

Variational Inference analysis on raw data

corrado

2023-09-15

```
library("here")
```

```
## here() starts at /Users/corrado/_repositories/surprise
```

```
suppressPackageStartupMessages(  
  {  
    library("tidyverse")  
    library("brms")  
    library("cmdstanr")  
    library("reshape")  
    library("devtools")  
    library("mice")  
    library("tidybayes")  
    library("emmeans")  
    library("broom.mixed")  
    library("rstanarm")  
  }  
)  
  
theme_set(bayesplot::theme_default(base_family = "sans", base_size = 14))  
set.seed(123)  
  
source(here("libraries", "functions.R"))
```

```
# Import complete data set
```

```
# Import the data that have been created by the previous scripts.  
# The data have been created with the 01_, 10_, 11_ scripts in  
# the present directory.  
data <- get_data()
```

```
## Rows: 64098 Columns: 23  
## -- Column specification -----  
## Delimiter: ","  
## chr  (10): subj_name, resp, movie_id, date, is_surprise_clip, is_clip_trial,...  
## dbl  (12): subject_number, trial, target_or, flanker_or, correct, rt, block,...  
## time (1): time_of_day  
##  
## i Use 'spec()' to retrieve the full column specification for this data.  
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
# Tidy data
```

```
# tidy the data frame  
data_tidy <- tidy_flanker(data)
```

```
## 'summarise()' has grouped output by 'subj_name'. You can override using the  
## '.groups' argument.  
## Joining with 'by = join_by(subj_name, block)'
```

```
# Perform some participants' flanker checks.  
flanker_accuracy_overall <- get_flanker_accuracy(data_tidy, overall = TRUE)
```

```
## 'summarise()' has grouped output by 'experiment'. You can override using the  
## '.groups' argument.
```

```
# Get a list of participants who scored below 80% accuracy.  
accuracy_removal <- flanker_accuracy_overall |>  
  filter(accuracy < 0.80) |>  
  pull(subj_id)  
  
length(accuracy_removal)
```

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

```
# Remove the <80% accuracy participants from the flanker data.  
flanker_data <- data_tidy |>  
  filter(!subj_id %in% accuracy_removal)  
  
# Check number of subjects by condition.  
flanker_data |>  
  group_by(experiment, is_surprise_clip) |>  
  summarize(  
    n = n_distinct(subj_id)  
  )
```

```
## 'summarise()' has grouped output by 'experiment'. You can override using the  
## '.groups' argument.
```

```
## # A tibble: 3 x 3  
## # Groups:   experiment [2]  
##   experiment is_surprise_clip    n  
##   <fct>      <fct>          <int>  
## 1 control   No                81  
## 2 surprise  No Surprise       120  
## 3 surprise  Surprise          120
```

```
# Select correct trials only
```

```

dt_cor <- flanker_data |>
  dplyr::filter(correct == 1)

nrow_total <- nrow(dt_cor)

# remove missing data on rt.
dt_cor <- dt_cor[!is.na(dt_cor$rt), ]

nrow_na_removed <- nrow(dt_cor)

# percent removed
(1 - nrow_na_removed / nrow_total) * 100

## [1] 0.07513148

nrow_total - nrow_na_removed

## [1] 45

nrow_total

## [1] 59895

# Select correct trials by experiment

# Select correct trials of the surprise experiment
surprise_cor_df <- dt_cor[dt_cor$experiment == "surprise", ]

# Select correct trials of the control experiment
control_cor_df <- dt_cor[dt_cor$experiment == "control", ]

# Data wrangling

surprise_cor_df$BL <- surprise_cor_df$block
surprise_cor_df$blk <- factor(surprise_cor_df$block)
surprise_cor_df$BF <- surprise_cor_df$blk

surprise_cor_df$zrt <- scale(surprise_cor_df$rt) |> as.numeric()

surprise_cor_df$CT <- surprise_cor_df$is_congruent_trial |>
  as.factor()

surprise_cor_df$SC <- surprise_cor_df$is_surprise_clip |>
  as.factor()

surprise_cor_df$movie_id <- factor(surprise_cor_df$movie_id)

d <- surprise_cor_df |>
  dplyr::select(rt, zrt, CT, SC, BL, BF, subj_id, movie_id)

## Adding missing grouping variables: 'subj_name'

```

```
# brm() analysis
```

```
m0 <- brm(  
  bf(  
    zrt ~ 1 + (1 | subj_id) + (1 | movie_id)  
  ),  
  algorithm = "meanfield",  
  family = asym_laplace(),  
  iter = 20000, # Increase the number of iterations  
  data = d  
)
```

```
## Compiling Stan program...
```

```
## Trying to compile a simple C file
```

```
## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c  
## using C compiler: 'Apple clang version 14.0.3 (clang-1403.0.22.14.1)'  
## using SDK: 'MacOSX13.3.sdk'  
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library/Frameworks/R.framework/Resources/include" -c foo.c  
## In file included from <built-in>:1:  
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/StanHeaders/StanHeaders.h:1:  
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:1:  
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Geometry:1:  
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Cholesky:1:  
## namespace Eigen {  
## ^  
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Geometry:1:  
## namespace Eigen {  
## ^  
## ;  
## In file included from <built-in>:1:  
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/StanHeaders/StanHeaders.h:1:  
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:1:  
## #include <complex>  
## ~~~~~  
## 3 errors generated.  
## make: *** [foo.o] Error 1
```

```
## Start sampling
```

```
## Chain 1: -----  
## Chain 1: EXPERIMENTAL ALGORITHM:  
## Chain 1: This procedure has not been thoroughly tested and may be unstable  
## Chain 1: or buggy. The interface is subject to change.  
## Chain 1: -----  
## Chain 1:  
## Chain 1:  
## Chain 1:  
## Chain 1: Gradient evaluation took 0.006438 seconds  
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 64.38 seconds.
```

```

## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Begin eta adaptation.
## Chain 1: Iteration: 1 / 250 [ 0%] (Adaptation)
## Chain 1: Iteration: 50 / 250 [ 20%] (Adaptation)
## Chain 1: Iteration: 100 / 250 [ 40%] (Adaptation)
## Chain 1: Iteration: 150 / 250 [ 60%] (Adaptation)
## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Iteration: 250 / 250 [100%] (Adaptation)
## Chain 1: Success! Found best value [eta = 0.1].
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1:      iter      ELBO  delta_ELBO_mean  delta_ELBO_med  notes
## Chain 1:      100     -64838.990           1.000           1.000
## Chain 1:      200     -53064.649           0.611           1.000
## Chain 1:      300     -46714.580           0.453           0.222
## Chain 1:      400     -43890.726           0.356           0.222
## Chain 1:      500     -41308.425           0.297           0.136
## Chain 1:      600     -39501.326           0.255           0.136
## Chain 1:      700     -38413.951           0.223           0.064
## Chain 1:      800     -37507.849           0.198           0.064
## Chain 1:      900     -36918.863           0.178           0.063
## Chain 1:     1000     -36447.570           0.161           0.063
## Chain 1:     1100     -36372.503           0.147           0.046
## Chain 1:     1200     -36033.955           0.135           0.046
## Chain 1:     1300     -35944.438           0.125           0.028
## Chain 1:     1400     -35794.259           0.116           0.028
## Chain 1:     1500     -35743.137           0.109           0.024
## Chain 1:     1600     -35697.972           0.102           0.024
## Chain 1:     1700     -35642.698           0.096           0.016
## Chain 1:     1800     -35625.928           0.091           0.016
## Chain 1:     1900     -35592.546           0.086           0.013
## Chain 1:     2000     -35575.157           0.082           0.013
## Chain 1:     2100     -35567.682           0.032           0.009  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

## Warning: Pareto k diagnostic value is 3.88. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```
loo_m0 <- loo(m0)
```

```

m1 <- brm(
  bf(zrt ~ CT * SC * BL +
    (1 | subj_id) + (1 | movie_id)
  ),
  algorithm = "meanfield",
  family = asym_laplace(),
  iter = 20000, # Increase the number of iterations
  data = d
)

