Supplement 6

Experiment 1 – Modelling the SPARS stimulus-response relationship

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Contents

This script is part 2 of our analysis of the stimulus-response characteristics of the SPARS. This script models the relationship between stimulus intensity and SPARS rating using linear mixed models and quantile mixed model regression.

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

Descriptive plots of the data are provided in *"outputs/supplement_5.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"*, the sensitivity of the scale to changes in stimulus intensity are described in *"outputs/supplement_9.pdf"*, and the variance in ratings at each stimulus intensity is described in *"outputs/supplement_10.pdf"*.

Import and clean/transform data

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

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

############################################################
#                                                          #
```

```
#                Calculate 'Tukey trimean'                #
#                                                         #
###########################################################
# Define 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
  tm <- (q2 + ((q1 + q3) / 2)) / 2
  # Convert to integer
  tm <- as.integer(round(tm))
  return(tm)
}

###########################################################
#                                                         #
#                    Generate core data                   #
#                                                         #
###########################################################
# Calculate the participant average
data_tm <- data %>%
  group_by(PID, intensity) %>%
  summarise(tri_mean = tri.mean(rating)) %>%
  ungroup()

# Calculate the group average
data_group <- data_tm %>%
  group_by(intensity) %>%
  summarise(median = median(tri_mean)) %>%
  ungroup()
```

Linear mixed model regression

To allow for a curvilinear relationship between stimulus intensity and rating, we modelled the data using polynomial regression, with 1st (linear), 2nd (quadratic), and 3rd (cubic) order orthogonal polynomials. For each polynomial expression, we modelled the random effects as random intercept only, and as random intercept and slope.

The random intercept only and random intercept and slope models were compared using the likelihood test, and the better model taken forward.

1st-order (linear) polynomial

```
# Intercept only
lmm1 <- lmer(tri_mean ~ intensity + (1 | PID),
             data = data_tm,
             REML = TRUE)
```

```r
# Intercept and slope
lmm1b <- lmer(tri_mean ~ intensity + (intensity | PID),
              data = data_tm,
              REML = TRUE)

# Better model?
anova(lmm1, lmm1b)
```

```
## Data: data_tm
## Models:
## lmm1: tri_mean ~ intensity + (1 | PID)
## lmm1b: tri_mean ~ intensity + (intensity | PID)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## lmm1   4 1814.7 1828.7 -903.37   1806.7
## lmm1b  6 1733.6 1754.6 -860.79   1721.6 85.146      2  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Anova of better model
Anova(lmm1b,
      type = 2,
      test.statistic = 'F')
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: tri_mean
##                F Df Df.res    Pr(>F)
## intensity 94.707  1 17.998 1.356e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Print better model
summary(lmm1b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: tri_mean ~ intensity + (intensity | PID)
##    Data: data_tm
##
## REML criterion at convergence: 1715.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0493 -0.4430  0.0157  0.5165  3.6042
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  PID      (Intercept) 633.16   25.163
##           intensity    36.17    6.014   -0.89
##  Residual              42.54    6.522
## Number of obs: 244, groups:  PID, 19
##
## Fixed effects:
##             Estimate Std. Error t value
```

```
## (Intercept)  -39.764      5.895  -6.746
## intensity     14.126      1.451   9.732
##
## Correlation of Fixed Effects:
##           (Intr)
## intensity -0.885
```

```r
# Doesn't work with LaTex
#tab_model(lmm1b,
#           auto.label = FALSE,
#           dv.labels = "Response",
#           string.pred = "Coefficients",
#           pred.labels = c('(Intercept)', 'Intensity'),
#           string.stat = 'Estimate',
#           string.ci = '95% CI',
#           string.p = 'p-value',
#           show.icc = FALSE,
#           show.r2 = FALSE)
```

2nd-order (quadratic) polynomial

```r
# Intercept only
lmm2 <- lmer(tri_mean ~ poly(intensity, 2) + (1 | PID),
             data = data_tm,
             REML = TRUE)

