S1: behavioural analysis with brms

I. S. Plank

2025-02-07

S1.1 Introduction

This R Markdown script analyses behavioural data from the FAB (face attention bias) paradigm of the EMBA project. The data was preprocessed before being read into this script.

The task is modeled after Jakobsen et al. (2021), *Attention, Perception, & Psychophysics* and the authors were kind enough to share their stimuli. Each trial starts with a black fixation cross on a white background. Then, a cue consisting of a pair of pictures, one object and one face, is shown with one picture on the left and one on the right of the previous location of the fixation cross. In line with Moore et al. (2012), *J Autism Dev Disord*, we set the duration of the cue presentation to 200ms. Afterwards, a target square appears either at the previous location of the face or the object. Subjects task is to determine the location (right or left) of the target as fast and accurate as possible. The target only disappears when the participant gives their answer.

The visual angle of the target was 1.17 degrees, the visual angle of the cues was 4.25 and the distance of the centre of the target and cue from the fixation cross was 2.67 degrees.

Some general settings

```
# number of simulations
nsim = 250

# set number of iterations and warmup for models
iter = 3000
warm = 1000

# set the seed
set.seed(2468)
```

Package versions

The following packages are used in this RMarkdown file:

```
## [1] "R version 4.4.2 (2024-10-31)"
```

```
## [1] "knitr version 1.46"
## [1] "ggplot2 version 3.5.1"
## [1] "brms version 2.21.0"
## [1] "designr version 0.1.13"
## [1] "bridgesampling version 1.1.2"
## [1] "tidyverse version 2.0.0"
## [1] "ggpubr version 0.6.0"
## [1] "ggrain version 0.0.4"
## [1] "bayesplot version 1.11.1"
## [1] "SBC version 0.3.0.9000"
```

```
## [1] "rstatix version 0.7.2"
## [1] "BayesFactor version 0.9.12.4.7"
## [1] "effectsize version 0.8.9"
## [1] "bayestestR version 0.15.0"
```

General info

We planned to determine the group-level effect subjects following Barr (2013). For each model, experiment specific priors were set based on previous literature or the task (see comments in the code).

We performed prior predictive checks as proposed in Schad, Betancourt and Vasishth (2020) using the SBC package based on the original design with three groups. To do so, we create 250 simulated datasets where parameters are simulated from the priors. These parameters are used to create one fake dataset. Both the true underlying parameters and the simulated discrimination values are saved.

Then, we create graphs showing the prior predictive distribution of the simulated discrimination threshold to check whether our priors fit our general expectations about the data. Next, we perform checks of computational faithfulness and model sensitivity as proposed by Schad, Betancourt and Vasishth (2020) and implemented in the SBC package. We create models for each of the simulated datasets. Last, we calculate performance metrics for each of these models, focusing on the population-level parameters. We did not rerun SBC after adding the exploratory sample of ADHD+ASD.

We base our assessment of the hypothesis on the posterior distributions. Therefore, we perform posterior prdictive checks and in some cases simplify the model by aggregating values to improve posterior fit.

Preparation and group comparisons

First, we load the data and combine it with demographic information including the diagnostic status of the subjects. Then, all predictors are set to sum contrasts. We have a look at the demographics describing our four diagnostic groups: adults with ADHD, autistic adults, autistic adults with ADHD (explorative) and adults without any neurological and psychiatric diagnoses.

Since this is sensitive data, we load the anonymised version of the processed data at this point but also leave the code we used to create it.

```
# check if the data file exists, if yes load it:
if (!file.exists("FAB_data.RData")) {

  # get demo info for subjects
  df.sub = read_csv(file.path("/home/emba/Documents/EMBA/CentraXX", "EMBA_centraXX.csv"),
                    show_col_types = F) %>%
    mutate(
      diagnosis = recode(diagnosis, "CTR" = "COMP"),
      adhd.meds.desc = adhd.meds,
      adhd.meds = if_else(is.na(adhd.meds), FALSE, TRUE)
    )

  # set the data path
  dt.path  = "/home/emba/Documents/EMBA/BVET"
  dt.explo = "/home/emba/Documents/EMBA/BVET-explo"

  # load excluded participants (low accuracy)
  exc = c(scan(file.path(dt.path, 'FAB_exc.txt'), what="character", sep=NULL),
          scan(file.path(dt.explo, 'FAB_exc.txt'), what="character", sep=NULL))
  df.exc = df.sub %>% filter(subID %in% exc) %>%
    select(diagnosis) %>%
    group_by(diagnosis) %>% count()
```

```r
# load the behavioral data and merge with group
df.fab = merge(df.sub %>% select(subID, diagnosis, RAADS_total, ASRS_total, adhd.meds),
               readRDS(file = paste0(dt.path, '/df_FAB.RDS')), all.y = T) %>%
  mutate_if(is.character, as.factor)
df.exp = merge(df.sub %>% select(subID, diagnosis, RAADS_total, ASRS_total, adhd.meds),
               readRDS(file = paste0(dt.explo, '/df_FAB.RDS')), all.y = T) %>%
  mutate_if(is.character, as.factor)

# only keep participants included in the study in the subject data frame
subIDs = as.character(c(unique(df.fab$subID), unique(df.exp$subID)))
df.sub = df.sub %>% filter(subID %in% subIDs)

df.med = df.sub %>% group_by(diagnosis) %>%
  summarise(
    adhd.meds = mean(adhd.meds)
  )

adhd.meds.desc = unique(df.sub[!is.na(df.sub$adhd.meds.desc),]$adhd.meds.desc)

# load the eye tracking data and only keep participants included in the study,
# so no people with more than 33% mistakes, no people without any saccades
# and no people with too many blinks
df.sac = rbind(readRDS(file.path(dt.explo, "FAB_ET_data.rds")),
               readRDS(file.path(dt.path,  "FAB_ET_data.rds"))) %>%
  merge(., df.sub %>% select(subID, diagnosis), keep.y = T)

# check groups of people who had no relevant saccades at all
df.nosac = df.sac %>% filter(is.na(trl)) %>%
  group_by(diagnosis) %>%
  count()

# anonymise the data
df.fab = df.fab %>%
  mutate(
    PID = subID,
    subID = as.factor(as.numeric(subID))
  )
df.exp = df.exp %>%
  mutate(
    PID = subID,
    subID = as.factor(as.numeric(subID) + length(unique(df.fab$subID)))
  )

# get a correspondence of original PIDs and anonymised subIDs
df.recode = rbind(df.fab %>% select(PID, subID) %>% distinct(),
                  df.exp %>% select(PID, subID) %>% distinct())
recode = as.character(df.recode$subID)
names(recode) = df.recode$PID
df.fab = df.fab %>% select(-PID)
df.exp = df.exp %>% select(-PID)

# anonymise ET data in the same way
df.sac$subID = str_replace_all(df.sac$subID, recode)
```

```r
# print gender frequencies and compare them across groups
tb.gen = xtabs(~ gender + diagnosis, data = df.sub)
ct.full = contingencyTableBF(tb.gen,
                             sampleType = "indepMulti",
                             fixedMargin = "cols")
# since only DAN in the ADHD group, we try again after excluding them
ct.mf = contingencyTableBF(tb.gen[2:3,],
                           sampleType = "indepMulti",
                           fixedMargin = "cols")
tb.gen = xtabs(~ gender + diagnosis + cis, data = df.sub)

# get the gender descriptions of the not-male and not-female participants
gen.desc = unique(tolower(df.sub[df.sub$gender == "dan",]$gender_desc))

# check which outcomes of interest are normally distributed
df.sht = df.sub %>%
  group_by(diagnosis) %>%
  shapiro_test(age, iq, BDI_total, ASRS_total, RAADS_total, TAS_total) %>%
  mutate(
    sig = if_else(p < 0.05, "*", "")
  )

# most of the measures are not normally distributed;
# therefore, we compute ranks for these outcomes
df.sub = df.sub %>%
  mutate(
    rage   = rank(age),
    rBDI   = rank(BDI_total),
    rRAADS = rank(RAADS_total),
    rTAS   = rank(TAS_total),
    diagnosis = as.factor(diagnosis)
  )

# now we can compute our ANOVAs
aov.age   = anovaBF(rage   ~ diagnosis, data = df.sub)
aov.iq    = anovaBF(iq     ~ diagnosis, data = df.sub)
aov.BDI   = anovaBF(rBDI   ~ diagnosis, data = df.sub)
aov.ASRS  = anovaBF(ASRS_total  ~ diagnosis, data = df.sub)
aov.RAADS = anovaBF(rRAADS ~ diagnosis, data = df.sub)
aov.TAS   = anovaBF(rTAS   ~ diagnosis, data = df.sub)

# ...and put everything in a new dataframe for printing
measurement  = "Age"
ADHD     = sprintf("%.2f (±%.2f)",
                   mean(df.sub[df.sub$diagnosis == "ADHD",]$age),
                   sd(df.sub[df.sub$diagnosis == "ADHD",]$age)/
                     sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",])))
ASD      = sprintf("%.2f (±%.2f)",
                   mean(df.sub[df.sub$diagnosis == "ASD",]$age),
                   sd(df.sub[df.sub$diagnosis == "ASD",]$age)/
                     sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",])))
`ADHD+ASD`     = sprintf("%.2f (±%.2f)",
                   mean(df.sub[df.sub$diagnosis == "BOTH",]$age),
```

```
                  sd(df.sub[df.sub$diagnosis == "BOTH",]$age)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",])))
COMP     = sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "COMP",]$age),
                  sd(df.sub[df.sub$diagnosis == "COMP",]$age)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",])))
logBF10 = sprintf("%.3f", aov.age@bayesFactor[["bf"]])
df.table = data.frame(measurement, ADHD, ASD, `ADHD+ASD`, COMP, logBF10)
df.table = rbind(df.table,
     c(
       "ASRS",
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "ADHD",]$ASRS_total),
               sd(df.sub[df.sub$diagnosis == "ADHD",]$ASRS_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",]))),
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "ASD",]$ASRS_total),
               sd(df.sub[df.sub$diagnosis == "ASD",]$ASRS_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",]))),
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "BOTH",]$ASRS_total),
               sd(df.sub[df.sub$diagnosis == "BOTH",]$ASRS_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",]))),
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "COMP",]$ASRS_total),
               sd(df.sub[df.sub$diagnosis == "COMP",]$ASRS_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",]))),
       sprintf("%.3f", aov.ASRS@bayesFactor[["bf"]])
     ),
     c(
       "BDI",
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "ADHD",]$BDI_total),
               sd(df.sub[df.sub$diagnosis == "ADHD",]$BDI_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",]))),
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "ASD",]$BDI_total),
               sd(df.sub[df.sub$diagnosis == "ASD",]$BDI_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",]))),
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "BOTH",]$BDI_total),
               sd(df.sub[df.sub$diagnosis == "BOTH",]$BDI_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",]))),
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "COMP",]$BDI_total),
               sd(df.sub[df.sub$diagnosis == "COMP",]$BDI_total)/
                 sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",]))),
       sprintf("%.3f", aov.BDI@bayesFactor[["bf"]])
     ),
     c(
       "BDI",
       sprintf("%.2f (±%.2f)",
               mean(df.sub[df.sub$diagnosis == "ADHD",]$BDI_total),
```

```
            sd(df.sub[df.sub$diagnosis == "ADHD",]$BDI_total)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",]))),
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "ASD",]$BDI_total),
            sd(df.sub[df.sub$diagnosis == "ASD",]$BDI_total)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",]))),
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "BOTH",]$BDI_total),
            sd(df.sub[df.sub$diagnosis == "BOTH",]$BDI_total)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",]))),
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "COMP",]$BDI_total),
            sd(df.sub[df.sub$diagnosis == "COMP",]$BDI_total)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",]))),
    sprintf("%.3f", aov.BDI@bayesFactor[["bf"]])
  ),
  c(
    "Gender (diverse/agender/non-binary - female - male)",
    sprintf("%d - %d - %d",
            nrow(df.sub[df.sub$diagnosis == "ADHD" & df.sub$gender == "dan",]),
            nrow(df.sub[df.sub$diagnosis == "ADHD" & df.sub$gender == "fem",]),
            nrow(df.sub[df.sub$diagnosis == "ADHD" & df.sub$gender == "mal",])),
    sprintf("%d - %d - %d",
            nrow(df.sub[df.sub$diagnosis == "ASD" & df.sub$gender == "dan",]),
            nrow(df.sub[df.sub$diagnosis == "ASD" & df.sub$gender == "fem",]),
            nrow(df.sub[df.sub$diagnosis == "ASD" & df.sub$gender == "mal",])),
    sprintf("%d - %d - %d",
            nrow(df.sub[df.sub$diagnosis == "BOTH" & df.sub$gender == "dan",]),
            nrow(df.sub[df.sub$diagnosis == "BOTH" & df.sub$gender == "fem",]),
            nrow(df.sub[df.sub$diagnosis == "BOTH" & df.sub$gender == "mal",])),
    sprintf("%d - %d - %d",
            nrow(df.sub[df.sub$diagnosis == "COMP" & df.sub$gender == "dan",]),
            nrow(df.sub[df.sub$diagnosis == "COMP" & df.sub$gender == "fem",]),
            nrow(df.sub[df.sub$diagnosis == "COMP" & df.sub$gender == "mal",])),
    sprintf("%.3f", ct.full@bayesFactor[["bf"]])
  ),
  c(
    "IQ",
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "ADHD",]$iq),
            sd(df.sub[df.sub$diagnosis == "ADHD",]$iq)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",]))),
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "ASD",]$iq),
            sd(df.sub[df.sub$diagnosis == "ASD",]$iq)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",]))),
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "BOTH",]$iq),
            sd(df.sub[df.sub$diagnosis == "BOTH",]$iq)/
              sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",]))),
    sprintf("%.2f (±%.2f)",
            mean(df.sub[df.sub$diagnosis == "COMP",]$iq),
            sd(df.sub[df.sub$diagnosis == "COMP",]$iq)/
```

```
                    sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",]))),
          sprintf("%.3f", aov.iq@bayesFactor[["bf"]])
        ),
        c(
          "RADS-R",
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "ADHD",]$RAADS_total),
                  sd(df.sub[df.sub$diagnosis == "ADHD",]$RAADS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",]))),
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "ASD",]$RAADS_total),
                  sd(df.sub[df.sub$diagnosis == "ASD",]$RAADS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",]))),
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "BOTH",]$RAADS_total),
                  sd(df.sub[df.sub$diagnosis == "BOTH",]$RAADS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",]))),
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "COMP",]$RAADS_total),
                  sd(df.sub[df.sub$diagnosis == "COMP",]$RAADS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",]))),
          sprintf("%.3f", aov.RAADS@bayesFactor[["bf"]])
        ),
        c(
          "TAS",
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "ADHD",]$TAS_total),
                  sd(df.sub[df.sub$diagnosis == "ADHD",]$TAS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "ADHD",]))),
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "ASD",]$TAS_total),
                  sd(df.sub[df.sub$diagnosis == "ASD",]$TAS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "ASD",]))),
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "BOTH",]$TAS_total),
                  sd(df.sub[df.sub$diagnosis == "BOTH",]$TAS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "BOTH",]))),
          sprintf("%.2f (±%.2f)",
                  mean(df.sub[df.sub$diagnosis == "COMP",]$TAS_total),
                  sd(df.sub[df.sub$diagnosis == "COMP",]$TAS_total)/
                    sqrt(nrow(df.sub[df.sub$diagnosis == "COMP",]))),
          sprintf("%.3f", aov.TAS@bayesFactor[["bf"]])
        )
    ) %>% arrange(measurement)

    # save it all
    save(df.fab, df.sac, df.exp, df.sht, ct.full, ct.mf, df.exc,
         df.nosac, gen.desc, tb.gen, df.table, adhd.meds.desc, df.med,
         file = "FAB_data.RData")

} else {

    load("FAB_data.RData")
```

```
}

# print the group of excluded participants based on low accuracy (< 2/3)
kable(df.exc)
```

diagnosis	n
ADHD	1
ASD	1

```
rm(df.exc)

# print the group of the participants included in behavioural and eye tracking
kable(merge(
  df.sac %>% filter(!is.na(trl)) %>% select(subID, diagnosis) %>% distinct() %>%
    group_by(diagnosis) %>% summarise(`sample size eye tracking` = n()),
  rbind(df.fab, df.exp) %>% select(subID, diagnosis) %>% distinct() %>%
    group_by(diagnosis) %>% summarise(`sample size behavioural` = n())
  ))
```

diagnosis	sample size eye tracking	sample size behavioural
ADHD	16	23
ASD	19	24
BOTH	22	23
COMP	21	24

```
# Note: eye-tracking only collected if calibration accuracy < 0.5, then exclusion:
# 1 due to more than 1/3 blinks
# 2 due to no relevant saccades
# how many have been removed due to no relevant saccades?
kable(df.nosac)
```

