Covariate Selection

Supplementary material

Contents

Data pre-processing

Packages & Options

```
library(tidyverse)
library(brms)
library(projpred)
library(bayesplot)

# retrieve # of cores
ncores <- parallel::detectCores()

# for output clarity
options(scipen = 999)
```

Data

```
# load data
apes1 <- read_csv("../../../data/laac_data_trial.csv")
apes2 <- read_csv("../../../data/laac_data_task.csv")

fn0 <- function(x, ...) {
  # helper function
  # sum over correct choice variable (code)
  to_return = tibble(cogn = sum(x$code))
  return(to_return)
}

code_sum <- apes1 %>%
  # contains summed code variable [for each task, time point, session and subject]
  group_by(time_point, session, subject, task) %>%
  group_modify(fn0)
```

```r
apes1_tmp <- apes1 %>%
  # helper for merging
  select(-c(date, trial_session, trial_time_point, code)) %>%
  unique(by = c("time_point", "session", "subject"))

apes1_new <-
  as_tibble(merge(apes1_tmp, code_sum, by = c("time_point", "session", "subject", "task"))) %>%
  mutate(across(c(subject, group, heat, test_day, le_present, dist_present, sex, rearing, observer), as
  mutate(observer = fct_relevel(observer, "no")) %>%
  jtools::center(.,vars = c("sick_severity",
                            "le_mean",
                            "time_outdoors",
                            "age",
                            "time_in_leipzig")) %>%
  group_by(group, time_point) %>%
  mutate(rank_gmc = rank - mean(rank, na.rm = TRUE)) %>%
  ungroup() %>%
  arrange(time_point)

grp_size <- tibble(
  # number of apes for each species
  a_chimp = 20,
  b_chimp = 6,
  bonobo = 12,
  gorilla = 6,
  orangutan = 6
)

apes1_new <- apes1_new %>%
  # create rank variable depending on species
  group_by(group, time_point) %>%
  mutate(
    rel_rank = case_when(
      group == "a_chimp" ~ percent_rank(grp_size$a_chimp:1)[rank],
      group == "b_chimp" ~ percent_rank(grp_size$b_chimp:1)[rank],
      group == "bonobo" ~ percent_rank(grp_size$bonobo:1)[rank],
      group == "gorilla" ~ percent_rank(grp_size$gorilla:1)[rank],
      group == "orangutan" ~ percent_rank(grp_size$orangutan:1)[rank]
    )
  ) %>%
  ungroup()

apes1_new <- apes1_new %>%
  # create coding for heat variable
  mutate(heat_mod = case_when(
    sex == "f" & heat == "yes" ~ "_f_fheat",
    sex == "m" & heat == "yes" ~ "_m_fheat",
    sex == "f" & heat == "no" ~ "_f_noheat",
    sex == "m" & heat == "no" ~ "_m_noheat"),
    heat_mod = as_factor(heat_mod)
  ) %>%
  mutate(heat_mod = fct_relevel(heat_mod, "_f_noheat"))
```

```r
apes1_new <- apes1_new %>%
  select(-heat, -heat_mod)

apes1_new <- apes1_new %>%
  # recode rearing categories: hand -> unknown
  mutate(rearing = fct_recode(rearing, "hand" = "unknown"))

apes1_new <-  apes1_new %>%
  mutate(observer_mod = case_when(
    observer == "yes" ~ "yes",
    observer == "no" ~ "no",
    observer != "no" & observer != "yes" & observer != "NA" ~ "yes",
    TRUE ~ "no"
  ), observer_mod =  as_factor(observer_mod))

t_cau <- filter(apes1_new, task == "causality")
t_inf <- filter(apes1_new, task == "inference")
t_quant <- filter(apes1_new, task == "quantity")
t_gaze <- filter(apes1_new, task == "gaze_following")
t_grat <- filter(apes1_new, task == "delay_of_gratification")

t_gaze <- t_gaze %>%
  # create dummy variable indicating if session 1 or 2
  group_by(time_point, session) %>%
  mutate(tp_mod = cur_group_id()) %>%
  ungroup() %>%
  mutate(day2 = case_when(session == 1 ~ "no",
                          session == 2 ~ "yes"),
         day2 = factor(day2)) %>%
  select(tp_mod, day2, everything())

t_gaze <- t_gaze %>%
  # remove duplicates created by day2
  group_by(subject) %>%
  filter(!duplicated(tp_mod)) %>%
  ungroup()
```

```r
# filter data to only include time points from phase 2
t_cau <- filter(t_cau, time_point >= 15)
t_inf <- filter(t_inf, time_point >= 15)
t_quant <- filter(t_quant, time_point >= 15)
t_gaze <- filter(t_gaze, time_point >= 15)
t_grat <- filter(t_grat, time_point >= 15)
```

Covariate selection

```r
# covariate needed for projection prediction
# placed here for easy editing of formula
all_fixed_effects <- c("sick_severity",
                       "test_day", "test_tp",
                       "rel_rank",
                       "observer_mod",
```

```
                      "age", "time_in_leipzig",
                      "sex", "group",
                      "rearing",
                      "le_mean",
                      "dist_mean",
                      "time_outdoors",
                      "sociality")

fm <- formula(cogn ~ sick_severity +
                test_day + test_tp +
                rel_rank + # rank_gmc +
                observer_mod +
                age + time_in_leipzig +
                sex + group +
                rearing +
                le_mean + # le_max + # le_present +
                dist_mean + # dist_max + # + dist_present +
                time_outdoors +
                sociality + # sociality_total
                # heat_mod + # heat +
                (1|subject)
              )

fm_gaze <- update(fm, . ~ . +day2 -test_day)
```

