

# Martel Paper - Daily OA Pain

2024-03-18

## Data Wrangling

```
## Load packages
library(tidyverse)
library(ggplot2)
library(tidyr)
library(haven) ## This library provides functions to read sav file into R
library(lme4)
library(lmerTest)

## Read data
data_paper <- read_sav("Dataset; 2024.1.sav")
checkdf3 <- data_paper |>
  subset(ID == 2072) |>
  select(c(ID,
           Level1_Even_DateIn,
           Level1_Even_TimeIn,
           Wave_Day))

## Delete Weird ID 2072 those weird reporting days
data_paper <- data_paper |>
  filter(!(ID == 2072 & Wave_Day >= 7))
```

## Adjusting Wave Day

- $DT_i$  combines  $D_i$  and  $T_i$ : 'DateTime' variable
- $DT_0$  is the first response 'DateTime' for each patient
- $W_i$  is the adjusted 'Wave\_Day' variable
- Add a grace period  $G$  for calculating the adjusted  $W_i$ , in our case  $G = 6$  hours
- Calculate the datetime difference  $H_i$  in \*\*hours\*\* from the first response, incorporating the grace period:

$$H_i = DT_i - DT_{i-1}$$

- Then apply the grace period indicator  $I_i$ :

$$I_i = \begin{cases} 1 & \text{if } H_i \leq 24 + G \\ \left\lceil \frac{H_i - G}{24} \right\rceil & \text{otherwise} \end{cases}$$

- The initial response for ‘Wave\_Day’ is 1, i.e.,  $W_0 = 1$ , then the adjusted ‘Wave\_Day’  $W_i$  is

$$W_i = \sum_{i=0}^{i-1} I_i$$

```
## Consecutive Days - Grace Period 6 hours
data_paper <- data_paper |>
  mutate(Lev1_DateTimeIn = as.POSIXct(strptime(paste(Level1_Even_DateIn,
                                                    Level1_Even_TimeIn),
                                                    format="%Y-%m-%d %H:%M:")) |>

  arrange(ID, Lev1_DateTimeIn) |>
  group_by(ID) |>
  mutate(
    TimeDiffHours = as.numeric(difftime(Lev1_DateTimeIn,
                                         lag(Lev1_DateTimeIn,
                                              default = first(Lev1_DateTimeIn)),
                                         units = "hours")), # T diff

    WithinGracePeriod = if_else(TimeDiffHours <= 30,
                                1,
                                ceiling((TimeDiffHours - 6) / 24)), # Check grace perio

    Wave_Day_Adjusted = cumsum(WithinGracePeriod) # Adjusted Wave_Day
  ) |>
  ungroup()

##### Check if the above approach is correct #####
checkdf <- data_paper |> select(c(ID,
                                Lev1_DateTimeIn,
                                TimeDiffHours,
                                WithinGracePeriod,
                                Wave_Day_Adjusted,
                                Baseline_Demog_BMI))

checkdf2 <- checkdf |> subset(ID == 2072) # Weird ID 2072
max(checkdf$Wave_Day_Adjusted, na.rm = TRUE)
```

```
## [1] 21
```

```
## Fill in the gap of Wave_Day
data_paper2 <- data_paper |>
  group_by(ID) |>
  complete(Wave_Day = 1:14) |>
  ungroup()
```

```
## Check the aberrant values
```

```
summary(data_paper2$IndexLev1_NegativeAffect_Total) # Lev 1 Negative Affect
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##    0.000   8.333  20.667  25.189  37.000  97.333   1228
```

```
summary(data_paper2$IndexLev1_Catastrophizing_Total) # Lev 1 Catas
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##    0.000   2.667  12.667  23.085  38.000 100.000   1228
```

```
summary(data_paper2$IndexLev2_QST_BaselinePPTTh) # Lev 2 PPTThs?
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##    67.0   235.5   369.0   395.8   482.5  1200.0   1321
```

```
summary(data_paper2$IndexLev2_QST_TSPAve) # Lev 2 TSP?
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##   -2.50    1.50    7.50   13.97   15.00   94.00   1284
```

```
summary(data_paper2$IndexLev2_QST_CpmTrialAve) # Lev 2 CPM?
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##    37.56  104.00  119.74  123.10  135.13  251.76   1329
```

```
summary(data_paper2$IndexLev1_PainAverage) # Lev 1 Pain?
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##     0.00   24.00   38.00   41.73   59.75  100.00   1234
```

```
##### Check if lagged value is correct #####
```

```
data_paper2_check <- data_paper2 |>
```

```
  select(c(ID, Wave_Day_Adjusted, IndexLev1_PainAverage, IndexLev1_PainAverage_Lagged))
```