diagnosis	n
ASD	1
COMP	1

```
rm(df.nosac)

# print the outcome of the shapiro tests
kable(df.sht %>% arrange(variable))
```

diagnosis	variable	statistic	p	sig
ADHD	ASRS_total	0.9304718	0.1119616	
ASD	ASRS_total	0.9512379	0.2881380	
BOTH	ASRS_total	0.9547574	0.3660251	
COMP	ASRS_total	0.9192136	0.0561186	
ADHD	BDI_total	0.8170622	0.0007279	*
ASD	BDI_total	0.8078769	0.0003974	*
BOTH	BDI_total	0.8324214	0.0013277	*

diagnosis	variable	statistic	p	sig
COMP	BDI_total	0.7421016	0.0000383	*
ADHD	RAADS_total	0.9257590	0.0885842	
ASD	RAADS_total	0.9449707	0.2103029	
BOTH	RAADS_total	0.9524787	0.3291283	
COMP	RAADS_total	0.8449398	0.0017635	*
ADHD	TAS_total	0.9593558	0.4504806	
ASD	TAS_total	0.9181140	0.0530706	
BOTH	TAS_total	0.9445280	0.2245560	
COMP	TAS_total	0.8727860	0.0059679	*
ADHD	age	0.9180376	0.0604839	
ASD	age	0.9492659	0.2611939	
BOTH	age	0.9503886	0.2981103	
COMP	age	0.8104190	0.0004382	*
ADHD	iq	0.9648751	0.5684099	
ASD	iq	0.9579062	0.3978177	
BOTH	iq	0.9583546	0.4309600	
COMP	iq	0.9505974	0.2791247	

```
rm(df.sht)

# print the outcome of the two contingency tables for comparison
# based on full sample with agender, diverse and non-binary in one category
ct.full@bayesFactor
```

```
##                          bf error                      time          code
## Non-indep. (a=1) -4.405795     0 Fri Feb  7 10:50:51 2025 265f6709666bb
```

```
# based on female and male participants only
ct.mf@bayesFactor
```

```
##                          bf error                      time          code
## Non-indep. (a=1) -2.737336     0 Fri Feb  7 10:50:51 2025 265f62c9f6dd7
```

```
# combine explorative and original data
df.fab = rbind(df.fab, df.exp)

# set the levels of the diagnosis factor
df.fab$diagnosis = factor(df.fab$diagnosis,
                          levels = c("ADHD", "ASD", "BOTH", "COMP"))

# set and print the contrasts
contrasts(df.fab$cue) = contr.sum(2)
contrasts(df.fab$cue)
```

```
##        [,1]
## face      1
## object   -1
```

```
contrasts(df.fab$diagnosis) = contr.sum(4)
contrasts(df.fab$diagnosis)
```

```
##      [,1] [,2] [,3]
## ADHD    1    0    0
## ASD     0    1    0
```

```
## BOTH    0    0    1
## COMP   -1   -1   -1
```

```
# print final group comparisons for the paper
kable(df.table)
```

measurement	ADHD	ASD	ADHD.ASD	COMP	logBF10
ASRS	43.39 (±2.61)	32.54 (±1.62)	46.43 (±1.94)	25.04 (±1.68)	20.618
Age	26.70 (±1.51)	28.58 (±1.46)	30.22 (±1.72)	27.42 (±1.15)	-1.726
BDI	8.09 (±1.77)	11.21 (±2.12)	8.61 (±1.71)	2.25 (±0.62)	7.763
BDI	8.09 (±1.77)	11.21 (±2.12)	8.61 (±1.71)	2.25 (±0.62)	7.763
Gender (diverse/agender/non-binary - female - male)	2 - 9 - 12	0 - 12 - 12	3 - 12 - 8	0 - 11 - 13	-4.406
IQ	108.35 (±2.46)	111.31 (±2.95)	112.93 (±2.34)	109.90 (±1.92)	-2.170
RADS-R	92.61 (±8.74)	152.92 (±8.32)	146.52 (±6.97)	44.58 (±7.15)	30.978
TAS	50.22 (±2.58)	63.17 (±1.48)	56.48 (±2.15)	39.08 (±1.93)	20.118

The three diagnostic groups are similar in age, IQ and gender distribution. However, they seem to differ in their questionnaire scores measuring ADHD (ASRS), depression (BDI), autism (RAADS) and alexithymia (TAS).

S1.2 Reaction times

First, we analyse the reaction times for all correctly answered trials to assess whether participants answer faster if the target appears at the previous location of the face, which we refer to as face attention bias (FAB). In our preregistration, we formulated the following hypotheses:

H1a) COMP participants react faster in response to targets appearing on the side of the face compared to targets appearing on the side of the object (face attention bias; Jakobsen et al., 2021). H1b) ADHD participants react slower than COMP participants in both cue conditions (Sonuga-Barke et al., 2004). H1c) ASD participants react slower than COMP participants in both cue conditions (Ghosn et al., 2018). H1d) Face attention bias is decreased in ASD participants compared to COMP participants (Moore et al., 2012). H1e) Face attention bias in ADHD participants differs from face attention bias in COMP participants.

Full model

Simulation-based calibration

First, we attempted to use a full model for the data. This model includes multiple instances of each stimulus per participant in each of the conditions (face cue or object cue). Therefore, we need slopes for the cue per subject as well as for cue, diagnosis and their interaction for the stimulus.

```
code = "FAB"

# full model formula
f.fab = brms::bf(rt.cor ~ diagnosis * cue + (cue | subID) + (cue * diagnosis | stm) )
```

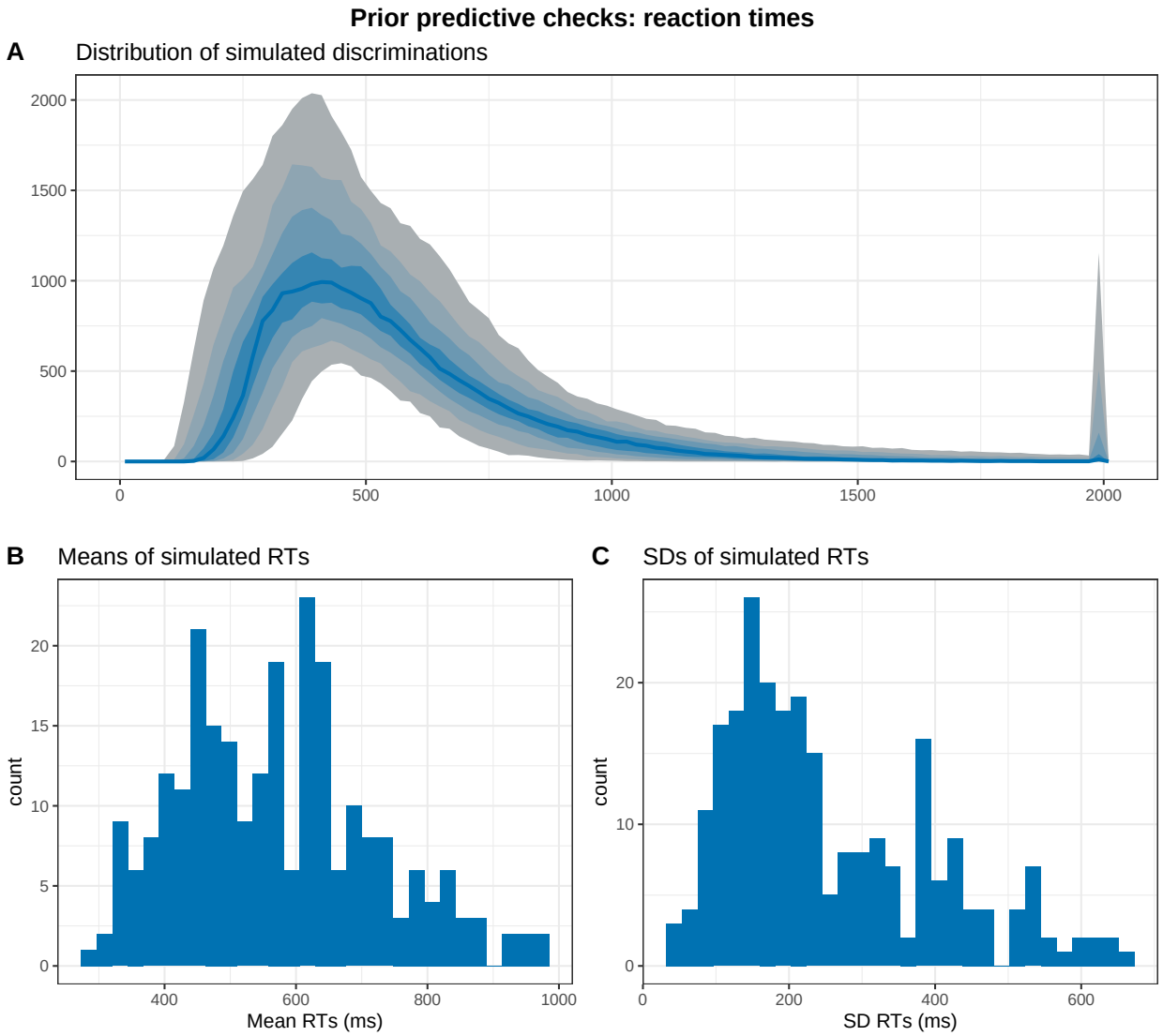
```r
# set informed priors based on previous results
priors = c(
  # general priors based on SBV
  prior(normal(6, 0.3),  class = Intercept),
  prior(normal(0, 0.5),  class = sigma),
  prior(normal(0, 0.1),  class = sd),
  prior(lkj(2),          class = cor),
  # face attention bias effect based on Jakobsen et al. (2021)
  prior(normal(-0.01, 0.04), class = b, coef = cue1),
  # ADHD subjects being slower based on Pievsky & McGrath (2018)
  prior(normal(0.025, 0.04),   class = b, coef = diagnosis1),
  # ASD subjects being slower based on Morrison et al. (2018)
  prior(normal(0.025, 0.04),   class = b, coef = diagnosis2),
  # decreased FAB in ASD subjects based on Moore et al. (2012)
  prior(normal(0.01,  0.04),   class = b, coef = diagnosis2:cue1),
  # no specific expectations for FAB in ADHD
  prior(normal(0,     0.04), class = b),
  # shift
  prior(normal(200,   100), class = ndt)
)

# check if the SBC already exists
if (file.exists(file.path(cache_dir, sprintf("df_res_%s.rds", code)))) {
  # load in the results of the SBC
  df.results = readRDS(file.path(cache_dir, sprintf("df_res_%s.rds", code)))
  df.backend = readRDS(file.path(cache_dir, sprintf("df_div_%s.rds", code)))
  dat        = readRDS(file.path(cache_dir, sprintf("dat_%s.rds", code)))
} else {
  # perform the SBC
  gen = SBC_generator_brms(f.fab, data = df.fab, prior = priors,
                           family = shifted_lognormal,
                           thin = 50, warmup = 20000, refresh = 2000)
  bck = SBC_backend_brms_from_generator(gen, chains = 4, thin = 1,
                                        init = 0.1, warmup = warm, iter = iter)
  dat = generate_datasets(gen, nsim)
  saveRDS(dat, file.path(cache_dir, sprintf("dat_%s.rds", code)))
  res = compute_SBC(dat,
        bck,
        cache_mode     = "results",
        cache_location = file.path(cache_dir, sprintf("res_%s", code)))
  df.results = res$stats
  df.backend = res$backend_diagnostics
  saveRDS(df.results, file = file.path(cache_dir, paste0("df_res_", code, ".rds")))
  saveRDS(df.backend, file = file.path(cache_dir, paste0("df_div_", code, ".rds")))
}
```

We start by investigating the rhats and the number of divergent samples. This shows that 6 of 250 simulations had at least one parameter that had an rhat of at least 1.05, and 1 model had divergent samples (mean number of samples of the simulations with divergent samples: 4). This suggests that this model performs well.

Next, we can plot the simulated values to perform prior predictive checks.

```r
# create a matrix out of generated data
dvname = gsub(" ", "", gsub("[\\|~].*", "", f.fab)[1])
```

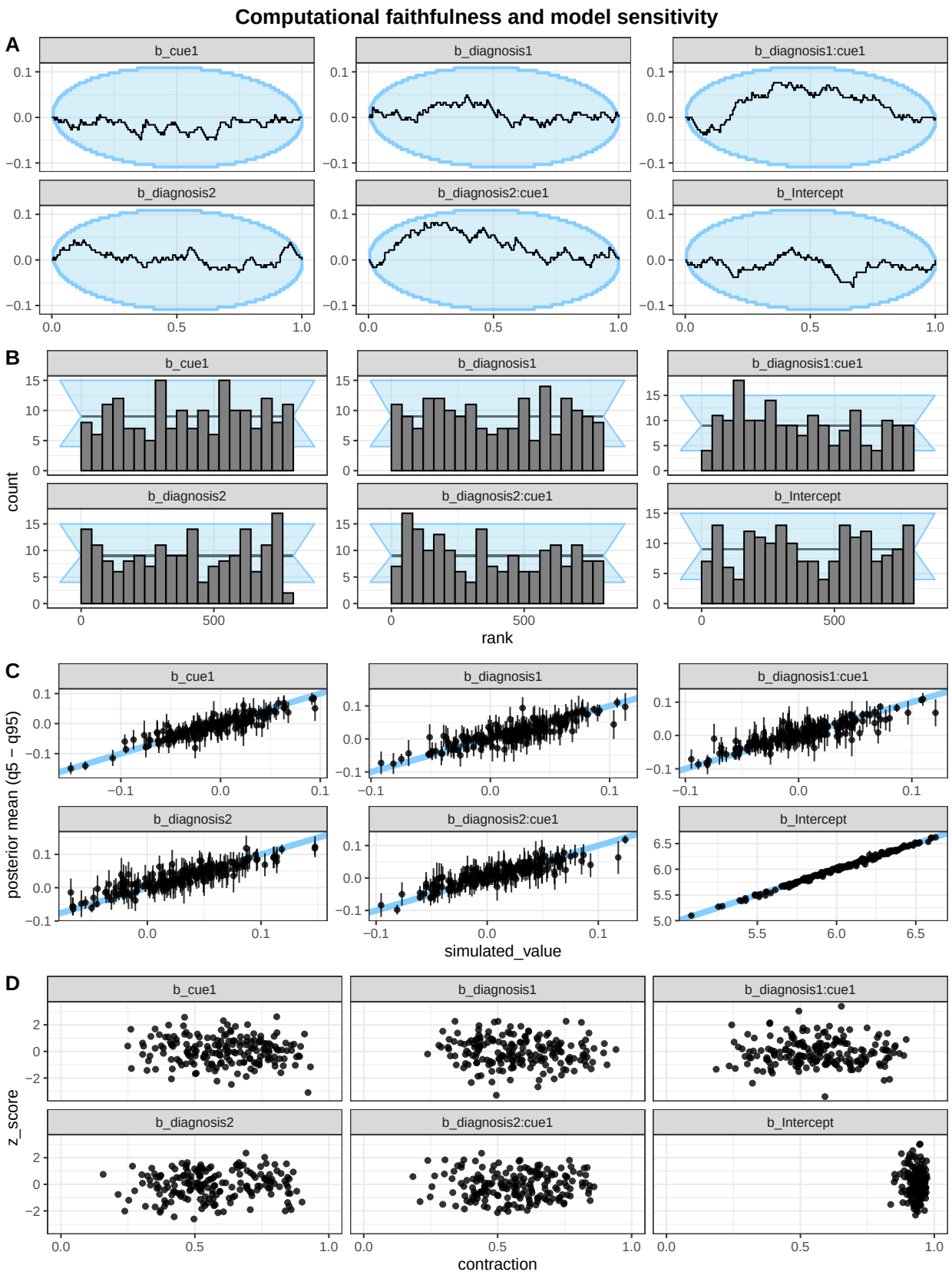
```
dvfakemat = matrix(NA, nrow(dat[['generated']][[1]]), length(dat[['generated']]))
for (i in 1:length(dat[['generated']])) {
  dvfakemat[,i] = dat[['generated']][[i]][[dvname]]
}
truePars = dat$variables

# set large values to a max
dvfakemat[dvfakemat > 2000] = 2000

# compute one histogram per simulated data-set
binwidth = 20
breaks = seq(0, max(dvfakemat, na.rm=T) + binwidth, binwidth)
histmat = matrix(NA, ncol = length(dat), nrow = length(breaks)-1)
for (i in 1:nrow(truePars)) {
  histmat[,i] = hist(dvfakemat[,i], breaks = breaks, plot = F)$counts
}
# for each bin, compute quantiles across histograms
probs = seq(0.1, 0.9, 0.1)
quantmat= as.data.frame(matrix(NA, nrow=dim(histmat)[1], ncol = length(probs)))
names(quantmat) = paste0("p", probs)
for (i in 1:dim(histmat)[1]) {
  quantmat[i,] = quantile(histmat[i,], p = probs)
}
quantmat$x = breaks[2:length(breaks)] - binwidth/2 # add bin mean
p1 = ggplot(data = quantmat, aes(x = x)) +
  geom_ribbon(aes(ymax = p0.9, ymin = p0.1), fill = c_light) +
  geom_ribbon(aes(ymax = p0.8, ymin = p0.2), fill = c_light_highlight) +
  geom_ribbon(aes(ymax = p0.7, ymin = p0.3), fill = c_mid) +
  geom_ribbon(aes(ymax = p0.6, ymin = p0.4), fill = c_mid_highlight) +
  geom_line(aes(y = p0.5), colour = c_dark, linewidth = 1) +
  labs(title = "Distribution of simulated discriminations", y = "", x = "") +
  theme_bw()

tmpM = apply(dvfakemat, 2, mean) # mean
tmpSD = apply(dvfakemat, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark)  +
  labs(x = "Mean RTs (ms)", title = "Means of simulated RTs") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD RTs (ms)", title = "SDs of simulated RTs") +
  theme_bw()
p = ggarrange(p1,
  ggarrange(p2, p3, ncol = 2, labels = c("B", "C")),
  nrow = 2, labels = "A")
annotate_figure(p,
                top = text_grob("Prior predictive checks: reaction times",
                face = "bold", size = 14))
```



