Study 4 Analysis: Perceptual Adaptation

Kelsey Neuenswander

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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_o), 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_o, a well-established sexually dimorphic aspect of voice, using PSOLA (Pitch Synchronous Overlap Add) resynthesis. For masculinized versions, f_o values were lowered to 90% of baseline. For feminized versions, f_o 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_o values were lowered to 70% of baseline. For feminized versions, f_o was increased to 140% of baseline.

Procedure. We recruited U.S. residents 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 fist heard an adapting voice followed by a test voice which they judged for attractiveness and masculinity/femininity (1 = *Not at all* to 9 = *Extremely*). We also collected perceptions of likability, friendliness, and typicality for future exploratory analyses not reported here. 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. Participants completed 20 trials in pseudo-randomized order in each block (40 trials total), 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("study4_data.csv", header = TRUE)
```

Factor

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

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

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

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

Filter
There were only 4 participants who did not identify as male or female. Because we were interested in investigating the interaction between condition, target sex, and participant sex, we filtered out participants who did not identify as male or female since the power for detecting an effect with a sample size of 4 is too low.

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

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

```r
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.

```r
# sample size before filtering
nrow(data)/40   # divide by number of trials since data is long form
```

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

```r
# 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
```

The original sample size was 178. After filtering participants whose responses did not meet our requirements, the final sample size is 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 (77.91%).

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 (59.88%).

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 25.38 years old, with a range from 18 - 63.

Multilevel Analyses (NCC Design)

The following analyses are done in a stepwise fashion.

Attraction

Main Effect - Attraction by Condition (Masculinized/Feminized)

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

# multilevel model
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 = "nlminb")))
```

```
## Loading required namespace: optimx
```

```r
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")

# multilevel model
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
```

```r
# 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
```

```r
# 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)

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

# multilevel model
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")

# multilevel model
model.4 <- lmer(attraction ~ condition * target.sex + (1|ID) + (1|trial), data=data, na.action = 'na.exc
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()))
```
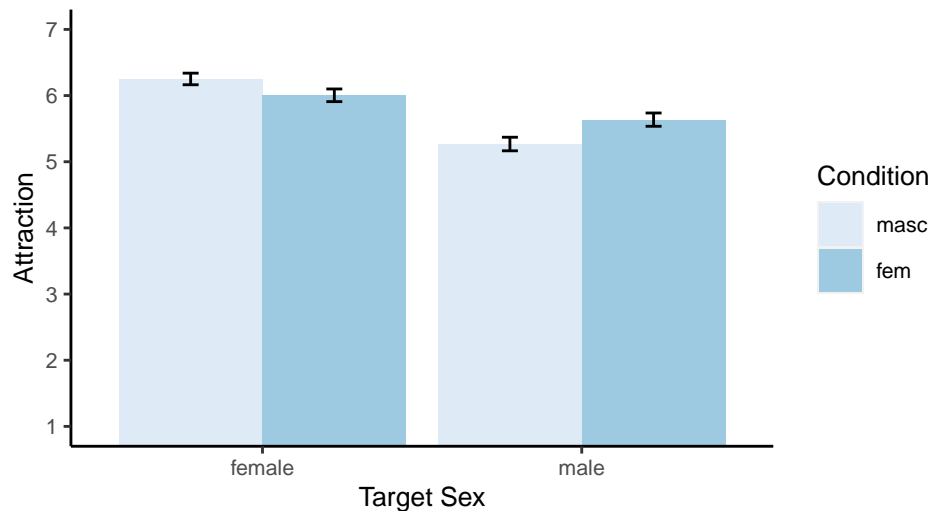
```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

```
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 with 95% CI
attraction_CxTS_plot <- data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = attraction, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "", x="Target Sex", y="Attraction", fill="Condition")
```

```
attraction_CxTS_plot
```

The interaction between target sex and condition is significant, $t(38) = 3.33$, $p = .002$. 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

```r
# 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 = "nlminb")))
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               0.000000000000151 ***
## 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
## targt.sxfml -0.404  0.468
## cndtnfm:tr.  0.366 -0.516 -0.906
```

The simple effect of condition centered at male targets is significant, $t(199) = 2.06$, $p = .040$.