$$APE(t_i) = I(PAIN(t_i) - PAIN(t_i - 1) \geq 20)$$

```
## APE index
```

```
data_paper2 <- data_paper2 |>
```

```
  group_by(ID) |>
```

```
  mutate(APE = ifelse(IndexLev1_PainAverage - IndexLev1_PainAverage_Lagged >= 20, 1, 0))
```

```
##### Check if it is correctly coded #####
```

```
data_paper2_check <- data_paper2 |>
```

```
  select(c(ID, Wave_Day_Adjusted,
           IndexLev1_PainAverage,
           IndexLev1_PainAverage_Lagged,
           APE))
```

For calculating the RPE based on the within person mean, define the indicator that the pain is above the average pain for person  $i$  on day  $t_i$ . Note that  $n_{t_i} = \max t_i$  for patient  $i$ .

$$A(t_i) = I\left(PAIN(t_i) > \frac{1}{n_{t_i}} \sum_{t_i=1}^{n_{t_i}} PAIN(t_i)\right)$$

Then define the RPE given  $A(t_i) = 1$  for person  $i$  on day  $t_i$ .

$$RPE(t_i) = I\left(PAIN(t_i) \leq \frac{1}{n_{t_i}} \sum_{t_i=1}^{n_{t_i}} PAIN(t_i)\right) \times A(t_i - 1)$$

```
## RPE Index using within person mean
data_paper2 <- data_paper2 |>
  group_by(ID) |>
  mutate(AVE = mean(IndexLev1_PainAverage, na.rm = TRUE),
         A = ifelse(IndexLev1_PainAverage > AVE, 1, 0),
         A_lag = lag(A),
         Lev1_RPE_useMean = ifelse(A_lag == 1,
                                   ifelse(IndexLev1_PainAverage <= AVE, 1, 0), 0))

##### Check #####
data_paper2_check <- data_paper2 |>
  select(c(ID, Wave_Day_Adjusted, IndexLev1_PainAverage, IndexLev1_PainAverage_Lagged,
          AVE, A, A_lag, Lev1_RPE_useMean))

# 203 RPEs
```

For calculating the RPE based on the APE,

$$RPE(t_i) = I\left(PAIN(t_i) \leq \frac{1}{n_{t_i}} \sum_{t_i=1}^{n_{t_i}} PAIN(t_i)\right) \times APE(t_i - 1)$$

```
## RPE Index using APE
data_paper2 <- data_paper2 |>
  group_by(ID) |>
  mutate(APE_lag = lag(APE),
         Lev1_RPE_useAPE = ifelse(APE_lag == 1,
                                   ifelse(IndexLev1_PainAverage <= 20, 1, 0), 0))

##### Check #####
data_paper2_check <- data_paper2 |>
  select(c(ID, Wave_Day_Adjusted, IndexLev1_PainAverage, IndexLev1_PainAverage_Lagged,
          APE, APE_lag, Lev1_RPE_useAPE))

# 4 RPEs
```

## Analysis of APE using the Table in the Manuscript

### ## Unadjusted APE to Negative Affect

```
model_APE.NA <- glmer(APE ~ IndexLev1_NegativeAffect_Total + (1|ID), family = binomial())
summary(model_APE.NA)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: APE ~ IndexLev1_NegativeAffect_Total + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##  451.6    465.7   -222.8    445.6      809
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.5907 -0.2780 -0.2335 -0.2048  3.9737
##
## Random effects:
##  Groups Name            Variance Std.Dev.
##  ID      (Intercept)  0.7268    0.8525
## Number of obs: 812, groups: ID, 157
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -3.124537   0.329004  -9.497   <2e-16 ***
## IndexLev1_NegativeAffect_Total  0.014167   0.006951   2.038   0.0415 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IndxL1_NA_T -0.732
```

