

Supplement 10

Experiment 1 – Rating variance in the SPARS

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This script is part 6 of our analysis of the stimulus-response characteristics of the SPARS. In these analyses we assessed intra-individual and inter-individual variability in scoring on the SPARS at each pain intensity.

We used the *median absolute deviation* (MAD), which is a robust measure of dispersion, to assess variance. To calculate intra-individual variance for each stimulus intensity, we calculated the MAD using the ratings from repeated stimuli at each stimulus intensity. We also used the MAD for calculating inter-individual variance for each scale and at each intensity, using the median ratings by individuals at each intensity as the input.

Median absolute deviation

$$MAD = \text{median}(|X_i - \text{median}(X)|)$$

Source URL: https://github.com/kamermanpr/SPARS/tree/supplementary_pdfs

Descriptive plots of the data are provided in “*outputs/supplement_5.pdf*”, modelling of the stimulus-response relationship is described in “*outputs/supplement_6.pdf*”, the diagnostics on the final linear mixed model are described in “*outputs/supplement_7.pdf*”, the stability of the model is described in “*outputs/supplement_8.pdf*”, and the sensitivity of the scale to changes in stimulus intensity are described in “*outputs/supplement_9.pdf*”.

Import and clean/transform data

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

```

#                               Clean                               #
#                               #
#####
data %<>%
  # Select required columns
  select(PID, intensity, rating)

```

Intra-individual variation (participant-level)

```

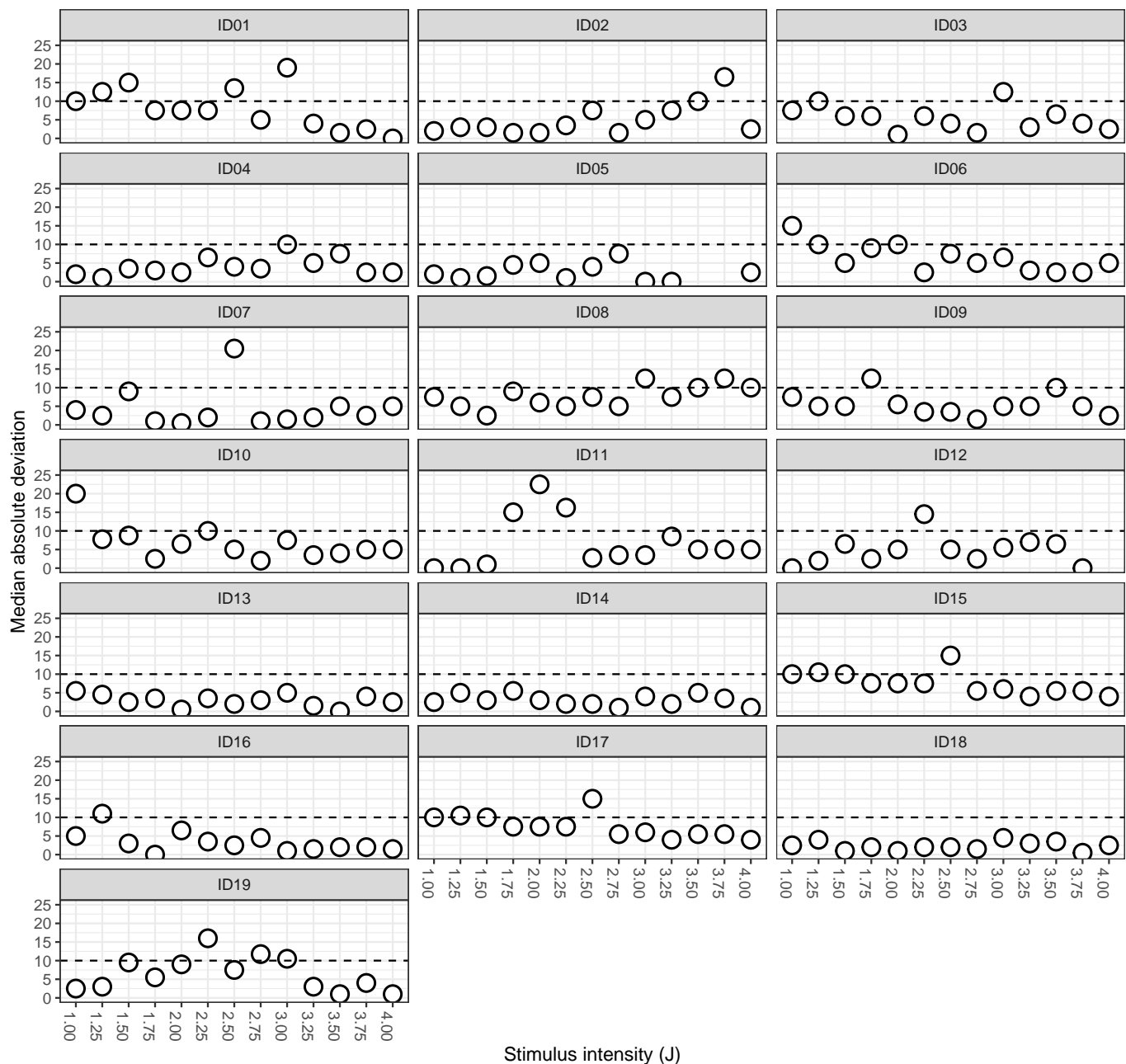
# Calculate MAD
data_varianceP <- data %>%
  group_by(PID, intensity) %>%
  summarise(MAD = mad(x = rating,
                     constant = 1,
                     na.rm = TRUE)) %>%
  ungroup()

# Plot
ggplot(data = data_varianceP) +
  aes(y = MAD,
      x = sprintf('%.02f', intensity)) +
  geom_point(shape = 21,
            size = 4,
            stroke = 1,
            fill = '#FFFFFF') +
  geom_hline(yintercept = 10,
            linetype = 2) +
  labs(title = 'Participant-level median absolute deviation (MAD) for the SPARS',
       subtitle = 'Dotted line: 10% of scale range (100 units)',
       y = 'Median absolute deviation',
       x = 'Stimulus intensity (J)') +
  scale_y_continuous(limits = c(0, 25)) +
  facet_wrap(~ PID, ncol = 3) +
  theme(axis.text.x = element_text(angle = -90))

