

Study 3 Analysis: Conceptual 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 and 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 the gender-atypical or gender-typical 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 gender-atypical adaptation condition would rate test voices as more attractive than participants in the gender-typical adaptation 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("study3_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 5 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 5 is too low.

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

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

```

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

```

```
## [1] 173
```

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] 173
```

```

# 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] 163
```

The original sample size was 178. After filtering participants whose responses did not meet our requirements, the final sample size is 163.

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
## 37 126  0  0
```

The majority of the sample is female (77.30%)

Race

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

```
##
##  1  2  3  4  5  8  9
## 17 16 14 104 10  1  1
```

The majority of the sample is White (63.80%).

Age

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

```
##      nbr.val      nbr.null      nbr.na      min      max
## 6520.00000000  0.00000000  0.00000000 18.00000000 57.00000000
##      range      sum      median      mean      SE.mean
## 39.00000000 167080.00000000 23.00000000 25.62576687  0.09521884
##  CI.mean.0.95      var      std.dev      coef.var
##  0.18666016  59.11441497  7.68858992  0.30003355
```

The average age is 25.63 years old, with a range from 18 - 57.

Multilevel Analyses (NCC Design)

The following analyses are done in a stepwise fashion.

Attraction

Main Effect - Attraction by Condition (Typical/Atypical)

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

# 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: 26946.7
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.1462 -0.6213 0.0838 0.6692 3.0953
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.1352 1.0654
## trial (Intercept) 0.0968 0.3111
## Residual 3.3787 1.8381
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.8444 0.1359 187.2979 43.006 <0.0000000000000002 ***
## conditiontypical -0.3157 0.1734 161.0029 -1.821 0.0705 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.681
```

```
# 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)    5.5780564 6.11075937
## conditiontypical -0.6555239 0.02417936
```

```
# 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 atypical   5.84  2.17  3040 0.0394
## 2 typical    5.53  2.12  3480 0.0359
```

There is no difference in attraction ratings of test voices after adaptation to atypical voices ($M = 5.84$, $SD = 2.17$) relative to typical voices ($M = 5.53$, $SD = 2.12$), $t(161) = -1.82$, $p = .071$.

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: 26815.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0331 -0.6259  0.0749  0.6531  3.1985
##
## Random effects:
## Groups   Name                Variance Std.Dev.
```

```
## ID      (Intercept) 1.15438  1.0744
## trial   (Intercept) 0.09326  0.3054
## Residual      3.30751  1.8187
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)    5.94142    0.10213  193.47710   58.18 <0.0000000000000002 ***
## target.sexmale -0.53100    0.04513  6326.64547  -11.77 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.221
```

```
# 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)    5.7412564  6.1415886
## target.sexmale -0.6194587 -0.4425503
```

```
# 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    5.95  2.06  3260 0.0360
## 2 male      5.40  2.20  3260 0.0386
```

Female test voices ($M = 5.95$, $SD = 2.06$) are rated as significantly more attractive than male test voices ($M = 5.40$, $SD = 2.20$), $t(6327) = -11.77$, $p < .001$.

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: 26947.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1494 -0.6213  0.0790  0.6663  3.1050
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.1438  1.0695
## trial   (Intercept) 0.0968  0.3111
## Residual                3.3787  1.8381
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.6067     0.1103 182.4222  50.827 <0.0000000000000002 ***
## Sex1          0.3047     0.2072 160.9955   1.471      0.143
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.426
```

```
# 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)  5.3905420 5.8229501
## Sex1        -0.1014258 0.7109067
```

```
# 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      5.61  2.18  5040 0.0307
## 2 1      5.91  2.02  1480 0.0526
```

There is no significant difference in attraction ratings between male participants ($M = 5.91$, $SD = 2.02$) and female participants ($M = 5.61$, $SD = 2.18$), $t(161) = 1.47$, $p = .143$.

Interaction - Attraction by Condition (Atypical/Typical) and Target Sex (Male/Female)

```
#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: 26811.7
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.0459 -0.6239 0.0741 0.6495 3.1817
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.13693 1.066
## trial (Intercept) 0.08585 0.293
## Residual 3.30751 1.819
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 6.0092 0.1464 196.1635 41.051
## conditiontypical -0.1167 0.2017 192.9771 -0.578
## target.sexmale -0.3296 0.1137 56.4327 -2.898
## conditiontypical:target.sexmale -0.3980 0.2061 38.0639 -1.931
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditiontypical 0.56364
## target.sexmale 0.00534 **
## conditiontypical:target.sexmale 0.06100 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnt trgt.s
## cndtnttypcl -0.726
## target.sxml -0.388 0.469
## cndtntypc:. 0.357 -0.511 -0.918
```