Debugging Area

```
#info <- debug_contr_error2(fm, t_cau)
#info
```

Reference Model: 2-level Multilevel Model (random intercepts only)

```
m_cau_2l <- brm(fm, data = t_cau,
                warmup = 1e3, iter = 4e3, cores = ncores, chains = 4,
                seed = 2021,
                save_pars = save_pars(all = TRUE)
                )
```

```
## Running /usr/lib/R/bin/R CMD SHLIB foo.c
## gcc -std=gnu99 -std=gnu11 -I"/usr/share/R/include" -DNDEBUG   -I"/home/ben/R/x86_64-pc-linux-gnu-libi
## In file included from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Core:88,
##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Dense:1,
##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/StanHeaders/include/stan/math/prim/
##                  from <command-line>:
## /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/src/Core/util/Macros.h:628:1: err
##   628 | namespace Eigen {
##       | ^~~~~~~~~
## /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/src/Core/util/Macros.h:628:17: e
##   628 | namespace Eigen {
##       |                 ^
## In file included from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Dense:1,
##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/StanHeaders/include/stan/math/prim/
##                  from <command-line>:
```

```
## /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Core:96:10: fatal error: complex
##    96 | #include <complex>
##       |          ^~~~~~~~~
## compilation terminated.
## make: *** [/usr/lib/R/etc/Makeconf:168: foo.o] Error 1
```

```
m_inf_2l <- brm(fm, data = t_inf,
                warmup = 1e3, iter = 4e3, cores = ncores, chains = 4,
                seed = 2021,
                save_pars = save_pars(all = TRUE)
                )
```

```
## Running /usr/lib/R/bin/R CMD SHLIB foo.c
## gcc -std=gnu99 -std=gnu11 -I"/usr/share/R/include" -DNDEBUG   -I"/home/ben/R/x86_64-pc-linux-gnu-libi
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##    96 | #include <complex>
##       |          ^~~~~~~~~
## compilation terminated.
## make: *** [/usr/lib/R/etc/Makeconf:168: foo.o] Error 1
```

```
m_quant_2l <- brm(fm, data = t_quant,
                  warmup = 1e3, iter = 4e3, cores = ncores, chains = 4,
                  seed = 2021,
                  save_pars = save_pars(all = TRUE)
                  )
```

```
## Running /usr/lib/R/bin/R CMD SHLIB foo.c
## gcc -std=gnu99 -std=gnu11 -I"/usr/share/R/include" -DNDEBUG   -I"/home/ben/R/x86_64-pc-linux-gnu-libi
## In file included from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Core:88,
##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Dense:1,
##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/StanHeaders/include/stan/math/prim/
##                  from <command-line>:
## /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/src/Core/util/Macros.h:628:1: err
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##    96 | #include <complex>
```

```
##       |          ^~~~~~~~
## compilation terminated.
## make: *** [/usr/lib/R/etc/Makeconf:168: foo.o] Error 1
```

```
m_gaze_2l <- brm(fm_gaze, data = t_gaze,
                 warmup = 1e3, iter = 4e3, cores = ncores, chains = 4,
                 seed = 2021,
                 save_pars = save_pars(all = TRUE)
                 )
```

```
## Running /usr/lib/R/bin/R CMD SHLIB foo.c
## gcc -std=gnu99 -std=gnu11 -I"/usr/share/R/include" -DNDEBUG   -I"/home/ben/R/x86_64-pc-linux-gnu-libi
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##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Dense:1,
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##       |                 ^
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## /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Core:96:10: fatal error: complex
##    96 | #include <complex>
##       |          ^~~~~~~~~
## compilation terminated.
## make: *** [/usr/lib/R/etc/Makeconf:168: foo.o] Error 1
```

```
m_grat_2l <- brm(fm, data = t_grat,
                 warmup = 1e3, iter = 4e3, cores = ncores, chains = 4,
                 seed = 2021,
                 save_pars = save_pars(all = TRUE)
                 )
```

```
## Running /usr/lib/R/bin/R CMD SHLIB foo.c
## gcc -std=gnu99 -std=gnu11 -I"/usr/share/R/include" -DNDEBUG   -I"/home/ben/R/x86_64-pc-linux-gnu-libi
## In file included from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Core:88,
##                  from /home/ben/R/x86_64-pc-linux-gnu-library/4.1/RcppEigen/include/Eigen/Dense:1,
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##    96 | #include <complex>
##       |          ^~~~~~~~~
## compilation terminated.
```

```
## make: *** [/usr/lib/R/etc/Makeconf:168: foo.o] Error 1
```

```
library(loo)
lapply(list(m_cau_2l, m_inf_2l, m_quant_2l, m_gaze_2l, m_grat_2l), loo)
```

```
summary(m_cau_2l)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: cogn ~ sick_severity + test_day + test_tp + rel_rank + observer_mod + age + time_in_leipzig
##    Data: t_cau (Number of observations: 1051)
##   Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
##          total post-warmup draws = 12000
##
## Group-Level Effects:
## ~subject (Number of levels: 43)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     2.37      0.30     1.87     3.05 1.00     5288     7473
##
## Population-Level Effects:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           7.54      1.47     4.64    10.42 1.00     8246     7779
## sick_severity       0.12      0.07    -0.01     0.25 1.00    21234     9175
## test_dayyes        -0.77      0.75    -2.25     0.72 1.00    17534    10102
## test_tp            -0.01      0.02    -0.05     0.03 1.00    20226     9633
## rel_rank            1.02      0.88    -0.67     2.74 1.00    17040     8305
## observer_modno     -0.10      0.14    -0.38     0.18 1.00    20814     8414
## age                -0.05      0.05    -0.14     0.05 1.00     8668     8179
## time_in_leipzig     0.07      0.08    -0.08     0.22 1.00     8278     8275
## sexf                0.18      0.88    -1.54     1.88 1.00     9043     8567
## groupb_chimp        2.70      1.65    -0.48     5.98 1.00     7602     8158
## groupa_chimp       -0.58      1.20    -2.90     1.84 1.00     6742     7359
## grouporangutan      2.30      1.75    -1.13     5.71 1.00     8256     8203
## groupbonobo         0.57      1.36    -2.13     3.27 1.00     7387     7361
## rearinghand         0.81      1.21    -1.60     3.16 1.00     8609     7976
## le_mean             0.08      0.34    -0.58     0.75 1.00    20966     8582
## dist_mean           0.61      0.27     0.09     1.12 1.00    18092     9895
## time_outdoors      -0.14      0.02    -0.17    -0.10 1.00    19472     9544
## sociality          -0.33      0.15    -0.63    -0.04 1.00    20214     8476
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     1.56      0.03     1.49     1.63 1.00    15205     8570
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
summary(m_inf_2l)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: cogn ~ sick_severity + test_day + test_tp + rel_rank + observer_mod + age + time_in_leipzig
##    Data: t_inf (Number of observations: 1063)
##   Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
##          total post-warmup draws = 12000
```

```