# Intercept and slope
lmm2b <- lmer(tri_mean ~ poly(intensity, 2) + (intensity | PID),
              data = data_tm,
              REML = TRUE)

# Better model?
anova(lmm2, lmm2b)
```

```
## Data: data_tm
## Models:
## lmm2: tri_mean ~ poly(intensity, 2) + (1 | PID)
## lmm2b: tri_mean ~ poly(intensity, 2) + (intensity | PID)
##       Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## lmm2   5 1816.7 1834.2 -903.35   1806.7
## lmm2b  7 1735.5 1760.0 -860.74   1721.5 85.22      2  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Anova for better model
Anova(lmm2b,
      type = 2,
      test.statistic = 'F')
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: tri_mean
##                          F Df Df.res    Pr(>F)
```

```
## poly(intensity, 2) 46.667  2 43.413 1.526e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Print better model
summary(lmm2b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: tri_mean ~ poly(intensity, 2) + (intensity | PID)
##    Data: data_tm
##
## REML criterion at convergence: 1704.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0263 -0.4333  0.0007  0.5147  3.6042
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  PID      (Intercept) 633.22   25.164
##           intensity    36.17    6.014   -0.89
##  Residual              42.73    6.537
## Number of obs: 244, groups:  PID, 19
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           -4.666      3.184  -1.465
## poly(intensity, 2)1  205.327     21.102   9.730
## poly(intensity, 2)2    2.061      6.553   0.315
##
## Correlation of Fixed Effects:
##             (Intr) p(,2)1
## ply(ntn,2)1 -0.505
## ply(ntn,2)2  0.001  0.002
```

```r
# Doesn't work with LaTex
#tab_model(lmm2b,
#          auto.label = FALSE,
#          dv.labels = "Response",
#          string.pred = "Coefficients",
#          pred.labels = c('(Intercept)',
#                          'Intensity (linear)',
#                          'Intensity (quadratic)'),
#          string.stat = 'Estimate',
#          string.ci = '95% CI',
#          string.p = 'p-value',
#          show.icc = FALSE,
#          show.r2 = FALSE)
```

3rd-order (cubic) polynomial

```r
# Intercept only
lmm3 <- lmer(tri_mean ~ poly(intensity, 3) + (1 | PID),
             data = data_tm,
             REML = TRUE)

# Intercept and slope
lmm3b <- lmer(tri_mean ~ poly(intensity, 3) + (intensity | PID),
              data = data_tm,
              REML = TRUE)

# Better model?
anova(lmm3, lmm3b)
```

```
## Data: data_tm
## Models:
## lmm3: tri_mean ~ poly(intensity, 3) + (1 | PID)
## lmm3b: tri_mean ~ poly(intensity, 3) + (intensity | PID)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## lmm3   6 1813.8 1834.8 -900.90   1801.8
## lmm3b  8 1727.0 1754.9 -855.48   1711.0 90.841      2  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Anova for better model
Anova(lmm3b,
      type = 2,
      test.statistic = 'F')
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: tri_mean
##                         F Df Df.res    Pr(>F)
## poly(intensity, 3) 34.148  3 71.491 8.318e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Print better model
summary(lmm3b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: tri_mean ~ poly(intensity, 3) + (intensity | PID)
##    Data: data_tm
##
## REML criterion at convergence: 1688.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0170 -0.4757  0.0340  0.4967  3.4425
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  PID      (Intercept) 639.31   25.285
##           intensity    36.93    6.077   -0.89
##  Residual              40.77    6.385
```

```
## Number of obs: 244, groups:  PID, 19
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           -4.666      3.178  -1.468
## poly(intensity, 3)1  205.350     21.255   9.661
## poly(intensity, 3)2    2.125      6.401   0.332
## poly(intensity, 3)3   20.946      6.399   3.273
##
## Correlation of Fixed Effects:
##             (Intr) p(,3)1 p(,3)2
## ply(ntn,3)1 -0.507
## ply(ntn,3)2  0.001  0.002
## ply(ntn,3)3  0.000  0.000  0.003
```