```
# 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)                   5.7223054  6.296115626
## conditiontypical              -0.5120377  0.278674075
## target.sexmale                -0.5525296 -0.106680886
## conditiontypical:target.sexmale -0.8020000  0.006038146
```

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

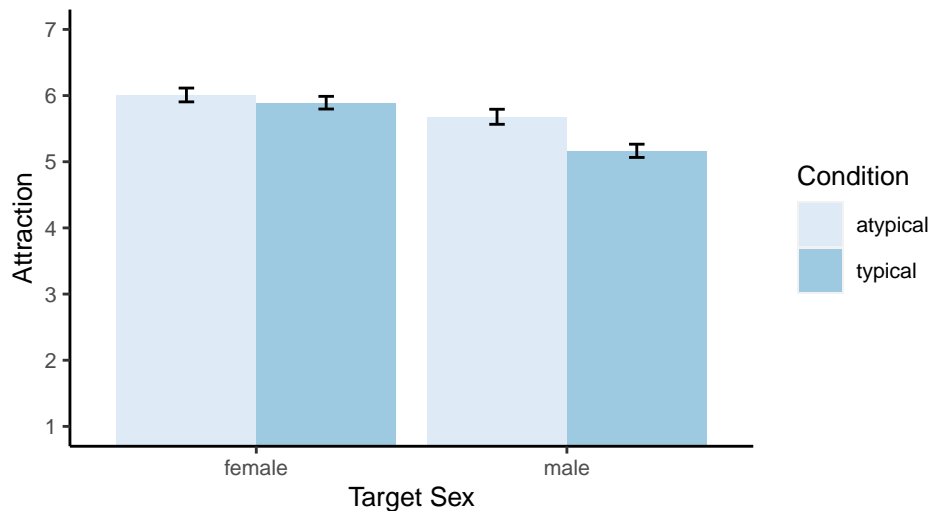
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
attraction_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 atypical  female     6.01  2.08  1520 0.0532
## 2 atypical  male      5.68  2.26  1520 0.0579
## 3 typical   female     5.89  2.04  1740 0.0489
## 4 typical   male      5.16  2.13  1740 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 not significant, $t(38) = -1.93$, $p = .061$.

Interaction - Attraction by Condition (Atypical/Typical) and Participant Sex (Male/Female)

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

# multilevel model
model.5 <- lmer(attraction ~ condition * Sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude',
summary(model.5)
```

```
## 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: 26944.3
##
## Scaled residuals:
## Min      1Q  Median      3Q      Max
## -4.1622 -0.6201  0.0796  0.6663  3.0975
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.1239  1.0601
## trial   (Intercept) 0.0968  0.3111
## Residual              3.3787  1.8381
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      5.7613    0.1459 184.1830  39.475 <0.0000000000000002
## conditiontypical -0.3142    0.1959 159.0000  -1.604      0.111
## Sex1              0.5262    0.3458 159.0000   1.522      0.130
## conditiontypical:Sex1 -0.2423    0.4329 159.0000  -0.560      0.576
```

```
##
## (Intercept)          ***
## conditiontypical
## Sex1
## conditiontypical:Sex1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) cndtnt Sex1
## condnttypcl -0.660
## Sex1        -0.374  0.279
## cndtntyp:S1  0.299 -0.452 -0.799
```

```
# 95% confidence interval
ci.5 <- confint(model.5,method="Wald", level=0.95)
ci.5
```

```
##                2.5 %      97.5 %
## .sig01          NA        NA
## .sig02          NA        NA
## .sigma          NA        NA
## (Intercept)     5.4752760 6.04738030
## conditiontypical -0.6980756 0.06977422
## Sex1            -0.1515836 1.20392737
## conditiontypical:Sex1 -1.0908165 0.60611793
```

```
# 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 atypical  2      5.76  2.18  2560 0.0432
## 2 atypical  1      6.29  2.06   480 0.0942
## 3 typical   2      5.45  2.16  2480 0.0435
## 4 typical   1      5.73  1.98  1000 0.0626
```

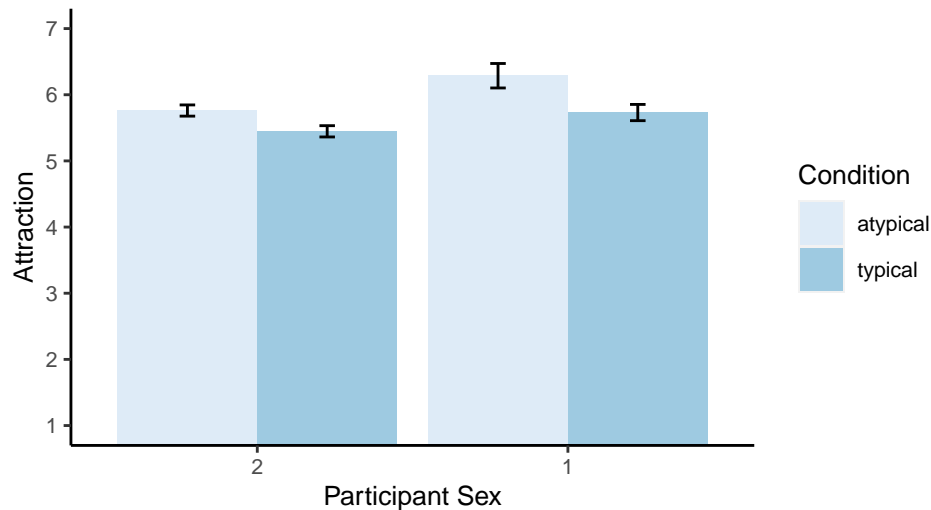
```
#plot with 95% CI
attraction_CxPS_plot <- data %>%
  group_by(condition, Sex) %>%
  phe_mean(x = attraction, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=Sex, y=value, fill=condition)) +
```

```

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", y="Attraction", fill="Condition")

attraction_CxPS_plot

```



The interaction between condition and participant sex is not significant, $t(159) = -0.56$, $p = .576$.

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

```

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

# multilevel model
model.6 <- lmer(attraction ~ Sex * target.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 ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26813.5
##
## Scaled residuals:
## Min      1Q  Median      3Q      Max
## -4.0919 -0.6235  0.0720  0.6510  3.2109
##
## Random effects:

```

```
## Groups      Name      Variance Std.Dev.
## ID          (Intercept) 1.14561  1.0703
## trial      (Intercept) 0.09475  0.3078
## Residual                    3.30572  1.8182
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.89623    0.11302  203.29792  52.171
## Sex1              0.19731    0.21422  183.83466   0.921
## target.sexmale    -0.57897    0.05123  6316.42370 -11.302
## Sex1:target.sexmale 0.21486    0.10858  6351.43658   1.979
##
##              Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## Sex1            0.3582
## target.sexmale  <0.0000000000000002 ***
## Sex1:target.sexmale 0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.430
## target.sxml -0.227  0.120
## Sx1:trgt.sx  0.107 -0.253 -0.474
```

```
# 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)      5.674723442  6.1177404
## Sex1            -0.222557721  0.6171782
## target.sexmale    -0.679371243 -0.4785723
## Sex1:target.sexmale 0.002056805  0.4276641
```

```
# 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
```