Subfigure A shows the distribution of the simulated data with bluer bands being more likely than greyer bands. It shows a distribution that fits our expectations about reaction times in a simple decision task. The same applies to the distribution of the means and standard deviations in the simulated datasets. We go ahead with these priors and check the results of the SBC. We only plot the results from the models that had no divergence issues.

```
# get simulation numbers with issues
rank = max(df.results$max_rank)
check = merge(df.results %>%
    group_by(sim_id) %>%
      summarise(
        rhat = max(rhat, na.rm = T),
        mean_rank = mean(max_rank)
        ) %>%
    filter(rhat >= 1.05 | mean_rank != rank),
  df.backend %>% filter(n_divergent > 0), all = T)

# plot SBC with functions from the SBC package focusing on population-level parameters
df.results.b = df.results %>%
```

```
  filter(substr(variable, 1, 2) == "b_") %>%
  filter(!(sim_id %in% check$sim_id))
p1 = plot_ecdf_diff(df.results.b) + theme_bw() + theme(legend.position = "none") +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p2 = plot_rank_hist(df.results.b, bins = 20) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p3 = plot_sim_estimated(df.results.b, alpha = .8) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p4 = plot_contraction(df.results.b,
                      prior_sd = setNames(
                        c(as.numeric(
                          gsub(".*, (.+)\\).*", "\\1",
                               priors[priors$class == "Intercept",]$prior)),
                          as.numeric(
                            gsub(".*, (.+)\\).*", "\\1",
                                 priors[priors$class == "b",]$prior))),
                                          unique(df.results.b$variable))) +
  theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))

p = ggarrange(p1, p2, p3, p4, labels = "AUTO", ncol = 1, nrow = 4)
annotate_figure(p, top =
                  text_grob("Computational faithfulness and model sensitivity",
                face = "bold", size = 14))
```



Next, we check the ranks of the parameters. If the model is unbiased, these should be uniformly distributed

(Schad, Betancourt and Vasishth, 2020). The sample empirical cumulative distribution function (ECDF) lies within the theoretical distribution (95%) and the rank histogram also shows ranks within the 95% expected range, although there are some small deviations. We judge this to be acceptable.

Then, we investigated the relationship between the simulated true parameters and the posterior estimates. Although there are individual values diverging from the expected pattern, most parameters were recovered successfully within an uncertainty interval of alpha = 0.05.

Last, we explore the z-score and the posterior contraction of our population-level predictors. The z-score "determines the distance of the posterior mean from the true simulating parameter", while the posterior contraction "estimates how much prior uncertainty is reduced in the posterior estimation" (Schad, Betancourt and Vasisth, 2020). All of this looks good for this model.

Posterior predictive checks

As the next step, we fit the model to the data, check whether there are divergence or rhat issues, and then check whether the chains have converged.

```
# fit the full model
set.seed(2469)
m.fab = brm(f.fab,
            df.fab, prior = priors,
            family = shifted_lognormal,
            iter = iter, warmup = warm,
            backend = "cmdstanr", threads = threading(8),
            file = "m_fab_full"
            )
rstan::check_hmc_diagnostics(m.fab$fit)
```

```
##
## Divergences:
```

```
## 0 of 8000 iterations ended with a divergence.
```

```
##
## Tree depth:
```

```
## 0 of 8000 iterations saturated the maximum tree depth of 10.
```

```
##
## Energy:
```

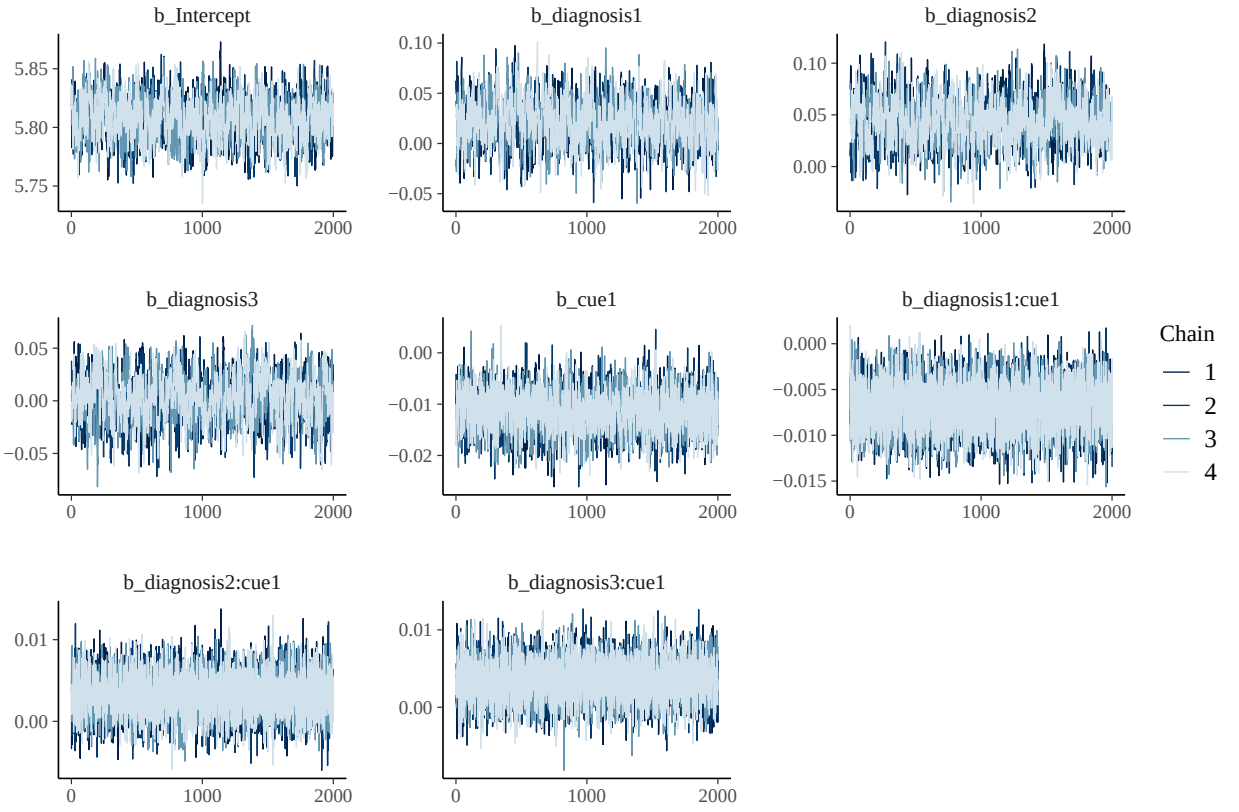
```
## E-BFMI indicated no pathological behavior.
```

```
# check that rhats are below 1.01
sum(brms::rhat(m.fab) >= 1.01, na.rm = T)
```

```
## [1] 0
```

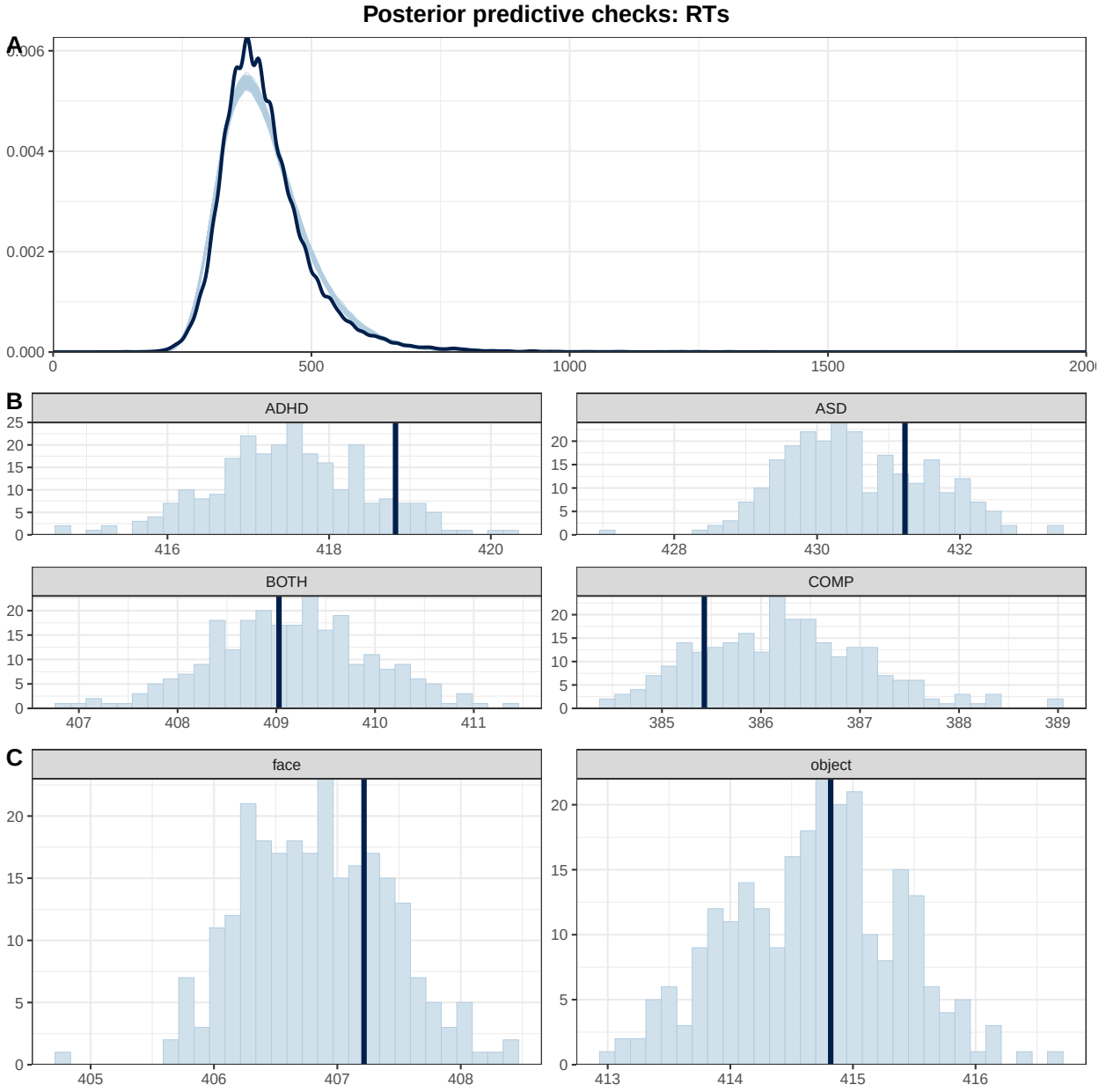
```
# check the trace plots
post.draws = as_draws_df(m.fab)
mcmc_trace(post.draws, regex_pars = "^b_",
           facet_args = list(ncol = 3)) +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
```

```
## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```



This model has no pathological behaviour with E-BFMI, no divergent samples and no rhat that is higher or equal to 1.01. Therefore, we go ahead and perform our posterior predictive checks.

```
# get posterior predictions
post.pred = posterior_predict(m.fab, ndraws = nsim)

# check the fit of the predicted data compared to the real data
p1 = pp_check(m.fab, ndraws = nsim) +
  theme_bw() + theme(legend.position = "none") + xlim(0, 2000)

# get rid of NAs in data frame for plotting
df.fab.na = df.fab[!is.na(df.fab$rt.cor),]

# distributions of means compared to the real values per group
p2 = ppc_stat_grouped(df.fab.na$rt.cor, post.pred, df.fab.na$diagnosis) +
  theme_bw() + theme(legend.position = "none")

# distributions of means compared to the real values per cue
p3 = ppc_stat_grouped(df.fab.na$rt.cor, post.pred, df.fab.na$cue) +
  theme_bw() + theme(legend.position = "none")

p = ggarrange(p1, p2, p3,
          nrow = 3, ncol = 1, labels = "AUTO")
annotate_figure(p,
                top = text_grob("Posterior predictive checks: RTs",
                face = "bold", size = 14))
```



Although the overall shape in subfigure A of the simulated data fits well with the real data, the model seems to underestimate the reaction times of the ADHD and ASD groups and overestimate the reaction times of the COMP group: the dark blue line shows the mean of the actual dataset while the light blue bars show the distribution of the predicted data.

Since we are interested in accurate estimates, we decide to aggregate with the median of the reaction times per stimulus (face-object cue combination) and cue. Then, there are no missing values in the data and we model an estimate for each specific stimulus and cue combination for each participant.

Aggregated model

First, we compute the aggregation and have a quick look at the resulting data.

```
# keep full dataframe
df.fab.full = df.fab

# aggregate reaction times
df.fab = df.fab %>%
  group_by(subID, diagnosis, stm, cue) %>%
  summarise(
    rt.cor = median(rt.cor, na.rm = T)
  ) %>% ungroup() %>%
  mutate_if(is.character, as.factor)

# set and print the contrasts
contrasts(df.fab$cue) = contr.sum(2)
contrasts(df.fab$cue)
```

```
##        [,1]
## face      1
## object   -1
```

```
contrasts(df.fab$diagnosis) = contr.sum(4)[c(1,2,4,3),]
contrasts(df.fab$diagnosis)
```

```
##      [,1] [,2] [,3]
## ADHD    1    0    0
## ASD     0    1    0
## BOTH   -1   -1   -1
## COMP    0    0    1
```

```
summary(df.fab)
```

```
##      subID      diagnosis        stm           cue           rt.cor
##  1      :  72   ADHD:1656   1_10   : 188   face  :3384   Min.   :256.0
##  2      :  72   ASD :1728   1_11   : 188   object:3384   1st Qu.:364.0
##  3      :  72   BOTH:1656   1_12   : 188                 Median :394.8
##  4      :  72   COMP:1728   1_7    : 188                 Mean   :406.6
##  5      :  72               1_8    : 188                 3rd Qu.:435.5
##  6      :  72               1_9    : 188                 Max.   :919.0
##  (Other):6336               (Other):5640
```

There are now no NAs in the data, because no one made an error on all instances of one stimulus combination.

Stimulation-based calibration

We again perform an SBC. The model formula and priors can stay the same.

