

Study 4: Mixed Masc-Fem Analysis

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This study investigates the social evaluative implications of sensory adaptation to men's *and* women's voices.

Stimuli. Test stimuli were audio recordings of 20 young adult men and 20 young adult women reciting the sentence "Hi, I'm a student at UCLA". Samples were recorded digitally (M-Audio Microtrack recorder, 16-bit amplitude resolution, 44.1 kHz sampling rate) using an AKG E535 condenser microphone placed approximately 15cm from the mouth. Stimuli varied naturally in duration, fundamental frequency (F_0), and voice quality.

Adapting stimuli. Adaptors included both masculinized and feminized exemplars that would be gender-typical or gender-atypical relative to test stimuli. Male adaptors were generated from recordings of 5 young adult men producing the same sentence as test stimuli. These recordings were manipulated to be more masculine or more feminine using the VT-Change script in Praat (Boersma & Weenink, 2021). We altered F_0 , a well-established sexually dimorphic aspect of voice, using PSOLA (Pitch Synchronous Overlap Add) resynthesis. For masculinized versions, F_0 values were lowered to 90% of baseline. For feminized versions, F_0 was increased to 175% of baseline. Female adaptors were generated from recordings of 5 young adult women producing the same sentence as test stimuli. For masculinized versions, F_0 values were lowered to 70% of baseline. For feminized versions, F_0 was increased to 140% of baseline.

Procedure. We recruited U.S. resident from Prolific. After providing consent, participants were randomly assigned to either a feminized or masculinized adaptation condition. In one block, participants listened to only male voices and in another block they listened to only female voices. On each trial, participants first heard an adapting voice followed by a test voice which they judged for attractiveness, masculinity/femininity, likability, friendliness, and typicality (1 = *Not at all* to 9 = *Extremely*). To maintain attention, participants also completed a secondary task rating whether the pitch of each adaptor was higher, lower, or identical to the previous adaptor. In total, participants completed 40 trials in pseudo-randomized order, with each adaptor presented four times.

Hypotheses. Variability in vocal tract length and laryngeal cavity size create large differences in fundamental frequency for male and female voices (Hillenbrand et al., 1995). Perceivers evaluate men and women with regard to these differences, rating men as more attractive when their voices have low fundamental frequency but women as more attractive when their voices have high fundamental frequency (Puts, 2005; Puts, Barndt, Welling, Dawood, & Burriss, 2011). Therefore, we predicted that participants in the feminized adaptation condition would rate male test voices as more attractive and female test voices as less attractive than participants in the masculinized adaptation condition. Furthermore, we predicted that participants in the masculinized adaptation condition would rate male test voices as less attractive and female test voices as more attractive than participants in the feminized condition. This is because adaptation to feminized male voices or masculinized female voices will make a neutral test voice sound more typical and therefore more favorable.

Load Data

```
data <- read.csv("/Users/kelse/Documents/UCLA/Projects/Auditory Aftereffects/Analysis/Prolific/Mixed/Ma
header = TRUE)
```

Factor

```
# test voice
data$voice <- factor(data$voice)

# condition
data$condition <- as.factor(data$condition)

# target sex
data$target.sex <- as.factor(data$target.sex)

# participant ID
data$ID <- factor(data$ID)

# participant sex
data$Sex <- as.factor(data$Sex)
```

Filter Filter out participants who do not identify as male or female.

```
nrow(data)/40
```

```
## [1] 178
```

```
data <- data %>%
  filter(Sex == "1" | Sex == "2")
nrow(data)/40
```

```
## [1] 174
```

Check Data Quality

Group by participant ID and filter out participants with a response range of 1 on any of the dependent variables.

```
# sample size before filtering
nrow(data)/40
```

```
## [1] 174
```

```
# attraction
data <- data %>%
  group_by(ID) %>%
  filter((max(attraction) - min(attraction) > 1))

# masculinity/femininity
data <- data %>%
  group_by(ID) %>%
  filter((max(masc.fem) - min(masc.fem) > 1))

# likability
data <- data %>%
  group_by(ID) %>%
```

```

    filter((max(likability) - min(likability) > 1))

# friends
data <- data %>%
  group_by(ID) %>%
  filter((max(friends) - min(friends) > 1))

# typicality
data <- data %>%
  group_by(ID) %>%
  filter((max(typicality) - min(typicality) > 1))

# sample size after filtering
nrow(data)/40

```

```
## [1] 172
```

Demographics After filtering participants, calculate the demographics of the final sample.

Sex

```
table(data$Sex)/40 # 1 = male, 2 = female, 3 = other 4 = prefer not to say
```

```
##
##  1  2  3  4
## 38 134  0  0
```

The majority of the sample is female (78%), followed by male (22%).

Race

```
table(data$Race)/40 # 1 = Asian, 2 = Black, 3 = Latino, 4 = White, 5 = Biracial/Other, 6 = prefer not
```

```
##
##  1  2  3  4  5  7
## 15 17 25 103 11  1
```

The majority of the sample is White (60%), followed by Latino (15%), Black (10%), Asian (9%), and Biracial/Other (3%).

Age

```
stat.desc(data$Age)
```

```
##      nbr.val      nbr.null      nbr.na      min      max
## 6880.0000000  0.0000000  0.0000000  18.0000000  63.0000000
##      range      sum      median      mean      SE.mean
## 45.0000000 174640.0000000  23.0000000  25.3837209  0.0848813
##  CI.mean.0.95      var      std.dev      coef.var
##    0.1663936    49.5692654    7.0405444    0.2773646
```

The average age is 25 years old, with a range from 18 - 63.

Politics

```
table(data$Politics)/40 # 1 = Very Conservative, 2 = Conservative, 3 = Moderat, 4 = Liberal, 5 = Very
```

```
##
##  1  2  3  4  5  6
##  2 19 28 73 48  2
```

The majority of the sample is moderate to liberal.

Sexual Orientation

```
table(data$SO)/40 # 1 = Heterosexual, 2 = Gay/Lesbian/Queer, 3 = Bisexual, 4 = Not Sure, 5 = prefer no
```

```
##
##   1   2   3   4   5   6
## 104  11  48   2   1   6
```

The majority of the sample is heterosexual (60%), followed by bisexual (28%) and gay (6%).

Education

```
table(data$Education)/40 # 1 = Less than high school, 2 = High school, 3 = Some college, 4 = Associate
```

```
##
##   1   2   3   4   5   6   7   8
##   1  21  60  12  48   9  17   4
```

Most participants have completed some college.

Multilevel Analyses (NCC Design)

The following analyses are done in a stepwise fashion.

Attraction

Main Effect - Attraction by Condition (Masculinized/Feminized)

```
# reference group - masc condition
data$condition <- relevel(data$condition, ref = "masc")

model.1 <- lmer(attraction ~ condition + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ condition + (1 | ID) + (1 | trial)
##   Data: data
## Control:
```

```
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28267.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5194 -0.6440  0.0862   0.6955   3.4953
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   ID          (Intercept) 0.92359  0.9610
##   trial       (Intercept) 0.08924  0.2987
##   Residual                3.31373  1.8204
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.75948   0.11747 195.11855  49.029 <0.0000000000000002 ***
## conditionfem  0.06081   0.15300 169.99997   0.397      0.692
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## conditionfm -0.644
```

```
# 95% confidence interval
ci.1 <- confint(model.1, method = "Wald", level = 0.95)
ci.1
```

```
##              2.5 %   97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)   5.5292458 5.989720
## conditionfem -0.2390603 0.360683
```

```
# group means
attraction_condition <- data %>%
  group_by(condition) %>%
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))
attraction_condition
```

```
## # A tibble: 2 x 5
##   condition mean    sd    n    se
##   <fct>     <dbl> <dbl> <int> <dbl>
## 1 masc     5.76  2.09  3480 0.0354
## 2 fem      5.82  2.07  3400 0.0355
```

There is no difference in attraction ratings of test voices after adaptation to masculinized voices ($M = 5.76$, $SD = 2.09$) relative to feminized voices ($M = 5.82$, $SD = 2.07$), $t(170) = 0.40$, $p = .692$.

Main Effect - Attraction by Target Sex (Male/Female)

```

# reference group - female targets
data$target.sex <- relevel(data$target.sex, ref = "female")

model.2 <- lmer(attraction ~ target.sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.2)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28028.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7752 -0.6437  0.0768  0.6882  3.3749
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.92146  0.9599
## trial   (Intercept) 0.08867  0.2978
## Residual              3.19656  1.7879
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)    6.12759    0.09221 189.02007   66.45 <0.0000000000000002 ***
## target.sexmale -0.67611    0.04311 6668.30201  -15.68 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.234

# 95% confidence interval
ci.2 <- confint(model.2, method = "Wald", level = 0.95)
ci.2

##              2.5 %    97.5 %
## .sig01          NA         NA
## .sig02          NA         NA
## .sigma          NA         NA
## (Intercept)    5.9468560  6.308324
## target.sexmale -0.7606091 -0.591612

# group means
attraction_sex <- data %>%

```

```

group_by(target.sex) %>%
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))
attraction_sex

```

```

## # A tibble: 2 x 5
##   target.sex mean    sd      n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female      6.13  1.94  3440 0.0331
## 2 male        5.45  2.15  3440 0.0367

```

Female test voices ($M = 6.13$, $SD = 1.94$) are rated as significantly more attractive than male test voices ($M = 5.45$, $SD = 2.15$), $t(6668) = -15.68$, $p < .001$.

Main Effect - Attraction by Participant Sex (Male/Female)

```

# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

```

```

model.3 <- lmer(attraction ~ Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.3)

```

```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28265.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5268 -0.6440  0.0846  0.6929  3.4853
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.91140 0.9547
## trial   (Intercept) 0.08924 0.2987
## Residual              3.31374 1.8204
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.72892    0.09824 181.71835  58.317 <0.0000000000000002 ***
## Sex1          0.27437    0.18326 170.00375   1.497      0.136
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.412

```

```
# 95% confidence interval
ci.3 <- confint(model.3, method = "Wald", level = 0.95)
ci.3
```

```
##                2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)  5.53637553 5.9214603
## Sex1        -0.08481019 0.6335533
```

```
# group means
attraction_Sex <- data %>%
  group_by(Sex) %>%
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))
attraction_Sex
```

```
## # A tibble: 2 x 5
##   Sex    mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.73  2.10  5360 0.0287
## 2 1      6.00  1.99  1520 0.0510
```

There is no significant difference in attraction ratings between male participants ($M = 6.00$, $SD = 1.99$) and female participants ($M = 5.73$, $SD = 2.10$), $t(170) = 1.50$, $p = .136$.

Interaction - Attraction by Condition (Masculinized/Feminized) and Target Sex (Male/Female)

```
# simple effects: relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.4 <- lmer(attraction ~ condition * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.4)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28021.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7594 -0.6437  0.0742  0.6874  3.3764
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## ID      (Intercept)  0.92652   0.9626
```



```
## trial      (Intercept) 0.06655 0.2580
## Residual          3.19655 1.7879
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      6.2511    0.1258 197.8487  49.709
## conditionfem     -0.2470    0.1787 198.6141  -1.383
## target.sexmale   -0.9833    0.1016  55.9216  -9.675
## conditionfem:target.sexmale  0.6157    0.1845  38.0014   3.336
##
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## conditionfem          0.16833
## target.sexmale    0.000000000000151 ***
## conditionfem:target.sexmale    0.00191 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxml -0.404  0.468
## cndtnfm:tr.  0.366 -0.516 -0.906
```

```
# 95% confidence interval
```

```
ci.4 <- confint(model.4, method = "Wald", level = 0.95)
ci.4
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      6.0046741  6.4976248
## conditionfem     -0.5972158  0.1031523
## target.sexmale   -1.1825309 -0.7841358
## conditionfem:target.sexmale  0.2539927  0.9773799
```

```
# group means
```

```
attraction_CxTS <- data %>%
  group_by(condition, target.sex) %>%
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))
```

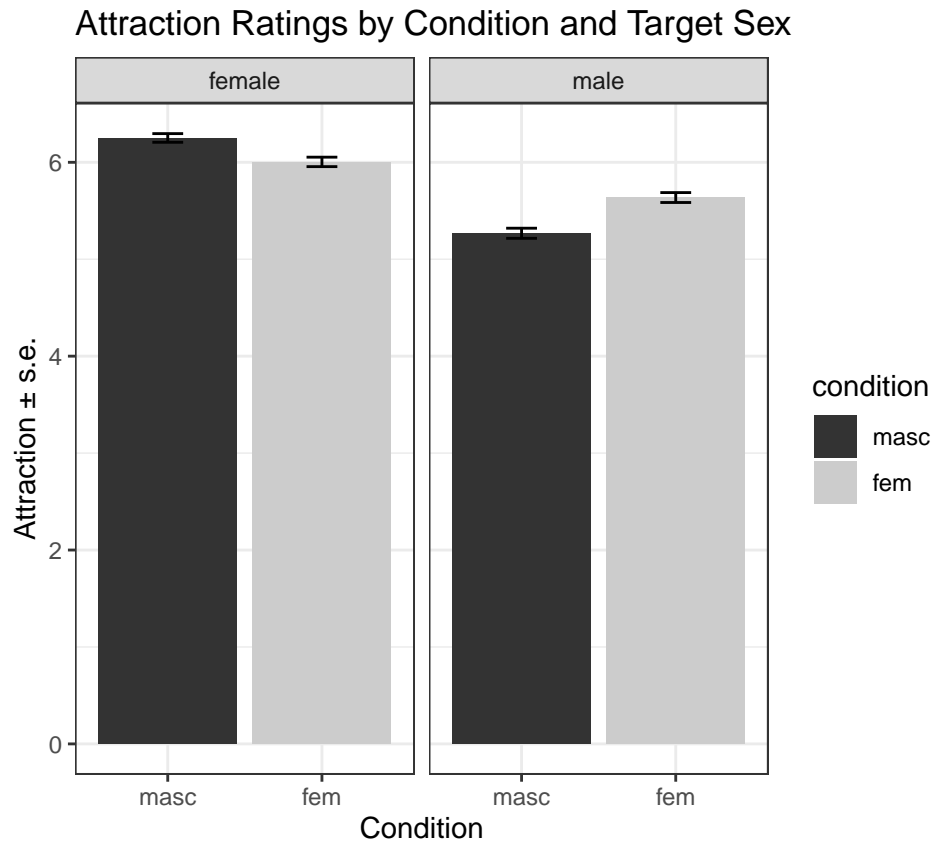
```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

```
attraction_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 masc      female      6.25  1.86  1740 0.0447
## 2 masc      male        5.27  2.18  1740 0.0522
## 3 fem       female      6.00  2.01  1700 0.0488
## 4 fem       male        5.64  2.11  1700 0.0511
```

```
# plot
attraction_CxTS_plot <- ggplot(attraction_CxTS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey()

attraction_CxTS_plot + labs(title = "Attraction Ratings by Condition and Target Sex",
  y = "Attraction ± s.e.", x = "Condition") + theme_bw()
```



The interaction between target sex and condition is significant, $t(38) = 3.33$, $p < .01$. Male test voices are rated as more attractive after adaptation to feminized voices, while female test voices are rated as more attractive after adaptation to masculinized voices. The simple effect of condition centered at female targets is not significant, $t(199) = -1.38$, $p = .168$.

Simple Effect - Attraction by Condition (Masculinized/Feminized) when Target Sex (Male/Female) is centered at Male

```
# simple effects: relevel so reference group = male
data$target.sex <- relevel(data$target.sex, ref = "male")

model.5 <- lmer(attraction ~ condition * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.5)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
```

```
## lmerModLmerTest]
## Formula: attraction ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28021.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7594 -0.6437  0.0742  0.6874  3.3764
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.92652 0.9626
## trial   (Intercept) 0.06655 0.2580
## Residual 3.19655 1.7879
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.2678     0.1258 197.8487  41.890
## conditionfem      0.3687     0.1787 198.6141   2.063
## target.sexfemale  0.9833     0.1016  55.9216   9.675
## conditionfem:target.sexfemale -0.6157     0.1845  38.0014  -3.336
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem      0.04038 *
## target.sexfemale  0.0000000000000151 ***
## conditionfem:target.sexfemale  0.00191 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxfml -0.404  0.468
## cndtnfm:tr.  0.366 -0.516 -0.906
```

The simple effect of condition centered at male targets is significant, $t(199) = 2.06$, $p < .05$.

Interaction - Attraction by Condition (Masculinized/Feminized) and Participant Sex (Male/Female)

```
# simple effects: relevel so reference group = female
data$Sex <- relevel(data$Sex, ref = "2")

model.6 <- lmer(attraction ~ condition * Sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.6)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
```

```
## Formula: attraction ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28266.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5236 -0.6421  0.0856  0.6918  3.4901
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.91887 0.9586
## trial   (Intercept) 0.08924 0.2987
## Residual 3.31373 1.8204
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      5.6789      0.1278 194.3742  44.426 <0.0000000000000002 ***
## conditionfem      0.1064      0.1732 168.0000   0.614      0.540
## Sex1              0.4383      0.2770 168.0000   1.583      0.115
## conditionfem:Sex1 -0.3032      0.3717 168.0000  -0.816      0.416
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf Sex1
## conditionfm -0.637
## Sex1         -0.398 0.294
## cndtnfm:Sex1 0.297 -0.466 -0.745

# 95% confidence interval
ci.6 <- confint(model.6, method = "Wald", level = 0.95)
ci.6

##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.4283381 5.9294084
## conditionfem  -0.2330808 0.4459692
## Sex1          -0.1045475 0.9811760
## conditionfem:Sex1 -1.0316610 0.4253067

# group means
attraction_CxPS <- data %>%
  group_by(condition, Sex) %>%
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))

