

Supplement 1

SPARS A: Width of the pain threshold

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Contents

Question	1
Import and inspect data	2
Data at the level of the individual	3
Bootstrapping procedure	3
Plots	4
Scatter plots	4
Trimean confidence interval plots	6
Data at the level of the group	9
Bootstrapping procedure	9
Plots	10
Scatter plots	10
Trimean confidence interval plots	11
Session information	13

Question

How wide is the pain threshold for participants taking part in the SPARS A trial?

To answer the question, we calculated the *Tukey Trimean* and bootstrapped 95% confidence interval (CI) for each individual, at each stimulus intensity. Next, we plotted these statistics to show the stimulus range over which each individual's CIs included zero on the SPARS (pain threshold).

To get an idea of the width of the stimulus range that included zero on the SPARS at the group level, we calculated the *Tukey trimean* for each individual, at each stimulus intensity, and then calculated the mean and bootstrapped 95% CI for the group at each stimulus intensity. These data were then plotted to show the stimulus range over which the group's CIs included zero (pain threshold).

The selection of the *tukey trimean* as the measure of central tendency at the individual level was based on the analysis of central tendency reported in the original description of the SPARS (Supplement_3.pdf). The *Tukey trimean* is defined as the weighted average of the distribution's median and its two quartiles, and is a robust measure of central tendency that unlike a median, takes the spread of the data into account.

$$T_{mean} = \frac{1}{2}(Q_2 + \frac{Q_1 + Q_3}{2})$$

Where:

- Q_1 = 25th percentile

- $Q_2 = 50^{\text{th}}$ percentile (median)
- $Q_3 = 75^{\text{th}}$ percentile

```
# Define the tri_mean function
tri_mean <- function(x) {
  # Calculate quantiles
  q1 <- quantile(x, probs = 0.25, na.rm = TRUE)[[1]]
  q2 <- median(x, na.rm = TRUE)
  q3 <- quantile(x, probs = 0.75, na.rm = TRUE)[[1]]
  # Calculate trimean
  tri_mean <- (q2 + ((q1 + q3) / 2)) / 2
  # Round to a whole number
  tri_mean <- round(tri_mean)
  return(tri_mean)
}
```

Note: No inspection of block and stimulus order effects were undertaken because analysis of these factors in the original description of the SPARS revealed no order effects (Supplement_4.pdf).

The experimental protocol called for participants to be exposed to 13 stimuli, evenly spaced at 0.25J intervals over the range 1.00J to 4.00J. Each stimulus intensity was applied 8 times, giving a total of 104 exposures (trials). To prevent learning effects, the 104 trials were randomised across 4 experimental blocks (26 trials per block).

Import and inspect data

```
# Import
data <- read_rds('data-cleaned/SPARS_A.rds')

# Inspect
glimpse(data)

## Observations: 1,927
## Variables: 6
## $ PID          <chr> "ID01", "ID01", "ID01", "ID01", "ID01", "ID01", "...
## $ block        <chr> "A", "A", "A", "A", "A", "A", "A", "A", "A", "A",...
## $ block_order  <dbl> 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4...
## $ trial_number <dbl> 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 9...
## $ intensity    <dbl> 3.00, 2.25, 4.00, 3.25, 2.75, 2.25, 2.75, 4.00, 2...
## $ rating       <dbl> -40, -25, 10, 2, -10, -25, -20, 10, -25, -50, -25...

data %>%
  select(intensity, rating) %>%
  skim()

## Skim summary statistics
##   n obs: 1927
##   n variables: 2
##
## -- Variable type:numeric -----
##   variable missing complete    n mean   sd  p0    p25 p50    p75 p100
##   intensity      0      1927 1927  2.47  0.93   1    1.75 2.5    3.25   4
##   rating         0      1927 1927 -4.45 22.31 -50 -20    2    10    45
```

```
##      hist
##
##
```