```
code = "FAB_agg"

# check if the SBC already exists
if (file.exists(file.path(cache_dir, sprintf("df_res_%s.rds", code)))) {
  # load in the results of the SBC
  df.results = readRDS(file.path(cache_dir, sprintf("df_res_%s.rds", code)))
  df.backend = readRDS(file.path(cache_dir, sprintf("df_div_%s.rds", code)))
  dat        = readRDS(file.path(cache_dir, sprintf("dat_%s.rds", code)))
} else {
  # perform the SBC
  gen = SBC_generator_brms(f.fab, data = df.fab, prior = priors,
                           family = shifted_lognormal,
```

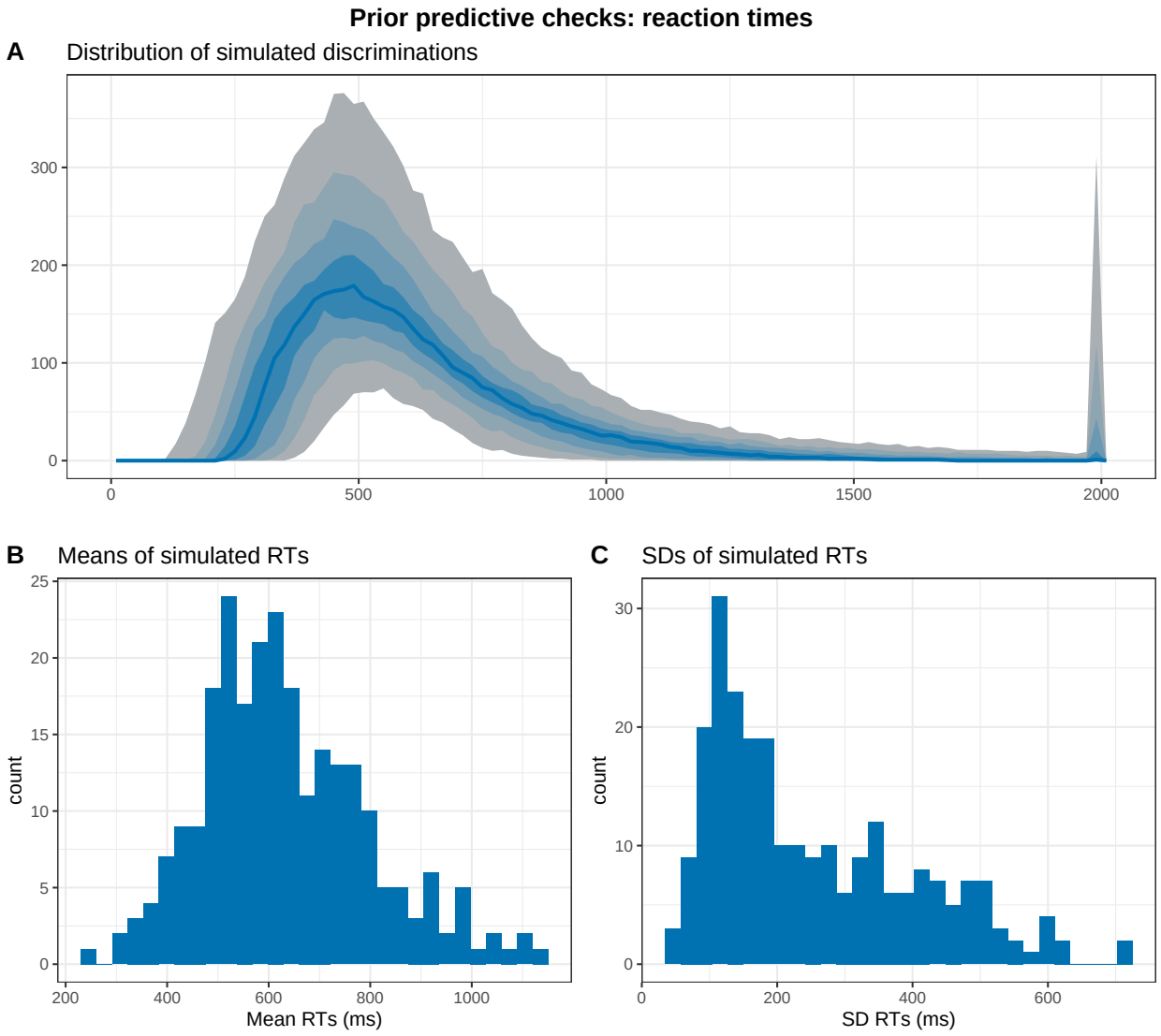
```
                              thin = 50, warmup = 20000, refresh = 2000)
  bck = SBC_backend_brms_from_generator(gen, chains = 4, thin = 1,
                                        init = 0.1, warmup = warm, iter = iter)
  set.seed(468)
  if (file.exists(file.path(cache_dir, sprintf("dat_%s.rds", code)))) {
    dat = readRDS(file.path(cache_dir, sprintf("dat_%s.rds", code)))
  } else {
    dat = generate_datasets(gen, nsim)
    saveRDS(dat, file.path(cache_dir, sprintf("dat_%s.rds", code)))
  }
  res = compute_SBC(dat,
        bck,
        cache_mode     = "results",
        cache_location = file.path(cache_dir, sprintf("res_%s", code)))
  df.results = res$stats
  df.backend = res$backend_diagnostics
  saveRDS(df.results, file = file.path(cache_dir, paste0("df_res_", code, ".rds")))
  saveRDS(df.backend, file = file.path(cache_dir, paste0("df_div_", code, ".rds")))
}

set.seed(4682)
```

We start by investigating the rhats and the number of divergent samples. This shows that 3 of 250 simulations had at least one parameter that had an rhat of at least 1.05, and 2 models had divergent samples (mean number of samples of the simulations with divergent samples: 17.5). This suggests that this model performs well enough and only few simulated models exhibit issues.

Next, we can plot the simulated values to perform prior predictive checks.

```
# create a matrix out of generated data
dvname = gsub(" ", "", gsub("[\\|~].*", "", f.fab)[1])
dvfakemat = matrix(NA, nrow(dat[['generated']][[1]]), length(dat[['generated']]))
for (i in 1:length(dat[['generated']])) {
  dvfakemat[,i] = dat[['generated']][[i]][[dvname]]
}
truePars = dat$variables

# set large values to a max
dvfakemat[dvfakemat > 2000] = 2000

# compute one histogram per simulated data-set
binwidth = 20
breaks = seq(0, max(dvfakemat, na.rm=T) + binwidth, binwidth)
histmat = matrix(NA, ncol = length(dat), nrow = length(breaks)-1)
for (i in 1:nrow(truePars)) {
  histmat[,i] = hist(dvfakemat[,i], breaks = breaks, plot = F)$counts
}
# for each bin, compute quantiles across histograms
probs = seq(0.1, 0.9, 0.1)
quantmat= as.data.frame(matrix(NA, nrow=dim(histmat)[1], ncol = length(probs)))
names(quantmat) = paste0("p", probs)
for (i in 1:dim(histmat)[1]) {
  quantmat[i,] = quantile(histmat[i,], p = probs)
}
quantmat$x = breaks[2:length(breaks)] - binwidth/2 # add bin mean
```

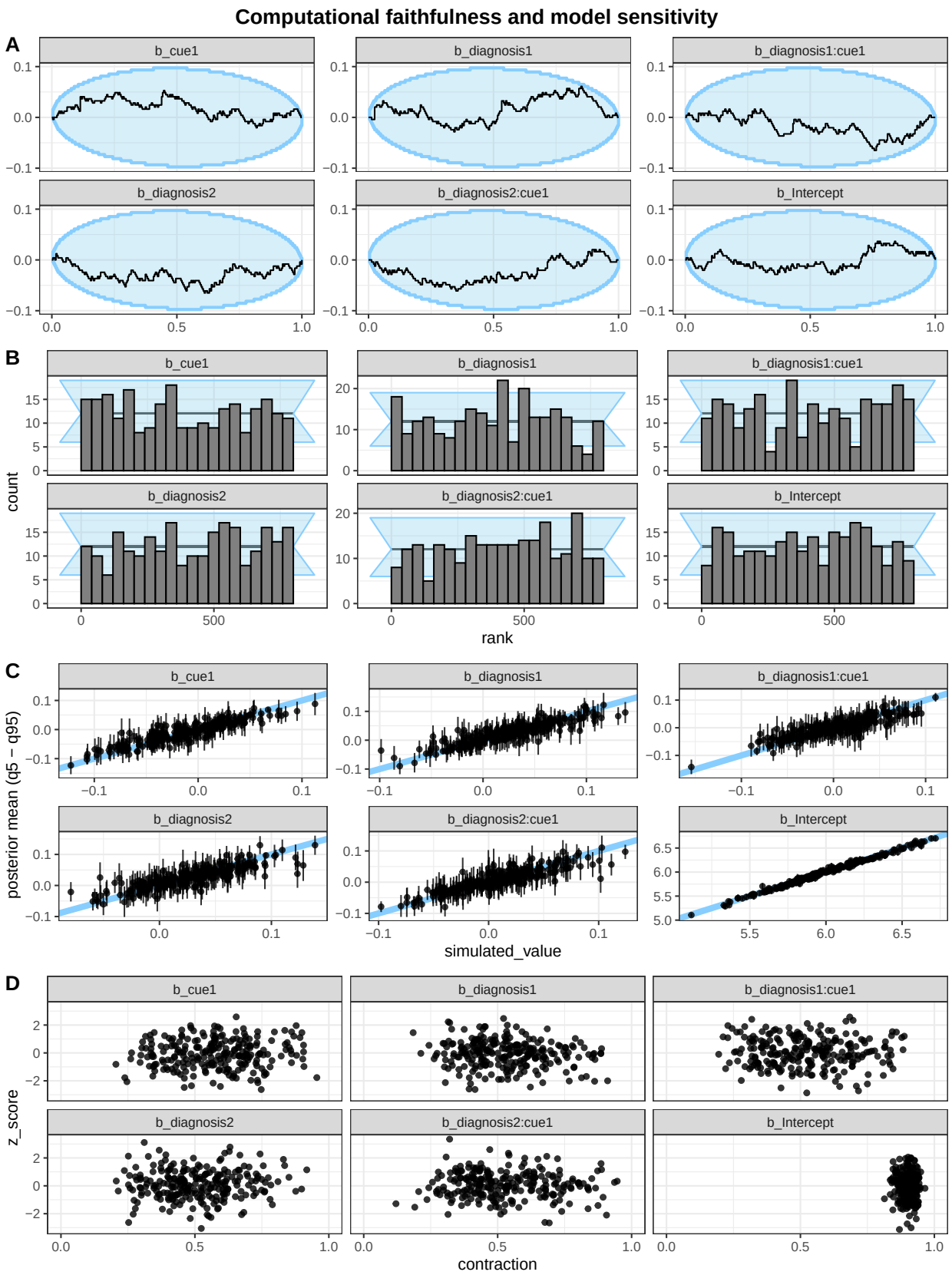
```r
p1 = ggplot(data = quantmat, aes(x = x)) +
  geom_ribbon(aes(ymax = p0.9, ymin = p0.1), fill = c_light) +
  geom_ribbon(aes(ymax = p0.8, ymin = p0.2), fill = c_light_highlight) +
  geom_ribbon(aes(ymax = p0.7, ymin = p0.3), fill = c_mid) +
  geom_ribbon(aes(ymax = p0.6, ymin = p0.4), fill = c_mid_highlight) +
  geom_line(aes(y = p0.5), colour = c_dark, linewidth = 1) +
  labs(title = "Distribution of simulated discriminations", y = "", x = "") +
  theme_bw()

tmpM = apply(dvfakemat, 2, mean) # mean
tmpSD = apply(dvfakemat, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark)  +
  labs(x = "Mean RTs (ms)", title = "Means of simulated RTs") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD RTs (ms)", title = "SDs of simulated RTs") +
  theme_bw()
p = ggarrange(p1,
  ggarrange(p2, p3, ncol = 2, labels = c("B", "C")),
  nrow = 2, labels = "A")
annotate_figure(p,
                top = text_grob("Prior predictive checks: reaction times",
                face = "bold", size = 14))
```



Again, this all looks good.

```
# get simulation numbers with issues
rank = max(df.results$max_rank)
check = merge(df.results %>%
    group_by(sim_id) %>%
      summarise(
        rhat = max(rhat, na.rm = T),
        mean_rank = mean(max_rank)
        ) %>%
    filter(rhat >= 1.05 | mean_rank != rank),
  df.backend %>% filter(n_divergent > 0), all = T)

# plot SBC with functions from the SBC package focusing on population-level parameters
df.results.b = df.results %>%
  filter(substr(variable, 1, 2) == "b_") %>%
  filter(!(sim_id %in% check$sim_id))
p1 = plot_ecdf_diff(df.results.b) + theme_bw() + theme(legend.position = "none") +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
```

```
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p2 = plot_rank_hist(df.results.b, bins = 20) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p3 = plot_sim_estimated(df.results.b, alpha = .8) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p4 = plot_contraction(df.results.b,
                      prior_sd = setNames(
                        c(as.numeric(
                          gsub(".*, (.+)\\).*", "\\1",
                               priors[priors$class == "Intercept",]$prior)),
                          as.numeric(
                            gsub(".*, (.+)\\).*", "\\1",
                                 priors[priors$class == "b",]$prior))),
                                          unique(df.results.b$variable))) +
  theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))

p = ggarrange(p1, p2, p3, p4, labels = "AUTO", ncol = 1, nrow = 4)
annotate_figure(p,
                top = text_grob("Computational faithfulness and model sensitivity",
                face = "bold", size = 14))
```



Rank histogramms, sample ECDF, the relationship between the simulated true parameters and the posterior

estimates as well as z-score and posterior contraction of our population-level predictors all are acceptable for this model as well.

Posterior predictive checks

As the next step, we fit the model to the data, check whether there are divergence or rhat issues, and then check whether the chains have converged.

```
# fit the final model
set.seed(6824)
m.fab = brm(f.fab,
            df.fab, prior = priors,
            family = shifted_lognormal,
            iter = iter, warmup = warm,
            backend = "cmdstanr", threads = threading(8),
            file = "m_fab_final"
            )
rstan::check_hmc_diagnostics(m.fab$fit)
```

```
##
## Divergences:
```

```
## 0 of 8000 iterations ended with a divergence.
```

```
##
## Tree depth:
```

```
## 0 of 8000 iterations saturated the maximum tree depth of 10.
```

```
##
## Energy:
```

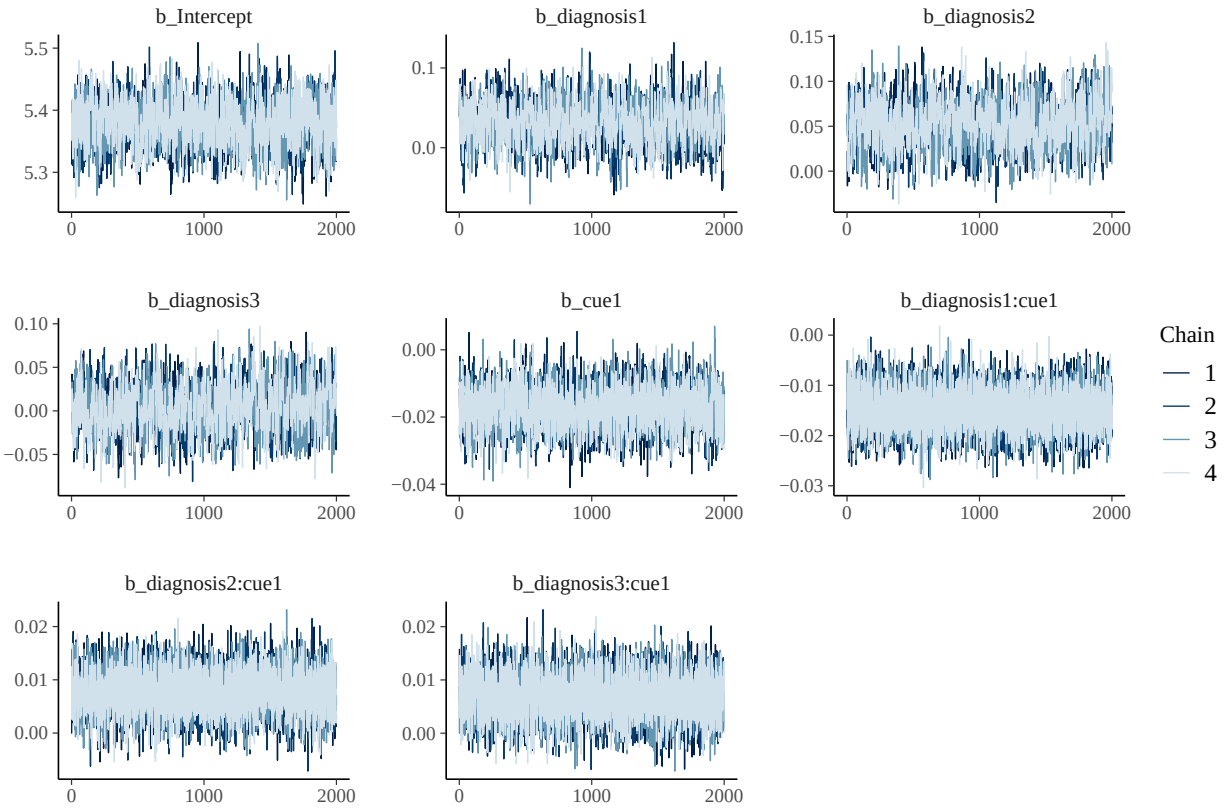
```
## E-BFMI indicated no pathological behavior.
```

```
# check that rhats are below 1.01
sum(brms::rhat(m.fab) >= 1.01, na.rm = T)
```

