> GSS2016 <- read\_csv("GSS\_2016.csv")

Parsed with column specification:

cols(

.default = col\_character(),

agekdbrn = col\_integer(),

babies = col\_integer(),

bigbang = col\_logical(),

bigbang1 = col\_logical(),

bigbang2 = col\_logical(),

boyorgrl = col\_logical(),

cohort = col\_integer(),

cohrs2 = col\_integer(),

condrift = col\_logical(),

coninc = col\_double(),

conrinc = col\_double(),

copres10 = col\_integer(),

copres105plus = col\_integer(),

cosei10 = col\_double(),

cosei10educ = col\_double(),

cosei10inc = col\_double(),

dateintv = col\_integer(),

earnrs = col\_integer(),

educ = col\_integer(),

electron = col\_logical()

# ... with 81 more columns

)

See spec(...) for full column specifications.

Warning: 2 parsing failures.

row # A tibble: 2 x 5 col row col expected actual file expected <int> <chr> <chr> <chr> <chr> actual 1 1210 old1 no trailing characters " or older" 'GSS\_2016.csv' file 2 2760 earnrs an integer eight or more 'GSS\_2016.csv'

> GSS2016$adults <- recode(GSS2016$adults,

+ "0" = 0,

+ "1" = 1,

+ "2" = 2,

+ "3" = 3,

+ "4" = 4,

+ "5" = 5,

+ "6" = 6,

+ "7" = 7,

+ "8 or more" = 8

+ )

> gssadults\_06 <- GSS2016 %>%

+ select(adults, sex) %>%

+ filter(!is.na(adults)) %>%

+ filter(!is.na(sex))

Warning message:

package ‘bindrcpp’ was built under R version 3.4.4

> gssadults\_06 %>%

+ summarise(mean.ad = mean(adults),

+ sd.ad = sd(adults),

+ n.ad = n()) %>%

+ mutate(se.ad = sd.ad / sqrt(n.ad),

+ "80%\_low.CI" = mean.ad - qt(1 - (0.20 / 2),

+ n.ad -1) \*se.ad,

+ "80%\_upp.CI" = mean.ad + qt(1 - (0.20 / 2),

+ n.ad -1) \*se.ad)

# A tibble: 1 x 6

mean.ad sd.ad n.ad se.ad `80%\_low.CI` `80%\_upp.CI`

<dbl> <dbl> <int> <dbl> <dbl> <dbl>

1 1.86 0.832 2866 0.0155 1.84 1.88

> # 95% Confidence Intervel

> gssadults\_06 %>%

+ summarise(mean.ad = mean(adults),

+ sd.ad = sd(adults),

+ n.ad = n()) %>%

+ mutate(se.ad = sd.ad / sqrt(n.ad),

+ "95%\_low.CI" = mean.ad - qt(1 - (0.05 / 2), n.ad -1) \*se.ad,

+ "95%\_upp.CI" = mean.ad + qt(1 - (0.05 / 2), n.ad -1) \*se.ad)

# A tibble: 1 x 6

mean.ad sd.ad n.ad se.ad `95%\_low.CI` `95%\_upp.CI`

<dbl> <dbl> <int> <dbl> <dbl> <dbl>

1 1.86 0.832 2866 0.0155 1.83 1.89

> gssadults\_06 %>%

+ summarise(mean.ad = mean(adults),

+ sd.ad = sd(adults),

+ n.ad = n()) %>%

+ mutate(se.ad = sd.ad / sqrt(n.ad),

+ "99%\_low.CI" = mean.ad - qt(1 - (0.01 / 2), n.ad -1) \*se.ad,

+ "99%\_upp.CI" = mean.ad + qt(1 - (0.01 / 2), n.ad -1) \*se.ad)

# A tibble: 1 x 6

mean.ad sd.ad n.ad se.ad `99%\_low.CI` `99%\_upp.CI`

<dbl> <dbl> <int> <dbl> <dbl> <dbl>

1 1.86 0.832 2866 0.0155 1.82 1.90

> gssadults\_06 %>%

+ group\_by(sex) %>% # this output gives us outputs based on `sex'

+ summarise(mean.ad = mean(adults),

+ sd.ad = sd(adults),

+ n.ad = n()) %>%

+ mutate(se.ad = sd.ad / sqrt(n.ad),

+ "80%\_low.CI" = mean.ad - qt(1 - (0.20 / 2),

+ n.ad -1) \*se.ad,

+ "80%\_upp.CI" = mean.ad + qt(1 - (0.20 / 2),

+ n.ad -1) \*se.ad)

# A tibble: 2 x 7

sex mean.ad sd.ad n.ad se.ad `80%\_low.CI` `80%\_upp.CI`

<chr> <dbl> <dbl> <int> <dbl> <dbl> <dbl>

1 female 1.83 0.812 1590 0.0204 1.80 1.86

2 male 1.90 0.855 1276 0.0239 1.87 1.93

> gssadults\_06 %>%

+ group\_by(sex) %>%

+ summarise(mean.ad = mean(adults),

+ sd.ad = sd(adults),

+ n.ad = n()) %>%

+ mutate(se.ad = sd.ad / sqrt(n.ad),

+ "95%\_low.CI" = mean.ad - qt(1 - (0.05 / 2), n.ad -1) \*se.ad,

+ "95%\_upp.CI" = mean.ad + qt(1 - (0.05 / 2), n.ad -1) \*se.ad)

# A tibble: 2 x 7

sex mean.ad sd.ad n.ad se.ad `95%\_low.CI` `95%\_upp.CI`

<chr> <dbl> <dbl> <int> <dbl> <dbl> <dbl>

1 female 1.83 0.812 1590 0.0204 1.79 1.87

2 male 1.90 0.855 1276 0.0239 1.86 1.95

> gssadults\_06 %>%

+ group\_by(sex) %>%

+ summarise(mean.ad = mean(adults),

+ sd.ad = sd(adults),

+ n.ad = n()) %>%

+ mutate(se.ad = sd.ad / sqrt(n.ad),

+ "99%\_low.CI" = mean.ad - qt(1 - (0.01 / 2), n.ad -1) \*se.ad,

+ "99%\_upp.CI" = mean.ad + qt(1 - (0.01 / 2), n.ad -1) \*se.ad)

# A tibble: 2 x 7

sex mean.ad sd.ad n.ad se.ad `99%\_low.CI` `99%\_upp.CI`

<chr> <dbl> <dbl> <int> <dbl> <dbl> <dbl>

1 female 1.83 0.812 1590 0.0204 1.78 1.88

2 male 1.90 0.855 1276 0.0239 1.84 1.96