50),ylab="change in testosterone")
barplot(highdiff$diff,main="High",ylim=c(-50,50),ylab="change in testosterone")
```

Low

High

Low
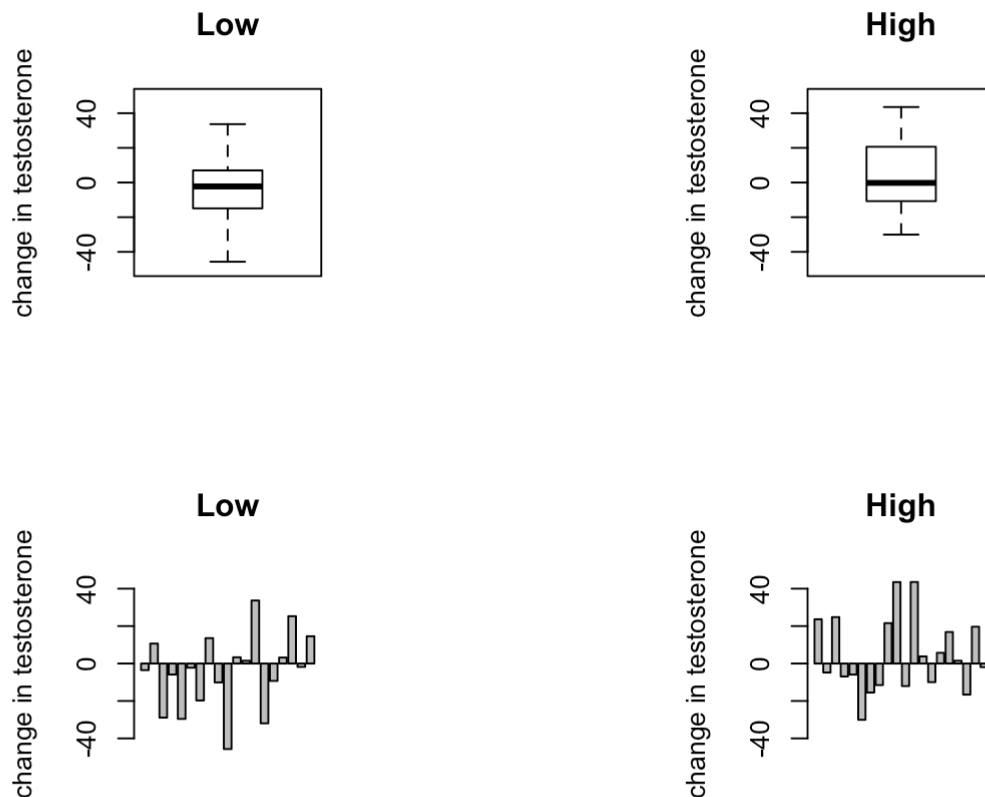
High

Two-sample t-test:

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

```
##
##   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
```

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
```

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~1,datc))
```

```
##
## Call:
## lm(formula = change ~ 1, data = datc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -45.859 -10.969  -2.099  13.904  43.386
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.164      3.267    0.05     0.96
##
## Residual standard error: 20.4 on 38 degrees of freedom
```

```
summary(m2a<-lm(change~chptreat,datc))
```

```
##
## 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
```

```
anova(m2,m2a)
```

```
## Analysis of Variance Table
##
## Model 1: change ~ 1
## Model 2: change ~ chptreat
##   Res.Df   RSS Df Sum of Sq      F Pr(>F)
## 1     38 15815
## 2     37 15055  1    760.49 1.8691 0.1798
```

```
## taking gender into account
summary(m3<-lm(change~female,datc))
```

```
##
## Call:
## lm(formula = change ~ female, data = datc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -47.603 -11.605  -1.227  13.467  44.258
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.6001     3.5048   0.171    0.865
## female       -1.3084     3.5048  -0.373    0.711
##
## Residual standard error: 20.64 on 37 degrees of freedom
## Multiple R-squared:  0.003752,   Adjusted R-squared:  -0.02317
## F-statistic: 0.1394 on 1 and 37 DF,  p-value: 0.7111
```