```
## [1] 0
```

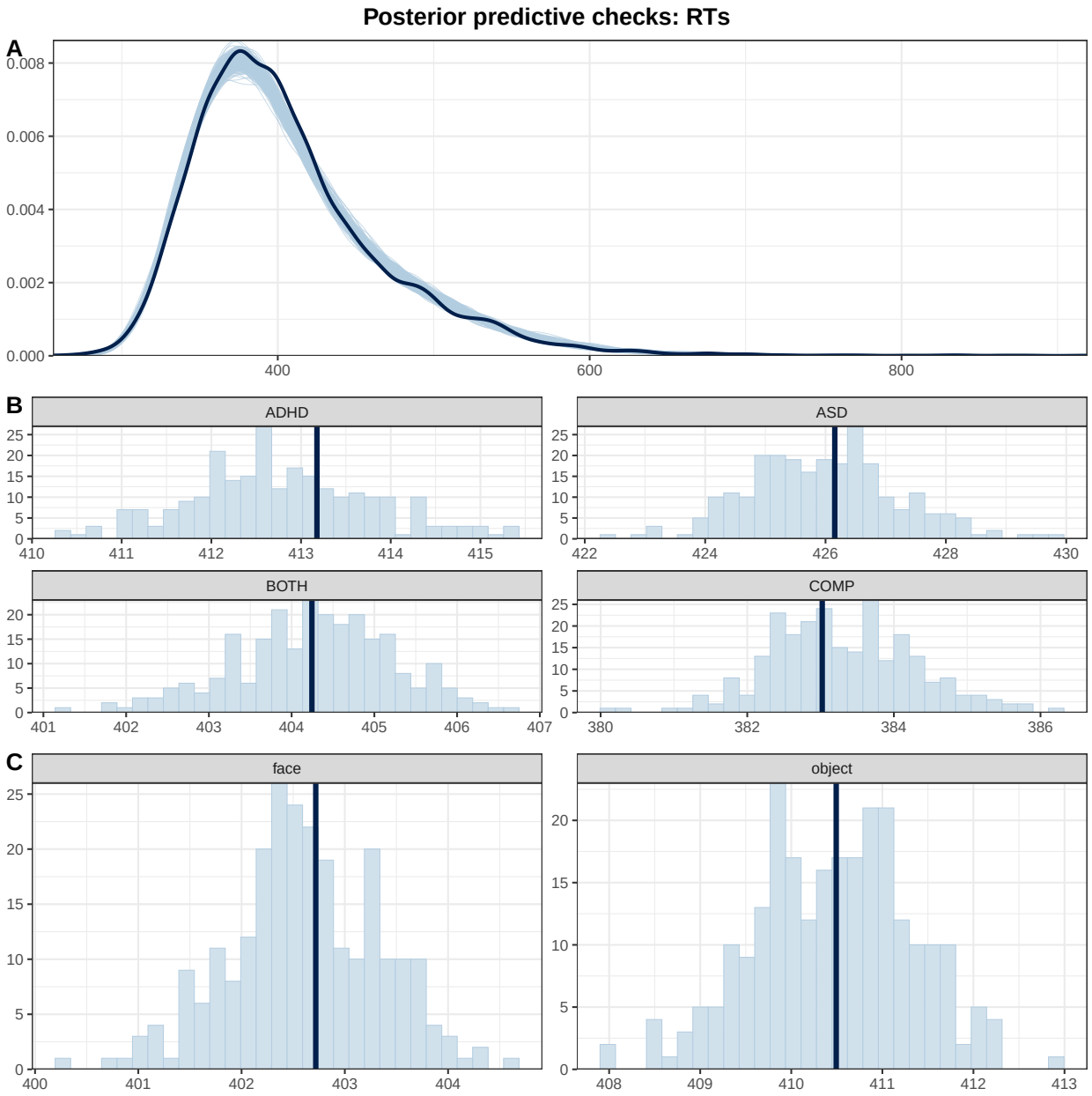
```
# check the trace plots
post.draws = as_draws_df(m.fab)
mcmc_trace(post.draws, regex_pars = "^b_",
           facet_args = list(ncol = 3)) +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
```

```
## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```



This model has no pathological behaviour with E-BFMI, no divergent samples and no rhat that is higher or equal to 1.01. Therefore, we go ahead and perform our posterior predictive checks.

```
# get posterior predictions
post.pred = posterior_predict(m.fab, ndraws = nsim)

# check the fit of the predicted data compared to the real data
p1 = pp_check(m.fab, ndraws = nsim) +
  theme_bw() + theme(legend.position = "none")

# distributions of means compared to the real values per group
p2 = ppc_stat_grouped(df.fab$rt.cor, post.pred, df.fab$diagnosis) +
  theme_bw() + theme(legend.position = "none")

# distributions of means compared to the real values per cue
p3 = ppc_stat_grouped(df.fab$rt.cor, post.pred, df.fab$cue) +
  theme_bw() + theme(legend.position = "none")

p = ggarrange(p1, p2, p3,
          nrow = 3, ncol = 1, labels = "AUTO")
annotate_figure(p,
                top = text_grob("Posterior predictive checks: RTs",
                face = "bold", size = 14))
```



This model fits our data much better.

Inferences

Now that we are convinced that we can trust our model, we have a look at its estimate and use the hypothesis function to assess our hypotheses and perform explorative tests.

```
# print a summary
summary(m.fab)
```

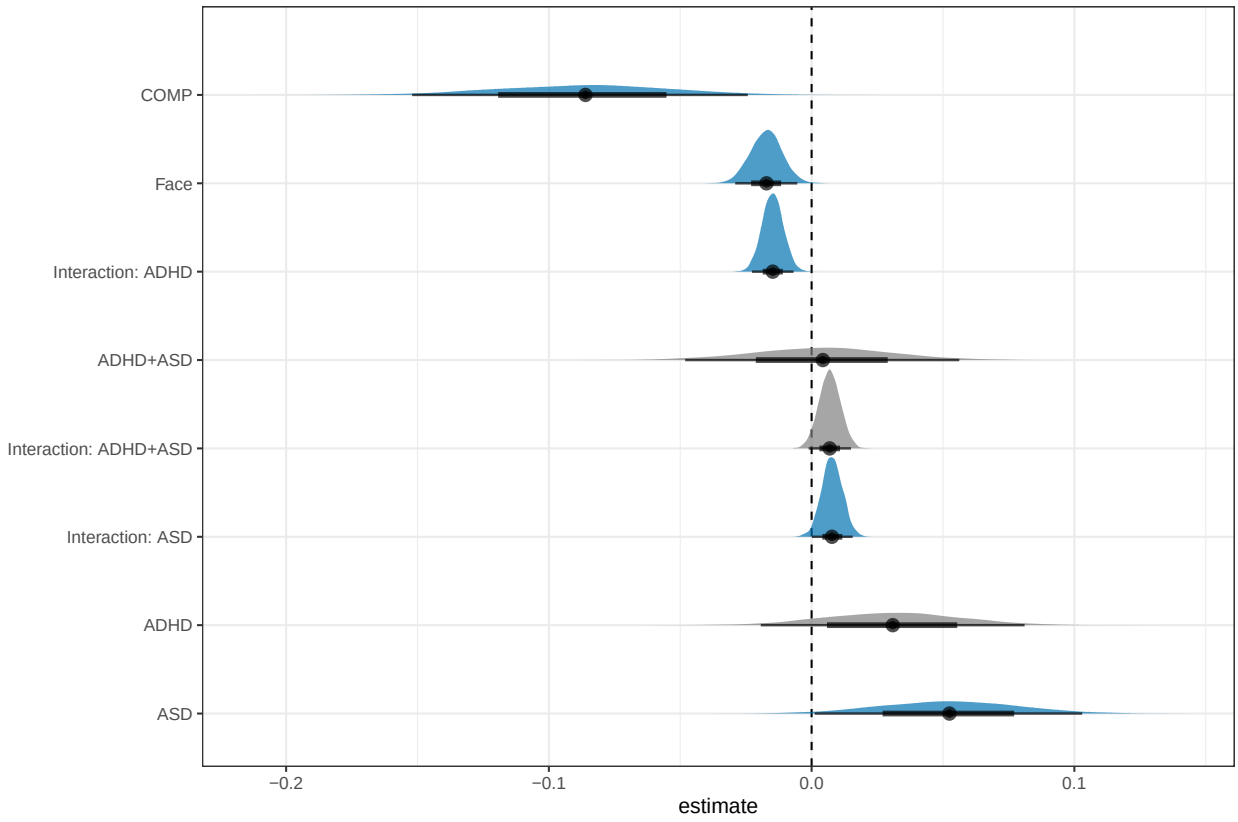
```
##  Family: shifted_lognormal
##   Links: mu = identity; sigma = identity; ndt = identity
## Formula: rt.cor ~ diagnosis * cue + (cue | subID) + (cue * diagnosis | stm)
##    Data: df.fab (Number of observations: 6768)
##   Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
```

```
##          total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~stm (Number of levels: 36)
##                                     Estimate Est.Error l-95% CI u-95% CI Rhat
## sd(Intercept)                           0.03      0.00     0.02     0.03 1.00
## sd(cue1)                                0.03      0.00     0.03     0.04 1.00
## sd(diagnosis1)                          0.01      0.00     0.00     0.02 1.00
## sd(diagnosis2)                          0.00      0.00     0.00     0.01 1.00
## sd(diagnosis3)                          0.01      0.00     0.00     0.01 1.00
## sd(cue1:diagnosis1)                     0.00      0.00     0.00     0.01 1.00
## sd(cue1:diagnosis2)                     0.00      0.00     0.00     0.01 1.00
## sd(cue1:diagnosis3)                     0.00      0.00     0.00     0.01 1.00
## cor(Intercept,cue1)                    -0.30      0.15    -0.57     0.03 1.00
## cor(Intercept,diagnosis1)              -0.12      0.26    -0.60     0.45 1.00
## cor(cue1,diagnosis1)                    0.01      0.26    -0.50     0.51 1.00
## cor(Intercept,diagnosis2)              -0.07      0.29    -0.60     0.51 1.00
## cor(cue1,diagnosis2)                   -0.05      0.29    -0.58     0.51 1.00
## cor(diagnosis1,diagnosis2)             -0.01      0.30    -0.58     0.57 1.00
## cor(Intercept,diagnosis3)               0.06      0.27    -0.49     0.57 1.00
## cor(cue1,diagnosis3)                    0.18      0.27    -0.41     0.66 1.00
## cor(diagnosis1,diagnosis3)             -0.12      0.30    -0.66     0.49 1.00
## cor(diagnosis2,diagnosis3)             -0.08      0.31    -0.65     0.54 1.00
## cor(Intercept,cue1:diagnosis1)          0.03      0.28    -0.51     0.55 1.00
## cor(cue1,cue1:diagnosis1)              -0.06      0.28    -0.58     0.49 1.00
## cor(diagnosis1,cue1:diagnosis1)         0.00      0.30    -0.56     0.57 1.00
## cor(diagnosis2,cue1:diagnosis1)        -0.00      0.30    -0.57     0.56 1.00
## cor(diagnosis3,cue1:diagnosis1)        -0.03      0.30    -0.59     0.54 1.00
## cor(Intercept,cue1:diagnosis2)         -0.21      0.28    -0.69     0.40 1.00
## cor(cue1,cue1:diagnosis2)              -0.01      0.28    -0.54     0.53 1.00
## cor(diagnosis1,cue1:diagnosis2)         0.03      0.29    -0.54     0.58 1.00
## cor(diagnosis2,cue1:diagnosis2)         0.04      0.30    -0.54     0.61 1.00
## cor(diagnosis3,cue1:diagnosis2)        -0.05      0.29    -0.59     0.53 1.00
## cor(cue1:diagnosis1,cue1:diagnosis2)   -0.09      0.31    -0.65     0.53 1.00
## cor(Intercept,cue1:diagnosis3)         -0.10      0.28    -0.62     0.46 1.00
## cor(cue1,cue1:diagnosis3)              -0.15      0.28    -0.65     0.43 1.00
## cor(diagnosis1,cue1:diagnosis3)         0.05      0.30    -0.52     0.61 1.00
## cor(diagnosis2,cue1:diagnosis3)         0.06      0.30    -0.53     0.62 1.00
## cor(diagnosis3,cue1:diagnosis3)        -0.02      0.30    -0.59     0.55 1.00
## cor(cue1:diagnosis1,cue1:diagnosis3)   -0.08      0.30    -0.63     0.52 1.00
## cor(cue1:diagnosis2,cue1:diagnosis3)   -0.01      0.30    -0.58     0.57 1.00
##                                     Bulk_ESS Tail_ESS
## sd(Intercept)                           2578     4611
## sd(cue1)                                2693     4533
## sd(diagnosis1)                          2411     3394
## sd(diagnosis2)                          4155     4612
## sd(diagnosis3)                          3402     4152
## sd(cue1:diagnosis1)                     3823     4565
## sd(cue1:diagnosis2)                     3982     4324
## sd(cue1:diagnosis3)                     3597     3381
## cor(Intercept,cue1)                     1826     3831
## cor(Intercept,diagnosis1)              13054     5814
## cor(cue1,diagnosis1)                   13349     6130
## cor(Intercept,diagnosis2)              16827     5305
```

```
## cor(cue1,diagnosis2)                    17348     5809
## cor(diagnosis1,diagnosis2)               9760     6457
## cor(Intercept,diagnosis3)               15806     5807
## cor(cue1,diagnosis3)                    12478     6278
## cor(diagnosis1,diagnosis3)               7439     6368
## cor(diagnosis2,diagnosis3)               7729     6017
## cor(Intercept,cue1:diagnosis1)          15320     6384
## cor(cue1,cue1:diagnosis1)               16067     5911
## cor(diagnosis1,cue1:diagnosis1)         10215     6390
## cor(diagnosis2,cue1:diagnosis1)          7492     6359
## cor(diagnosis3,cue1:diagnosis1)          7425     7042
## cor(Intercept,cue1:diagnosis2)          11799     6187
## cor(cue1,cue1:diagnosis2)               15752     5325
## cor(diagnosis1,cue1:diagnosis2)         10817     6320
## cor(diagnosis2,cue1:diagnosis2)          8245     6495
## cor(diagnosis3,cue1:diagnosis2)          6974     6717
## cor(cue1:diagnosis1,cue1:diagnosis2)     6068     6426
## cor(Intercept,cue1:diagnosis3)          14585     6447
## cor(cue1,cue1:diagnosis3)               11674     6152
## cor(diagnosis1,cue1:diagnosis3)          8962     5900
## cor(diagnosis2,cue1:diagnosis3)          6889     6461
## cor(diagnosis3,cue1:diagnosis3)          8014     7067
## cor(cue1:diagnosis1,cue1:diagnosis3)     6829     6746
## cor(cue1:diagnosis2,cue1:diagnosis3)     6471     6914
##
## ~subID (Number of levels: 94)
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)           0.21      0.02     0.18     0.24 1.00     1249     2259
## sd(cue1)                0.02      0.00     0.01     0.02 1.00     3696     5257
## cor(Intercept,cue1)    -0.04      0.14    -0.32     0.24 1.00     7658     6980
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           5.38      0.03     5.31     5.45 1.00     1000     1967
## diagnosis1          0.03      0.03    -0.02     0.08 1.00     1053     1809
## diagnosis2          0.05      0.03     0.00     0.10 1.00      959     1959
## diagnosis3          0.00      0.03    -0.05     0.06 1.00     1055     2006
## cue1               -0.02      0.01    -0.03    -0.01 1.00     2074     3747
## diagnosis1:cue1    -0.01      0.00    -0.02    -0.01 1.00     8305     7001
## diagnosis2:cue1     0.01      0.00     0.00     0.02 1.00     8591     7066
## diagnosis3:cue1     0.01      0.00    -0.00     0.01 1.00     8207     7062
##
## Further Distributional Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.13      0.00     0.13     0.14 1.00     5963     5842
## ndt     183.19      5.64   171.94   193.62 1.00     5982     5698
##
## Draws were sampled using sample(hmc). 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).
```

```
# get the estimates and compute groups
df.m.fab = as_draws_df(m.fab) %>%
  select(starts_with("b_")) %>%
```

```
  mutate(
    b_COMP    = - b_diagnosis1 - b_diagnosis2 - b_diagnosis3,
    ASD       = b_Intercept + b_diagnosis2,
    ADHD      = b_Intercept + b_diagnosis1,
    BOTH      = b_Intercept + b_diagnosis3,
    COMP      = b_Intercept + b_COMP
    )

# plot the posterior distributions
df.m.fab %>%
  select(starts_with("b_")) %>%
  pivot_longer(cols = starts_with("b_"), names_to = "coef", values_to = "estimate") %>%
  filter(coef != "b_Intercept") %>%
  mutate(
    coef = case_match(coef,
      "b_diagnosis1" ~ "ADHD",
      "b_diagnosis2" ~ "ASD",
      "b_diagnosis3" ~ "ADHD+ASD",
      "b_COMP"       ~ "COMP",
      "b_cue1"       ~ "Face",
      "b_diagnosis1:cue1" ~ "Interaction: ADHD",
      "b_diagnosis2:cue1" ~ "Interaction: ASD",
      "b_diagnosis3:cue1" ~ "Interaction: ADHD+ASD"
    ),
    coef = fct_reorder(coef, desc(estimate))
  ) %>%
  group_by(coef) %>%
  mutate(
    cred = case_when(
      (mean(estimate) < 0 & quantile(estimate, probs = 0.975) < 0) |
        (mean(estimate) > 0 & quantile(estimate, probs = 0.025) > 0) ~ "credible",
      T ~ "not credible"
    )
  ) %>% ungroup() %>%
  ggplot(aes(x = estimate, y = coef, fill = cred)) +
  geom_vline(xintercept = 0, linetype = 'dashed') +
  ggdist::stat_halfeye(alpha = 0.7) + ylab(NULL) + theme_bw() +
  scale_fill_manual(values = c(credible = c_dark, c_light)) +
  theme(legend.position = "none")
```




```
# H1a: FAB effect in COMP
h1a = hypothesis(m.fab,
                 "0 < 2*(diagnosis1:cue1 + diagnosis2:cue1 + diagnosis3:cue1 - cue1)")
h1a
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*(diagnosis... < 0    -0.03      0.02    -0.06    -0.01      77.43
##   Post.Prob Star
## 1      0.99    *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1b: ADHD slower than COMP
h1b = hypothesis(m.fab,
                 "0 < 2*diagnosis1 + diagnosis2 + diagnosis3")
h1b
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis1... < 0    -0.12      0.05     -0.2    -0.04     139.35
##   Post.Prob Star
## 1      0.99    *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
```

```
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1c: ASD slower than COMP
h1c = hypothesis(m.fab,
                 "0 < 2*diagnosis2 + diagnosis1 + diagnosis3")
h1c
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis2... < 0    -0.14      0.05    -0.22    -0.06     443.44
##   Post.Prob Star
## 1         1    *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1d: FAB in ASD decreased compared to COMP
h1d = hypothesis(m.fab,
                 "0 < 4*diagnosis2:cue1 + 2*diagnosis1:cue1 + 2*diagnosis3:cue1")
h1d
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(4*diagnosis2... < 0    -0.02      0.01    -0.04     0.01        6.9
##   Post.Prob Star
## 1      0.87
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1e: FAB in ADHD differs from FAB in COMP (undirected)
h1e = hypothesis(m.fab,
                 "0 > 4*diagnosis1:cue1 + 2*diagnosis2:cue1 + 2*diagnosis3:cue1",
                 alpha = 0.025)
h1e
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(4*diagnosis1... > 0     0.03      0.01        0     0.06      71.73
##   Post.Prob Star
## 1      0.99    *
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# Exploration

# E1: FAB generally
e1 = hypothesis(m.fab, "2*cue1 < 0", alpha = 0.025)
e1
```

```
## Hypothesis Tests for class b:
##     Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob Star
## 1 (2*cue1) < 0    -0.03      0.01    -0.06    -0.01     306.69         1    *
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E2: FAB effect in ADHD
e2 = hypothesis(m.fab, "0 < -2*cue1 - 2*diagnosis1:cue1", alpha = 0.025)
e2
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(-2*cue1-2*di... < 0    -0.06      0.01    -0.09    -0.04        Inf
##   Post.Prob Star
## 1         1    *
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E3: FAB effect in ASD
e3 = hypothesis(m.fab, "0 < -2*cue1 - 2*diagnosis2:cue1", alpha = 0.025)
e3
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(-2*cue1-2*di... < 0    -0.02      0.01    -0.05     0.01       9.39
##   Post.Prob Star
## 1       0.9
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E4: FAB effect in ADHD+ASD
e4 = hypothesis(m.fab, "0 < -2*cue1 - 2*diagnosis3:cue1", alpha = 0.025)
e4
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(-2*cue1-2*di... < 0    -0.02      0.01    -0.05     0.01      12.84
##   Post.Prob Star
## 1      0.93
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E5: FAB in ADHD differs from FAB in ASD
e5 = hypothesis(m.fab,
                "0 < -2*diagnosis1:cue1 + 2*diagnosis2:cue1", alpha = 0.025)
```

```
e5
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(-2*diagnosis... < 0    -0.05      0.01    -0.07    -0.02       7999
##   Post.Prob Star
## 1         1    *
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E6: FAB in ADHD differs from FAB in BOTH
e6 = hypothesis(m.fab,
                "0 < -2*diagnosis1:cue1 + 2*diagnosis3:cue1", alpha = 0.025)
e6
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(-2*diagnosis... < 0    -0.04      0.01    -0.07    -0.02    2665.67
##   Post.Prob Star
## 1         1    *
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E7: FAB in ASD differs from FAB in BOTH
e7 = hypothesis(m.fab,
                "0 < -2*diagnosis2:cue1 + 2*diagnosis3:cue1", alpha = 0.025)
e7
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(-2*diagnosis... < 0        0      0.01    -0.02     0.03       0.79
##   Post.Prob Star
## 1      0.44
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# E8: FAB in COMP differs from FAB in BOTH
e8 = hypothesis(m.fab,
                "0 < 2*diagnosis1:cue1 + 2*diagnosis2:cue1 + 4*diagnosis3:cue1",
                alpha = 0.025)
e8
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis1... < 0    -0.01      0.01    -0.04     0.01       5.26
##   Post.Prob Star
## 1      0.84
## ---
```

