

Auditory Aftereffects Men's Voices Analysis

Kelsey Neuenswander

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Introduction

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

Stimuli. Test stimuli were audio recordings of 20 young adult men 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, respectively, relative to test stimuli. 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.

Procedure. We recruited U.S. resident from Prolific. After providing consent, participants were randomly assigned to either the gender-atypical (feminized) or gender-typical (masculinized) adaptation condition. On each trial, participants first heard an adapting voice followed by a test voice which they judged for attractiveness, masculinity, 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 feminized voices would produce contrastive aftereffects, making neutral male test voices sound more gender-typical and therefore more attractive. Conversely, adaptation to masculinized voices should make neutral male 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/Men/Real")
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] 179
```

```

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

```

```
## [1] 175
```

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] 175
```

```

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

# masculinity
data <- data %>%
  group_by(ID) %>%
  filter((max(masculinity) - min(masculinity) > 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] 166
```

The original sample size was 175. After filtering participants whose responses did not meet the requirements of the data quality check, the final sample size is 166.

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
## 30 136  0
```

The majority of the sample is female (82%), followed by male (18%).

Race

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

```
##
##  1  2  3  4  5
## 10 14 17 113 12
```

The majority of the sample is White (69%), followed by Latino (10%), Black (8%), Biracial/Other (8%), and Asian (6%).

Age

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

```
##      nbr.val      nbr.null      nbr.na      min      max
## 3320.0000000  0.0000000  0.0000000  18.0000000  72.0000000
##      range      sum      median      mean      SE.mean
## 54.0000000 84160.0000000 23.0000000 25.3493976  0.1472108
## CI.mean.0.95      var      std.dev      coef.var
##  0.2886331  71.9477851  8.4822040  0.3346117
```

The average age is 25 years old, with a range from 18 - 72.

Politics

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

```
##
##  1  2  3  4  5
##  1  9 47 68 41
```

The majority of the sample is moderate to liberal.

Sexual Orientation

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

```
##
##  1  2  3  4
## 103 15 42  6
```

The majority of the sample is heterosexual (62%) followed by bisexual (25%) and gay (9%).

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
##  1 31 50 17 40 10 14  3
```

Most participants have attended at least some college.

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 = "nlminb")))
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: 13758.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.03988 -0.68186  0.02833  0.69512  2.75984
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0979  1.0478
## trial   (Intercept) 0.2737  0.5231
## Residual              3.2805  1.8112
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      5.5655      0.1694  64.8571  32.848 < 0.0000000000000002 ***
## conditiontypical -0.6466      0.1744 164.0000  -3.708    0.000286 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## condntntypcl -0.508

# 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)    5.2333986  5.8975538
## conditiontypical -0.9883759 -0.3047716

# 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    5.57  2.17 1680 0.0531
## 2 typical     4.92  2.13 1640 0.0525

```

Test voices were rated as more attractive after adaptation to feminized voices ($M = 5.57$, $SD = 2.17$) relative to masculinized voices ($M = 4.92$, $SD = 2.13$), $t(164) = -3.71$, $p < .001$.

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: 13760.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.00845 -0.67281  0.03536  0.70415  2.74799
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.1168  1.0568
## trial   (Intercept) 0.2737  0.5231
## Residual                 3.2805  1.8112
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)   5.1085     0.1520 44.9564  33.610 < 0.0000000000000002 ***
## Sex1          0.7615     0.2283 163.9986   3.336    0.00105 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.271

# 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) 4.810558 5.406354
## Sex1        0.314126 1.208962
```

```
# 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      5.11  2.17  2720 0.0416
## 2 1      5.87  2.10   600 0.0856
```

Male participants ($M = 5.87$, $SD = 2.10$) rated test voices as significantly more attractive than female participants ($M = 5.11$, $SD = 2.17$), $t(164) = 3.34$, $p < .01$.