```
summary(m3a<-lm(change~chptreat+female,datc))
```

```
##
## 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
```

```
anova(m3,m3a) ## no effect
```

```
## Analysis of Variance Table
##
## Model 1: change ~ female
## Model 2: change ~ chptreat + female
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1     37 15756
## 2     36 15010  1    746.13 1.7896 0.1894
```

```
## taking interaction between treatment and gender into account
summary(m4<-lm(change~female,datc))
```

```
##
## Call:
## lm(formula = change ~ female, data = datc)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -47.603 -11.605  -1.227  13.467  44.258
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.6001     3.5048   0.171    0.865
## female       -1.3084     3.5048  -0.373    0.711
##
## Residual standard error: 20.64 on 37 degrees of freedom
## Multiple R-squared:  0.003752,   Adjusted R-squared:  -0.02317
## F-statistic: 0.1394 on 1 and 37 DF,  p-value: 0.7111
```

```
summary(m4a<-lm(change~chptreat*female,datc))
```

```
##
## 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
```

```
anova(m4,m4a) ## no effect
```

```
## Analysis of Variance Table
##
## Model 1: change ~ female
## Model 2: change ~ chptreat * female
##   Res.Df   RSS Df Sum of Sq      F Pr(>F)
## 1     37 15756
## 2     35 14256  2      1500 1.8414 0.1736
```

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

Stan analysis

For now, I just fit the change model, with gender as predictor (including interaction with treatment). The priors probably need some more thought.

```
dat<-list(change=datc$change,
          female=datc$female,
          treatment=datc$chptreat,
          N=length(datc$change))

library(rstan)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: StanHeaders
```

```
## rstan (Version 2.12.1, packaged: 2016-09-11 13:07:50 UTC, GitRev: 85f7a56811da)
```

```
## For execution on a local, multicore CPU with excess RAM we recommend calling
## rstan_options(auto_write = TRUE)
## options(mc.cores = parallel::detectCores())
```

```
library(parallel)
rstan_options(auto_write=TRUE)
options(mc.cores=parallel::detectCores())

## cauchy priors on beta params:
#output <- stanc("linearmodel.stan")
## normal priors N(0,20) on beta params:
output <- stanc("linearmodel_normalpriors.stan")

fit <- stan(file='linearmodel_normalpriors.stan', data=dat,
            iter=2000, chains=4, seed=4938483,
            control = list(adapt_delta = 0.8))

paramnames<-c("alpha","beta_female","beta_treatment","beta_interaction","sigma")
```