Table 6: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	398	4.9	379	388	408	418
object	406	5.2	387	395	416	427
FAB	7.6	2.7	-2.9	2.1	13	17

```
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# extract predicted differences in ms instead of log data
df.new = df.fab %>%
  select(diagnosis, cue) %>%
  distinct() %>%
  mutate(
    condition = paste(diagnosis, cue, sep = "_")
  )
df.ms = as.data.frame(
  fitted(m.fab, summary = F,
              newdata = df.new %>% select(diagnosis, cue),
              re_formula = NA))
colnames(df.ms) = df.new$condition

# calculate our difference columns
df.ms = df.ms %>%
  mutate(
    COMP = rowMeans(select(., matches("COMP_.*")), na.rm = T),
    ADHD = rowMeans(select(., matches("ADHD_.*")), na.rm = T),
    ASD  = rowMeans(select(., matches("ASD_.*")), na.rm = T),
    BOTH = rowMeans(select(., matches("BOTH_.*")), na.rm = T),
    FAB  = rowMeans(select(., matches(".*_object")), na.rm = T) -
      rowMeans(select(., matches(".*_face")), na.rm = T),
    FAB_COMP = COMP_object - COMP_face,
    FAB_ADHD = ADHD_object - ADHD_face,
    FAB_ASD  = ASD_object  - ASD_face,
    FAB_BOTH = BOTH_object - BOTH_face,
    h1b  = ADHD - COMP,
    h1c  = ASD - COMP,
    h1d  = FAB_COMP - FAB_ASD,
    h1e  = FAB_ADHD - FAB_COMP,
    BOTH_COMP = BOTH - COMP
  )

vtable::st(df.ms %>%
  mutate(
    face   = rowMeans(select(., matches(".*_face")), na.rm = T),
    object = rowMeans(select(., matches(".*_object")), na.rm = T)
  ) %>% select(face, object, FAB),
  summ = c('mean(x)','sd(x)','min(x)','pctile(x)[2.5]','pctile(x)[97.5]','max(x)'))
```

As hypothesised, both autistic adults and adults with ADHD exhibited increased overall reaction times

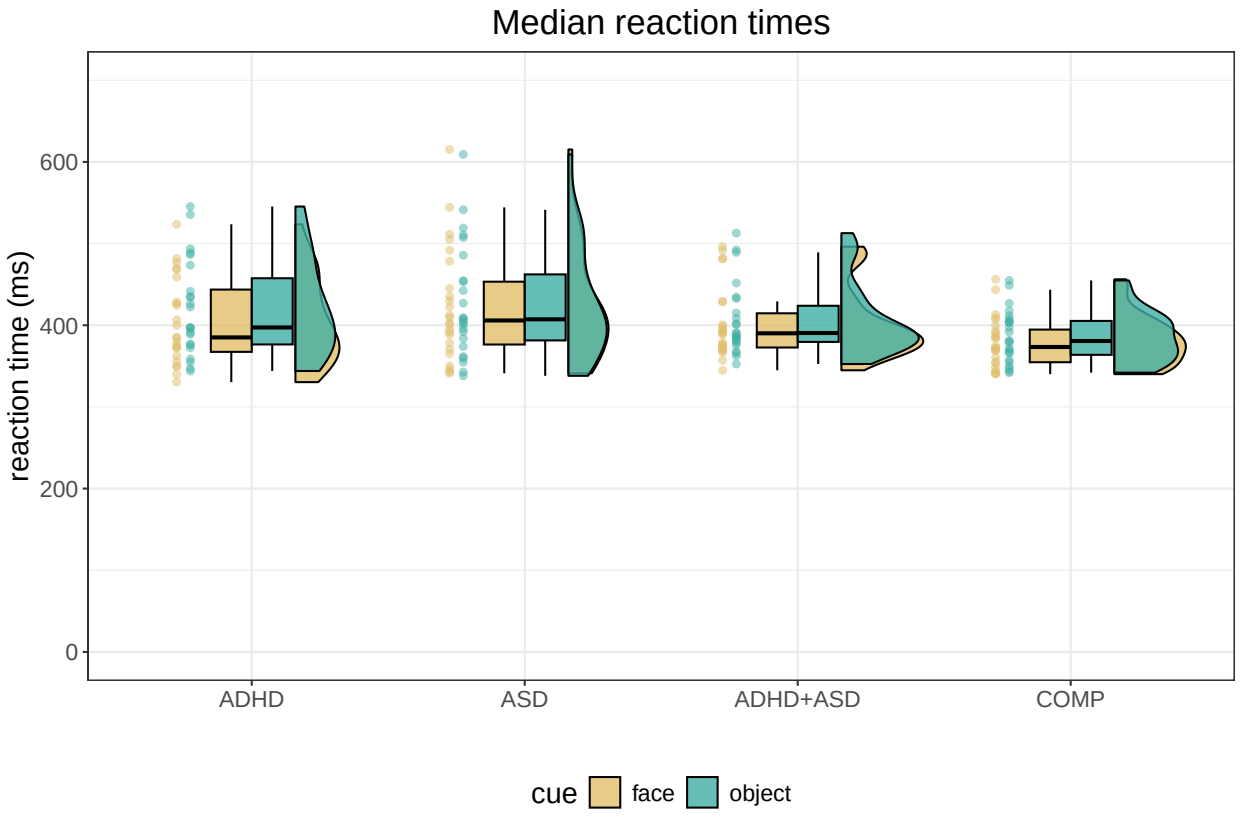
compared with the COMP group (COMP - ADHD: *estimate* = -0.12 [-0.2, -0.04], *posterior probability* = 99.29%; COMP - ASD: *estimate* = -0.14 [-0.22, -0.06], *posterior probability* = 99.78%). The model predicts that participants in the comparison group react 25.08ms [5.02, 45.75] faster than the participants in the ADHD group and 29.91ms [9.08, 50.83] faster than autistic participants. Additionally, the model predicts that the participants in the comparison group react 19.02ms [-1.55, 38.96] faster than adults in the ADHD+ASD group.

Our Bayesian linear mixed model with the median of correct reaction times as the outcome and diagnostic status, cue (face or object) and their interaction confirmed a face attention bias in our comparison group: COMP participants reacted faster in response to targets appearing on the side of the face compared to targets appearing on the side of the object (*estimate* = -0.03 [-0.06, -0.01], *posterior probability* = 98.72%). FAB was not credibly decreased in ASD participants compared to COMP participants (*estimate* = -0.02 [-0.04, 0.01], *posterior probability* = 87.34%). However, FAB was credibly higher in the ADHD than the COMP group (*estimate* = 0.03 [0, 0.06], *posterior probability* = 98.62%). Specifically, predicted reaction times based on the model estimate a FAB of 6.88ms [1.07, 12.92] in the COMP group, 14.47ms [8.08, 21.21] in the ADHD group, 4.37ms [-2.19, 10.97] in the ASD group as well as 4.57ms [-1.62, 10.71] in the ADHD+ASD group. These estimates are reflected in our exploration of FAB over all groups (*estimate* = -0.03 [-0.06, -0.01], *posterior probability* = 99.67%) as well as in the separate clinical groups with our model revealing a credible FAB effect in the ADHD (*estimate* = -0.06 [-0.09, -0.04], *posterior probability* = 100%) but not the ASD (*estimate* = -0.02 [-0.05, 0.01], *posterior probability* = 90.38%) and the ADHD+ASD group (*estimate* = -0.02 [-0.05, 0.01], *posterior probability* = 92.77%). Furthermore, FAB in the ASD and the ADHD+ASD group was equivalent ().

Plots

```
# overall median reaction times
df.fab %>%
  group_by(subID, diagnosis, cue) %>%
  summarise(
    rt.cor = mean(rt.cor, na.rm = T)
    ) %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD")
  ) %>%
  ggplot(aes(diagnosis, rt.cor, fill = cue, colour = cue)) + #
  geom_rain(rain.side = 'r',
boxplot.args = list(color = "black", outlier.shape = NA, show_guide = FALSE, alpha = .8),
violin.args = list(color = "black", outlier.shape = NA, alpha = .8),
boxplot.args.pos = list(
  position = ggpp::position_dodgenudge(x = 0, width = 0.3), width = 0.3
),
point.args = list(show_guide = FALSE, alpha = .5),
violin.args.pos = list(
  width = 0.6, position = position_nudge(x = 0.16)),
point.args.pos = list(position = ggpp::position_dodgenudge(x = -0.25, width = 0.1))) +
  ylim(0, 700) +
  scale_fill_manual(values = custom.col2) +
  scale_color_manual(values = custom.col2) +
  labs(title = "Median reaction times",
       x = "",
       y = "reaction time (ms)") +
  theme_bw() +
  theme(legend.position = "bottom",
        plot.title = element_text(hjust = 0.5),
```

```
        legend.direction = "horizontal",
        text = element_text(size = 15))
```




```
ggsave("Fig3_rts.pdf",
       units = "mm",
       width  = 170,
       height = 100,
       dpi    = 300)
```

S1.3 Explorative analysis of RTs considering number of saccades

Since saccadic behaviour may have influenced reaction times, we rerun the model concerning reaction times with a separate predictor coding the number of saccades of this stimulus pair.

```
# merge behaviour and saccades together
df.sac.fab = merge(df.fab.full,
                   df.sac %>% group_by(subID, diagnosis, trl) %>% summarise(n.sac = n()),
                   all.x = T) %>%
  # compute median rt.cor
  group_by(subID, diagnosis, cue, stm) %>%
  summarise(
    rt.cor = median(rt.cor, na.rm = T),
    n.sac  = sum(n.sac, na.rm = T)
  )
```

```
## `summarise()` has grouped output by 'subID', 'diagnosis'. You can override
```

```
## using the `.groups` argument.
## `summarise()` has grouped output by 'subID', 'diagnosis', 'cue'. You can
## override using the `.groups` argument.
```

```
# set the contrasts
contrasts(df.sac.fab$cue) = contr.sum(2)
contrasts(df.sac.fab$cue)
```

```
##        [,1]
## face      1
## object   -1
```

```
contrasts(df.sac.fab$diagnosis) = contr.sum(4)
contrasts(df.sac.fab$diagnosis)
```

```
##      [,1] [,2] [,3]
## ADHD    1    0    0
## ASD     0    1    0
## BOTH    0    0    1
## COMP   -1   -1   -1
```

```
# run the model > more iterations due to some suboptimal rhats in the first try
set.seed(1357)
m.rtsac = brm(rt.cor ~ diagnosis * cue + n.sac + (cue | subID) + (cue * diagnosis | stm),
            df.sac.fab, prior = priors,
            family = shifted_lognormal,
            iter = iter*2, warmup = warm*2,
            backend = "cmdstanr", threads = threading(8), file = "m_fab_sac"
            )
rstan::check_hmc_diagnostics(m.rtsac$fit)
```

```
##
## Divergences:
```

```
## 0 of 16000 iterations ended with a divergence.
```

```
##
## Tree depth:
```

```
## 0 of 16000 iterations saturated the maximum tree depth of 10.
```

```
##
## Energy:
```

