

Auditory Aftereffects - Women's Voices Analysis

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Introduction

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

Stimuli. Test stimuli were audio recordings of 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-atypical and gender-typical, respectively, relative to test stimuli. Adaptors were generated from recordings of 5 young adult women 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 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-typical (feminized) or gender-atypical (masculinized) adaptation condition. On each trial, participants first heard an adapting voice followed by a test voice which they judged for attractiveness, 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 20 trials in pseudo-randomized order, with each adaptor presented four times.

Hypotheses. Variability in vocal tract length and laryngeal cavity size create large differences in fundamental frequency for male and female voices (Hillenbrand et al., 1995). Perceivers evaluate men and women with regard to these differences, rating men as more attractive when their voices have low fundamental frequency but women as more attractive when their voices have high fundamental frequency (Puts, 2005; Puts, Barndt, Welling, Dawood, & Burriss, 2011). Therefore, we predicted that adaptation to masculinized voices would produce contrastive aftereffects, making neutral female test voices sound more gender-typical and therefore more attractive. Conversely, adaptation to feminized voices should make neutral female test voices sound less gender-typical and therefore less attractive.

Analysis

Load Data

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

Factor

```

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

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

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

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

```

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

```
nrow(data)/20
```

```
## [1] 182
```

```

data <- data %>%
  filter(Sex == "1" | Sex == "2")
nrow(data)/20

```

```
## [1] 179
```

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)/20

```

```
## [1] 179
```

```

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

# femininity
data <- data %>%
  group_by(ID) %>%
  filter((max(femininity) - min(femininity) > 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)/20

```

```
## [1] 153
```

The original sample size was 179. After filtering participants whose responses did not meet the requirements of the data quality check, the final sample size is 153.

Demographics

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

Sex

```
table(data$Sex)/20 # 1 = male, 2 = female, 3 = other
```

```
##
##  1  2  3
## 81 72  0
```

The majority of the sample is male (52%), followed by female (46%) and other (1%).

Race

```
table(data$Race)/20 # 1 = Asian, 2 = Black, 3 = Latino, 4 = White, 5 = Biracial/Other
```

```
##
##  1  2  3  4  5
## 24 15 13 96  5
```

The majority of the sample is White (63%), followed by Asian (16%), Black (10%), Latino (8%), and Biracial/Other (3%).

Age

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

```
##      nbr.val      nbr.null      nbr.na      min      max
## 3060.000000    0.000000    0.000000   18.000000   66.000000
##      range      sum      median      mean      SE.mean
## 48.000000 95900.000000 30.000000 31.3398693  0.1930486
##  CI.mean.0.95      var      std.dev      coef.var
##    0.3785182   114.0394037  10.6789233    0.3407456
```

The average age is 31 years old, with a range from 18 - 66.

Politics

```
table(data$Politics)/20 # 1 = Very Conservative, 2 = Conservative, 3 = Moderat, 4 = Liberal, 5 = Very
```

```
##
##  1  2  3  4  5
##  3 18 43 56 33
```

There is a decent spread of political identities, with the majority leaning liberal.

Sexual Orientation

```
table(data$S0)/20 # 1 = Heterosexual, 2 = Gay/Lesbian/Queer, 3 = Bisexual, 4 = Not Sure
```

```
##
##  1  2  3  4
## 118  9 25  1
```

The majority of the sample is heterosexual (76%).

Education

```
table(data$Education)/20 # 1 = Less than high school, 2 = High school, 3 = Some college, 4 = Associate
```

```
##
##  1  2  3  4  5  6  7  8
##  3 27 38 11 42  3 21  8
```

Most participants have obtained a bachelor's degree.

Multilevel Analyses

The following analyses are done in a step-wise fashion.

Attraction

Two Independent Variables (Condition, Participant Sex) and One Independent Variable (Attraction)

Main Effect: Attraction by Condition (Atypical/Typical)

```
# 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: 11988.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6689 -0.5874  0.0478  0.6831  2.9483
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## ID       (Intercept)  1.0308     1.0153
## trial    (Intercept)  0.1487     0.3856
## Residual                    2.5999     1.6124
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      6.0130     0.1500  99.0022  40.077 <0.0000000000000002 ***
## conditiontypical -0.3636     0.1742 150.9987  -2.087      0.0385 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## condntntypcl -0.577
```

```
# 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)    5.7189225  6.30705153
## conditiontypical -0.7050844 -0.02220539
```