### ## Unadjusted APE to Catastrophizing

```
model_APE.Cata <- glmer(APE ~ IndexLev1_Catastrophizing_Total + (1|ID), family = binomial())
summary(model_APE.Cata)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: APE ~ IndexLev1_Catastrophizing_Total + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
```

```
##      444.2      458.3     -219.1      438.2          809
##
## Scaled residuals:
##      Min        1Q    Median        3Q        Max
## -0.6057 -0.2835 -0.2176 -0.1865  3.9271
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   ID       (Intercept) 0.7367    0.8583
## Number of obs: 812, groups: ID, 157
##
## Fixed effects:
##                                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)                      -3.252303   0.316962 -10.261 < 2e-16 ***
## IndexLv1_Catastrophizing_Total    0.019020   0.005777   3.292 0.000994 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IndxLv1_C_T -0.720

## Unadjusted APE to PPThs
model_APE.PPThs <- glmer(APE ~ IndexLv2_QST_BaselinePPT + (1|ID), family = binomial())

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00456606 (tol = 0.002, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
## - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?

summary(model_APE.PPThs)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: APE ~ IndexLv2_QST_BaselinePPT + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##   415.4    429.2  -204.7   409.4      726
##
## Scaled residuals:
##      Min        1Q    Median        3Q        Max
## -0.4954 -0.2973 -0.2563 -0.2168  4.4125
##
```

```

## Random effects:
##   Groups Name      Variance Std.Dev.
##   ID      (Intercept) 0.49      0.7
## Number of obs: 729, groups: ID, 142
##
## Fixed effects:
##
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -1.7980758  0.3779866  -4.757 1.97e-06 ***
## IndexLev2_QST_BaselinePPTh -0.0021978  0.0009134  -2.406  0.0161 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IL2_QST_BPP -0.807
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.00456606 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?

## Unadjusted APE to TSP
model_APE.TSP <- glmer(APE ~ IndexLev2_QST_TSPAve + (1|ID), family = binomial(), data =
summary(model_APE.TSP)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: APE ~ IndexLev2_QST_TSPAve + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC  logLik deviance df.resid
##  433.9   447.8  -213.9   427.9     758
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -0.4841 -0.2851 -0.2630 -0.2260  5.6749
##
## Random effects:
##   Groups Name      Variance Std.Dev.
##   ID      (Intercept) 0.512    0.7155
## Number of obs: 761, groups: ID, 146
##
## Fixed effects:

```

```

##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -2.40370    0.24326  -9.881  <2e-16 ***
## IndexLev2_QST_TSPAve -0.01805    0.01029  -1.754   0.0794 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IL2_QST_TSP -0.450

## Unadjusted APE to CPM
model_APE.CPM <- glmer(APE ~ IndexLev2_QST_CpmTrialAve + (1|ID), family = binomial(), data = data_paper2)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
## - Rescale variables?

summary(model_APE.CPM)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: APE ~ IndexLev2_QST_CpmTrialAve + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##  415.4    429.2  -204.7   409.4     719
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.4942 -0.2957 -0.2365 -0.2284  3.3972
##
## Random effects:
## Groups Name      Variance Std.Dev.
## ID      (Intercept) 0.7285   0.8536
## Number of obs: 722, groups: ID, 141
##
## Fixed effects:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -2.895586    0.682383  -4.243  2.2e-05 ***
## IndexLev2_QST_CpmTrialAve  0.001580    0.005063   0.312   0.755
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IL2_QST_CTA -0.939

```



```

## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

## Adjusted APE
model_APE <- glmer(APE ~ IndexLev1_Catastrophizing_Total + IndexLev1_NegativeAffect_Total +
summary(model_APE)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## APE ~ IndexLev1_Catastrophizing_Total + IndexLev1_NegativeAffect_Total +
## (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##    445.9    464.7   -219.0    437.9      807
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6339 -0.2812 -0.2176 -0.1846  3.9902
##
## Random effects:
##  Groups Name      Variance Std.Dev.
##  ID      (Intercept) 0.7666   0.8755
## Number of obs: 811, groups: ID, 157
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -3.326941    0.364315  -9.132  < 2e-16 ***
## IndexLev1_Catastrophizing_Total    0.017634    0.006465   2.728  0.00638 **
## IndexLev1_NegativeAffect_Total     0.003769    0.008028   0.470  0.63869
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) IL1_C_
## IndxLv1_C_T -0.361
## IndxL1_NA_T -0.481 -0.434

model_APE_2 <- glmer(APE ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve + IndexLev2_

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0082882 (tol = 0.002, component 1)
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model