##
## Group-Level Effects:
## ~subject (Number of levels: 43)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     2.29      0.30     1.78     2.95 1.00     4899     7011
##
## Population-Level Effects:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           7.40      1.51     4.47    10.44 1.00     7815     7543
## sick_severity      -0.06      0.08    -0.22     0.09 1.00    17812     7754
## test_dayyes        -0.42      0.91    -2.21     1.36 1.00    17050     9673
## test_tp             0.05      0.02     0.00     0.10 1.00    16442     9759
## rel_rank            0.64      0.98    -1.27     2.57 1.00    14287     8711
## observer_modno      0.10      0.17    -0.24     0.44 1.00    18357     8618
## age                -0.05      0.05    -0.14     0.04 1.00     8031     7157
## time_in_leipzig     0.37      0.08     0.23     0.53 1.00     7822     6805
## sexf                0.82      0.85    -0.85     2.46 1.00     8441     7656
## groupb_chimp        1.75      1.59    -1.37     4.89 1.00     7856     7307
## groupa_chimp       -1.75      1.18    -4.04     0.54 1.00     6838     7650
## grouporangutan     -2.35      1.70    -5.76     0.93 1.00     7490     6744
## groupbonobo        -1.18      1.32    -3.76     1.45 1.00     7733     7831
## rearinghand        -1.08      1.21    -3.52     1.24 1.00     8112     7152
## le_mean             0.16      0.41    -0.64     0.98 1.00    18499     8084
## dist_mean          -0.20      0.33    -0.86     0.45 1.00    17806     8957
## time_outdoors      -0.13      0.02    -0.17    -0.09 1.00    15273     9173
## sociality          -0.49      0.18    -0.86    -0.13 1.00    19108     8808
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     1.91      0.04     1.83     2.00 1.00    15903     8101
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
summary(m_quant_2l)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: cogn ~ sick_severity + test_day + test_tp + rel_rank + observer_mod + age + time_in_leipzig
##    Data: t_quant (Number of observations: 1004)
##   Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
##          total post-warmup draws = 12000
##
## Group-Level Effects:
## ~subject (Number of levels: 43)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     1.56      0.21     1.21     2.03 1.00     4552     6743
##
## Population-Level Effects:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           7.02      1.11     4.81     9.21 1.00     6374     7711
## sick_severity       0.13      0.07    -0.01     0.28 1.00    20363     8548
## test_dayyes         0.88      0.62    -0.36     2.09 1.00    22958     8686
## test_tp             0.02      0.02    -0.01     0.06 1.00    16317    10267
```

```
## rel_rank            2.38      0.79     0.82     3.93 1.00    11526     8819
## observer_modno      0.13      0.17    -0.19     0.46 1.00    19091     8113
## age                -0.02      0.03    -0.08     0.05 1.00     7367     7810
## time_in_leipzig     0.14      0.05     0.04     0.25 1.00     6097     7340
## sexf                0.04      0.59    -1.10     1.21 1.00     6842     7467
## groupb_chimp        1.76      1.10    -0.40     3.93 1.00     5848     7618
## groupa_chimp        0.13      0.83    -1.49     1.76 1.00     5008     6722
## grouporangutan     -0.56      1.22    -2.94     1.83 1.00     5660     6785
## groupbonobo         0.94      0.93    -0.92     2.77 1.00     5394     7273
## rearinghand        -2.11      0.82    -3.76    -0.52 1.00     6820     7306
## le_mean            -0.64      0.32    -1.27    -0.00 1.00    20803     8852
## dist_mean           1.19      0.29     0.62     1.77 1.00    18419     9458
## time_outdoors      -0.09      0.02    -0.13    -0.06 1.00    16390     9198
## sociality           0.14      0.16    -0.18     0.46 1.00    20704     7972
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     1.65      0.04     1.58     1.73 1.00    18875     8142
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
summary(m_gaze_21)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: cogn ~ sick_severity + test_tp + rel_rank + observer_mod + age + time_in_leipzig + sex + gr
##    Data: t_gaze (Number of observations: 1083)
##   Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
##          total post-warmup draws = 12000
##
## Group-Level Effects:
## ~subject (Number of levels: 43)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.66      0.09     0.51     0.85 1.00     4561     7261
##
## Population-Level Effects:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           0.30      0.42    -0.52     1.13 1.00     7037     7679
## sick_severity       0.00      0.02    -0.04     0.05 1.00    17583     8751
## test_tp            -0.01      0.01    -0.02     0.00 1.00    15983     9819
## rel_rank           -0.03      0.26    -0.54     0.48 1.00    14321     8642
## observer_modno      0.07      0.05    -0.04     0.17 1.00    17981     8591
## age                 0.02      0.01    -0.00     0.05 1.00     8134     7235
## time_in_leipzig    -0.01      0.02    -0.05     0.04 1.00     8140     8397
## sexf                0.14      0.24    -0.33     0.61 1.00     7322     7628
## groupb_chimp        0.03      0.46    -0.86     0.94 1.00     6704     7332
## groupa_chimp        0.36      0.34    -0.31     1.04 1.00     5789     6739
## grouporangutan     -0.24      0.49    -1.22     0.71 1.00     7179     7834
## groupbonobo         0.32      0.38    -0.43     1.06 1.00     6380     7169
## rearinghand        -0.48      0.34    -1.14     0.19 1.00     7627     7380
## le_mean            -0.06      0.11    -0.28     0.16 1.00    18055     8125
## dist_mean          -0.09      0.10    -0.28     0.10 1.00    16178     9170
## time_outdoors       0.00      0.01    -0.01     0.02 1.00    16329     9994
```

```
## sociality          -0.12      0.06    -0.22    -0.01 1.00    16565     8040
## day2yes            -0.03      0.03    -0.10     0.03 1.00    16744     7502
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.56      0.01     0.54     0.59 1.00    15358     7755
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
summary(m_grat_21)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: cogn ~ sick_severity + test_day + test_tp + rel_rank + observer_mod + age + time_in_leipzig
##    Data: t_grat (Number of observations: 2041)
##   Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
##          total post-warmup draws = 12000
##
## Group-Level Effects:
## ~subject (Number of levels: 43)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     3.03      0.39     2.38     3.90 1.00     4494     6554
##
## Population-Level Effects:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           6.23      1.80     2.71     9.90 1.00     7917     8157
## sick_severity       0.09      0.06    -0.04     0.22 1.00    21594     8819
## test_dayyes        -1.12      0.59    -2.28     0.03 1.00    21851     8176
## test_tp            -0.10      0.02    -0.14    -0.06 1.00    19107     9579
## rel_rank            0.96      0.88    -0.78     2.69 1.00    18046     7968
## observer_modno     -0.11      0.16    -0.42     0.19 1.00    21689     8551
## age                 0.03      0.06    -0.09     0.14 1.00     8220     7670
## time_in_leipzig     0.23      0.10     0.04     0.43 1.00     8039     7898
## sexf               -2.19      1.12    -4.41     0.01 1.00     8560     7618
## groupb_chimp        0.34      2.11    -3.83     4.47 1.00     7331     7664
## groupa_chimp       -0.28      1.53    -3.29     2.69 1.00     6624     7718
## grouporangutan     -1.51      2.22    -5.89     2.77 1.00     7601     7463
## groupbonobo        -1.33      1.73    -4.76     2.04 1.00     7412     7594
## rearinghand        -0.49      1.53    -3.58     2.49 1.00     8376     7904
## le_mean             0.01      0.45    -0.86     0.88 1.00    21047     8516
## dist_mean          -0.02      0.29    -0.58     0.53 1.00    19833     9230
## time_outdoors      -0.11      0.02    -0.14    -0.07 1.00    18892     9994
## sociality          -0.28      0.16    -0.60     0.04 1.00    22494     8449
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     2.17      0.03     2.11     2.24 1.00    21383     8538
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Predictive Projection