```
# Doeasn't work with LaTex
#tab_model(lmm3b,
#           auto.label = FALSE,
#           dv.labels = "Response",
#           string.pred = "Coefficients",
#           pred.labels = c('(Intercept)',
#                           'Intensity (linear)',
#                           'Intensity (quadratic)',
#                           'Intensity (cubic)'),
#           string.stat = 'Estimate',
#           string.ci = '95% CI',
#           string.p = 'p-value',
#           show.icc = FALSE,
#           show.r2 = FALSE)
```

Compare models

```
knitr::kable(broom::tidy(anova(lmm1b, lmm2b, lmm3b)),
             caption = 'Linear model vs quadratic model and cubic model')
```

Table 1: Linear model vs quadratic model and cubic model

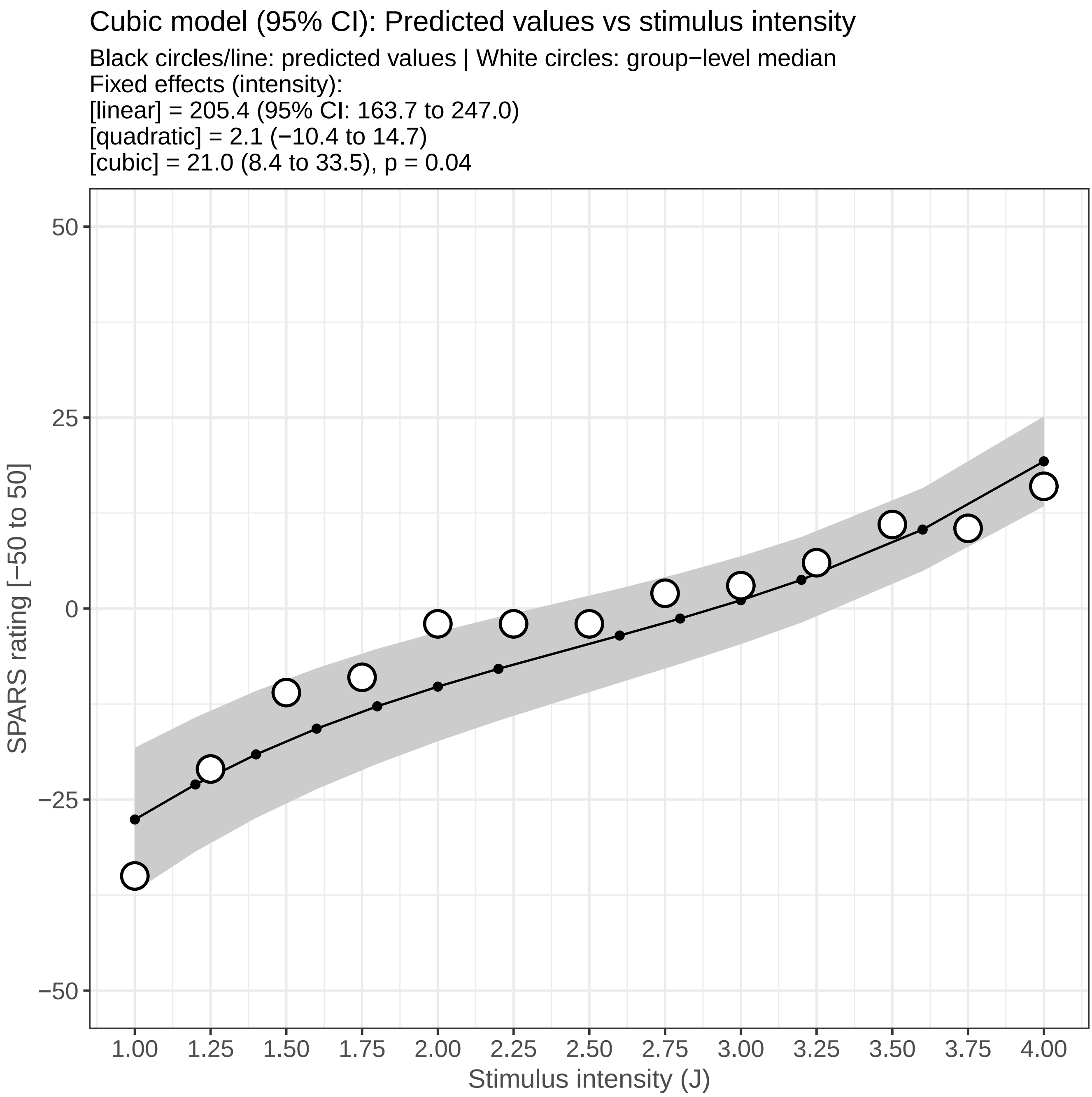
term	df	AIC	BIC	logLik	deviance	statistic	Chi.Df	p.value
lmm1b	6	1733.586	1754.569	-860.7930	1721.586	NA	NA	NA
lmm2b	7	1735.487	1759.967	-860.7434	1721.487	0.0991866	1	0.7528079
lmm3b	8	1726.958	1754.936	-855.4791	1710.958	10.5285980	1	0.0011754

PLot the model