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: 13746.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.02936 -0.68547  0.03129  0.69776  2.76663
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0135  1.0067
## trial   (Intercept) 0.2737  0.5231
## Residual              3.2805  1.8112
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      5.4846     0.1761  72.9144  31.150 < 0.0000000000000002
## conditiontypical -0.7522     0.1861 162.0007  -4.042    0.0000817
## Sex1              0.4248     0.3015 162.0007   1.409     0.161
## conditiontypical:Sex1 0.6678     0.4386 162.0007   1.523     0.130
##
## (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 -0.528
## Sex1        -0.326  0.309
## cndtntyp:S1  0.224 -0.424 -0.688
```

```
# 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)     5.1394731  5.8296445
## conditiontypical -1.1169549 -0.3874569
## Sex1            -0.1661447  1.0157771
## conditiontypical:Sex1 -0.1917372  1.5273989
```

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

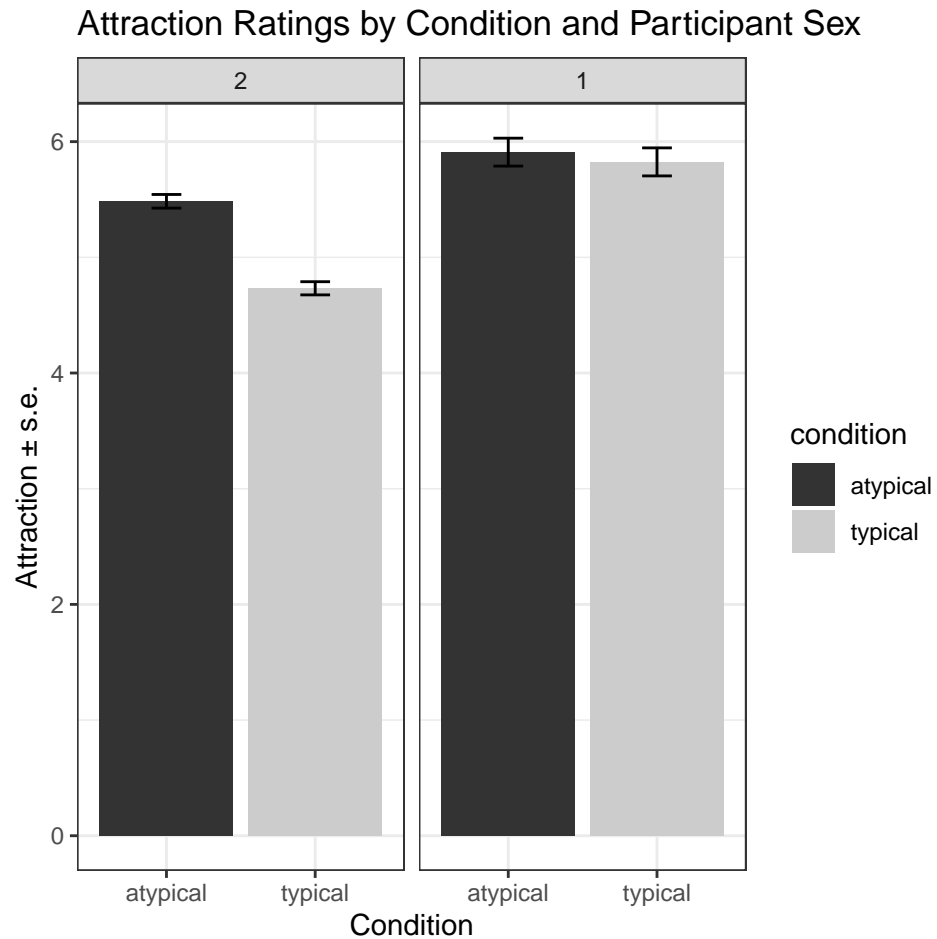
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
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      5.48  2.17  1360 0.0589
## 2 atypical  1      5.91  2.16   320 0.121
## 3 typical   2      4.73  2.10  1360 0.0569
## 4 typical   1      5.82  2.03   280 0.121
```

```
# 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, $t(162) = 1.52$, $p = .130$.

Masculinity

Main Effect: Masculinity by Condition

```
model.5 <- lmer(masculinity ~ 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: masculinity ~ condition + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 12858.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -4.0522 -0.6320 0.0302 0.6474 3.2915
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.9611 0.9803
## trial (Intercept) 0.1593 0.3992
## Residual 2.4890 1.5777
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.9119 0.1445 87.0086 40.904 < 0.0000000000000002 ***
## conditiontypical -0.9747 0.1617 164.0008 -6.026 0.0000000107 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.553
```

```
# 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) 5.628630 6.1951793
## conditiontypical -1.291722 -0.6576974
```

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