```
# group means
attraction_condition <- data %>%
  group_by(condition) %>%
  summarise(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    6.01  1.96 1540 0.0499
## 2 typical     5.65  1.92 1520 0.0492
```

Test voices were rated as more attractive after adaptation to masculinized voices ($M = 6.01$, $SD = 1.96$) relative to feminized voices ($M = 5.64$, $SD = 1.92$), $t(153) = -2.09$, $p < .05$.

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

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

model.2 <- 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.2)

## 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: 11992.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6570 -0.5918  0.0495  0.6852  2.9422
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0637  1.0314
## trial   (Intercept) 0.1487  0.3856
## Residual                2.5999  1.6124
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.85625    0.15497 106.15891  37.791 <0.0000000000000002 ***
## Sex1          -0.04514    0.17696 151.00554  -0.255      0.799
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.605

# 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)  5.552524 6.1599759
## Sex1        -0.391983 0.3017052
```

```
# group means
attraction_Sex <- data %>%
  group_by(Sex) %>%
  summarise(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      5.86  1.93  1440 0.0508
## 2 1      5.81  1.96  1620 0.0488
```

There is no difference in attraction ratings between male participants ($M = 5.81$, $SD = 1.96$) and female participants ($M = 5.86$, $SD = 1.93$), $t(151) = -0.26$, $p = .799$.

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

```
model.3 <- 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.3)
```

```
## 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: 11989.5
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -3.6742 -0.5863  0.0520  0.6865  2.9558
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)  1.0385     1.0191
##   trial    (Intercept)  0.1487     0.3856
##   Residual                    2.5999     1.6124
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      5.9408    0.1954 146.4071  30.401 <0.0000000000000002
## conditiontypical -0.1790    0.2552 149.0004  -0.702      0.484
## Sex1              0.1425    0.2464 149.0004   0.579      0.564
## conditiontypical:Sex1 -0.3460    0.3506 149.0004  -0.987      0.325
##
## (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 -0.617
## Sex1        -0.639  0.489
## cndtntyp:S1  0.449 -0.728 -0.703
```

```
# 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)     5.5577892 6.3237898
## conditiontypical -0.6791701 0.3211206
## Sex1            -0.3403843 0.6254720
## conditiontypical:Sex1 -1.0330815 0.3411310
```

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

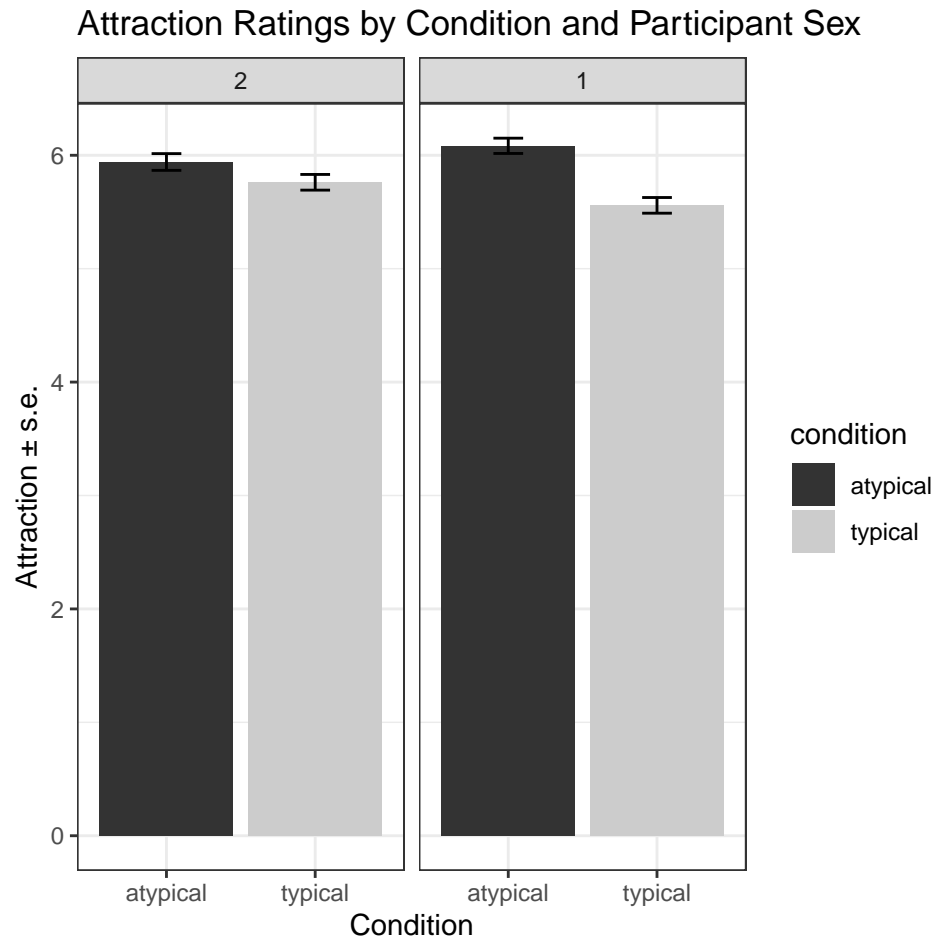
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
attraction_total
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n     se
##   <fct>     <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      5.94  2.03  760 0.0738
## 2 atypical  1      6.08  1.88  780 0.0674
## 3 typical   2      5.76  1.80  680 0.0691
## 4 typical   1      5.56  2.00  840 0.0691
```