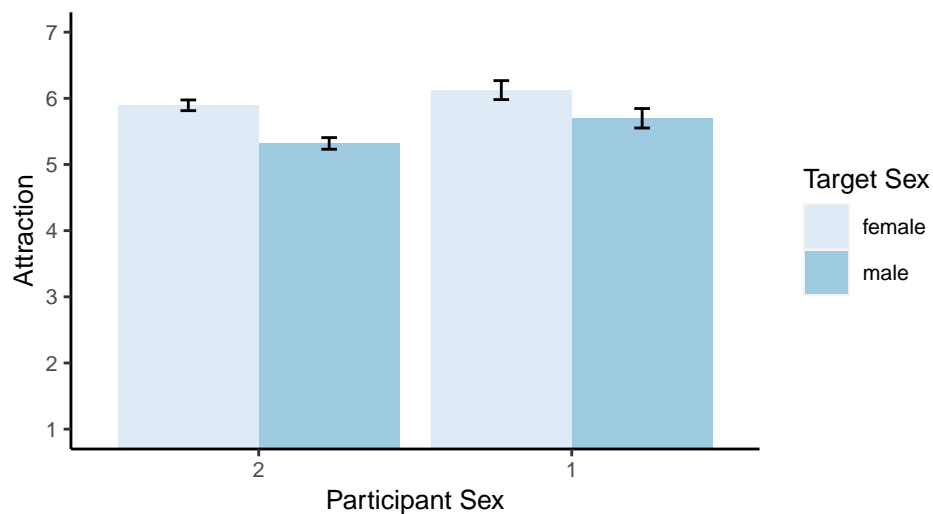
```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
```

```
##   Sex  target.sex  mean    sd     n    se
##   <fct> <fct>      <dbl> <dbl> <int> <dbl>
## 1 2    female      5.89  2.08  2520 0.0413
## 2 2    male       5.32  2.24  2520 0.0447
## 3 1    female      6.12  1.98   740 0.0729
## 4 1    male       5.70  2.04   740 0.0750
```

#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=Sex, y=value, fill=target.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="Participant Sex", y="Attraction", fill="Target Sex")

attraction_PSxTS_plot
```



The interaction between target sex and participant sex is significant, $t(6351) = 1.98$, $p = .048$. The simple effect of participant sex when target sex is centered at female is not significant, $t(184) = 0.92$, $p = .358$.

Simple Effect - Attraction by Participant Sex (Male/Female) when Target Sex (Male/Female) is Centered at Male

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

# multilevel model
model.7 <- lmer(attraction ~ Sex * target.sex + (1 | ID) + (1 | trial),
  data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlsminb")))
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: 26813.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0919 -0.6235  0.0720  0.6510  3.2109
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.14561 1.0703
## trial   (Intercept) 0.09475 0.3078
## Residual 3.30572 1.8182
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)    5.31726    0.11302 203.29792  47.048
## Sex1           0.41217    0.21422 183.83468   1.924
## target.sexfemale 0.57897    0.05123 6316.42369 11.302
## Sex1:target.sexfemale -0.21486    0.10858 6351.43657 -1.979
##
##              Pr(>|t|)
## (Intercept) <0.0000000000000002 ***
## Sex1        0.0559 .
## target.sexfemale <0.0000000000000002 ***
## Sex1:target.sexfemale 0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1        -0.430
## target.sxfml -0.227  0.120
## Sx1:trgt.sx  0.107 -0.253 -0.474
```

```
# 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)    5.095751674  5.538768617
## Sex1          -0.007697244  0.832038612
## target.sexfemale 0.478572301  0.679371243
## Sex1:target.sexfemale -0.427664110 -0.002056807
```

The simple effect of participant sex when target sex is centered at male is not significant, $t(184) = 1.92$, p

= .056.