```

```

## Compiling Stan program...

## Trying to compile a simple C file

## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## using C compiler: 'Apple clang version 14.0.3 (clang-1403.0.22.14.1)'
## using SDK: 'MacOSX13.3.sdk'
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library/Frameworks/R.framework/Resources/include"
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/Stancpp/Eigen/Core:96:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/Matrix.h:27:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/MatrixBase.h:27:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/Matrix.h:27:
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/Matrix.h:27:1: error: unknown type name 'Eigen::Matrix'
## namespace Eigen {
## ^
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/MatrixBase.h:27:1: error: unknown type name 'Eigen::MatrixBase'
## namespace Eigen {
## ^
## ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/Stancpp/Eigen/Core:96:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/Matrix.h:27:
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/MatrixBase.h:27:1: error: unknown type name 'Eigen::MatrixBase'
## #include <complex>
## ^~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

## Start sampling

## Chain 1: -----
## Chain 1: EXPERIMENTAL ALGORITHM:
## Chain 1: This procedure has not been thoroughly tested and may be unstable
## Chain 1: or buggy. The interface is subject to change.
## Chain 1: -----
## Chain 1:
## Chain 1:
## Chain 1:
## Chain 1: Gradient evaluation took 0.007534 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 75.34 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Begin eta adaptation.
## Chain 1: Iteration: 1 / 250 [ 0%] (Adaptation)
## Chain 1: Iteration: 50 / 250 [ 20%] (Adaptation)
## Chain 1: Iteration: 100 / 250 [ 40%] (Adaptation)
## Chain 1: Iteration: 150 / 250 [ 60%] (Adaptation)
## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Success! Found best value [eta = 1] earlier than expected.
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1: iter ELBO delta_ELBO_mean delta_ELBO_med notes

```

```

## Chain 1:    100      -43344.856          1.000          1.000
## Chain 1:    200      -35981.350          0.602          1.000
## Chain 1:    300      -35342.905          0.408          0.205
## Chain 1:    400      -36782.953          0.315          0.205
## Chain 1:    500      -36734.259          0.253          0.039
## Chain 1:    600      -35009.725          0.219          0.049
## Chain 1:    700      -34941.284          0.188          0.039
## Chain 1:    800      -35363.621          0.166          0.039
## Chain 1:    900      -34970.158          0.149          0.018
## Chain 1:   1000      -35598.362          0.136          0.018
## Chain 1:   1100      -35064.395          0.125          0.018
## Chain 1:   1200      -34868.101          0.115          0.018
## Chain 1:   1300      -35238.346          0.107          0.015
## Chain 1:   1400      -34864.103          0.100          0.015
## Chain 1:   1500      -34720.122          0.093          0.012
## Chain 1:   1600      -34984.200          0.088          0.012
## Chain 1:   1700      -34640.099          0.083          0.011
## Chain 1:   1800      -34616.734          0.079          0.011
## Chain 1:   1900      -35187.764          0.076          0.011
## Chain 1:   2000      -34624.619          0.073          0.012
## Chain 1:   2100      -34577.506          0.023          0.011
## Chain 1:   2200      -34782.792          0.013          0.011
## Chain 1:   2300      -35000.670          0.012          0.011
## Chain 1:   2400      -34666.471          0.011          0.010  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

```

```

## Warning: Pareto k diagnostic value is 10.07. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```

loo_m1 <- loo(m1)

comp <- loo_compare(loo_m0, loo_m1)
print(comp, digits = 2)

```

```

##      elpd_diff se_diff
## m1      0.00      0.00
## m0 -1009.17    55.04

```

```

m2 <- brm(
  bf(zrt ~ CT * SC * BF +
     (1 + CT * SC * BF | subj_id) + (1 | movie_id)
  ),
  algorithm = "meanfield",
  family = asym_laplace(),
  iter = 20000, # Increase the number of iterations
  data = d
)

```

```

## Compiling Stan program...

```



```

## Chain 1:    200      -74693.885          0.632          1.000
## Chain 1:    300      -63948.696          0.477          0.264
## Chain 1:    400      -56278.678          0.392          0.264
## Chain 1:    500      -51370.599          0.333          0.168
## Chain 1:    600      -47427.613          0.291          0.168
## Chain 1:    700      -44805.837          0.258          0.136
## Chain 1:    800      -42725.292          0.232          0.136
## Chain 1:    900      -40514.278          0.212          0.096
## Chain 1:   1000      -39736.673          0.193          0.096
## Chain 1:   1100      -38532.088          0.178          0.083
## Chain 1:   1200      -37957.374          0.165          0.083
## Chain 1:   1300      -37064.266          0.154          0.059
## Chain 1:   1400      -36407.065          0.144          0.059
## Chain 1:   1500      -36030.097          0.135          0.055
## Chain 1:   1600      -35517.196          0.128          0.055
## Chain 1:   1700      -35108.074          0.121          0.049
## Chain 1:   1800      -34928.275          0.114          0.049
## Chain 1:   1900      -34657.303          0.109          0.031
## Chain 1:   2000      -34334.634          0.104          0.031
## Chain 1:   2100      -34257.042          0.054          0.024
## Chain 1:   2200      -34024.182          0.041          0.020
## Chain 1:   2300      -33927.681          0.033          0.018
## Chain 1:   2400      -33814.622          0.026          0.015
## Chain 1:   2500      -33698.340          0.022          0.014
## Chain 1:   2600      -33628.717          0.017          0.012
## Chain 1:   2700      -33526.929          0.015          0.010
## Chain 1:   2800      -33467.605          0.012          0.009  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

```

```

## Warning: Pareto k diagnostic value is 17. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```

loo_m2 <- loo(m2)

comp <- loo_compare(loo_m1, loo_m2)
print(comp, digits = 2)

```

```

##      elpd_diff se_diff
## m2      0.00      0.00
## m1 -1258.82     68.60

```

```

print(loo_m2)

```

```

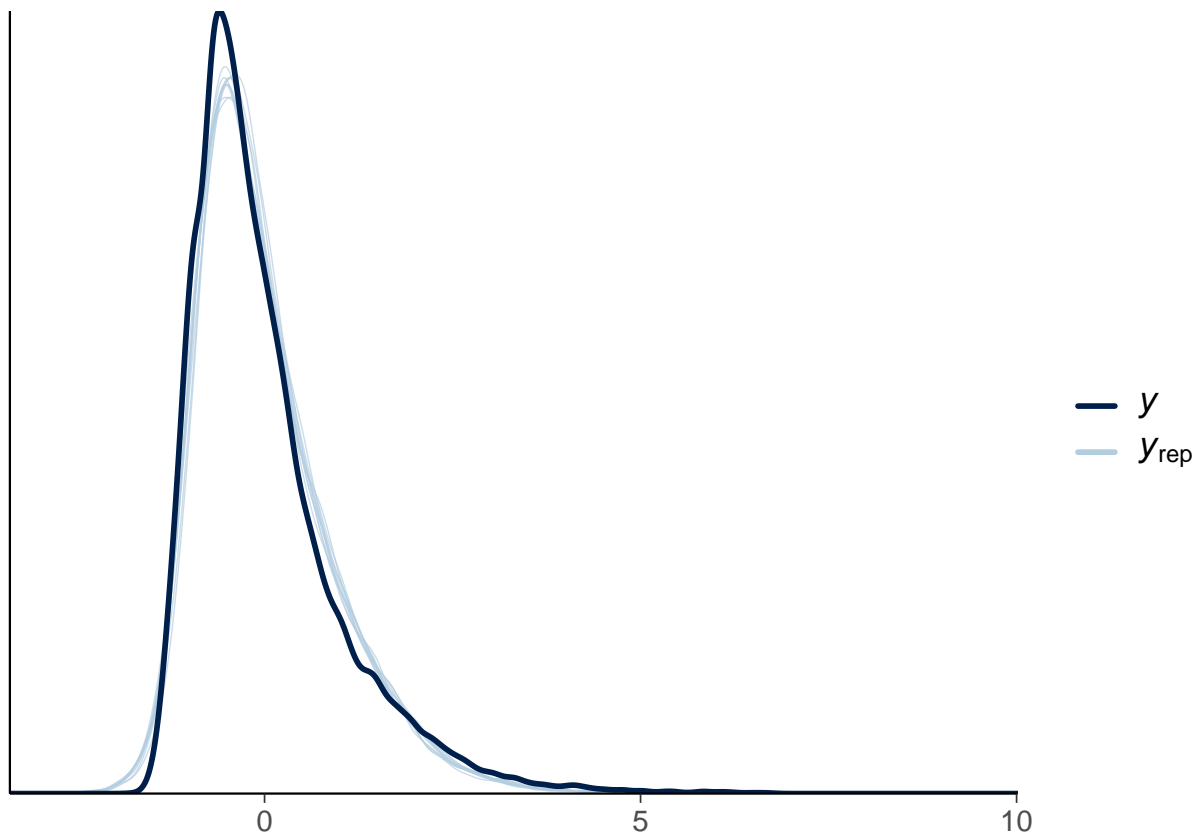
##
## Computed from 1000 by 36032 log-likelihood matrix
##
##      Estimate      SE
## elpd_loo -33108.7 190.9
## p_loo      1594.4  11.0

