

Study 3: Mixed Atypical-Typical Analysis

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

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

Adapting stimuli. Adaptors included both masculinized and feminized exemplars that would be gender-typical 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_0 , a well-established sexually dimorphic aspect of voice, using PSOLA (Pitch Synchronous Overlap Add) resynthesis. For masculinized versions, F_0 values were lowered to 90% of baseline. For feminized versions, F_0 was increased to 175% of baseline. Female adaptors were generated from recordings of 5 young adult women producing the same sentence as test stimuli. For masculinized versions, F_0 values were lowered to 70% of baseline. For feminized versions, F_0 was increased to 140% of baseline.

Procedure. We recruited U.S. resident from Prolific. After providing consent, participants were randomly assigned to either 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, masculinity/femininity, likability, friendliness, and typicality (1 = *Not at all* to 9 = *Extremely*). To maintain attention, participants also completed a secondary task rating whether the pitch of each adaptor was higher, lower, or identical to the previous adaptor. In total, participants completed 40 trials in pseudo-randomized order, with each adaptor presented four times.

Hypotheses. Variability in vocal tract length and laryngeal cavity size create large differences in fundamental frequency for male and female voices (Hillenbrand et al., 1995). Perceivers evaluate men and women with regard to these differences, rating men as more attractive when their voices have low fundamental frequency but women as more attractive when their voices have high fundamental frequency (Puts, 2005; Puts, Barndt, Welling, Dawood, & Burriess, 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("/Users/kelse/Documents/UCLA/Projects/Auditory Aftereffects/Analysis/Prolific/Mixed/Atypical-Typical/LoadData.csv",  
  header = TRUE)
```

Factor

```

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

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

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

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

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

```

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

```
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

```

```
## [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
```

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%), followed by male (23%).

Race

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

```
##
##  1  2  3  4  5  6  7
## 17 16 14 104 10  1  1
```

The majority of the sample is White (64%), followed by Asian (10%), Black (10%), Latino (9%), and Biracial/Other (6%).

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 26 years old, with a range from 18 - 57.

Politics

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

```
##
##  1  2  3  4  5  6
##  4 15 32 60 47  5
```

The majority of the sample is moderate to liberal.

Sexual Orientation

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

```
##
##  1  2  3  4  5  6
## 93  9 48  5  1  7
```

The majority of the sample is heterosexual (57%), followed by bisexual (29%) and gay (6%).

Education

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

```
##
##  1  2  3  4  5  6  7  8
##  1 19 56  9 48  6 18  6
```

Most participants have obtained a bachelor's degree.

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")

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

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

```
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 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")

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 = "nloptn"))
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 = "nloptn"))
##
## 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")

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")

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 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
## condnttypcl -0.726
## target.sxml -0.388  0.469
## cndnttypc:.  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()))
```

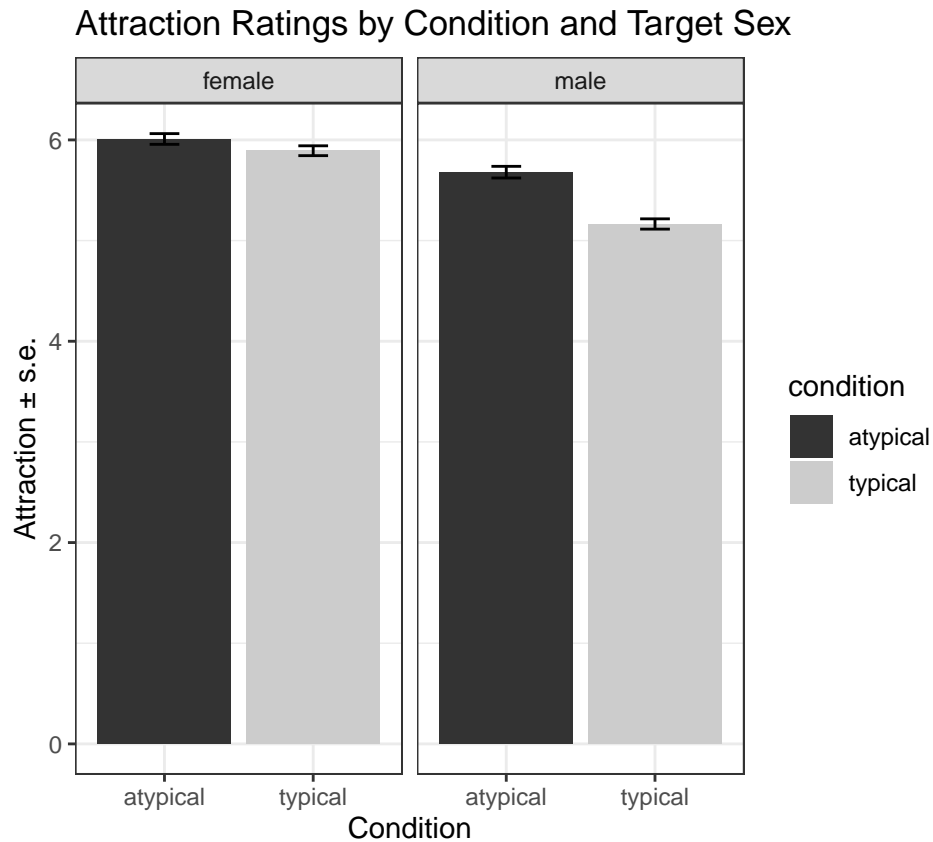
```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

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

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



The interaction between target sex and condition is 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")

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

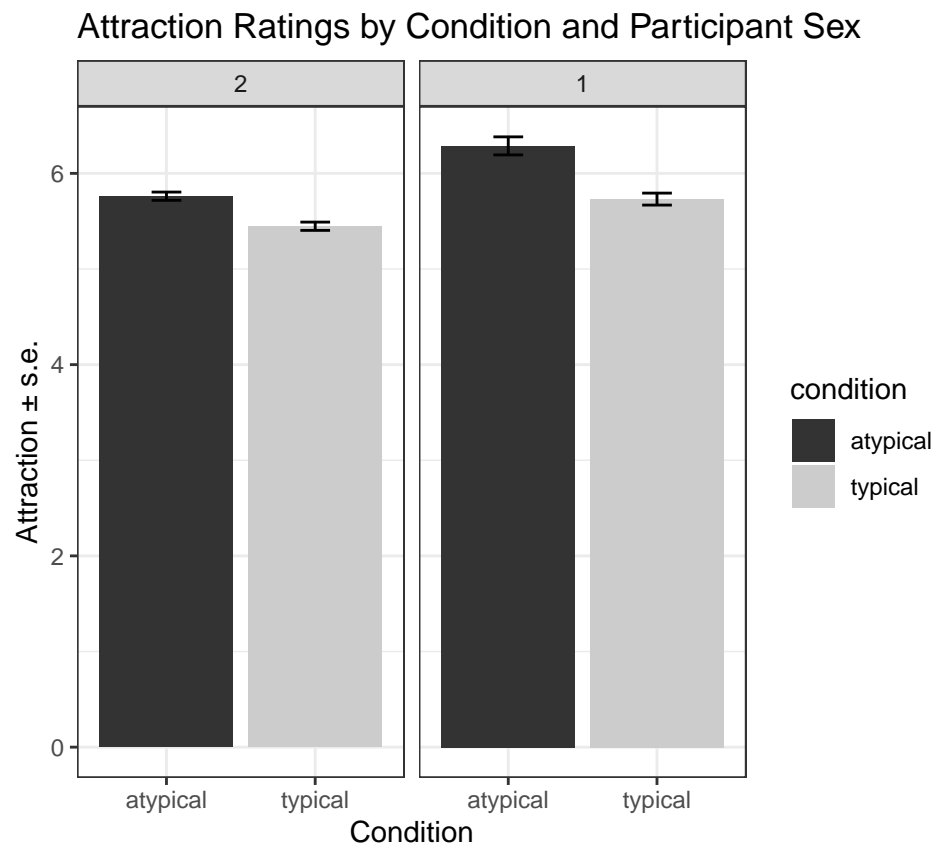
```
attraction_CxPS
```

```
## # 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
```

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

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



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

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")

model.6 <- 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.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 = "nlsminb"))
##
## 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.

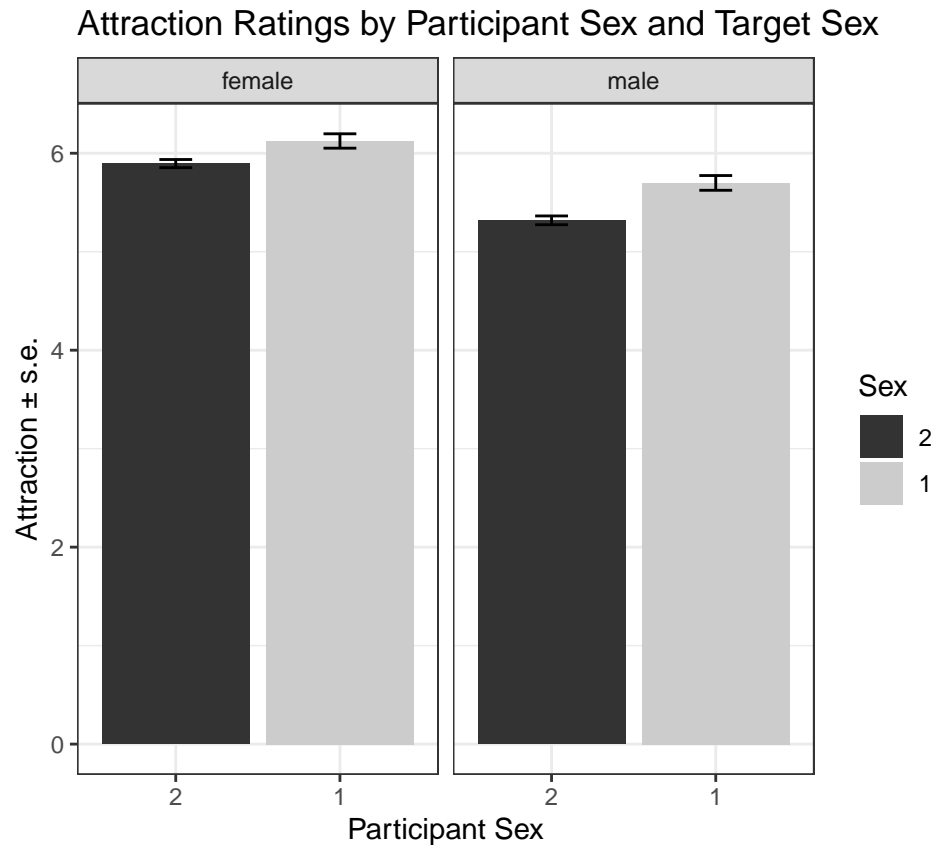
```
attraction_PSxTS
```

```
## # 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

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

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



The interaction between 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")

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 = "nlsminb"))
##
## 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")

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