Data at the level of the individual

Bootstrapping procedure

```
# Nest data in preparation for bootstrapping at each stimulus intensity
data_boot <- data %>%
  group_by(PID, intensity) %>%
  nest()

# Define bootstrap function
boot_tri_mean <- function(d,i){
  tri_mean(d[i])
}

# Perform bootstrap
set.seed(123456789)
data_boot %<>%
  mutate(boot = map(.x = data,
                    ~ boot(data = .x$rating,
                          statistic = boot_tri_mean,
                          R = 10000, # For small sample size
                          stype = 'i'))))

# Remove NULL bootstrap row 56 (ID05, only one value = 20)
data_boot <- data_boot[-56, ]

# Extract CI from boot object
data_boot %<>%
  mutate(boot_ci = map(.x = boot,
                      ~ boot.ci(.x,
                                type = 'basic'))))

# Extract the data, giving original trimean and bootstrapped CI
data_boot %<>%
  mutate(tri_mean = map_dbl(.x = boot_ci,
                           ~ .x$t0),
         lower_ci = map_dbl(.x = boot_ci,
                           ~ .x$basic[[4]]),
         upper_ci = map_dbl(.x = boot_ci,
                           ~ .x$basic[[5]]))

# Delete unwanted columns
data_boot %<>%
  select(-data, -boot, -boot_ci)

# Clip CI intervals (SPARS ranges from -50 to 50)
data_boot %<>%
```

```

mutate(upper_ci = ifelse(upper_ci > 50,
                        yes = 50,
                        no = upper_ci),
      lower_ci = ifelse(lower_ci < -50,
                        yes = -50,
                        no = lower_ci))

# Add fill column for plot
data_boot %<>%
  mutate(fill = ifelse(upper_ci >= 0 & lower_ci <= 0,
                      yes = 'inclusive',
                      no = 'exclusive'),
         fill = factor(fill,
                      levels = c('inclusive', 'exclusive'),
                      ordered = TRUE))

```

Plots

Scatter plots

```

# Plot scatter plot of ratings for each individual at every intensity
ggplot(data = data) +
  aes(x = intensity,
      y = rating,
      fill = intensity,
      colour = intensity) +
  geom_hline(yintercept = 0,
            size = 1) +
  geom_hline(yintercept = 25,
            linetype = 2) +
  geom_hline(yintercept = -25,
            linetype = 2) +
  geom_hline(yintercept = 50,
            linetype = 2) +
  geom_hline(yintercept = -50,
            linetype = 2) +
  geom_point(shape = 21,
            size = 4,
            stroke = 0.3) +
  scale_fill_gradient(low = '#CCCCCC', high = '#000000') +
  scale_colour_gradient(low = '#000000', high = '#CCCCCC') +
  scale_y_continuous(limits = c(-50, 50),
                    breaks = c(-50, 0, 50)) +
  scale_x_continuous(breaks = seq(from = 1,
                                to = 4,
                                by = 0.25),
                    labels = sprintf('%0.2f', round(seq(from = 1,
                                                        to = 4,
                                                        by = 0.25), 2))) +
  facet_wrap(~ PID, ncol = 4) +
  labs(title = "Individuals: Scatter plots of SPARS ratings at each stimulus intensity",
       subtitle = "- Dashed line: pain threshold\n- Colour gradient: stimulus intensity",
       x = 'Stimulus intensity (J)',