```

```
## looic      66217.4 381.8
## -----
## Monte Carlo SE of elpd_loo is 1.4.
##
## Pareto k diagnostic values:
##           Count Pct.    Min. n_eff
## (-Inf, 0.5] (good)  35986 99.9%    407
## (0.5, 0.7]  (ok)     46  0.1%     705
## (0.7, 1]    (bad)     0  0.0%    <NA>
## (1, Inf)    (very bad) 0  0.0%    <NA>
##
## All Pareto k estimates are ok (k < 0.7).
## See help('pareto-k-diagnostic') for details.
```

```
pp_check(m2)
```

```
## Using 10 posterior draws for ppc type 'dens_overlay' by default.
```



```
m3 <- brm(
  bf(zrt ~ CT * SC * BL +
     (1 + CT * SC * BL | subj_id) + (1 | movie_id)
  ),
  algorithm = "meanfield",
  family = asym_laplace(),
  iter = 20000, # Increase the number of iterations
```



```

## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Iteration: 250 / 250 [100%] (Adaptation)
## Chain 1: Success! Found best value [eta = 0.1].
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1:      iter      ELBO  delta_ELBO_mean  delta_ELBO_med  notes
## Chain 1:    100    -89242.372          1.000          1.000
## Chain 1:    200    -69762.930          0.640          1.000
## Chain 1:    300    -59435.485          0.484          0.279
## Chain 1:    400    -52369.742          0.397          0.279
## Chain 1:    500    -47080.961          0.340          0.174
## Chain 1:    600    -44839.808          0.292          0.174
## Chain 1:    700    -42276.676          0.259          0.135
## Chain 1:    800    -40885.306          0.231          0.135
## Chain 1:    900    -39443.867          0.209          0.112
## Chain 1:   1000    -38534.916          0.191          0.112
## Chain 1:   1100    -37962.628          0.175          0.061
## Chain 1:   1200    -36940.742          0.162          0.061
## Chain 1:   1300    -36521.419          0.151          0.050
## Chain 1:   1400    -36020.410          0.141          0.050
## Chain 1:   1500    -35625.508          0.132          0.037
## Chain 1:   1600    -35322.309          0.125          0.037
## Chain 1:   1700    -35285.399          0.117          0.034
## Chain 1:   1800    -34956.527          0.111          0.034
## Chain 1:   1900    -34710.912          0.106          0.028
## Chain 1:   2000    -34530.643          0.101          0.028
## Chain 1:   2100    -34466.292          0.051          0.024
## Chain 1:   2200    -34341.981          0.037          0.015
## Chain 1:   2300    -34272.140          0.029          0.014
## Chain 1:   2400    -34198.874          0.022          0.011
## Chain 1:   2500    -34117.966          0.016          0.011
## Chain 1:   2600    -34061.827          0.014          0.009  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

## Warning: Pareto k diagnostic value is 13.53. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```

loo_m3 <- loo(m3)

comp <- loo_compare(loo_m3, loo_m2)
print(comp, digits = 2)

```

```

##      elpd_diff se_diff
## m2      0.00      0.00
## m3 -738.09     48.10

```

```

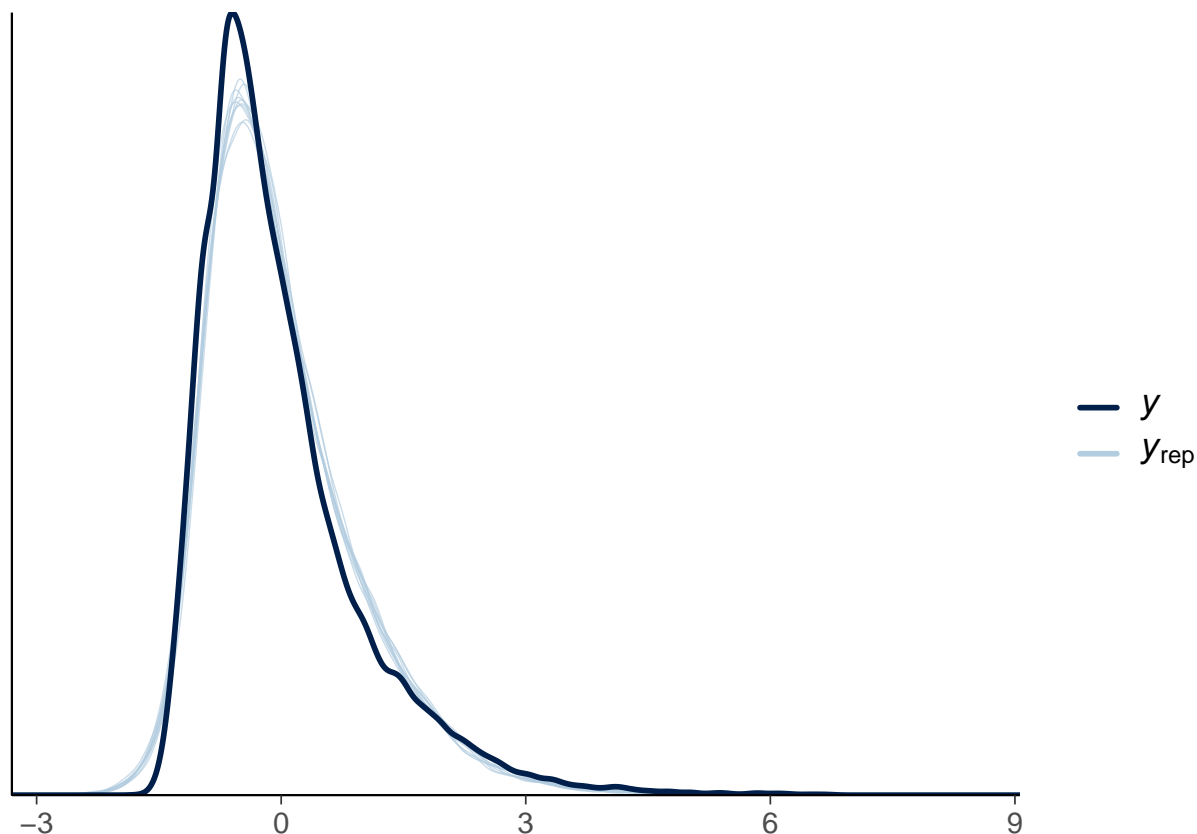
pp_check(m3)

```

```

## Using 10 posterior draws for ppc type 'dens_overlay' by default.

```



```
print(loo_m3)
```

```
##
## Computed from 1000 by 36032 log-likelihood matrix
##
##      Estimate      SE
## elpd_loo -33846.8 190.3
## p_loo      932.3   6.2
## looic      67693.6 380.6
## -----
## Monte Carlo SE of elpd_loo is 1.0.
##
## Pareto k diagnostic values:
##      Count Pct.    Min. n_eff
## (-Inf, 0.5] (good) 36025 100.0% 524
## (0.5, 0.7]  (ok)    7    0.0% 551
## (0.7, 1]   (bad)    0    0.0% <NA>
## (1, Inf)   (very bad) 0    0.0% <NA>
##
## All Pareto k estimates are ok (k < 0.7).
## See help('pareto-k-diagnostic') for details.
```

```
# Test whether the kind of video is important within the surprise experiment.
```

```
m4 <- brm(
```

```

bf(zrt ~ CT * BL +
  (1 + CT * BL | subj_id) + (1 | movie_id)
),
algorithm = "meanfield",
family = asym_laplace(),
iter = 20000, # Increase the number of iterations
init = 0.01,
data = d
)

```

```
## Compiling Stan program...
```

```
## Trying to compile a simple C file
```

```

## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## using C compiler: 'Apple clang version 14.0.3 (clang-1403.0.22.14.1)'
## using SDK: 'MacOSX13.3.sdk'
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library/Frameworks/R.framework/Resources/include"
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/stan/math/rev/core.hpp:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:96:
## namespace Eigen {
## ~
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/Matrix.h:1:
## namespace Eigen {
## ~
## ~
## ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/stan/math/rev/core.hpp:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:96:
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:96:
## #include <complex>
## ~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

```

```
## Start sampling
```

```

## Chain 1: -----
## Chain 1: EXPERIMENTAL ALGORITHM:
## Chain 1:   This procedure has not been thoroughly tested and may be unstable
## Chain 1:   or buggy. The interface is subject to change.
## Chain 1: -----
## Chain 1:
## Chain 1:
## Chain 1:
## Chain 1: Gradient evaluation took 0.012266 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 122.66 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:

```

```

## Chain 1:
## Chain 1: Begin eta adaptation.
## Chain 1: Iteration: 1 / 250 [ 0%] (Adaptation)
## Chain 1: Iteration: 50 / 250 [ 20%] (Adaptation)
## Chain 1: Iteration: 100 / 250 [ 40%] (Adaptation)
## Chain 1: Iteration: 150 / 250 [ 60%] (Adaptation)
## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Success! Found best value [eta = 1] earlier than expected.
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1:      iter      ELBO  delta_ELBO_mean  delta_ELBO_med  notes
## Chain 1:    100    -40570.431          1.000          1.000
## Chain 1:    200    -34800.329          0.583          1.000
## Chain 1:    300    -34610.230          0.390          0.166
## Chain 1:    400    -33765.720          0.299          0.166
## Chain 1:    500    -34145.628          0.241          0.025
## Chain 1:    600    -33967.189          0.202          0.025
## Chain 1:    700    -33555.053          0.175          0.012
## Chain 1:    800    -33882.057          0.154          0.012
## Chain 1:    900    -33524.302          0.138          0.011
## Chain 1:   1000    -33239.053          0.125          0.011
## Chain 1:   1100    -33588.039          0.115          0.011
## Chain 1:   1200    -33403.783          0.106          0.011
## Chain 1:   1300    -33480.677          0.098          0.010
## Chain 1:   1400    -33341.290          0.091          0.010
## Chain 1:   1500    -33198.028          0.085          0.010  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

## Warning: Pareto k diagnostic value is 7.23. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```
loo_m4 <- loo(m4)
```

```
comp <- loo_compare(loo_m3, loo_m4)
print(comp, digits = 2)
```

```

##      elpd_diff se_diff
## m4      0.00      0.00
## m3 -1212.31     52.57

```

```
# Remove the three-way interaction
```

```

m5 <- brm(
  bf(zrt ~ CT * SC + CT * BL + SC * BL +
    (1 + CT * SC + CT * BL + SC * BL | subj_id) + (1 | movie_id)
  ),
  algorithm = "meanfield",
  family = brms::asym_laplace(),
  iter = 20000, # Increase the number of iterations

```

```

init = 0.01,
data = d
)

```

```
## Compiling Stan program...
```

```
## Trying to compile a simple C file
```

```

## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## using C compiler: 'Apple clang version 14.0.3 (clang-1403.0.22.14.1)'
## using SDK: 'MacOSX13.3.sdk'
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include"
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core:1:
## namespace Eigen {
## ^
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core:1:
## namespace Eigen {
## ^
## ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include:1:
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:96:
## #include <complex>
## ^~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

```

```
## Start sampling
```

```

## Chain 1: -----
## Chain 1: EXPERIMENTAL ALGORITHM:
## Chain 1:   This procedure has not been thoroughly tested and may be unstable
## Chain 1:   or buggy. The interface is subject to change.
## Chain 1: -----
## Chain 1:
## Chain 1:
## Chain 1:
## Chain 1: Gradient evaluation took 0.014241 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 142.41 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Begin eta adaptation.
## Chain 1: Iteration:   1 / 250 [  0%] (Adaptation)
## Chain 1: Iteration:  50 / 250 [ 20%] (Adaptation)
## Chain 1: Iteration: 100 / 250 [ 40%] (Adaptation)
## Chain 1: Iteration: 150 / 250 [ 60%] (Adaptation)

```



```

## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Iteration: 250 / 250 [100%] (Adaptation)
## Chain 1: Success! Found best value [eta = 0.1].
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1:      iter      ELBO  delta_ELBO_mean  delta_ELBO_med  notes
## Chain 1:    100    -207014.447      1.000      1.000
## Chain 1:    200    -122442.623      0.845      1.000
## Chain 1:    300    -98153.633      0.646      0.691
## Chain 1:    400    -83033.265      0.530      0.691
## Chain 1:    500    -71462.777      0.456      0.247
## Chain 1:    600    -63569.721      0.401      0.247
## Chain 1:    700    -57622.000      0.359      0.182
## Chain 1:    800    -53208.407      0.324      0.182
## Chain 1:    900    -50186.756      0.295      0.162
## Chain 1:   1000    -48587.525      0.269      0.162
## Chain 1:   1100    -45945.649      0.249      0.124
## Chain 1:   1200    -44571.188      0.231      0.124
## Chain 1:   1300    -43124.783      0.216      0.103
## Chain 1:   1400    -42257.253      0.202      0.103
## Chain 1:   1500    -41121.245      0.190      0.083
## Chain 1:   1600    -40378.575      0.180      0.083
## Chain 1:   1700    -39909.204      0.170      0.060
## Chain 1:   1800    -39233.737      0.161      0.060
## Chain 1:   1900    -38708.476      0.154      0.058
## Chain 1:   2000    -38414.435      0.146      0.058
## Chain 1:   2100    -38064.603      0.097      0.034
## Chain 1:   2200    -37716.130      0.063      0.033
## Chain 1:   2300    -37522.596      0.050      0.031
## Chain 1:   2400    -37267.549      0.042      0.028
## Chain 1:   2500    -36987.929      0.034      0.021
## Chain 1:   2600    -36934.083      0.028      0.018
## Chain 1:   2700    -36714.540      0.023      0.017
## Chain 1:   2800    -36588.581      0.019      0.014
## Chain 1:   2900    -36478.459      0.016      0.012
## Chain 1:   3000    -36375.133      0.015      0.009  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

```

```

## Warning: Pareto k diagnostic value is 25.03. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```

loo_m5 <- loo(m5)

# Test of the three-way interaction
comp <- loo_compare(loo_m3, loo_m5)
print(comp, digits = 2)

```

```

##      elpd_diff se_diff
## m3      0.00      0.00
## m5 -2405.31     80.41

```

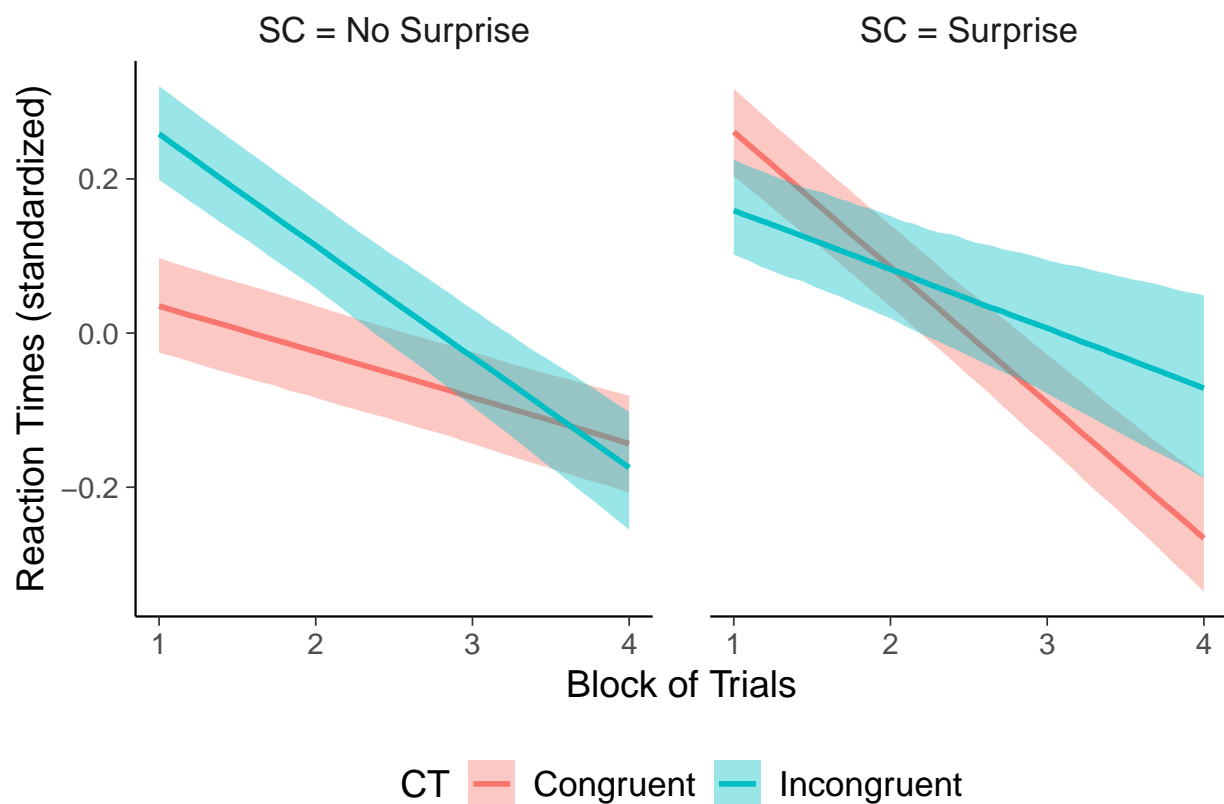
```

# Conditional plot.

mod <- m3

# Three-way interaction
conditions <- make_conditions(mod, "SC")
c_eff <- conditional_effects(mod, "BL:CT", conditions=conditions)
plot(c_eff, plot = FALSE)[[1]] +
  theme(legend.position = "bottom") +
  labs(
    y = "Reaction Times (standardized)",
    x = "Block of Trials"
  )
)