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")

# multilevel model
model.6 <- lmer(attraction ~ condition * Sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude',
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 ***
```

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```
## 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:Sx1  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 with 95% CI
attraction_CxPS_plot <- data %>%
  group_by(condition, Sex) %>%
  phe_mean(x = attraction, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=Sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
```

```
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "", x="Participant Sex (1 = Male, 2 = Female)", y="Attraction", fill="Condition")

attraction_CxPS_plot
```
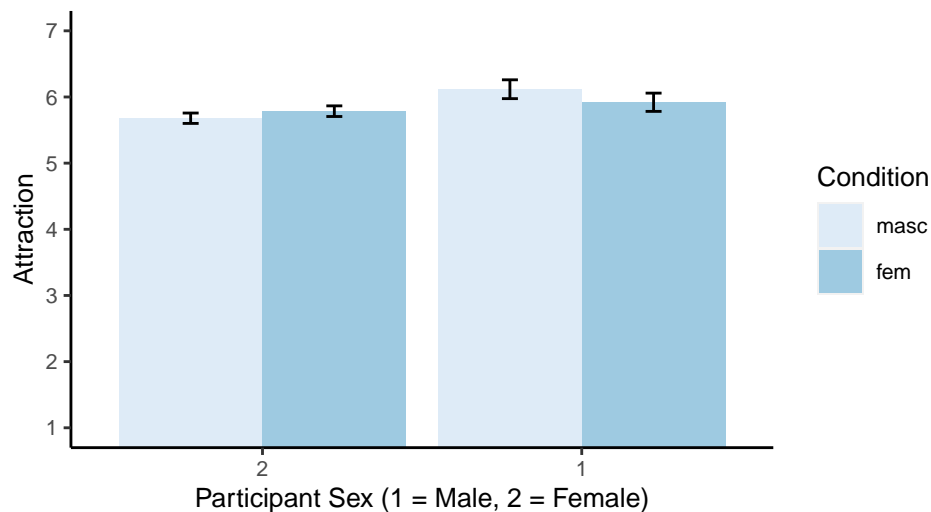

The interaction between condition and participant sex is not significant, $t(168) = $ -0.82, $p = .416$.

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

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

# multilevel model
model.7 <- lmer(attraction ~ Sex * target.sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude'
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
```

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```
## 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
```

```r
# 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
```

```r
# 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.
```

```r
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
```

```r
#plot with 95% CI
attraction_PSxTS_plot <- data %>%
  group_by(Sex, target.sex) %>%
  phe_mean(x = attraction, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=Sex)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "", x="Target Sex", y="Attraction", fill="Participant Sex")

attraction_PSxTS_plot
```
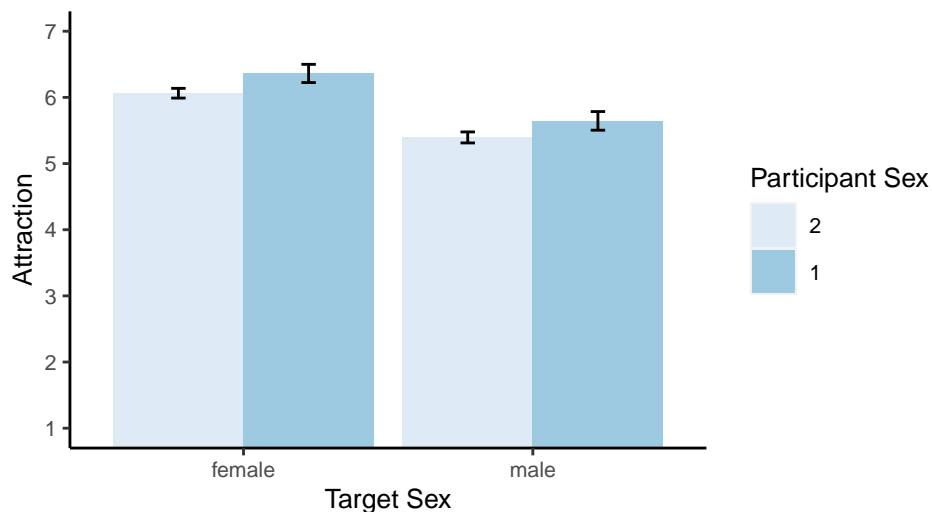