```
# delay random intercept to last place so that it doesn't soak up all the variance
s_terms <- c("1", all_fixed_effects,
             paste0(paste(all_fixed_effects, collapse = " + "), " + (1 | subject)"))
tmp <- all_fixed_effects[-2]
s_terms_gaze <- c("1", c(tmp, "day2"),
                  paste0(paste(c(tmp, "day2"), collapse = " + "), " + (1 | subject)"))
```

```
refM_cau <- get_refmodel(m_cau_21)
refM_inf <- get_refmodel(m_inf_21)
refM_quant <- get_refmodel(m_quant_21)
refM_gaze <- get_refmodel(m_gaze_21)
refM_grat <- get_refmodel(m_grat_21)
```

```
vs_cau <- varsel(refM_cau, search_terms = s_terms)
summary(vs_cau); plot(vs_cau, stats = c('elpd', 'rmse'))

randint_ind_vscau <- length(solution_terms(vs_cau))
relevant_cov_vscau <- c(1, 2, 3, 4, 5, randint_ind_vscau)

# proj_cau <- project(vs_cau, solution_terms = relevant_cov_vscau)
# mcmc_areas(as.matrix(proj_cau), pars = solution_terms(vs_cau)[relevant_cov_vscau])
```

```
vs_inf <- varsel(refM_inf, search_terms = s_terms)
summary(vs_inf); plot(vs_inf, stats = c('elpd', 'rmse'))

randint_ind_vsinf <- length(solution_terms(vs_inf))
relevant_cov_vsinf <- c(1, 2, 3, 4, 5, randint_ind_vsinf)

#proj_inf <- project(vs_inf, solution_terms = relevant_cov_vsinf, ndraws = 10)
#mcmc_areas(as.matrix(proj_inf), pars = solution_terms(vs_inf)[relevant_cov_vsinf])
```