```



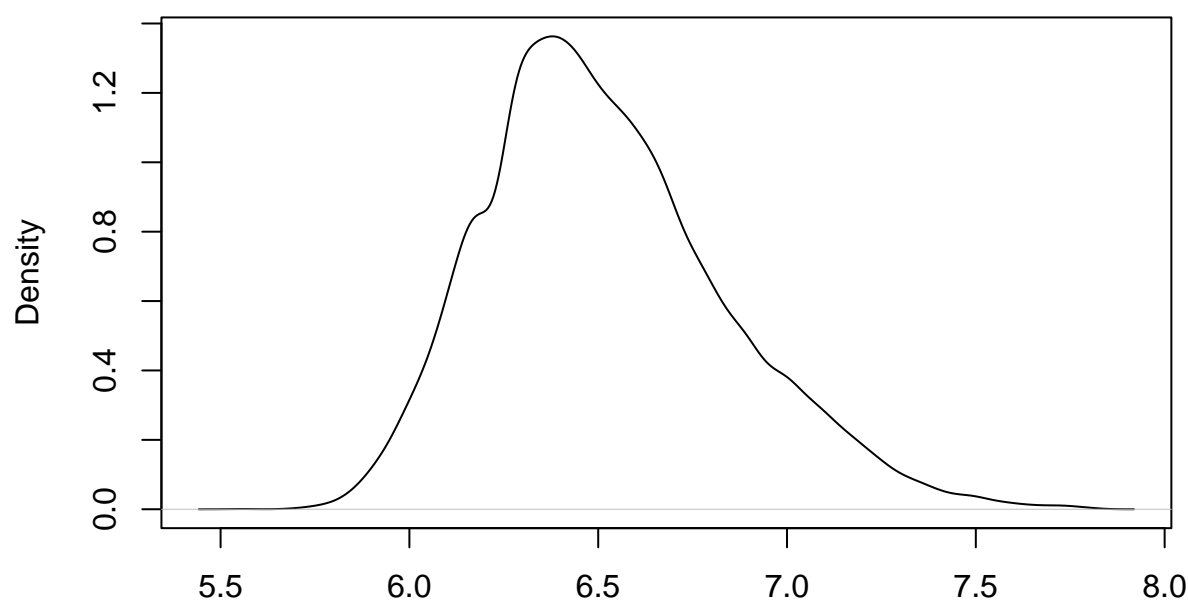
```

# Plot of the raw data means

plot(density(log(surprise_cor_df$rt)))

```

density(x = log(surprise_cor_df\$rt))



N = 36032 Bandwidth = 0.03425

```
surprise_cor_df$lrt <- log(surprise_cor_df$rt)

# Calculate the within-subject mean and standard error for each condition
subject_summary <- surprise_cor_df %>%
  group_by(subj_id, SC, CT, BL) %>%
  summarize(
    subj_mean = mean(lrt, na.rm = TRUE),
    .groups = 'drop'
  )

# Calculate the overall mean and within-subject standard error for each condition
plot_df <- subject_summary %>%
  group_by(SC, CT, BL) %>%
  summarize(
    m = mean(subj_mean, na.rm = TRUE),
    stderr = sd(subj_mean, na.rm = TRUE) / sqrt(n()),
    .groups = 'drop'
  )

# Create the lower and upper bounds for the error bars
plot_df$lower <- plot_df$m - plot_df$stderr
plot_df$upper <- plot_df$m + plot_df$stderr

plot_df$m <- exp(plot_df$m)
plot_df$stderr <- exp(plot_df$stderr)
plot_df$lower <- exp(plot_df$lower)
```

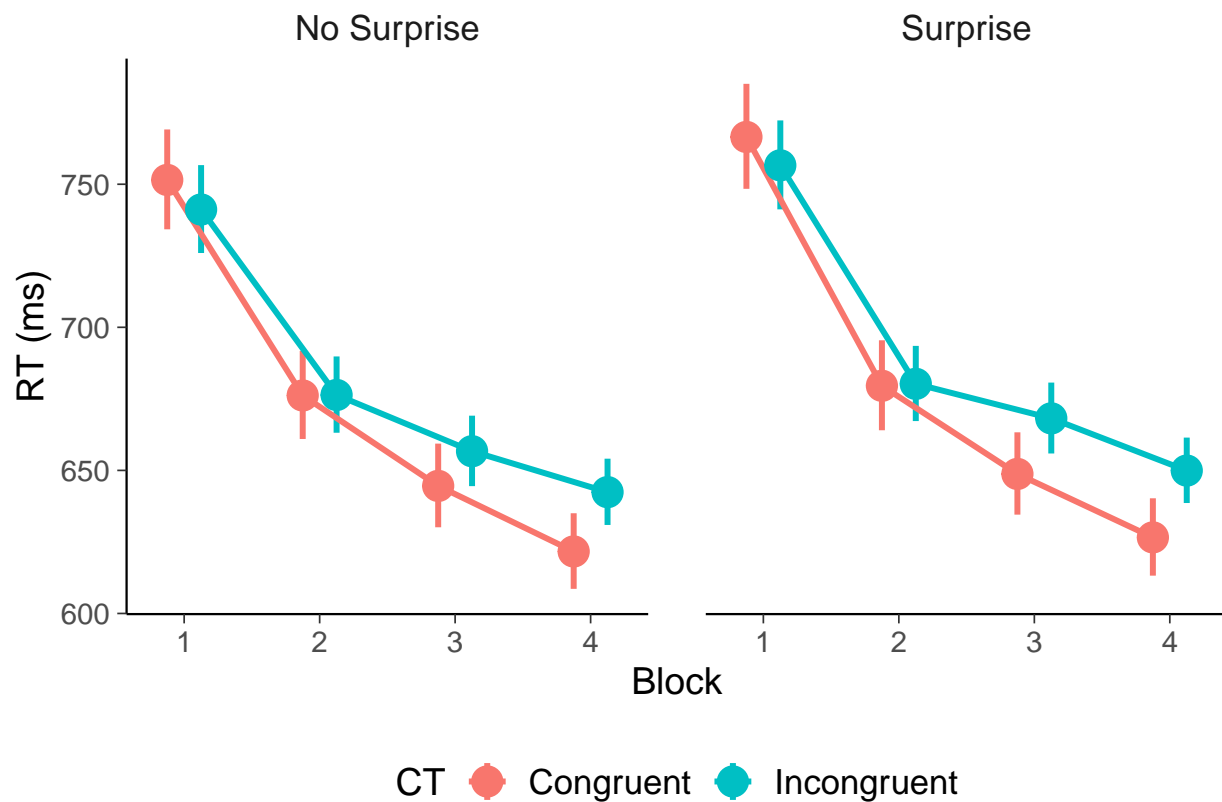
```

plot_df$upper <- exp(plot_df$upper)

# Create the plot
pd <- position_dodge(0.5)

ggplot(plot_df, aes(x = BL, y = m, color = CT)) +
  geom_pointrange(aes(ymin = lower, ymax = upper), lwd = 1.05, position = pd) +
  geom_line(position = pd, lwd = 1.05) +
  geom_point(position = pd, size = 5) +
  facet_grid(~SC) +
  xlab("Block") +
  ylab("RT (ms)") +
  theme(legend.position = "bottom")

```



```

# Compute contrasts.

mod <- m2 # Use block as factor

#get the adjusted means
em <- emmeans (mod, ~ BF:CT | SC)
em

## SC = No Surprise:
## BF CT          emmean lower.HPD upper.HPD
## 1 Congruent    -0.000897 -0.032312    0.0406

