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
```

```
# Doesn't work with LaTex
# sjt.lmer(lmm1b,
#          show.header = TRUE,
#          string.dv = "Response",
#          string.pred = "Coefficients",
#          depvar.labels = '',
#          pred.labels = 'intensity',
#          string.est = 'Estimate',
#          string.ci = '95% CI',
#          string.p = 'p-value',
#          show.icc = FALSE,
#          show.r2 = FALSE)
```

2nd-order (quadratic) polynomial

```
# 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
```

```
# 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
# sjt.lmer(lmm2b,
#          show.header = TRUE,
#          string.dv = "Response",
#          string.pred = "Coefficients",
#          depvar.labels = '',
#          pred.labels = 'intensity',
#          string.est = '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
# sjt.lmer(lmm3b,
#          show.header = TRUE,
#          string.dv = "Response",
#          string.pred = "Coefficients",
#          depvar.labels = '',
#          pred.labels = 'intensity',
#          string.est = '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')
```

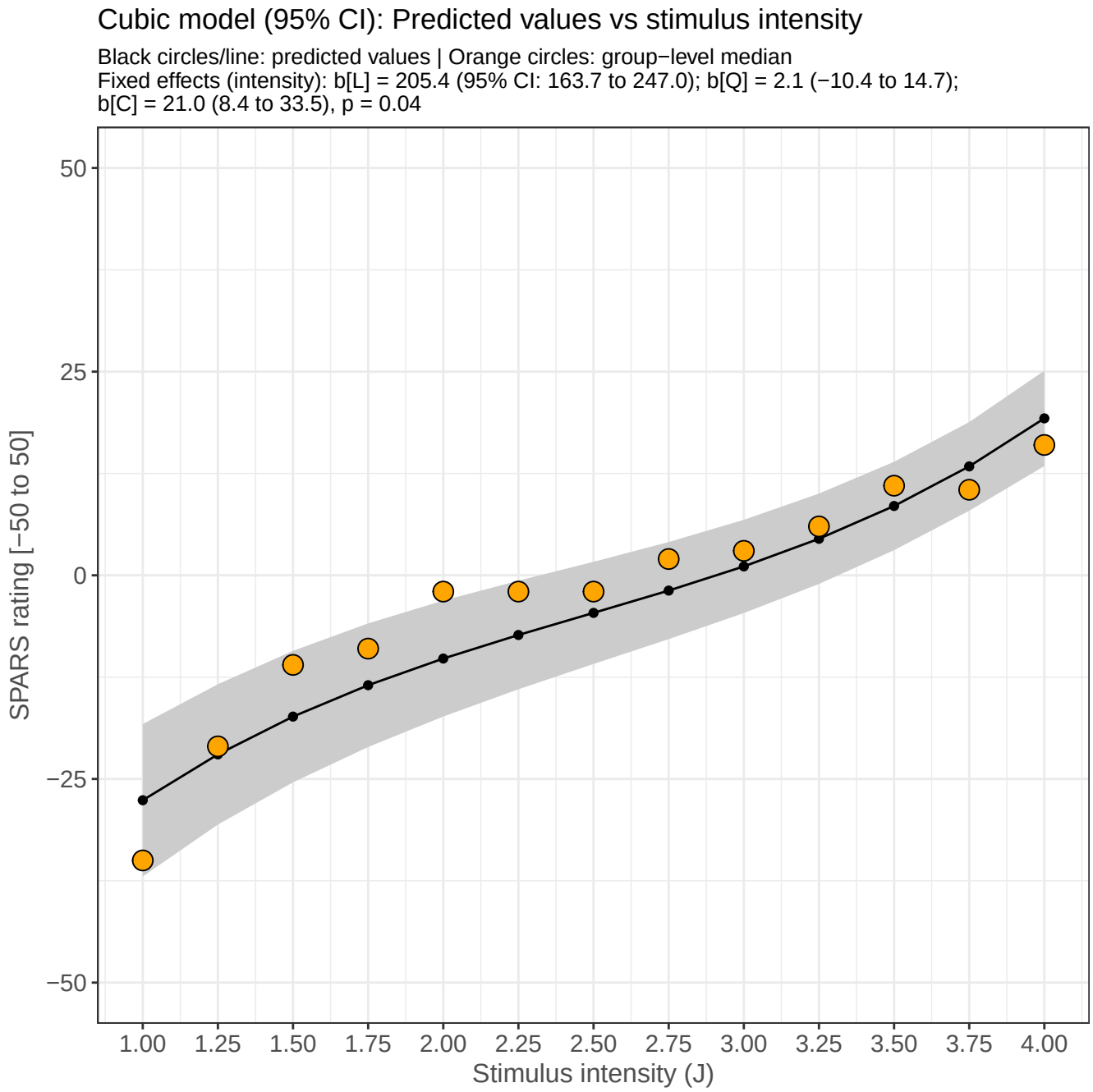
Table 1: Linear model vs quadratic model and cubic model

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 <- ggeffects::ggpredict(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 = 4,
             fill = '#FFA500') +
labs(title = 'Cubic model (95% CI): Predicted values vs stimulus intensity',
     subtitle = 'Black circles/line: predicted values | Orange circles: group-level medi
     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   29.49292   -95.64061      22.896  0.22336
## poly(intensity, 3)1 204.70791   14.74668   175.07335     234.343  < 2e-16
## poly(intensity, 3)2  11.54948   18.70429   -26.03821      49.137  0.53978
## poly(intensity, 3)3  