```
print(fit,pars=paramnames)
```

```
## Inference for Stan model: linearmodel_normalpriors.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##                   mean se_mean   sd   2.5%   25%   50%   75% 97.5% n_eff
## alpha             0.17    0.06 3.29  -6.20 -2.01  0.22  2.43  6.45  2972
## beta_female      -0.88    0.06 3.30  -7.38 -3.11 -0.93  1.31  5.59  2971
## beta_treatment    5.62    0.06 3.30  -0.78  3.36  5.58  7.75 12.11  2797
## beta_interaction -4.43    0.06 3.34 -11.06 -6.57 -4.39 -2.18  2.19  3061
## sigma            20.31    0.04 2.32  16.35 18.73 20.09 21.68 25.35  2888
##                   Rhat
## alpha                1
## beta_female          1
## beta_treatment       1
## beta_interaction     1
## sigma                1
##
## Samples were drawn using NUTS(diag_e) at Thu Oct  6 11:57:26 2016.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```
fit_matrix<-as.matrix(fit)
(prob<-mean(fit_matrix[,3]>0))
```
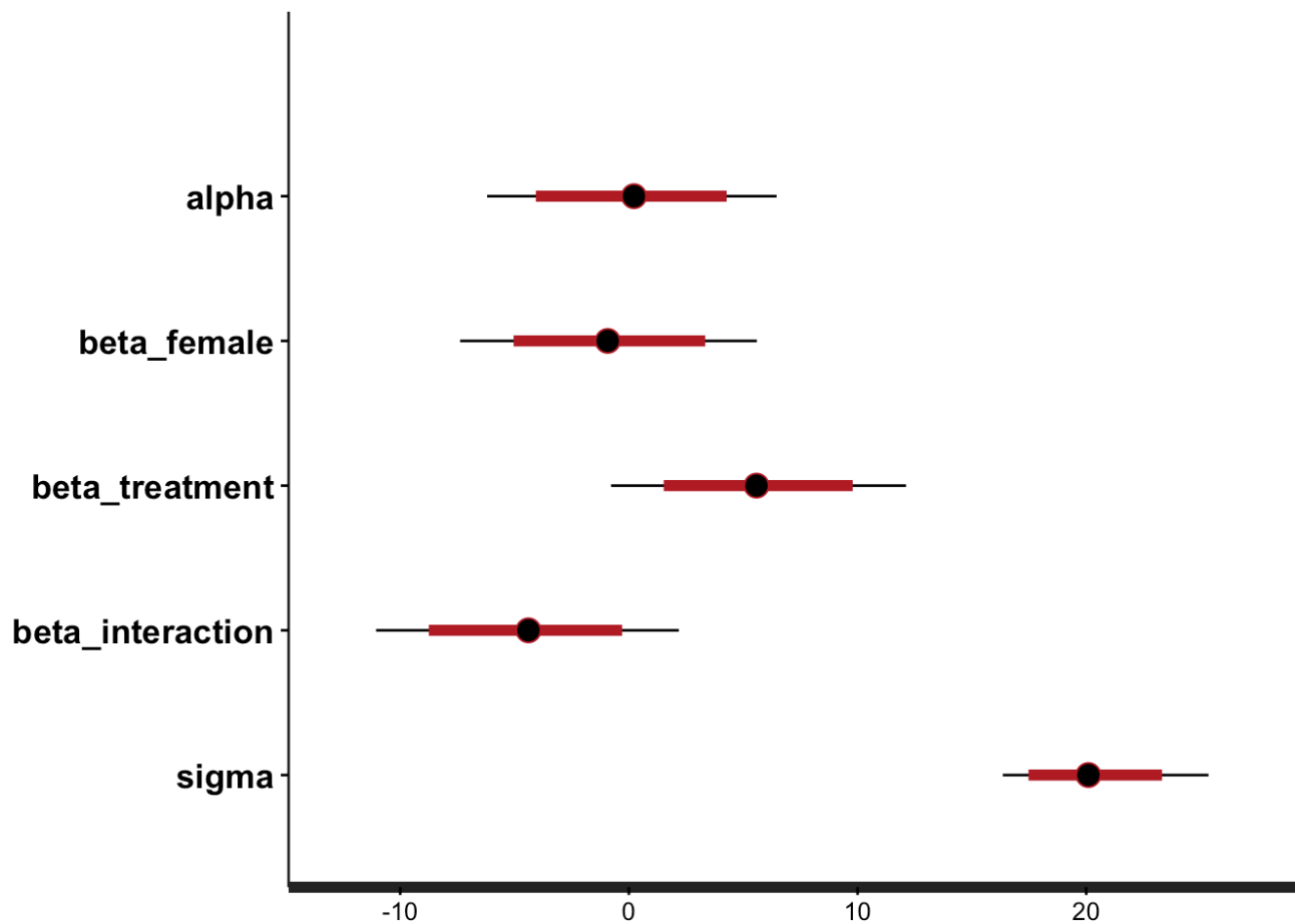
```
## [1] 0.96
```