```
## # A tibble: 2 x 5
##   condition mean    sd    n    se
##   <fct>      <dbl> <dbl> <int> <dbl>
## 1 atypical  5.91  1.90 1680 0.0463
## 2 typical   4.94  1.89 1640 0.0467
```

Test voices were rated as more masculine after adaptation to feminized voices ($M = 5.91$, $SD = 1.90$) relative to masculinized voices ($M = 4.94$, $SD = 1.89$), $t(164) = -6.03$, $p < .01$.

Main Effect: Masculinity by Participant Sex

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

model.6 <- lmer(masculinity ~ 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: masculinity ~ Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 12882.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0323 -0.6384  0.0294  0.6424  3.2786
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.1400  1.0677
## trial   (Intercept) 0.1594  0.3992
## Residual                2.4890  1.5777
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)   5.3147     0.1314  65.8453  40.447 < 0.0000000000000002 ***
## Sex1          0.6403     0.2268 163.9989   2.823    0.00535 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.312

```

```

# 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) 5.057166 5.572245
## Sex1       0.195738 1.084850

```

```

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

```

```
## # A tibble: 2 x 5
##   Sex    mean    sd      n      se
##   <fct> <dbl> <dbl> <int> <dbl>
## 1 2      5.31  1.94  2720 0.0373
## 2 1      5.96  1.93   600 0.0787
```

Male participants ($M = 5.96$, $SD = 1.93$) rated test voices as significantly more masculine than female participants ($M = 5.31$, $SD = 1.94$), $t(164) = 2.82$, $p < .01$.

Interaction: Masculinity by Condition and Participant Sex

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

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: masculinity ~ condition * Sex + (1 | ID) + (1 | trial)
## Data: data
## Control:
## lmerControl(optimizer = "optimx", calc.derivs = FALSE, optCtrl = list(method = "nlminb"))
##
## REML criterion at convergence: 12847.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0408 -0.6345  0.0325  0.6434  3.3000
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.8974  0.9473
## trial   (Intercept) 0.1594  0.3992
## Residual                2.4890  1.5777
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      5.8632    0.1516  98.0136  38.665 < 0.0000000000000002
## conditiontypical -1.0971    0.1734 161.9996  -6.328  0.000000000233
## Sex1              0.2555    0.2809 161.9996   0.910    0.3643
## conditiontypical:Sex1 0.7462    0.4085 161.9996   1.826    0.0696
##
## (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 -0.572
## Sex1          -0.353  0.309
```

