

Study 4 Analysis: Perceptual Adaptation

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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 first 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

```
# 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.

```
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 # divide by number of trials since data is long form
```

```
## [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
```

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
## 6880.00000000    0.00000000    0.00000000    18.0000000    63.0000000
##           range           sum           median           mean           SE.mean
## 45.00000000 174640.00000000    23.00000000    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)

```
# 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

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
```

```
# 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")

# 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.exclude')
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 = "nlsminb"))
##
## 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 0.0000000000000151 ***
## 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()))
```

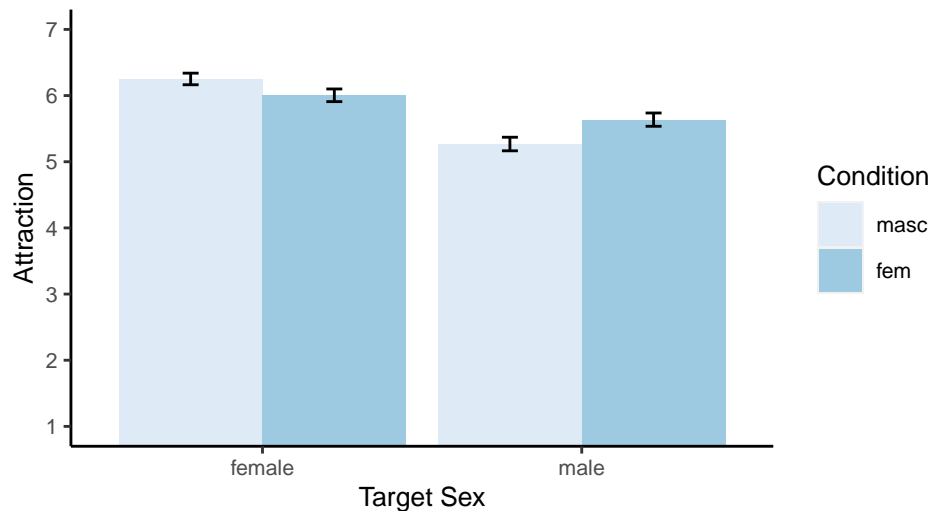
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
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

```
# simple effects: releveel so reference group = male
data$target.sex <- releveel(data$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 = "nlsminb"))
##
## 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, $t(199) = 2.06$, $p = .040$.

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 ***
```

```
## 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
```

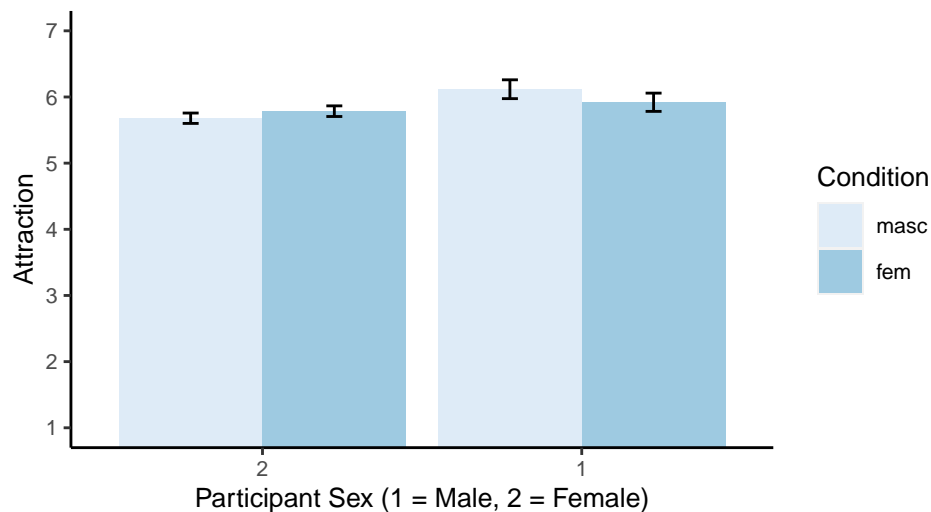
```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n     se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 masc      2      5.68  2.13  2840 0.0400
## 2 masc      1      6.12  1.83   640 0.0725
## 3 fem       2      5.79  2.06  2520 0.0411
## 4 fem       1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

```
#plot 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 = "nlsminb"))
##
## 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.

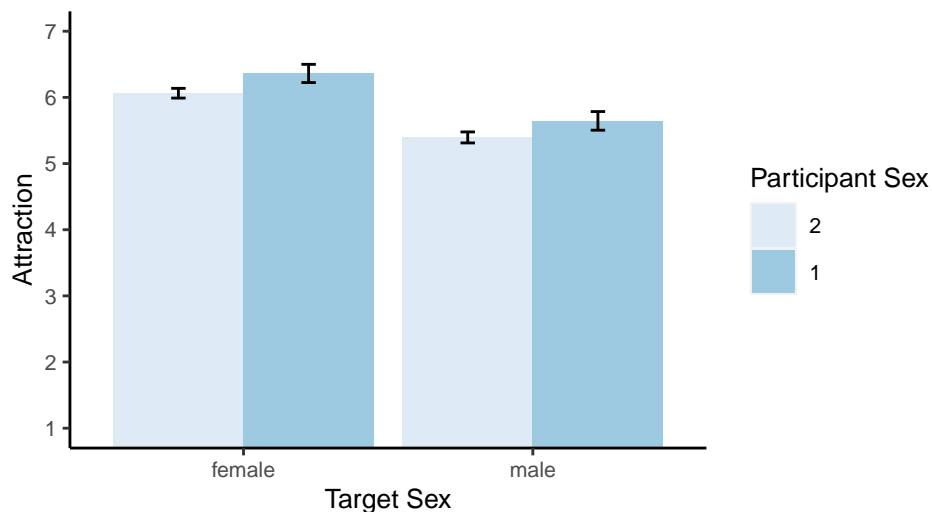
```
attraction_PSxTS
```