```
predicted <- ggeffect(model = lmm3b,
                      terms = 'intensity',
                      ci.lvl = 0.95)

ggplot(data = predicted) +
```

```
  geom_ribbon(aes(x = x,
                  ymin = conf.low,
                  ymax = conf.high),
              fill = '#CCCCCC') +
  geom_line(aes(x = x,
                y = predicted)) +
  geom_point(aes(x = x,
                 y = predicted)) +
  geom_point(data = data_group,
             aes(x = intensity,
                 y = median),
             shape = 21,
             size = 5,
             stroke = 1,
             fill = '#FFFFFF') +
labs(title = 'Cubic model (95% CI): Predicted values vs stimulus intensity',
     subtitle = 'Black circles/line: predicted values | White circles: group-level media
     x = 'Stimulus intensity (J)',
     y = 'SPARS rating [-50 to 50]') +
scale_y_continuous(limits = c(-50, 50)) +
scale_x_continuous(breaks = seq(from = 1, to = 4, by = 0.25))
```



The cubic model has the best fit. The resulting curvilinear response function is *steepest* at the extremes and *flattens out* in the mid-ranges of stimulus intensity. We performed diagnostics on this model to confirm that the model was properly specified.

Quantile mixed model regression

```
# Quantile model with 2.5, 25, 50, 75, and 97.5% quantiles
qmm <- lqmm(fixed = tri_mean ~ poly(intensity, 3),
            random = ~ intensity,
            group = PID,
            data = data_tm,
            tau = c(0.025, 0.25, 0.5, 0.75, 0.975))
```