```
## cndtntyp:S1 0.243 -0.424 -0.688
```

```
# 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)    5.56602046 6.1604501
## conditiontypical -1.43683541 -0.7572822
## Sex1           -0.29498628 0.8060157
## conditiontypical:Sex1 -0.05455211 1.5468840
```

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

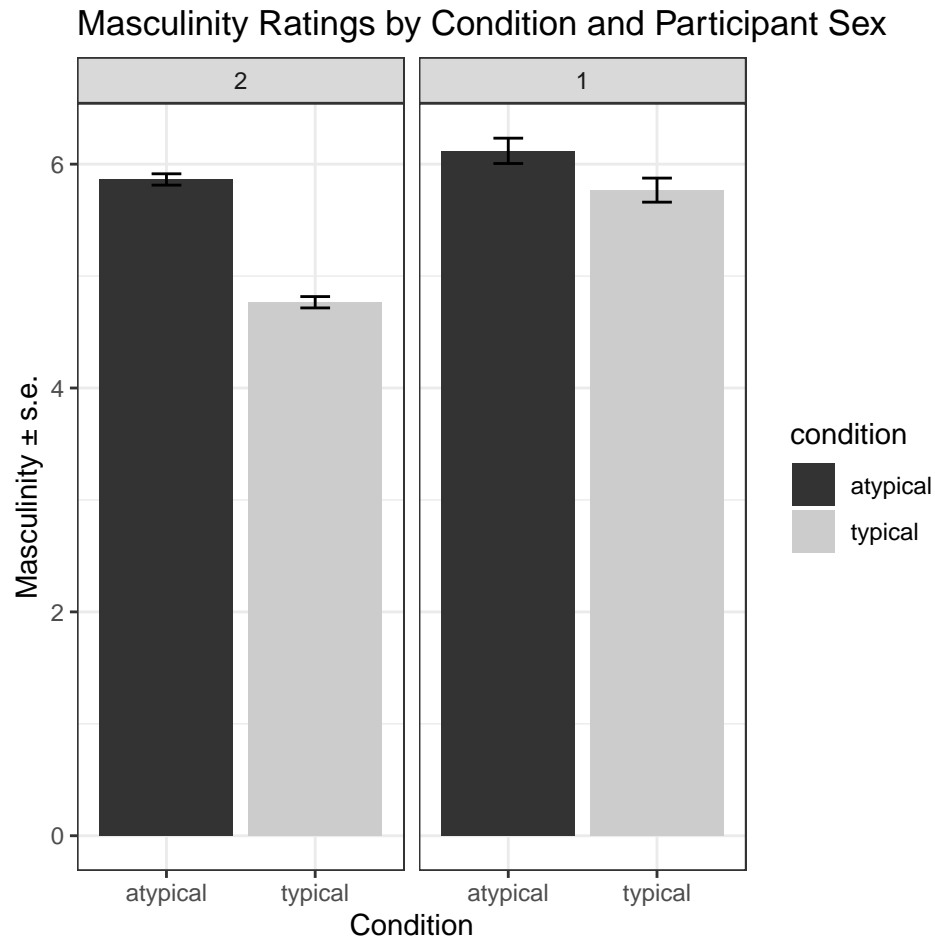
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
masculinity_total
```

```
## # A tibble: 4 x 6
## # Groups:   condition [2]
##   condition Sex    mean    sd     n    se
##   <fct>      <fct> <dbl> <dbl> <int> <dbl>
## 1 atypical  2      5.86  1.86  1360 0.0505
## 2 atypical  1      6.12  2.02   320 0.113
## 3 typical   2      4.77  1.87  1360 0.0506
## 4 typical   1      5.77  1.80   280 0.107
```

```
# plot
masculinity_inx2_plot <- ggplot(masculinity_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()

masculinity_inx2_plot + labs(title = "Masculinity Ratings by Condition and Participant Sex",
  y = "Masculinity ± s.e.", x = "Condition") + theme_bw()
```



The interaction between condition and participant sex is not significant, $t(162) = 1.83$, $p = .070$.

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: 12896.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -3.2769 -0.5664 0.0719 0.6561 2.9580
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.7622 0.8730
## trial (Intercept) 0.2330 0.4827
## Residual 2.5408 1.5940
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.9012 0.1491 56.2065 39.574 <0.0000000000000002 ***
## conditiontypical -0.3006 0.1464 163.9980 -2.053 0.0416 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.485
```

```
# 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) 5.6089233 6.19345768
## conditiontypical -0.5874969 -0.01366457
```

```
# 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  5.90  1.91 1680 0.0466
## 2 typical   5.60  1.84 1640 0.0454
```

Test voices were rated as significantly more likable after adaptation to feminized voices ($M = 5.90$, $SD = 1.91$) relative to masculinized voices ($M = 5.60$, $SD = 1.84$), $t(164) = -2.05$, $p < .05$.

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: 12896.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2898 -0.5652  0.0667  0.6575  2.9506
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.7613  0.8726
## trial   (Intercept) 0.2330  0.4827
## Residual                2.5408  1.5940
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.6809     0.1348   39.4815  42.129 <0.0000000000000002 ***
## Sex1          0.3975     0.1901  163.9983   2.091    0.0381 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.255

```

```

# 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) 5.41659326 5.9451714
## Sex1       0.02482591 0.7700761

```

```

# 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      5.68  1.86  2720 0.0356
## 2 1      6.08  1.95   600 0.0797
```

Male participants ($M = 6.08$, $SD = 1.95$) rate test voices as significantly more likable than female participants ($M = 5.68$, $SD = 1.86$), $t(164) = 2.09$, $p < .05$.