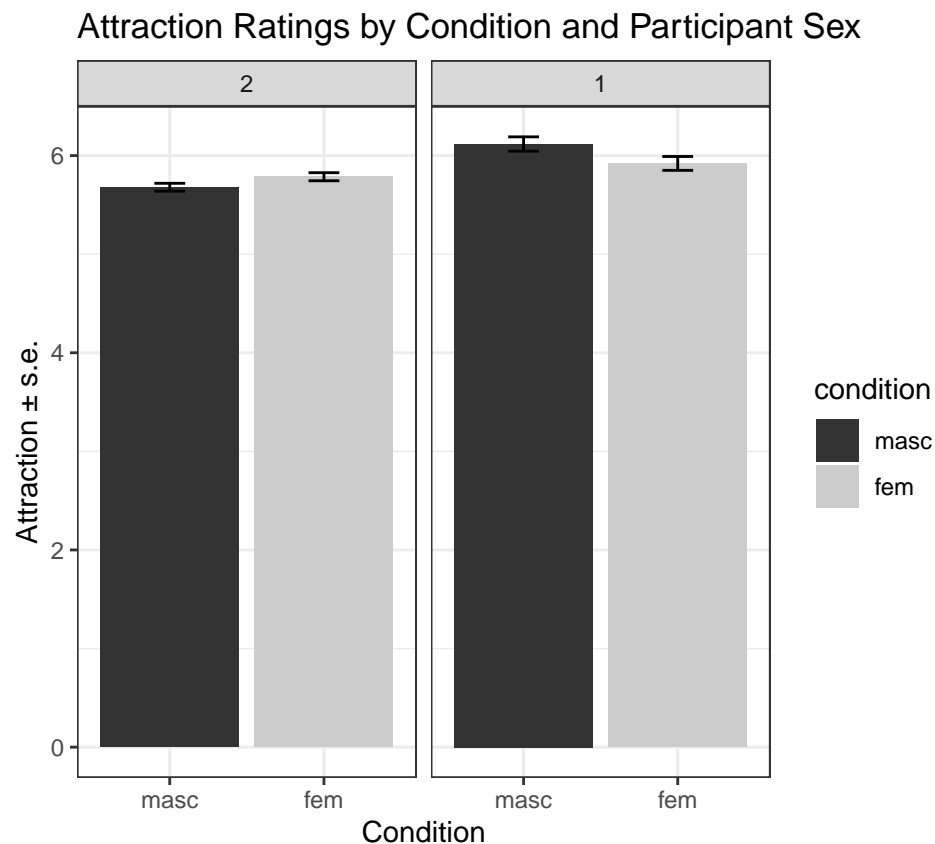
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

```
attraction_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      2      5.68  2.13  2840 0.0400
## 2 masc      1      6.12  1.83   640 0.0725
## 3 fem       2      5.79  2.06  2520 0.0411
## 4 fem       1      5.92  2.09   880 0.0704
```

```
# plot
attraction_CxPS_plot <- ggplot(attraction_CxPS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~Sex) + scale_fill_grey()

attraction_CxPS_plot + labs(title = "Attraction Ratings by Condition and Participant Sex",
  y = "Attraction ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(168) = -0.82$, $p=.416$.

Interaction - Attraction by Participant Sex (Male/Female) and Target Sex (Male/Female)

```

# releve so reference group = female
data$target.sex <- releve(data$target.sex, ref = "female")

model.7 <- lmer(attraction ~ Sex * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.7)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 28029.6
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.8063 -0.6451 0.0761 0.6895 3.3428
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.91435 0.9562
## trial (Intercept) 0.08929 0.2988
## Residual 3.19643 1.7879
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 6.0554 0.1012 205.7938 59.811 <0.0000000000000002
## Sex1 0.3269 0.1905 198.5922 1.716 0.0878
## target.sexmale -0.6529 0.0489 6673.1700 -13.352 <0.0000000000000002
## Sex1:target.sexmale -0.1050 0.1043 6683.5882 -1.007 0.3140
##
## (Intercept) ***
## Sex1 .
## target.sexmale ***
## Sex1:target.sexmale
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Sex1 trgt.s
## Sex1 -0.416
## target.sxml -0.241 0.129
## Sx1:trgt.sx 0.114 -0.274 -0.472

# 95% confidence interval
ci.7 <- confint(model.7, method = "Wald", level = 0.95)
ci.7

## 2.5 % 97.5 %

```

```
## .sig01                NA        NA
## .sig02                NA        NA
## .sigma                NA        NA
## (Intercept)          5.85692589  6.25378691
## Sex1                  -0.04657521  0.70029303
## target.sexmale       -0.74871336 -0.55704060
## Sex1:target.sexmale  -0.30932289  0.09937349
```

```
# group means
```

```
attraction_PSxTS <- data %>%
  group_by(Sex, target.sex) %>%
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))
```

'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.

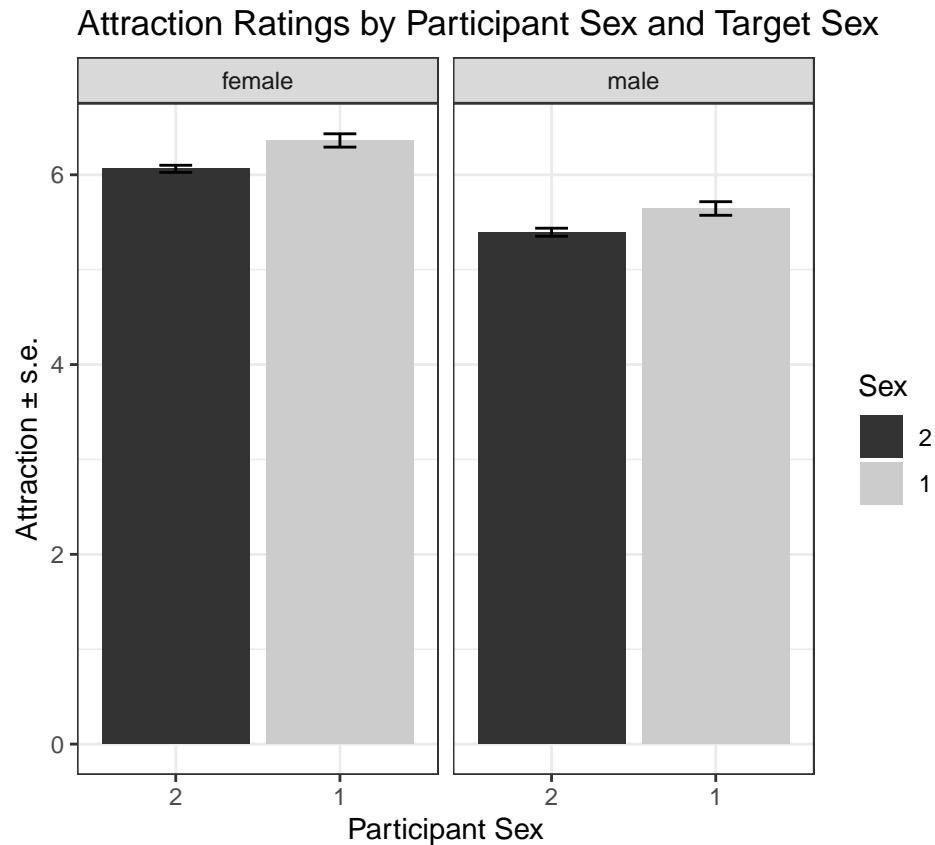
```
attraction_PSxTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex  target.sex mean    sd    n    se
##   <fct> <fct>     <dbl> <dbl> <int> <dbl>
## 1 2    female     6.06  1.94  2680 0.0375
## 2 2    male       5.39  2.20  2680 0.0424
## 3 1    female     6.36  1.93   760 0.0701
## 4 1    male       5.64  1.98   760 0.0717
```

```
# plot
```

```
attraction_PSxTS_plot <- ggplot(attraction_PSxTS, aes(x = Sex, y = mean,
  fill = Sex)) + geom_bar(position = "dodge", stat = "identity") + geom_errorbar(aes(ymin = mean -
  se, ymax = mean + se), width = 0.2) + facet_wrap(~target.sex) + scale_fill_grey()

attraction_PSxTS_plot + labs(title = "Attraction Ratings by Participant Sex and Target Sex",
  y = "Attraction ± s.e.", x = "Participant Sex") + theme_bw()
```



The interaction between participant sex and target sex is not significant, $t(6684) = -1.01, p = .314$.

Three Way Interaction - Attraction by Condition (Masculinized/Feminized), Target Sex (Male/Female), and Participant Sex (Male/Female)

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.8 <- lmer(attraction ~ condition * target.sex * Sex + (1 | ID) +
  (1 | trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.8)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 28022.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8082 -0.6449  0.0754  0.6883  3.3268
##
```



```
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept) 0.92181  0.9601
##   trial    (Intercept) 0.06655  0.2580
##   Residual                3.19637  1.7878
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##               Estimate Std. Error      df t value
## (Intercept)      6.171127    0.136241  207.341015  45.296
## conditionfem     -0.229857    0.197630  209.903258  -1.163
## target.sexmale   -0.984507    0.105626   65.228868  -9.321
## Sex1              0.435123    0.287812  195.839240   1.512
## conditionfem:target.sexmale  0.672602    0.190251   42.930817   3.535
## conditionfem:Sex1 -0.192302    0.386224  195.839240  -0.498
## target.sexmale:Sex1  0.006382    0.156458 6666.000350   0.041
## conditionfem:target.sexmale:Sex1 -0.221750    0.209957 6666.000350  -1.056
##                                     Pr(>|t|)
## (Intercept)                < 0.0000000000000002 ***
## conditionfem                  0.24612
## target.sexmale                0.000000000000131 ***
## Sex1                          0.13219
## conditionfem:target.sexmale    0.00099 ***
## conditionfem:Sex1              0.61911
## target.sexmale:Sex1            0.96746
## conditionfem:target.sexmale:Sex1 0.29093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnf trgt.s Sex1  cndt:. cnd:S1 tr.:S1
## conditionfm -0.689
## target.sxml -0.388  0.427
## Sex1        -0.389  0.268  0.074
## cndtnfm:tr.  0.344 -0.481 -0.886 -0.041
## cndtnfm:Sx1  0.290 -0.425 -0.055 -0.745  0.065
## trgt.sxm:S1  0.106 -0.073 -0.272 -0.272  0.151  0.203
## cndtnf:.:S1 -0.079  0.115  0.203  0.203 -0.240 -0.272 -0.745
```

95% confidence interval

```
ci.8 <- confint(model.8, method = "Wald", level = 0.95)
ci.8
```

```
##               2.5 %      97.5 %
## .sig01          NA         NA
## .sig02          NA         NA
## .sigma          NA         NA
## (Intercept)     5.9040990  6.4381545
## conditionfem    -0.6172055  0.1574916
## target.sexmale  -1.1915309 -0.7774832
## Sex1            -0.1289778  0.9992242
## conditionfem:target.sexmale  0.2997168  1.0454878
## conditionfem:Sex1 -0.9492877  0.5646833
## target.sexmale:Sex1 -0.3002709  0.3130350
```

```
## conditionfem:target.sexmale:Sex1 -0.6332576 0.1897575
```

```
# group means
```

```
attraction_total <- data %>%  
  group_by(condition, target.sex, Sex) %>%  
  summarize(mean = mean(attraction), sd = sd(attraction), n = n(), se = sd(attraction)/sqrt(n()))
```

'summarise()' has grouped output by 'condition', 'target.sex'. You can override using the '.groups' argument.

```
attraction_total
```

```
## # A tibble: 8 x 7
```

```
## # Groups:   condition, target.sex [4]
```

```
##   condition target.sex Sex    mean    sd     n    se  
##   <fct>      <fct>    <fct> <dbl> <dbl> <int> <dbl>  
## 1 masc      female    2     6.17 1.88  1420 0.0499  
## 2 masc      female    1     6.61 1.74   320 0.0974  
## 3 masc      male      2     5.19 2.25  1420 0.0597  
## 4 masc      male      1     5.63 1.80   320 0.100  
## 5 fem       female    2     5.94 2.00  1260 0.0563  
## 6 fem       female    1     6.18 2.04   440 0.0974  
## 7 fem       male      2     5.63 2.11  1260 0.0595  
## 8 fem       male      1     5.66 2.10   440 0.100
```

```
# subset means for male and female participants
```

```
male_attraction <- attraction_total %>%  
  filter(Sex == "1")
```

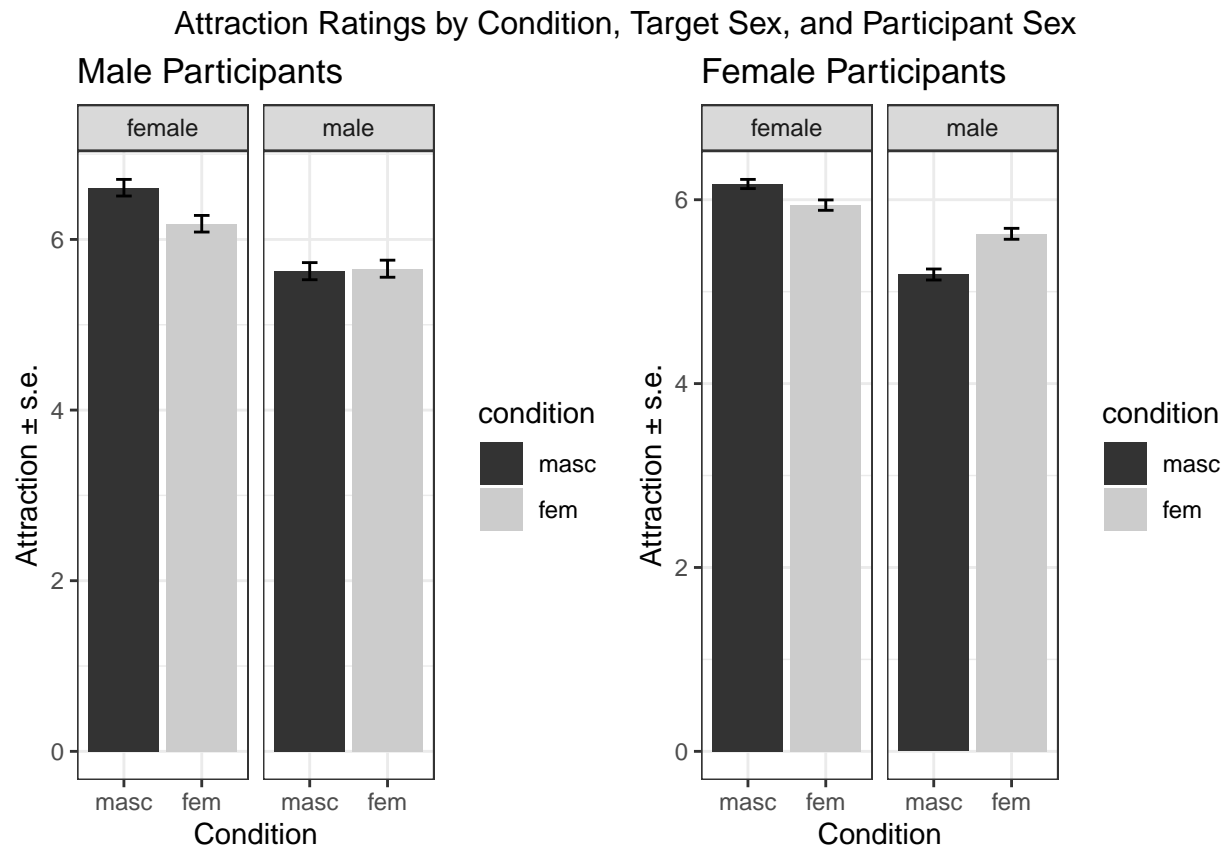
```
female_attraction <- attraction_total %>%  
  filter(Sex == "2")
```

```
# plot
```

```
male_attraction_plot <- ggplot(male_attraction, aes(x = condition, y = mean,  
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +  
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +  
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Male Participants",  
  y = "Attraction ± s.e.", x = "Condition") + theme_bw()
```

```
female_attraction_plot <- ggplot(female_attraction, aes(x = condition,  
  y = mean, fill = condition)) + geom_bar(position = "dodge", stat = "identity") +  
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +  
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",  
  y = "Attraction ± s.e.", x = "Condition") + theme_bw()
```

```
grid.arrange(male_attraction_plot, female_attraction_plot, nrow = 1, top = textGrob("Attraction Ratings"))
```



The three way interaction is not significant, $t(6666) = 1.06$, $p = .291$.

Masculinity/Femininity

Main Effect - Masc/Fem by Condition

```
# reference group - masc condition
data$condition <- relevel(data$condition, ref = "masc")

model.9 <- lmer(masc.fem ~ condition + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.9)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27485.6
##
## Scaled residuals:
## Min 1Q Median 3Q Max
```

```
## -3.5787 -0.6811 0.0517 0.6952 3.5486
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.7510 0.8666
## trial (Intercept) 0.1115 0.3339
## Residual 2.9592 1.7202
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.9060 0.1108 189.5063 53.317 <0.0000000000000002 ***
## conditionfem 0.0472 0.1385 169.9982 0.341 0.734
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## conditionfm -0.618
```

```
# 95% confidence interval
ci.9 <- confint(model.9, method = "Wald", level = 0.95)
ci.9
```

```
##          2.5 %    97.5 %
## .sig01      NA      NA
## .sig02      NA      NA
## .sigma      NA      NA
## (Intercept) 5.6889264 6.1231426
## conditionfem -0.2242928 0.3186945
```

```
# group means
mascfem_condition <- data %>%
  group_by(condition) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))
mascfem_condition
```

```
## # A tibble: 2 x 5
##   condition mean    sd    n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 masc      5.91  1.90  3480 0.0321
## 2 fem       5.95  2.01  3400 0.0344
```

There is no difference in masc/fem ratings after adaptation to feminized voices ($M = 5.95$, $SD = 2.01$) relative to masculinized voices ($M = 5.91$, $SD = 1.90$), $t(170) = 0.341$, $p = .734$.

Main Effect - Masc/Fem by Target Sex

```
# reference group - female targets
data$target.sex <- relevel(data$target.sex, ref = "female")

model.10 <- lmer(masc.fem ~ target.sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx"),
```

```

      calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.10)

```

```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ target.sex + (1 | ID) + (1 | trial)
##   Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27295.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5570 -0.6637  0.0623  0.7050  3.4349
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.7488   0.8653
##   trial    (Intercept) 0.1103   0.3321
##   Residual                2.8755   1.6957
## Number of obs: 6880, groups:  ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)    6.21523    0.08915 161.23036   69.72 <0.0000000000000002 ***
## target.sexmale -0.57173    0.04089 6668.23634  -13.98 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.229

```

```

# 95% confidence interval
ci.10 <- confint(model.10, method = "Wald", level = 0.95)
ci.10

```

```

##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    6.0405039  6.3899503
## target.sexmale -0.6518767 -0.4915898

```

```

# group means
mascfem_sex <- data %>%
  group_by(target.sex) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))
mascfem_sex

```

```

## # A tibble: 2 x 5

```

```
## target.sex mean sd n se
## <fct> <dbl> <dbl> <int> <dbl>
## 1 female 6.22 1.94 3440 0.0331
## 2 male 5.64 1.92 3440 0.0327
```

Female test voices ($M = 6.22$, $SD = 1.94$) are rated as significantly more feminine than male test voices are rated masculine ($M = 5.64$, $SD = 1.92$), $t(6668) = -13.98$, $p < .001$.