The interaction between participant sex and target sex is not significant, $t(6684) = -1.01$, $p = .314$.

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

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

# multilevel model
model.8 <- lmer(attraction ~ condition * target.sex * Sex + (1|ID) + (1|trial), data=data, na.action =
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 = "nlminb"))
##
## 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
```

```r
# 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`
```

```r
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
```

```r
# subset means for male and female participants
male_data <- data %>% filter(Sex == "1")
female_data <- data %>% filter(Sex == "2")

#plot with 95% CI
male_attraction_plot <- male_data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = attraction, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
```

```
    labs(title = "Male Participants", x="Target Sex", y="Attraction", fill="Condition")

female_attraction_plot <- female_data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = attraction, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "Female Participants", x="Target Sex", y="Attraction", fill="Condition")

grid.arrange(male_attraction_plot, female_attraction_plot, nrow=1)
```
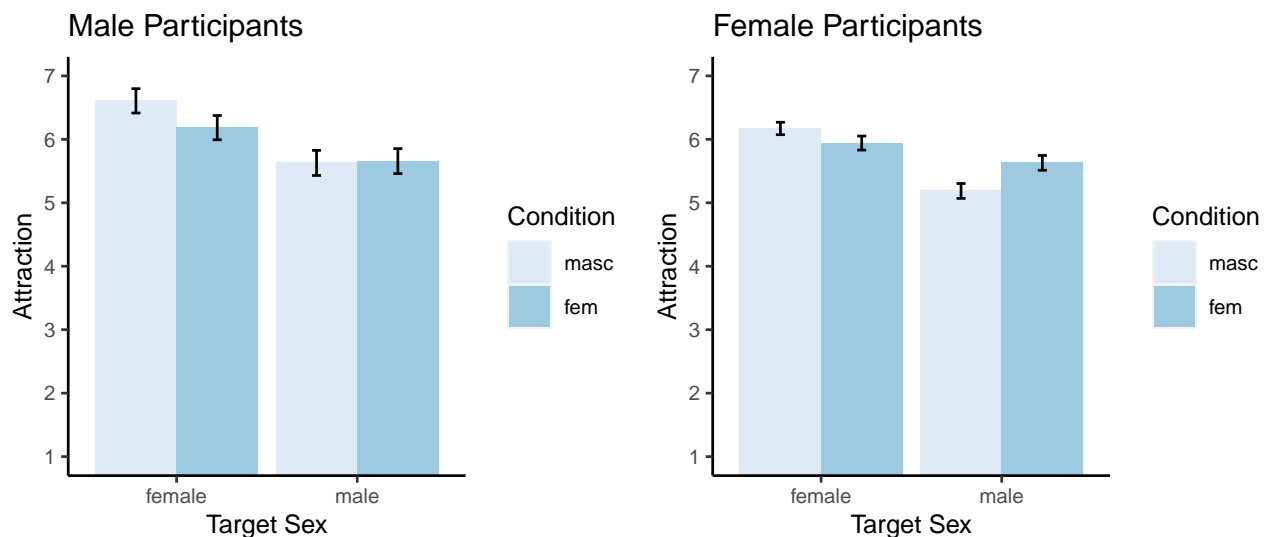

The three way interaction is not significant, $t(6666) = 1.06$, $p = .291$.

Masculinity/Femininity

Main Effect - Masc/Fem by Condition

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

# multilevel model
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 [
```

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```
## 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
```