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: 12893.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2936 -0.5668  0.0715  0.6607  2.9632
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   ID       (Intercept)         0.7478   0.8647
##   trial    (Intercept)         0.2330   0.4827
##   Residual                        2.5408   1.5940
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)      5.8507    0.1566   65.7949   37.367 <0.0000000000000002
## conditiontypical -0.3397    0.1604  162.0003   -2.118    0.0357
## Sex1              0.2649    0.2599  162.0003    1.019    0.3096
## conditiontypical:Sex1 0.2598    0.3780  162.0003    0.687    0.4929
##
## (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 -0.512
## Sex1          -0.316  0.309
## cndntntyp:S1  0.217 -0.424 -0.688
```

```
# 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)      5.5438564  6.15761418
## conditiontypical -0.6540969 -0.02531488
## Sex1             -0.2444819  0.77426134
## conditiontypical:Sex1 -0.4810992  1.00068952
```

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

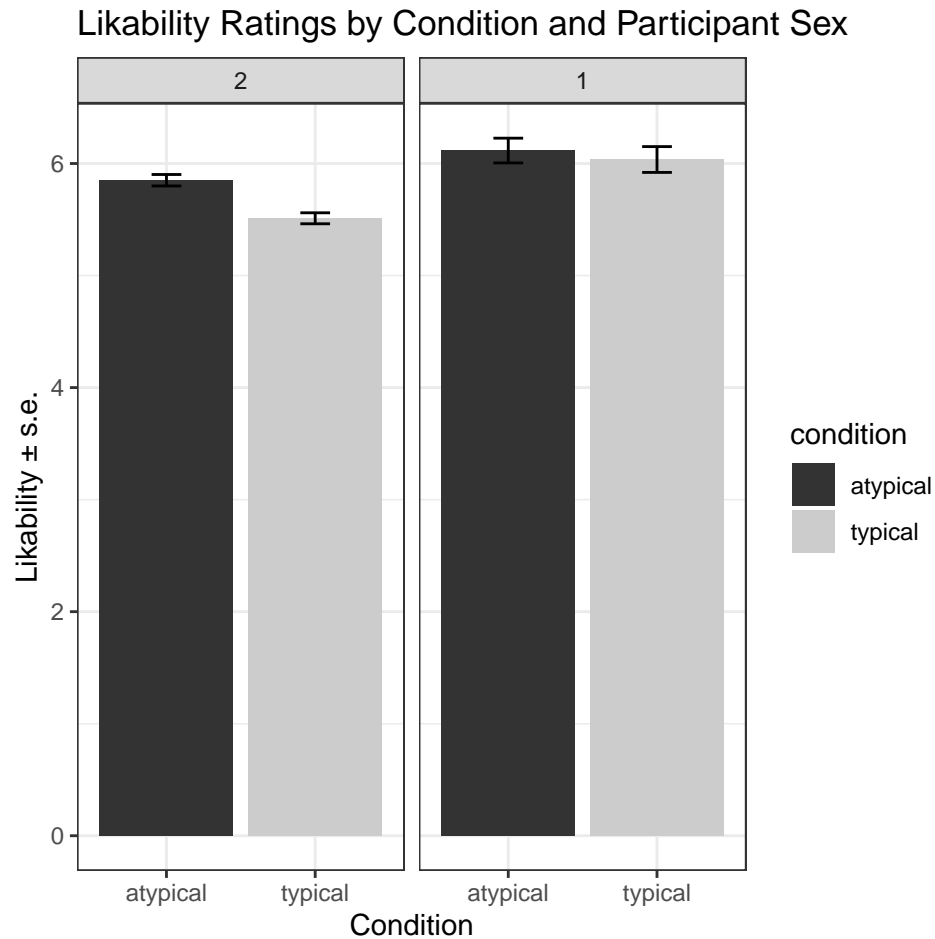
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
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      5.85  1.89  1360 0.0512
## 2 atypical 1      6.12  1.98   320 0.110
## 3 typical  2      5.51  1.81  1360 0.0491
## 4 typical  1      6.04  1.93   280 0.115
```

```
# 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, $t(162) = 0.69$, $p = .493$.

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: 13368.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -3.2709 -0.6011 0.0450 0.6499 3.3173
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 1.0677 1.0333
## trial (Intercept) 0.1802 0.4245
## Residual 2.9094 1.7057
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 5.6399 0.1531 85.7267 36.828 <0.0000000000000002 ***
## conditiontypical -0.3167 0.1710 164.0000 -1.852 0.0658 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.552
```

```
# 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) 5.3397322 5.94002970
## conditiontypical -0.6518426 0.01842214
```

```
# 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  5.64  2.10  1680 0.0511
## 2 typical   5.32  1.97  1640 0.0486
```

There was no significant difference in friends ratings between participants after adaptation to feminized voices ($M = 5.64$, $SD = 2.10$) relative to masculinized voices ($M = 5.32$, $SD = 1.97$), $t(164) = -1.85$, $p = .066$.