Three Way Interaction - Attraction by Condition (Atypical/Typical), 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 = "nlsminb"))
##
## REML criterion at convergence: 26804.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0470 -0.6282  0.0670  0.6514  3.1824
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## ID       (Intercept)  1.12579   1.061
## trial    (Intercept)  0.08586   0.293
## Residual                    3.30393   1.818
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df
## (Intercept)    5.602344   0.156412 200.632743
## conditiontypical -0.576537   0.222665 201.089562
## target.sexfemale  0.317969   0.117253  63.740676
## Sex1            0.489323   0.357427 181.452164
## conditiontypical:target.sexfemale  0.524773   0.211742  42.388686
## conditiontypical:Sex1 -0.005129   0.447455 181.452164
## target.sexfemale:Sex1  0.073698   0.180818 6315.000919
## conditiontypical:target.sexfemale:Sex1 -0.474440   0.226362 6315.000919
##              t value      Pr(>|t|)
## (Intercept)   35.818 < 0.0000000000000002 ***
## conditiontypical -2.589      0.01032 *
## target.sexfemale  2.712      0.00859 **
## Sex1            1.369      0.17269
## conditiontypical:target.sexfemale  2.478      0.01726 *
## conditiontypical:Sex1 -0.011      0.99087
## target.sexfemale:Sex1  0.408      0.68360
## conditiontypical:target.sexfemale:Sex1 -2.096      0.03613 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```



```
## Correlation of Fixed Effects:
##      (Intr) cndtnt trgt.s Sex1   cndt:. cnd:S1 tr.:S1
## condnttypcl -0.702
## trgt.sxfml -0.375  0.428
## Sex1      -0.361  0.253  0.062
## cndnttypc:. 0.337 -0.475 -0.900 -0.034
## cndnttyp:S1 0.288 -0.411 -0.049 -0.799  0.055
## trgt.sxf:S1 0.091 -0.064 -0.243 -0.253  0.135  0.202
## cndtnt:.:S1 -0.073  0.104  0.195  0.202 -0.219 -0.253 -0.799
```

```
# 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)    5.29578260  5.90890490
## conditiontypical -1.01295351 -0.14012109
## target.sexfemale 0.08815775  0.54777975
## Sex1           -0.21122126  1.18986709
## conditiontypical:target.sexfemale 0.10976739  0.93977898
## conditiontypical:Sex1 -0.88212524  0.87186651
## target.sexfemale:Sex1 -0.28069907  0.42809490
## conditiontypical:target.sexfemale:Sex1 -0.91810165 -0.03077805
```

```
# 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 atypical  male       2     5.60  2.27  1280  0.0635
## 2 atypical  male       1     6.09  2.14   240  0.138
## 3 atypical  female     2     5.92  2.08  1280  0.0582
## 4 atypical  female     1     6.48  1.97   240  0.127
## 5 typical   male       2     5.03  2.18  1240  0.0618
## 6 typical   male       1     5.51  1.97   500  0.0879
## 7 typical   female     2     5.87  2.07  1240  0.0587
## 8 typical   female     1     5.95  1.97   500  0.0880
```

```

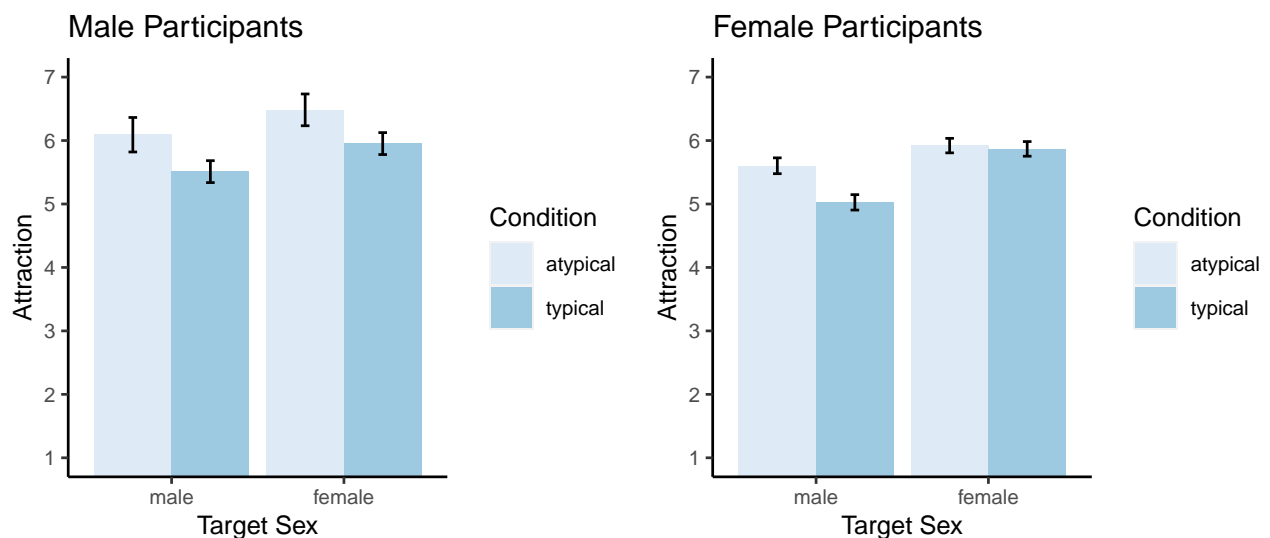
# subset means for male and female participants
male_data <- data %>% filter(Sex == "1")
female_data <- data %>% filter(Sex == "2")

#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 significant, $t(6315) = -2.10$, $p = .036$. The simple effect of target sex and condition on attraction ratings centered at female participants is significant, $t(42) = 2.48$, $p = .017$.

Simple Effect - Attraction by Condition (Atypical/Typical) and Target Sex (Male/Female) when Participant Sex (Male/Female) is centered at Male

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

# multilevel model
model.9 <- lmer(attraction ~ condition * target.sex * Sex + (1 | ID) +
  (1 | trial), data = data, na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.9)
```

```
## 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: 26804.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0470 -0.6282  0.0670  0.6514  3.1824
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  ID       (Intercept)  1.12579   1.061
##  trial    (Intercept)  0.08586   0.293
##  Residual                    3.30393   1.818
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df
## (Intercept)    6.091667   0.334478 193.975109
## conditiontypical -0.581667   0.409643 197.370289
## target.sexfemale  0.391667   0.190049 425.378827
## Sex2            -0.489323   0.357427 181.452142
## conditiontypical:target.sexfemale  0.050333   0.274029 118.488173
## conditiontypical:Sex2    0.005129   0.447455 181.452142
## target.sexfemale:Sex2   -0.073698   0.180818 6315.000920
## conditiontypical:target.sexfemale:Sex2  0.474440   0.226362 6315.000931
##              t value      Pr(>|t|)
## (Intercept)    18.212 <0.0000000000000002 ***
## conditiontypical   -1.420      0.1572
## target.sexfemale    2.061      0.0399 *
## Sex2              -1.369      0.1727
## conditiontypical:target.sexfemale    0.184      0.8546
## conditiontypical:Sex2    0.011      0.9909
## target.sexfemale:Sex2   -0.408      0.6836
## conditiontypical:target.sexfemale:Sex2  2.096      0.0361 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation of Fixed Effects:
##          (Intr) cndtnt trgt.s Sex2   cndt:. cnd:S2 tr.:S2
## condntypcl -0.817
## trgt.sxfml -0.284  0.287
## Sex2       -0.900  0.735  0.203
## cndntypc:.  0.244 -0.334 -0.858 -0.141
## cndntyp:S2  0.719 -0.869 -0.162 -0.799  0.166
## trgt.sxf:S2  0.228 -0.186 -0.801 -0.253  0.556  0.202
## cndtnt:..S2 -0.182  0.220  0.640  0.202 -0.657 -0.253 -0.799
```

```
# 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) 5.43610249 6.7472308
## conditiontypical -1.38455309 0.2212198
## target.sexfemale 0.01917769 0.7641556
## Sex2          -1.18986712 0.2112213
## conditiontypical:target.sexfemale -0.48675292 0.5874196
## conditiontypical:Sex2 -0.87186654 0.8821253
## target.sexfemale:Sex2 -0.42809490 0.2806991
## conditiontypical:target.sexfemale:Sex2 0.03077805 0.9181017
```

The simple effect of target sex and condition on attraction ratings centered at male participants is not significant, $t(118) = 0.18$, $p = .855$.