```r
# Summary
summary(qmm)
```

```
## Call: lqmm(fixed = tri_mean ~ poly(intensity, 3), random = ~intensity,
##     group = PID, tau = c(0.025, 0.25, 0.5, 0.75, 0.975), data = data_tm)
##
## tau = 0.025
##
## Fixed effects:
##                          Value Std. Error lower bound upper bound  Pr(>|t|)
## (Intercept)          -36.37236    9.70619   -55.87768     -16.867 0.0004716
## poly(intensity, 3)1 204.70791   22.36297   159.76785     249.648 3.481e-12
## poly(intensity, 3)2  11.54948   22.14290   -32.94835      56.047 0.6043068
## poly(intensity, 3)3  26.76290   12.91830     0.80262      52.723 0.0435784
##
## (Intercept)         ***
## poly(intensity, 3)1 ***
## poly(intensity, 3)2
## poly(intensity, 3)3 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## tau = 0.25
##
## Fixed effects:
##                          Value Std. Error lower bound upper bound  Pr(>|t|)
## (Intercept)          -16.06242    6.98392   -30.09713     -2.0277   0.02575
## poly(intensity, 3)1 205.06628   23.47942   157.88262    252.2500 1.475e-11
## poly(intensity, 3)2   0.84314   12.42679   -24.12943     25.8157   0.94618
## poly(intensity, 3)3  21.92427    8.75776     4.32489     39.5237   0.01568
##
## (Intercept)         *
## poly(intensity, 3)1 ***
## poly(intensity, 3)2
## poly(intensity, 3)3 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## tau = 0.5
##
## Fixed effects:
##                         Value Std. Error lower bound upper bound  Pr(>|t|)
## (Intercept)            3.2873     7.2773    -11.3370      17.912   0.65347
## poly(intensity, 3)1 204.0394    23.9347    155.9408     252.138 3.045e-11
## poly(intensity, 3)2   2.2389    11.9844    -21.8447      26.322   0.85258
## poly(intensity, 3)3  22.1176     8.6720      4.6905      39.545   0.01393
##
## (Intercept)
## poly(intensity, 3)1 ***
## poly(intensity, 3)2
## poly(intensity, 3)3 *
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## tau = 0.75