```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: attraction ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "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)    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
## condntypc1 -0.702
## trgt.sxfml -0.375  0.428
## Sex1       -0.361  0.253  0.062
## cndntypc:. 0.337 -0.475 -0.900 -0.034
## cndntyp: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
## cndntnt:.: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_attraction <- attraction_total %>%
  filter(Sex == "1")
female_attraction <- attraction_total %>%
  filter(Sex == "2")
```

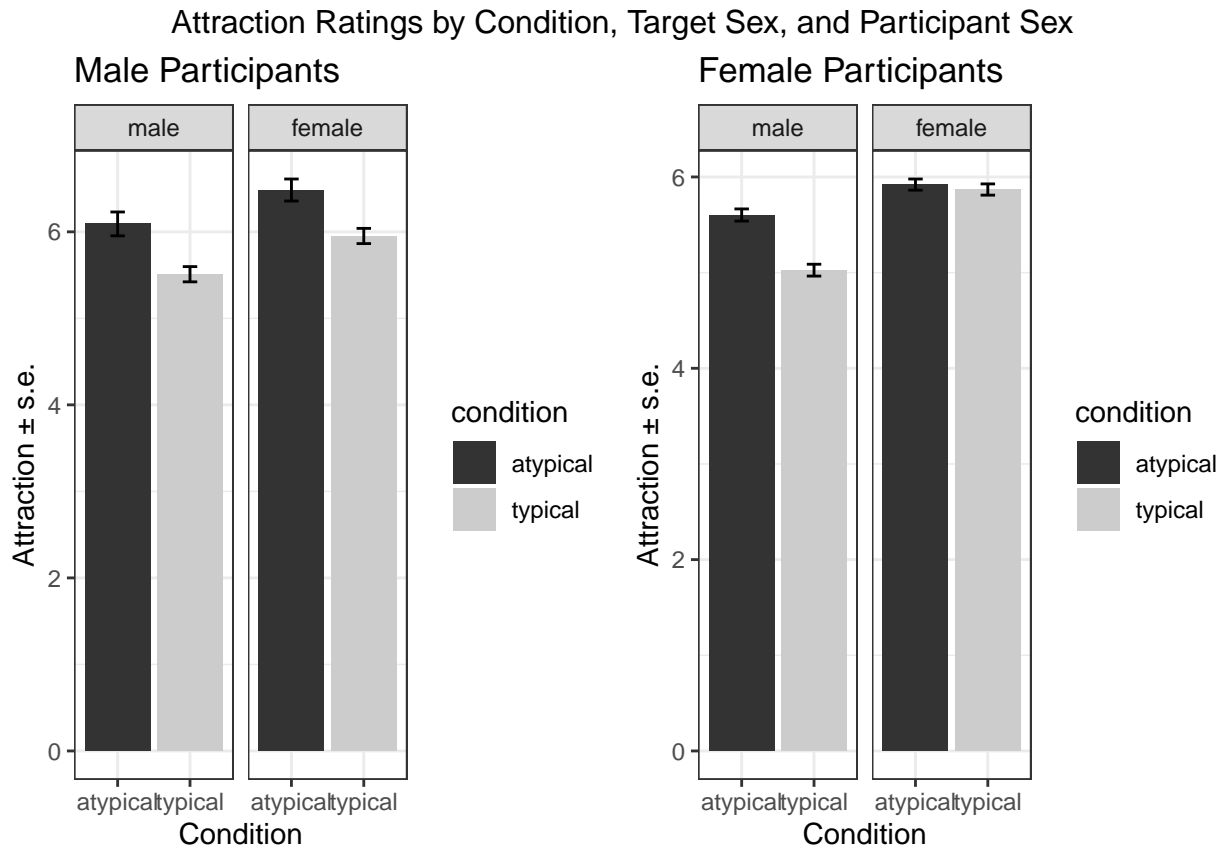
```
# plot
```

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

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

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

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



The three way interaction is significant, $t(6315) = -2.10$, $p < .05$. The simple effect of target sex and condition on attraction ratings centered at female participants is significant, $t(42) = 2.48$, $p < .05$.

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")

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 = "nllminb")))
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
## cndtntypcl -0.817
## targt.sxfml -0.284  0.287
## Sex2        -0.900  0.735  0.203
## cndtntypc:.  0.244 -0.334 -0.858 -0.141
## cndtntyp: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")

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 = "nlsminb")))
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 = "nlsminb"))
##
## 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")

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 = "nlminb")))
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 = "nlminb"))
##
## 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)    5.848184  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")
```

```
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 = "nlsminb")))
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")

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masc.fem ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 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
## cndtntypcl -0.725
## target.sxml -0.412 0.495
## cndtntypc:. 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
```

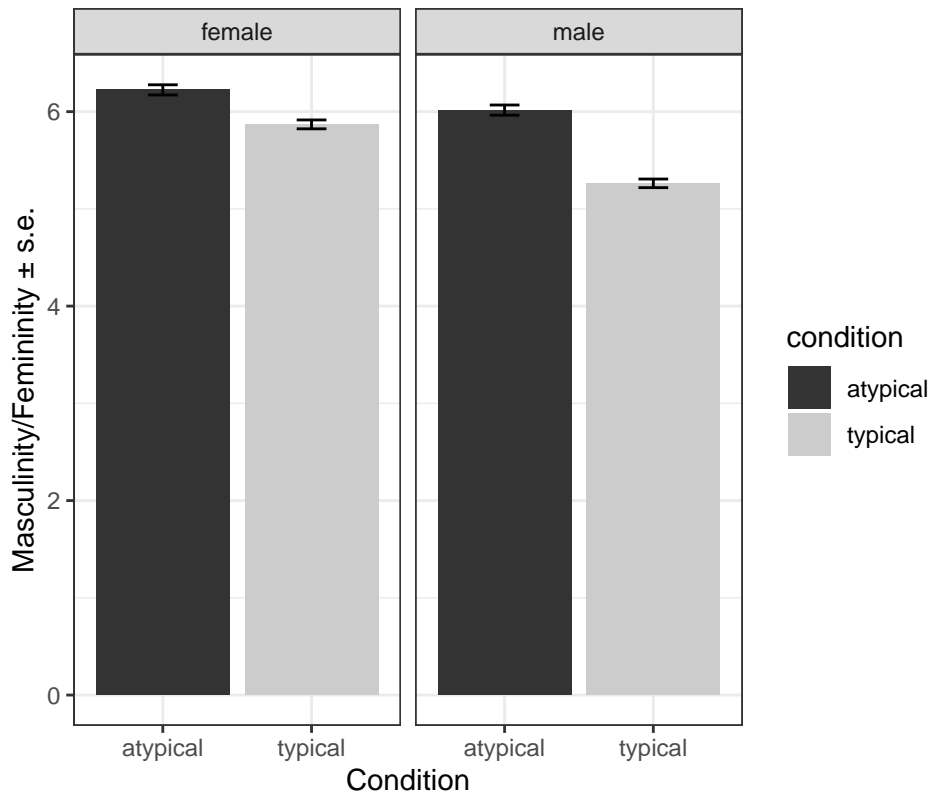
```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 atypical  female      6.22  2.04  1520 0.0523
## 2 atypical  male       6.02  2.04  1520 0.0524
## 3 typical   female      5.87  1.91  1740 0.0457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

```
# plot
```

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

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

Masculinity/Femininity Ratings by Condition and Target Sex



The interaction between condition and target sex is significant, $t(38) = -2.08$, $p < .05$. The simple effect of condition when target sex is centered at female is significant, $t(187) = -2.00$, $p < .05$.

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

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

model.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 = "nlsminb")))
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 = "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)      6.0158      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
## cndtntypc1 -0.725
## trgt.sxfml -0.412  0.495
## cndtntypc:. 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")

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

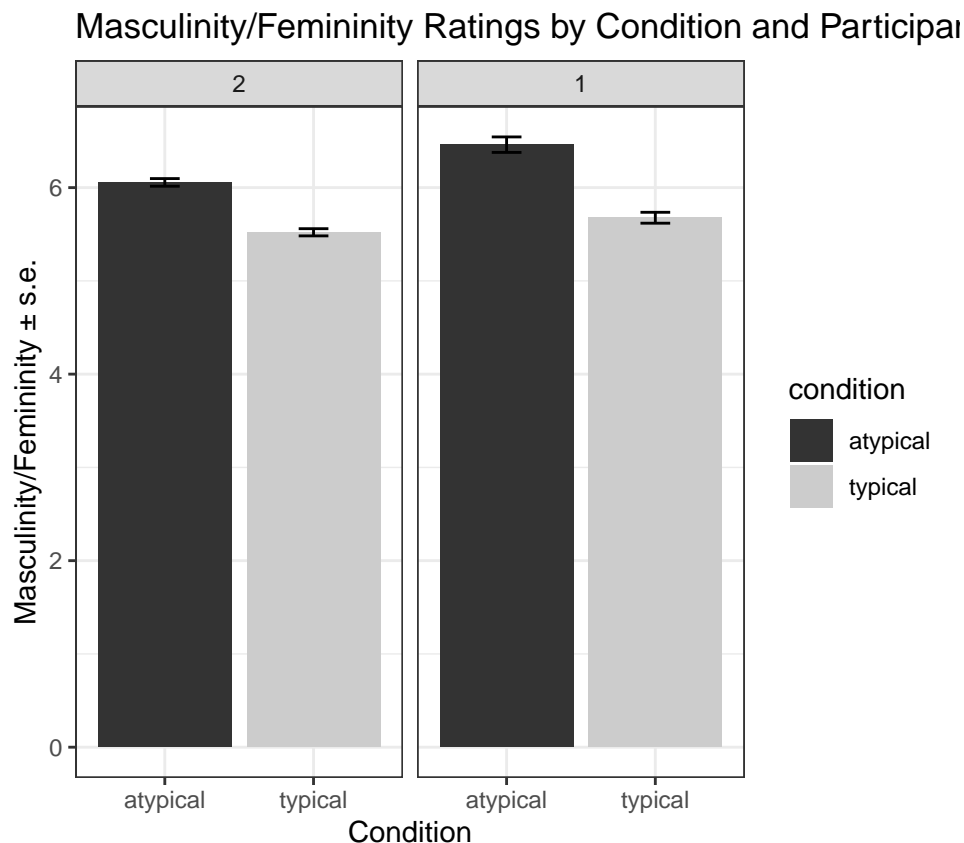
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

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

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



The interaction between condition and participant sex is not significant, $t(159) = -0.66$, $p = .508$.

Interaction - Masc/Fem by Participant Sex and Target Sex

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

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: 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.
```

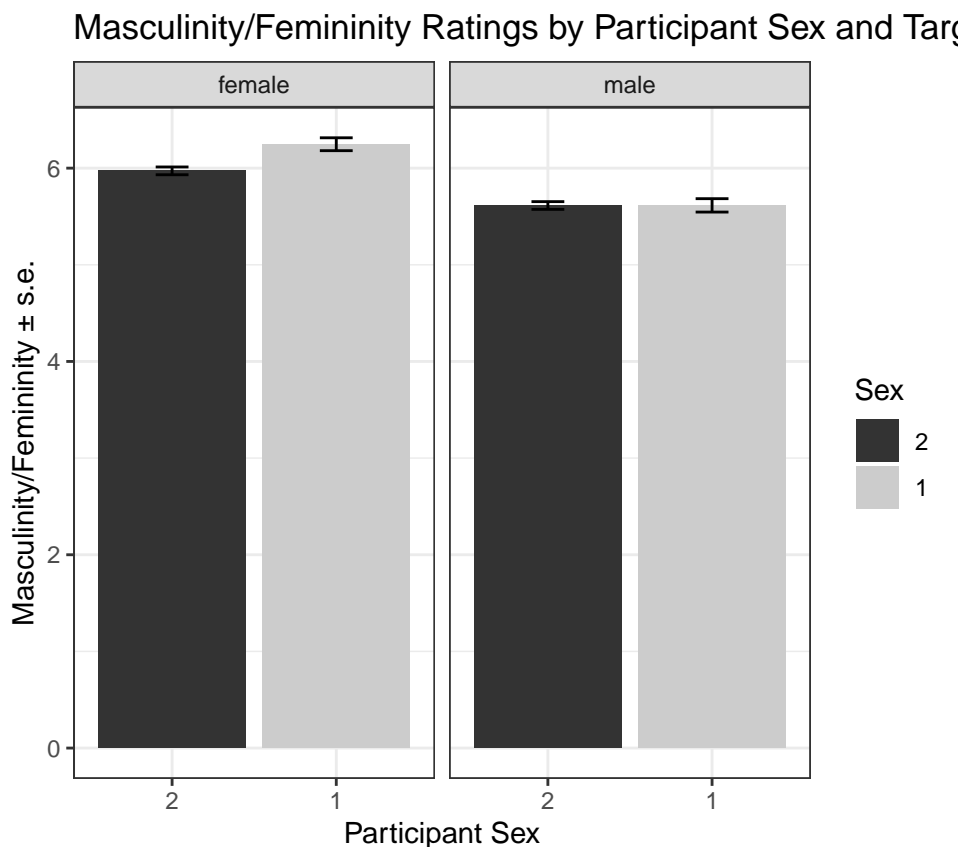
```
mascfem_PSxTS
```

```
## # 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
```