```r
# 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
```

```r
# 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

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

# multilevel model
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
```

```r
# 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")
```

```
# multilevel model
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")
```

```
# multilevel model
model.12 <- lmer(masc.fem ~ condition * target.sex + (1|ID) + (1|trial), data=data, na.action = 'na.excl
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
```

```r
# 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
```

```r
# 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 with 95% CI
mascfem_CxTS_plot <- data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "", x="Target Sex", y="Masc/Fem", fill="Condition")

mascfem_CxTS_plot
```
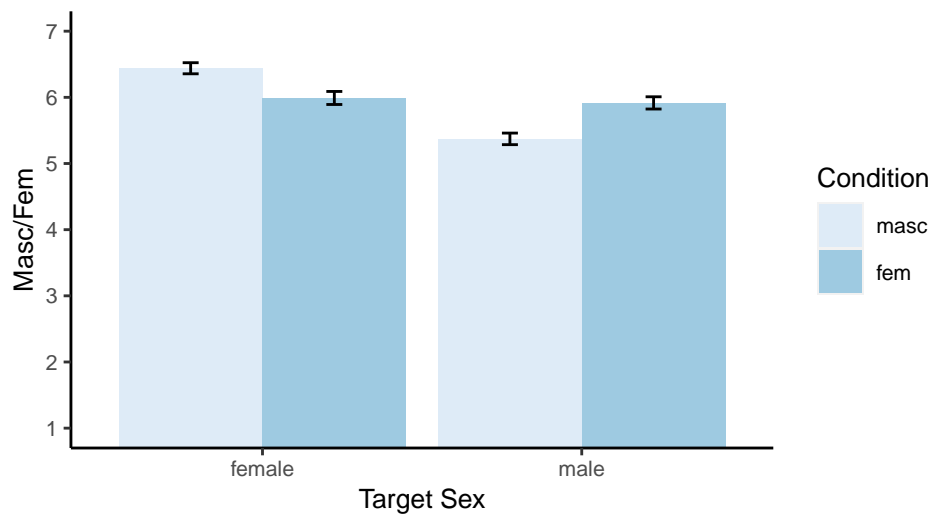

The interaction between target sex and condition is significant, $t(38)=6.13$, $p<.001$. Male test voices are rated as significantly more masculine after adaptation to feminized voices, while female test voices are rated as significantly more feminine after adaptation to masculinized voices. Furthermore,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

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

# multilevel model
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 = "nlminb")))
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
## targt.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")

# multilevel model
model.14 <- lmer(masc.fem ~ condition * Sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude',
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:Sx1  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 with 95% CI
mascfem_CxPS_plot <- data %>%
  group_by(condition, Sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=Sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "", x="Participant Sex", y="Masc/Fem", fill="Condition")
```

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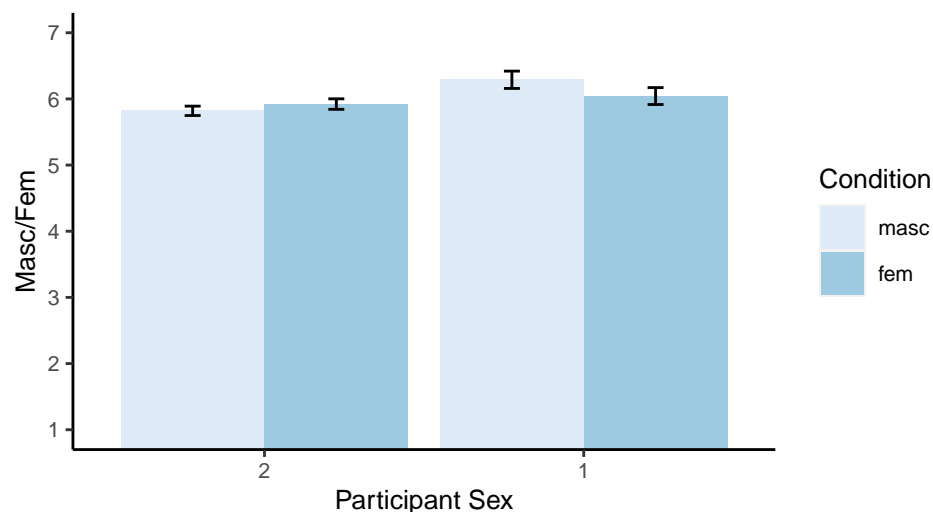
The interaction between condition and participant sex is not significant, $t(168)$ = -1.04, p = .301.