##
## Fixed effects:
##                          Value Std. Error lower bound upper bound  Pr(>|t|)
## (Intercept)            19.0218     7.2020      4.5489      33.495   0.01105
## poly(intensity, 3)1 203.2674    24.4777    154.0776     252.457 6.572e-11
## poly(intensity, 3)2   5.9630    12.1237    -18.4004      30.326   0.62502
## poly(intensity, 3)3  22.6834     8.8776      4.8432      40.524   0.01377
##
## (Intercept)         *
## poly(intensity, 3)1 ***
## poly(intensity, 3)2
## poly(intensity, 3)3 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## tau = 0.975
##
## Fixed effects:
##                          Value Std. Error lower bound upper bound  Pr(>|t|)
## (Intercept)            22.0604    14.8642     -7.8104      51.931   0.14418
## poly(intensity, 3)1 188.9824    23.8309    141.0923     236.872 2.444e-10
## poly(intensity, 3)2  22.3598    13.3181     -4.4040      49.123   0.09954
## poly(intensity, 3)3  12.1005     8.3818     -4.7433      28.944   0.15520
##
## (Intercept)
## poly(intensity, 3)1 ***
## poly(intensity, 3)2 .
## poly(intensity, 3)3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## AIC:
## [1] 2304 (df = 7) 1892 (df = 7) 1858 (df = 7) 1913 (df = 7) 2212 (df = 7)
```

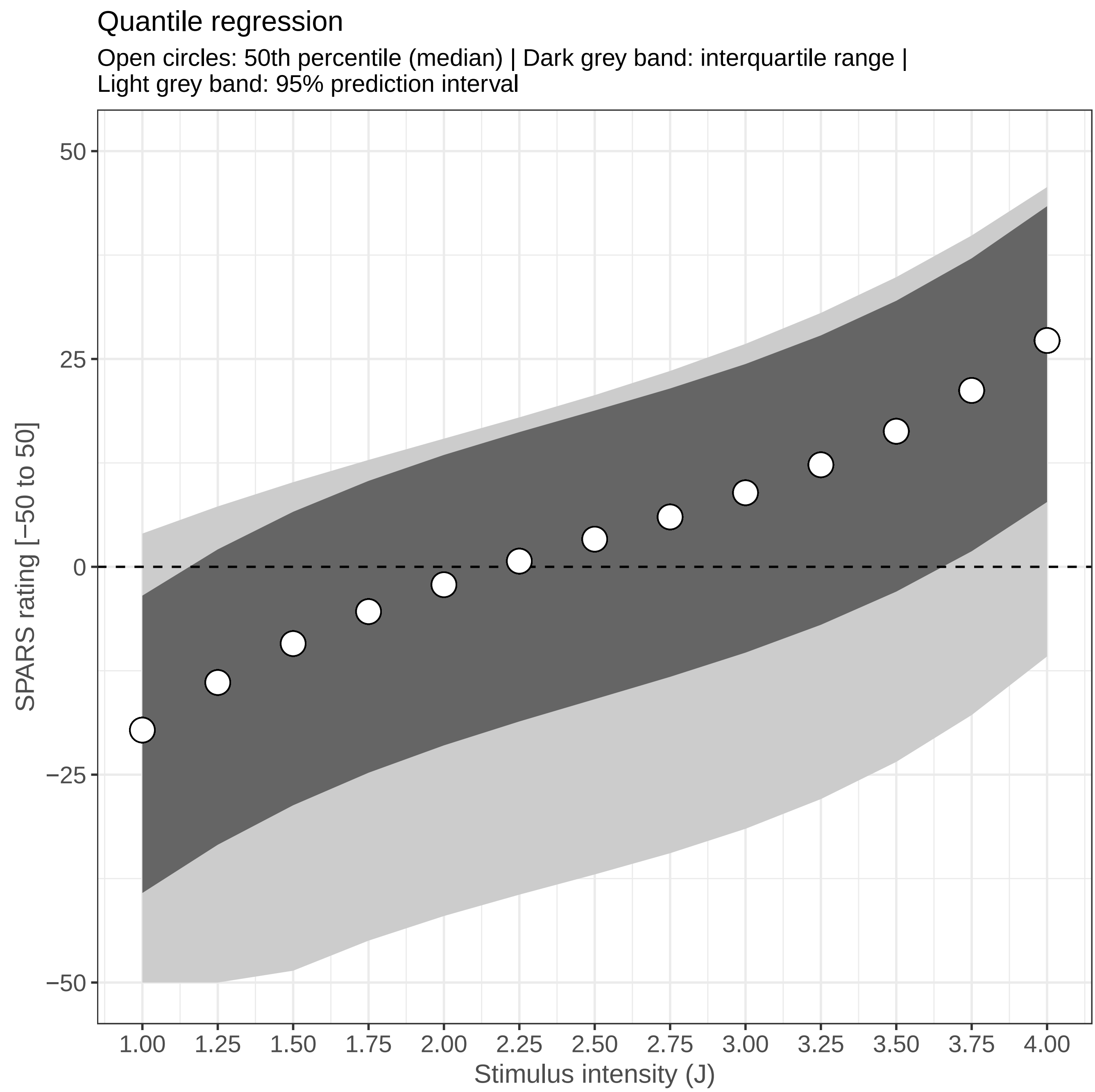
```r
# Get predicted values
## Level 0 (conditional, note difference to the lmer diagnostics)
quant_predict <- as.data.frame(predict(qmm, level = 0))
names(quant_predict) <- paste0('Q', c(2.5, 25, 50, 75, 97.5))