```

```
## - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

```
summary(model_APE_2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## APE ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve + IndexLev2_QST_BaselinePPTh +
## (1 | ID)
## Data: data_paper2
##
##          AIC          BIC    logLik deviance df.resid
##    395.4      418.1   -192.7    385.4      679
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.4812 -0.3194 -0.2721 -0.2041  6.7952
##
## Random effects:
## Groups Name          Variance Std.Dev.
## ID      (Intercept) 0.2546    0.5046
## Number of obs: 684, groups: ID, 132
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.8004089   0.8281877  -0.966   0.33381
## IndexLev2_QST_CpmTrialAve -0.0025796   0.0048251  -0.535   0.59291
## IndexLev2_QST_TSPAve     -0.0250571   0.0106213  -2.359   0.01832 *
## IndexLev2_QST_BaselinePPTh -0.0028134   0.0009779  -2.877   0.00401 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) IL2_QST_C IL2_QST_T
## IL2_QST_CTA -0.864
## IL2_QST_TSP -0.236  0.030
## IL2_QST_BPP -0.631  0.275    0.176
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0082882 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

## Analysis of RPE using the Table of Manuscript

### ## Unadjusted RPE to Negative Affect

```
model_RPE.NA <- glmer(Lev1_RPE_useMean ~ IndexLev1_NegativeAffect_Total + (1|ID), family
```

```
## boundary (singular) fit: see help('isSingular')
```

```
summary(model_RPE.NA)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev1_NegativeAffect_Total + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##  923.8    937.9   -458.9   917.8      814
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.5986 -0.5882 -0.5715 -0.5178  1.9000
##
## Random effects:
## Groups Name          Variance Std.Dev.
## ID      (Intercept) 3.535e-15 5.946e-08
## Number of obs: 817, groups: ID, 157
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.026494    0.127343  -8.061 7.58e-16 ***
## IndexLev1_NegativeAffect_Total -0.002979    0.004024  -0.740    0.459
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IndxL1_NA_T -0.773
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

### ## Unadjusted RPE to Catastrophizing

```
model_RPE.Cata <- glmer(Lev1_RPE_useMean ~ IndexLev1_Catastrophizing_Total + (1|ID), fam
```

```
## boundary (singular) fit: see help('isSingular')
```

```
summary(model_RPE.Cata)
```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev1_Catastrophizing_Total + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##    920.2    934.3   -457.1    914.2     814
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6210 -0.6084 -0.5641 -0.4431  2.2700
##
## Random effects:
## Groups Name             Variance Std.Dev.
## ID      (Intercept) 0         0
## Number of obs: 817, groups: ID, 157
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.952720   0.107572  -8.857   <2e-16 ***
## IndexLev1_Catastrophizing_Total -0.006868   0.003466  -1.981   0.0475 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IndxLv1_C_T -0.658
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

## Unadjusted RPE to PPTs
model_RPE.PPTs <- glmer(Lev1_RPE_useMean ~ IndexLev2_QST_BaselinePPT + (1|ID), family

## boundary (singular) fit: see help('isSingular')

summary(model_RPE.PPTs)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev2_QST_BaselinePPT + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##    837.0    850.8   -415.5    831.0     731