Interaction - Masc/Fem by Participant Sex and Target Sex

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

# multilevel model
model.15 <- lmer(masc.fem ~ Sex * target.sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude',
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
```

```r
# 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
```

```r
# 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.
```

```r
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
```

```r
#plot with 95% CI
mascfem_PSxTS_plot <- data %>%
  group_by(Sex, target.sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=Sex)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "", x="Target Sex", y="Masc/Fem", fill="Participant Sex")

mascfem_PSxTS_plot
```
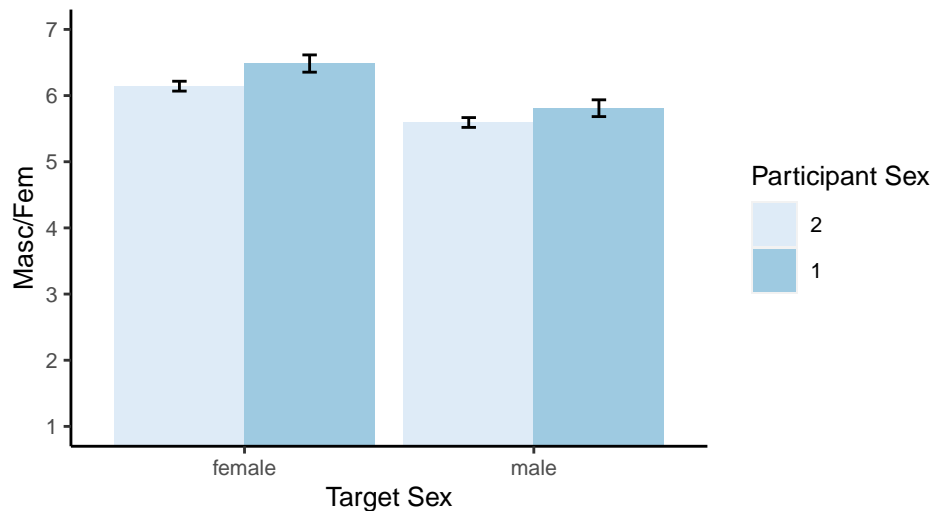
The interaction between participant sex and target sex is significant, $t(6680) = -2.24$, $p = .025$. The simple effect of participant sex when target sex is centered at female is also signficant, $t(202) = 2.26$, $p = .025$.

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")

# multilevel model
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
```