Main Effect - Masc/Fem by Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.11 <- lmer(masc.fem ~ Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.11)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27482.6
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.5821 -0.6818 0.0535 0.6962 3.5359
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.7380 0.8591
## trial (Intercept) 0.1115 0.3339
## Residual 2.9592 1.7202
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.86772 0.09406 162.55095 62.382 <0.0000000000000002 ***
## Sex1 0.27899 0.16561 170.00045 1.685 0.0939 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## Sex1 -0.389

# 95% confidence interval
ci.11 <- confint(model.11, method = "Wald", level = 0.95)
ci.11

## 2.5 % 97.5 %
```

```
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.68336825 6.0520795
## Sex1           -0.04560392 0.6035772
```

```
# group means
mascfem_Sex <- data %>%
  group_by(Sex) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))
mascfem_Sex
```

```
## # A tibble: 2 x 5
##   Sex    mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.87  1.98  5360 0.0270
## 2 1      6.15  1.83  1520 0.0471
```

There is no significant difference in masc/fem ratings between male participants ($M = 6.15$, $SD = 1.83$) and female participants ($M = 5.87$, $SD = 1.98$), $t(170) = 1.69$, $p = .094$.

Interaction - Masc/Fem by Condition and Target Sex

```
# relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.12 <- lmer(masc.fem ~ condition * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.12)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27272.5
##
## Scaled residuals:
##    Min      1Q  Median      3Q     Max
## -3.5363 -0.6610  0.0587  0.7018  3.4355
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.75307 0.8678
## trial   (Intercept) 0.04884 0.2210
## Residual 2.87552 1.6957
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
```

```
## (Intercept)          6.43966    0.11292 200.29820  57.029
## conditionfem         -0.44907    0.16045 201.02624  -2.799
## target.sexmale       -1.06724    0.09049  59.27099 -11.794
## conditionfem:target.sexmale  0.99254    0.16194  38.00093   6.129
##                               Pr(>|t|)
## (Intercept)          < 0.0000000000000002 ***
## conditionfem          0.00563 **
## target.sexmale        < 0.0000000000000002 ***
## conditionfem:target.sexmale  0.000000379 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxml -0.401  0.450
## cndtnfm:tr.  0.357 -0.505 -0.892
```

```
# 95% confidence interval
```

```
ci.12 <- confint(model.12, method = "Wald", level = 0.95)
ci.12
```

```
##                               2.5 %    97.5 %
## .sig01                       NA        NA
## .sig02                       NA        NA
## .sigma                       NA        NA
## (Intercept)                  6.2183390  6.6609713
## conditionfem                 -0.7635402 -0.1345936
## target.sexmale              -1.2446059 -0.8898769
## conditionfem:target.sexmale  0.6751432  1.3099278
```

```
# group means
```

```
mascfem_CxTS <- data %>%
  group_by(condition, target.sex) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))
```

'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
mascfem_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 masc      female    6.44  1.78  1740 0.0427
## 2 masc      male      5.37  1.86  1740 0.0445
## 3 fem       female    5.99  2.07  1700 0.0502
## 4 fem       male      5.92  1.94  1700 0.0471
```

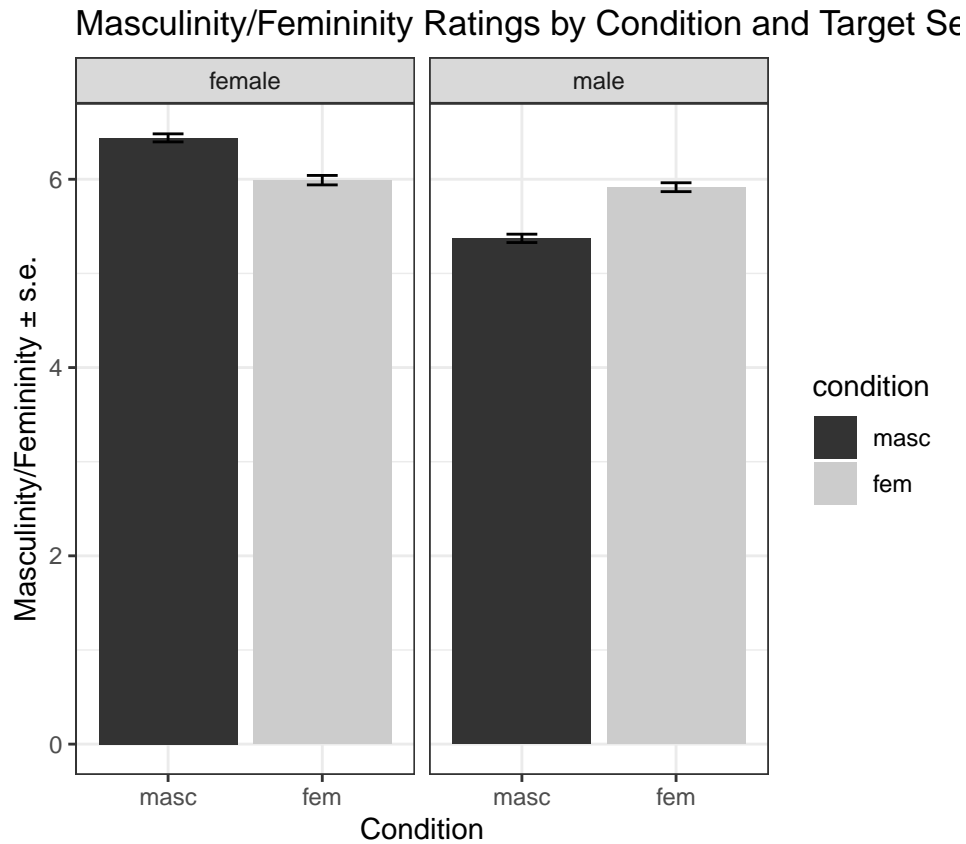
```
# plot
```

```
mascfem_CxTS_plot <- ggplot(mascfem_CxTS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
```



```
geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
facet_wrap(~target.sex) + scale_fill_grey()

mascfem_CxTS_plot + labs(title = "Masculinity/Femininity Ratings by Condition and Target Sex",
y = "Masculinity/Femininity  $\pm$  s.e.", x = "Condition") + theme_bw()
```



The interaction between target sex and condition is significant, $t(38)=6.13$, $p<.001$. Male test voices are rated as significantly more masculine after adaptation to feminized voices, while female test voices are rated as significantly more feminine after adaptation to masculinized voices. Furthermore, the simple effect of condition centered at female voices is significant, $t(201)=-2.80$, $p<.01$.

Simple Effect - Masc/Fem by Condition when Target Sex is centered at Male

```
# simple effects: relevel so reference group = male
data$target.sex <- relevel(data$target.sex, ref = "male")

model.13 <- lmer(masc.fem ~ condition * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.13)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
```

```
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27272.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5363 -0.6610  0.0587  0.7018  3.4355
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept) 0.75307  0.8678
##   trial    (Intercept) 0.04884  0.2210
##   Residual                    2.87552  1.6957
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      5.37241    0.11292 200.29820  47.578
## conditionfem      0.54347    0.16045 201.02624   3.387
## target.sexfemale  1.06724    0.09049  59.27099  11.794
## conditionfem:target.sexfemale -0.99254    0.16194  38.00093  -6.129
##
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## conditionfem      0.000849 ***
## target.sexfemale  < 0.0000000000000002 ***
## conditionfem:target.sexfemale  0.000000379 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxfml -0.401  0.450
## cndtnfm:tr.  0.357 -0.505 -0.892
```

The effect of condition and target sex centered at male targets is also significant, $t(201)=3.39$, $p<.001$.

Interaction - Masc/Fem by Condition and Participant Sex

```
# relevel so reference group = female
data$Sex <- relevel(data$Sex, ref = "2")

model.14 <- lmer(masc.fem ~ condition * Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.14)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
```

```
## REML criterion at convergence: 27483.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5768 -0.6802  0.0527  0.6938  3.5423
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.7423   0.8616
##   trial    (Intercept) 0.1115   0.3339
##   Residual                2.9592   1.7202
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      5.8197      0.1195 193.8827  48.692 <0.0000000000000002 ***
## conditionfem      0.1021      0.1564 167.9712   0.653      0.5147
## Sex1              0.4693      0.2500 167.9712   1.877      0.0622 .
## conditionfem:Sex1 -0.3480      0.3355 167.9712  -1.037      0.3012
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf Sex1
## conditionfm -0.615
## Sex1        -0.385  0.294
## cndtnfm:Sex1 0.287 -0.466 -0.745
```

```
# 95% confidence interval
```

```
ci.14 <- confint(model.14, method = "Wald", level = 0.95)
ci.14
```

```
##              2.5 %    97.5 %
## .sig01          NA        NA
## .sig02          NA        NA
## .sigma          NA        NA
## (Intercept)    5.5854595 6.0539771
## conditionfem  -0.2043936 0.4086078
## Sex1          -0.0207155 0.9594039
## conditionfem:Sex1 -1.0056148 0.3096393
```

```
# group means
```

```
mascfem_CxPS <- data %>%
  group_by(condition, Sex) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))
```

```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

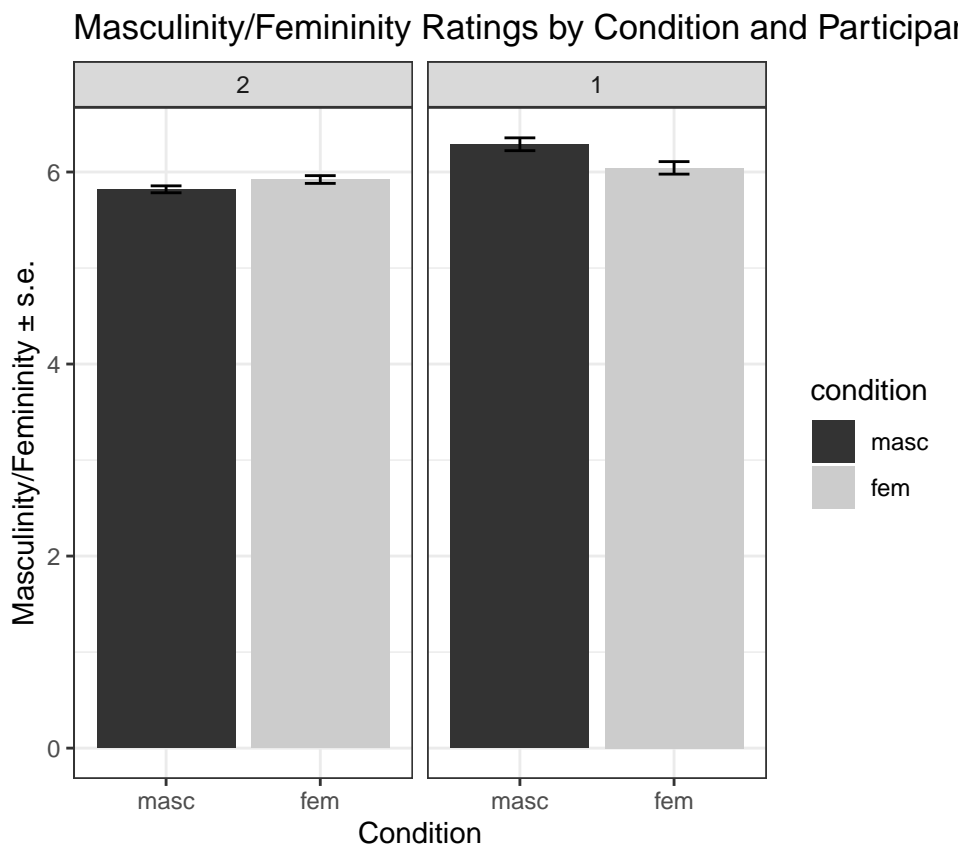
```
mascfem_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
```

```
##   condition Sex    mean    sd     n     se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      2      5.82  1.93  2840 0.0362
## 2 masc      1      6.29  1.68   640 0.0666
## 3 fem       2      5.92  2.03  2520 0.0405
## 4 fem       1      6.04  1.93   880 0.0651
```

```
# plot
mascfem_CxPS_plot <- ggplot(mascfem_CxPS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~Sex) + scale_fill_grey()

mascfem_CxPS_plot + labs(title = "Masculinity/Femininity Ratings by Condition and Participant Sex",
  y = "Masculinity/Femininity ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(168) = -1.04$, $p = .301$.

Interaction - Masc/Fem by Participant Sex and Target Sex

```
# relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.15 <- lmer(masc.fem ~ Sex * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.15)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27292.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6175 -0.6699  0.0607  0.6994  3.3752
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.7401  0.8603
## trial   (Intercept) 0.1124  0.3353
## Residual                2.8735  1.6951
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      6.12905    0.09700  183.01414  63.189
## Sex1              0.38984    0.17283  201.60540   2.256
## target.sexmale    -0.52265    0.04636 6671.66368 -11.273
## Sex1:target.sexmale -0.22171    0.09887 6679.86513  -2.242
##
##              Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## Sex1           0.0252 *
## target.sexmale <0.0000000000000002 ***
## Sex1:target.sexmale 0.0250 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.394
## target.sxml -0.239  0.135
## Sx1:trgt.sx  0.113 -0.286 -0.472
```

95% confidence interval

```
ci.15 <- confint(model.15, method = "Wald", level = 0.95)
ci.15
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.93894375  6.31915788
## Sex1           0.05109727  0.72858494
## target.sexmale -0.61352592 -0.43178182
## Sex1:target.sexmale -0.41549432 -0.02792353
```

```

# group means
mascfem_PSxTS <- data %>%
  group_by(Sex, target.sex) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))

## 'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.

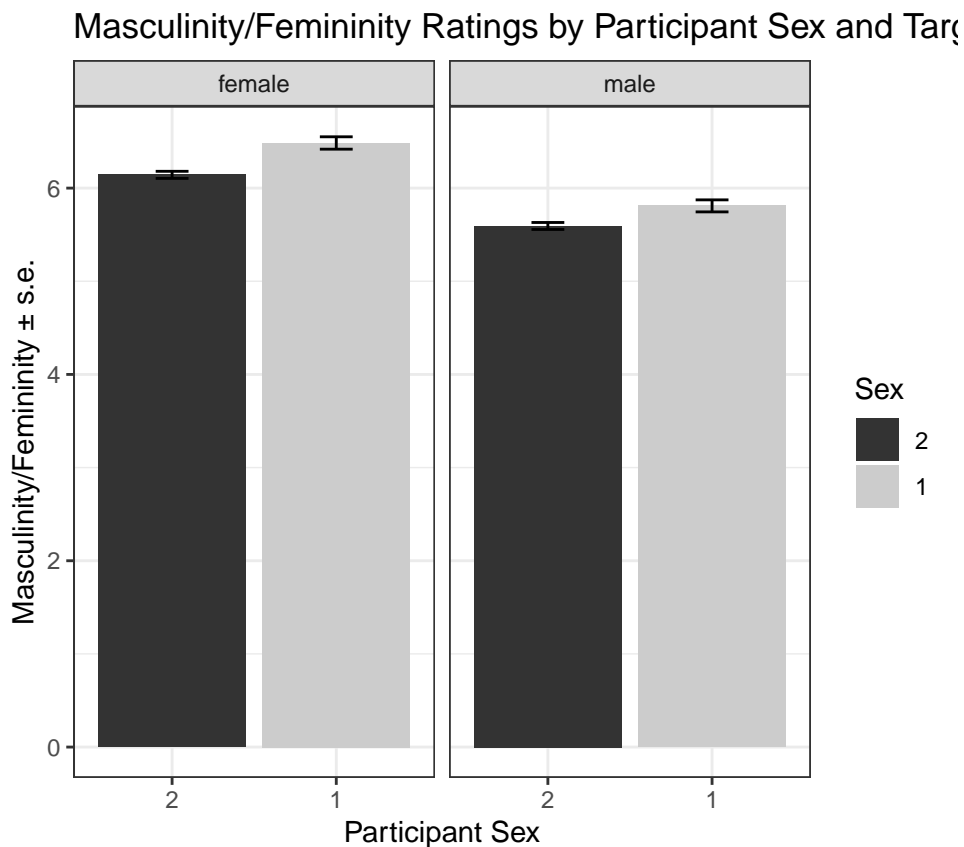
mascfem_PSxTS

## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd    n    se
##   <fct> <fct>    <dbl> <dbl> <int> <dbl>
## 1 2     female    6.14  1.97  2680 0.0380
## 2 2     male     5.59  1.95  2680 0.0377
## 3 1     female    6.48  1.83   760 0.0663
## 4 1     male     5.81  1.78   760 0.0645

# plot
mascfem_PSxTS_plot <- ggplot(mascfem_PSxTS, aes(x = Sex, y = mean, fill = Sex)) +
  geom_bar(position = "dodge", stat = "identity") + geom_errorbar(aes(ymin = mean -
    se, ymax = mean + se), width = 0.2) + facet_wrap(~target.sex) + scale_fill_grey()

mascfem_PSxTS_plot + labs(title = "Masculinity/Femininity Ratings by Participant Sex and Target Sex",
  y = "Masculinity/Femininity ± s.e.", x = "Participant Sex") + theme_bw()

```



The interaction between participant sex and target sex is significant, $t(6680) = -2.24$, $p < .05$. The simple effect of participant sex when target sex is centered at female is also significant, $t(202) = 2.26$, $p < .05$.

Simple Effect - Masc/Fem by Participant Sex when Target Sex is Centered at Male

```
# relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "male")

model.16 <- lmer(masc.fem ~ Sex * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.16)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27292.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6175 -0.6699  0.0607  0.6994  3.3752
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.7401  0.8603
## trial   (Intercept) 0.1124  0.3353
## Residual                2.8735  1.6951
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value
## (Intercept)    5.60640    0.09700 183.01414  57.801
## Sex1            0.16813    0.17283 201.60540   0.973
## target.sexfemale 0.52265    0.04636 6671.66368 11.273
## Sex1:target.sexfemale 0.22171    0.09887 6679.86513   2.242
##
##              Pr(>|t|)
## (Intercept) <0.0000000000000002 ***
## Sex1        0.332
## target.sexfemale <0.0000000000000002 ***
## Sex1:target.sexfemale 0.025 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1        -0.394
## target.sxfml -0.239  0.135
## Sx1:trgt.sx  0.113 -0.286 -0.472
```

```
# 95% confidence interval
ci.16 <- confint(model.16, method = "Wald", level = 0.95)
ci.16
```

```
##                2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)     5.41628988 5.7965040
## Sex1            -0.17061165 0.5068760
## target.sexfemale 0.43178182 0.6135259
## Sex1:target.sexfemale 0.02792353 0.4154943
```

The simple effect of participant sex when target sex is centered at male is not significant, $t(202) = 0.97$, $p = .332$.