```
## # 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 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)

```
# 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.sxm1 -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_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
```

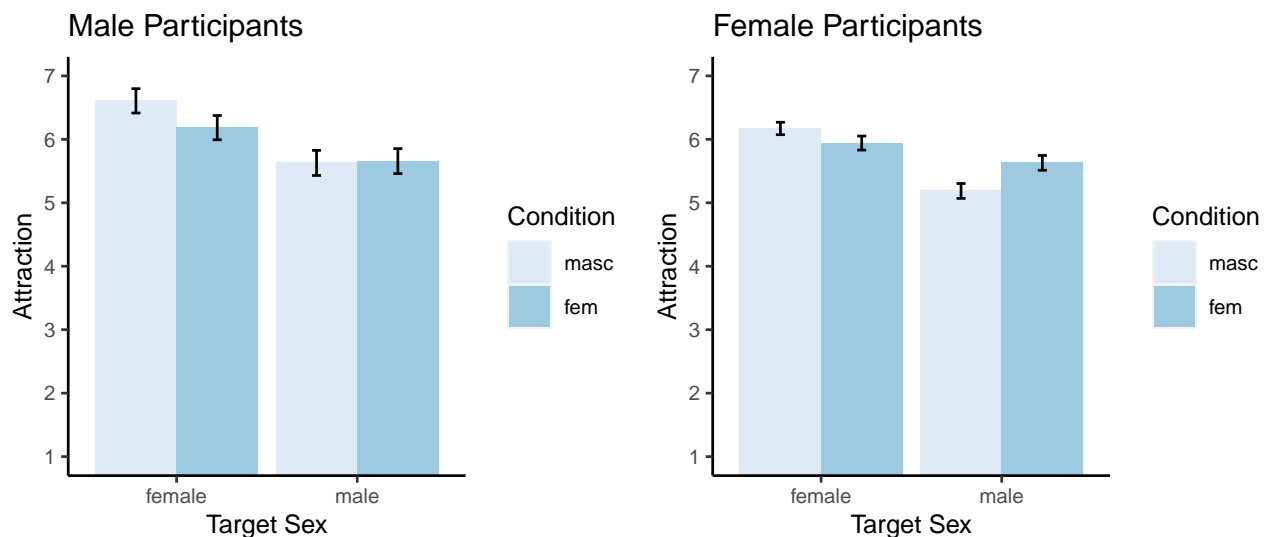
```

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 = "nlnminb")))
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")

# 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

# 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.exclude')
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()))
```