Masculinity/Femininity

Main Effect - Masc/Fem by Condition

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

# multilevel model
model.10 <- 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.10)

## 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: 26088.5
##
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7520 -0.6260  0.0608  0.6747  2.9392
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.83273  0.9125
##   trial    (Intercept) 0.08451  0.2907
##   Residual                2.97443  1.7247
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      6.1197     0.1185 187.2284  51.633 < 0.0000000000000002 ***
## conditiontypical -0.5539     0.1495 160.9991  -3.704    0.000291 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## condntntypcl -0.673
```

```
# 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)    5.8874327  6.3520409
## conditiontypical -0.8470229 -0.2608416
```

```
# 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 atypical  6.12  2.04  3040 0.0371
## 2 typical   5.57  1.90  3480 0.0322
```

Test voices are rated as significantly more masculine/feminine after adaptation to atypical voices ($M = 6.12$, $SD = 2.04$) relative to typical voices ($M = 5.57$, $SD = 1.90$), $t(161) = -3.70$, $p < .001$.

Main Effect - Masc/Fem by Target Sex

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

```

# multilevel model
model.11 <- 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 = "nlsminb")))
summary(model.11)

## 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 = "nlsminb"))
##
## REML criterion at convergence: 26012.1
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.6453 -0.6255 0.0612 0.6691 2.8794
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.90501 0.9513
## trial (Intercept) 0.08175 0.2859
## Residual 2.93233 1.7124
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 6.02885 0.09218 189.07596 65.403 <0.0000000000000002 ***
## target.sexmale -0.40954 0.04249 6326.72832 -9.638 <0.0000000000000002 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## target.sxml -0.230

# 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) 5.8481814 6.209520
## target.sexmale -0.4928284 -0.326256

# 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    6.03  1.98  3260 0.0347
## 2 male      5.61  1.98  3260 0.0346
```

Female test voices ($M = 6.03$, $SD = 1.98$) are rated as significantly more feminine than male test voices are rated masculine ($M = 5.61$, $SD = 1.98$), $t(6327) = -9.64$, $p < .001$.

Main Effect - Masc/Fem by Participant Sex

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

```
# multilevel model
model.12 <- 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.12)
```

```
## 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: 26100.8
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -3.7487 -0.6292  0.0621  0.6751  2.9284
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.90664 0.9522
## trial   (Intercept) 0.08451 0.2907
## Residual                2.97443 1.7247
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.79266    0.09949 179.53046  58.223 <0.0000000000000002 ***
## Sex1          0.13842    0.18520 160.99998   0.747      0.456
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.423
```

```
# 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) 5.5976611 5.9876564
## Sex1       -0.2245635 0.5014082
```

```
# 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      5.79  2.02  5040 0.0285
## 2 1      5.93  1.87  1480 0.0487
```

There is no significant difference in masc/fem ratings between male participants ($M = 5.93$, $SD = 1.87$) and female participants ($M = 5.79$, $SD = 2.02$), $t(161) = 0.75$, $p = .456$.

Interaction - Masc/Fem by Condition and Target Sex

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

# multilevel model
model.13 <- lmer(masc.fem ~ condition * target.sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude')
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: 25998.1
##
## Scaled residuals:
##    Min      1Q  Median      3Q     Max
## -3.6648 -0.6252  0.0655  0.6728  2.8969
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.83378 0.9131
## trial (Intercept) 0.07395 0.2719
## Residual 2.93233 1.7124
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
```



```
## (Intercept)                6.2237      0.1288 191.1829 48.309
## conditiontypical           -0.3547      0.1777 186.9102 -1.997
## target.sexmale             -0.2079      0.1061  56.9134 -1.960
## conditiontypical:target.sexmale -0.3984      0.1919  38.0680 -2.077
##                               Pr(>|t|)
## (Intercept)                <0.0000000000000002 ***
## conditiontypical            0.0473 *
## target.sexmale              0.0549 .
## conditiontypical:target.sexmale 0.0446 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) cndtnt trgt.s
## condnttypcl -0.725
## target.sxml -0.412  0.495
## cndnttypc:.  0.377 -0.540 -0.916
```

```
# 95% confidence interval
ci.13 <- confint(model.13,method="Wald", level=0.95)
ci.13
```

```
##                               2.5 %      97.5 %
## .sig01                       NA        NA
## .sig02                       NA        NA
## .sigma                       NA        NA
## (Intercept)                  5.9711812 6.47618717483
## conditiontypical             -0.7029283 -0.00650906796
## target.sexmale               -0.4158070 0.00001750019
## conditiontypical:target.sexmale -0.7744494 -0.02240483917
```

```
# 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
```

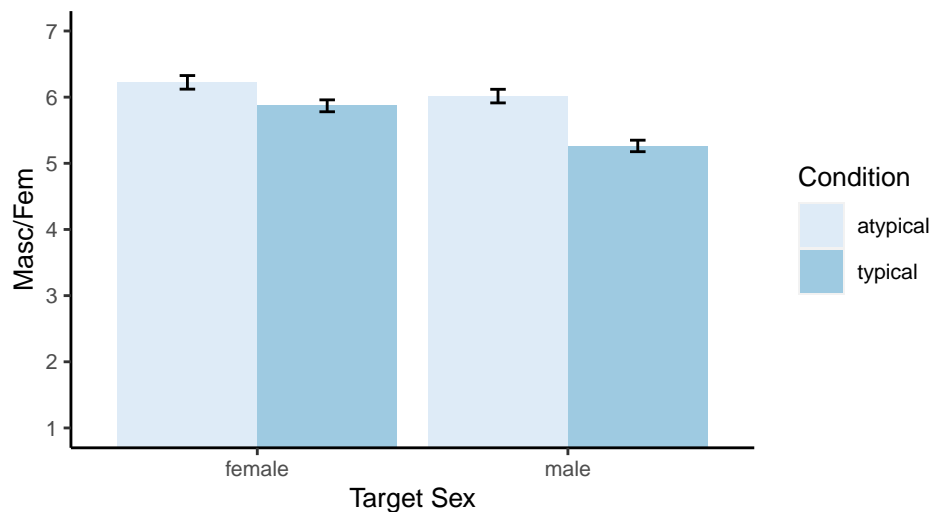
```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 atypical  female      6.22  2.04 1520 0.0523
## 2 atypical  male       6.02  2.04 1520 0.0524
## 3 typical   female      5.87  1.91 1740 0.0457
## 4 typical   male       5.26  1.85 1740 0.0443
```

```

#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 condition and target sex is significant, $t(38) = -2.08$, $p = .045$. The simple effect of condition when target sex is centered at female is significant, $t(187) = -2.00$, $p = .047$.

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.14 <- 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.14)

## 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: 25998.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6648 -0.6252  0.0655   0.6728  2.8969
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##    ID      (Intercept) 0.83378  0.9131
##   trial    (Intercept) 0.07395  0.2719
##   Residual                2.93233  1.7124
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##                                Estimate Std. Error      df t value
## (Intercept)                   6.0158      0.1288 191.1829  46.695
## conditiontypical              -0.7531      0.1777 186.9102  -4.239
## target.sexfemale               0.2079      0.1061  56.9134   1.960
## conditiontypical:target.sexfemale  0.3984      0.1919  38.0680   2.077
##                                Pr(>|t|)
## (Intercept)                   < 0.0000000000000002 ***
## conditiontypical               0.0000352 ***
## target.sexfemale               0.0549 .
## conditiontypical:target.sexfemale  0.0446 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnt trgt.s
## condnttypcl -0.725
## targt.sxfml -0.412  0.495
## cndnttypc:.  0.377 -0.540 -0.916
```

```
# 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)                   5.76328650926  6.2682924
## conditiontypical              -1.10135542099 -0.4049362
## target.sexfemale              -0.00001749974  0.4158070
## conditiontypical:target.sexfemale  0.02240484017  0.7744494
```