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

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

The interaction between 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

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

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 = "nlsminb")))
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 = "nlsminb"))
##
## 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")

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: 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
## cndtntypcl -0.703
## trgt.sxfml -0.397  0.451
## Sex1 -0.357  0.251  0.067
## cndtntypc:. 0.356 -0.503 -0.898 -0.037
## cndtntyp: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
```

subset means for male and female participants

```
male_mascfem <- mascfem_total %>%
  filter(Sex == "1")
female_mascfem <- mascfem_total %>%
  filter(Sex == "2")
```

plot

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

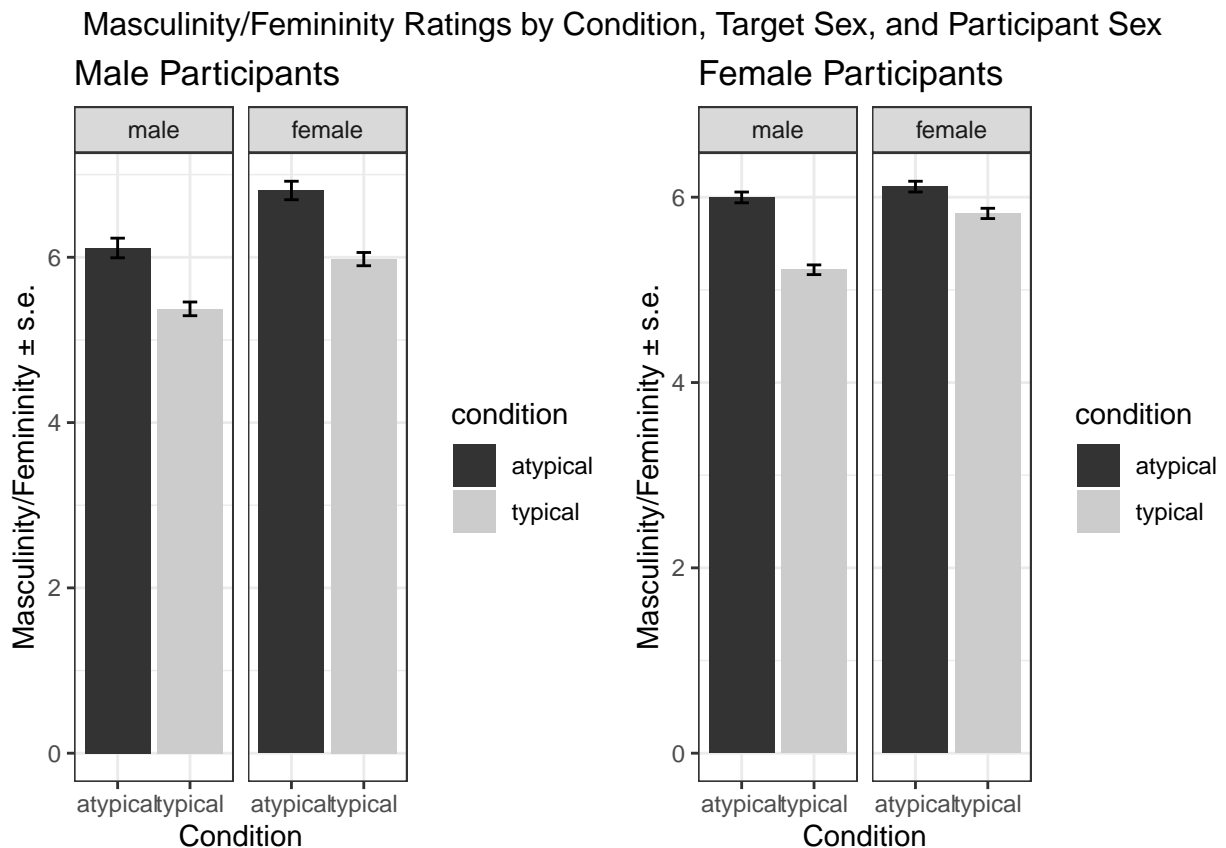
female_mascfem_plot <- ggplot(female_mascfem, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",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

```

y = "Masculinity/Femininity ± s.e.", x = "Condition") + theme_bw()

grid.arrange(male_mascfem_plot, female_mascfem_plot, nrow = 1, top = textGrob("Masculinity/Femininity Ratings by Condition, Target Sex, and Participant Sex"))

```



The three way interaction is significant, $t(6315) = -2.75, p < .01$. The simple effect of target sex and condition on masc/fem ratings centered at female participants is significant $t(42) = 2.49, p < .05$.

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

```

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

model.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 = "nlsminb")))
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 = "nlsminb"))
##

```

```
## 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
## cndtntypcl -0.816
## trgt.sxfml -0.305  0.307
## Sex2       -0.898  0.732  0.220
## cndtntypc:. 0.262 -0.358 -0.858 -0.153
## cndtntyp: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 $t(121) = -0.37, p=.715$.

Likability

Main Effect - Likability by Condition

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25263
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.6504 -0.5447 0.0794 0.6409 3.5848
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.9934 0.9967
## trial (Intercept) 0.0695 0.2636
## Residual 2.6028 1.6133
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.9862 0.1252 185.6353 47.829 <0.0000000000000002 ***
## conditiontypical -0.1649 0.1615 160.9991 -1.021 0.309
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.689
```

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

```
##                2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)    5.7408814 6.2314871
## conditiontypical -0.4815163 0.1516766
```

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

```
## # A tibble: 2 x 5
##   condition mean    sd     n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 atypical   5.99  1.98  3040 0.0359
## 2 typical    5.82  1.85  3480 0.0313
```

There was no significant difference in likability ratings of test voices after adaptation to atypical voices ($M = 5.99$, $SD = 1.98$) relative to typical voices ($M = 5.82$, $SD = 1.85$), $t(161) = -1.02$, $p = .309$.

Main Effect - Likability by Target Sex

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nloptn"))
##
## REML criterion at convergence: 25191
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7423 -0.5367  0.0728  0.6304  3.7251
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## ID       (Intercept) 0.99439   0.9972
```



```
## trial      (Intercept) 0.06978  0.2642
## Residual                2.57215  1.6038
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      6.07200    0.09293  197.41333  65.341 <0.0000000000000002 ***
## target.sexmale   -0.34768    0.03980  6326.93498  -8.736 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.214
```

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

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.8898660  6.2541338
## target.sexmale -0.4256836 -0.2696779
```

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

```
## # A tibble: 2 x 5
##   target.sex mean    sd      n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female    6.07  1.88  3260 0.0328
## 2 male      5.72  1.93  3260 0.0339
```

Female test voices ($M = 6.07$, $SD = 1.88$) were rated as significantly more likable than male test voices ($M = 5.72$, $SD = 1.93$), $t(6327) = -8.74$, $p < .001$.

Main Effect - Likability by Participant Sex

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

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

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

```
## lmerModLmerTest]
## Formula: likability ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25263.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6460 -0.5441  0.0805  0.6401  3.5897
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.9970  0.9985
## trial   (Intercept) 0.0695  0.2636
## Residual                2.6028  1.6133
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.8675     0.1008 185.1018  58.193 <0.0000000000000002 ***
## Sex1          0.1352     0.1927 161.0000   0.702      0.484
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.434
```

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

```
##              2.5 %   97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)  5.6698406 6.065080
## Sex1        -0.2424372 0.512922
```

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

```
## # A tibble: 2 x 5
##   Sex mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.87  1.94  5040  0.0273
## 2 1      6.00  1.83  1480  0.0476
```

There is no significant difference in likability ratings between male participants ($M = 6.00$, $SD = 1.83$) and female participants ($M = 5.87$, $SD = 1.94$), $t(161) = 0.70$, $p = .484$.

Interaction - Likability by Condition and Target Sex

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 25193.2
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.7381 -0.5349 0.0724 0.6313 3.7229
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.99415 0.9971
## trial (Intercept) 0.07193 0.2682
## Residual 2.57215 1.6038
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 6.16974 0.13553 197.23998 45.522
## conditiontypical -0.18410 0.18674 194.46127 -0.986
## target.sexmale -0.36711 0.10284 55.25801 -3.570
## conditiontypical:target.sexmale 0.03837 0.18738 38.06757 0.205
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditiontypical 0.325407
## target.sexmale 0.000749 ***
## conditiontypical:target.sexmale 0.838844
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnt trgt.s
## cndtntypcl -0.726
## target.sxml -0.379 0.463
## cndtntypc:. 0.350 -0.502 -0.922
```

```
# 95% confidence interval
ci.23 <- confint(model.23, method = "Wald", level = 0.95)
ci.23
```

```
##                2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)    5.9040957 6.4353780
## conditiontypical -0.5501035 0.1818942
## target.sexmale  -0.5686773 -0.1655332
## conditiontypical:target.sexmale -0.3288894 0.4056287
```

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

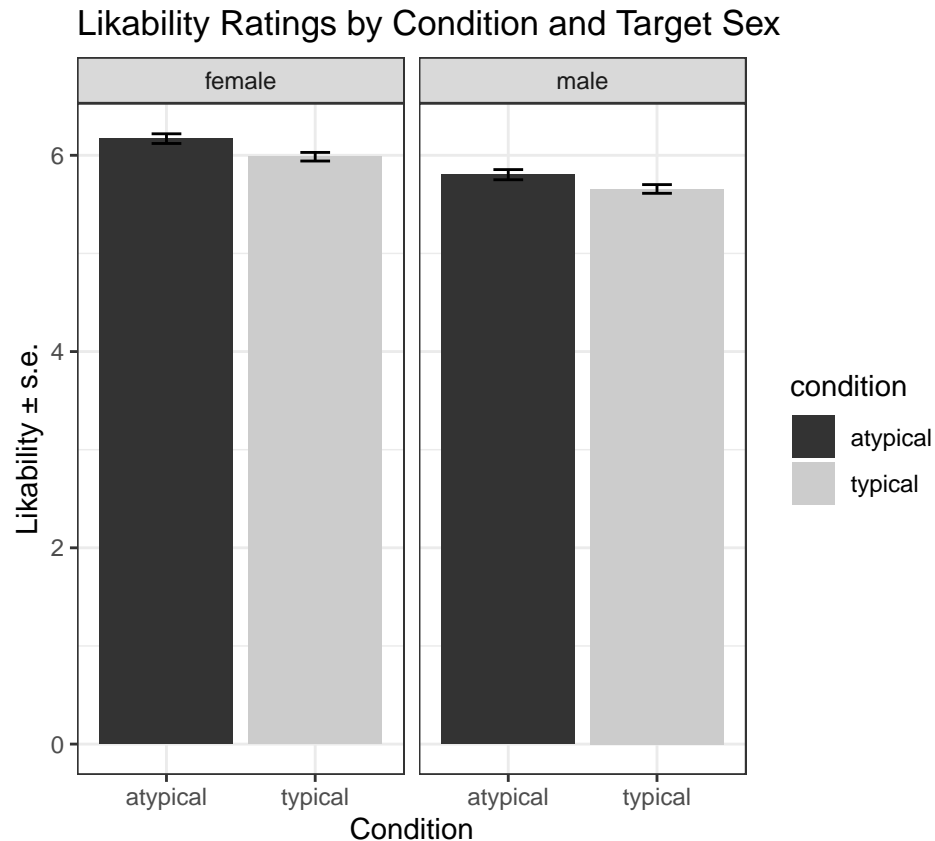
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
likability_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 atypical  female      6.17  1.92  1520 0.0493
## 2 atypical  male       5.80  2.02  1520 0.0518
## 3 typical   female      5.99  1.83  1740 0.0439
## 4 typical   male       5.66  1.85  1740 0.0444
```

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

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



The interaction between condition and target sex is not significant, $t(38) = .21, p = .839$.

Interaction - Likability by Condition and Participant Sex

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25263.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6487 -0.5441  0.0791  0.6418  3.5874
##
## Random effects:
## Groups   Name                Variance Std.Dev.
```

```
## ID      (Intercept) 0.9991  0.9996
## trial   (Intercept) 0.0695  0.2636
## Residual      2.6028  1.6133
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      5.9344      0.1355 181.7287  43.790 <0.0000000000000002
## conditiontypical -0.1360      0.1838 159.0000  -0.740      0.461
## Sex1              0.3281      0.3245 159.0000   1.011      0.313
## conditiontypical:Sex1 -0.2485      0.4063 159.0000  -0.612      0.542
##
## (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 -0.667
## Sex1          -0.378  0.279
## cndntntyp:S1  0.302 -0.452 -0.799
```

```
# 95% confidence interval
ci.24 <- confint(model.24, method = "Wald", level = 0.95)
ci.24
```

```
##              2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)      5.6687624 6.1999876
## conditiontypical -0.4962810 0.2243052
## Sex1             -0.3079124 0.9641624
## conditiontypical:Sex1 -1.0447533 0.5477292
```