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 = "nlminb")))
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: 13361.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2425 -0.5991  0.0431  0.6543  3.3275
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0214  1.0106
## trial   (Intercept) 0.1802  0.4245
## Residual                2.9094  1.7057
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.3585     0.1326   55.3247  40.404 <0.0000000000000002 ***
## Sex1          0.6915     0.2179  164.0006   3.174      0.0018 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.297
```

```
# 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) 5.098519 5.618392
## Sex1        0.264489 1.118599
```

```
# 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      5.36  2.02  2720 0.0387
## 2 1      6.05  2.05   600 0.0838
```

Male participants ($M = 6.05$, $SD = 2.05$) rated test voices as significantly more friendly than female participants ($M = 5.36$, $SD = 2.02$), $t(164) = 3.17$, $p < .01$.

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 = "nloptnlopt")))
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 = "nloptnlopt"))
##
## REML criterion at convergence: 13358.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2534 -0.6016  0.0462  0.6519  3.3087
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 1.0025  1.0013
## trial   (Intercept) 0.1802  0.4245
## Residual                2.9094  1.7057
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)      5.5559     0.1609  97.1127  34.528 <0.0000000000000002
## conditiontypical -0.3949     0.1838 161.9965  -2.149    0.0331
## Sex1              0.4410     0.2977 161.9965   1.481    0.1405
## conditiontypical:Sex1 0.5087     0.4330 161.9965   1.175    0.2418
##
## (Intercept)      ***
## conditiontypical  *
## Sex1
## conditiontypical:Sex1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnt Sex1
## cndtnttypcl -0.571
## Sex1        -0.352  0.309
## cndtntyp:S1 0.242 -0.424 -0.688
```

```
# 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)    5.2405088  5.87125593
## conditiontypical -0.7549968 -0.03470908
## Sex1           -0.1425071  1.02449239
## conditiontypical:Sex1 -0.3400234  1.35740785
```

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

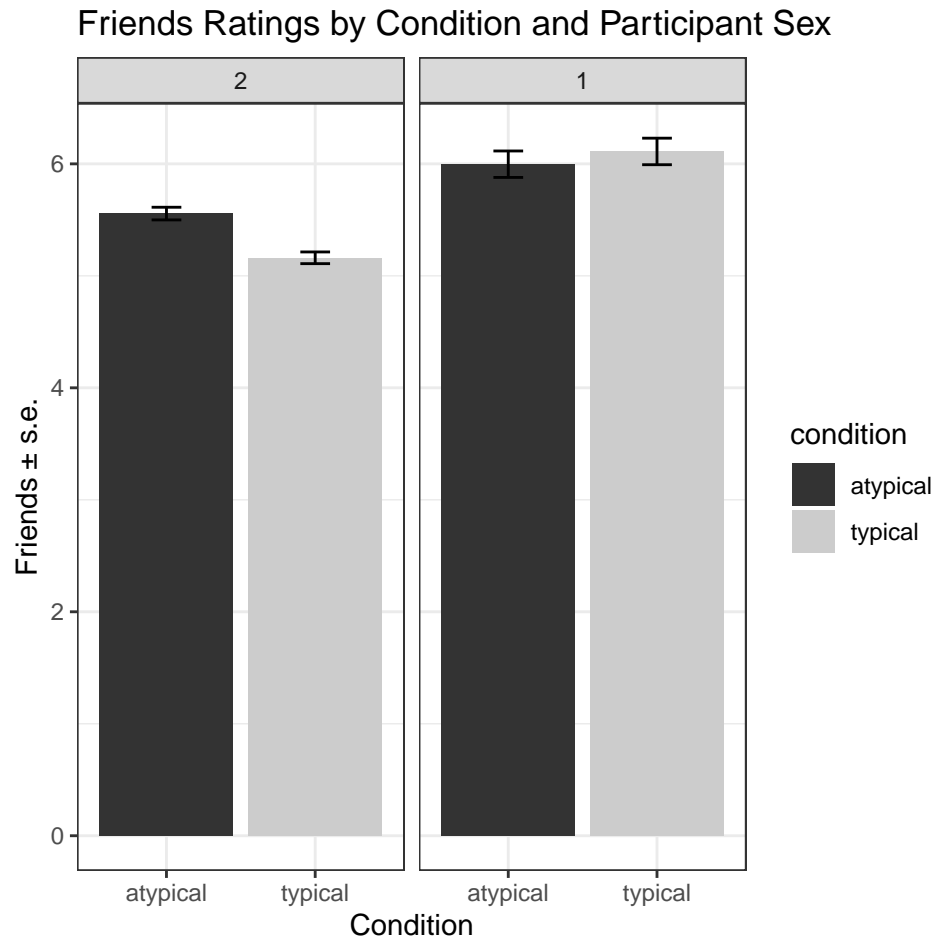
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
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      5.56  2.08  1360 0.0565
## 2 atypical  1      6.00  2.11   320 0.118
## 3 typical   2      5.16  1.93  1360 0.0522
## 4 typical   1      6.11  1.98   280 0.119
```