The simple effect of condition when target sex is centered at male is significant, $t(187) = -4.24$, $p < .001$.

Interaction - Masc/Fem by Condition and Participant Sex

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

```
# multilevel model
```

```
model.15 <- lmer(masc.fem ~ condition * 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 ~ condition * Sex + (1 | ID) + (1 | trial)  
## Data: data  
## Control:  
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))  
##  
## REML criterion at convergence: 26088  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -3.7681 -0.6260  0.0603  0.6759  2.9338  
##  
## Random effects:  
## Groups   Name      Variance Std.Dev.  
## ID       (Intercept) 0.8310   0.9116  
## trial    (Intercept) 0.0845   0.2907  
## Residual                2.9744   1.7247  
## Number of obs: 6520, groups: ID, 163; trial, 40  
##  
## Fixed effects:  
##              Estimate Std. Error    df t value      Pr(>|t|)  
## (Intercept)      6.0559     0.1275 185.1370  47.492 < 0.0000000000000002  
## conditiontypical -0.5349     0.1696 158.9949  -3.155     0.00192  
## Sex1              0.4046     0.2993 158.9949   1.352     0.17844  
## conditiontypical:Sex1 -0.2485     0.3747 158.9949  -0.663     0.50814  
##  
## (Intercept)      ***  
## conditiontypical  **  
## Sex1  
## conditiontypical:Sex1  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Correlation of Fixed Effects:  
##              (Intr) cndtnt Sex1  
## condntntypcl -0.654  
## Sex1          -0.371  0.279  
## cndntntyp:S1  0.296 -0.452 -0.799
```

```
# 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)    5.8059401  6.3057786
```

```
## conditiontypical      -0.8672188 -0.2025645
## Sex1                   -0.1821109  0.9912255
## conditiontypical:Sex1 -0.9829621  0.4859120
```

```
# 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()))
```

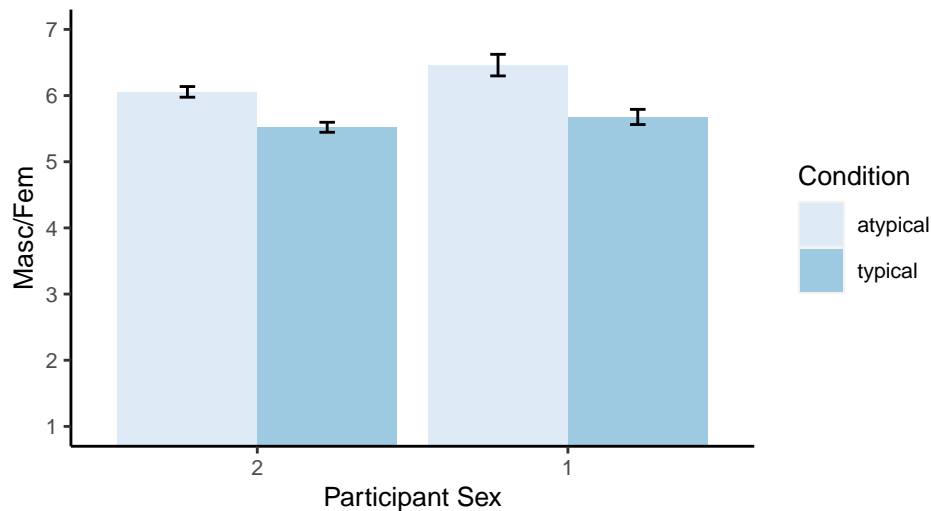
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
mascfem_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      6.06  2.08  2560 0.0411
## 2 atypical  1      6.46  1.82   480 0.0830
## 3 typical   2      5.52  1.92  2480 0.0386
## 4 typical   1      5.68  1.85  1000 0.0584
```

```
#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, $t(159) = -0.66$, $p = .508$.