```
# plot
attraction_inx2_plot <- ggplot(attraction_total, 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_inx2_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, $t(149) = -0.99$, $p = .325$.

Femininity

Main Effect: Femininity by Condition

```
model.5 <- lmer(femininity ~ condition + (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: femininity ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 11978.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -3.7384 -0.6263 0.0773 0.6935 2.4891
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.8790 0.9375
## trial (Intercept) 0.2252 0.4745
## Residual 2.6032 1.6134
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 6.2981 0.1561 67.0358 40.348 < 0.0000000000000002 ***
## conditiontypical -0.4941 0.1624 150.9995 -3.042 0.00277 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.517
```

```
# 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) 5.992118 6.6039860
## conditiontypical -0.812465 -0.1757441
```

```
# group means
femininity_condition <- data %>%
  group_by(condition) %>%
  summarise(mean = mean(femininity), sd = sd(femininity), n = n(), se = sd(femininity)/sqrt(n()))
femininity_condition
```

```
## # A tibble: 2 x 5
##   condition mean    sd    n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 atypical    6.30  1.91 1540 0.0486
## 2 typical     5.80  1.93 1520 0.0496
```

Test voices were rated as more feminine after adaptation to masculinized voices ($M = 6.30$, $SD = 1.91$) relative to feminized voices ($M = 5.79$, $SD = 1.94$), $t(153) = 3.15$, $p < .01$.

Main Effect: Femininity by Participant Sex

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

model.6 <- lmer(femininity ~ Sex + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx"),
```

```

      calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.6)

```

```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: femininity ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 11987.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7261 -0.6256  0.0743  0.6913  2.4753
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.9393  0.9692
## trial   (Intercept) 0.2252  0.4745
## Residual                2.6032  1.6134
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   6.0111     0.1616   74.2788  37.199 <0.0000000000000002 ***
## Sex1          0.0784     0.1675  150.9999   0.468      0.64
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.549

```

```

# 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)  5.6943943 6.3278279
## Sex1        -0.2498985 0.4066887

```

```

# group means
femininity_Sex <- data %>%
  group_by(Sex) %>%
  summarise(mean = mean(femininity), sd = sd(femininity), n = n(), se = sd(femininity)/sqrt(n()))
femininity_Sex

```

```

## # A tibble: 2 x 5

```

```
##   Sex    mean    sd     n     se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      6.01  1.96  1440 0.0516
## 2 1      6.09  1.91  1620 0.0475
```

There was no significant difference in femininity ratings between male participants ($M = 6.09$, $SD = 1.91$) and female participants ($M = 6.01$, $SD = 1.96$), $t(151) = 0.47$, $p = .64$.

Interaction: Femininity by Condition and Participant Sex

```
model.7 <- lmer(femininity ~ 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.7)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: femininity ~ condition * Sex + (1 | ID) + (1 | trial)
##   Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlsminb"))
##
## REML criterion at convergence: 11980
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -3.7453 -0.6279  0.0734  0.6912  2.4912
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)         0.8889   0.9428
##   trial    (Intercept)         0.2252   0.4745
##   Residual                        2.6032   1.6134
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      6.2158    0.1951 115.5703  31.854 <0.0000000000000002
## conditiontypical -0.4334    0.2383 149.0000  -1.819    0.071
## Sex1             0.1624    0.2301 149.0000   0.706    0.481
## conditiontypical:Sex1 -0.1233    0.3274 149.0000  -0.377    0.707
##
## (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 -0.577
## Sex1         -0.597  0.489
## cndntntyp:S1  0.420 -0.728 -0.703
```

```
# 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)    5.8333343 6.59824460
## conditiontypical -0.9005148 0.03364174
## Sex1          -0.2885837 0.61341502
## conditiontypical:Sex1 -0.7650183 0.51833826
```