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

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

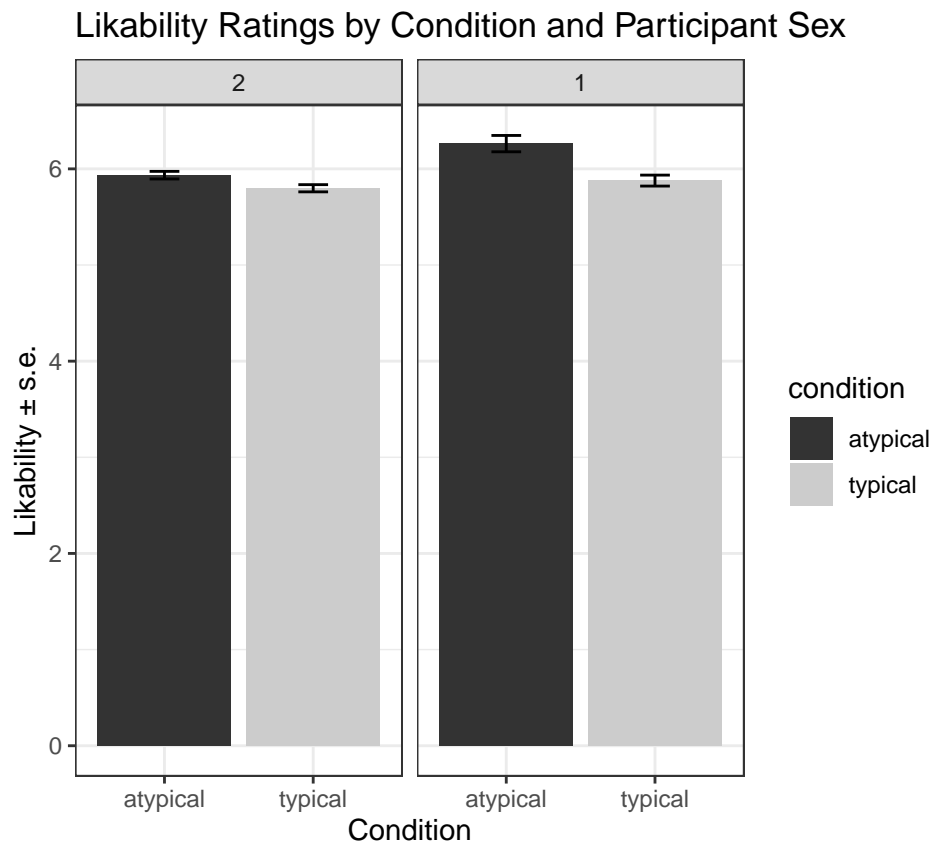
```
likability_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd      n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      5.93  2.00  2560 0.0395
```

```
## 2 atypical 1      6.26  1.86   480 0.0849
## 3 typical  2      5.80  1.87  2480 0.0375
## 4 typical  1      5.88  1.80  1000 0.0570
```

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

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



The interaction between condition and participant sex is not significant, $t(159) = -0.62$, $p = .542$.

Interaction - Likability by Participant Sex and Target Sex

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

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

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

```
## lmerModLmerTest]
## Formula: likability ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25194.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7452 -0.5372  0.0719  0.6301  3.7290
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.99772 0.9989
## trial   (Intercept) 0.06976 0.2641
## Residual                2.57245 1.6039
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      6.04672    0.10336 204.33929  58.501
## Sex1              0.11098    0.19856 181.48014   0.559
## target.sexmale    -0.35852    0.04519 6316.48454 -7.934
## Sex1:target.sexmale 0.04852    0.09577 6352.16094   0.507
##
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## Sex1              0.577
## target.sexmale    0.00000000000000249 ***
## Sex1:target.sexmale 0.612
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.436
## target.sxml -0.219  0.114
## Sx1:trgt.sx  0.104 -0.241 -0.474
```

95% confidence interval

```
ci.25 <- confint(model.25, method = "Wald", level = 0.95)
ci.25
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.8441394  6.2493039
## Sex1          -0.2781858  0.5001465
## target.sexmale -0.4470896 -0.2699557
## Sex1:target.sexmale -0.1391813  0.2362294
```



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

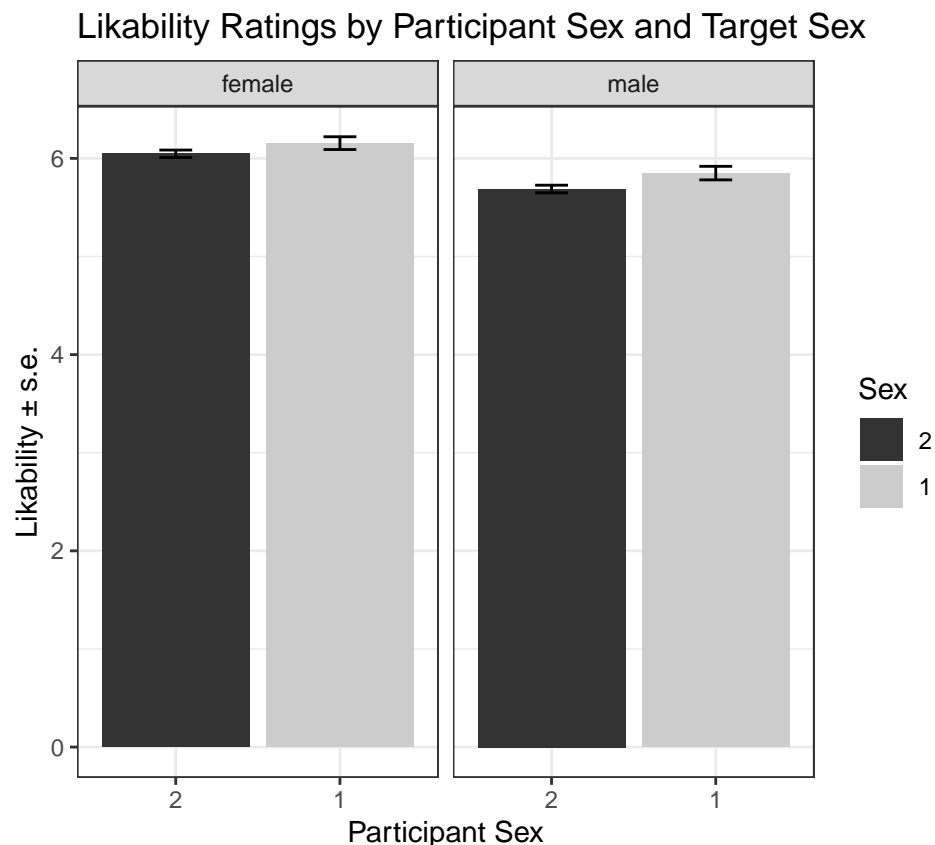
'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.

```
likability_PSxTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd    n    se
##   <fct> <fct>     <dbl> <dbl> <int> <dbl>
## 1 2     female     6.05  1.91  2520 0.0380
## 2 2     male      5.69  1.95  2520 0.0388
## 3 1     female     6.16  1.77   740 0.0650
## 4 1     male      5.85  1.88   740 0.0691
```

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

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



The interaction between participant sex and target sex is not significant, $t(6352) = 0.51$, $p = .612$.

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

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: likability ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlopt"))
##
## REML criterion at convergence: 25197.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7436 -0.5358  0.0714  0.6297  3.7249
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.99984 0.9999
## trial   (Intercept) 0.07193 0.2682
## Residual                2.57281 1.6040
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error df
## (Intercept)    6.1179688    0.1457018 200.7490677
## conditiontypical -0.1445817    0.2074291 201.0987051
## target.sexmale -0.3671875    0.1058910  62.0727813
## Sex1           0.3278646    0.3341752 178.7895664
## conditiontypical:target.sexmale 0.0171875    0.1922011  42.1273070
## conditiontypical:Sex1 -0.2852517    0.4183465 178.7895667
## target.sexmale:Sex1 0.0005208    0.1595622 6314.9980633
## conditiontypical:target.sexmale:Sex1 0.0734792    0.1997524 6314.9980626
##              t value      Pr(>|t|)
## (Intercept)   41.990 < 0.0000000000000002 ***
## conditiontypical -0.697      0.486597
## target.sexmale -3.468      0.000959 ***
## Sex1           0.981      0.327861
## conditiontypical:target.sexmale 0.089      0.929168
## conditiontypical:Sex1 -0.682      0.496213
## target.sexmale:Sex1 0.003      0.997396
## conditiontypical:target.sexmale:Sex1 0.368      0.712996
## ---
## 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
## target.sxml -0.363  0.419
## Sex1        -0.362  0.254  0.057
## cndnttypc:.  0.329 -0.463 -0.904 -0.031
## cndnttyp:S1  0.289 -0.413 -0.045 -0.799  0.051
## trgt.sxm:S1  0.086 -0.061 -0.238 -0.239  0.131  0.191
## cndtnt:..S1 -0.069  0.099  0.190  0.191 -0.213 -0.239 -0.799
```

```
# 95% confidence interval
```

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

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.8323984  6.4035391
## conditiontypical -0.5511353  0.2619720
## target.sexmale   -0.5747300 -0.1596450
## Sex1            -0.3271067  0.9828359
## conditiontypical:target.sexmale -0.3595197  0.3938947
## conditiontypical:Sex1 -1.1051958  0.5346925
## target.sexmale:Sex1 -0.3122153  0.3132569
## conditiontypical:target.sexmale:Sex1 -0.3180283  0.4649866
```

```
# group means
```

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

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

```
likability_total
```

```
## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex   mean    sd     n    se
##   <fct>      <fct>   <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  female     2     6.12  1.95  1280  0.0544
## 2 atypical  female     1     6.45  1.77   240  0.114
## 3 atypical  male       2     5.75  2.03  1280  0.0568
## 4 atypical  male       1     6.08  1.94   240  0.125
## 5 typical   female     2     5.97  1.86  1240  0.0528
## 6 typical   female     1     6.02  1.75   500  0.0784
## 7 typical   male       2     5.62  1.86  1240  0.0528
## 8 typical   male       1     5.74  1.84   500  0.0824
```