Interaction - Masc/Fem by Participant Sex and Target Sex

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

# multilevel model
model.16 <- lmer(masc.fem ~ Sex * target.sex + (1|ID) + (1|trial), data=data, na.action = 'na.exclude',
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: 26011.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5979 -0.6229  0.0637  0.6705  2.9219
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.90771 0.9527
## trial   (Intercept) 0.08037 0.2835
## Residual                2.93093 1.7120
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value
## (Intercept)    5.97302    0.10187 202.52490  58.637
## Sex1           0.24773    0.19212 186.43752   1.289
## target.sexmale -0.36073    0.04823 6316.44169 -7.479
## Sex1:target.sexmale -0.21861    0.10223 6352.01584 -2.138
```

```
##                                Pr(>|t|)
## (Intercept)                  < 0.0000000000000002 ***
## Sex1                          0.1988
## target.sexmale                0.00000000000000852 ***
## Sex1:target.sexmale          0.0325 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) Sex1  trgt.s
## Sex1      -0.428
## target.sxml -0.237  0.126
## Sx1:trgt.sx  0.112 -0.266 -0.474
```

```
# 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)     5.7733724  6.17267682
## Sex1            -0.1288269  0.62428208
## target.sexmale  -0.4552686 -0.26619495
## Sex1:target.sexmale -0.4189722 -0.01824884
```

```
# 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    5.97  2.02  2520 0.0403
## 2 2    male      5.61  2.00  2520 0.0399
## 3 1    female    6.25  1.81   740 0.0666
## 4 1    male      5.61  1.88   740 0.0692
```

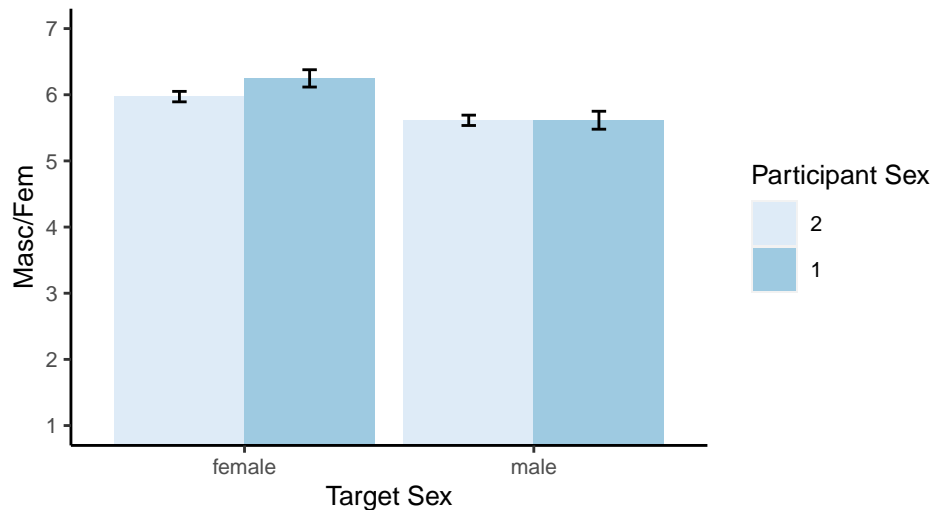
```
#plot with 95% CI
mascfem_PSxTS_plot <- data %>%
  group_by(target.sex, Sex) %>%
  phe_mean(x = masc.fem, type = "full", confidence = 0.95) %>%
  ggplot(aes(x=target.sex, y=value, fill=Sex)) +
```

```

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 target sex and participant sex is significant, $t(6352) = 2.14$, $p = .033$. The simple effect of participant sex when target sex is centered at female is not significant, $t(186) = 1.29$, $p = .199$.

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

```

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

# multilevel model
model.17 <- 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.17)

```

```

## 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: 26011.2
##
## Scaled residuals:
## Min      1Q  Median      3Q      Max

```



```
## -3.5979 -0.6229 0.0637 0.6705 2.9219
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.90771 0.9527
## trial (Intercept) 0.08037 0.2835
## Residual 2.93093 1.7120
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 5.61229 0.10187 202.52491 55.095
## Sex1 0.02912 0.19212 186.43753 0.152
## target.sexfemale 0.36073 0.04823 6316.44169 7.479
## Sex1:target.sexfemale 0.21861 0.10223 6352.01584 2.138
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## Sex1 0.8797
## target.sexfemale 0.00000000000000852 ***
## Sex1:target.sexfemale 0.0325 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Sex1 trgt.s
## Sex1 -0.428
## target.sxfml -0.237 0.126
## Sx1:trgt.sx 0.112 -0.266 -0.474
```

```
# 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) 5.41264064 5.8119450
## Sex1 -0.34743737 0.4056716
## target.sexfemale 0.26619495 0.4552686
## Sex1:target.sexfemale 0.01824885 0.4189722
```

The simple effect of participant sex when target sex is centered at male is not significant, $t(186) = 0.15$, $p = .880$.

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.18 <- lmer(masc.fem ~ condition * target.sex * Sex + (1|ID) + (1|trial), data=data, na.action = 'na.omit')
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: 25989.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6216 -0.6230  0.0622  0.6696  2.8925
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.83218  0.9122
## trial   (Intercept) 0.07397  0.2720
## Residual                2.92789  1.7111
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      5.99766    0.13780 198.69626  43.524
## conditiontypical -0.78072    0.19614 199.39362  -3.980
## target.sexfemale  0.11641    0.10942  64.40527   1.064
## Sex1              0.11484    0.31119 185.71769   0.369
## conditiontypical:target.sexfemale 0.49166    0.19720  42.48978   2.493
## conditiontypical:Sex1  0.04422    0.38957 185.71769   0.114
## target.sexfemale:Sex1  0.57943    0.17022 6315.00017   3.404
## conditiontypical:target.sexfemale:Sex1 -0.58549    0.21309 6315.00018  -2.748
##
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditiontypical 0.0000963 ***
## target.sexfemale 0.291357
## Sex1 0.712511
## conditiontypical:target.sexfemale 0.016635 *
## conditiontypical:Sex1 0.909747
## target.sexfemale:Sex1 0.000668 ***
## conditiontypical:target.sexfemale:Sex1 0.006020 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnt trgt.s Sex1  cndt:. cnd:S1 tr.:S1
## condntypcl -0.703
## trgt.sxfml -0.397  0.451
## Sex1 -0.357  0.251  0.067
## cndntypc:.  0.356 -0.503 -0.898 -0.037
## cndntyp:S1  0.285 -0.407 -0.054 -0.799  0.061
## trgt.sxf:S1  0.098 -0.069 -0.246 -0.273  0.136  0.218
## cndtnt:.:S1 -0.078  0.111  0.196  0.218 -0.221 -0.273 -0.799