Three Way Interaction - Masc/Fem by Condition, Target Sex, and Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.17 <- lmer(masc.fem ~ condition * target.sex * Sex + (1 | ID) + (1 |
  trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nloptn"))
summary(model.17)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nloptn"))
##
## REML criterion at convergence: 27264.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6346 -0.6652  0.0601  0.7004  3.3396
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  ID       (Intercept) 0.74443  0.8628
##  trial    (Intercept) 0.04886  0.2210
##  Residual                    2.87206  1.6947
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##                Estimate Std. Error    df t value
## (Intercept)      5.286620   0.122272 208.999227  43.236
## conditionfem      0.652269   0.177452 211.415820   3.676
## target.sexfemale  1.066197   0.094504  70.470148  11.282
## Sex1              0.466505   0.260787 198.815143   1.789
## conditionfem:target.sexfemale -1.100324   0.167773  43.779844  -6.558
```



```
## conditionfem:Sex1 -0.555394 0.349958 198.815143 -1.587
## target.sexfemale:Sex1 0.005678 0.148309 6666.001819 0.038
## conditionfem:target.sexfemale:Sex1 0.414813 0.199021 6666.001819 2.084
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem 0.000301 ***
## target.sexfemale < 0.0000000000000002 ***
## Sex1 0.075163 .
## conditionfem:target.sexfemale 0.0000000052 ***
## conditionfem:Sex1 0.114095
## target.sexfemale:Sex1 0.969463
## conditionfem:target.sexfemale:Sex1 0.037174 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnf trgt.s Sex1 cndt:. cnd:S1 tr.:S1
## conditionfm -0.689
## target.sxfml -0.386 0.412
## Sex1 -0.392 0.270 0.082
## cndtnfm:tr. 0.337 -0.473 -0.871 -0.046
## cndtnfm:Sx1 0.292 -0.428 -0.061 -0.745 0.073
## trgt.sxf:S1 0.112 -0.077 -0.289 -0.284 0.163 0.212
## cndtnf:..S1 -0.083 0.122 0.215 0.212 -0.258 -0.284 -0.745
```

```
# 95% confidence interval
```

```
ci.17 <- confint(model.17, method = "Wald", level = 0.95)
ci.17
```

```
## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.04697058 5.5262689
## conditionfem 0.30446945 1.0000689
## target.sexfemale 0.88097186 1.2514225
## Sex1 -0.04462716 0.9776377
## conditionfem:target.sexfemale -1.42915288 -0.7714955
## conditionfem:Sex1 -1.24129942 0.1305111
## target.sexfemale:Sex1 -0.28500235 0.2963580
## conditionfem:target.sexfemale:Sex1 0.02473964 0.8048860
```

```
# group means
```

```
mascfem_total <- data %>%
  group_by(condition, target.sex, Sex) %>%
  summarize(mean = mean(masc.fem), sd = sd(masc.fem), n = n(), se = sd(masc.fem)/sqrt(n()))
```

```
## 'summarise()' has grouped output by 'condition', 'target.sex'. You can override using the '.groups' argument
```

```
mascfem_total
```

```
## # A tibble: 8 x 7
```

```
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex    mean    sd     n     se
##   <fct>      <fct>    <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      male      2     5.29 1.91  1420 0.0508
## 2 masc      male      1     5.75 1.52   320 0.0852
## 3 masc      female    2     6.35 1.80  1420 0.0477
## 4 masc      female    1     6.82 1.67   320 0.0932
## 5 fem       male      2     5.94 1.94  1260 0.0547
## 6 fem       male      1     5.85 1.94   440 0.0927
## 7 fem       female    2     5.90 2.12  1260 0.0597
## 8 fem       female    1     6.24 1.90   440 0.0907
```

```
# subset means for male and female participants
```

```
male_mascfem <- mascfem_total %>%
```

```
  filter(Sex == "1")
```

```
female_mascfem <- mascfem_total %>%
```

```
  filter(Sex == "2")
```

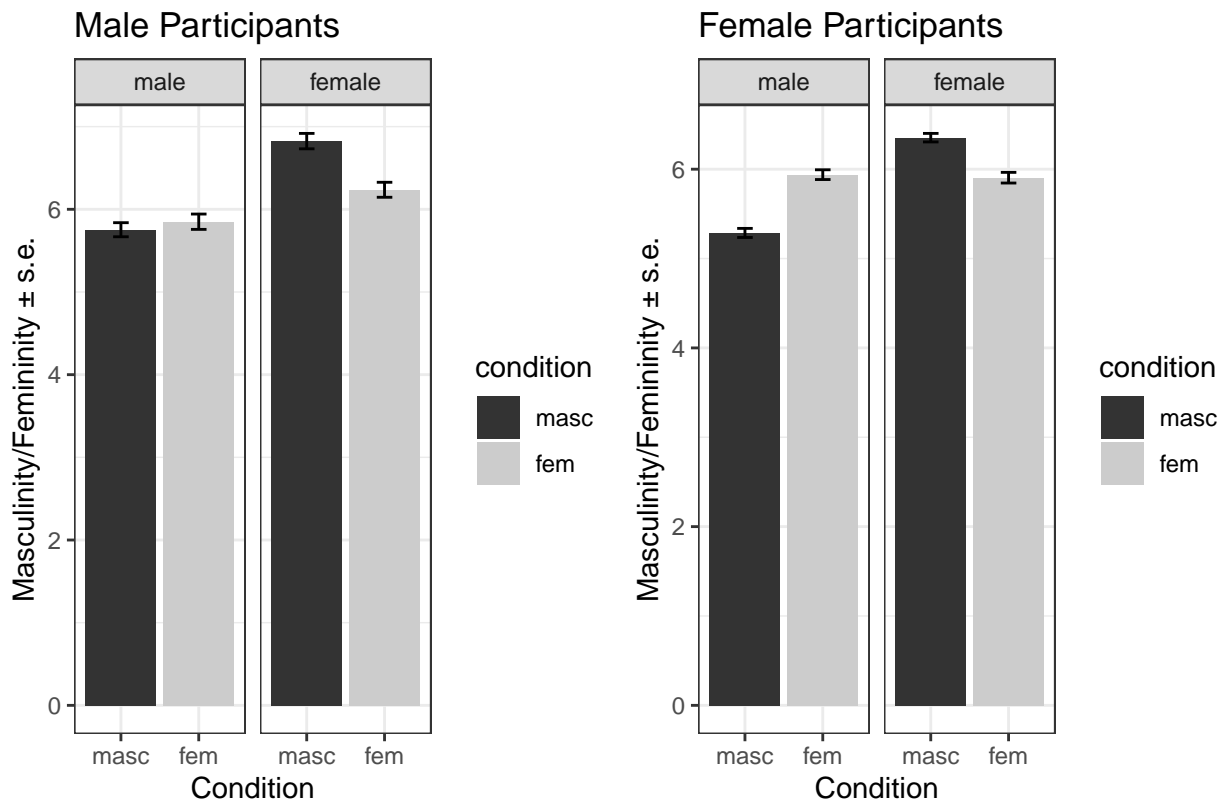
```
# plot
```

```
male_mascfem_plot <- ggplot(male_mascfem, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Male Participants",
  y = "Masculinity/Femininity ± s.e.", x = "Condition") + theme_bw()
```

```
female_mascfem_plot <- ggplot(female_mascfem, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",
  y = "Masculinity/Femininity ± s.e.", x = "Condition") + theme_bw()
```

```
grid.arrange(male_mascfem_plot, female_mascfem_plot, nrow = 1, top = textGrob("Masculinity/Femininity R
```

Masculinity/Femininity Ratings by Condition, Target Sex, and Participant Sex



The three way interaction is significant, $t(6666) = 2.08, p < .05$. The simple effect of target sex and condition on masc/fem ratings centered at female participants is also significant $t(44) = -6.56, p < .001$.

Simple Effect - Masc/Fem by Condition and Target Sex when Participant Sex is centered at Male

```
# reference group - male participants
data$Sex <- relevel(data$Sex, ref = "1")

model.18 <- lmer(masc.fem ~ condition * target.sex * Sex + (1 | ID) + (1 | trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.18)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27264.9
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.6346 -0.6652 0.0601 0.7004 3.3396
```

```
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## ID          (Intercept) 0.74443  0.8628
## trial       (Intercept) 0.04886  0.2210
## Residual                2.87206  1.6947
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)    5.753125   0.240718 212.832246  23.900
## conditionfem    0.096875   0.317417 214.368067   0.305
## target.sexfemale 1.071875   0.151117 445.417812   7.093
## Sex2           -0.466505   0.260787 198.815138  -1.789
## conditionfem:target.sexfemale -0.685511   0.224831 140.507677  -3.049
## conditionfem:Sex2  0.555394   0.349958 198.815140   1.587
## target.sexfemale:Sex2 -0.005678   0.148309 6666.001853  -0.038
## conditionfem:target.sexfemale:Sex2 -0.414813   0.199021 6666.001829  -2.084
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## conditionfem              0.76051
## target.sexfemale    0.000000000000519 ***
## Sex2                0.07516 .
## conditionfem:target.sexfemale    0.00274 **
## conditionfem:Sex2    0.11409
## target.sexfemale:Sex2    0.96946
## conditionfem:target.sexfemale:Sex2 0.03717 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf trgt.s Sex2   cndt:. cnd:S2 tr.:S2
## conditionfm -0.758
## trgt.sxfml -0.314  0.289
## Sex2        -0.884  0.670  0.228
## cndtnfm:tr.  0.256 -0.354 -0.816 -0.153
## cndtnfm:Sx2  0.659 -0.863 -0.170 -0.745  0.197
## trgt.sxf:S2  0.251 -0.191 -0.801 -0.284  0.538  0.212
## cndtnf:..S2 -0.187  0.245  0.597  0.212 -0.693 -0.284 -0.745
```

95% confidence interval

```
ci.18 <- confint(model.18, method = "Wald", level = 0.95)
ci.18
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.2813265  6.22492346
## conditionfem   -0.5252501  0.71900007
## target.sexfemale  0.7756913  1.36805868
## Sex2           -0.9776377  0.04462716
## conditionfem:target.sexfemale -1.1261719 -0.24485084
## conditionfem:Sex2 -0.1305111  1.24129942
```

```
## target.sexfemale:Sex2          -0.2963580  0.28500235
## conditionfem:target.sexfemale:Sex2 -0.8048860 -0.02473964
```

The simple effect of target sex and condition on masc/fem ratings centered at male participants is significant $t(141) = -3.05$, $p < .01$.

Likability

Main Effect - Likability by Condition

```
# reference group - masc condition
data$condition <- relevel(data$condition, ref = "masc")

model.19 <- lmer(likability ~ condition + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.19)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26432.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8867 -0.5840  0.0777  0.6614  3.6829
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.80052  0.8947
## trial   (Intercept) 0.07056  0.2656
## Residual                2.53009  1.5906
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.92385    0.10813 196.31700   54.78 <0.0000000000000002 ***
## conditionfem  0.07791    0.14174 170.00018    0.55      0.583
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## conditionfm -0.648

# 95% confidence interval
ci.19 <- confint(model.19, method = "Wald", level = 0.95)
ci.19
```

```
##                2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)    5.7119165 6.1357846
## conditionfem -0.1998933 0.3557216
```

```
# group means
likability_condition <- data %>%
  group_by(condition) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))
likability_condition
```

```
## # A tibble: 2 x 5
##   condition mean    sd     n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 masc      5.92  1.81  3480 0.0307
## 2 fem       6.00  1.87  3400 0.0321
```

There is no significant difference in likability ratings of test voices after adaptation to masculinized voices ($M = 5.92$, $SD = 1.81$) relative to feminized voices ($M = 6.00$, $SD = 1.87$), $t(170) = 0.55$, $p = .583$.

Main Effect - Likability by Target Sex

```
# reference group - female targets
data$target.sex <- relevel(data$target.sex, ref = "female")

model.20 <- lmer(likability ~ target.sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.20)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26270.5
##
## Scaled residuals:
##    Min      1Q  Median      3Q     Max
## -4.0914 -0.5943  0.0801  0.6409  3.5760
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  0.7984     0.8935
##   trial    (Intercept)  0.0702     0.2650
##   Residual                    2.4687     1.5712
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
```

```
##               Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      6.20726    0.08435  194.09737    73.59 <0.0000000000000002 ***
## target.sexmale   -0.48981    0.03789  6668.29341   -12.93 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr)
## target.sxml -0.225
```

```
# 95% confidence interval
ci.20 <- confint(model.20, method = "Wald", level = 0.95)
ci.20
```

```
##               2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)     6.0419409  6.3725807
## target.sexmale -0.5640704 -0.4155542
```

```
# group means
likability_sex <- data %>%
  group_by(target.sex) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))
likability_sex
```

```
## # A tibble: 2 x 5
##   target.sex mean    sd     n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female    6.21  1.80  3440 0.0306
## 2 male      5.72  1.85  3440 0.0316
```

Female test voices ($M = 6.21$, $SD = 1.80$) are rated as significantly more likable than male test voices ($M = 5.72$, $SD = 1.85$), $t(6668) = -12.93$, $p < .001$.

Main Effect - Likability by Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.21 <- lmer(likability ~ Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.21)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
```

```
##
## REML criterion at convergence: 26428.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8960 -0.5832  0.0765  0.6626  3.6694
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.78177  0.8842
##   trial    (Intercept) 0.07056  0.2656
##   Residual                2.53009  1.5906
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.88694    0.08983 185.82982   65.53 <0.0000000000000002 ***
## Sex1          0.34135    0.16895 170.00000    2.02      0.0449 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.415
```

```
# 95% confidence interval
ci.21 <- confint(model.21, method = "Wald", level = 0.95)
ci.21
```

```
##              2.5 %    97.5 %
## .sig01          NA         NA
## .sig02          NA         NA
## .sigma          NA         NA
## (Intercept) 5.71086964 6.0630110
## Sex1        0.01021658 0.6724818
```

```
# group means
likability_Sex <- data %>%
  group_by(Sex) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))
likability_Sex
```

```
## # A tibble: 2 x 5
##   Sex   mean    sd     n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.89  1.86  5360 0.0254
## 2 1      6.23  1.74  1520 0.0447
```

Male participants ($M = 6.23$, $SD = 1.74$) rated test voices as more likable than female participants ($M = 5.89$, $SD = 1.86$), $t(170) = 2.02$, $p < .05$.

Interaction - Likability by Condition and Target Sex


```
# simple effects: relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.22 <- lmer(likability ~ condition * target.sex + (1 | ID) + (1 |
  trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.22)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26266.4
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.0789 -0.5886 0.0780 0.6435 3.5835
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.80205 0.8956
## trial (Intercept) 0.05698 0.2387
## Residual 2.46871 1.5712
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 6.28966 0.11613 198.87955 54.159
## conditionfem -0.16436 0.16500 199.59277 -0.996
## target.sexmale -0.73161 0.09239 54.39764 -7.919
## conditionfem:target.sexmale 0.48455 0.16892 38.00213 2.869
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem 0.3204
## target.sexmale 0.000000000127 ***
## conditionfem:target.sexmale 0.0067 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxml -0.398 0.467
## cndtnfm:tr. 0.363 -0.512 -0.912
```

```
# 95% confidence interval
ci.22 <- confint(model.22, method = "Wald", level = 0.95)
ci.22
```

```
## 2.5 % 97.5 %
```

```
## .sig01                NA        NA
## .sig02                NA        NA
## .sigma                NA        NA
## (Intercept)           6.0620401  6.5172702
## conditionfem          -0.4877474  0.1590253
## target.sexmale        -0.9126848 -0.5505336
## conditionfem:target.sexmale 0.1534780 0.8156227
```

```
# group means
likability_CxTS <- data %>%
  group_by(condition, target.sex) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))
```

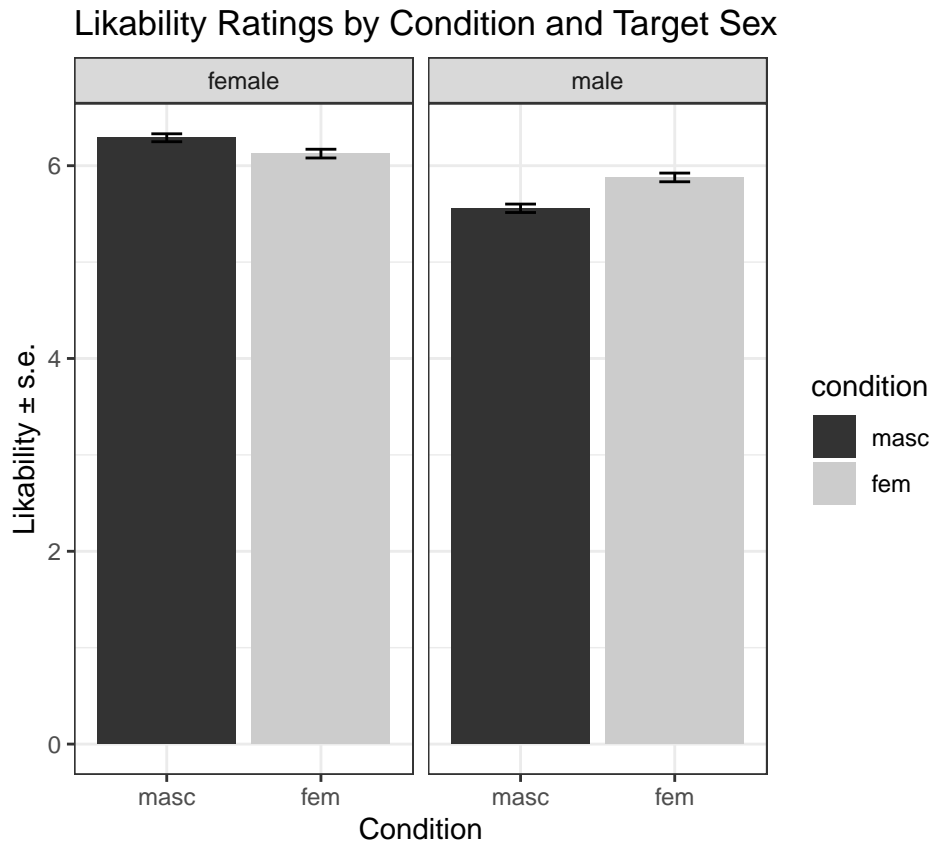
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
likability_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 masc      female      6.29  1.71  1740 0.0410
## 2 masc      male       5.56  1.83  1740 0.0439
## 3 fem       female      6.13  1.87  1700 0.0454
## 4 fem       male       5.88  1.86  1700 0.0452
```

```
# plot
likability_CxTS_plot <- ggplot(likability_CxTS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey()

likability_CxTS_plot + labs(title = "Likability Ratings by Condition and Target Sex",
  y = "Likability ± s.e.", x = "Condition") + theme_bw()
```



The interaction between target sex and condition is significant, $t(38)=2.87$, $p<.01$. Male test voices are rated as significantly more likable after adaptation to feminized voices, while female test voices are rated as significantly more likable after adaptation to masculinized voices. The simple effect of condition when target sex is centered at female is not significant, $t(200) = -1.00$, $p=.320$.

Simple Effect - Likability by Condition when Target Sex is centered at Male