```

Participant-level median absolute deviation (MAD) for the SPARS

Dotted line: 10% of scale range (100 units)



There is no clear pattern in intra-individual variance in intensity rating within the scale. Variance can be high on a case-by-case basis, but most MAD value are < 10% of the scale range (100 units, -50 to 50).

Inter-individual variation (group-level)

```
# Process data for plotting
data_varianceG <- data %>%
  # Calculate median rating at each stimulus intensity for each scale per PID
  group_by(PID, intensity) %>%
  summarise(median = median(rating,
                             na.rm = TRUE)) %>%

  # Calculate group MAD
  group_by(intensity) %>%
```

```

summarise(MAD = mad(median,
                    constant = 1,
                    na.rm = TRUE)) %>%

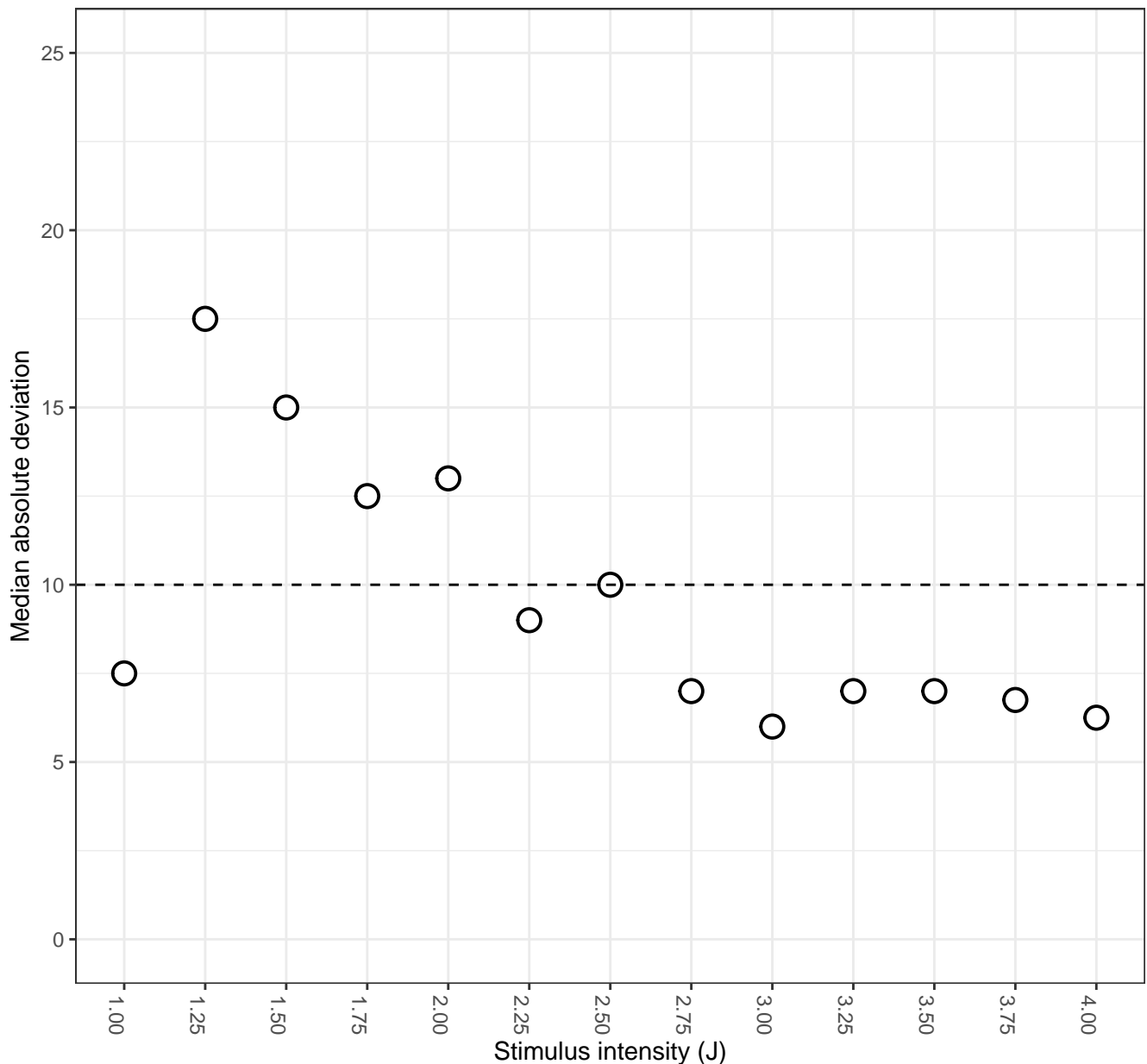
ungroup()

# Plot
ggplot(data = data_varianceG) +
  aes(y = MAD,
      x = sprintf('%.02f', intensity)) +
  geom_point(shape = 21,
            size = 4,
            stroke = 1,
            fill = '#FFFFFF') +
  geom_hline(yintercept = 10,
            linetype = 2) +
  labs(title = 'Group-level median absolute deviation (MAD) for the SPARS',
       subtitle = 'Dotted line: 10% of scale range (100 units)',
       y = 'Median absolute deviation',