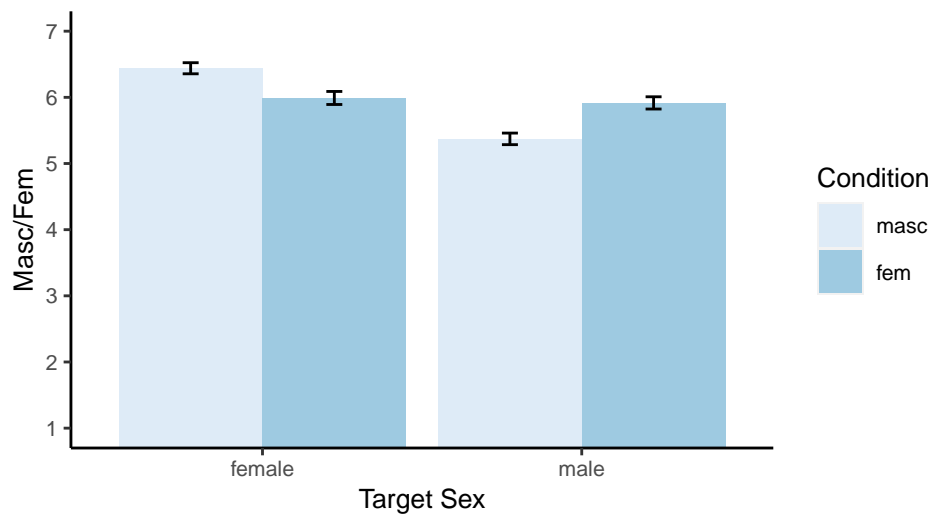
```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

```
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 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


```

# 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 = "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 = "nlsminb"))
##
## 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()))
```

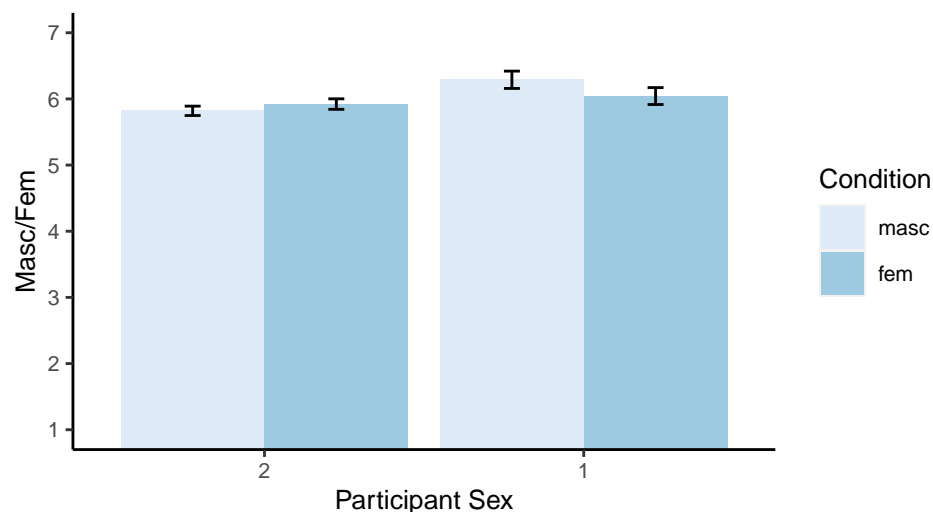
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
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

```
#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

# 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()))
```

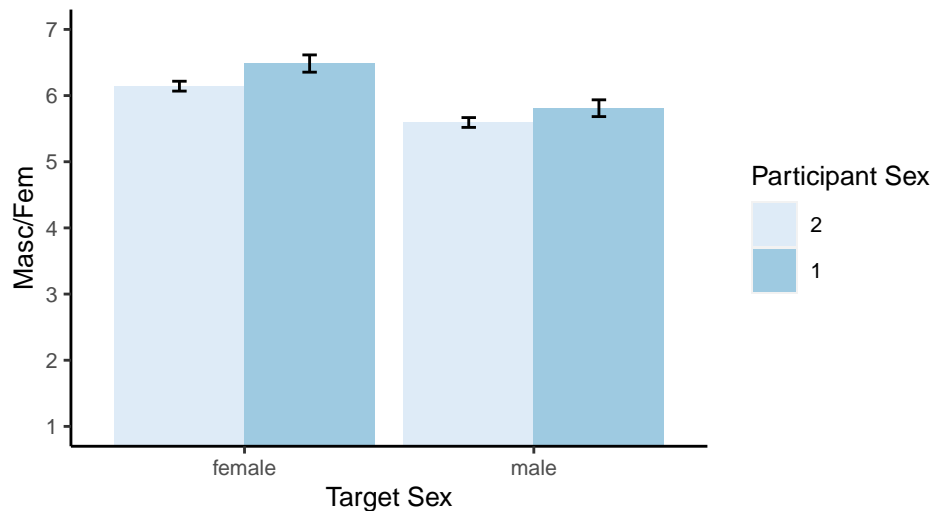
'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.

```
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 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 significant, $t(202) = 2.26$, $p = .025$.

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
```

```
## 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")
```

```
# multilevel model
```