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

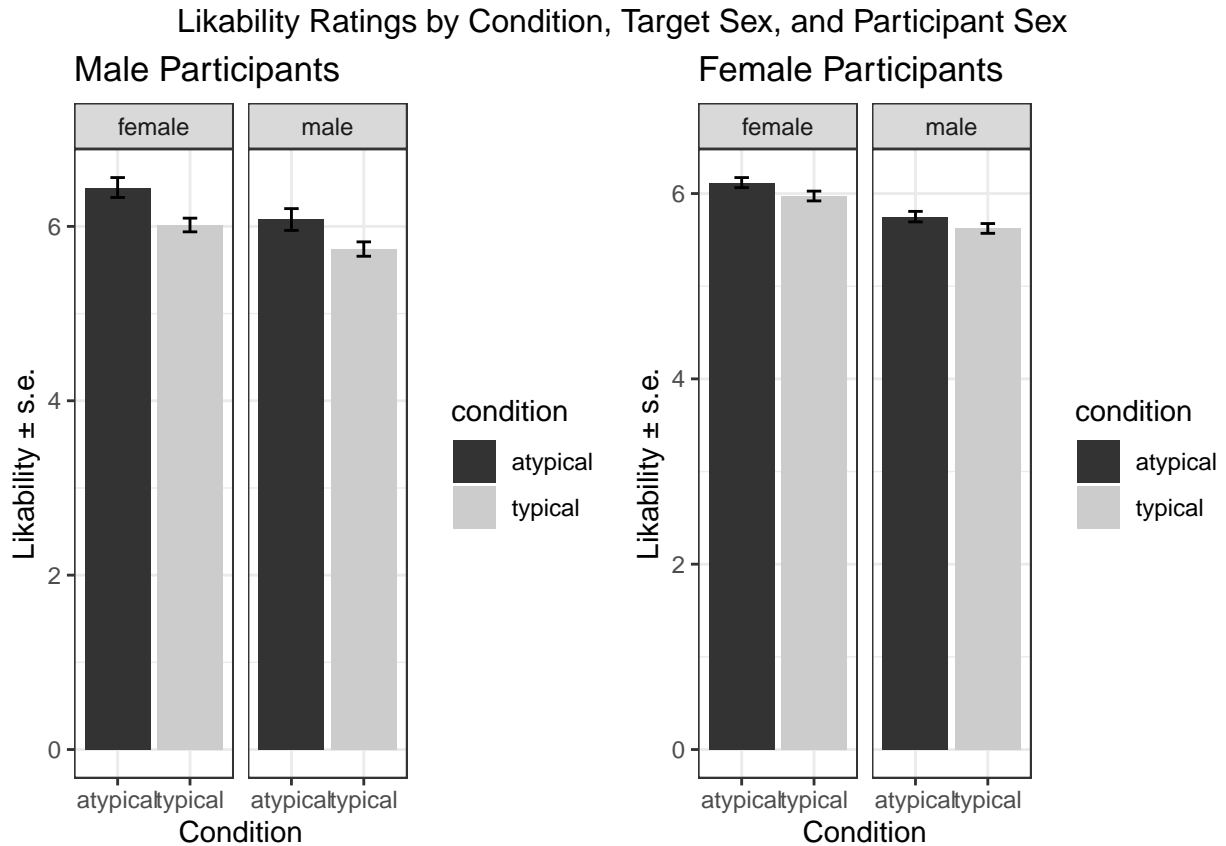
```
male_likability <- likability_total %>%
  filter(Sex == "1")
```

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

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

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

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



The three way interaction is not significant $t(6315) = -0.37, p = .713$.

Friends

Main Effect - Friends by Condition

```

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26343.5
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.5678 -0.5846 0.0525 0.6551 3.6028
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.16121 1.0776
## trial (Intercept) 0.07812 0.2795
## Residual 3.07358 1.7532
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.7227 0.1351 184.9991 42.369 <0.0000000000000002 ***
## conditiontypical -0.0862 0.1747 161.0012 -0.493 0.622
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.690

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

## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.4579716 5.9874232
## conditiontypical -0.4286109 0.2562047

# group means
friends_condition <- data %>%

```

```

group_by(condition) %>%
  summarize(mean = mean(friends), sd = sd(friends), n = n(), se = sd(friends)/sqrt(n()))
friends_condition

```

```

## # A tibble: 2 x 5
##   condition mean    sd      n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 atypical  5.72  2.14  3040 0.0388
## 2 typical   5.64  2.02  3480 0.0342

```

There is no difference in friendliness ratings after adaptation to atypical voices ($M = 5.72$, $SD = 2.14$) versus typical voices ($M = 5.63$, $SD = 2.02$), $t(161) = -0.49$, $p = .622$.

Main Effect - Friends by Target Sex

```

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26257.9
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -3.4678 -0.5785  0.0527  0.6470  3.7542
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.1565  1.0754
## trial   (Intercept) 0.0787  0.2805
## Residual                 3.0312  1.7410
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)    5.88076    0.09997 197.96041  58.825 <0.0000000000000002 ***
## target.sexmale -0.40814    0.04320 6327.26891  -9.447 <0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## target.sxml -0.216

```

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

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.6848192  6.0766959
## target.sexmale -0.4928171 -0.3234645
```

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

```
## # A tibble: 2 x 5
##   target.sex mean    sd     n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female     5.88  2.03  3260 0.0355
## 2 male       5.47  2.10  3260 0.0368
```

Female test voices ($M = 5.88$, $SD = 2.03$) are rated as significantly more friendly than male test voices ($M = 5.47$, $SD = 2.10$), $t(6327) = -9.45$, $p < .001$.

Main Effect - Friends by Participant Sex

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26342.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5646 -0.5824  0.0514  0.6543  3.6055
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## ID       (Intercept)  1.15800   1.0761
## trial    (Intercept)  0.07812   0.2795
```

```
## Residual          3.07358  1.7532
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##           Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)  5.6383      0.1084 184.8509  52.008 <0.0000000000000002 ***
## Sex1         0.1691      0.2078 161.0000   0.814      0.417
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.435
```

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

```
##           2.5 %    97.5 %
## .sig01         NA         NA
## .sig02         NA         NA
## .sigma         NA         NA
## (Intercept)  5.4258093 5.850778
## Sex1        -0.2381114 0.576389
```

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

```
## # A tibble: 2 x 5
##   Sex    mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.64  2.12  5040 0.0298
## 2 1      5.81  1.91  1480 0.0496
```

There is no significant difference in friends ratings between male participants ($M = 5.81$, $SD = 1.91$) and female participants ($M = 5.64$, $SD = 2.11$), $t(161) = 0.81$, $p = .417$.

Interaction - Friends by Condition and Target Sex

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

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

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



```
## Formula: friends ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26260.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.4675 -0.5790  0.0525  0.6482  3.7553
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  1.16222   1.0781
##   trial    (Intercept)  0.08091   0.2844
##   Residual                    3.03118   1.7410
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.94539    0.14605 197.89849  40.707
## conditiontypical -0.12298    0.20119 195.27768  -0.611
## target.sexmale   -0.44539    0.10991  55.98101  -4.053
## conditiontypical:target.sexmale  0.07356    0.19959  38.06366   0.369
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## conditiontypical    0.541738
## target.sexmale     0.000158 ***
## conditiontypical:target.sexmale  0.714517
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) cndtnt trgt.s
## condntypcl -0.726
## target.sxml -0.376  0.456
## cndntypc:.  0.346 -0.496 -0.919
```

```
# 95% confidence interval
```

```
ci.30 <- confint(model.30, method = "Wald", level = 0.95)
ci.30
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.6591327  6.2316567
## conditiontypical -0.5173105  0.2713486
## target.sexmale   -0.6608061 -0.2299834
## conditiontypical:target.sexmale -0.3176330  0.4647443
```

```
# group means
```

```
friends_CxTS <- data %>%
```

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

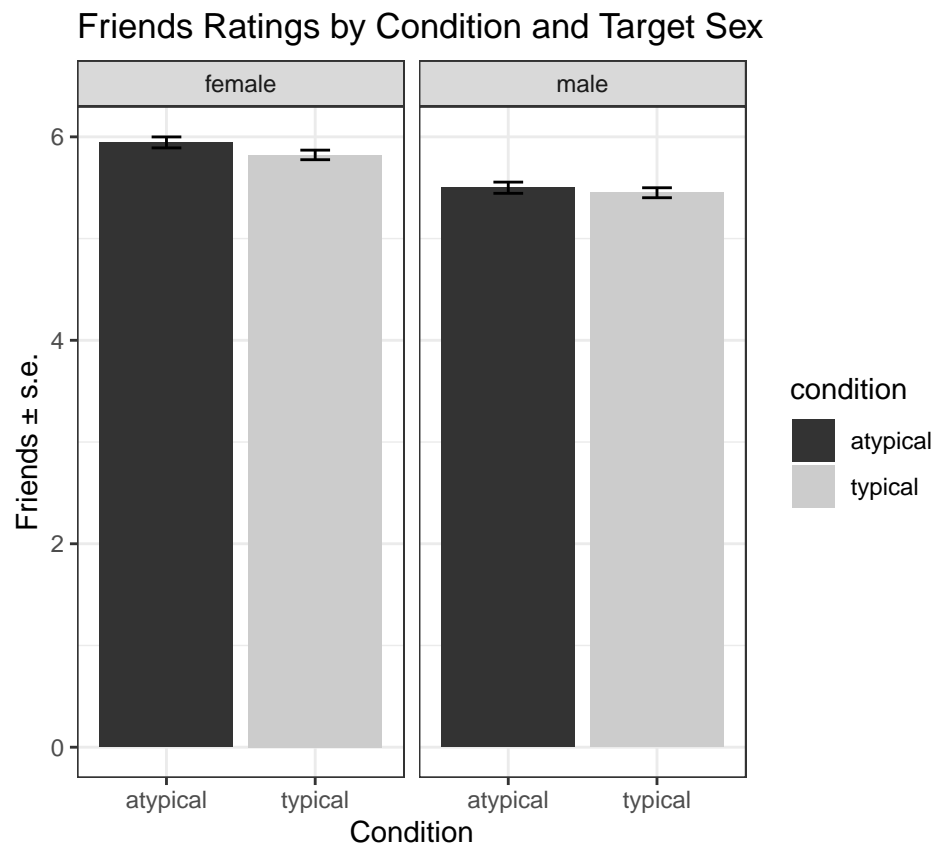
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
friends_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
##   <fct>      <fct>    <dbl> <dbl> <int> <dbl>
## 1 atypical  female     5.95  2.10  1520 0.0538
## 2 atypical  male       5.5   2.15  1520 0.0553
## 3 typical   female     5.82  1.96  1740 0.0471
## 4 typical   male       5.45  2.05  1740 0.0491
```

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

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



The interaction between condition and target sex is not significant, $t(38) = 0.37$, $p = .715$.

Interaction - Friends by Condition and Participant Sex

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26343.6
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.5664 -0.5835 0.0523 0.6556 3.6052
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.16911 1.0813
## trial (Intercept) 0.07812 0.2795
## Residual 3.07358 1.7532
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 5.67422 0.14636 181.05000 38.769
## conditiontypical -0.07301 0.19891 158.99924 -0.367
## Sex1 0.30703 0.35114 158.99924 0.874
## conditiontypical:Sex1 -0.18424 0.43958 158.99924 -0.419
## Pr(>|t|)
## (Intercept) <0.0000000000000002 ***
## conditiontypical 0.714
## Sex1 0.383
## conditiontypical:Sex1 0.676
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnt Sex1
## cndtnttypcl -0.669
## Sex1 -0.379 0.279
## cndtntyp:S1 0.303 -0.452 -0.799
```

```
# 95% confidence interval
ci.31 <- confint(model.31, method = "Wald", level = 0.95)
ci.31
```

```
##                2.5 %    97.5 %
## .sig01                NA        NA
## .sig02                NA        NA
## .sigma                NA        NA
## (Intercept)      5.3873611 5.9610764
## conditiontypical -0.4628589 0.3168408
## Sex1             -0.3811838 0.9952463
## conditiontypical:Sex1 -1.0458022 0.6773203
```