```
# group means
femininity_total <- data %>%
  group_by(condition, Sex) %>%
  summarise(mean = mean(femininity), sd = sd(femininity), n = n(), se = sd(femininity)/sqrt(n()))
```

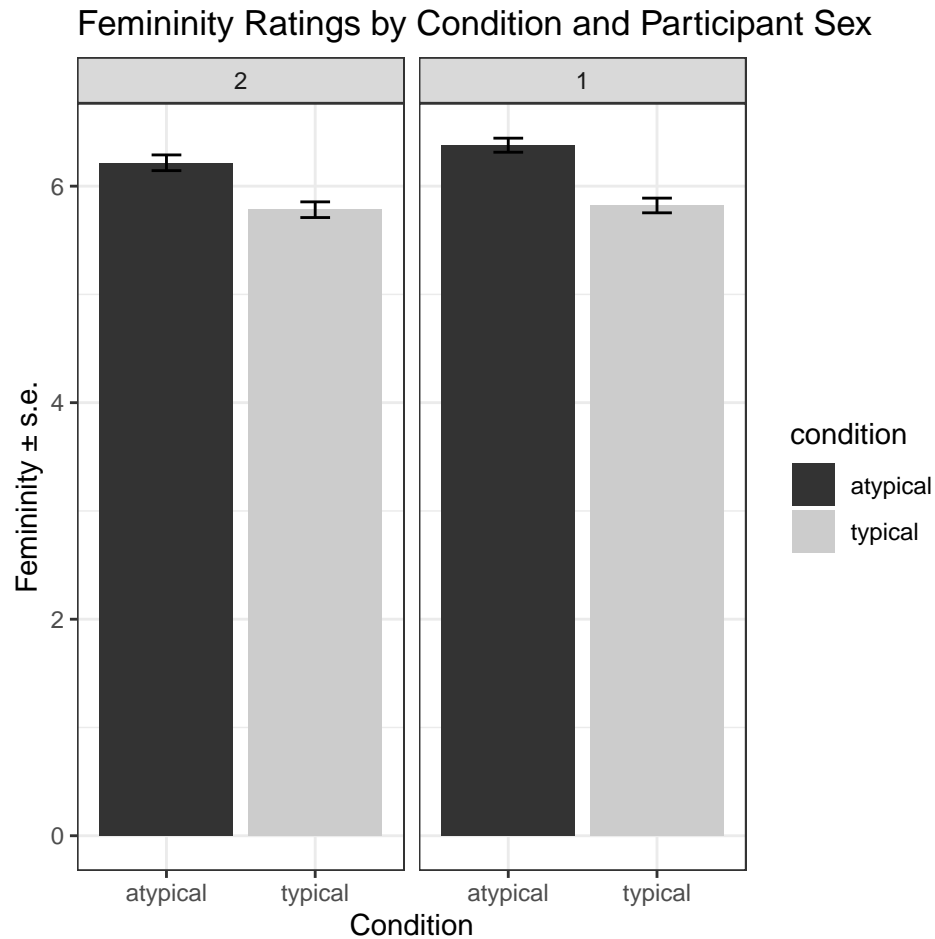
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
femininity_total
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd      n    se
##   <fct>    <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical 2      6.22  2.00   760 0.0725
## 2 atypical 1      6.38  1.81   780 0.0649
## 3 typical 2      5.78  1.89   680 0.0725
## 4 typical 1      5.82  1.97   840 0.0679
```

```
# plot
femininity_inx2_plot <- ggplot(femininity_total, 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()

femininity_inx2_plot + labs(title = "Femininity Ratings by Condition and Participant Sex",
  y = "Femininity ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(149) = -0.38$, $p = .707$.

Likability

Main Effect: Likability by Condition

```
model.9 <- 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.9)
```

```
## 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: 11341.9
##
## Scaled residuals:
## Min      1Q  Median      3Q      Max
```

```
## -3.8062 -0.5674 0.0724 0.6502 3.5064
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.83136 0.9118
## trial (Intercept) 0.08684 0.2947
## Residual 2.10863 1.4521
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 6.1773 0.1285 117.8380 48.078 <0.0000000000000002 ***
## conditiontypical -0.2062 0.1565 150.9985 -1.318 0.19
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.605
```

```
# 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) 5.9254481 6.4290974
## conditiontypical -0.5129544 0.1005142
```

```
# group means
likability_condition <- data %>%
  group_by(condition) %>%
  summarise(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    6.18  1.75 1540 0.0447
## 2 typical     5.97  1.72 1520 0.0441
```

There was no significant difference in ratings of likability between participants after adaptation to masculinized voices ($M = 6.18$, $SD = 1.75$) relative to feminized voices ($M = 5.97$, $SD = 1.72$), $t(151) = -1.32$, $p = .19$.

Main Effect: Likability by Participant Sex

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

model.10 <- lmer(likability ~ Sex + (1 | ID) + (1 | trial), data = data,
```

```

na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
  calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.10)