```
params<-extract(fit,pars=paramnames)

stan_plot(fit,pars=paramnames)
```
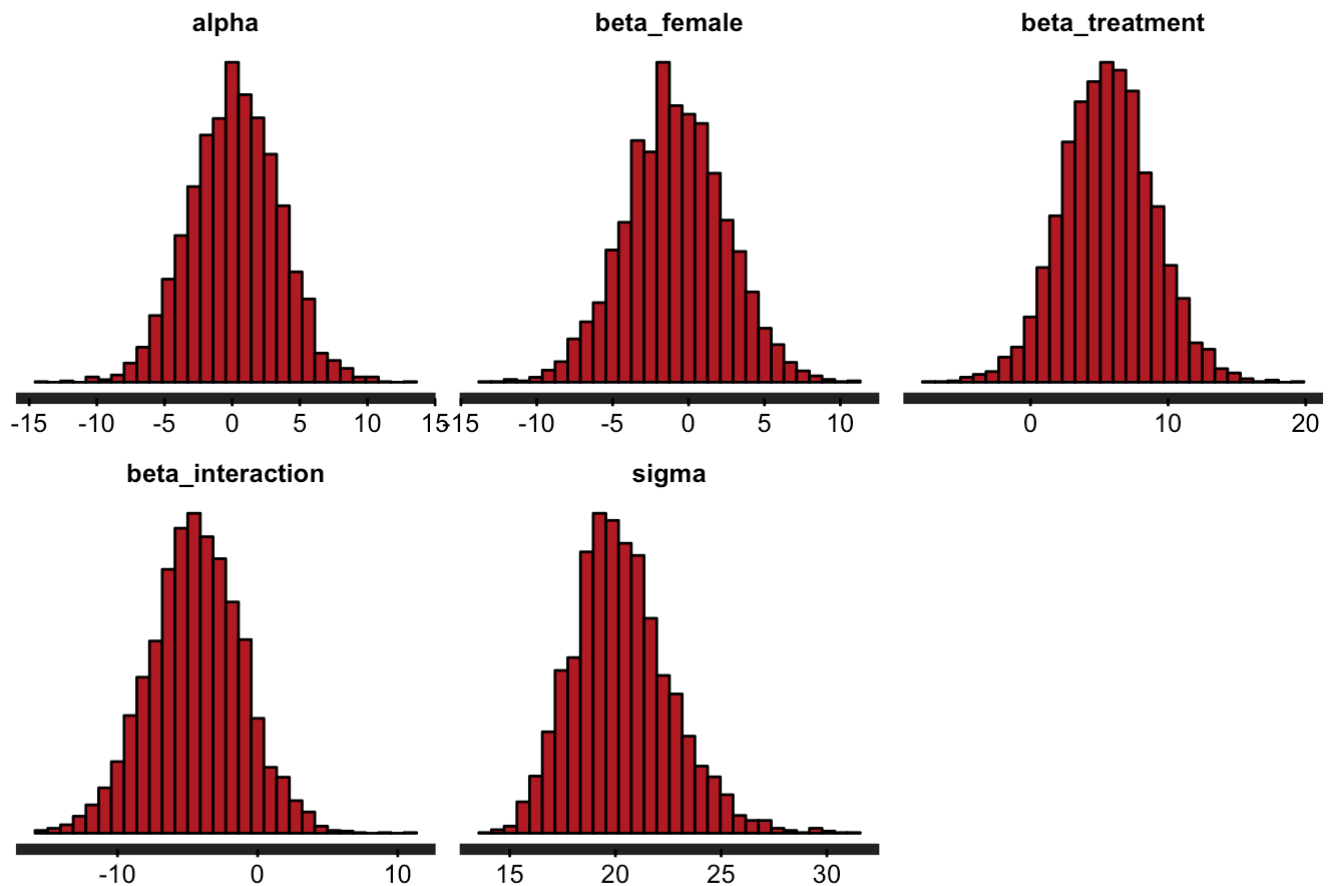
```
## ci_level: 0.8 (80% intervals)
```

```
## outer_level: 0.95 (95% intervals)
```

```
stan_hist(fit,pars=paramnames)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

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.

The Stan model shows that one could argue that there is some weak evidence for testosterone going up when one holds a high power pose. There is a 95% probability of the treatment coefficient being positive, with 95% credible interval [-0.78, 12.11].