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

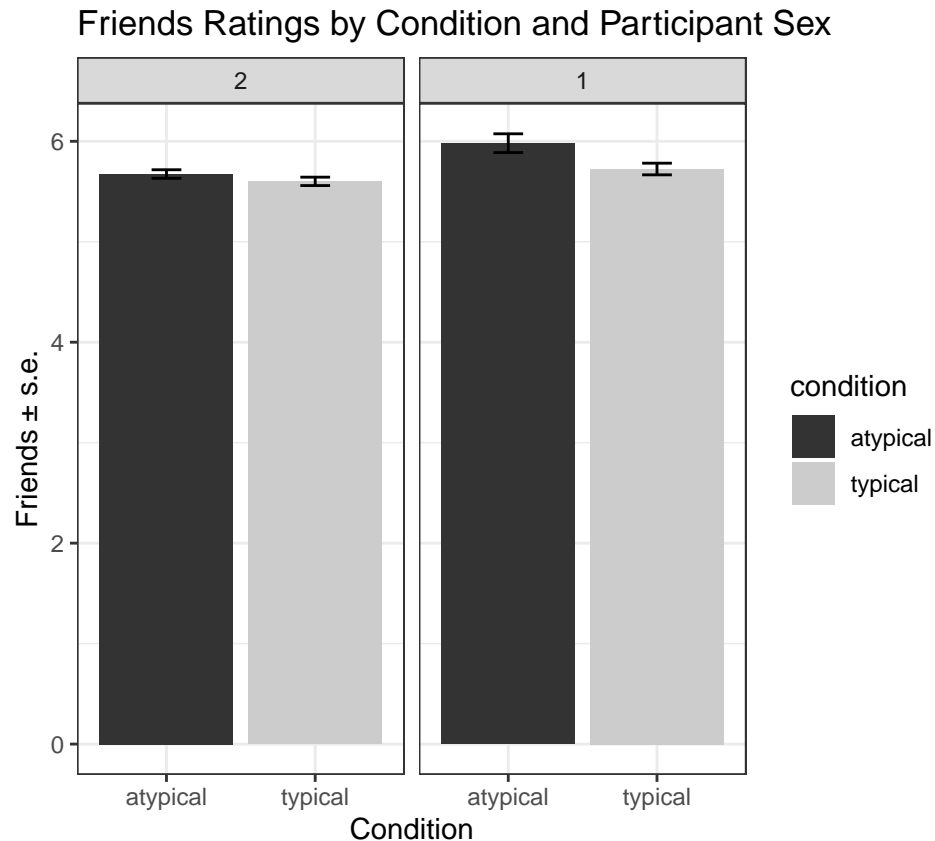
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
friends_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>    <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical 2      5.67  2.15  2560 0.0425
## 2 atypical 1      5.98  2.04   480 0.0932
## 3 typical 2      5.60  2.08  2480 0.0418
## 4 typical 1      5.72  1.83  1000 0.0580
```

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

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



The interaction between condition and participant sex is not significant, $t(159) = -0.42$, $p = .676$.

Interaction - Friends by Participant Sex and Target Sex

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: friends ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 26259.3
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.4598 -0.5744 0.0498 0.6479 3.7632
##
## Random effects:
## Groups Name Variance Std.Dev.
```

```
## ID      (Intercept) 1.15907  1.0766
## trial   (Intercept) 0.07856  0.2803
## Residual      3.03076  1.7409
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.85855    0.11120  204.47329  52.684
## Sex1              0.09669    0.21419  181.75668   0.451
## target.sexmale   -0.44052    0.04905  6316.50156 -8.981
## Sex1:target.sexmale  0.14491    0.10394  6352.70394   1.394
##              Pr(>|t|)
## (Intercept)      <0.0000000000000002 ***
## Sex1              0.652
## target.sexmale   <0.0000000000000002 ***
## Sex1:target.sexmale  0.163
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.437
## target.sxml -0.221  0.115
## Sx1:trgt.sx  0.104 -0.243 -0.474
```

```
# 95% confidence interval
ci.32 <- confint(model.32, method = "Wald", level = 0.95)
ci.32
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.64060288  6.0765061
## Sex1            -0.32311039  0.5164814
## target.sexmale  -0.53665484 -0.3443885
## Sex1:target.sexmale -0.05881736  0.3486305
```

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

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

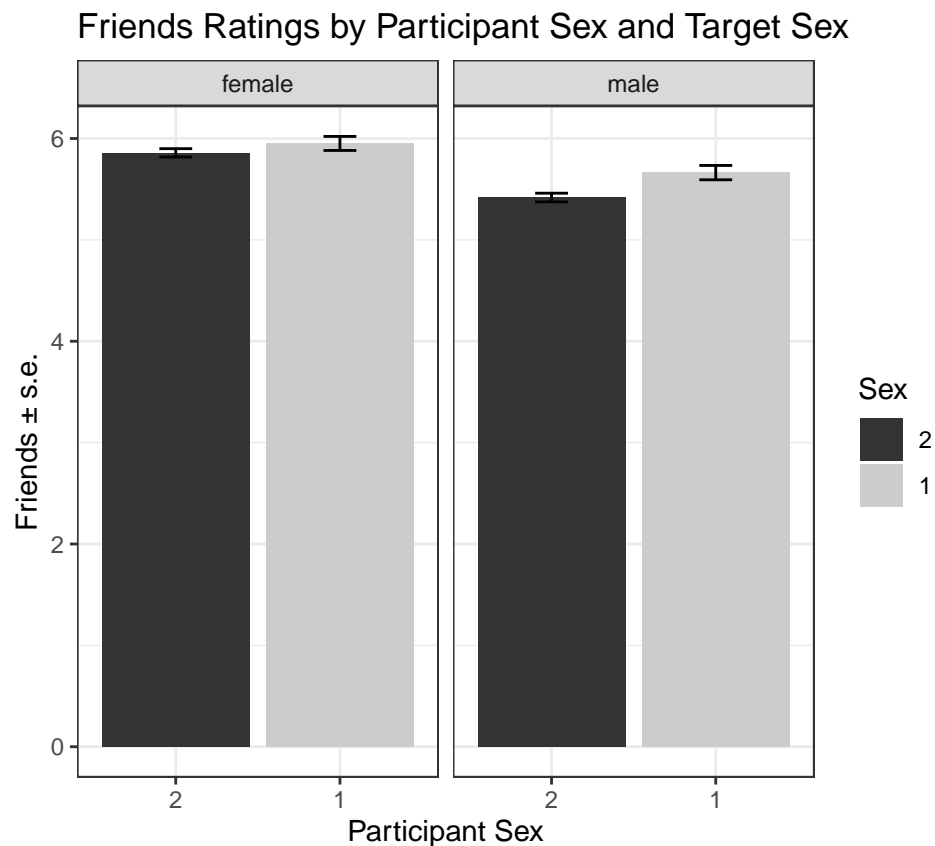
```
friends_PsTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd      n    se
##   <fct> <fct>    <dbl> <dbl> <int> <dbl>
## 1 2     female      5.86  2.07  2520 0.0412
```

```
## 2 2    male      5.42  2.14 2520 0.0427
## 3 1    female    5.95  1.88  740 0.0691
## 4 1    male      5.66  1.92  740 0.0707
```

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

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



The interaction between participant sex and target sex is not significant, $t(6353) = 1.39$, $p = .163$.

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

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

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

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

```

## Formula: friends ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 26262.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.4608 -0.5740  0.0498  0.6469  3.7631
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.1702  1.0818
## trial   (Intercept) 0.0809  0.2844
## Residual                 3.0312  1.7410
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      5.90625    0.15715 200.96944  37.582
## conditiontypical -0.09657    0.22374 201.28610  -0.432
## target.sexmale   -0.46406    0.11325  63.11923 -4.098
## Sex1              0.24792    0.36166 178.90683   0.685
## conditiontypical:target.sexmale 0.04713    0.20491  42.29130   0.230
## conditiontypical:Sex1 -0.20359    0.45275 178.90683 -0.450
## target.sexmale:Sex1  0.11823    0.17319 6315.00117   0.683
## conditiontypical:target.sexmale:Sex1 0.03871    0.21682 6315.00117   0.179
##
##              Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditiontypical 0.666479
## target.sexmale 0.000121 ***
## Sex1 0.493918
## conditiontypical:target.sexmale 0.819206
## conditiontypical:Sex1 0.653487
## target.sexmale:Sex1 0.494862
## conditiontypical:target.sexmale:Sex1 0.858321
## ---
## 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 -0.702
## target.sxm1 -0.360  0.413
## Sex1 -0.363  0.255  0.058
## cndntypc:.  0.325 -0.458 -0.901 -0.032
## cndntyp:S1  0.290 -0.414 -0.046 -0.799  0.052
## trgt.sxm:S1  0.087 -0.061 -0.241 -0.239  0.133  0.191
## cndntnt:.:S1 -0.069  0.099  0.193  0.191 -0.217 -0.239 -0.799

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

```



```
##                2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)     5.5982330 6.2142670
## conditiontypical -0.5351022 0.3419570
## target.sexmale   -0.6860375 -0.2420875
## Sex1            -0.4609247 0.9567580
## conditiontypical:target.sexmale -0.3544824 0.4487364
## conditiontypical:Sex1 -1.0909770 0.6837888
## target.sexmale:Sex1 -0.2212266 0.4576849
## conditiontypical:target.sexmale:Sex1 -0.3862509 0.4636635
```

group means

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

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

```
friends_total
```

```
## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex    mean    sd     n    se
##   <fct>      <fct>   <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  female     2     5.91  2.11  1280 0.0590
## 2 atypical  female     1     6.15  2.02   240 0.130
## 3 atypical  male       2     5.44  2.17  1280 0.0606
## 4 atypical  male       1     5.81  2.05   240 0.133
## 5 typical   female     2     5.81  2.02  1240 0.0575
## 6 typical   female     1     5.85  1.80   500 0.0807
## 7 typical   male       2     5.39  2.12  1240 0.0602
## 8 typical   male       1     5.59  1.85   500 0.0829
```

subset means for male and female participants

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

plot

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

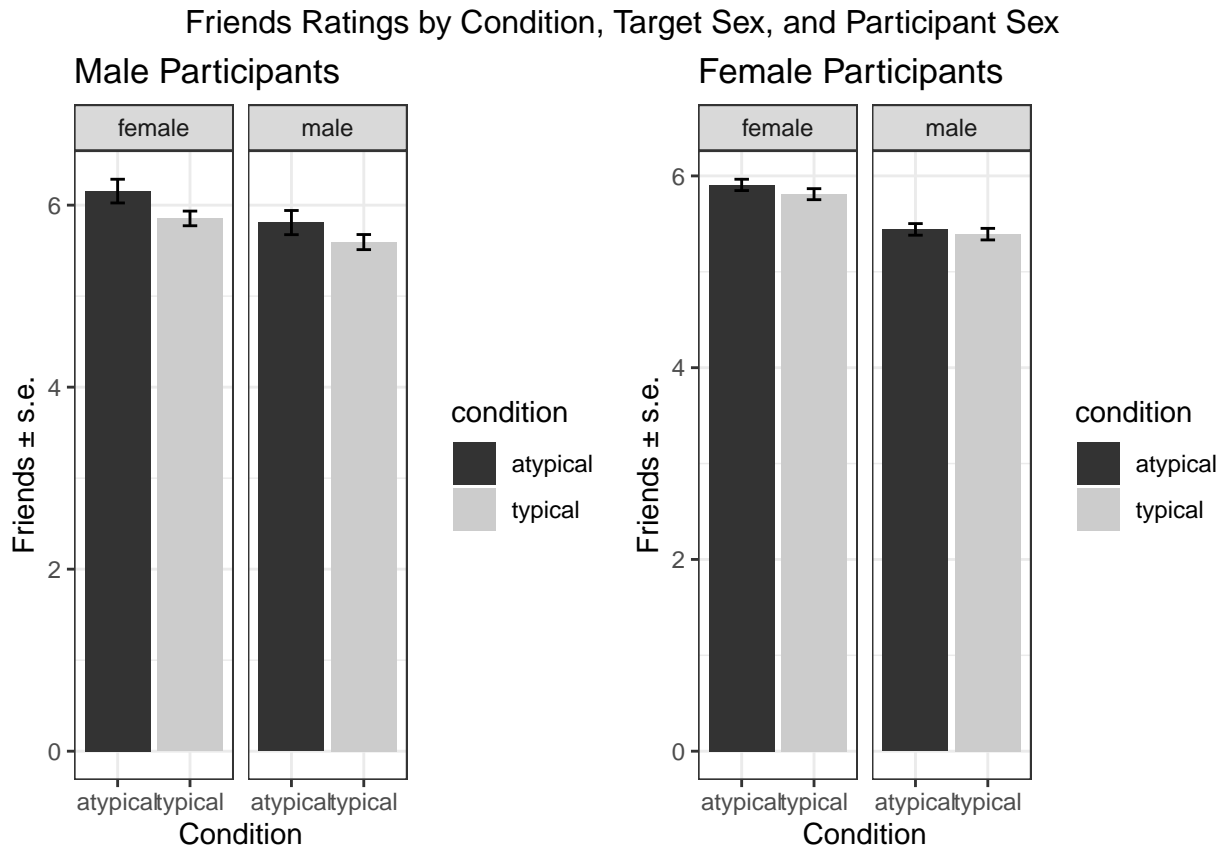
female_friends_plot <- ggplot(female_friends, aes(x = condition, y = mean,
  fill = condition)) + geom_bar(position = "dodge", stat = "identity") +
  geom_errorbar(aes(ymin = mean - se, ymax = mean + se), width = 0.2) +
  facet_wrap(~target.sex) + scale_fill_grey() + labs(title = "Female Participants",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

```

y = "Friends ± s.e.", x = "Condition") + theme_bw()

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

```



The three way interaction is not significant, $t(6315) = -0.18, p = .858$.