26.76290   12.89966     0.84007      52.686  0.04329
##
## (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    8.34122   -32.82474      0.6999  0.059959
## poly(intensity, 3)1 205.06628   14.58453   175.75758    234.3750 < 2.2e-16
## poly(intensity, 3)2   0.84314   13.35216   -25.98903     27.6753  0.949907
## poly(intensity, 3)3  21.92427    7.52232     6.80761     37.0409  0.005356
##
## (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     8.1325    -13.0555      19.630  0.687812
## poly(intensity, 3)1 204.0394    14.7300    174.4383     233.641 < 2.2e-16
## poly(intensity, 3)2   2.2389    12.8770    -23.6384      28.116  0.862688
## poly(intensity, 3)3  22.1176     7.8359      6.3708      37.864  0.006865
##
## (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     7.6863      3.5757      34.468  0.016840
## poly(intensity, 3)1 203.2674    15.5063    172.1063     234.428 < 2.2e-16
## poly(intensity, 3)2   5.9630    12.0117    -18.1755      30.102  0.621809
## poly(intensity, 3)3  22.6834     7.5058      7.5999      37.767  0.003984
##
## (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    11.8678     -1.7888      45.910   0.06906
## poly(intensity, 3)1 188.9824    16.7261    155.3700     222.595 2.999e-15
## poly(intensity, 3)2  22.3598    13.4991     -4.7676      49.487   0.10403
## poly(intensity, 3)3  12.1005     9.2630     -6.5143      30.715   0.19754
##
## (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)
```

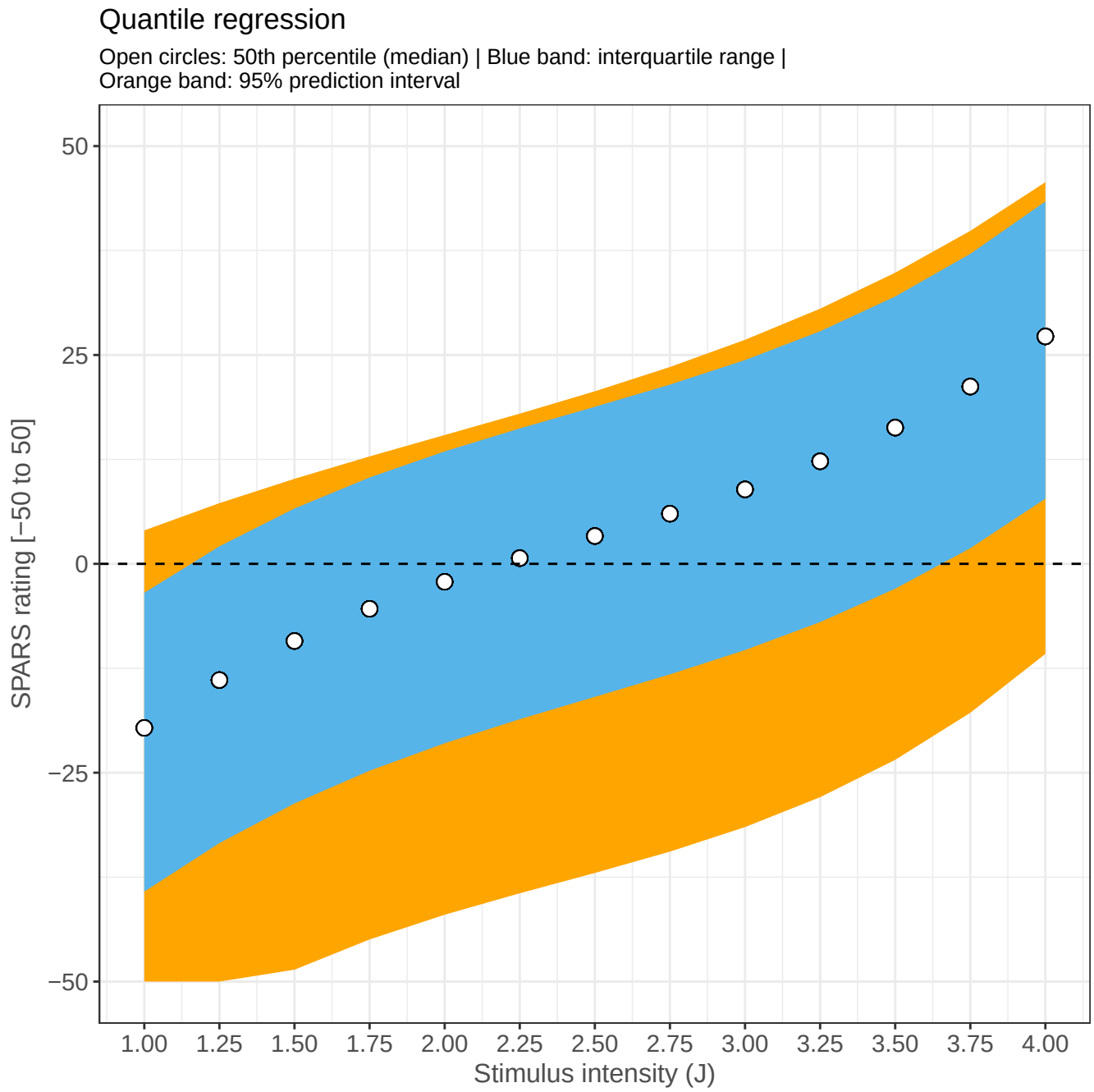
```
# Get predicted values
## Level 0 (conditional, note difference to the lmer diagnostics)
quant_predict <- as.data.frame(predict(qmm, level = 0))
names(quant_predict) <- paste0('Q', c(2.5, 25, 50, 75, 97.5))

# 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,
```

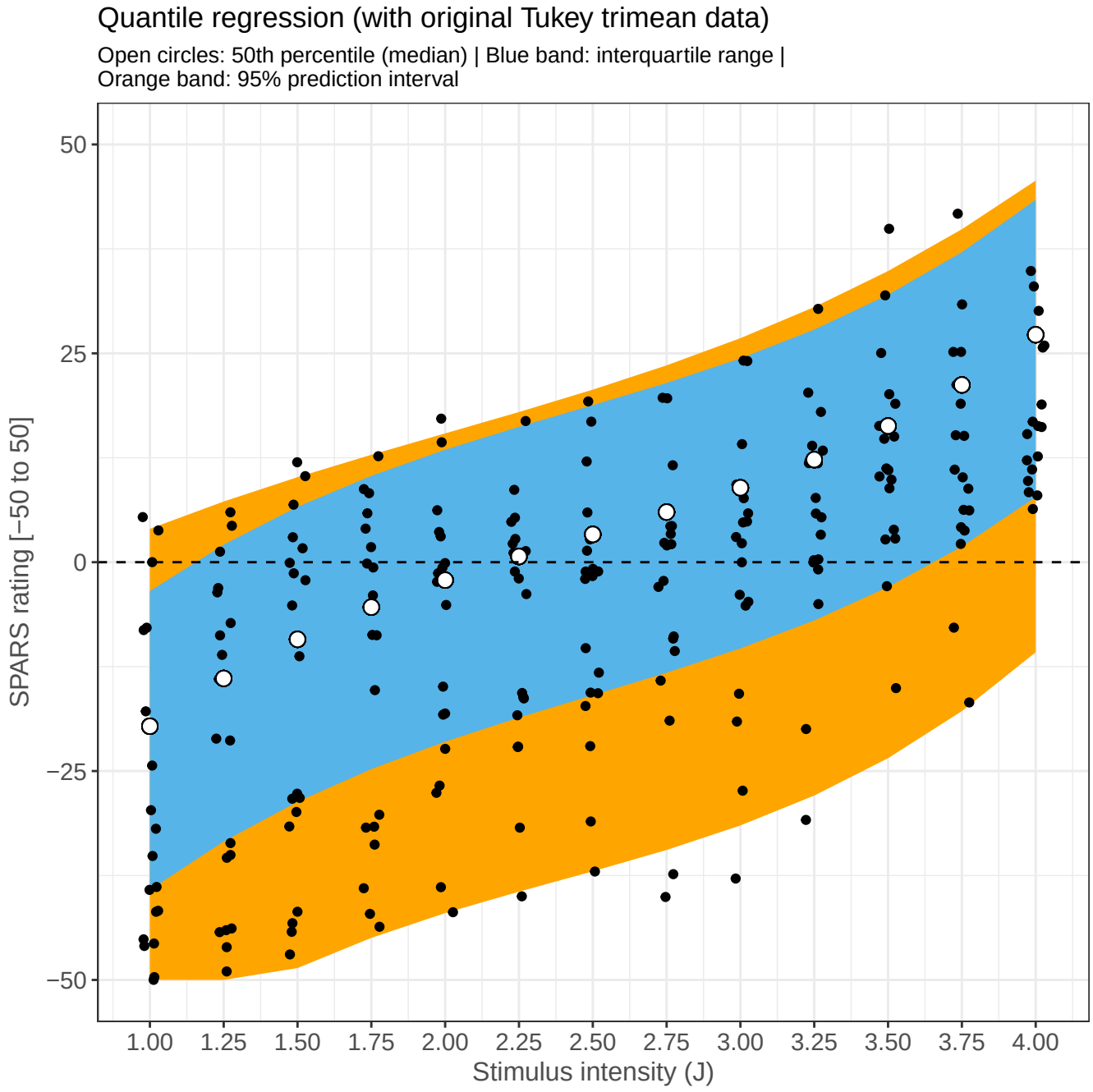
```
                                    no = .))))