```
vs_quant <- varsel(refM_quant, search_terms = s_terms)
summary(vs_quant); plot(vs_quant, stats = c('elpd', 'rmse'))

randint_ind_vsquant <- length(solution_terms(vs_quant))
relevant_cov_vsquant <- c(1, 2, 3, 4, 5, randint_ind_vsquant)

# proj_quant <- project(vs_quant, solution_terms = relevant_cov_vsquant)
# mcmc_areas(as.matrix(proj_quant), pars = solution_terms(vs_quant)[relevant_cov_vsquant])
```

```
vs_gaze <- varsel(refM_gaze, search_terms = s_terms_gaze)
summary(vs_gaze); plot(vs_gaze, stats = c('elpd', 'rmse'))

randint_ind_vsgaze <- length(solution_terms(vs_gaze))
relevant_cov_vsgaze <- c(1, 2, 3, 4, 5, randint_ind_vsgaze)

# proj_gaze <- project(vs_gaze, solution_terms = relevant_cov_vsgaze)
# mcmc_areas(as.matrix(proj_gaze), pars = solution_terms(vs_gaze)[relevant_cov_vsgaze])
```

```
vs_grat <- varsel(refM_grat, search_terms = s_terms)
summary(vs_grat); plot(vs_grat, stats = c('elpd', 'rmse'))

randint_ind_vsgrat <- length(solution_terms(vs_grat))
```

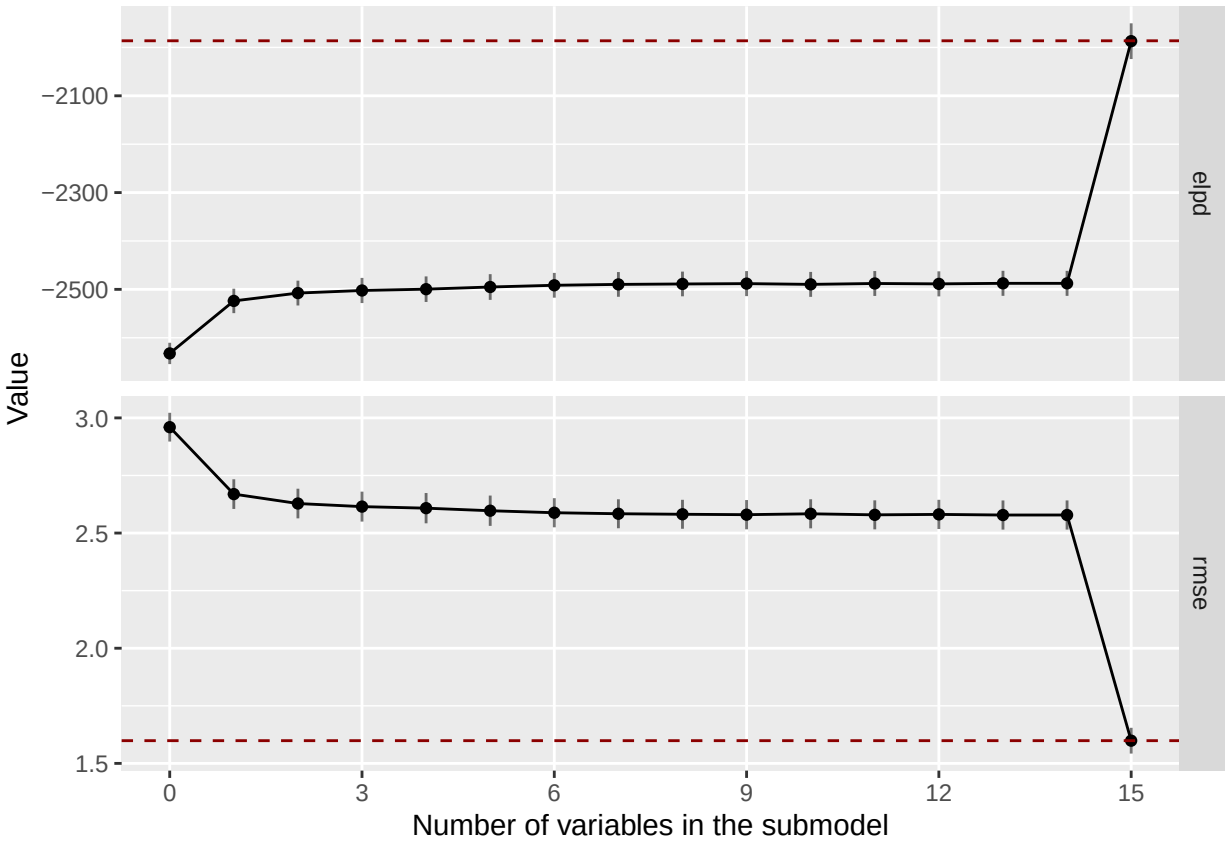
```
relevant_cov_vsgrat <- c(1, 2, 3, 4, 5, randint_ind_vsgrat)
```

```
cvs_cau <- cv_varsel(refM_cau,
                     search_terms = s_terms, cv_method = "LOO", method = "forward",
                     seed = 2020)
```

```
## [1] "Computing LOOs..."
##   |                                                                      |
```

```
summary(cvs_cau); plot(cvs_cau, stats = c('elpd', 'rmse'))
```

```
##    size  solution_terms      elpd  elpd.se
## 2     0            <NA> -2632.381 22.17875
## 3     1           group -2523.896 25.40957
## 4     2   time_outdoors -2507.663 25.81262
## 5     3    observer_mod -2502.323 26.15601
## 6     4 time_in_leipzig -2499.616 26.56242
## 7     5             age -2495.134 26.70207
## 8     6         rearing -2491.561 25.78467
## 9     7   sick_severity -2489.756 25.69297
## 10    8       sociality -2488.840 25.68971
## 11    9             sex -2488.112 26.04062
## 12   10        rel_rank -2489.686 25.90108
## 13   11        test_day -2487.843 25.88234
## 14   12       dist_mean -2488.633 26.02771
## 15   13         test_tp -2487.511 26.00442
## 16   14         le_mean -2487.586 26.00413
## 17   15   (1 | subject) -1987.106 37.12607
```