```

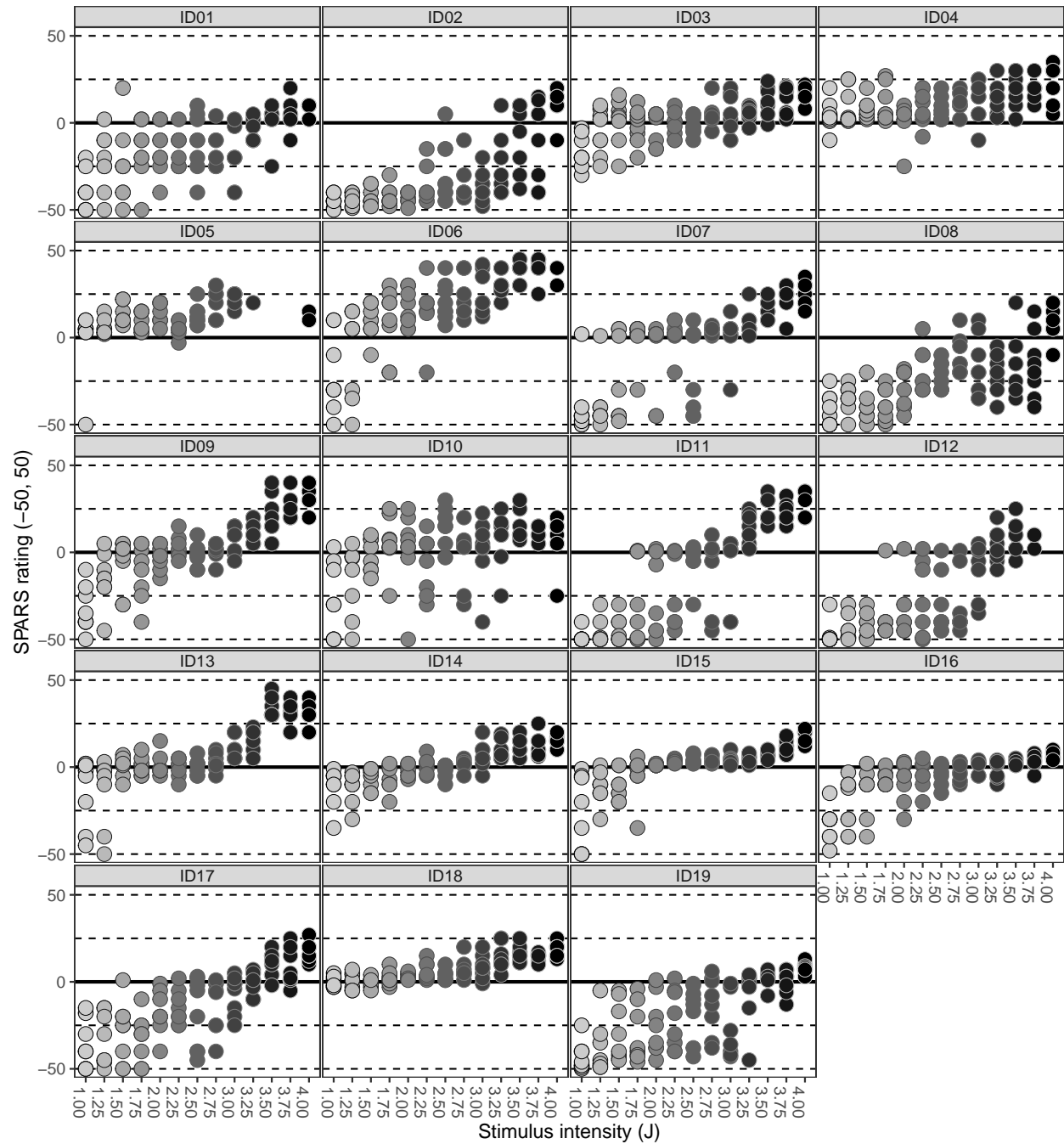
```

y = 'SPARS rating (-50, 50)' +
theme(legend.position = 'none',
      panel.grid = element_blank(),
      panel.spacing = unit(0.1, 'lines'),
      strip.text = element_text(margin = margin(t = 0.1,
                                                  b = 0.1,
                                                  r = 1,
                                                  l = 1,
                                                  'lines'))),
      axis.text.x = element_text(angle = -90))