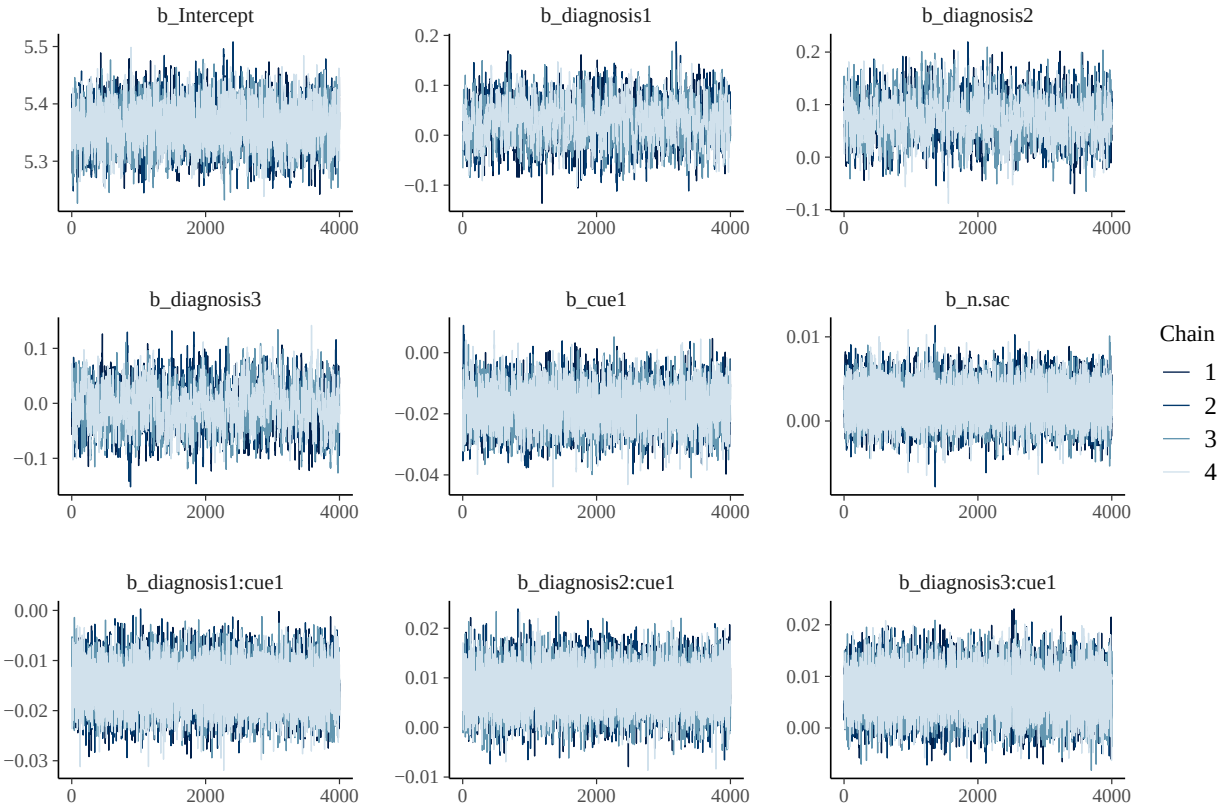
```
## E-BFMI indicated no pathological behavior.
```

```
# check that rhats are below 1.01
sum(brms::rhat(m.rtsac) >= 1.01, na.rm = T)
```

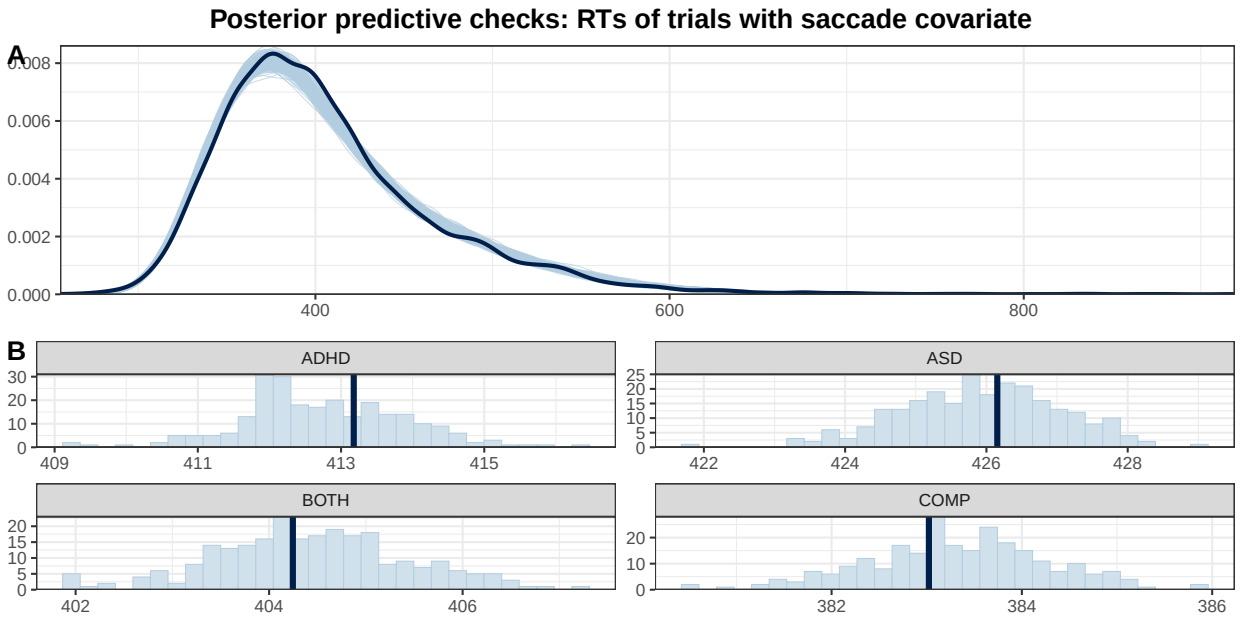
```
## [1] 0
```

```
# check the trace plots
post.draws = as_draws_df(m.rtsac)
mcmc_trace(post.draws, regex_pars = "^b_",
           facet_args = list(ncol = 3)) +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
```

```
## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```




```
# get posterior predictions
post.pred = posterior_predict(m.rtsac, ndraws = nsim)

# check the fit of the predicted data compared to the real data
p1 = pp_check(m.rtsac, ndraws = nsim) +
  theme_bw() + theme(legend.position = "none")

df.sac.fab = df.sac.fab %>% drop_na()

# distributions of means compared to the real values per group
p2 = ppc_stat_grouped(df.sac.fab$rt.cor, post.pred, df.sac.fab$diagnosis) +
  theme_bw() + theme(legend.position = "none")

p = ggarrange(p1, p2,
          nrow = 2, ncol = 1, labels = "AUTO")
annotate_figure(p,
                top = text_grob("Posterior predictive checks: RTs of trials with saccade covariate",
                face = "bold", size = 14))
```




```
# print a summary
summary(m.rtsac)
```

```
##  Family: shifted_lognormal
##   Links: mu = identity; sigma = identity; ndt = identity
## Formula: rt.cor ~ diagnosis * cue + n.sac + (cue | subID) + (cue * diagnosis | stm)
##    Data: df.sac.fab (Number of observations: 6768)
##   Draws: 4 chains, each with iter = 6000; warmup = 2000; thin = 1;
##          total post-warmup draws = 16000
##
## Multilevel Hyperparameters:
## ~stm (Number of levels: 36)
##                                     Estimate Est.Error l-95% CI u-95% CI Rhat
## sd(Intercept)                           0.03      0.00     0.02     0.04 1.00
## sd(cue1)                                0.03      0.00     0.03     0.05 1.00
## sd(diagnosis1)                          0.01      0.00     0.00     0.02 1.00
## sd(diagnosis2)                          0.00      0.00     0.00     0.01 1.00
## sd(diagnosis3)                          0.01      0.00     0.00     0.01 1.00
## sd(cue1:diagnosis1)                     0.00      0.00     0.00     0.01 1.00
## sd(cue1:diagnosis2)                     0.00      0.00     0.00     0.01 1.00
## sd(cue1:diagnosis3)                     0.01      0.00     0.00     0.01 1.00
## cor(Intercept,cue1)                    -0.32      0.15    -0.60    -0.00 1.00
## cor(Intercept,diagnosis1)              -0.13      0.28    -0.65     0.45 1.00
## cor(cue1,diagnosis1)                    0.00      0.28    -0.54     0.55 1.00
## cor(Intercept,diagnosis2)              -0.09      0.31    -0.65     0.53 1.00
## cor(cue1,diagnosis2)                   -0.07      0.31    -0.64     0.56 1.00
## cor(diagnosis1,diagnosis2)             -0.00      0.33    -0.62     0.63 1.00
## cor(Intercept,diagnosis3)               0.08      0.29    -0.51     0.62 1.00
## cor(cue1,diagnosis3)                    0.21      0.29    -0.43     0.71 1.00
## cor(diagnosis1,diagnosis3)             -0.15      0.33    -0.73     0.54 1.00
## cor(diagnosis2,diagnosis3)             -0.10      0.33    -0.70     0.56 1.00
## cor(Intercept,cue1:diagnosis1)          0.04      0.31    -0.56     0.62 1.00
## cor(cue1,cue1:diagnosis1)              -0.07      0.31    -0.63     0.54 1.00
## cor(diagnosis1,cue1:diagnosis1)         0.00      0.33    -0.62     0.63 1.00
```

```
## cor(diagnosis2,cue1:diagnosis1)          0.01      0.33    -0.62     0.64 1.00
## cor(diagnosis3,cue1:diagnosis1)         -0.04      0.33    -0.65     0.60 1.00
## cor(Intercept,cue1:diagnosis2)          -0.24      0.31    -0.76     0.42 1.00
## cor(cue1,cue1:diagnosis2)               -0.01      0.30    -0.58     0.56 1.00
## cor(diagnosis1,cue1:diagnosis2)          0.04      0.33    -0.59     0.65 1.00
## cor(diagnosis2,cue1:diagnosis2)          0.05      0.33    -0.59     0.67 1.00
## cor(diagnosis3,cue1:diagnosis2)         -0.06      0.33    -0.67     0.60 1.00
## cor(cue1:diagnosis1,cue1:diagnosis2)    -0.11      0.34    -0.72     0.58 1.00
## cor(Intercept,cue1:diagnosis3)          -0.11      0.30    -0.66     0.50 1.00
## cor(cue1,cue1:diagnosis3)               -0.18      0.30    -0.70     0.46 1.00
## cor(diagnosis1,cue1:diagnosis3)          0.06      0.32    -0.58     0.66 1.00
## cor(diagnosis2,cue1:diagnosis3)          0.08      0.33    -0.58     0.68 1.00
## cor(diagnosis3,cue1:diagnosis3)         -0.02      0.33    -0.65     0.61 1.00
## cor(cue1:diagnosis1,cue1:diagnosis3)    -0.09      0.34    -0.69     0.58 1.00
## cor(cue1:diagnosis2,cue1:diagnosis3)    -0.02      0.33    -0.63     0.61 1.00
##                                    Bulk_ESS Tail_ESS
## sd(Intercept)                          5427     8841
## sd(cue1)                               4975     8785
## sd(diagnosis1)                         4471     6339
## sd(diagnosis2)                         7691     8290
## sd(diagnosis3)                         5667     7105
## sd(cue1:diagnosis1)                    6625     8074
## sd(cue1:diagnosis2)                    7312     7797
## sd(cue1:diagnosis3)                    7569     8869
## cor(Intercept,cue1)                    3331     6448
## cor(Intercept,diagnosis1)             21004    11804
## cor(cue1,diagnosis1)                  24252    11892
## cor(Intercept,diagnosis2)             26451    11698
## cor(cue1,diagnosis2)                  28940    12033
## cor(diagnosis1,diagnosis2)            18957    13099
## cor(Intercept,diagnosis3)             23840    11742
## cor(cue1,diagnosis3)                  21027    10744
## cor(diagnosis1,diagnosis3)            12065    12836
## cor(diagnosis2,diagnosis3)            12939    13289
## cor(Intercept,cue1:diagnosis1)        27241    12327
## cor(cue1,cue1:diagnosis1)             27888    11914
## cor(diagnosis1,cue1:diagnosis1)       16607    13583
## cor(diagnosis2,cue1:diagnosis1)       13948    12579
## cor(diagnosis3,cue1:diagnosis1)       14351    13095
## cor(Intercept,cue1:diagnosis2)        21038    11053
## cor(cue1,cue1:diagnosis2)             24812    11038
## cor(diagnosis1,cue1:diagnosis2)       15771    13103
## cor(diagnosis2,cue1:diagnosis2)       14324    13425
## cor(diagnosis3,cue1:diagnosis2)       14336    13229
## cor(cue1:diagnosis1,cue1:diagnosis2)  10937    13282
## cor(Intercept,cue1:diagnosis3)        22736    11119
## cor(cue1,cue1:diagnosis3)             24013    11918
## cor(diagnosis1,cue1:diagnosis3)       17144    12753
## cor(diagnosis2,cue1:diagnosis3)       14349    13395
## cor(diagnosis3,cue1:diagnosis3)       14434    13178
## cor(cue1:diagnosis1,cue1:diagnosis3)  11799    13519
## cor(cue1:diagnosis2,cue1:diagnosis3)  12178    13171
##
## ~subID (Number of levels: 94)
```

```
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)           0.22      0.02     0.19     0.26 1.00     2188     4453
## sd(cue1)                0.02      0.00     0.01     0.02 1.00     7455     9127
## cor(Intercept,cue1)    -0.05      0.15    -0.34     0.24 1.00    13863    13088
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           5.36      0.04     5.29     5.43 1.00     2277     5948
## diagnosis1          0.03      0.04    -0.05     0.11 1.00     1144     2287
## diagnosis2          0.07      0.04    -0.00     0.15 1.00     1262     2630
## diagnosis3         -0.01      0.04    -0.08     0.07 1.00     1135     2355
## cue1               -0.02      0.01    -0.03    -0.01 1.00     3645     6361
## n.sac               0.00      0.00    -0.00     0.01 1.00    37709    11098
## diagnosis1:cue1    -0.02      0.00    -0.02    -0.01 1.00    12937    12763
## diagnosis2:cue1     0.01      0.00    -0.00     0.02 1.00    12764    12960
## diagnosis3:cue1     0.01      0.00    -0.00     0.02 1.00    12667    12837
##
## Further Distributional Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.13      0.00     0.13     0.14 1.00     9913    10935
## ndt     185.16      5.49   173.87   195.41 1.00    10117    10800
##
## Draws were sampled using sample(hmc). 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).
```

```
# H1a: FAB effect in COMP
h1a = hypothesis(m.rtsac,
                 "0 < 2*(diagnosis1:cue1 + diagnosis2:cue1 + diagnosis3:cue1 - cue1)")
h1a
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*(diagnosis... < 0    -0.03      0.02    -0.06    -0.01      83.66
##   Post.Prob Star
## 1      0.99    *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1b: ADHD slower than COMP
h1b = hypothesis(m.rtsac,
                 "0 < 2*diagnosis1 + diagnosis2 + diagnosis3")
h1b
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis1... < 0    -0.12      0.07    -0.23    -0.02      32.61
##   Post.Prob Star
## 1      0.97    *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
```

```
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1c: ASD slower than COMP
h1c = hypothesis(m.rtsac,
                 "0 < 2*diagnosis2 + diagnosis1 + diagnosis3")
h1c
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis2... < 0    -0.17      0.06    -0.28    -0.06     227.57
##   Post.Prob Star
## 1         1    *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# H1d: FAB in ASD decreased compared to COMP
h1d = hypothesis(m.rtsac,
                 "0 < 4*diagnosis2:cue1 + 2*diagnosis1:cue1 + 2*diagnosis3:cue1")
h1d
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(4*diagnosis2... < 0    -0.02      0.01    -0.04     0.01       6.86
##   Post.Prob Star
## 1      0.87
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

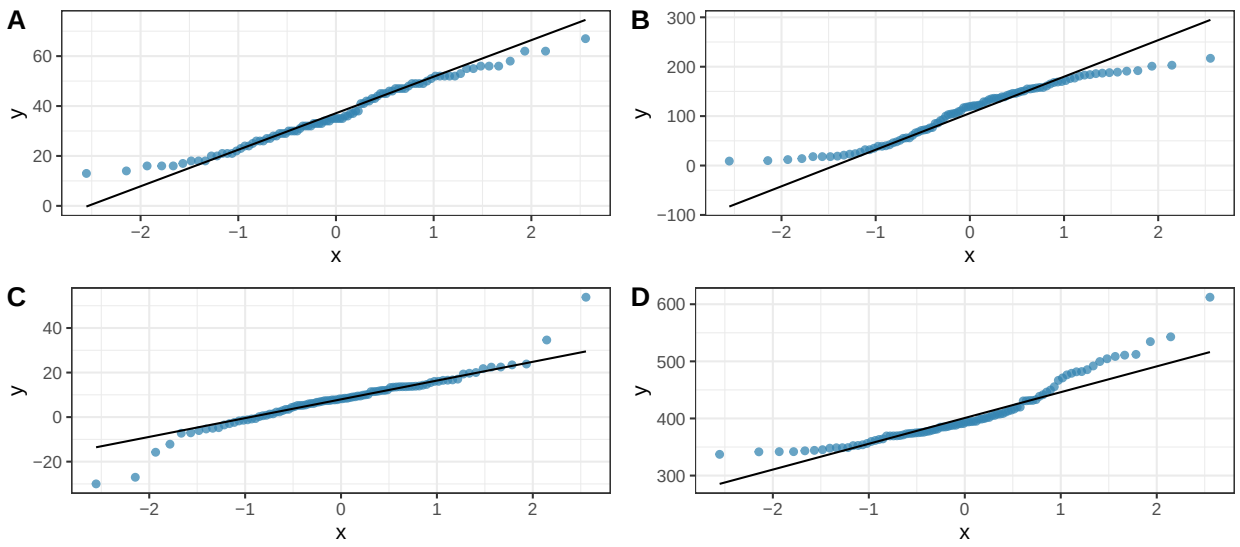
```
# H1e: FAB in ADHD differs from FAB in COMP (undirected)
h1e = hypothesis(m.rtsac,
                 "0 > 4*diagnosis1:cue1 + 2*diagnosis2:cue1 + 2*diagnosis3:cue1",
                 alpha = 0.025)
h1e
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(4*diagnosis1... > 0     0.03      0.01        0     0.06      73.07
##   Post.Prob Star
## 1      0.99    *
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

This model confirmed the same hypotheses.

S1.4 Explorative analysis of subject-specific FAB with overall RT, RADS and ASRS