```
# 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, $t(162) = 1.18$, $p = .242$.

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: 12852.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```



```
## -3.5872 -0.6251 0.0440 0.6695 3.3036
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.7820 0.8843
## trial (Intercept) 0.2579 0.5079
## Residual 2.5012 1.5815
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 6.0524 0.1539 53.3789 39.318 < 0.0000000000000002 ***
## conditiontypical -0.4756 0.1479 164.0050 -3.216 0.00156 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## condntntypcl -0.474
```

```
# 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) 5.7506762 6.3540857
## conditiontypical -0.7653395 -0.1857639
```

```
# 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 6.05 1.88 1680 0.0458
## 2 typical 5.58 1.87 1640 0.0463
```

People rated voices as significantly more typical after adaptation to feminized voices ($M = 6.05$, $SD = 1.88$) relative to masculinized voices ($M = 5.58$, $SD = 1.87$), $t(164) = -3.22$, $p < 0.01$.

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: 12859.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5628 -0.6284  0.0504  0.6626  3.2932
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID      (Intercept) 0.8216  0.9064
## trial   (Intercept) 0.2579  0.5078
## Residual                2.5012  1.5815
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value      Pr(>|t|)
## (Intercept)   5.7555     0.1409   39.0409  40.845 <0.0000000000000002 ***
## Sex1          0.3428     0.1963  164.0011   1.747      0.0826 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Sex1 -0.252

```

```

# 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)  5.47933106 6.0316984
## Sex1        -0.04184403 0.7274813

```

```

# 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 5.76 1.88 2720 0.0361
## 2 1 6.10 1.90 600 0.0778
```

There is no difference in typicality ratings between female ($M = 5.76$, $SD = 1.88$) and male ($M = 6.10$, $SD = 1.90$) participants, $t(164) = 1.75$, $p = .083$.

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 = "nloptn"))
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 = "nloptn"))
##
## REML criterion at convergence: 12846.5
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.5881 -0.6261 0.0444 0.6652 3.3116
##
## Random effects:
## Groups Name Variance Std.Dev.
## ID (Intercept) 0.7500 0.8660
## trial (Intercept) 0.2579 0.5079
## Residual 2.5012 1.5815
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 6.06618 0.16051 61.30941 37.792
## conditiontypical -0.62132 0.16043 161.99924 -3.873
## Sex1 -0.07243 0.25992 161.99924 -0.279
## conditiontypical:Sex1 0.84543 0.37807 161.99924 2.236
## Pr(>|t|)
## (Intercept) < 0.0000000000000002 ***
## conditiontypical 0.000156 ***
## Sex1 0.780872
## conditiontypical:Sex1 0.026704 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) cndtnt Sex1
## cndtnttypcl -0.500
## Sex1 -0.308 0.309
## cndtnttyp:S1 0.212 -0.424 -0.688
```

```
# 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)    5.7515766  6.3807763
## conditiontypical -0.9357573 -0.3068898
## Sex1          -0.5818674  0.4370145
## conditiontypical:Sex1 0.1044355  1.5864258
```