```

```
## 2 Congruent -0.152757 -0.192000 -0.1037
## 3 Congruent -0.267424 -0.308094 -0.2225
## 4 Congruent -0.327470 -0.365367 -0.2880
## 1 Incongruent 0.039031 0.000861 0.0746
## 2 Incongruent -0.105621 -0.160468 -0.0412
## 3 Incongruent -0.204678 -0.261306 -0.1553
## 4 Incongruent -0.256855 -0.315761 -0.2029
##
## SC = Surprise:
## BF CT emmean lower.HPD upper.HPD
## 1 Congruent 0.410658 0.375315 0.4449
## 2 Congruent 0.154978 0.103596 0.2113
## 3 Congruent 0.049769 0.000821 0.0988
## 4 Congruent -0.020332 -0.066870 0.0301
## 1 Incongruent 0.385291 0.348062 0.4273
## 2 Incongruent 0.221274 0.134159 0.3028
## 3 Incongruent 0.139107 0.059979 0.2150
## 4 Incongruent 0.109118 0.028787 0.1885
##
## Point estimate displayed: median
## HPD interval probability: 0.95
```

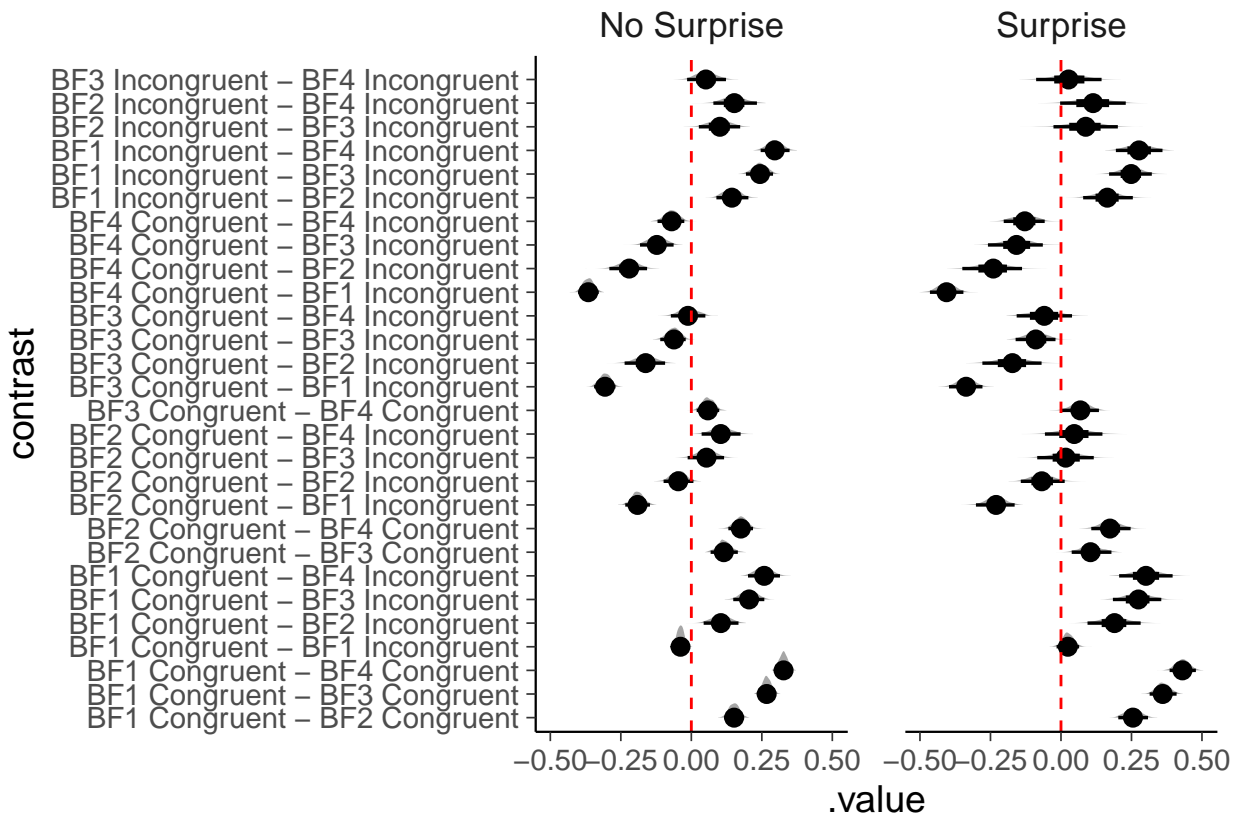
```
#get all possible contrasts
cont <- contrast(em, "tukey")
cont
```

```
## SC = No Surprise:
## contrast estimate lower.HPD upper.HPD
## BF1 Congruent - BF2 Congruent 0.1517 0.11712 0.1873
## BF1 Congruent - BF3 Congruent 0.2672 0.23908 0.3008
## BF1 Congruent - BF4 Congruent 0.3271 0.29705 0.3527
## BF1 Congruent - BF1 Incongruent -0.0384 -0.06414 -0.0172
## BF1 Congruent - BF2 Incongruent 0.1047 0.04086 0.1645
## BF1 Congruent - BF3 Incongruent 0.2048 0.14835 0.2578
## BF1 Congruent - BF4 Incongruent 0.2583 0.19999 0.3126
## BF2 Congruent - BF3 Congruent 0.1152 0.06729 0.1615
## BF2 Congruent - BF4 Congruent 0.1756 0.13128 0.2188
## BF2 Congruent - BF1 Incongruent -0.1908 -0.23335 -0.1458
## BF2 Congruent - BF2 Incongruent -0.0464 -0.09265 0.0107
## BF2 Congruent - BF3 Incongruent 0.0537 -0.01071 0.1193
## BF2 Congruent - BF4 Incongruent 0.1043 0.03420 0.1704
## BF3 Congruent - BF4 Congruent 0.0588 0.01845 0.0980
## BF3 Congruent - BF1 Incongruent -0.3061 -0.34778 -0.2723
## BF3 Congruent - BF2 Incongruent -0.1621 -0.23261 -0.0920
## BF3 Congruent - BF3 Incongruent -0.0617 -0.10611 -0.0182
## BF3 Congruent - BF4 Incongruent -0.0119 -0.06913 0.0529
## BF4 Congruent - BF1 Incongruent -0.3653 -0.40390 -0.3315
## BF4 Congruent - BF2 Incongruent -0.2204 -0.29316 -0.1582
## BF4 Congruent - BF3 Incongruent -0.1224 -0.17890 -0.0609
## BF4 Congruent - BF4 Incongruent -0.0697 -0.11884 -0.0240
## BF1 Incongruent - BF2 Incongruent 0.1438 0.08799 0.2000
## BF1 Incongruent - BF3 Incongruent 0.2435 0.19492 0.2899
## BF1 Incongruent - BF4 Incongruent 0.2957 0.24368 0.3449
## BF2 Incongruent - BF3 Incongruent 0.1013 0.02934 0.1738
```

```
## BF2 Incongruent - BF4 Incongruent 0.1524 0.07600 0.2293
## BF3 Incongruent - BF4 Incongruent 0.0516 -0.01850 0.1191
##
## SC = Surprise:
## contrast estimate lower.HPD upper.HPD
## BF1 Congruent - BF2 Congruent 0.2552 0.20116 0.3061
## BF1 Congruent - BF3 Congruent 0.3607 0.31800 0.4112
## BF1 Congruent - BF4 Congruent 0.4308 0.38522 0.4784
## BF1 Congruent - BF1 Incongruent 0.0244 -0.01648 0.0619
## BF1 Congruent - BF2 Incongruent 0.1898 0.09369 0.2826
## BF1 Congruent - BF3 Incongruent 0.2747 0.19121 0.3616
## BF1 Congruent - BF4 Incongruent 0.3013 0.21352 0.3998
## BF2 Congruent - BF3 Congruent 0.1047 0.03761 0.1781
## BF2 Congruent - BF4 Congruent 0.1738 0.10725 0.2468
## BF2 Congruent - BF1 Incongruent -0.2302 -0.29010 -0.1587
## BF2 Congruent - BF2 Incongruent -0.0681 -0.14027 0.0140
## BF2 Congruent - BF3 Incongruent 0.0168 -0.08702 0.1098
## BF2 Congruent - BF4 Incongruent 0.0469 -0.05754 0.1469
## BF3 Congruent - BF4 Congruent 0.0686 0.00805 0.1367
## BF3 Congruent - BF1 Incongruent -0.3365 -0.39746 -0.2790
## BF3 Congruent - BF2 Incongruent -0.1722 -0.28552 -0.0772
## BF3 Congruent - BF3 Incongruent -0.0893 -0.16195 -0.0213
## BF3 Congruent - BF4 Incongruent -0.0593 -0.15902 0.0363
## BF4 Congruent - BF1 Incongruent -0.4058 -0.46263 -0.3442
## BF4 Congruent - BF2 Incongruent -0.2400 -0.34569 -0.1359
## BF4 Congruent - BF3 Incongruent -0.1577 -0.26298 -0.0704
## BF4 Congruent - BF4 Incongruent -0.1283 -0.20336 -0.0587
## BF1 Incongruent - BF2 Incongruent 0.1642 0.07679 0.2521
## BF1 Incongruent - BF3 Incongruent 0.2489 0.17045 0.3220
## BF1 Incongruent - BF4 Incongruent 0.2767 0.19663 0.3616
## BF2 Incongruent - BF3 Incongruent 0.0877 -0.03519 0.1919
## BF2 Incongruent - BF4 Incongruent 0.1139 0.00548 0.2377
## BF3 Incongruent - BF4 Incongruent 0.0269 -0.10537 0.1244
##
## Point estimate displayed: median
## HPD interval probability: 0.95
```

```
#get the posterior draws from the contrasts
cont_posterior <- gather_emmeans_draws(cont)

#plot
ggplot(cont_posterior,
  aes(y = contrast, x = .value)) +
  stat_halfeye() +
  facet_wrap(~SC) +
  geom_vline(xintercept = 0, color = "red", lty = 2)
```



```
# Control experiment
```

```
control_cor_df$blk <- factor(control_cor_df$block)

control_cor_df$zrt <- scale(control_cor_df$rt) |>
  as.numeric()

control_cor_df$CT <- control_cor_df$is_congruent_trial |>
  as.factor()

control_cor_df$BF <- control_cor_df$blk
control_cor_df$BL <- control_cor_df$block

control_cor_df$movie_id <- factor(control_cor_df$movie_id)
control_cor_df$subj_id <- factor(control_cor_df$subj_id)

dc <- control_cor_df |>
  dplyr::select(zrt, CT, BL, BF, subj_id, movie_id)
```

```
## Adding missing grouping variables: 'subj_name'
```

```
c3 <- brm(
  bf(zrt ~ CT * BL +
    (1 + CT * BL | subj_id) + (1 | movie_id)
```



```

## Chain 1: Iteration: 1 / 250 [ 0%] (Adaptation)
## Chain 1: Iteration: 50 / 250 [ 20%] (Adaptation)
## Chain 1: Iteration: 100 / 250 [ 40%] (Adaptation)
## Chain 1: Iteration: 150 / 250 [ 60%] (Adaptation)
## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Success! Found best value [eta = 1] earlier than expected.
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1:      iter      ELBO  delta_ELBO_mean  delta_ELBO_med  notes
## Chain 1:    100    -26834.126      1.000      1.000
## Chain 1:    200    -26134.424      0.513      1.000
## Chain 1:    300    -25621.156      0.349      0.027
## Chain 1:    400    -25513.701      0.263      0.027
## Chain 1:    500    -25239.639      0.212      0.020
## Chain 1:    600    -25221.502      0.177      0.020
## Chain 1:    700    -25255.717      0.152      0.011
## Chain 1:    800    -25050.032      0.134      0.011
## Chain 1:    900    -25031.850      0.119      0.008  MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

## Warning: Pareto k diagnostic value is 7.11. Resampling is disabled. Decreasing
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.