```

Individuals: Scatter plots of SPARS ratings at each stimulus intensity

- Dashed line: pain threshold
- Colour gradient: stimulus intensity



Trimean confidence interval plots

```
# Plot individual CIs at every intensity
ggplot(data = data_boot) +
  aes(x = intensity,
      fill = fill,
      colour = fill) +
```

```

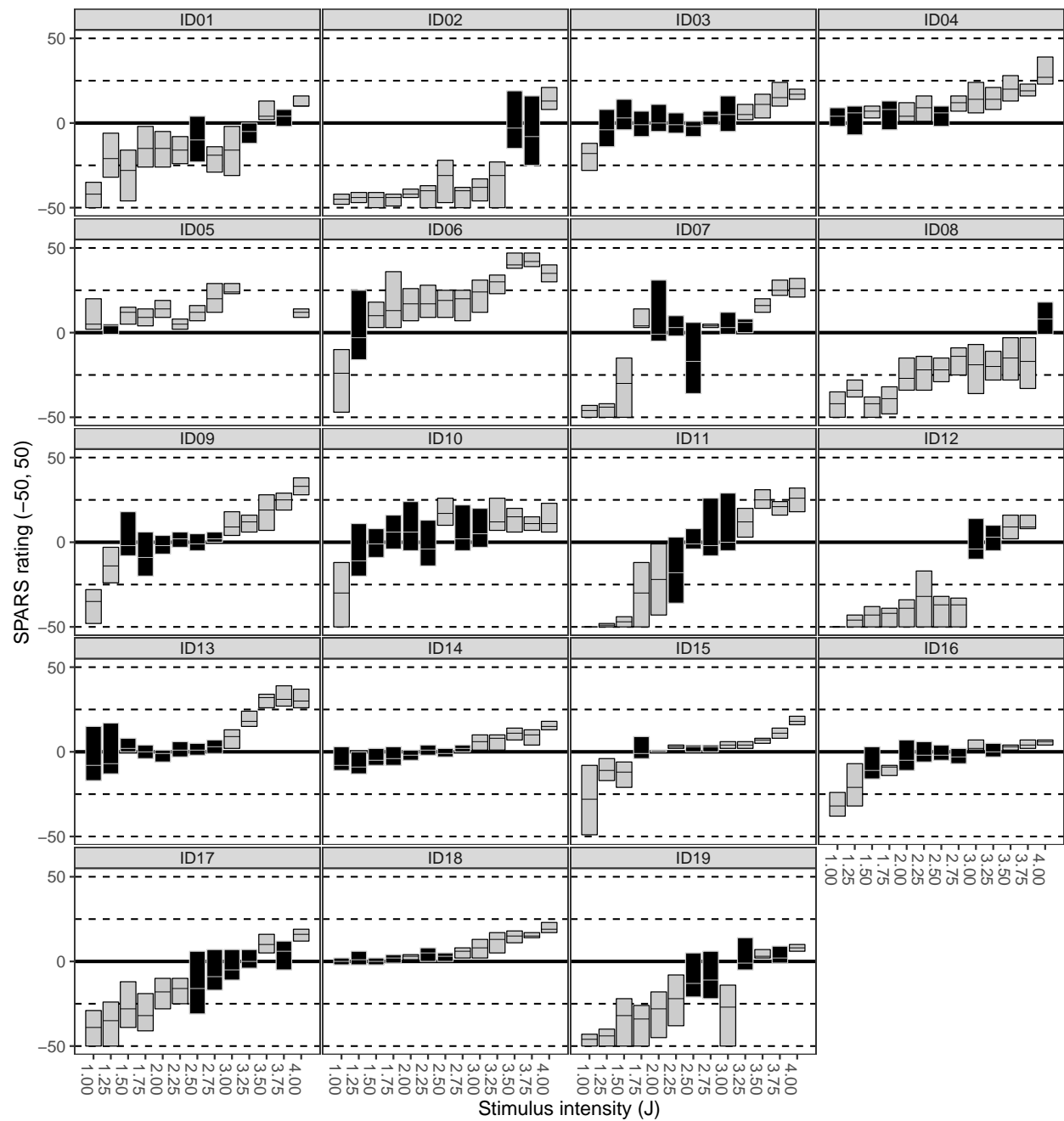
geom_hline(yintercept = 0,
           size = 1) +
geom_hline(yintercept = -25,
           linetype = 2) +
geom_hline(yintercept = 25,
           linetype = 2) +
geom_hline(yintercept = 50,
           linetype = 2) +
geom_hline(yintercept = -50,
           linetype = 2) +
geom_crossbar(aes(y = tri_mean,
                  ymin = lower_ci,
                  ymax = upper_ci),
              fatten = 0,
              size = 0.3) +
scale_fill_manual(values = c('#000000', '#CCCCCC')) +
scale_colour_manual(values = c('#CCCCCC', '#000000')) +
scale_y_continuous(limits = c(-50, 50),
                   breaks = c(-50, 0, 50)) +
scale_x_continuous(breaks = seq(from = 1,
                                to = 4,
                                by = 0.25),
                  labels = sprintf('%0.2f', round(seq(from = 1,
                                                         to = 4,
                                                         by = 0.25), 2))) +

facet_wrap(~ PID, ncol = 4) +
labs(title = "Individuals: Crossbar plots of 95% CI of Tukey trimeans for SPARS ratings\nat each st.",
     subtitle = '- Basic bootstrap 95% CI with 10,000 resamples\n- Dashed line: pain threshold | - 1',
     x = 'Stimulus intensity (J)',
     y = 'SPARS rating (-50, 50)') +
theme(legend.position = 'none',
      panel.grid = element_blank(),
      panel.spacing = unit(0.1, 'lines'),
      strip.text = element_text(margin = margin(t = 0.1,
                                                  b = 0.1,
                                                  r = 1,
                                                  l = 1,
                                                  'lines'))),
      axis.text.x = element_text(angle = -90))