```

```

## 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: 11342.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.8090 -0.5641  0.0753  0.6481  3.5046
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.83660 0.9147
## trial   (Intercept) 0.08684 0.2947
## Residual                2.10864 1.4521
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   6.1528     0.1320 123.1410  46.610 <0.0000000000000002 ***
## Sex1          -0.1472     0.1572 151.0118  -0.936      0.351
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.630

```

```

# 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)  5.8940491 6.4115065
## Sex1        -0.4553407 0.1608962

```

```

# group means
likability_Sex <- data %>%
  group_by(Sex) %>%
  summarise(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      6.15  1.70  1440 0.0449
## 2 1      6.01  1.77  1620 0.0439
```

There is no difference in likability ratings by male ($M = 6.01$, $SD = 1.77$) and female ($M = 6.15$, $SD = 1.70$) participants, $t(151) = -0.94$, $p = .351$.

Interaction: Likability by Condition and Participant Sex

```
model.11 <- 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.11)
```

```
## 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: 11341.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7937 -0.5673  0.0744  0.6495  3.5181
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept) 0.82722   0.9095
##   trial    (Intercept) 0.08684   0.2947
##   Residual                    2.10864   1.4521
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value
## (Intercept)    6.13947    0.16996 155.22978  36.124
## conditiontypical  0.02817    0.22798 149.00534   0.124
## Sex1            0.07463    0.22013 149.00534   0.339
## conditiontypical:Sex1 -0.43037    0.31320 149.00534  -1.374
##
##              Pr(>|t|)
## (Intercept) <0.0000000000000002 ***
## conditiontypical    0.902
## Sex1                0.735
## conditiontypical:Sex1 0.171
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnt Sex1
## condntntypcl -0.633
## Sex1         -0.656  0.489
```

```
## cndtntyp:Sex1 0.461 -0.728 -0.703
```

```
# 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)      5.8063625 6.4725849
## conditiontypical -0.4186578 0.4750046
## Sex1             -0.3568204 0.5060782
## conditiontypical:Sex1 -1.0442338 0.1834914
```

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

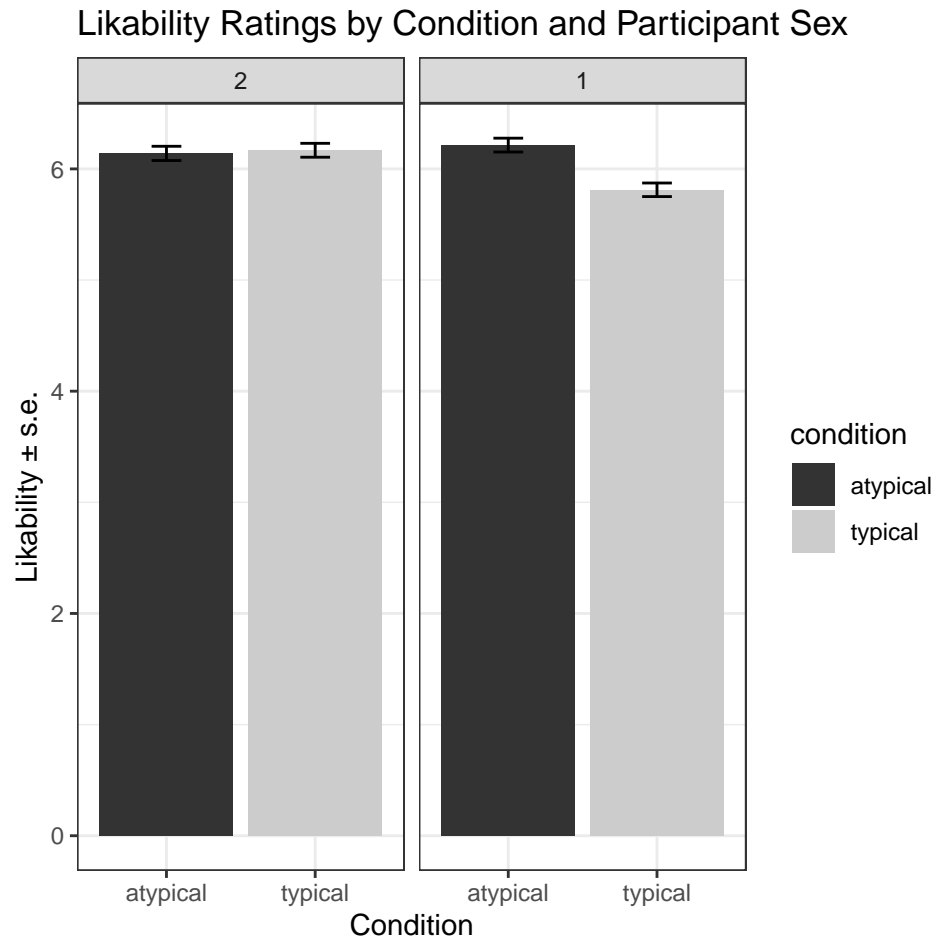
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
likability_total
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n     se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      6.14  1.77  760 0.0641
## 2 atypical  1      6.21  1.74  780 0.0623
## 3 typical   2      6.17  1.63  680 0.0625
## 4 typical   1      5.81  1.77  840 0.0611
```