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

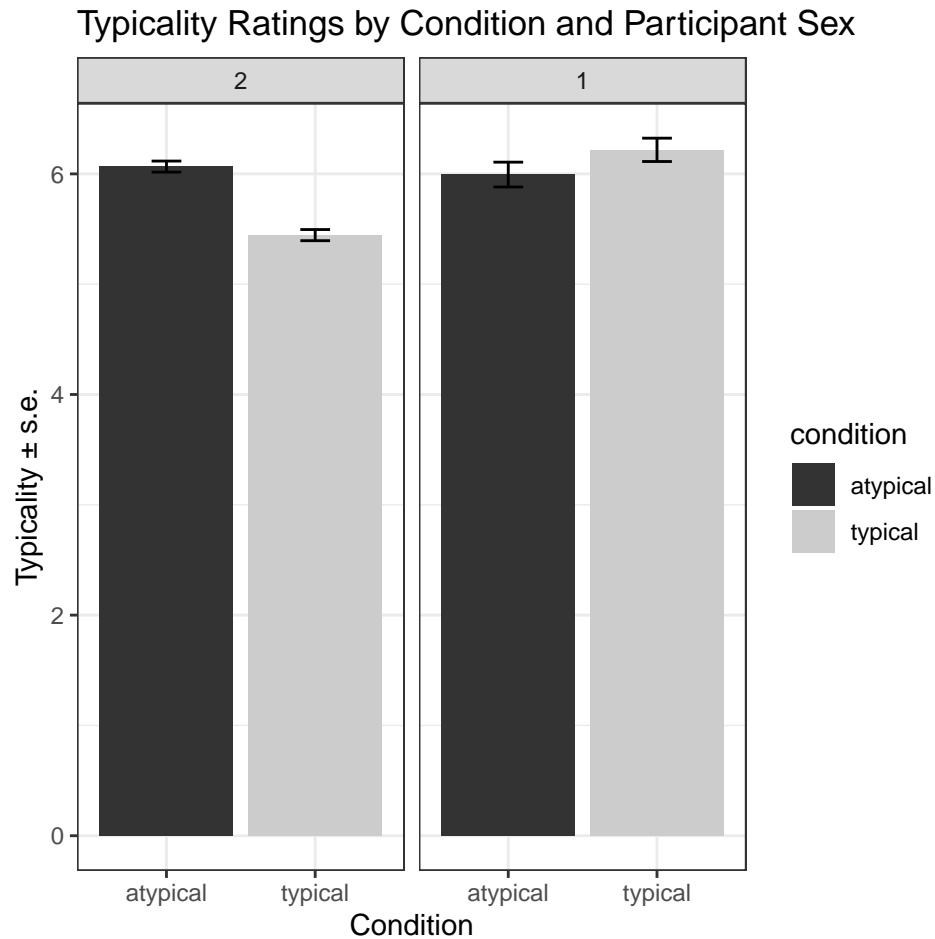
'summarise()' has grouped output by 'condition'. You can override using the '.groups' argument.

```
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      6.07  1.85  1360 0.0501
## 2 atypical 1      5.99  2.01   320 0.113
## 3 typical  2      5.44  1.87  1360 0.0506
## 4 typical  1      6.22  1.77   280 0.106
```

```
# 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 significant, $t(162) = 2.24$, $p < .05$. The simple effect of condition when participant sex is centered at female is also significant, $t(162) = -3.87$, $p < .001$.

Simple Effect: Typicality by Condition when Participant Sex is centered at Male

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

model.20 <- lmer(typicality ~ 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.20)

## 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: 12846.5
##
## Scaled residuals:
## Min 1Q Median 3Q Max
```

```

## -3.5881 -0.6261 0.0444 0.6652 3.3116
##
## Random effects:
## Groups   Name            Variance Std.Dev.
## ID       (Intercept) 0.7500   0.8660
## trial    (Intercept) 0.2579   0.5079
## Residual                2.5012   1.5815
## Number of obs: 3320, groups: ID, 166; trial, 20
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      5.99375    0.25998 161.59243  23.055
## conditiontypical  0.22411    0.34234 161.99924   0.655
## Sex2              0.07243    0.25992 161.99924   0.279
## conditiontypical:Sex2 -0.84543    0.37807 161.99924  -2.236
##
##              Pr(>|t|)
## (Intercept)    <0.0000000000000002 ***
## conditiontypical  0.5136
## Sex2            0.7809
## conditiontypical:Sex2 0.0267 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) cndtnt Sex2
## condntntypcl -0.615
## Sex2          -0.809 0.615
## cndntntyp:S2  0.556 -0.906 -0.688

```

The simple effect of condition when participant sex is centered at male is not significant, $t(162) = 0.66$, $p=.514$.