# Plot
ggplot(data = data_lqmm) +
  aes(x = intensity,
      y = Q50) +
  geom_ribbon(aes(ymin = `Q2.5`,
                  ymax = `Q97.5`),
              fill = '#FFA500') +
  geom_ribbon(aes(ymin = `Q25`,
                  ymax = `Q75`),
              fill = '#56B4E9') +
  geom_point(size = 3,
             shape = 21,
             fill = '#FFFFFF',
             colour = '#000000') +
  geom_hline(yintercept = 0,
             linetype = 2) +
  labs(title = paste('Quantile regression'),
       subtitle = 'Open circles: 50th percentile (median) | Blue band: interquartile range
       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 = '#FFA500') +
  geom_ribbon(aes(ymin = `Q25`,
                  ymax = `Q75`),
              fill = '#56B4E9') +
  geom_point(data = data_tm,
             aes(y = tri_mean),
             position = position_jitter(width = 0.03)) +
  geom_point(size = 3,
             shape = 21,
             fill = '#FFFFFF',
             colour = '#000000') +
```

```
  geom_hline(yintercept = 0,
             linetype = 2) +
  labs(title = paste('Quantile regression (with original Tukey trimean data)'),
       subtitle = 'Open circles: 50th percentile (median) | Blue band: interquartile range
       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

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS High Sierra 10.13.5
##
## 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     car_3.0-0          carData_3.0-1
##  [4] sjPlot_2.4.1       HLMdiag_0.3.1      lqmm_1.5.4
##  [7] lme4_1.1-17        Matrix_1.2-14      forcats_0.3.0
## [10] stringr_1.3.1      dplyr_0.7.5        purrr_0.2.5
## [13] readr_1.1.1        tidyr_0.8.1        tibble_1.4.2
## [16] ggplot2_2.2.1.9000 tidyverse_1.2.1    magrittr_1.5
##
## loaded via a namespace (and not attached):
##   [1] TH.data_1.0-8      minqa_1.2.4        colorspace_1.3-2
##   [4] rio_0.5.10         modeltools_0.2-21  ggridges_0.5.0
##   [7] sjlabelled_1.0.11  rprojroot_1.3-2    estimability_1.3
##  [10] snakecase_0.9.1    rstudioapi_0.7     glmmTMB_0.2.1.0
##  [13] DT_0.4             mvtnorm_1.0-8      lubridate_1.7.4
##  [16] coin_1.2-2         xml2_1.2.0         codetools_0.2-15
##  [19] splines_3.5.0      mnormt_1.5-5       knitr_1.20
##  [22] sjmisc_2.7.2       effects_4.0-1      bayesplot_1.5.0
##  [25] jsonlite_1.5       nloptr_1.0.4       ggeffects_0.3.4
##  [28] pbkrtest_0.4-7     broom_0.4.4        shiny_1.1.0
##  [31] compiler_3.5.0     httr_1.3.1         sjstats_0.15.0
##  [34] emmeans_1.2.1      backports_1.1.2    assertthat_0.2.0
##  [37] lazyeval_0.2.1     survey_3.33-2      cli_1.0.0
##  [40] later_0.7.3        htmltools_0.3.6    tools_3.5.0
##  [43] SparseGrid_0.8.2   coda_0.19-1        gtable_0.2.0
##  [46] glue_1.2.0         reshape2_1.4.3     merTools_0.4.1
##  [49] Rcpp_0.12.17       cellranger_1.1.0   nlme_3.1-137
##  [52] psych_1.8.4        lmtest_0.9-36      openxlsx_4.1.0
##  [55] rvest_0.3.2        mime_0.5           stringdist_0.9.5.1
##  [58] MASS_7.3-50        zoo_1.8-1          scales_0.5.0.9000
##  [61] promises_1.0.1     hms_0.4.2          parallel_3.5.0
##  [64] sandwich_2.4-0     pwr_1.2-2          TMB_1.7.13
##  [67] curl_3.2           yaml_2.1.19        stringi_1.2.2
##  [70] highr_0.6          blme_1.0-4         zip_1.0.0
##  [73] rlang_0.2.1        pkgconfig_2.0.1    arm_1.10-1
```

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##  [76] evaluate_0.10.1    lattice_0.20-35    prediction_0.3.6
##  [79] bindr_0.1.1        labeling_0.3       htmlwidgets_1.2
##  [82] tidyselect_0.2.4   plyr_1.8.4         R6_2.2.2
##  [85] multcomp_1.4-8     RLRsim_3.1-3       pillar_1.2.3
##  [88] haven_1.1.1        foreign_0.8-70     withr_2.1.2
##  [91] mgcv_1.8-23        survival_2.42-3    abind_1.4-5
##  [94] nnet_7.3-12        modelr_0.1.2       crayon_1.3.4
##  [97] rmarkdown_1.9      grid_3.5.0         readxl_1.1.0
## [100] data.table_1.11.4  digest_0.6.15      xtable_1.8-2
## [103] httpuv_1.4.3       stats4_3.5.0       munsell_0.4.3
```