# Join with 'central_lmm'
data_lqmm <- data_tm %>%
  bind_cols(quant_predict)

# Trim prediction to upper and lower limits of the scale
data_lqmm %<>%
  mutate_if(is.numeric,
            funs(ifelse(. > 50,
                        yes = 50,
                        no = ifelse(. < -50,
                                    yes = -50,
```

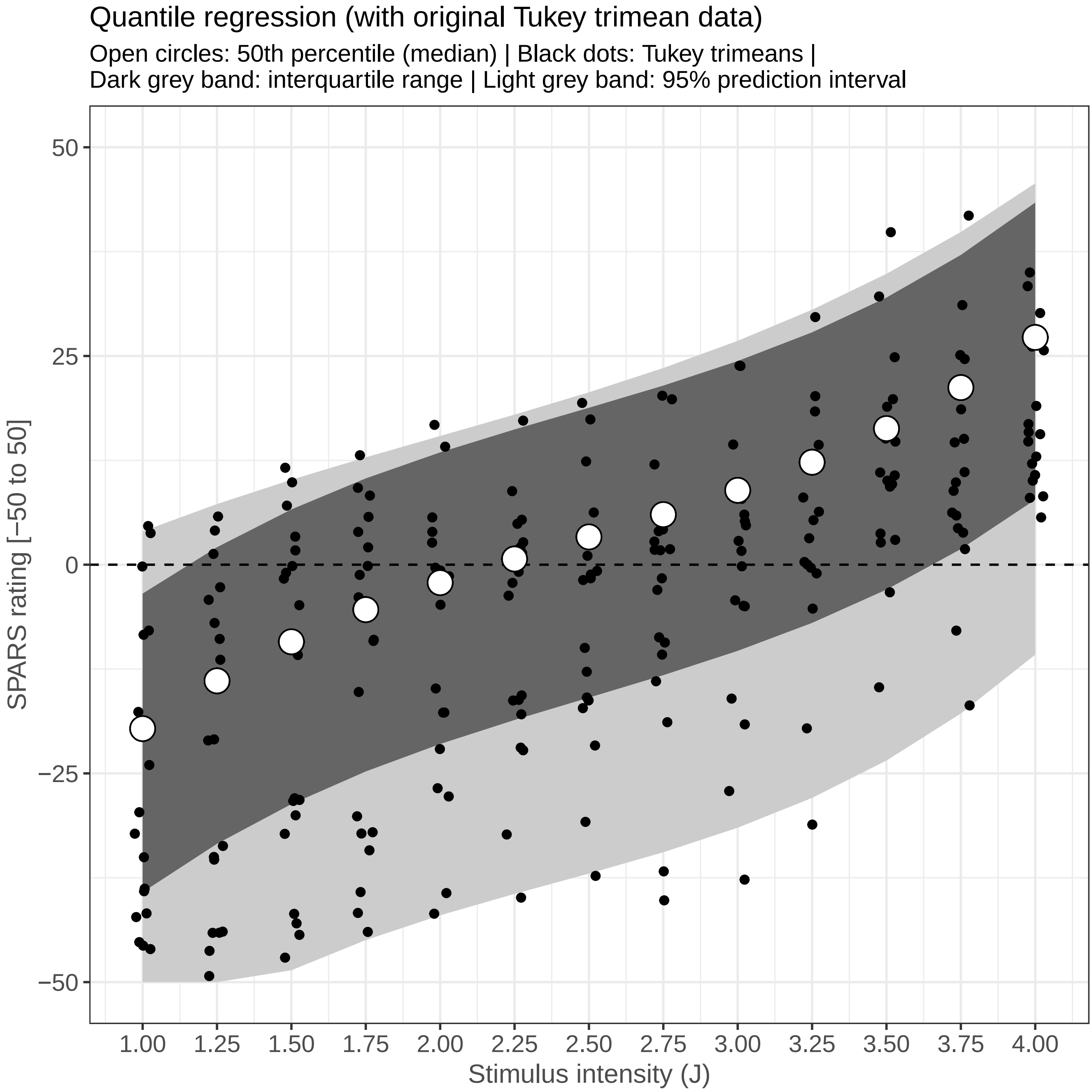
```
                                    no = .))))

# Plot
ggplot(data = data_lqmm) +
  aes(x = intensity,
      y = Q50) +
  geom_ribbon(aes(ymin = `Q2.5`,
                  ymax = `Q97.5`),
              fill = '#CCCCCC') +
  geom_ribbon(aes(ymin = `Q25`,
                  ymax = `Q75`),
              fill = '#656565') +
  geom_hline(yintercept = 0,
             linetype = 2) +
  geom_point(size = 5,
             shape = 21,
             fill = '#FFFFFF',
             colour = '#000000') +
  labs(title = paste('Quantile regression'),
       subtitle = 'Open circles: 50th percentile (median) | Dark grey band: interquartile
       x = 'Stimulus intensity (J)',
       y = 'SPARS rating [-50 to 50]') +
  scale_y_continuous(limits = c(-50, 50)) +
  scale_x_continuous(breaks = unique(data_lqmm$intensity))
```




```
## With original data
ggplot(data = data_lqmm) +
  aes(x = intensity,
      y = Q50) +
  geom_ribbon(aes(ymin = `Q2.5`,
                  ymax = `Q97.5`),
              fill = '#CCCCCC') +
  geom_ribbon(aes(ymin = `Q25`,
                  ymax = `Q75`),
              fill = '#656565') +
  geom_point(data = data_tm,
             aes(y = tri_mean),
             position = position_jitter(width = 0.03)) +
  geom_hline(yintercept = 0,
             linetype = 2) +
  geom_point(size = 5,
             shape = 21,
```