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

```
#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")
```

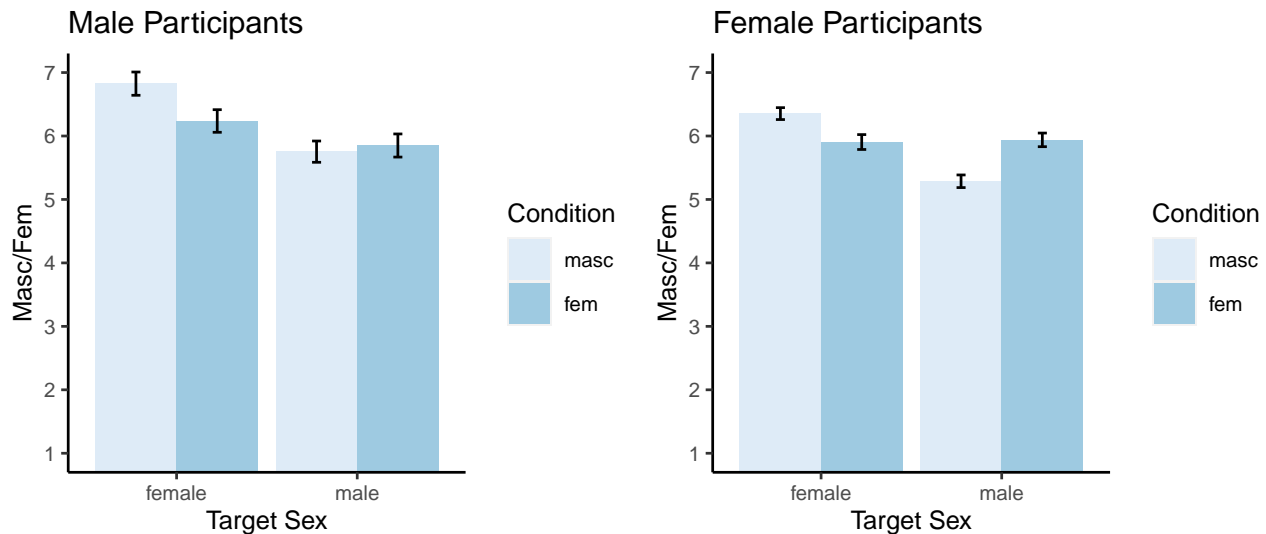
```
female_mascfem_plot <- female_data %>%
  group_by(condition, target.sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=condition)) +
  geom_bar(stat = "identity", position = "dodge", width = .90) +
  geom_errorbar(aes(ymin = lowercl, ymax = 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   0.000000000000519 ***
## 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 $t(141) = -3.05$, $p < .003$.

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            -0.2511206   -0.4145246      -0.08   0.002 **
## ADE              -0.0000528   -0.2189132       0.22   0.996
## Total Effect    -0.2511734   -0.5233010       0.02   0.086 .
## Prop. Mediated   0.9465535   -2.5833691       5.60   0.088 .
## ---
## 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 [-0.42, -0.07].

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              0.35864      0.13624      0.58 <0.0000000000000002 ***
## ADE               0.00601     -0.23690      0.24      0.984
## Total Effect      0.36465      0.04957      0.69      0.024 *
## Prop. Mediated    0.98384      0.46059      3.18      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 = "nlsminb")))
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 = "nlsminb"))
##
## 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 [0.15, 0.59].