```
# plot
likability_inx2_plot <- ggplot(likability_total, 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_inx2_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, $t(149) = -1.37, p=.171$.

Friends

Main Effect: Friends by Condition

```
model.13 <- 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.13)
```

```
## 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: 11765
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -3.6742 -0.5556 0.0715 0.6501 3.8974
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.87738 0.9367
## trial (Intercept) 0.08237 0.2870
## Residual 2.43351 1.5600
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.9792 0.1307 122.4651 45.733 <0.0000000000000002 ***
## conditiontypical -0.2049 0.1616 151.0096 -1.268 0.207
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.614
```

```
# 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) 5.7229727 6.2354688
## conditiontypical -0.5216432 0.1118859
```

```
# group means
friends_condition <- data %>%
  group_by(condition) %>%
  summarise(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 5.98 1.88 1540 0.0479
## 2 typical 5.77 1.80 1520 0.0461
```

There was no significant difference in friends ratings between participants after adaptation to masculinized voices ($M = 5.98$, $SD = 1.88$) relative to feminized voices ($M = 5.77$, $SD = 1.80$), $t(151) = -1.27$, $p = .207$.

Main Effect: Friends by Participant Sex

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

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

```
## 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: 11766.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6673 -0.5503  0.0701  0.6476  3.8914
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.88803  0.9424
## trial   (Intercept) 0.08237  0.2870
## Residual                2.43351  1.5600
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)  5.873611    0.134692 127.906124  43.608 <0.0000000000000002 ***
## Sex1         0.007253    0.162755 151.002639   0.045      0.965
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.640
```

```
# 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)  5.6096191 6.1376032
## Sex1        -0.3117412 0.3262473
```

```
# group means
friends_Sex <- data %>%
  group_by(Sex) %>%
  summarise(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      5.87  1.80  1440 0.0475
## 2 1      5.88  1.87  1620 0.0466
```

There is no difference in friends ratings between male participants ($M = 5.88$, $SD = 1.87$) and female participants ($M = 5.87$, $SD = 1.80$), $t(151) = 0.05$, $p = .965$.

Interaction: Friends by Condition and Participant Sex

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

```
## 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 = "nloptnlo"))
##
## REML criterion at convergence: 11764.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6844 -0.5569  0.0726  0.6549  3.9052
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.87392 0.9348
## trial   (Intercept) 0.08237 0.2870
## Residual                2.43350 1.5600
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.84211    0.17412 156.38069  33.552
## conditiontypical    0.06672    0.23555 148.99677   0.283
## Sex1              0.27072    0.22744 148.99677   1.190
## conditiontypical:Sex1 -0.51406    0.32360 148.99677  -1.589
##              Pr(>|t|)
## (Intercept)      <0.0000000000000002 ***
## conditiontypical      0.777
## Sex1                0.236
## conditiontypical:Sex1  0.114
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnt Sex1
## condntntypcl -0.639
## Sex1         -0.662  0.489
## cndntntyp:S1  0.465 -0.728 -0.703
```

```
# 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)    5.5008342 6.1833763
## conditiontypical -0.3949434 0.5283800
## Sex1           -0.1750540 0.7164845
## conditiontypical:Sex1 -1.1482995 0.1201744
```