```

```

loo_c3 <- loo(c3)

print(loo_c3)

```

```

##
## Computed from 1000 by 23818 log-likelihood matrix
##
##      Estimate      SE
## elpd_loo -24703.5 150.0
## p_loo      360.2   2.9
## looic      49407.0 300.1
## -----
## Monte Carlo SE of elpd_loo is 0.6.
##
## Pareto k diagnostic values:
##      Count Pct.    Min. n_eff
## (-Inf, 0.5] (good)  23817 100.0%  550
## (0.5, 0.7]  (ok)     1   0.0%   889
## (0.7, 1]    (bad)     0   0.0%  <NA>
## (1, Inf)    (very bad) 0   0.0%  <NA>
##
## All Pareto k estimates are ok (k < 0.7).
## See help('pareto-k-diagnostic') for details.

```

```

summary(c3)

```

```

## Family: asym_laplace

```

```

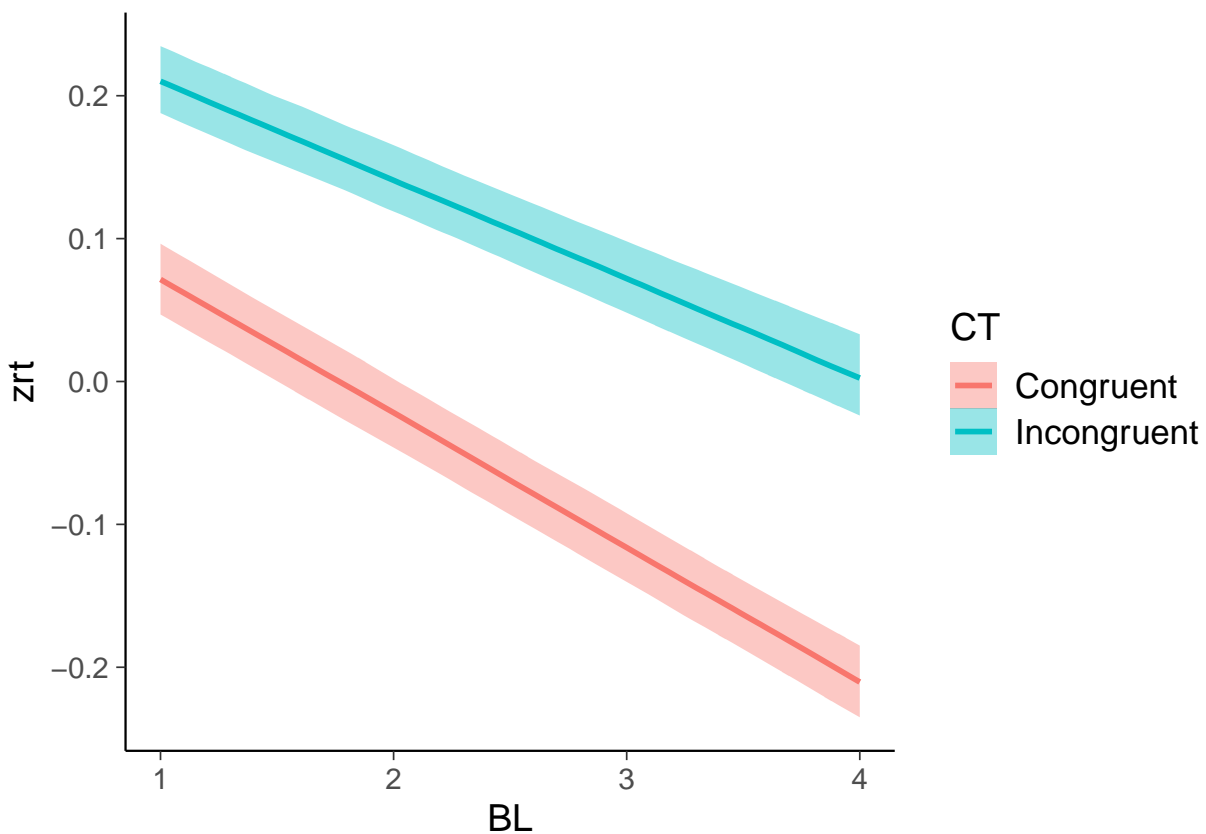
## Links: mu = identity; sigma = identity; quantile = identity
## Formula: zrt ~ CT * BL + (1 + CT * BL | subj_id) + (1 | movie_id)
## Data: dc (Number of observations: 23818)
## Draws: 1 chains, each with iter = 1000; warmup = 0; thin = 1;
## total post-warmup draws = 1000
##
## Group-Level Effects:
## ~movie_id (Number of levels: 10)
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)      0.01      0.00      0.00      0.01 1.00      1006      982
##
## ~subj_id (Number of levels: 81)
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)      0.50      0.00      0.50      0.51 1.00
## sd(CTIncongruent)   0.28      0.00      0.27      0.29 1.00
## sd(BL)              0.06      0.00      0.06      0.06 1.00
## sd(CTIncongruent:BL) 0.00      0.00      0.00      0.00 1.00
## cor(Intercept,CTIncongruent) -0.66      0.01     -0.68     -0.63 1.00
## cor(Intercept,BL)      -0.63      0.02     -0.67     -0.58 1.00
## cor(CTIncongruent,BL)   0.07      0.03      0.01      0.12 1.00
## cor(Intercept,CTIncongruent:BL) 0.11      0.38     -0.60      0.80 1.00
## cor(CTIncongruent,CTIncongruent:BL) -0.13      0.44     -0.86      0.71 1.00
## cor(BL,CTIncongruent:BL) -0.00      0.43     -0.78      0.79 1.00
##           Bulk_ESS Tail_ESS
## sd(Intercept)      938      994
## sd(CTIncongruent)   977      868
## sd(BL)             1126      992
## sd(CTIncongruent:BL) 915      981
## cor(Intercept,CTIncongruent) 1003      972
## cor(Intercept,BL)      921     1009
## cor(CTIncongruent,BL)   1002      981
## cor(Intercept,CTIncongruent:BL) 1082      983
## cor(CTIncongruent,CTIncongruent:BL) 881     1017
## cor(BL,CTIncongruent:BL) 1015      871
##
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      -0.37      0.01     -0.39     -0.36 1.00      952      944
## CTIncongruent    0.11      0.01      0.09      0.14 1.00      982      944
## BL              -0.09      0.00     -0.10     -0.09 1.00      992      923
## CTIncongruent:BL  0.02      0.00      0.02      0.03 1.00     1041      858
##
## Family Specific Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma        0.20      0.00      0.20      0.20 1.00      842      890
## quantile      0.25      0.00      0.24      0.25 1.00     1046      871
##
## Draws were sampled using variational(meanfield).