```
# simple effects: relevel so reference group = male
data$target.sex <- relevel(data$target.sex, ref = "male")

model.23 <- lmer(likability ~ condition * target.sex + (1 | ID) + (1 |
  trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.23)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 26266.4
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.0789 -0.5886 0.0780 0.6435 3.5835
```

```
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept) 0.80205  0.8956
##   trial    (Intercept) 0.05698  0.2387
##   Residual                2.46871  1.5712
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##               Estimate Std. Error      df t value
## (Intercept)      5.55805    0.11613 198.87955  47.860
## conditionfem      0.32019    0.16500 199.59278   1.941
## target.sexfemale  0.73161    0.09239  54.39764   7.919
## conditionfem:target.sexfemale -0.48455    0.16892  38.00213  -2.869
##               Pr(>|t|)
## (Intercept)      < 0.0000000000000002 ***
## conditionfem              0.0537 .
## target.sexfemale      0.000000000127 ***
## conditionfem:target.sexfemale      0.0067 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxfml -0.398  0.467
## cndtnfm:tr.  0.363 -0.512 -0.912
```

The effect of condition when target sex is centered at male is not significant, $t(200)=1.94$, $p=.054$.

Interaction - Likability by Condition and Participant Sex

```
# relevel so reference group = female
data$Sex <- relevel(data$Sex, ref = "2")

model.24 <- lmer(likability ~ condition * Sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.24)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * Sex + (1 | ID) + (1 | trial)
##   Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26429.9
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -3.8923 -0.5834  0.0747  0.6599  3.6742
##
## Random effects:
```

```
## Groups      Name      Variance Std.Dev.
## ID          (Intercept) 0.78645  0.8868
## trial       (Intercept) 0.07056  0.2656
## Residual                2.53009  1.5906
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      5.8285      0.1172 194.5764  49.739 <0.0000000000000002 ***
## conditionfem      0.1243      0.1595 168.0001   0.779      0.4372
## Sex1              0.5184      0.2551 168.0001   2.032      0.0437 *
## conditionfem:Sex1 -0.3291      0.3423 168.0001  -0.961      0.3378
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf Sex1
## conditionfm -0.640
## Sex1        -0.400  0.294
## cndtnfm:Sex1 0.298 -0.466 -0.745
```

```
# 95% confidence interval
```

```
ci.24 <- confint(model.24, method = "Wald", level = 0.95)
ci.24
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.5988492 6.0581930
## conditionfem     -0.1884475 0.4369608
## Sex1             0.0183755 1.0183322
## conditionfem:Sex1 -1.0000234 0.3418510
```

```
# group means
```

```
likability_CxPS <- data %>%
  group_by(condition, Sex) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))
```

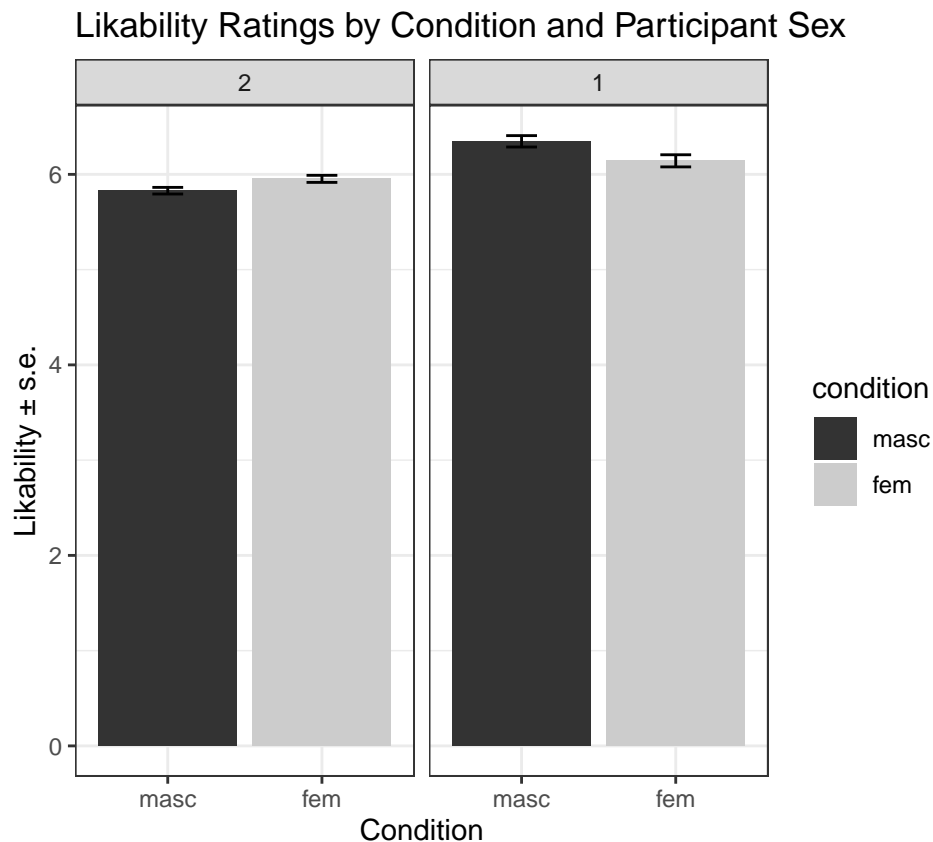
```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

```
likability_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      2      5.83  1.86  2840 0.0349
## 2 masc      1      6.35  1.51   640 0.0598
## 3 fem       2      5.95  1.86  2520 0.0371
## 4 fem       1      6.14  1.89   880 0.0637
```

```
# plot
likability_CxPS_plot <- ggplot(likability_CxPS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~Sex) + scale_fill_grey()

likability_CxPS_plot + labs(title = "Likability Ratings by Condition and Participant Sex",
  y = "Likability ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(168) = -0.96, p = .338$.

Interaction - Likability by Participant Sex and Target Sex

```
# relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.25 <- lmer(likability ~ Sex * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.25)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
```

```
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26270.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1183 -0.5921  0.0805  0.6436  3.5457
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept) 0.78330  0.8850
##   trial    (Intercept) 0.07051  0.2655
##   Residual                    2.46883  1.5713
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      6.12453    0.09236 208.25778  66.311
## Sex1              0.37442    0.17505 195.89549   2.139
## target.sexmale   -0.47517    0.04297 6673.06743 -11.057
## Sex1:target.sexmale -0.06615    0.09163 6683.33057  -0.722
##
##              Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## Sex1              0.0337 *
## target.sexmale   <0.0000000000000002 ***
## Sex1:target.sexmale 0.4704
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.419
## target.sxml -0.233  0.123
## Sx1:trgt.sx  0.110 -0.262 -0.472

# 95% confidence interval
ci.25 <- confint(model.25, method = "Wald", level = 0.95)
ci.25

##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.94350241  6.3055512
## Sex1           0.03132984  0.7175141
## target.sexmale -0.55939891 -0.3909472
## Sex1:target.sexmale -0.24573867  0.1134474

# group means
likability_PSxTS <- data %>%
  group_by(Sex, target.sex) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))

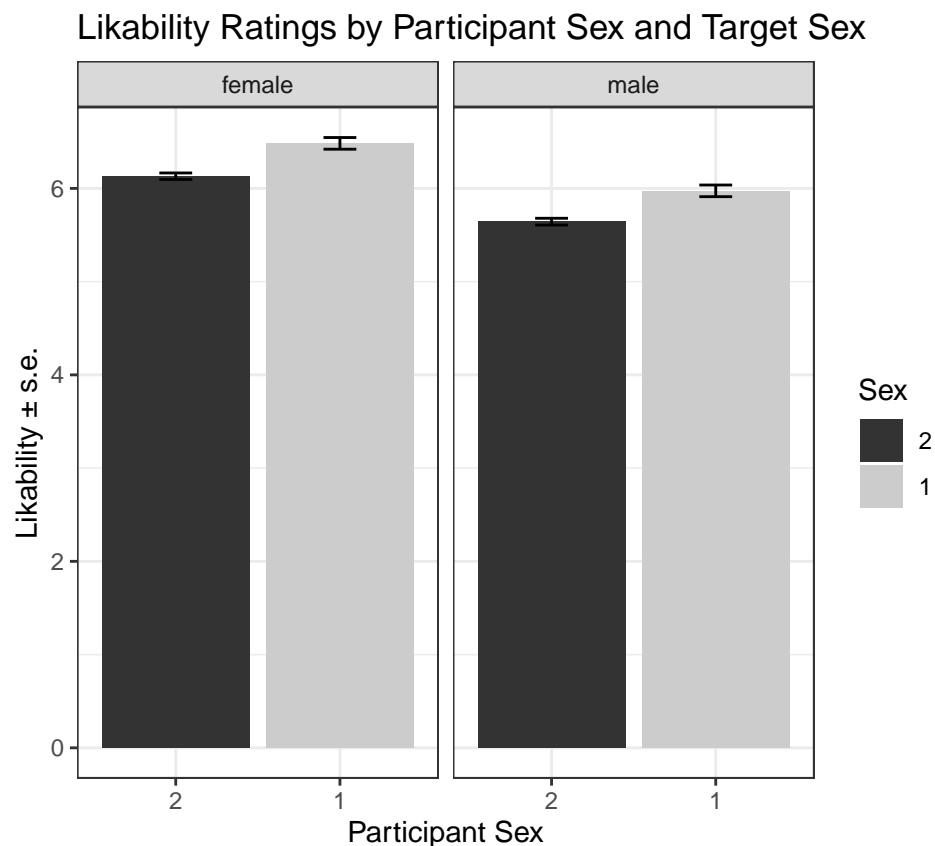
## 'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.
```

```
likability_PSxTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd    n    se
##   <fct> <fct>     <dbl> <dbl> <int> <dbl>
## 1 2     female     6.13  1.81  2680 0.0349
## 2 2     male      5.64  1.88  2680 0.0364
## 3 1     female     6.48  1.73   760 0.0626
## 4 1     male      5.97  1.73   760 0.0626
```

```
# plot
likability_PSxTS_plot <- ggplot(likability_PSxTS, aes(x = Sex, y = mean,
  fill = Sex)) + geom_bar(position = "dodge", stat = "identity") + geom_errorbar(aes(ymin = mean -
  se, ymax = mean + se), width = 0.2) + facet_wrap(~target.sex) + scale_fill_grey()

likability_PSxTS_plot + labs(title = "Likability Ratings by Participant Sex and Target Sex",
  y = "Likability ± s.e.", x = "Participant Sex") + theme_bw()
```



The interaction between participant sex and target sex is not significant, $t(6683) = -0.72, p = .470$.

Three Way Interaction - Likability by Condition, Target Sex, and Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")
```



```

model.26 <- lmer(likability ~ condition * target.sex * Sex + (1 | ID) +
  (1 | trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.26)

```

```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26263.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1419 -0.5884  0.0790  0.6470  3.5191
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.78801 0.8877
## trial   (Intercept) 0.05698 0.2387
## Residual                2.46771 1.5709
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      6.20634    0.12524 207.23313 49.555
## conditionfem     -0.16110    0.18166 209.60833 -0.887
## target.sexmale   -0.75563    0.09578  62.82673 -7.889
## Sex1              0.45304    0.26419 193.25528  1.715
## conditionfem:target.sexmale  0.57071    0.17374  42.53192  3.285
## conditionfem:Sex1 -0.14373    0.35453 193.25528 -0.405
## target.sexmale:Sex1  0.13063    0.13747 6666.00001  0.950
## conditionfem:target.sexmale:Sex1 -0.37071    0.18448 6666.00001 -2.010
##
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem      0.37620
## target.sexmale    0.000000000567 ***
## Sex1              0.08799 .
## conditionfem:target.sexmale  0.00205 **
## conditionfem:Sex1  0.68563
## target.sexmale:Sex1 0.34202
## conditionfem:target.sexmale:Sex1 0.04452 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf trgt.s Sex1  cndt:. cnd:S1 tr.:S1
## conditionfm -0.689
## target.sxml -0.382  0.427
## Sex1        -0.388  0.267  0.069
## cndtnfm:tr.  0.342 -0.478 -0.894 -0.038

```

```
## cndtnfm:Sex1  0.289 -0.424 -0.051 -0.745  0.060
## trgt.sxm:S1  0.101 -0.070 -0.264 -0.260  0.146  0.194
## cndtnf:..S1 -0.075  0.110  0.197  0.194 -0.231 -0.260 -0.745
```

```
# 95% confidence interval
```

```
ci.26 <- confint(model.26, method = "Wald", level = 0.95)
ci.26
```

```
##                2.5 %      97.5 %
## .sig01          NA         NA
## .sig02          NA         NA
## .sigma          NA         NA
## (Intercept)    5.96086703  6.451809022
## conditionfem   -0.51715291  0.194953048
## target.sexmale -0.94336143 -0.567906173
## Sex1           -0.06477406  0.970848004
## conditionfem:target.sexmale  0.23018562  0.911240719
## conditionfem:Sex1 -0.83859707  0.551137847
## target.sexmale:Sex1 -0.13880817  0.400075774
## conditionfem:target.sexmale:Sex1 -0.73228611 -0.009140226
```

```
# group means
```

```
likability_total <- data %>%
  group_by(condition, target.sex, Sex) %>%
  summarize(mean = mean(likability), sd = sd(likability), n = n(), se = sd(likability)/sqrt(n()))
```

```
## 'summarise()' has grouped output by 'condition', 'target.sex'. You can override using the '.groups' argument.
```

```
likability_total
```

```
## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex    mean    sd     n    se
##   <fct>      <fct>   <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      female    2     6.21  1.74  1420  0.0462
## 2 masc      female    1     6.66  1.51   320  0.0846
## 3 masc      male      2     5.45  1.89  1420  0.0502
## 4 masc      male      1     6.03  1.45   320  0.0809
## 5 fem       female    2     6.05  1.87  1260  0.0528
## 6 fem       female    1     6.35  1.86   440  0.0886
## 7 fem       male      2     5.86  1.85  1260  0.0521
## 8 fem       male      1     5.93  1.90   440  0.0907
```

```
# subset means for male and female participants
```

```
male_likability <- likability_total %>%
  filter(Sex == "1")
female_likability <- likability_total %>%
  filter(Sex == "2")
```

```
# plot
```

```
male_likability_plot <- ggplot(male_likability, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
```

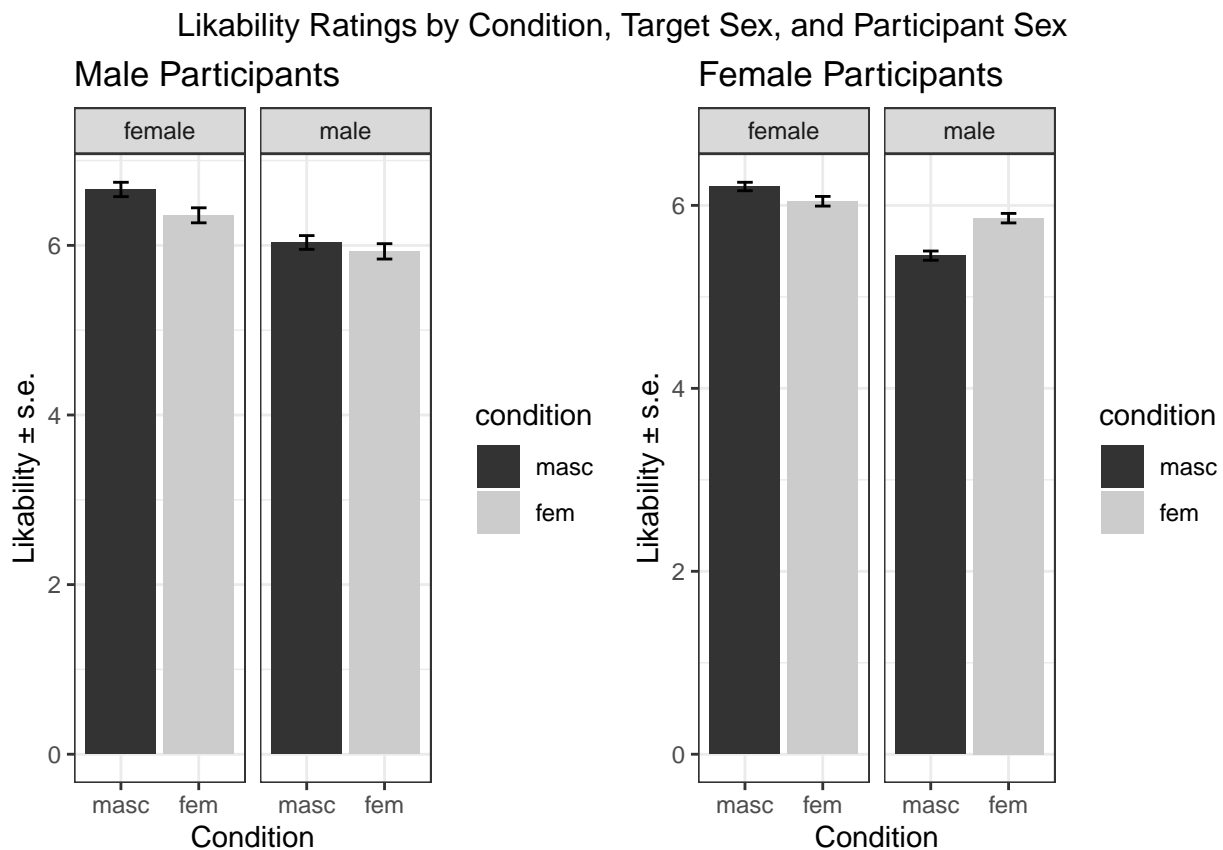
```

geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Male Participants",
y = "Likability ± s.e.", x = "Condition") + theme_bw()

female_likability_plot <- ggplot(female_likability, aes(x = condition,
y = mean, fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",
y = "Likability ± s.e.", x = "Condition") + theme_bw()

grid.arrange(male_likability_plot, female_likability_plot, nrow = 1, top = textGrob("Likability Ratings

```



The three way interaction is significant $t(6666) = 2.01, p < .05$. The simple effect of target sex and condition on likability ratings centered at female participants is also significant $t(43) = -3.29, p < .01$.