```

```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6444 -0.6050 -0.5738  1.5684  2.1812
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   ID      (Intercept) 0          0
## Number of obs: 734, groups: ID, 142
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -0.8386985   0.1835062  -4.570 4.87e-06 ***
## IndexLev2_QST_BaselinePPTh -0.0006009   0.0004239  -1.418   0.156
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IL2_QST_BPP -0.887
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

## Unadjusted RPE to TSP
model_RPE.TSP <- glmer(Lev1_RPE_useMean ~ IndexLev2_QST_TSPAve + (1|ID), family = binomial)

## boundary (singular) fit: see help('isSingular')

summary(model_RPE.TSP)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev2_QST_TSPAve + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##    868.0    881.9   -431.0    862.0     762
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.5804 -0.5799 -0.5790  1.7229  1.7501
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   ID      (Intercept) 0          0
```

```

## Number of obs: 765, groups: ID, 146
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.0888762  0.1040628 -10.464  <2e-16 ***
## IndexLev2_QST_TSPAve -0.0003236  0.0044722  -0.072    0.942
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## IL2_QST_TSP -0.598
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

## Unadjusted RPE to CPM
model_RPE.CPM <- glmer(Lev1_RPE_useMean ~ IndexLev2_QST_CpmTrialAve + (1|ID), family = b

## boundary (singular) fit: see help('isSingular')

summary(model_RPE.CPM)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev2_QST_CpmTrialAve + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##  828.3    842.1  -411.1    822.3     724
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6344 -0.5849 -0.5771  1.5998  1.8201
##
## Random effects:
## Groups Name      Variance Std.Dev.
## ID      (Intercept) 0        0
## Number of obs: 727, groups: ID, 141
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.248189  0.345373  -3.614 0.000301 ***
## IndexLev2_QST_CpmTrialAve  0.001342  0.002699   0.497 0.618950
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
##
## Correlation of Fixed Effects:
##      (Intr)
## IL2_QST_CTA -0.969
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

## Adjusted RPE
model_RPE <- glmer(Lev1_RPE_useMean ~ IndexLev1_Catastrophizing_Total + IndexLev1_Negat

## boundary (singular) fit: see help('isSingular')

summary(model_RPE)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## Lev1_RPE_useMean ~ IndexLev1_Catastrophizing_Total + IndexLev1_NegativeAffect_Total +
##      (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##    919.5    938.4   -455.8    911.5      812
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6507 -0.6074 -0.5641 -0.4285  2.3095
##
## Random effects:
## Groups Name      Variance Std.Dev.
## ID      (Intercept) 0        0
## Number of obs: 816, groups: ID, 157
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.985040   0.130399  -7.554 4.22e-14 ***
## IndexLev1_Catastrophizing_Total -0.007347   0.004012  -1.831  0.0671 .
## IndexLev1_NegativeAffect_Total  0.001537   0.004684   0.328  0.7428
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) IL1_C_
## IndxLv1_C_T -0.189
## IndxL1_NA_T -0.562 -0.502
```

```

## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
model_RPE_2 <- glmer(Lev1_RPE_useMean ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve
## boundary (singular) fit: see help('isSingular')
summary(model_RPE_2)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve +
## IndexLev2_QST_BaselinePPTh + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##  786.9    809.6   -388.4    776.9      683
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6359 -0.5949 -0.5740  1.5799  2.0883
##
## Random effects:
## Groups Name      Variance Std.Dev.
## ID      (Intercept) 3.809e-16 1.952e-08
## Number of obs: 688, groups: ID, 132
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -0.8913559   0.4717071  -1.890   0.0588 .
## IndexLev2_QST_CpmTrialAve  0.0001801   0.0028856   0.062   0.9502
## IndexLev2_QST_TSPAve    -0.0010464   0.0046924  -0.223   0.8235
## IndexLev2_QST_BaselinePPTh -0.0005068   0.0004886  -1.037   0.2996
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) IL2_QST_C IL2_QST_T
## IL2_QST_CTA -0.878
## IL2_QST_TSP -0.281  0.055
## IL2_QST_BPP -0.645  0.278  0.227
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