30

```
## 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
## targt.sxfml -0.239  0.135
## Sx1:trgt.sx  0.113 -0.286 -0.472
```

```r
# 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

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

# multilevel model
model.17 <- lmer(masc.fem ~ condition * target.sex * Sex + (1|ID) + (1|trial), data=data, na.action = '
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 = "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)                           5.286620    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           0.000000052 ***
## 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
## targt.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
```

```r
# 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
```

```r
# 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` a
```

```r
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
```

```r
#plot with 95% CI
male_mascfem_plot <- male_data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "Male Participants", x="Target Sex", y="Masc/Fem", fill="Condition")

female_mascfem_plot <- female_data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = uppercl), position = position_dodge(.90), width = 0.1) +
  scale_y_continuous(limits=c(1,7), breaks=seq(1,7,by=1), oob = rescale_none) +
  scale_fill_brewer(palette = 1) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        panel.background = element_blank(), axis.line = element_line(colour = "black"),
```
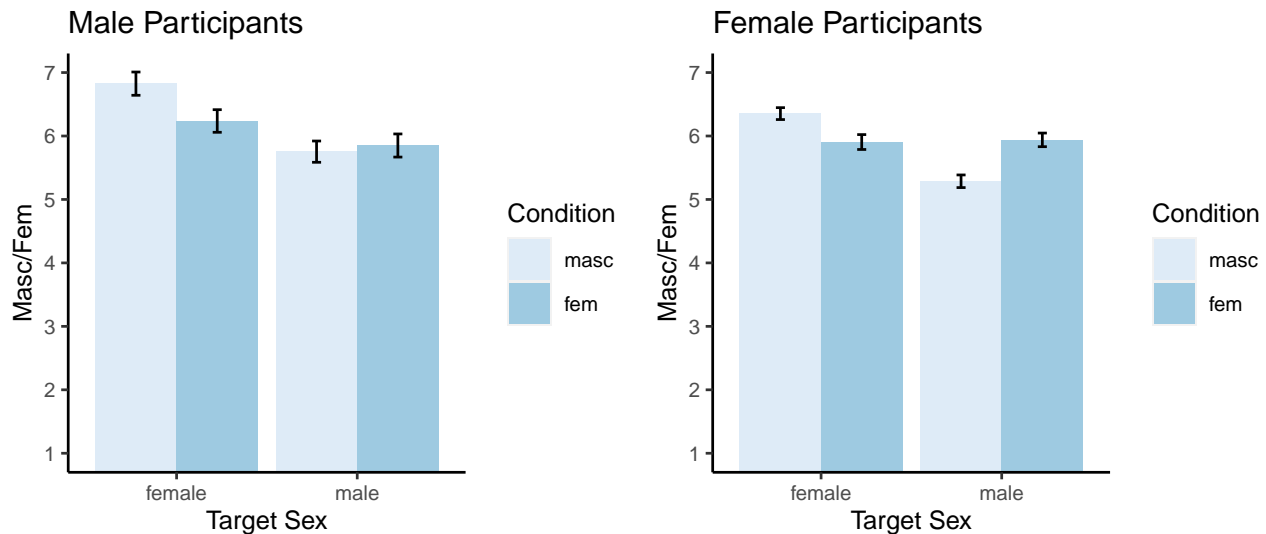
```
        text = element_text(size = 10)) + # apply custom minimal theme
  labs(title = "Female Participants", x="Target Sex", y="Masc/Fem", fill="Condition")


grid.arrange(male_mascfem_plot, female_mascfem_plot, nrow=1)
```


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")

# multilevel model
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                      0.00000000000519 ***
## 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
## targt.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
```

```r
# 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 $t(141) = -3.05$, $p < .003$.

Mediation

Multilevel Moderated Mediation - Interaction Between Condition and Target Sex on Attractiveness Mediated by Perceived Masculinity/Femininity

```
# group data into male and female targets
male_targ_data <- data %>%
    dplyr::filter(target.sex == "male")
female_targ_data <- data %>%
    dplyr::filter(target.sex == "female")
```

Female Targets

```
# detach lmerTest package (will not run otherwise)
detach("package:lmerTest", unload = TRUE)

# mediator model
med.fit.fem <- lmer(masc.fem ~ condition + (1 | ID), data = female_targ_data)

# outcome model
out.fit.fem <- lmer(attraction ~ condition + masc.fem + (1 | ID), data = female_targ_data)

# function to calculate indirect effect (ACME) and direct effect
# (ADE)
med.out.fem <- mediate(med.fit.fem, out.fit.fem, treat = "condition", mediator = "masc.fem",
    sims = 1000)
```

```
## Warning in mediate(med.fit.fem, out.fit.fem, treat = "condition", mediator =
## "masc.fem", : treatment and control values do not match factor levels; using
## masc and fem as control and treatment, respectively
```

```
summary(med.out.fem)
```

```
##
## Causal Mediation Analysis
##
## Quasi-Bayesian Confidence Intervals
##
## Mediator Groups: ID
##
## Outcome Groups: ID
##
```

```
## Output Based on Overall Averages Across Groups
##
##                 Estimate 95% CI Lower 95% CI Upper p-value
## ACME            -0.24638      -0.41848        -0.07   0.008 **
## ADE             -0.00538      -0.21509         0.20   0.920
## Total Effect    -0.25177      -0.51204         0.03   0.076 .
## Prop. Mediated   0.92366      -2.23988         3.92   0.076 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Sample Size Used: 3440
##
##
## Simulations: 1000
```