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

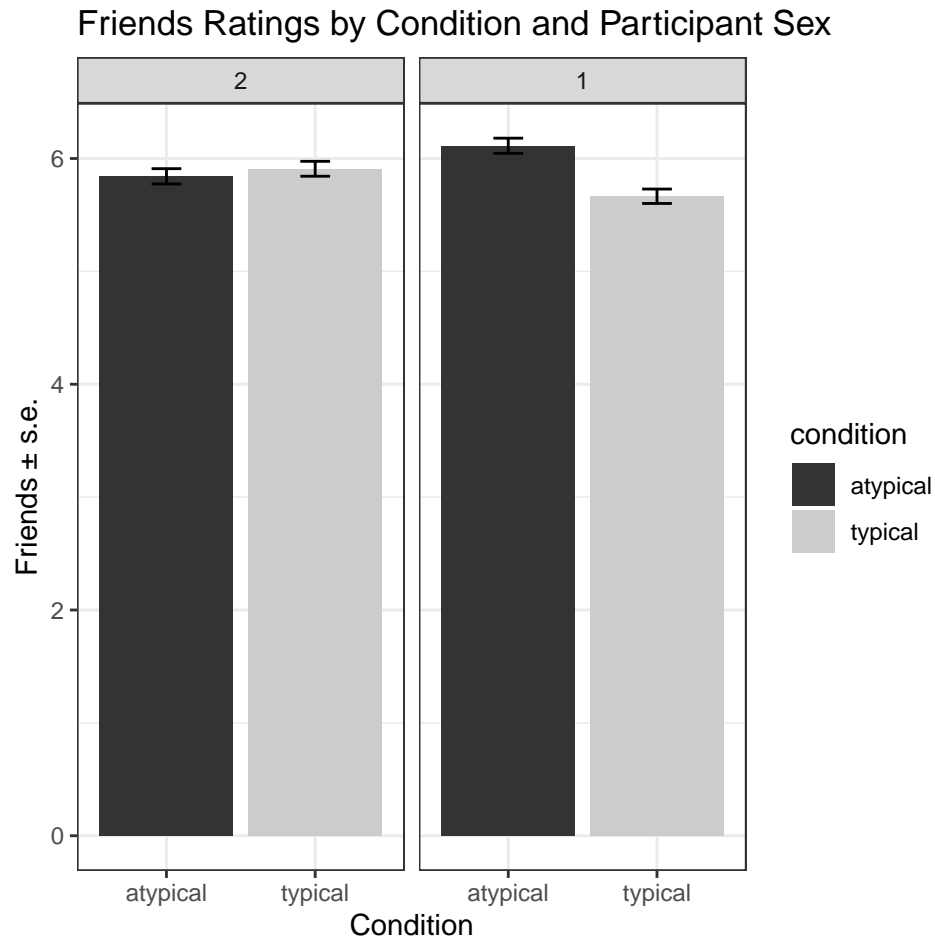
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
friends_total
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      5.84  1.87   760 0.0679
## 2 atypical  1      6.11  1.88   780 0.0672
## 3 typical   2      5.91  1.72   680 0.0661
## 4 typical   1      5.67  1.85   840 0.0637
```

```
# plot
friends_inx2_plot <- ggplot(friends_total, 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_inx2_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, $t(149) = -1.59$, $p = .114$.

Typicality

Main Effect: Typicality by Condition

```
model.17 <- lmer(typicality ~ condition + (1 | ID) + (1 | trial), data = data,
  na.action = "na.exclude", control = lmerControl(optimizer = "optimx",
    calc.derivs = FALSE, optCtrl = list(method = "nlminb")))
summary(model.17)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: typicality ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 11783.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```



```
## -3.3696 -0.5808 0.0653 0.6233 3.5505
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.0309 1.0153
## trial (Intercept) 0.1867 0.4321
## Residual 2.4195 1.5555
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.74156 0.15587 85.79474 36.84 <0.0000000000000002 ***
## conditiontypical 0.04857 0.17354 151.00000 0.28 0.78
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.553
```

```
# 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) 5.4360504 6.0470665
## conditiontypical -0.2915603 0.3887066
```

```
# group means
typicality_condition <- data %>%
  group_by(condition) %>%
  summarise(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  5.74  1.91 1540 0.0487
## 2 typical   5.79  1.89 1520 0.0485
```

There was no significant difference in ratings of typicality between participants after adaptation to masculinized voices ($M = 5.74$, $SD = 1.91$) relative to feminized voices ($M = 5.79$, $SD = 1.90$), $t(151) = 0.28$, $p = .78$.

Main Effect: Typicality by Participant Sex

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

model.18 <- 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.18)

```

```

## 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: 11783.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3703 -0.5817  0.0654  0.6226  3.5482
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0314  1.0156
## trial   (Intercept) 0.1867  0.4321
## Residual                2.4195  1.5555
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.75278    0.15919  90.51500   36.14 <0.0000000000000002 ***
## Sex1          0.02438    0.17387 150.99991    0.14      0.889
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.578

```

```

# 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)  5.4407684 6.0647871
## Sex1        -0.3163997 0.3651651

```

```

# group means
typicality_Sex <- data %>%
  group_by(Sex) %>%
  summarise(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  1.86  1440  0.0490
## 2 1      5.78  1.94  1620  0.0481
```

There is no difference in typicality ratings between female ($M = 5.75$, $SD = 1.86$) and male ($M = 5.78$, $SD = 1.94$) participants, $t(151) = 0.14$, $p = .889$.