Simple Effect - Likability by Condition and Target Sex when Participant Sex is centered at Male

```

# reference group - male participants
data$Sex <- relevel(data$Sex, ref = "1")

model.27 <- lmer(likability ~ condition * target.sex * Sex + (1 | ID) +
  (1 | trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.27)

```

```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26263.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1419 -0.5884  0.0790  0.6470  3.5191
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.78801 0.8877
## trial   (Intercept) 0.05698 0.2387
## Residual                2.46771 1.5709
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      6.6594      0.2446 208.9158  27.230
## conditionfem     -0.3048      0.3226 210.6685  -0.945
## target.sexmale   -0.6250      0.1453 326.0319  -4.300
## Sex2             -0.4530      0.2642 193.2553  -1.715
## conditionfem:target.sexmale  0.2000      0.2223 113.7166   0.900
## conditionfem:Sex2  0.1437      0.3545 193.2553   0.405
## target.sexmale:Sex2 -0.1306      0.1375 6666.0000  -0.950
## conditionfem:target.sexmale:Sex2  0.3707      0.1845 6666.0000   2.010
##
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem      0.3458
## target.sexmale    0.0000225 ***
## Sex2              0.0880 .
## conditionfem:target.sexmale  0.3703
## conditionfem:Sex2  0.6856
## target.sexmale:Sex2  0.3420
## conditionfem:target.sexmale:Sex2  0.0445 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnf trgt.s Sex2  cndt:. cnd:S2 tr.:S2
## conditionfm -0.758
## target.sxm1 -0.297  0.286
## Sex2        -0.882  0.668  0.201
## cndtnfm:tr.  0.247 -0.345 -0.830 -0.131
## cndtnfm:Sx2  0.657 -0.860 -0.150 -0.745  0.169
## trgt.sxm:S2  0.229 -0.174 -0.772 -0.260  0.505  0.194
## cndtnf:.:S2 -0.171  0.224  0.575  0.194 -0.649 -0.260 -0.745

# 95% confidence interval
ci.27 <- confint(model.27, method = "Wald", level = 0.95)

```

ci.27

```
##                                2.5 %      97.5 %
## .sig01                        NA        NA
## .sig02                        NA        NA
## .sigma                        NA        NA
## (Intercept)                   6.180039644  7.13871036
## conditionfem                  -0.937164358  0.32750527
## target.sexmale                 -0.909846568 -0.34015343
## Sex2                          -0.970848004  0.06477406
## conditionfem:target.sexmale    -0.235771724  0.63577172
## conditionfem:Sex2             -0.551137847  0.83859707
## target.sexmale:Sex2           -0.400075774  0.13880817
## conditionfem:target.sexmale:Sex2 0.009140226  0.73228611
```

The simple effect of target sex and condition on likability ratings centered at male participants is not significant $t(114) = -0.90$, $p = .370$.

Friends

Main Effect - Friends by Condition

```
# reference group - masc condition
data$condition <- relevel(data$condition, ref = "masc")

model.28 <- lmer(friends ~ condition + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.28)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27303.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8902 -0.6106  0.0674  0.6671  3.4983
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  ID       (Intercept)         1.0371   1.018
##  trial    (Intercept)         0.0992   0.315
##  Residual                        2.8596   1.691
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
```

```
## (Intercept)      5.65862      0.12338 198.03022    45.86 <0.0000000000000002 ***
## conditionfem     0.06256      0.16058 170.00043      0.39              0.697
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## conditionfm -0.643
```

```
# 95% confidence interval
ci.28 <- confint(model.28, method = "Wald", level = 0.95)
ci.28
```

```
##              2.5 %    97.5 %
## .sig01          NA         NA
## .sig02          NA         NA
## .sigma          NA         NA
## (Intercept)    5.4167988 5.900443
## conditionfem -0.2521735 0.377285
```

```
# group means
friends_condition <- data %>%
  group_by(condition) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
friends_condition
```

```
## # A tibble: 2 x 5
##   condition mean    sd      n    se
##   <fct>     <dbl> <dbl> <int> <dbl>
## 1 masc      5.66   1.96  3480 0.0332
## 2 fem       5.72   2.03  3400 0.0348
```

There is no difference in friendliness ratings after adaptation to masculinized voices ($M = 5.66$, $SD = 1.96$) relative to feminized voices ($M = 5.72$, $SD = 2.03$), $t(170) = 0.39$, $p = .697$.

Main Effect - Friends by Target Sex

```
# reference group - female targets
data$target.sex <- relevel(data$target.sex, ref = "female")

model.29 <- lmer(friends ~ target.sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.29)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
```

```
## REML criterion at convergence: 27101.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7810 -0.6033  0.0648  0.6596  3.3808
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 1.03372  1.0167
##   trial    (Intercept) 0.09875  0.3143
##   Residual                2.77358  1.6654
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)    5.97919    0.09636  190.74998   62.05 <0.0000000000000002 ***
## target.sexmale -0.57931    0.04016  6668.24505  -14.43 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.208
```

```
# 95% confidence interval
ci.29 <- confint(model.29, method = "Wald", level = 0.95)
ci.29
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.7903270  6.1680496
## target.sexmale -0.6580168 -0.5005969
```

```
# group means
friends_sex <- data %>%
  group_by(target.sex) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
friends_sex
```

```
## # A tibble: 2 x 5
##   target.sex mean    sd      n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female    5.98  1.92  3440 0.0327
## 2 male      5.40  2.03  3440 0.0346
```

Female test voices ($M = 5.98$, $SD = 1.92$) are rated as significantly more friendly than male test voices ($M = 5.40$, $SD = 2.03$), $t(6668) = -14.41$, $p < .001$.

Main Effect - Friends by Participant Sex

```

# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.30 <- lmer(friends ~ Sex + (1 | ID) + (1 | trial), data = data, na.action = "na.exclude",
  control = lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.30)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 27297.3
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.8847 -0.6088 0.0677 0.6682 3.4819
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.00003 1.000
## trial (Intercept) 0.09919 0.315
## Residual 2.85957 1.691
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.5862 0.1024 185.6653 54.577 <0.0000000000000002 ***
## Sex1 0.4678 0.1902 170.0000 2.459 0.0149 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## Sex1 -0.411

# 95% confidence interval
ci.30 <- confint(model.30, method = "Wald", level = 0.95)
ci.30

## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.38558440 5.7868037
## Sex1 0.09487357 0.8406331

# group means
friends_Sex <- data %>%
  group_by(Sex) %>%

```



```
summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
friends_Sex
```

```
## # A tibble: 2 x 5
##   Sex    mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.59  2.02  5360 0.0276
## 2 1      6.05  1.86  1520 0.0477
```

Male participants ($M = 6.05$, $SD = 1.86$) rated test voices as significantly more friendly than female participants ($M = 5.59$, $SD = 2.02$), $t(170) = 2.50$, $p < .05$.

Interaction - Friends by Condition and Target Sex

```
# simple effects: relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.31 <- lmer(friends ~ condition * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.31)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27097.7
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -3.7664 -0.6021  0.0669  0.6584  3.3886
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  1.039      1.0195
##   trial    (Intercept)  0.083      0.2881
##   Residual                    2.774      1.6654
## Number of obs: 6880, groups:  ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      6.0816    0.1330 195.3868  45.725
## conditionfem     -0.2046    0.1889 196.1527  -1.083
## target.sexmale   -0.8460    0.1072  51.0348 -7.893
## conditionfem:target.sexmale  0.5342    0.1991  38.0043   2.683
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem      0.2803
## target.sexmale    0.000000000213 ***
## conditionfem:target.sexmale  0.0108 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxml -0.403  0.489
## cndtnfm:tr.  0.374 -0.527 -0.927
```

```
# 95% confidence interval
```

```
ci.31 <- confint(model.31, method = "Wald", level = 0.95)
ci.31
```

```
##                2.5 %    97.5 %
## .sig01           NA        NA
## .sig02           NA        NA
## .sigma           NA        NA
## (Intercept)      5.8209245  6.3422939
## conditionfem     -0.5748703  0.1657696
## target.sexmale   -1.0560535 -0.6359005
## conditionfem:target.sexmale 0.1439260  0.9244987
```

```
# group means
```

```
friends_CxTS <- data %>%
  group_by(condition, target.sex) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
```

'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

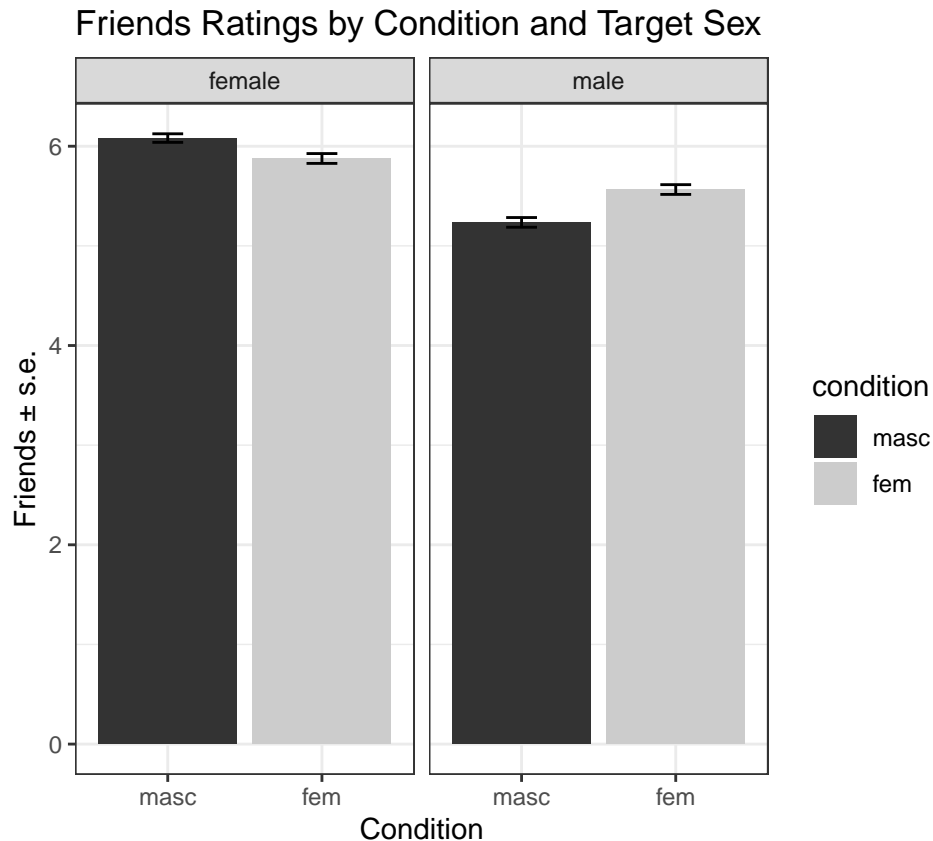
```
friends_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd     n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 masc      female      6.08  1.79  1740 0.0430
## 2 masc      male       5.24  2.03  1740 0.0486
## 3 fem       female      5.88  2.03  1700 0.0493
## 4 fem       male       5.57  2.02  1700 0.0489
```

```
# plot
```

```
friends_CxTS_plot <- ggplot(friends_CxTS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey()
```

```
friends_CxTS_plot + labs(title = "Friends Ratings by Condition and Target Sex",
  y = "Friends ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and target sex is significant, $t(38) = 2.68$, $p < .05$. Male test voices are rated as significantly more friendly after adaptation to feminized voices, while female test voices are rated as significantly more friendly after adaptation to masculinized voices. The simple effect of condition when target sex is centered at female is not significant, $t(196) = -1.08$, $p = .280$.

Simple Effect - Friends by Condition When Target Sex is centered at Male

```
# simple effects: relevel so reference group = male
data$target.sex <- relevel(data$target.sex, ref = "male")

model.32 <- lmer(friends ~ condition * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.32)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 27097.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7664 -0.6021  0.0669  0.6584  3.3886
```

```
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.039 1.0195
## trial (Intercept) 0.083 0.2881
## Residual 2.774 1.6654
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 5.2356 0.1330 195.3868 39.364
## conditionfem 0.3297 0.1889 196.1527 1.745
## target.sexfemale 0.8460 0.1072 51.0348 7.893
## conditionfem:target.sexfemale -0.5342 0.1991 38.0043 -2.683
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem 0.0826 .
## target.sexfemale 0.0000000000213 ***
## conditionfem:target.sexfemale 0.0108 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxfml -0.403 0.489
## cndtnfm:tr. 0.374 -0.527 -0.927
```

The simple effect of condition when target sex is centered at male is not significant, $t(196) = 1.75$, $p=.083$.

Interaction - Friends by Condition and Participant Sex

```
# relevel so reference group = female
data$Sex <- relevel(data$Sex, ref = "2")

model.33 <- lmer(friends ~ condition * Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.33)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27297.2
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.8820 -0.6087 0.0690 0.6664 3.4884
##
## Random effects:
```

```
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.00015 1.000
## trial (Intercept) 0.09919 0.315
## Residual 2.85957 1.691
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.5183 0.1326 196.5733 41.627 < 0.0000000000000002 ***
## conditionfem 0.1444 0.1792 168.0000 0.806 0.42147
## Sex1 0.7629 0.2865 168.0000 2.663 0.00849 **
## conditionfem:Sex1 -0.5370 0.3844 168.0000 -1.397 0.16430
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnf Sex1
## conditionfm -0.635
## Sex1 -0.397 0.294
## cndtnfm:Sex1 0.296 -0.466 -0.745
```

```
# 95% confidence interval
ci.33 <- confint(model.33, method = "Wald", level = 0.95)
ci.33
```

```
## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.2584883 5.7781314
## conditionfem -0.2067876 0.4955647
## Sex1 0.2014496 1.3244307
## conditionfem:Sex1 -1.2904847 0.2164803
```

```
# group means
friends_CxPS <- data %>%
  group_by(condition, Sex) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
```

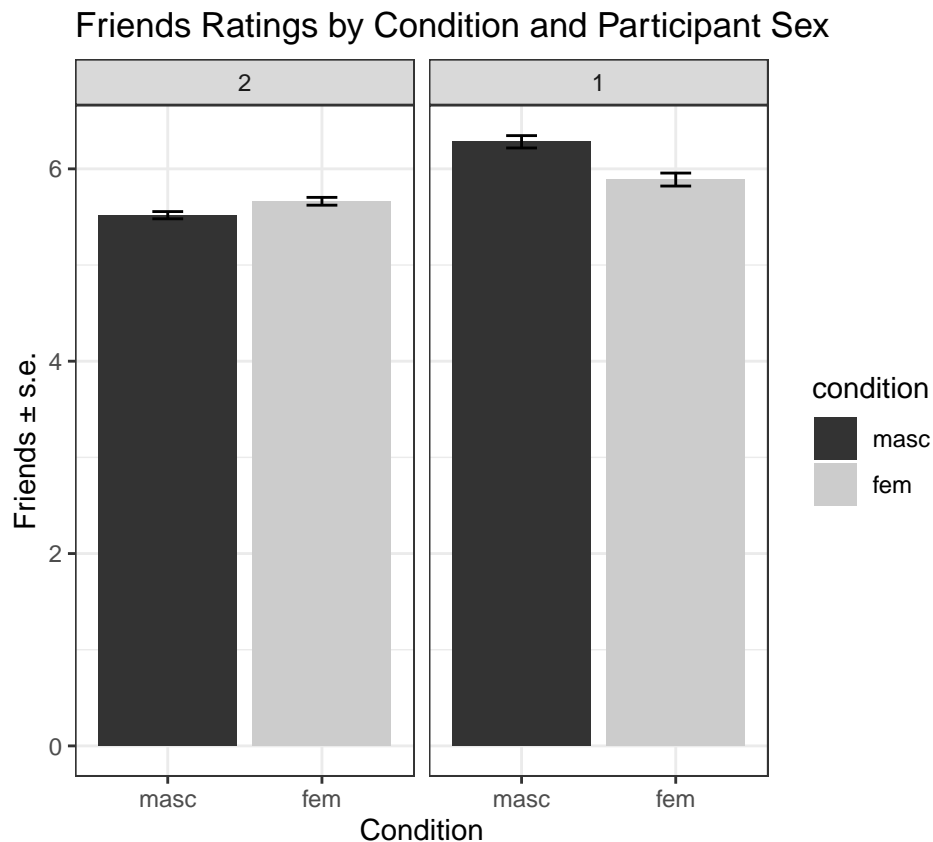
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
friends_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
## condition Sex mean sd n se
## <fct> <fct> <dbl> <dbl> <int> <dbl>
## 1 masc 2 5.52 2.00 2840 0.0376
## 2 masc 1 6.28 1.62 640 0.0641
## 3 fem 2 5.66 2.04 2520 0.0406
## 4 fem 1 5.89 2.00 880 0.0675
```

```
# plot
friends_CxPS_plot <- ggplot(friends_CxPS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~Sex) + scale_fill_grey()

friends_CxPS_plot + labs(title = "Friends Ratings by Condition and Participant Sex",
  y = "Friends  $\pm$  s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(168) = -1.40$, $p = .164$.

Interaction - Friends by Participant Sex and Target Sex

```
# relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.34 <- lmer(friends ~ Sex * target.sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.34)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
```

```
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 27099.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7729 -0.6054  0.0657   0.6591   3.3700
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  1.00218   1.001
##   trial    (Intercept)  0.09862   0.314
##   Residual                2.77398   1.666
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)    5.87900    0.10479  205.32058  56.103
## Sex1            0.45353    0.19635  192.86100   2.310
## target.sexmale -0.58560    0.04555 6672.08154 -12.855
## Sex1:target.sexmale  0.02845    0.09714 6680.88059   0.293
##              Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## Sex1            0.022 *
## target.sexmale  <0.0000000000000002 ***
## Sex1:target.sexmale  0.770
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.414
## target.sxml -0.217  0.117
## Sx1:trgt.sx  0.103 -0.247 -0.472
```

```
# 95% confidence interval
```

```
ci.34 <- confint(model.34, method = "Wald", level = 0.95)
ci.34
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.67361391  6.0843775
## Sex1            0.06868889  0.8383686
## target.sexmale -0.67488631 -0.4963205
## Sex1:target.sexmale -0.16194157  0.2188400
```