```
              fill = '#FFFFFF',
              colour = '#000000') +
  labs(title = paste('Quantile regression (with original Tukey trimean data)'),
       subtitle = 'Open circles: 50th percentile (median) | Black dots: Tukey trimeans |\n
       x = 'Stimulus intensity (J)',
       y = 'SPARS rating [-50 to 50]') +
  scale_y_continuous(limits = c(-50, 50)) +
  scale_x_continuous(breaks = unique(data_lqmm$intensity))
```



There is good stability in the shape of the response characteristics across the quantiles. For all stimulus intensities, the distribution is left skewed (long tail towards lower ratings).

Session information

```r
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  ggeffects_0.5.0 car_3.0-2       carData_3.0-2
##  [5] sjPlot_2.6.0    HLMdiag_0.3.1   lqmm_1.5.4      lme4_1.1-18-1
##  [9] Matrix_1.2-14   forcats_0.3.0   stringr_1.3.1   dplyr_0.7.6
## [13] purrr_0.2.5     readr_1.1.1     tidyr_0.8.1     tibble_1.4.2
## [17] ggplot2_3.0.0   tidyverse_1.2.1 magrittr_1.5
##
## loaded via a namespace (and not attached):
##  [1] TH.data_1.0-9      minqa_1.2.4        colorspace_1.3-2
##  [4] modeltools_0.2-22  rio_0.5.10         ggridges_0.5.1
##  [7] sjlabelled_1.0.14  rprojroot_1.3-2    estimability_1.3
## [10] snakecase_0.9.2    rstudioapi_0.8     glmmTMB_0.2.2.0
## [13] mvtnorm_1.0-8      lubridate_1.7.4    coin_1.2-2
## [16] xml2_1.2.0         codetools_0.2-15   splines_3.5.1
## [19] mnormt_1.5-5       knitr_1.20         sjmisc_2.7.5
## [22] effects_4.0-3      bayesplot_1.6.0    jsonlite_1.5
## [25] nloptr_1.2.1       pbkrtest_0.4-7     broom_0.5.0
## [28] compiler_3.5.1     httr_1.3.1         sjstats_0.17.1
## [31] emmeans_1.2.4      backports_1.1.2    assertthat_0.2.0
## [34] lazyeval_0.2.1     survey_3.33-2      cli_1.0.1
## [37] htmltools_0.3.6    tools_3.5.1        SparseGrid_0.8.2
## [40] coda_0.19-1        gtable_0.2.0       glue_1.3.0
## [43] reshape2_1.4.3     Rcpp_0.12.19       cellranger_1.1.0
## [46] nlme_3.1-137       psych_1.8.4        openxlsx_4.1.0
## [49] rvest_0.3.2        stringdist_0.9.5.1 MASS_7.3-50
## [52] zoo_1.8-4          scales_1.0.0       hms_0.4.2
## [55] parallel_3.5.1     sandwich_2.5-0     pwr_1.2-2
## [58] TMB_1.7.14         yaml_2.2.0         curl_3.2
## [61] stringi_1.2.4      highr_0.7          zip_1.0.0
## [64] rlang_0.2.2        pkgconfig_2.0.2    evaluate_0.11
## [67] lattice_0.20-35    prediction_0.3.6   bindr_0.1.1
## [70] labeling_0.3       tidyselect_0.2.4   plyr_1.8.4
## [73] R6_2.2.2           multcomp_1.4-8     RLRsim_3.1-3
## [76] pillar_1.3.0       haven_1.1.2        foreign_0.8-71
```

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## [79] withr_2.1.2        mgcv_1.8-24        abind_1.4-5
## [82] survival_2.42-6    nnet_7.3-12        modelr_0.1.2
## [85] crayon_1.3.4       rmarkdown_1.10     grid_3.5.1
## [88] readxl_1.1.0       data.table_1.11.8  digest_0.6.17
## [91] xtable_1.8-3       stats4_3.5.1       munsell_0.5.0
```