Interaction: Typicality by Condition and Participant Sex

```
model.19 <- 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.19)
```

```
## 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 = "nlsminb"))
##
## REML criterion at convergence: 11785.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3731 -0.5834  0.0648  0.6254  3.5553
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0427  1.0211
## trial   (Intercept) 0.1867  0.4321
## Residual                2.4195  1.5555
## Number of obs: 3060, groups: ID, 153; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value
## (Intercept)    5.78947    0.19990 136.56921  28.962
## conditiontypical -0.07771    0.25465 148.99900  -0.305
## Sex1           -0.09460    0.24589 148.99900  -0.385
## conditiontypical:Sex1  0.23641    0.34985 148.99900   0.676
##
##              Pr(>|t|)
## (Intercept) <0.0000000000000002 ***
## conditiontypical      0.761
## Sex1                  0.701
## conditiontypical:Sex1  0.500
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnt Sex1
## condntntypcl -0.602
## Sex1         -0.623  0.489
```

```
## cndtntyp:S1 0.438 -0.728 -0.703
```

```
# 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)    5.3976771 6.1812702
## conditiontypical -0.5768224 0.4214044
## Sex1          -0.5765336 0.3873298
## conditiontypical:Sex1 -0.4492800 0.9220972
```

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

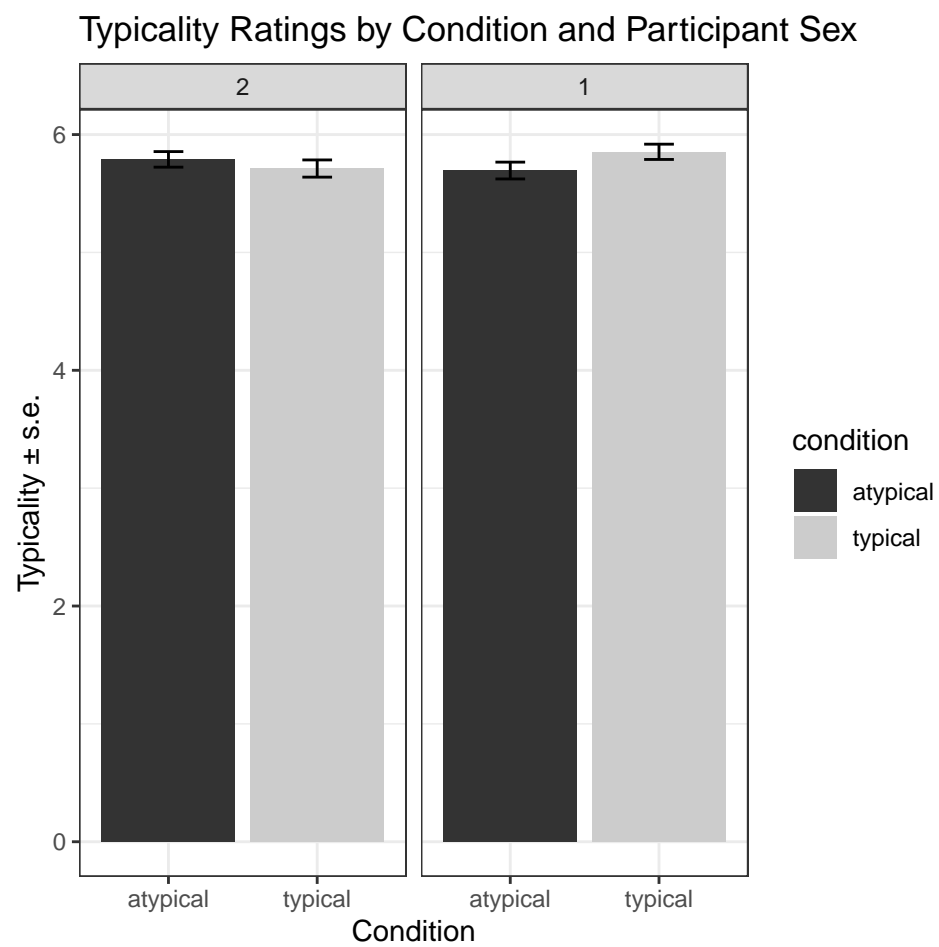
```
## 'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.
```

```
typicality_total
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      5.79  1.82  760 0.0662
## 2 atypical  1      5.69  1.99  780 0.0714
## 3 typical   2      5.71  1.90  680 0.0729
## 4 typical   1      5.85  1.88  840 0.0649
```

```
# plot
typicality_inx2_plot <- ggplot(typicality_total, 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_inx2_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, $t(149) = 0.68$, $p = .500$.