       x = 'Stimulus intensity (J)') +
  scale_y_continuous(limits = c(0, 25)) +
  theme(axis.text.x = element_text(angle = -90))

```

Group-level median absolute deviation (MAD) for the SPARS

Dotted line: 10% of scale range (100 units)



Other than an 'odd' value at 1J, there is a trend for high inter-individual MAD values at low stimulus intensities, and for this variance to decrease as stimulus intensity increases.

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
##
## 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  forcats_0.3.0  stringr_1.3.1  dplyr_0.7.6
## [5] purrr_0.2.5    readr_1.1.1    tidyr_0.8.1    tibble_1.4.2
## [9] ggplot2_3.0.0  tidyverse_1.2.1 magrittr_1.5
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.19    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_0.6.17
## [9] lubridate_1.7.4 jsonlite_1.5     evaluate_0.11    nlme_3.1-137
## [13] gtable_0.2.0    lattice_0.20-35 pkgconfig_2.0.2 rlang_0.2.2
## [17] cli_1.0.1        rstudioapi_0.8  yaml_2.2.0      haven_1.1.2
## [21] withr_2.1.2     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_0.2.4
## [29] glue_1.3.0       R6_2.2.2        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 labeling_0.3
## [41] stringi_1.2.4    lazyeval_0.2.1  munsell_0.5.0    broom_0.5.0
## [45] crayon_1.3.4
```