```
# proj_cau_cv <- project(cvs_cau, solution_terms = c(1, 2, 3, 14))
# mcmc_areas(as.matrix(proj_cau_cv), pars = solution_terms(cvs_cau)[c(1, 2, 3, 14)])
```

relevant covariates: (1 | subject), group

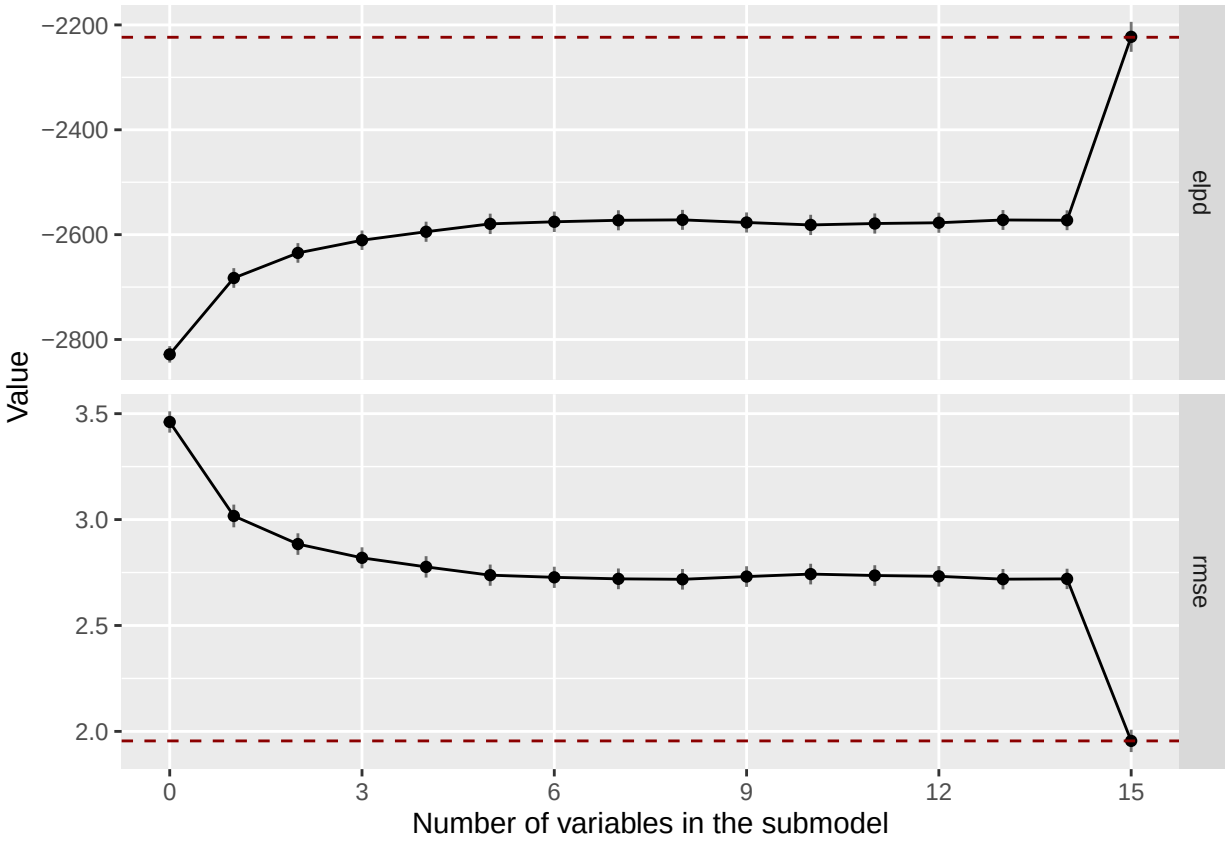
```
cvs_inf <- cv_varsel(refM_inf,
                     search_terms = s_terms, cv_method = "LOO", method = "forward",
                     seed = 2020)
```

```
## [1] "Computing LOOs..."
##   |                                                                      |
```

```
summary(cvs_inf); plot(cvs_inf, stats = c('elpd', 'rmse'))
```

```
##    size  solution_terms      elpd  elpd.se
## 2     0            <NA> -2828.352 15.82216
## 3     1 time_in_leipzig -2682.695 18.91740
```

```
## 4     2           group -2634.904 18.81065
## 5     3             age -2610.675 18.71129
## 6     4   time_outdoors -2594.494 19.32609
## 7     5             sex -2579.451 19.57018
## 8     6      sociality -2575.496 19.58552
## 9     7   sick_severity -2572.666 19.22843
## 10    8         rearing -2571.815 19.16138
## 11    9       dist_mean -2576.845 19.32863
## 12   10         test_tp -2581.475 19.43935
## 13   11        rel_rank -2578.800 19.34059
## 14   12         le_mean -2577.327 19.25856
## 15   13        test_day -2572.052 19.05043
## 16   14    observer_mod -2572.573 19.03634
## 17   15   (1 | subject) -2222.716 28.76281
```