```

Individuals: Crossbar plots of 95% CI of Tukey trimeans for SPARS ratings at each stimulus intensity

- Basic bootstrap 95% CI with 10,000 resamples
- Dashed line: pain threshold | – Black fill: 95% CI includes zero



Data at the level of the group

Bootstrapping procedure

```
# Calculate individual trimeans at each stimulus intensity
data_group <- data %>%
  group_by(PID, intensity) %>%
  summarise(tri_mean = tri_mean(rating)) %>%
  ungroup()

# Nest data in preparation for bootstrapping at each stimulus intensity
data_boot_group <- data_group %>%
  group_by(intensity) %>%
  nest()

# Perform bootstrap
set.seed(987654321)
data_boot_group %<>% mutate(boot = map(.x = data,
  ~ boot(data = .x$tri_mean,
    statistic = boot_tri_mean,
    R = 10000, # For small sample size
    stype = 'i'))))

# Extract CI from boot object
data_boot_group %<>% mutate(boot_ci = map(.x = boot,
  ~ boot.ci(.x,
    type = 'basic'))))

# Extract the data, giving original median and bootstrapped CI
data_boot_group %<>% mutate(tri_mean = map(.x = boot_ci,
  ~ .x$t0),
  lower_ci = map(.x = boot_ci,
  ~ .x$basic[[4]]),
  upper_ci = map(.x = boot_ci,
  ~ .x$basic[[5]]))

# Delete unwanted columns
data_boot_group %<>% select(-data, -boot, -boot_ci) %>%
  unnest()

# Clip CI intervals (SPARS ranges from -50 to 50)
data_boot_group %<>%
  mutate(upper_ci = ifelse(upper_ci > 50,
    yes = 50,
    no = upper_ci),
  lower_ci = ifelse(lower_ci < -50,
    yes = -50,
    no = lower_ci))

# Add fill column for plot
data_boot_group %<>%
  mutate(fill = ifelse(upper_ci >= 0 & lower_ci <= 0,
    yes = 'inclusive',
```

```

        no = 'exclusive'),
fill = factor(fill,
              levels = c('inclusive', 'exclusive'),
              ordered = TRUE))