```

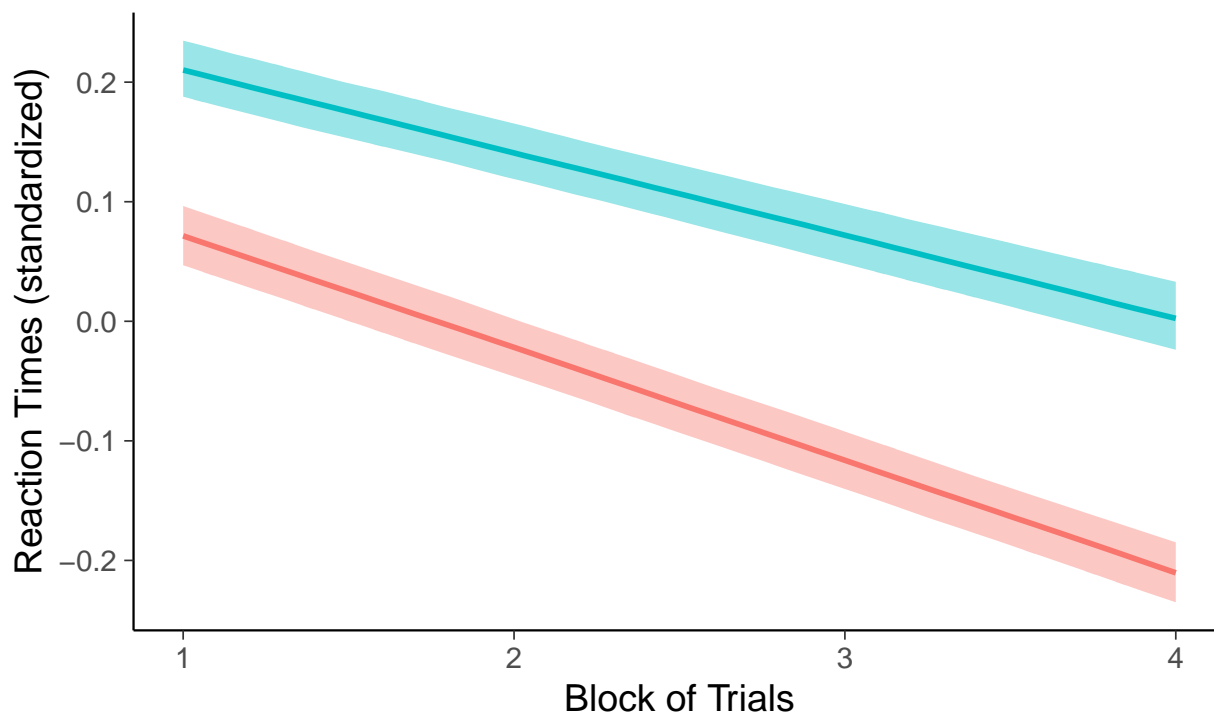
```

mod_c <- c3
conditional_effects(mod_c, "BL:CT")

```



```
# Two-way interaction
c_eff <- conditional_effects(mod_c, "BL:CT")
plot(c_eff, plot = FALSE)[[1]] +
  theme(legend.position = "bottom") +
  labs(
    y = "Reaction Times (standardized)",
    x = "Block of Trials"
  )
```



CT — Congruent — Incongruent

```
# No interaction
c4 <- brm(
  bf(zrt ~ CT + BL +
    (1 + CT + BL | subj_id) + (1 | movie_id)
  ),
  algorithm = "meanfield",
  family = brms::asym_laplace(),
  iter = 20000, # Increase the number of iterations
  init = 0.1,
  data = dc
)
```

```
## Compiling Stan program...
```

```
## Trying to compile a simple C file
```

```
## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## using C compiler: 'Apple clang version 14.0.3 (clang-1403.0.22.14.1)'
## using SDK: 'MacOSX13.3.sdk'
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include"
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeaders/include/StanHeaders/math.hpp:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:1:
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core/Matrix.h:1:10: fatal error: 'Eigen/Core' file not found
```

```

## namespace Eigen {
## ^
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/src/Core
## namespace Eigen {
## ^
## ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/StanHeader:
## In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen:
## /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/Core:96
## #include <complex>
## ^~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

## Start sampling

## Chain 1: -----
## Chain 1: EXPERIMENTAL ALGORITHM:
## Chain 1:   This procedure has not been thoroughly tested and may be unstable
## Chain 1:   or buggy. The interface is subject to change.
## Chain 1: -----
## Chain 1:
## Chain 1:
## Chain 1:
## Chain 1: Gradient evaluation took 0.016007 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 160.07 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Begin eta adaptation.
## Chain 1: Iteration:   1 / 250 [  0%] (Adaptation)
## Chain 1: Iteration:  50 / 250 [ 20%] (Adaptation)
## Chain 1: Iteration: 100 / 250 [ 40%] (Adaptation)
## Chain 1: Iteration: 150 / 250 [ 60%] (Adaptation)
## Chain 1: Iteration: 200 / 250 [ 80%] (Adaptation)
## Chain 1: Success! Found best value [eta = 1] earlier than expected.
## Chain 1:
## Chain 1: Begin stochastic gradient ascent.
## Chain 1:   iter          ELBO   delta_ELBO_mean   delta_ELBO_med   notes
## Chain 1:   100        -26378.298           1.000           1.000
## Chain 1:   200        -26012.581           0.507           1.000
## Chain 1:   300        -26083.200           0.339           0.014
## Chain 1:   400        -25528.815           0.260           0.022
## Chain 1:   500        -25169.292           0.211           0.014
## Chain 1:   600        -25122.351           0.176           0.014
## Chain 1:   700        -25148.635           0.151           0.014
## Chain 1:   800        -25078.506           0.132           0.014
## Chain 1:   900        -25048.131           0.118           0.003   MEDIAN ELBO CONVERGED
## Chain 1:
## Chain 1: Drawing a sample of size 1000 from the approximate posterior...
## Chain 1: COMPLETED.

## Warning: Pareto k diagnostic value is 4.96. Resampling is disabled. Decreasing

```

```
## tol_rel_obj may help if variational algorithm has terminated prematurely.
## Otherwise consider using sampling instead.
```

```
loo_c4 <- loo(c4)

# Test of the interaction
comp <- loo_compare(loo_c3, loo_c4)
print(comp, digits = 2)
```

```
##      elpd_diff se_diff
## c3    0.00      0.00
## c4 -92.39     22.90
```

```
message("\n20_variational_inference.R: done!")
```

```
##
## 20_variational_inference.R: done!
```

```
# Accuracy modeling
```

```
# TODO
```

```
# Get the accuracy split by congruency.
flanker_accuracy <- get_flanker_accuracy(flanker_data, overall = FALSE)
```

```
## 'summarise()' has grouped output by 'experiment', 'subj_id'. You can override
## using the '.groups' argument.
```

```
flanker_accuracy |>
  group_by(experiment, is_congruent_trial) |>
  summarize(
    acc = mean(accuracy)
  )
```

```
## 'summarise()' has grouped output by 'experiment'. You can override using the
## '.groups' argument.
```

```
## # A tibble: 4 x 3
## # Groups:   experiment [2]
##   experiment is_congruent_trial  acc
##   <fct>      <chr>              <dbl>
## 1 control   Congruent              0.967
## 2 control   Incongruent             0.954
## 3 surprise  Congruent              0.963
## 4 surprise  Incongruent             0.961
```

```
# eof ----
```