```
# group means
```

```
friends_PSxTS <- data %>%
  group_by(Sex, target.sex) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
```

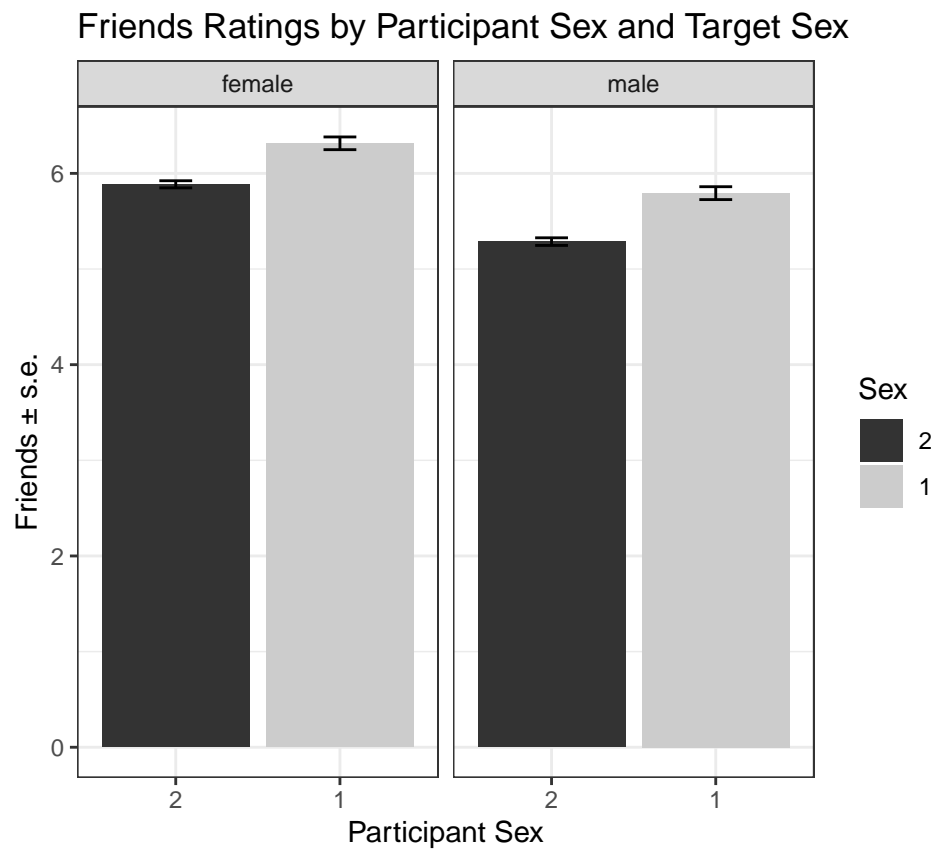
```
## 'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.
```

```
friends_PSxTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd    n    se
##   <fct> <fct>     <dbl> <dbl> <int> <dbl>
## 1 2     female     5.89  1.93  2680 0.0373
## 2 2     male       5.29  2.06  2680 0.0398
## 3 1     female     6.31  1.83   760 0.0664
## 4 1     male       5.79  1.86   760 0.0673
```

```
# plot
friends_PSxTS_plot <- ggplot(friends_PSxTS, aes(x = Sex, y = mean, fill = Sex)) +
  geom_bar(position = "dodge", stat = "identity") + geom_errorbar(aes(ymin = mean -
    se, ymax = mean + se), width = 0.2) + facet_wrap(~target.sex) + scale_fill_grey()

friends_PSxTS_plot + labs(title = "Friends Ratings by Participant Sex and Target Sex",
  y = "Friends ± s.e.", x = "Participant Sex") + theme_bw()
```



The interaction between participant sex and target sex is not significant, $t(6681) = 0.29$, $p = .770$.

Three Way Interaction - Friends by Condition, Target Sex, and Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")
```



```
model.35 <- lmer(friends ~ condition * target.sex * Sex + (1 | ID) + (1 |
  trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nloptnlo"))
summary(model.35)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nloptnlo"))
##
## REML criterion at convergence: 27093.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7482 -0.5983  0.0654  0.6576  3.3538
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  ID       (Intercept)         1.002    1.0012
##  trial    (Intercept)         0.083    0.2881
##  Residual                    2.773    1.6654
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      5.9585     0.1422  204.1731  41.902
## conditionfem     -0.1545     0.2061  206.9373  -0.750
## target.sexmale   -0.8803     0.1105   57.6089  -7.968
## Sex1              0.6697     0.2956  190.4115   2.265
## conditionfem:target.sexmale  0.5977     0.2037   41.6496   2.934
## conditionfem:Sex1 -0.3873     0.3967  190.4115  -0.976
## target.sexmale:Sex1  0.1865     0.1457 6666.0017   1.280
## conditionfem:target.sexmale:Sex1 -0.2994     0.1956 6666.0017  -1.531
##
##              Pr(>|t|)
## (Intercept) < 0.00000000000000002 ***
## conditionfem      0.45440
## target.sexmale    0.0000000000726 ***
## Sex1              0.02461 *
## conditionfem:target.sexmale  0.00542 **
## conditionfem:Sex1  0.33016
## target.sexmale:Sex1  0.20063
## conditionfem:target.sexmale:Sex1  0.12579
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf trgt.s Sex1   cndt:. cnd:S1 tr.:S1
## conditionfm -0.690
## target.sxml -0.388  0.450
## Sex1        -0.382  0.264  0.060
## cndtnfm:tr.  0.354 -0.494 -0.911 -0.032
```

```
## cndtnfm:Sex1  0.285 -0.418 -0.045 -0.745  0.051
## trgt.sxm:S1  0.094 -0.065 -0.243 -0.247  0.132  0.184
## cndtnf:..S1 -0.070  0.103  0.181  0.184 -0.209 -0.247 -0.745
```

```
# 95% confidence interval
```

```
ci.35 <- confint(model.35, method = "Wald", level = 0.95)
ci.35
```

```
##                                2.5 %      97.5 %
## .sig01                        NA         NA
## .sig02                        NA         NA
## .sigma                        NA         NA
## (Intercept)                   5.67974474  6.23715667
## conditionfem                  -0.55845439  0.24948949
## target.sexmale                -1.09682407 -0.66373931
## Sex1                          0.09029417  1.24905442
## conditionfem:target.sexmale    0.19842165  0.99706236
## conditionfem:Sex1             -1.16476794  0.39021011
## target.sexmale:Sex1           -0.09911279  0.47217617
## conditionfem:target.sexmale:Sex1 -0.68276217  0.08386907
```

```
# group means
```

```
friends_total <- data %>%
  group_by(condition, target.sex, Sex) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
```

'summarise()' has grouped output by 'condition', 'target.sex'. You can override using the '.groups' argument.

```
friends_total
```

```
## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex    mean    sd     n    se
##   <fct>      <fct>   <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      female    2     5.96  1.81  1420  0.0480
## 2 masc      female    1     6.63  1.60   320  0.0894
## 3 masc      male      2     5.08  2.09  1420  0.0554
## 4 masc      male      1     5.93  1.57   320  0.0877
## 5 fem       female    2     5.80  2.06  1260  0.0580
## 6 fem       female    1     6.09  1.95   440  0.0931
## 7 fem       male      2     5.52  2.01  1260  0.0566
## 8 fem       male      1     5.69  2.03   440  0.0970
```

```
# subset means for male and female participants
```

```
male_friends <- friends_total %>%
  filter(Sex == "1")
female_friends <- friends_total %>%
  filter(Sex == "2")
```

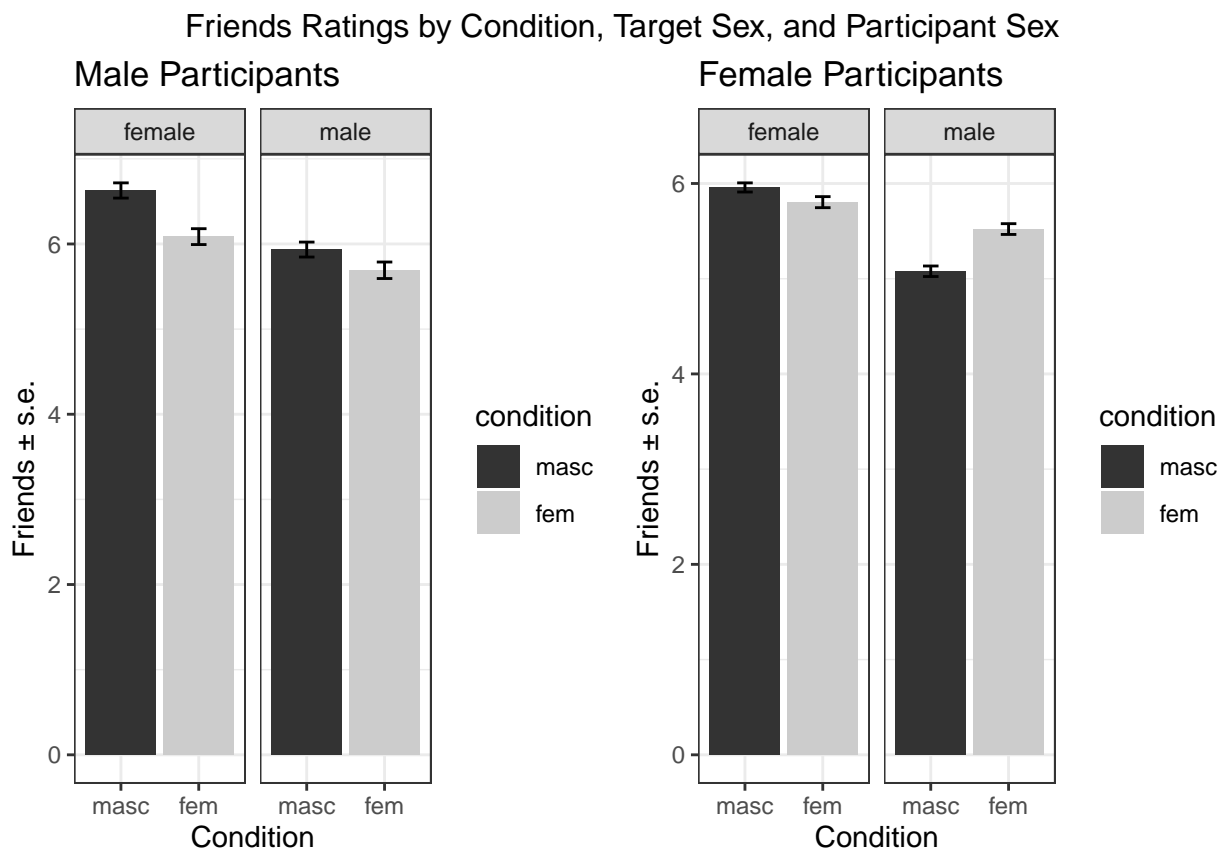
```
# plot
```

```
male_friends_plot <- ggplot(male_friends, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
```

```
geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Male Participants",
y = "Friends ± s.e.", x = "Condition") + theme_bw()

female_friends_plot <- ggplot(female_friends, aes(x = condition, y = mean,
fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",
y = "Friends ± s.e.", x = "Condition") + theme_bw()
```

```
grid.arrange(male_friends_plot, female_friends_plot, nrow = 1, top = textGrob("Friends Ratings by Condi"))
```



The three way interaction is not significant, $t(6666) = 1.53$, $p=.126$.

Typicality

Main Effect - Typicality by Condition

```
# reference group - masc condition
data$condition <- relevel(data$condition, ref = "masc")

model.36 <- lmer(typicality ~ condition + (1 | ID) + (1 | trial), data = data,
na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
summary(model.36)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26848.6
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.9162 -0.6223 0.0728 0.6652 3.5396
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.84840 0.9211
## trial (Intercept) 0.07112 0.2667
## Residual 2.68864 1.6397
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.82241 0.11092 195.99789 52.494 <0.0000000000000002 ***
## conditionfem 0.07229 0.14593 169.99323 0.495 0.621
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## conditionfm -0.650
```

```
# 95% confidence interval
ci.36 <- confint(model.36, method = "Wald", level = 0.95)
ci.36
```

```
## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.6050219 6.0398057
## conditionfem -0.2137299 0.3583141
```

```
# group means
typicality_condition <- data %>%
  group_by(condition) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
typicality_condition
```

```
## # A tibble: 2 x 5
## condition mean sd n se
## <fct> <dbl> <dbl> <int> <dbl>
## 1 masc 5.82 1.82 3480 0.0308
## 2 fem 5.89 1.97 3400 0.0339
```

There is no difference in typicality ratings after adaptation to feminized voices ($M = 5.89$, $SD = 1.97$) relative to masculinized voices ($M = 5.82$, $SD = 1.82$), $t(170) = 0.50$, $p = .621$.

Main Effect - Typicality by Target Sex

```
# reference group - female targets
data$target.sex <- relevel(data$target.sex, ref = "female")

model.37 <- lmer(typicality ~ target.sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.37)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26843.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8818 -0.6188  0.0760  0.6641  3.5081
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.84440  0.9189
## trial   (Intercept) 0.07098  0.2664
## Residual                2.68583  1.6389
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)    5.91424    0.08640  195.90692  68.453 < 0.0000000000000002
## target.sexmale -0.11220    0.03952  6668.32428  -2.839    0.00454
##
## (Intercept)    ***
## target.sexmale **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.229

# 95% confidence interval
ci.37 <- confint(model.37, method = "Wald", level = 0.95)
ci.37

##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
```

```
## .sigma          NA          NA
## (Intercept)    5.744904  6.08357806
## target.sexmale -0.189658 -0.03474872
```

```
# group means
typicality_sex <- data %>%
  group_by(target.sex) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
typicality_sex
```

```
## # A tibble: 2 x 5
##   target.sex mean    sd      n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female     5.92  1.90  3440 0.0324
## 2 male       5.80  1.89  3440 0.0323
```

Female test voices ($M = 5.92$, $SD = 1.90$) are rated as significantly more friendly than male test voices ($M = 5.80$, $SD = 1.90$), $t(6668) = -2.84$, $p < .01$.

Main Effect - Typicality by Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.38 <- lmer(typicality ~ Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.38)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26846.5
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -3.9114 -0.6230  0.0736  0.6642  3.5313
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  0.83913   0.9160
##   trial    (Intercept)  0.07113   0.2667
##   Residual                    2.68865   1.6397
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.80373    0.09242 187.20555  62.795 <0.0000000000000002 ***
## Sex1          0.24627    0.17497 169.99978   1.407      0.161
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.418
```

```
# 95% confidence interval
ci.38 <- confint(model.38, method = "Wald", level = 0.95)
ci.38
```

```
##              2.5 %    97.5 %
## .sig01          NA         NA
## .sig02          NA         NA
## .sigma          NA         NA
## (Intercept)  5.62258602 5.9848767
## Sex1        -0.09666974 0.5892071
```

```
# group means
typicality_Sex <- data %>%
  group_by(Sex) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
typicality_Sex
```

```
## # A tibble: 2 x 5
##   Sex   mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.80  1.91  5360 0.0261
## 2 1      6.05  1.84  1520 0.0473
```

There is no significant difference in friends ratings between male participants ($M = 6.05$, $SD = 1.84$) and female participants ($M = 5.80$, $SD = 1.91$), $t(170) = 1.41$, $p = .161$.

Interaction - Typicality by Condition and Target Sex

```
# simple effects: relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.39 <- lmer(typicality ~ condition * target.sex + (1 | ID) + (1 |
  trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.39)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26839.3
##
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8954 -0.6173  0.0785  0.6600  3.5193
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.84845  0.9211
##   trial    (Intercept) 0.05751  0.2398
##   Residual                2.68583  1.6389
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      6.00057    0.11904 200.16391  50.407
## conditionfem     -0.17234    0.16914 200.84879  -1.019
## target.sexmale   -0.35632    0.09401  55.49520  -3.790
## conditionfem:target.sexmale  0.48926    0.17103  38.00154   2.861
##
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## conditionfem      0.309471
## target.sexmale    0.000373 ***
## conditionfem:target.sexmale  0.006834 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnf trgt.s
## conditionfm -0.704
## target.sxml -0.395  0.459
## cndtnfm:tr.  0.358 -0.506 -0.907
```

```
# 95% confidence interval
ci.39 <- confint(model.39, method = "Wald", level = 0.95)
ci.39
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.7672535  6.2338959
## conditionfem     -0.5038490  0.1591701
## target.sexmale   -0.5405818 -0.1720619
## conditionfem:target.sexmale  0.1540503  0.8244757
```

```
# group means
typicality_CxTS <- data %>%
  group_by(condition, target.sex) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
```

```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

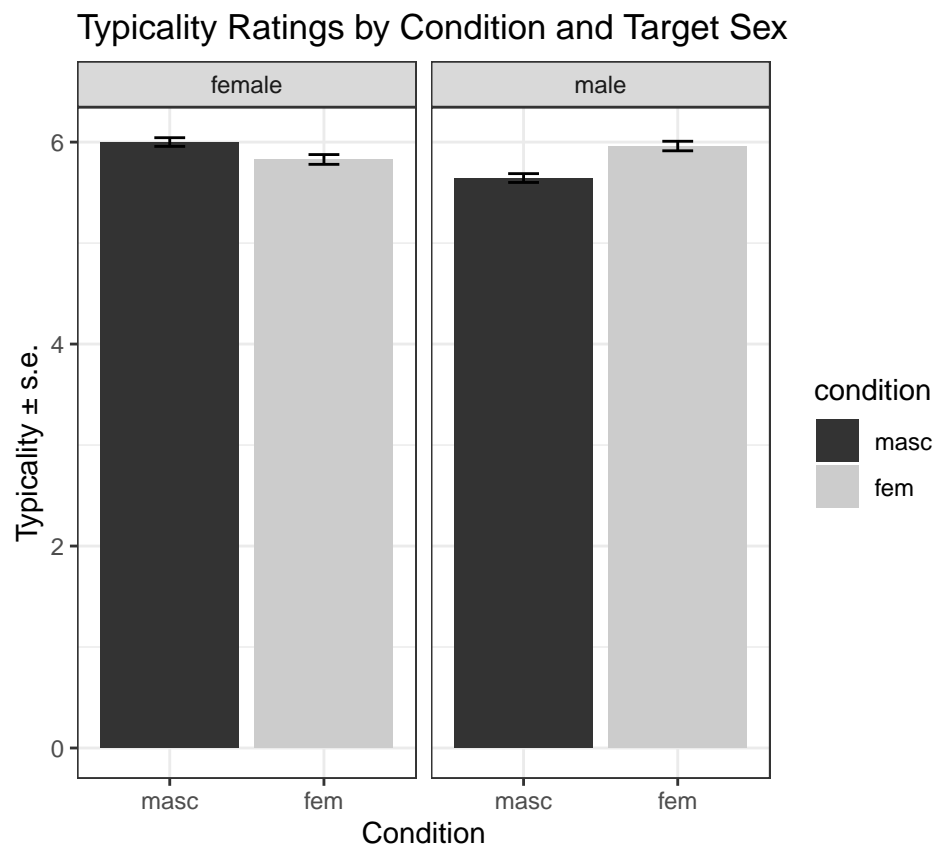


```
typicality_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd     n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 masc      female      6.00  1.79  1740 0.0430
## 2 masc      male       5.64  1.82  1740 0.0437
## 3 fem       female      5.83  2.00  1700 0.0484
## 4 fem       male       5.96  1.95  1700 0.0473
```

```
# plot
typicality_CxTS_plot <- ggplot(typicality_CxTS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey()

typicality_CxTS_plot + labs(title = "Typicality Ratings by Condition and Target Sex",
  y = "Typicality ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and target sex is significant, $t(38) = 2.86$, $p < .01$. Male voices are rated as significantly more typical after adaptation to feminized voices, while female voices are rated as significantly more typical after adaptation to masculinized voices. The simple effect of condition on typicality when target sex is centered at female is not significant, $t(201) = -1.02$, $p = .309$.

Simple Effect - Typicality by Condition when Target Sex is centered at Male