For female targets, the effect of condition on attraction ratings was fully mediated via perceived femininity. The indirect effect is -0.25 (ACME), which is significant insofar as the confidence interval does not contain zero [-0.41, -0.09].

Relationship between perceived femininity and attraction for female targets

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

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: attraction ~ masc.fem + (1 | ID) + (1 | trial)
##    Data: female_targ_data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 12353.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.8461 -0.5436  0.0664  0.5990  3.8885
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  ID       (Intercept) 0.39467  0.6282
##  trial    (Intercept) 0.09143  0.3024
##  Residual             1.91714  1.3846
## Number of obs: 3440, groups:  ID, 172; trial, 40
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  2.65382    0.11504   23.07
## masc.fem     0.55893    0.01447   38.62
##
## Correlation of Fixed Effects:
##         (Intr)
## masc.fem -0.782
```

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

```
##                    2.5 %      97.5 %
## .sig01                NA          NA
## .sig02                NA          NA
## .sigma                NA          NA
## (Intercept) 2.4283507 2.8792972
## masc.fem     0.5305578 0.5872954
```

Male Targets

```
# mediator model
med.fit.male <- lmer(masc.fem ~ condition + (1 | ID), data = male_targ_data)

# outcome model
out.fit.male <- lmer(attraction ~ condition + masc.fem + (1 | ID), data = male_targ_data)

# function to calculate indirect effect (ACME) and direct effect
# (ADE)
med.out.male <- mediate(med.fit.male, out.fit.male, treat = "condition",
    mediator = "masc.fem", sims = 1000)
```

```
## Warning in mediate(med.fit.male, out.fit.male, treat = "condition", mediator
## = "masc.fem", : treatment and control values do not match factor levels; using
## masc and fem as control and treatment, respectively
```

```
summary(med.out.male)
```

```
##
## Causal Mediation Analysis
##
## Quasi-Bayesian Confidence Intervals
##
## Mediator Groups: ID
##
## Outcome Groups: ID
##
## Output Based on Overall Averages Across Groups
##
##                Estimate 95% CI Lower 95% CI Upper p-value
## ACME            0.36043      0.14650         0.59   0.006 **
## ADE             0.00951     -0.22927         0.24   0.942
## Total Effect    0.36994      0.05458         0.68   0.022 *
## Prop. Mediated  0.96479      0.45061         3.23   0.024 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Sample Size Used: 3440
```

```
##
##
## Simulations: 1000
```

Relationship between perceived masculinity and attraction for male targets

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

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: attraction ~ masc.fem + (1 | ID) + (1 | trial)
##    Data: male_targ_data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 12727.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1968 -0.5492  0.0404  0.5922  3.9753
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  ID       (Intercept) 0.4779   0.6913
##  trial    (Intercept) 0.1618   0.4022
##  Residual             2.1208   1.4563
## Number of obs: 3440, groups:  ID, 172; trial, 40
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  1.71436    0.12320   13.92
## masc.fem     0.66224    0.01559   42.48
##
## Correlation of Fixed Effects:
##          (Intr)
## masc.fem -0.714
```

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

```
##                   2.5 %    97.5 %
## .sig01               NA        NA
## .sig02               NA        NA
## .sigma               NA        NA
## (Intercept) 1.4728993 1.9558246
## masc.fem    0.6316813 0.6927908
```

For male targets, the effect of condition on attraction ratings was fully mediated via perceived masculinity. The indirect effect is .36 (ACME), which is significant insofar as the confidence interval does not contain zero [0.14, 0.57].