Typicality

Main Effect - Typicality by Condition

```

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

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

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

```

```
##
## REML criterion at convergence: 25811.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.2158 -0.5855  0.0458  0.6699  3.1598
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.90466  0.9511
##   trial    (Intercept) 0.07411  0.2722
##   Residual                2.84341  1.6862
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      5.9128     0.1212 186.3613  48.782 <0.0000000000000002 ***
## conditiontypical -0.2260     0.1551 160.9998  -1.457      0.147
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## condntntypcl -0.683
```

```
# 95% confidence interval
ci.34 <- confint(model.34, method = "Wald", level = 0.95)
ci.34
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)    5.675265 6.15039338
## conditiontypical -0.530027 0.07793229
```

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

```
## # A tibble: 2 x 5
##   condition mean    sd    n    se
##   <fct>    <dbl> <dbl> <int> <dbl>
## 1 atypical  5.91  2.03  3040 0.0368
## 2 typical   5.69  1.88  3480 0.0319
```

There is no difference in typicality ratings after adaptation to atypical voices ($M = 5.91$, $SD = 2.03$) versus typical voices ($M = 5.69$, $SD = 1.88$), $t(161) = -1.46$, $p = .147$.

Main Effect - Typicality by Target Sex

```

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

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25806.6
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.1743 -0.5838 0.0388 0.6699 3.2078
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.91153 0.9547
## trial (Intercept) 0.07399 0.2720
## Residual 2.83971 1.6851
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.85599 0.09118 192.98229 64.222 < 0.0000000000000002
## target.sexmale -0.12762 0.04182 6327.24313 -3.052 0.00228
##
## (Intercept) ***
## target.sexmale **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## target.sxml -0.229

# 95% confidence interval
ci.35 <- confint(model.35, method = "Wald", level = 0.95)
ci.35

## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.6772690 6.03470448
## target.sexmale -0.2095759 -0.04565934

```

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

```
## # A tibble: 2 x 5
##   target.sex mean    sd    n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 female     5.86  1.96  3260 0.0343
## 2 male       5.73  1.95  3260 0.0341
```

Female test voices ($M = 5.86$, $SD = 1.96$) were rated as significantly more friendly than male test voices ($M = 5.73$, $SD = 1.95$), $t(6327) = -3.052$, $p < .01$.

Main Effect - Typicality by Participant Sex

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25812
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -4.2097 -0.5873  0.0447  0.6691  3.1675
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  0.9121    0.9550
##   trial    (Intercept)  0.0741    0.2722
##   Residual                    2.8434    1.6862
## Number of obs: 6520, groups:  ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.75238    0.09826 181.90531  58.541 <0.0000000000000002 ***
## Sex1          0.17532    0.18540 161.00000   0.946      0.346
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
```

```
##      (Intr)
## Sex1 -0.428
```

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

```
##              2.5 %    97.5 %
## .sig01          NA        NA
## .sig02          NA        NA
## .sigma          NA        NA
## (Intercept)  5.5597903 5.9449716
## Sex1        -0.1880643 0.5387078
```

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

```
## # A tibble: 2 x 5
##   Sex    mean    sd      n    se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.75  1.97  5040 0.0278
## 2 1      5.93  1.88  1480 0.0490
```

There is no significant difference in friends ratings between male participants ($M = 5.93$, $SD = 1.88$) and female participants ($M = 5.75$, $SD = 1.97$), $t(161) = 0.95$, $p = .346$.

Interaction - Typicality by Condition and Target Sex

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25807.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1803 -0.5855  0.0395  0.6712  3.2000
##
```

```
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   ID       (Intercept) 0.90476  0.9512
##   trial    (Intercept) 0.07619  0.2760
##   Residual                2.83971  1.6851
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##               Estimate Std. Error      df t value
## (Intercept)      5.96250    0.13260 193.17403  44.967
## conditiontypical -0.19813    0.18282 189.34750  -1.084
## target.sexmale   -0.09934    0.10656  55.90149  -0.932
## conditiontypical:target.sexmale -0.05583    0.19358  38.06484  -0.288
##
##               Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## conditiontypical      0.280
## target.sexmale      0.355
## conditiontypical:target.sexmale      0.775
## ---
## 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 -0.402  0.487
## cndnttypc:.  0.370 -0.529 -0.920
```

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

```
##               2.5 %    97.5 %
## .sig01          NA      NA
## .sig02          NA      NA
## .sigma          NA      NA
## (Intercept)     5.7026129 6.2223871
## conditiontypical -0.5564519 0.1601876
## target.sexmale   -0.3081960 0.1095118
## conditiontypical:target.sexmale -0.4352485 0.3235879
```

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

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

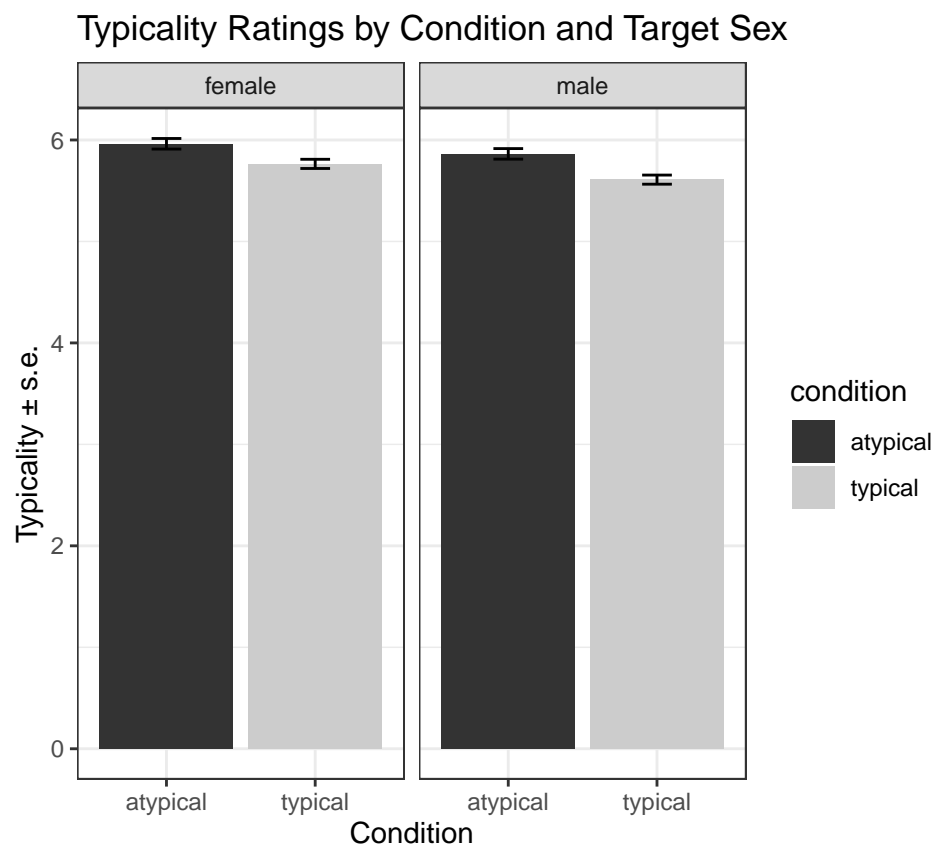
```
typicality_CxTS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition target.sex mean    sd    n    se
```

```
##   <fct>      <fct>      <dbl> <dbl> <int> <dbl>
## 1 atypical  female      5.96  2.03  1520 0.0521
## 2 atypical  male       5.86  2.03  1520 0.0519
## 3 typical   female      5.76  1.89  1740 0.0453
## 4 typical   male       5.61  1.87  1740 0.0448
```

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

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



The interaction between condition and target sex is not significant, $t(38) = -0.29$, $p = .775$.

Interaction - Typicality by Condition and Participant Sex

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

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



```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25811.2
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.2151 -0.5869 0.0446 0.6701 3.1612
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.9078 0.9528
## trial (Intercept) 0.0741 0.2722
## Residual 2.8434 1.6862
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.8887 0.1309 183.1292 44.969 <0.0000000000000002
## conditiontypical -0.2770 0.1763 159.0000 -1.571 0.118
## Sex1 0.1530 0.3112 159.0000 0.492 0.624
## conditiontypical:Sex1 0.1083 0.3896 159.0000 0.278 0.781
##
## (Intercept) ***
## conditiontypical
## Sex1
## conditiontypical:Sex1
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnt Sex1
## cndtntypcl -0.662
## Sex1 -0.375 0.279
## cndtntyp:S1 0.300 -0.452 -0.799
```

95% confidence interval

```
ci.38 <- confint(model.38, method = "Wald", level = 0.95)
ci.38
```

```
## 2.5 % 97.5 %
## .sig01 NA NA
## .sig02 NA NA
## .sigma NA NA
## (Intercept) 5.6320164 6.14532740
## conditiontypical -0.6225299 0.06857328
## Sex1 -0.4570190 0.76300859
## conditiontypical:Sex1 -0.6553512 0.87197455
```

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

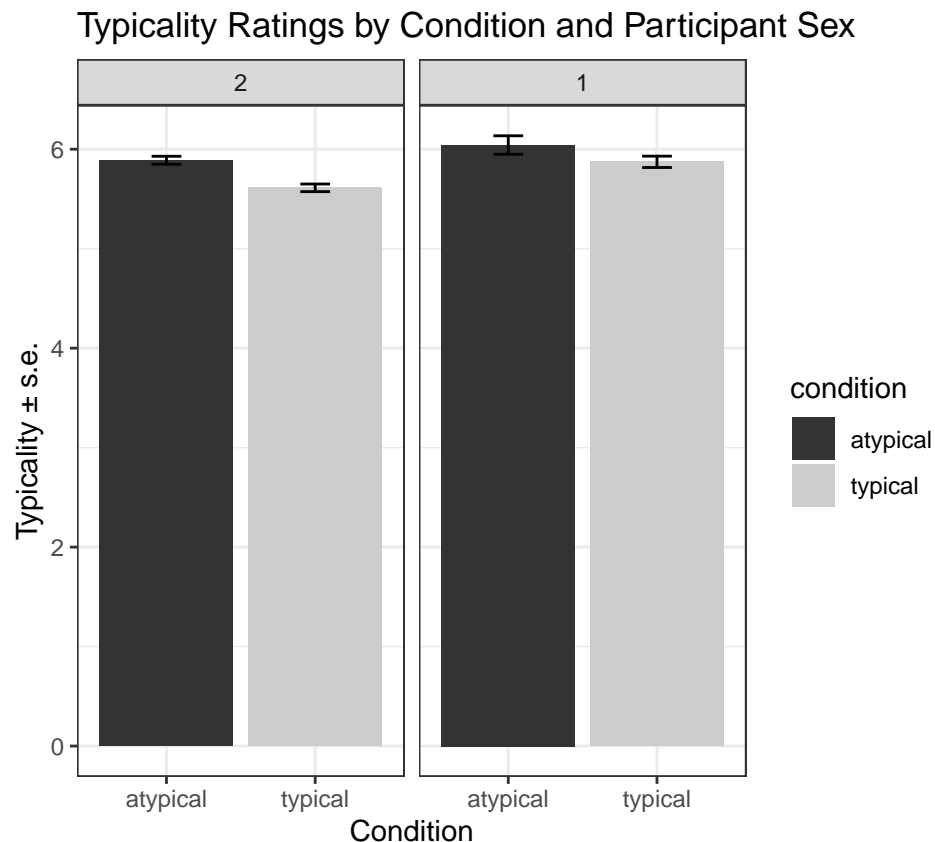
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
typicality_CxPS
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      5.89  2.03  2560 0.0401
## 2 atypical  1      6.04  2.04   480 0.0932
## 3 typical   2      5.61  1.91  2480 0.0383
## 4 typical   1      5.87  1.80  1000 0.0570
```

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

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



The interaction between condition and participant sex is not significant, $t(159) = 0.28$, $p = .781$.

Interaction - Typicality by Participant Sex and Target Sex

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ Sex * target.sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 25809.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.1707 -0.5827  0.0384  0.6697  3.2111
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.91216 0.9551
## trial   (Intercept) 0.07403 0.2721
## Residual                2.84009 1.6853
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)    5.82003    0.10108 203.80609  57.578
## Sex1           0.15811    0.19211 185.55758   0.823
## target.sexmale -0.13531    0.04748 6316.49914 -2.850
## Sex1:target.sexmale 0.03441    0.10062 6352.63975   0.342
##              Pr(>|t|)
## (Intercept)    < 0.0000000000000002 ***
## Sex1           0.41154
## target.sexmale 0.00439 **
## Sex1:target.sexmale 0.73235
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Sex1  trgt.s
## Sex1          -0.431
## target.sxml -0.235  0.124
## Sx1:trgt.sx  0.111 -0.262 -0.474
```