```
# proj_inf_cv <- project(cvs_inf, solution_terms = c(1, 2, 14))
# mcmc_areas(as.matrix(proj_inf_cv), pars = solution_terms(cvs_inf)[c(1, 2, 14)])
```

relevant covariates: (1 | subject), time_in_leipzig, group, age

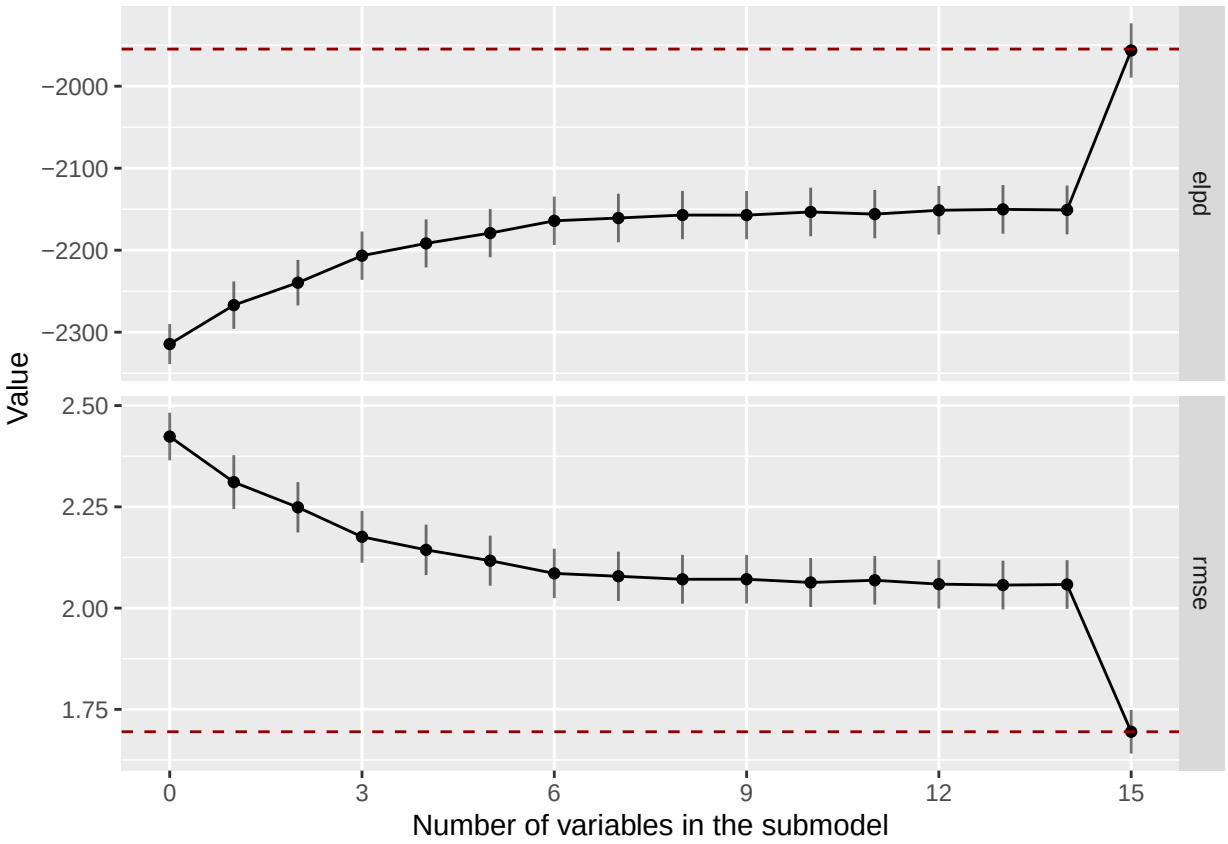
```
cvs_quant <- cv_varsel(refM_quant,
                       search_terms = s_terms, cv_method = "LOO", method = "forward",
                       seed = 2020)
```

```
## [1] "Computing LOOs..."
##   |                                                                              |
```

```
## [1] "20% of terms selected."
## [1] "30% of terms selected."
## [1] "40% of terms selected."
## [1] "50% of terms selected."
## [1] "60% of terms selected."
## [1] "70% of terms selected."
## [1] "80% of terms selected."
## [1] "90% of terms selected."
## [1] "100% of terms selected."
## [1] "Done."
```

```
summary(cvs_quant); plot(cvs_quant, stats = c('elpd', 'rmse'))
```

```
##    size  solution_terms      elpd  elpd.se
## 2     0            <NA> -2314.440 24.60445
## 3     1        rel_rank -2267.022 29.08643
## 4     2         rearing -2239.612 27.93706
## 5     3 time_in_leipzig -2206.693 29.65681
## 6     4           group -2191.728 29.49371
## 7     5   time_outdoors -2179.124 29.60804
## 8     6    observer_mod -2164.195 29.74271
## 9     7       dist_mean -2160.771 29.75924
## 10    8         test_tp -2157.152 29.65326
## 11    9        test_day -2157.242 29.63068
## 12   10   sick_severity -2153.379 29.77315
## 13   11             age -2156.008 29.67334
## 14   12             sex -2151.314 29.78852
## 15   13         le_mean -2150.254 29.87548
## 16   14       sociality -2150.911 29.92237
## 17   15   (1 | subject) -1956.428 33.29908
```




```
# proj_quant_cv <- project(cvs_quant, solution_terms = c(1, 2, 3, 15))
# mcmc_areas(as.matrix(proj_quant_cv), pars = solution_terms(cvs_quant)[c(1, 2, 3, 15)])
```

relevant covariates: (1 | subject), rel_rank, rearing, time_in_leipzig, group, time_outdoors