```

Plots

Scatter plots

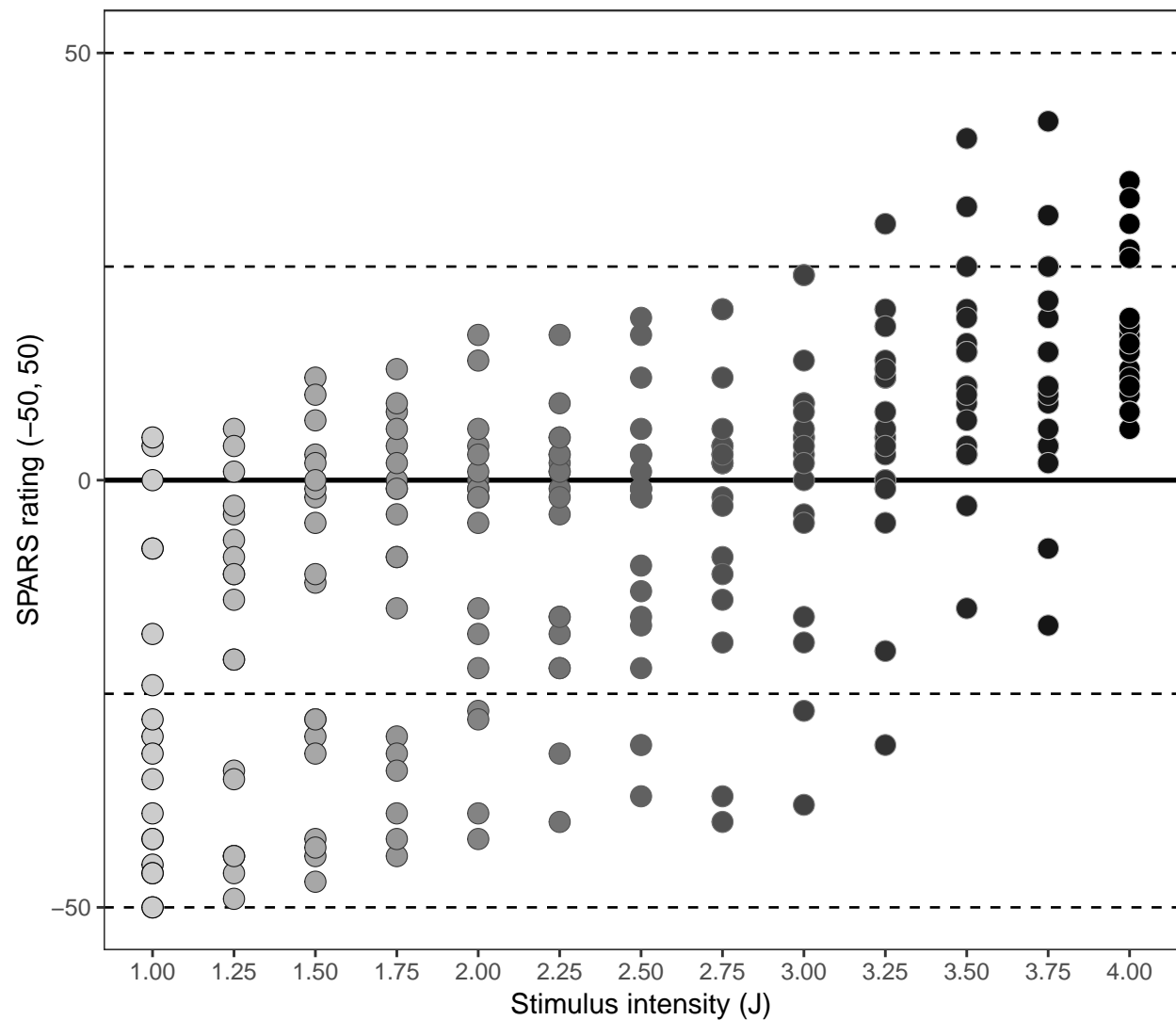
```

# Plot scatter plot of ratings for the group at every intensity
ggplot(data = data_group) +
  aes(x = intensity,
      y = tri_mean,
      fill = intensity,
      colour = intensity) +
  geom_hline(yintercept = 0,
            size = 1) +
  geom_hline(yintercept = -25,
            linetype = 2) +
  geom_hline(yintercept = 25,
            linetype = 2) +
  geom_hline(yintercept = 50,
            linetype = 2) +
  geom_hline(yintercept = -50,
            linetype = 2) +
  geom_point(shape = 21,
            size = 4,
            stroke = 0.3) +
  scale_fill_gradient(low = '#CCCCCC', high = '#000000') +
  scale_colour_gradient(low = '#000000', high = '#CCCCCC') +
  scale_y_continuous(limits = c(-50, 50),
                    breaks = c(-50, 0, 50)) +
  scale_x_continuous(breaks = seq(from = 1,
                                to = 4,
                                by = 0.25),
                    labels = sprintf('%0.2f', round(seq(from = 1,
                                                        to = 4,
                                                        by = 0.25), 2))) +
  labs(title = "Group: Scatter plots of SPARS Tukey trimean ratings\nat each stimulus intensity",
       subtitle = "- Dashed line: pain threshold\n- Colour gradient: stimulus intensity",
       x = 'Stimulus intensity (J)',
       y = 'SPARS rating (-50, 50)') +
  theme(legend.position = 'none',
        panel.grid = element_blank())