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

```
##                2.5 %      97.5 %
## .sig01          NA        NA
## .sig02          NA        NA
## .sigma          NA        NA
## (Intercept)    5.6219213  6.01814822
## Sex1          -0.2184122  0.53464214
## target.sexmale -0.2283678 -0.04224735
## Sex1:target.sexmale -0.1628003  0.23162746
```

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

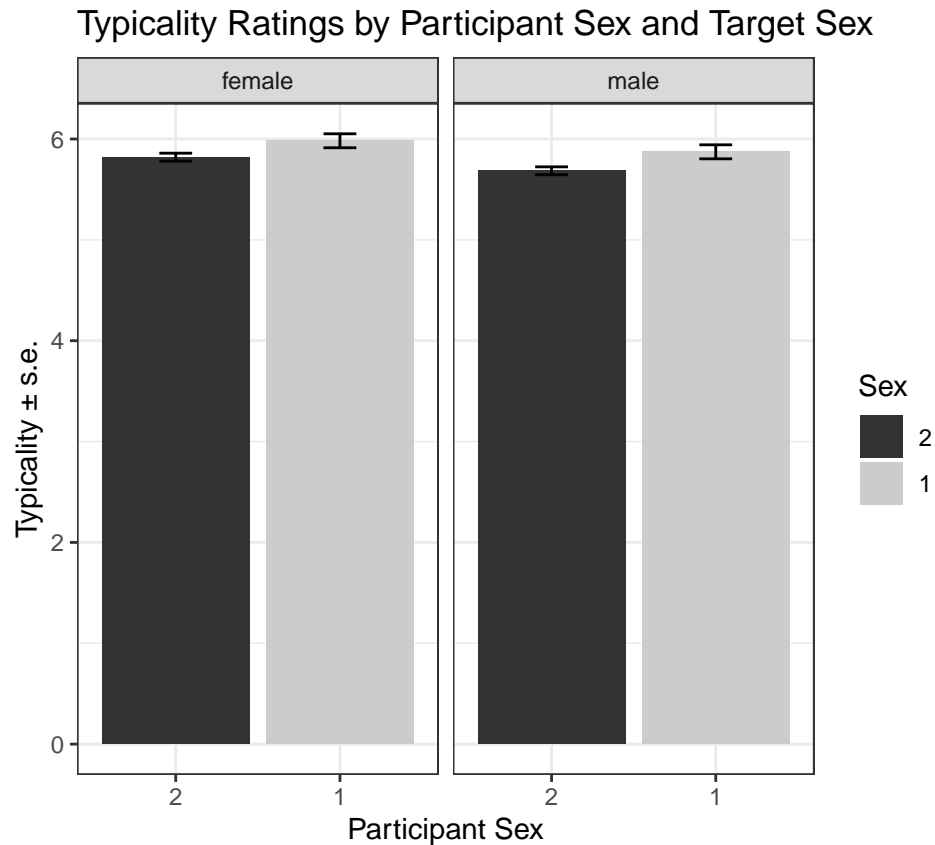
'summarise()' has grouped output by 'Sex'. You can override using the '.groups' argument.

```
typicality_PSxTS
```

```
## # A tibble: 4 x 6
## # Groups:   Sex [2]
##   Sex target.sex mean    sd    n    se
##   <fct> <fct>    <dbl> <dbl> <int> <dbl>
## 1 2     female    5.82  1.98  2520 0.0395
## 2 2     male     5.68  1.96  2520 0.0391
## 3 1     female    5.98  1.88   740 0.0690
## 4 1     male     5.87  1.89   740 0.0695
```

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

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



The interaction between participant sex and target sex is not significant, $t(6353) = 0.34$, $p = .732$.

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

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

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition * target.sex * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlopt"))
##
## REML criterion at convergence: 25811.4
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -4.1735 -0.5862 0.0394 0.6677 3.2065
##
## Random effects:
```

```
## Groups      Name      Variance Std.Dev.
## ID          (Intercept) 0.90787  0.9528
## trial       (Intercept) 0.07618  0.2760
## Residual                2.84038  1.6853
## Number of obs: 6520, groups: ID, 163; trial, 40
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      5.94766    0.14217 199.52816  41.833
## conditiontypical -0.25975    0.20238 200.11035  -1.284
## target.sexmale    -0.11797    0.10980  63.00479  -1.074
## Sex1              0.09401    0.32233 182.88027   0.292
## conditiontypical:target.sexmale -0.03445    0.19873  42.27232  -0.173
## conditiontypical:Sex1 0.17209    0.40352 182.88027   0.426
## target.sexmale:Sex1 0.11797    0.16765 6315.00005   0.704
## conditiontypical:target.sexmale:Sex1 -0.12755    0.20988 6315.00005  -0.608
##
##              Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## conditiontypical      0.201
## target.sexmale      0.287
## Sex1                0.771
## conditiontypical:target.sexmale 0.863
## conditiontypical:Sex1 0.670
## target.sexmale:Sex1 0.482
## conditiontypical:target.sexmale:Sex1 0.543
## ---
## 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
## condntypc1 -0.703
## target.sxm1 -0.386  0.443
## Sex1        -0.358  0.251  0.063
## cndntypc:.  0.348 -0.491 -0.902 -0.035
## cndntyp:S1  0.286 -0.408 -0.050 -0.799  0.056
## trgt.sxm:S1 0.093 -0.065 -0.241 -0.260  0.133  0.208
## cndntnt:.:S1 -0.074  0.106  0.193  0.208 -0.216 -0.260 -0.799
```

```
# 95% confidence interval
```

```
ci.40 <- confint(model.40, method = "Wald", level = 0.95)
ci.40
```

```
##              2.5 %      97.5 %
## .sig01          NA          NA
## .sig02          NA          NA
## .sigma          NA          NA
## (Intercept)      5.6689987 6.2263138
## conditiontypical -0.6564051 0.1368990
## target.sexmale    -0.3331749 0.0972374
## Sex1              -0.5377420 0.7257628
## conditiontypical:target.sexmale -0.4239467 0.3550455
## conditiontypical:Sex1 -0.6187906 0.9629633
## target.sexmale:Sex1 -0.2106274 0.4465649
## conditiontypical:target.sexmale:Sex1 -0.5389117 0.2838129
```

```

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

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

typicality_total

## # A tibble: 8 x 7
## # Groups:   condition, target.sex [4]
##   condition target.sex Sex    mean    sd     n    se
##   <fct>      <fct>    <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  female      2     5.95  2.02  1280 0.0564
## 2 atypical  female      1     6.04  2.11   240 0.136
## 3 atypical  male        2     5.83  2.03  1280 0.0568
## 4 atypical  male        1     6.04  1.98   240 0.128
## 5 typical   female      2     5.69  1.94  1240 0.0550
## 6 typical   female      1     5.95  1.76   500 0.0787
## 7 typical   male        2     5.54  1.88  1240 0.0533
## 8 typical   male        1     5.79  1.84   500 0.0825

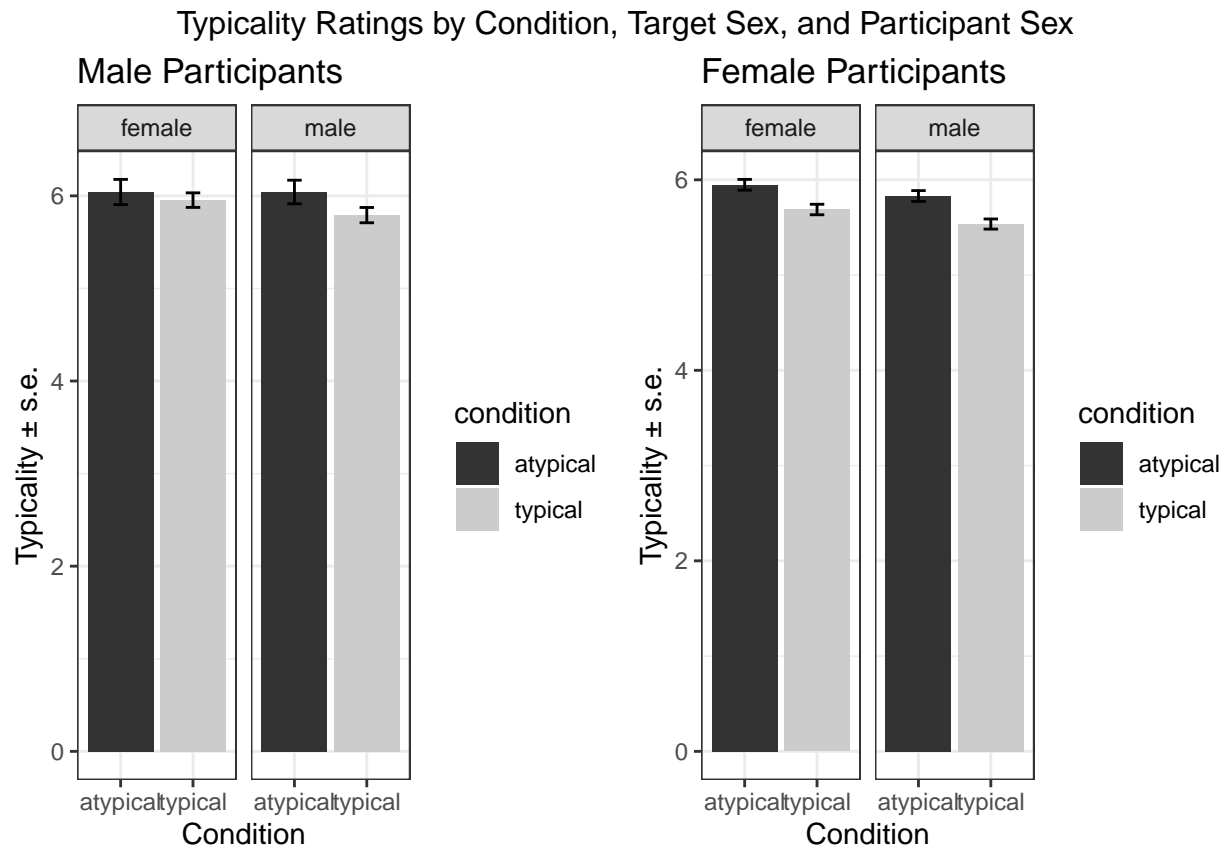
# subset means for male and female participants
male_typicality <- typicality_total %>%
  filter(Sex == "1")
female_typicality <- typicality_total %>%
  filter(Sex == "2")

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

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

grid.arrange(male_typicality_plot, female_typicality_plot, nrow = 1, top = textGrob("Typicality Ratings

```



The three way interaction is not significant, $t(6315) = .608$, $p = .543$.