```
cvs_gaze <- cv_varsel(refM_gaze,
                      search_terms = s_terms_gaze, cv_method = "LOO", method = "forward",
                      seed = 2020)
summary(cvs_gaze); plot(cvs_gaze, stats = c('elpd', 'rmse'))
# proj_gaze_cv <- project(cvs_gaze, solution_terms = c(1, 2, 3, 4, 5, 6, 7, 15))
# mcmc_areas(as.matrix(proj_gaze_cv), pars = solution_terms(cvs_gaze)[c(1, 2, 3, 4, 5, 6, 7, 15)])
```

relevant covariates:

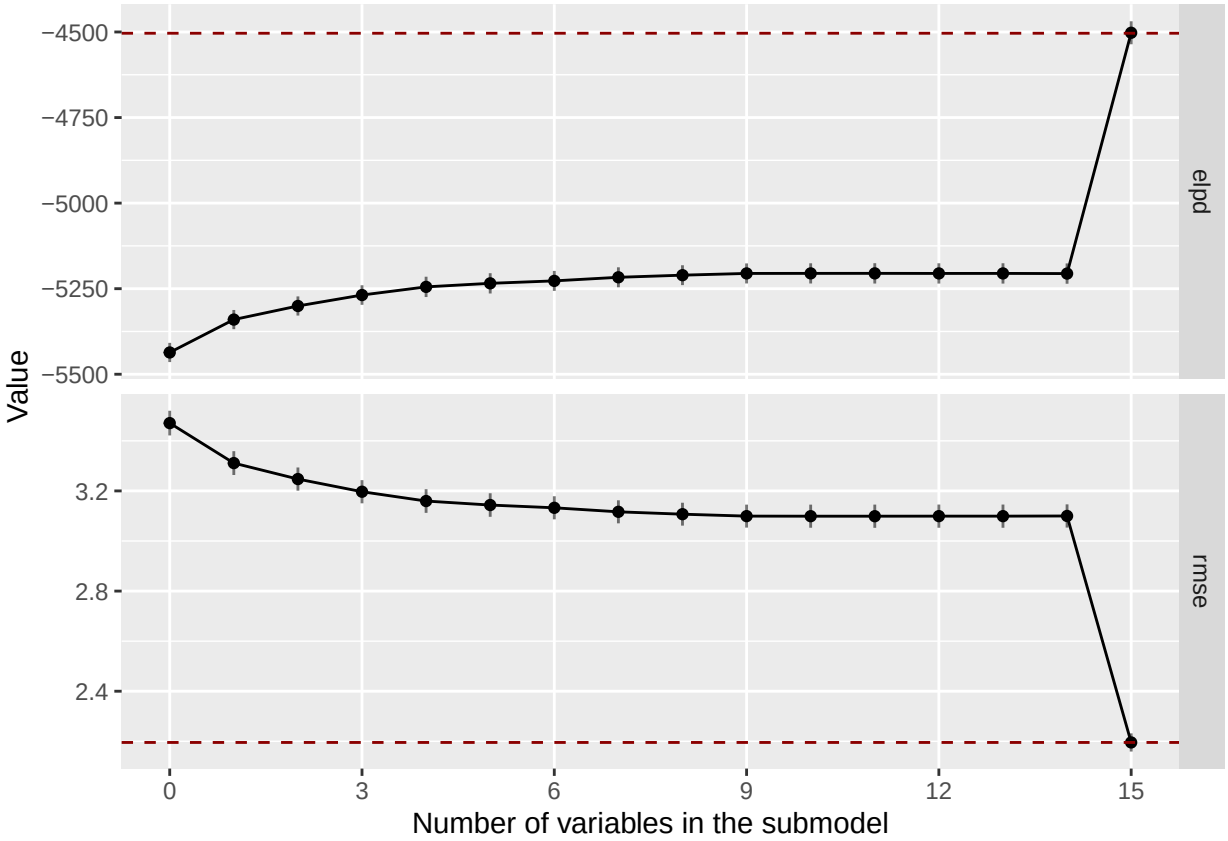
```
cvs_grat <- cv_varsel(refM_grat,
                      search_terms = s_terms, cv_method = "LOO", method = "forward",
                      seed = 2020)
```

```
## [1] "Computing LOOs..."
##   |                                                                      |
```

```
## [1] "90% of terms selected."
## [1] "100% of terms selected."
## [1] "Done."
```

```
summary(cvs_grat); plot(cvs_grat, stats = c('elpd', 'rmse'))
```

```
##    size  solution_terms      elpd  elpd.se
## 2     0            <NA> -5436.348 28.22279
## 3     1        rel_rank -5340.265 28.21010
## 4     2    observer_mod -5300.551 28.14984
## 5     3             sex -5268.591 28.76628
## 6     4           group -5244.726 29.81364
## 7     5 time_in_leipzig -5234.392 29.81946
## 8     6   time_outdoors -5227.208 29.35141
## 9     7         test_tp -5216.730 29.35081
## 10    8   sick_severity -5210.542 29.18732
## 11    9       sociality -5205.454 29.44042
## 12   10       dist_mean -5205.300 29.72444
## 13   11             age -5205.259 29.86887
## 14   12        test_day -5205.431 29.83157
## 15   13         le_mean -5205.401 29.88028
## 16   14         rearing -5205.862 29.89071
## 17   15   (1 | subject) -4502.324 33.76243
```




```
# proj_gaze_cv <- project(cvs_gaze, solution_terms = c(1, 2, 3, 4, 5, 6, 7, 15))
# mcmc_areas(as.matrix(proj_gaze_cv), pars = solution_terms(cvs_gaze)[c(1, 2, 3, 4, 5, 6, 7, 15)])
```

relevant covariates: (1 | subject), rel_rank, observer_mod, sex, group