```

Group: Scatter plots of SPARS Tukey trimean ratings
at each stimulus intensity

- Dashed line: pain threshold
- Colour gradient: stimulus intensity



Trimean confidence interval plots

```
# Plot group CIs at every intensity
ggplot(data = data_boot_group) +
  aes(x = intensity) +
  geom_hline(yintercept = 0,
             size = 1) +
  geom_hline(yintercept = -25,
             linetype = 2) +
  geom_hline(yintercept = 25,
             linetype = 2) +
  geom_hline(yintercept = 50,
             linetype = 2) +
```

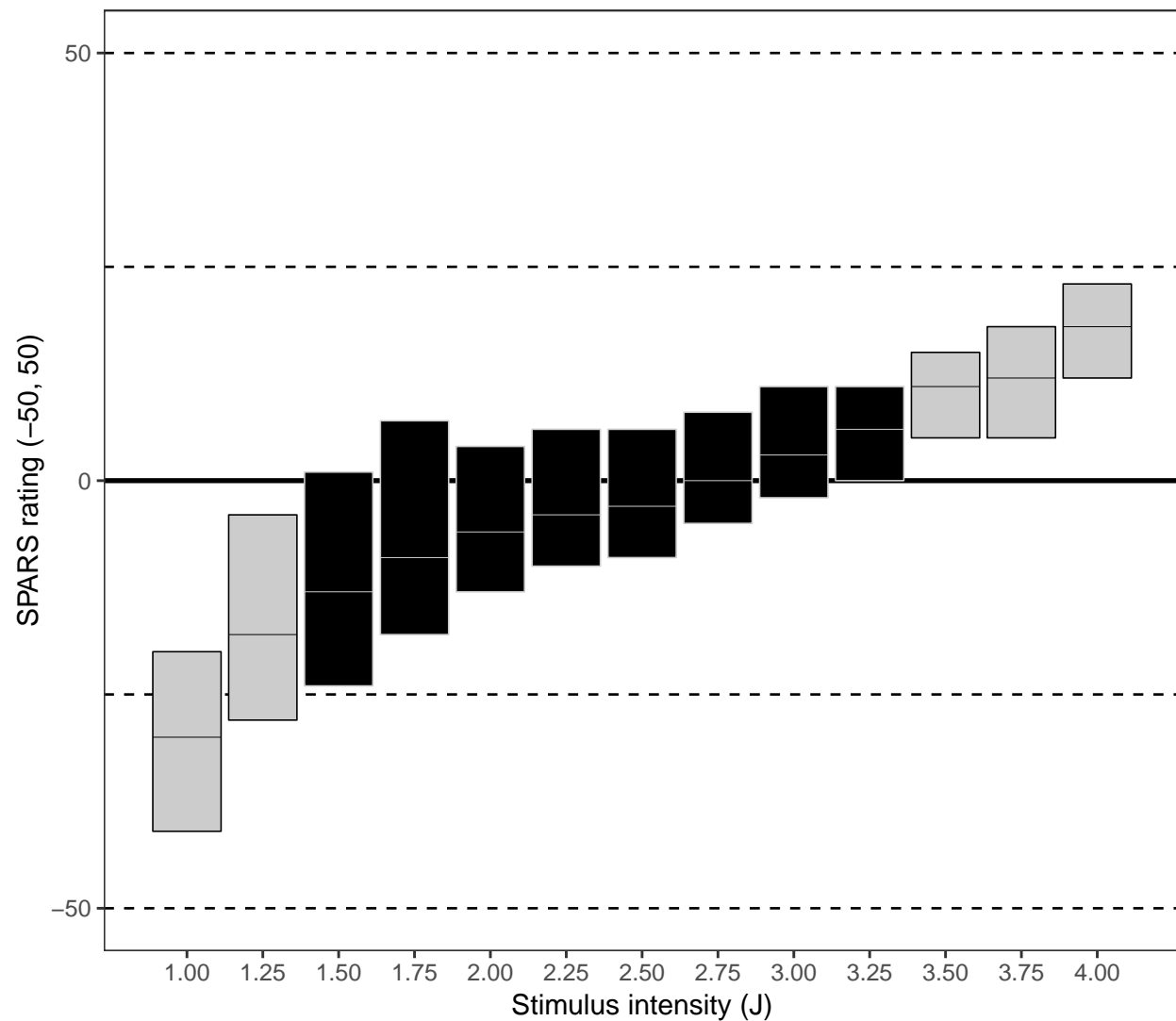
```

geom_hline(yintercept = -50,
           linetype = 2) +
geom_crossbar(aes(y = tri_mean,
                  ymin = lower_ci,
                  ymax = upper_ci,
                  fill = fill,
                  colour = fill),
              fatten = 0,
              size = 0.3) +
scale_fill_manual(values = c('#000000', '#CCCCCC')) +
scale_colour_manual(values = c('#CCCCCC', '#000000')) +
scale_y_continuous(limits = c(-50, 50),
                   breaks = c(-50, 0, 50)) +
scale_x_continuous(breaks = seq(from = 1,
                                to = 4,
                                by = 0.25),
                   labels = sprintf('%0.2f', round(seq(from = 1,
                                                         to = 4,
                                                         by = 0.25), 2))) +
labs(title = "Group: Crossbar plots of 95% CI of Tukey trimeans for SPARS ratings\nat each stimulus",
     subtitle = "- Basic bootstrap 95% CI with 10,000 resamples\n- Dashed line: pain threshold | - (",
     x = 'Stimulus intensity (J)',
     y = 'SPARS rating (-50, 50)') +
theme(legend.position = 'none',
      panel.grid = element_blank())