# 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)        5.72757346  6.2677390
## conditiontypical   -1.16514781 -0.3962937
## target.sexfemale   -0.09804725  0.3308597
## Sex1                -0.49507282  0.7247603
## conditiontypical:target.sexfemale  0.10516103  0.8781555
## conditiontypical:Sex1 -0.71932040  0.8077619
## target.sexfemale:Sex1  0.24580753  0.9130466
## conditiontypical:target.sexfemale:Sex1 -1.00314260 -0.1678406
```

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

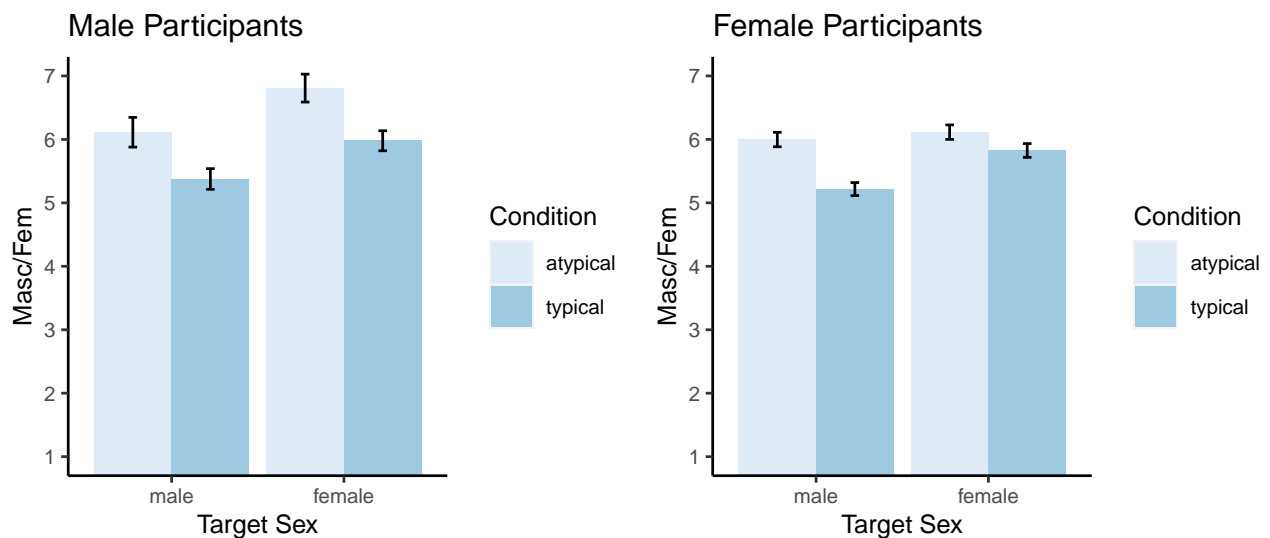
```
## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex   mean    sd     n    se
##   <fct>      <fct>   <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  male       2     6.00  2.08  1280 0.0581
## 2 atypical  male       1     6.11  1.84   240 0.119
## 3 atypical  female     2     6.11  2.08  1280 0.0580
## 4 atypical  female     1     6.81  1.73   240 0.112
## 5 typical   male       2     5.22  1.84  1240 0.0524
## 6 typical   male       1     5.38  1.86   500 0.0830
## 7 typical   female     2     5.82  1.95  1240 0.0554
## 8 typical   female     1     5.98  1.79   500 0.0801
```

#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, $t(6315) = -2.75$, $p = .006$. The simple effect of target sex and condition on masc/fem ratings centered at female participants is significant $t(42) = 2.49$, $p = .017$.

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.19 <- 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 = "nlmminb")))
summary(model.19)

## 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: 25989.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6216 -0.6230  0.0622  0.6696  2.8925
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept) 0.83218  0.9122
##   trial    (Intercept) 0.07397  0.2720
##   Residual                2.92789  1.7111
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##                                     Estimate Std. Error      df t value
## (Intercept)                       6.11250    0.29197  199.85181  20.935
## conditiontypical                   -0.73650    0.35789  203.42424  -2.058
## target.sexfemale                    0.69583    0.17832  438.58942   3.902
## Sex2                               -0.11484    0.31119  185.71769  -0.369
## conditiontypical:target.sexfemale  -0.09383    0.25632  120.84054  -0.366
## conditiontypical:Sex2              -0.04422    0.38957  185.71769  -0.114
## target.sexfemale:Sex2              -0.57943    0.17022  6315.00015  -3.404
## conditiontypical:target.sexfemale:Sex2  0.58549    0.21309  6315.00016   2.748
##                                     Pr(>|t|)
## (Intercept)                       < 0.0000000000000002 ***
## conditiontypical                   0.040877 *
## target.sexfemale                   0.000110 ***
## Sex2                               0.712511
## conditiontypical:target.sexfemale  0.714946
## conditiontypical:Sex2              0.909747
## target.sexfemale:Sex2              0.000668 ***
## conditiontypical:target.sexfemale:Sex2 0.006020 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnt trgt.s Sex2   cndt:. cnd:S2 tr.:S2
## condntypcl -0.816
## trgt.sxfml -0.305  0.307
## Sex2       -0.898  0.732  0.220
## cndntypc:.  0.262 -0.358 -0.858 -0.153
## cndntyp:S2  0.717 -0.866 -0.176 -0.799  0.181
## trgt.sxf:S2 0.245 -0.200 -0.804 -0.273  0.559  0.218
## cndtnt:.:S2 -0.196  0.237  0.642  0.218 -0.661 -0.273 -0.799

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

##                                     2.5 %      97.5 %
## .sig01                             NA         NA

```

## .sig02	NA	NA
## .sigma	NA	NA
## (Intercept)	5.5402502	6.68474978
## conditiontypical	-1.4379582	-0.03504184
## target.sexfemale	0.3463418	1.04532483
## Sex2	-0.7247603	0.49507282
## conditiontypical:target.sexfemale	-0.5962103	0.40854367
## conditiontypical:Sex2	-0.8077619	0.71932040
## target.sexfemale:Sex2	-0.9130466	-0.24580753
## conditiontypical:target.sexfemale:Sex2	0.1678406	1.00314260

The simple effect of target sex and condition on masc/fem ratings centered at male participants is not significant $t(121) = -0.37, p = .715$.

Since not significant, did not run mediation models