```



## Adjusting more confounding factors

```
## Consider age, sex, BMI,... (Lvl2) for APE
model_APE_2_conf <- glmer(APE ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve + IndexLev2_QST_BaselinePPTH +
  Baseline_Demog_Ethnicity + Baseline_Demog_Age + Baseline_Demog_BMI +
  Baseline_Demog_Sex + (1 | ID)
  Data: data_paper2

## boundary (singular) fit: see help('isSingular')

summary(model_APE_2_conf)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## APE ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve + IndexLev2_QST_BaselinePPTH +
## Baseline_Demog_Ethnicity + Baseline_Demog_Age + Baseline_Demog_BMI +
## Baseline_Demog_Sex + (1 | ID)
## Data: data_paper2
##
##          AIC          BIC    logLik deviance df.resid
##    335.7      374.6   -158.8    317.7      552
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.6638 -0.3659 -0.2685 -0.1813  5.9336
##
## Random effects:
## Groups Name          Variance Std.Dev.
## ID      (Intercept)  0          0
## Number of obs: 561, groups: ID, 107
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.687274   2.279250   0.740  0.45913
## IndexLev2_QST_CpmTrialAve -0.007839   0.005166  -1.517  0.12918
## IndexLev2_QST_TSPAve     -0.027360   0.010483  -2.610  0.00906 **
## IndexLev2_QST_BaselinePPTH -0.003491   0.001206  -2.894  0.00380 **
## Baseline_Demog_Ethnicity  -0.042890   0.245212  -0.175  0.86115
## Baseline_Demog_Age       -0.029515   0.018728  -1.576  0.11504
## Baseline_Demog_BMI        0.017727   0.025088   0.707  0.47984
## Baseline_Demog_Sex        0.017862   0.354976   0.050  0.95987
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) IL2_QST_C IL2_QST_T IL2_QST_B Bs_D_E Bs_D_A B_D_BM
```

```
## IL2_QST_CTA -0.466
## IL2_QST_TSP -0.206 0.117
## IL2_QST_BPP -0.359 0.336 0.146
## Bsln_Dmg_Et -0.294 -0.066 0.013 -0.142
## Bsln_Dmg_Ag -0.763 0.127 0.140 -0.003 0.146
## Bsln_Dm_BMI -0.609 0.165 0.026 0.103 0.188 0.288
## Bsln_Dmg_Sx -0.409 0.042 0.030 0.336 -0.097 0.204 -0.024
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

## Consider age, sex, BMI,... (Lvl2) for RPE
model_RPE_2_conf <- glmer(Lev1_RPE_useMean ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_T
## boundary (singular) fit: see help('isSingular')

summary(model_RPE_2_conf)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Lev1_RPE_useMean ~ IndexLev2_QST_CpmTrialAve + IndexLev2_QST_TSPAve +
## IndexLev2_QST_BaselinePPTh + Baseline_Demog_Ethnicity + Baseline_Demog_Age +
## Baseline_Demog_BMI + Baseline_Demog_Sex + (1 | ID)
## Data: data_paper2
##
##      AIC      BIC   logLik deviance df.resid
##  649.9    689.0   -316.0   631.9     556
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.7452 -0.6046 -0.5488  1.3418  2.2168
##
## Random effects:
##  Groups Name      Variance Std.Dev.
##  ID      (Intercept) 0         0
## Number of obs: 565, groups: ID, 107
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.2049867  1.5253835  -0.134   0.893
## IndexLev2_QST_CpmTrialAve  0.0007705  0.0032598   0.236   0.813
## IndexLev2_QST_TSPAve    -0.0006723  0.0049791  -0.135   0.893
## IndexLev2_QST_BaselinePPTh -0.0003639  0.0005917  -0.615   0.539
## Baseline_Demog_Ethnicity  0.0330458  0.1258920   0.262   0.793
## Baseline_Demog_Age     -0.0068997  0.0121735  -0.567   0.571
## Baseline_Demog_BMI     -0.0262475  0.0174921  -1.501   0.133
```

```

## Baseline_Demog_Sex          0.2288033  0.2218753   1.031    0.302
##
## Correlation of Fixed Effects:
##      (Intr) IL2_QST_C IL2_QST_T IL2_QST_B Bs_D_E Bs_D_A B_D_BM
## IL2_QST_CTA -0.510
## IL2_QST_TSP -0.299  0.155
## IL2_QST_BPP -0.409  0.288    0.206
## Bsln_Dmg_Et -0.300  0.026    0.065   -0.071
## Bsln_Dmg_Ag -0.789  0.242    0.210    0.060    0.132
## Bsln_Dm_BMI -0.607  0.103    0.127    0.210    0.210  0.282
## Bsln_Dmg_Sx -0.431  0.100    0.026    0.355   -0.062  0.223  0.027
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

```