```

Group: Crossbar plots of 95% CI of Tukey trimeans for SPARS ratings at each stimulus intensity

- Basic bootstrap 95% CI with 10,000 resamples
- Dashed line: pain threshold | – Grey fill: 95% CI includes zero



Session information

```
sessionInfo()

## R version 3.5.1 (2018-07-02)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS 10.14.1
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
```

```

##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] bindrcpp_0.2.2  skimr_1.0.3    boot_1.3-20    magrittr_1.5
## [5] forcats_0.3.0  stringr_1.3.1  dplyr_0.7.8    purrr_0.2.5
## [9] readr_1.2.1     tidyr_0.8.2    tibble_1.4.2   ggplot2_3.1.0
## [13] tidyverse_1.2.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.0      cellranger_1.1.0 pillar_1.3.0    compiler_3.5.1
## [5] plyr_1.8.4      bindr_0.1.1     tools_3.5.1     digest_0.6.18
## [9] lubridate_1.7.4 jsonlite_1.5     evaluate_0.12    nlme_3.1-137
## [13] gtable_0.2.0    lattice_0.20-38 pkgconfig_2.0.2 rlang_0.3.0.1
## [17] cli_1.0.1       rstudioapi_0.8  yaml_2.2.0      haven_2.0.0
## [21] withr_2.1.2.9000 xml2_1.2.0      httr_1.3.1      knitr_1.20
## [25] hms_0.4.2       rprojroot_1.3-2 grid_3.5.1       tidyselect_0.2.5
## [29] glue_1.3.0      R6_2.3.0        readxl_1.1.0    rmarkdown_1.10
## [33] modelr_0.1.2    backports_1.1.2 scales_1.0.0     htmltools_0.3.6
## [37] rvest_0.3.2     assertthat_0.2.0 colorspace_1.3-2 stringi_1.2.4
## [41] lazyeval_0.2.1  munsell_0.5.0   broom_0.5.0     crayon_1.3.4

```