Appendix D

Below is the R-code that we used to specify our models and obtain our $p$-values of Study 2.

```r
#set the working directory
setwd('path to working directory')

#read data
data1 = read.csv2("Data_Study_2_collabra.csv")

#load the library
library(afex)

# the variables contain the following values:
# DyadID: the unique id for each Dyad
# Treatment_name: low or high behavioral norm
# total_trials: always 20
# total_doubles: the total reported number of doubles for each dyad
# proportion_doubles: the variable “total_doubles” divided by “total_trials” (i.e., 20)

#First get model 1 with the mixed function. As the dependent variable we specified the
#proportion of doubles for each dyad, and Treatment_name (i.e., the behavioral condition)
#was the predictor. Furthermore, we wanted to obtain our $p$-values, hence we used the PB
#function, with 1000 simulations. Lastly, we also specified that the data was binomial.

model1 <- mixed(proportion_doubles ~ Treatment_name + (1 | DyadID), method = "PB",
                 family = binomial, data = data1, args.test = list(nsim = 1000))

#Now get the other model with the mixed function. The only difference with the first model is
#that instead of using the proportions as dependent variable, we used the cbind function. This
#function requires the hits (i.e., the number of doubles) and misses (i.e., the total number of
#trials minus the total number of doubles) as the dependent variable for each dyad. The rest is
#still the same.

model2 <- mixed(cbind(total_doubles,total_trials - total_doubles) ~ Treatment_name + (1 | DyadID), method = "PB", family = binomial, data = data1, args.test = list(nsim = 1000))

#get the p-values with the anova function
anova(model1)
anova(model2)
```
Lastly, below is Figure D1, which shows the output of the R-Code.

```r
> anova(model1)
Mixed Model Anova Table (Type 3 tests)
Model: proportion_doubles ~ Treatment_name + (1 | DyadID)
Data: datal
    Chisq Chi Df Pr(>Chisq) Pr(>P8)
Treatment_name 4.1822 1 0.04085 0.03696 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> anova(model2)
Mixed Model Anova Table (Type 3 tests)
Model: cbind(total_doubles, total_trials - total_doubles) ~ Treatment_name +
Model:   (1 | DyadID)
Data: datal
    Chisq Chi Df Pr(>Chisq) Pr(>P8)
Treatment_name 3.0407 1 0.081198 0.08735 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

*Figure D1.* Screenshot of the output of model 1 and model 2.