```

# simple effects: relevel so reference group = male
data$target.sex <- relevel(data$target.sex, ref = "male")

model.40 <- lmer(typicality ~ condition * target.sex + (1 | ID) + (1 |
  trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.40)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26839.3
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.8954 -0.6173 0.0785 0.6600 3.5193
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.84845 0.9211
## trial (Intercept) 0.05751 0.2398
## Residual 2.68583 1.6389
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 5.64425 0.11904 200.16391 47.413
## conditionfem 0.31692 0.16914 200.84879 1.874
## target.sexfemale 0.35632 0.09401 55.49520 3.790
## conditionfem:target.sexfemale -0.48926 0.17103 38.00154 -2.861
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem 0.062420 .
## target.sexfemale 0.000373 ***
## conditionfem:target.sexfemale 0.006834 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnf trgt.s
## conditionfm -0.704
## targt.sxfml -0.395 0.459
## cndtnfm:tr. 0.358 -0.506 -0.907

```

The simple effect of condition when target sex is centered at male is not significant, $t(201) = 1.87$, $p = .062$.

Interaction - Typicality by Condition and Participant Sex

```
# relevelevel so reference group = female
data$Sex <- relevelevel(data$Sex, ref = "2")
```

```
model.41 <- lmer(typicality ~ condition * Sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.41)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26848.3
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.9143 -0.6232 0.0730 0.6641 3.5343
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.84767 0.9207
## trial (Intercept) 0.07113 0.2667
## Residual 2.68864 1.6397
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.75880 0.12109 193.88216 47.556 <0.0000000000000002
## conditionfem 0.09556 0.16555 167.98699 0.577 0.565
## Sex1 0.34588 0.26470 167.98699 1.307 0.193
## conditionfem:Sex1 -0.19002 0.35521 167.98699 -0.535 0.593
##
## (Intercept) ***
## conditionfem
## Sex1
## conditionfem:Sex1
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnf Sex1
## conditionfm -0.643
## Sex1 -0.402 0.294
## cndtnfm:Sex1 0.300 -0.466 -0.745
```

```
# 95% confidence interval
ci.41 <- confint(model.41, method = "Wald", level = 0.95)
ci.41
```

```
## 2.5 % 97.5 %
```

```
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)    5.5214613 5.9961443
## conditionfem   -0.2289144 0.4200389
## Sex1           -0.1729164 0.8646858
## conditionfem:Sex1 -0.8862186 0.5061736
```

```
# group means
typicality_CxPS <- data %>%
  group_by(condition, Sex) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
```

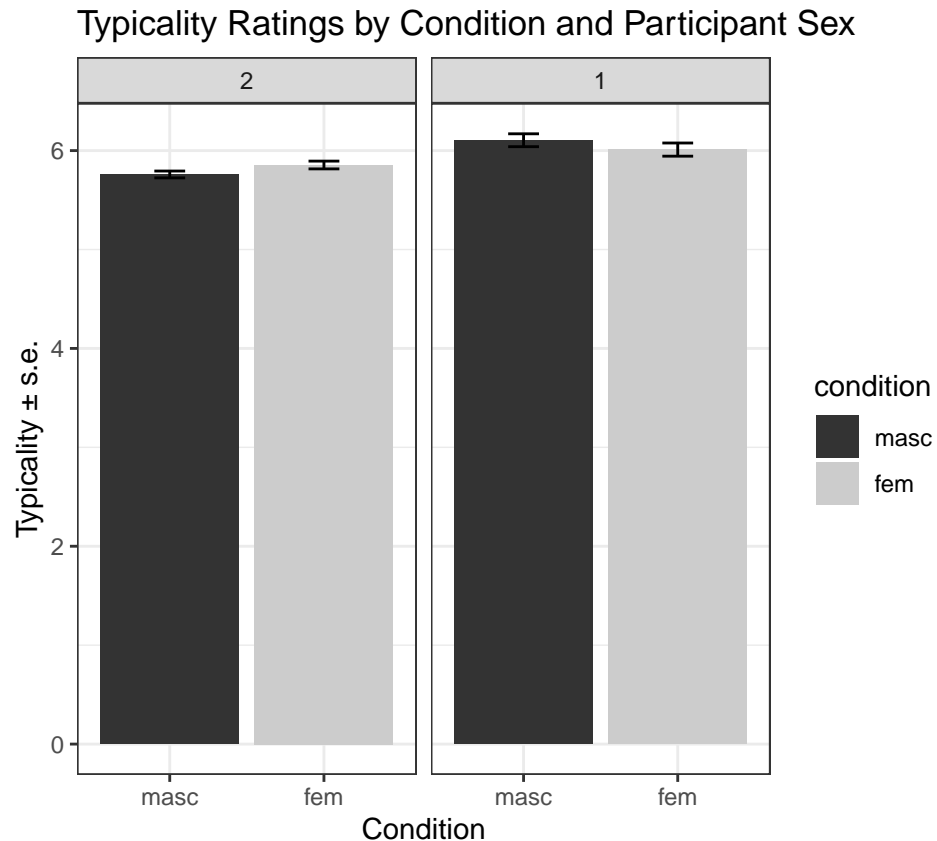
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
typicality_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n     se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      2      5.76  1.85  2840 0.0347
## 2 masc      1      6.10  1.65   640 0.0650
## 3 fem       2      5.85  1.97  2520 0.0393
## 4 fem       1      6.01  1.98   880 0.0666
```

```
# plot
typicality_CxPS_plot <- ggplot(typicality_CxPS, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~Sex) + scale_fill_grey()

typicality_CxPS_plot + labs(title = "Typicality Ratings by Condition and Participant Sex",
  y = "Typicality ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(168) = -0.54$, $p = .593$.

Interaction - Typicality by Participant Sex and Target Sex

```
# relevel so reference group = female
data$target.sex <- relevel(data$target.sex, ref = "female")

model.42 <- lmer(typicality ~ Sex * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.42)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26845.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8743 -0.6187  0.0755  0.6596  3.5113
##
## Random effects:
## Groups   Name                Variance Std.Dev.
```

```
## ID      (Intercept) 0.83921 0.9161
## trial   (Intercept) 0.07072 0.2659
## Residual      2.68614 1.6389
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.86609    0.09505  209.98725  61.717
## Sex1              0.21802    0.18138  196.27550   1.202
## target.sexmale   -0.12471    0.04482 6673.47134  -2.782
## Sex1:target.sexmale  0.05650    0.09557 6684.30415   0.591
##              Pr(>|t|)
## (Intercept)      < 0.0000000000000002 ***
## Sex1              0.23082
## target.sexmale    0.00541 **
## Sex1:target.sexmale 0.55442
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.422
## target.sxml -0.236  0.124
## Sx1:trgt.sx  0.111 -0.263 -0.472
```

```
# 95% confidence interval
ci.42 <- confint(model.42, method = "Wald", level = 0.95)
ci.42
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.6797949  6.05237571
## Sex1            -0.1374819  0.57351784
## target.sexmale   -0.2125610 -0.03685495
## Sex1:target.sexmale -0.1308198  0.24382264
```

```
# group means
typicality_PSxTS <- data %>%
  group_by(Sex, target.sex) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
```

'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.

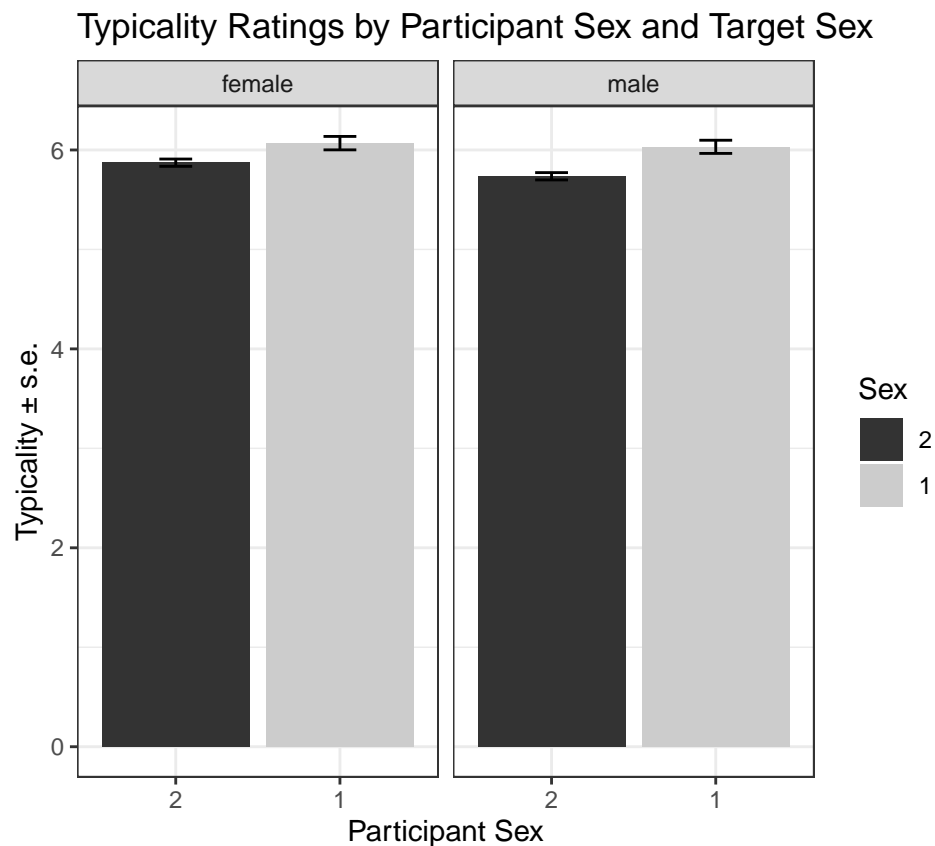
```
typicality_PSxTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd    n    se
##   <fct> <fct>    <dbl> <dbl> <int> <dbl>
## 1 2     female      5.87  1.91  2680 0.0368
```

```
## 2 2    male      5.74  1.91  2680 0.0369
## 3 1    female    6.07  1.86   760 0.0676
## 4 1    male      6.03  1.83   760 0.0662
```

```
# plot
typicality_PSxTS_plot <- ggplot(typicality_PSxTS, aes(x = Sex, y = mean,
  fill = Sex)) + geom_bar(position = "dodge", stat = "identity") + geom_errorbar(aes(ymin = mean -
  se, ymax = mean + se), width = 0.2) + facet_wrap(~target.sex) + scale_fill_grey()

typicality_PSxTS_plot + labs(title = "Typicality Ratings by Participant Sex and Target Sex",
  y = "Typicality ± s.e.", x = "Participant Sex") + theme_bw()
```



The interaction between participant sex and target sex is not significant, $t(6684) = 0.59$, $p = .554$.

Three Way Interaction - Typicality by Condition, Target Sex, and Participant Sex

```
# reference group - female participants
data$Sex <- relevel(data$Sex, ref = "2")

model.43 <- lmer(typicality ~ condition * target.sex * Sex + (1 | ID) +
  (1 | trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nllminb")))
summary(model.43)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
```

```

## Formula: typicality ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26843.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8900 -0.6209  0.0785  0.6592  3.5222
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.84767 0.9207
## trial   (Intercept) 0.05751 0.2398
## Residual                2.68654 1.6391
## Number of obs: 6880, groups: ID, 172; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      5.94225    0.12925 208.27510  45.974
## conditionfem     -0.14940    0.18753 210.41560  -0.797
## target.sexmale   -0.36690    0.09764  64.56529  -3.758
## Sex1              0.31712    0.27424 193.54540   1.156
## conditionfem:target.sexmale  0.48992    0.17621  42.82016   2.780
## conditionfem:Sex1 -0.18043    0.36801 193.54540  -0.490
## target.sexmale:Sex1  0.05753    0.14344 6666.00083   0.401
## conditionfem:target.sexmale:Sex1 -0.01918    0.19249 6666.00084  -0.100
##
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditionfem      0.426560
## target.sexmale    0.000371 ***
## Sex1              0.248953
## conditionfem:target.sexmale  0.008039 **
## conditionfem:Sex1  0.624479
## target.sexmale:Sex1  0.688395
## conditionfem:target.sexmale:Sex1  0.920636
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnf trgt.s Sex1  cndt:. cnd:S1 tr.:S1
## conditionfm -0.689
## target.sxm1 -0.378  0.417
## Sex1        -0.390  0.269  0.071
## cndtnfm:tr.  0.336 -0.470 -0.888 -0.039
## cndtnfm:Sx1  0.291 -0.426 -0.053 -0.745  0.062
## trgt.sxm:S1  0.102 -0.070 -0.270 -0.262  0.150  0.195
## cndtnf:.:S1 -0.076  0.111  0.201  0.195 -0.237 -0.262 -0.745

# 95% confidence interval
ci.43 <- confint(model.43, method = "Wald", level = 0.95)
ci.43

```



```
##                                2.5 %    97.5 %
## .sig01                        NA        NA
## .sig02                        NA        NA
## .sigma                        NA        NA
## (Intercept)                   5.6889223  6.1955848
## conditionfem                  -0.5169562  0.2181635
## target.sexmale                -0.5582820 -0.1755208
## Sex1                          -0.2203736  0.8546165
## conditionfem:target.sexmale    0.1445467  0.8352879
## conditionfem:Sex1             -0.9017153  0.5408489
## target.sexmale:Sex1           -0.2236085  0.3386614
## conditionfem:target.sexmale:Sex1 -0.3964428  0.3580855
```

```
# group means
```

```
typicality_total <- data %>%
  group_by(condition, target.sex, Sex) %>%
  summarize(mean = mean(typicality), sd = sd(typicality), n = n(), se = sd(typicality)/sqrt(n()))
```

'summarise()' has grouped output by 'condition', 'target.sex'. You can override using the '.groups' argument.

```
typicality_total
```

```
## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex    mean    sd     n    se
##   <fct>      <fct>   <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      female     2     5.94  1.81  1420  0.0480
## 2 masc      female     1     6.26  1.69   320  0.0943
## 3 masc      male       2     5.58  1.87  1420  0.0495
## 4 masc      male       1     5.95  1.59   320  0.0889
## 5 fem       female     2     5.79  2.00  1260  0.0565
## 6 fem       female     1     5.93  1.97   440  0.0940
## 7 fem       male       2     5.92  1.94  1260  0.0546
## 8 fem       male       1     6.09  1.98   440  0.0943
```

```
# subset means for male and female participants
```

```
male_typicality <- typicality_total %>%
  filter(Sex == "1")
female_typicality <- typicality_total %>%
  filter(Sex == "2")
```

```
# plot
```

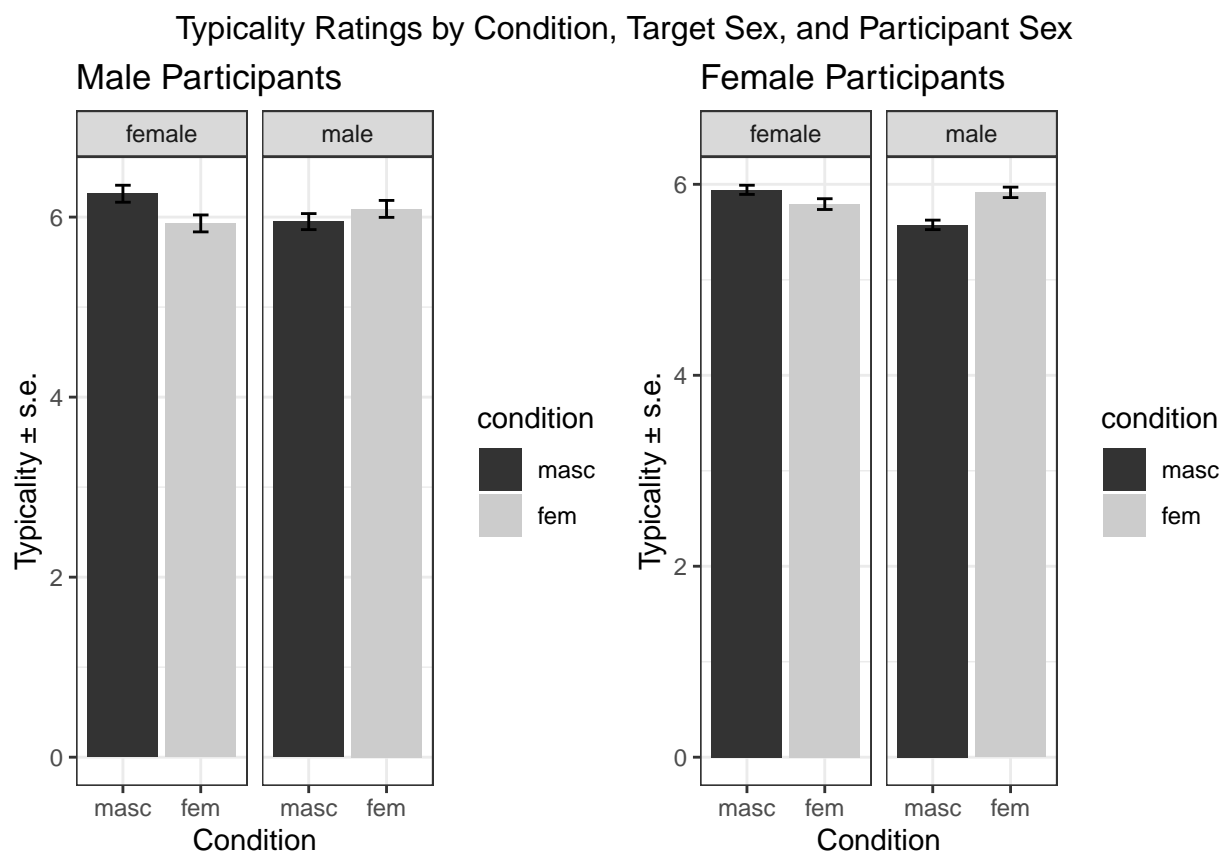
```
male_typicality_plot <- ggplot(male_typicality, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Male Participants",
  y = "Typicality ± s.e.", x = "Condition") + theme_bw()

female_typicality_plot <- ggplot(female_typicality, aes(x = condition,
  y = mean, fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",
```

```

y = "Typicality ± s.e.", x = "Condition") + theme_bw()
grid.arrange(male_typicality_plot, female_typicality_plot, nrow = 1, top = textGrob("Typicality Ratings

```



The three way interaction is not significant, $t(6666) = 0.10$, $p = .921$.