```
# merge with the questionnaire values
df.que = df.fab.full %>%
  group_by(subID, diagnosis, stm, cue, ASRS_total, RAADS_total, adhd.meds) %>%
  # summarise the median reaction time for each stimulus pair
  summarise(
    rt.cor = median(rt.cor, na.rm = T)
  ) %>%
  pivot_wider(names_from = cue, values_from = rt.cor) %>%
  # calculate the fab purely based on reaction times
  mutate(
    fab     = object - face,
    overall = (object + face) / 2
  ) %>% group_by(subID, diagnosis, ASRS_total, RAADS_total, adhd.meds) %>%
  # calculate the mean FAB per person
  summarise(
    fab     = mean(fab),
    overall = mean(overall)
  ) %>% ungroup() %>%
  select(subID, diagnosis, overall, fab, ASRS_total, RAADS_total, adhd.meds)

# check normal distributions
p1 = ggplot(df.que, aes(sample = ASRS_total)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()
p2 = ggplot(df.que, aes(sample = RAADS_total)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()
p3 = ggplot(df.que, aes(sample = fab)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()
p4 = ggplot(df.que, aes(sample = overall)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()
ggarrange(p1, p2, p3, p4,
          nrow = 2, ncol = 2, labels = "AUTO")
```

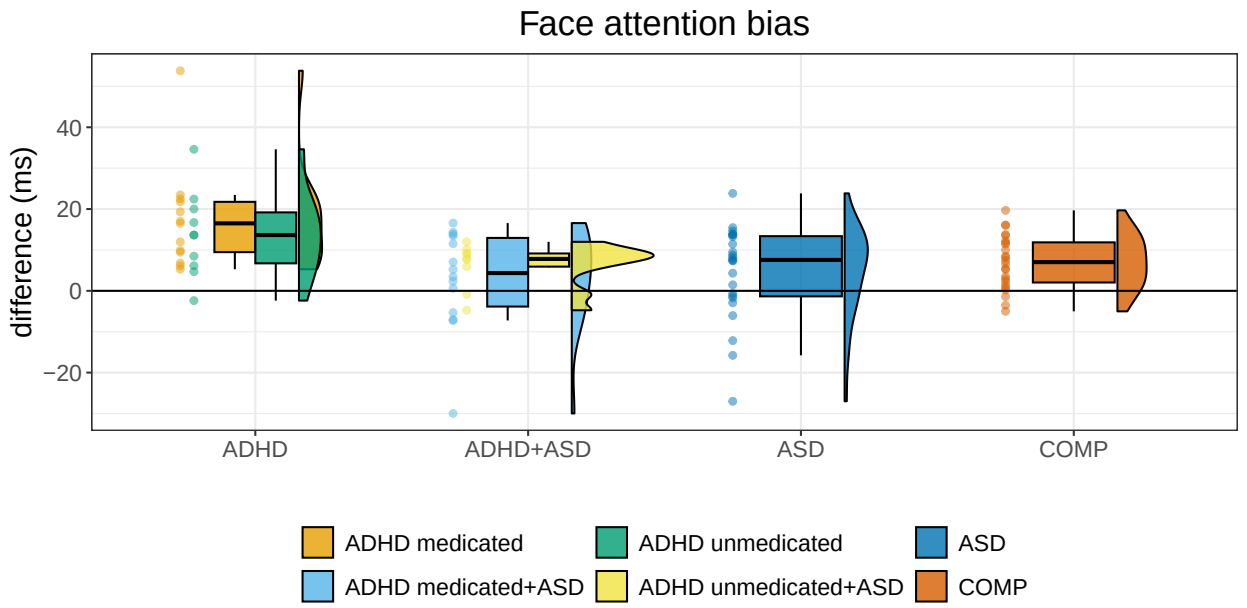



```
# do a Bayesian Spearman correlation: https://osf.io/j5wud
source("./helpers/rankBasedCommonFunctions.R")
source("./helpers/spearmanSampler.R")

# Default beta prior width is set to a = b = 1 for the sampler
if (file.exists("rho_ASRS.rds")) {
  rhoSamples.asrs = readRDS("rho_ASRS.rds")
} else {
  set.seed(5468)
  rhoSamples.asrs =
    spearmanGibbsSampler(xVals = df.que$ASRS_total,
                         yVals = df.que$fab,
                         nSamples = 5e3)
  saveRDS(rhoSamples.asrs, file = "rho_ASRS.rds")
}
if (file.exists("rho_RADS.rds")) {
  rhoSamples.rads = readRDS("rho_RADS.rds")
} else {
  set.seed(5468)
  rhoSamples.rads =
    spearmanGibbsSampler(xVals = df.que$RAADS_total,
                         yVals = df.que$fab,
                         nSamples = 5e3)
  saveRDS(rhoSamples.rads, file = "rho_RADS.rds")
}
if (file.exists("rho_RT.rds")) {
  rhoSamples.rt = readRDS("rho_RT.rds")
} else {
  set.seed(5478)
  rhoSamples.rt =
    spearmanGibbsSampler(xVals = df.que$overall,
                         yVals = df.que$fab,
                         nSamples = 5e3)
  saveRDS(rhoSamples.rt, file = "rho_RT.rds")
}
```

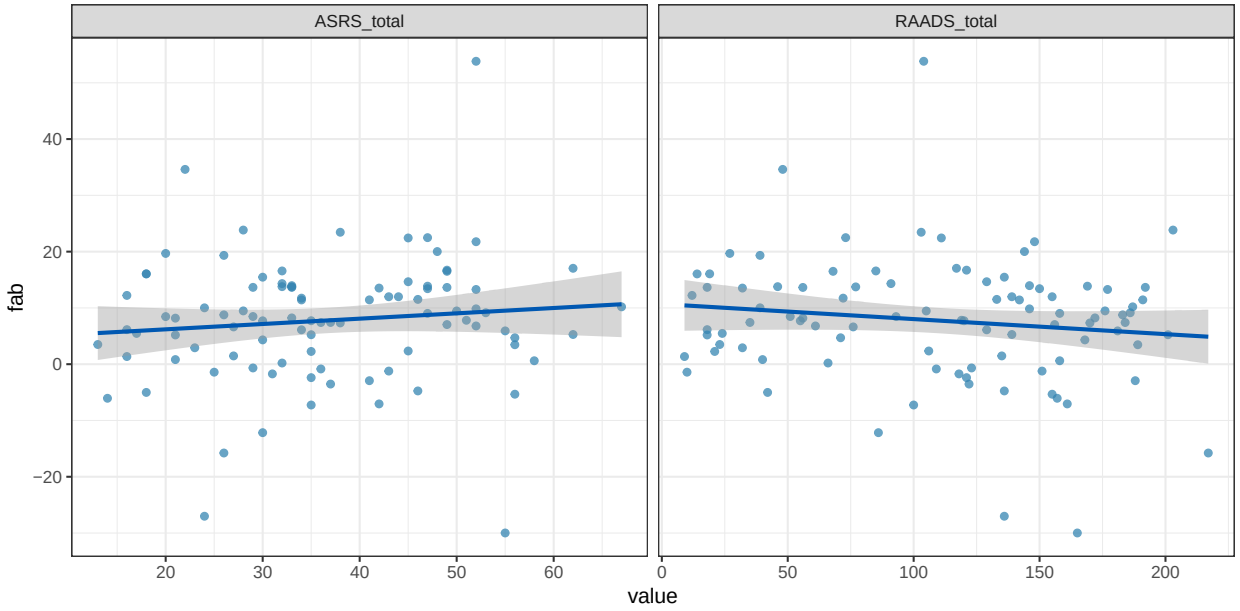
```
# give the posterior samples for rho to the function below to compute BF01
asrs.bf = computeBayesFactorOneZero(rhoSamples.asrs$rhoSamples,
                            whichTest = "Spearman",
                            priorParameter = 1)
rads.bf = computeBayesFactorOneZero(rhoSamples.rads$rhoSamples,
                            whichTest = "Spearman",
                            priorParameter = 1)
RT.bf = computeBayesFactorOneZero(rhoSamples.rt$rhoSamples,
                            whichTest = "Spearman",
                            priorParameter = 1)
```

Furthermore, Bayesian Spearman correlations revealed moderate evidence against associations between FAB and questionnaires assessing ASD (RADS: $\log(BF)$ = -1.63) or ADHD (ASRS: $\log(BF)$ = -1.61). Last, we explored whether FAB was associated with overall reaction times to assess whether attenuated FAB leads to better or worse task performance. A Bayesian Spearman correlation revealed moderate evidence against an association ($\log(BF)$ = -1.17).

```
# focus on the FAB effect
df.que %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD"),
    diagnosis = factor(diagnosis, levels = c("ADHD", "ADHD+ASD", "ASD", "COMP")),
    diagnosis_med = as.factor(case_when(
      adhd.meds & diagnosis == "ADHD" ~ "ADHD medicated",
      adhd.meds & diagnosis == "ADHD+ASD" ~ "ADHD medicated+ASD",
      diagnosis == "ADHD" ~ "ADHD unmedicated",
      diagnosis == "ADHD+ASD" ~ "ADHD unmedicated+ASD",
      T ~ diagnosis
    ))
  ) %>%
  ggplot(aes(diagnosis, fab, fill = diagnosis_med, colour = diagnosis_med)) + #
  geom_rain(rain.side = 'r',
boxplot.args = list(color = "black", outlier.shape = NA, show_guide = FALSE, alpha = .8),
violin.args = list(color = "black", outlier.shape = NA, alpha = .8),
boxplot.args.pos = list(
  position = ggpp::position_dodgenudge(x = 0, width = 0.3), width = 0.3
),
point.args = list(show_guide = FALSE, alpha = .5),
violin.args.pos = list(
  width = 0.6, position = position_nudge(x = 0.16)),
point.args.pos = list(position = ggpp::position_dodgenudge(x = -0.25, width = 0.1))) +
  geom_hline(yintercept = 0) +
  scale_fill_manual(values = custom.col) +
  scale_color_manual(values = custom.col) +
  labs(title = "Face attention bias",
       x = "",
       y = "difference (ms)") +
  theme_bw() +
  theme(legend.position = "bottom",
        plot.title = element_text(hjust = 0.5),
        legend.direction = "horizontal",
        text = element_text(size = 15),
        legend.title=element_blank())
```




```
ggsave("Fig4_FAB.pdf",
       units = "mm",
       width  = 170,
       height = 100,
       dpi    = 300)

# plot the associations
df.que %>%
  pivot_longer(cols = c(ASRS_total, RAADS_total), names_to = "questionnaire") %>%
  ggplot(., aes(y = fab, x = value)) +
  geom_point(colour = c_mid_highlight, alpha = 0.75) +
  geom_smooth(method = "lm",
              formula = y ~ x,
              colour = c_dark_highlight) +
  facet_grid(. ~ questionnaire, scale = "free_x") +
  theme_bw()
```



S1.5 Explorative analysis of errors

Last but not least, we are going to explore possible differences with regards to mean accuracies using a bernoulli distribution.

Next, we are going to explore possible differences with regards to accuracy. We use a bernoulli distribution to model the threshold between correct and incorrect trials. We computed the SBC outside of this script in batches to avoid running out of memory. Then, we combined it and load the results in here.

Simulation-based calibration

```
# figure out slopes for subject
kable(head(df.fab.full %>% count(subID, cue)))
```

subID	cue	n
1	face	216
1	object	216
2	face	216
2	object	216
3	face	216
3	object	216

```
kable(head(df.fab.full %>% count(stm, cue, diagnosis)))
```

stm	cue	diagnosis	n
1_10	face	ADHD	138
1_10	face	ASD	144
1_10	face	BOTH	138
1_10	face	COMP	144
1_10	object	ADHD	138

stm	cue	diagnosis	n
1_10	object	ASD	144

```
code = "FAB_err"

# increase iterations a bit to improve rhats
iter = 4000
warm = 2000

# code accuracy to track errors
df.fab.full = df.fab.full %>%
  mutate(
    error = if_else(acc,0,1)
  )

# set the formula
f.err = brms::bf(error ~ diagnosis * cue + (cue | subID) + (diagnosis * cue | stm) )

# set weakly informed priors
priors = c(
  prior(normal(6.0,   1.00), class = Intercept),
  prior(normal(1.0,   0.50), class = sd),
  prior(lkj(2),  class = cor),
  # no specific expectations for the rest of the effects
  prior(normal(0,     1.00), class = b)
)
```

```
# check if the SBC already exists
if (file.exists(file.path(cache_dir, sprintf("df_res_%s.rds", code)))) {
  # load in the resultsn of the SBC
  df.results = readRDS(file.path(cache_dir, sprintf("df_res_%s.rds", code)))
  df.backend = readRDS(file.path(cache_dir, sprintf("df_div_%s.rds", code)))
  dat        = readRDS(file.path(cache_dir, sprintf("dat_%s.rds", code)))
} else {
  # perform SBC
  gen = SBC_generator_brms(f.err, data = df.fab.full, prior = priors,
   thin = 50, warmup = 10000, refresh = 2000,
   generate_lp = TRUE, family = bernoulli, init = 0.1)
  bck = SBC_backend_brms_from_generator(gen, chains = 4, thin = 1,
    warmup = warm, iter = iter)
  if (!file.exists(file.path(cache_dir, sprintf("dat_%s.rds", code)))) {
    dat = generate_datasets(gen, nsim)
    saveRDS(dat, file.path(cache_dir, sprintf("dat_%s.rds", code)))
  } else {
    dat = readRDS(file.path(cache_dir, sprintf("dat_%s.rds", code)))
  }
  res = compute_SBC(dat,
        bck,
        cache_mode     = "results",
        cache_location = file.path(cache_dir, sprintf("res_%s", code)))
  df.results = res$stats
  df.backend = res$backend_diagnostics
  saveRDS(df.results, file = file.path(cache_dir, paste0("df_res_", code, ".rds")))
```

```
  saveRDS(df.backend, file = file.path(cache_dir, paste0("df_div_", code, ".rds")))
}
```

Looking at the rhats and divergent transitions shows that 0 of 250 simulations had at least one parameter that had an rhat of at least 1.05 and 2 had divergent samples. Therefore, we continue with this model and plot the simulated values to perform prior predictive checks.

```
# create a matrix out of generated data
dvname = gsub(" ", "", gsub("[\\|~].*", "", f.err)[1])
dvfakemat = matrix(NA, nrow(dat[['generated']][[1]]), length(dat[['generated']]))
for (i in 1:length(dat[['generated']])) {
  dvfakemat[,i] = dat[['generated']][[i]][[dvname]]
}
truePars = dat$variables

# compute one histogram per simulated data-set
options = c(0, 1)
histmat = matrix(NA, ncol = nrow(truePars), length(options))
for (i in 1:nrow(truePars)) {
  for (j in 1:length(options))
  {
    histmat[j,i] = sum(dvfakemat[,i] == options[j])
  }
}
# for each bin, compute quantiles across histograms
probs = seq(0.1, 0.9, 0.1)
quantmat= as.data.frame(matrix(NA, nrow=dim(histmat)[1], ncol = length(probs)))
names(quantmat) = paste0("p", probs)
for (i in 1:dim(histmat)[1]) {
  quantmat[i,] = quantile(histmat[i,], p = probs)
}
quantmat$x = c("error", "correct")
p0 = ggplot(data = quantmat, aes(x = x)) +
  geom_bar(aes(y = p0.9), fill = c_light, stat = "identity") +
  geom_bar(aes(y = p0.8), fill = c_light_highlight, stat = "identity") +
  geom_bar(aes(y = p0.7), fill = c_mid, stat = "identity") +
  geom_bar(aes(y = p0.6), fill = c_mid_highlight, stat = "identity") +
  geom_bar(aes(y = p0.5), fill = c_dark, stat = "identity") +
  labs(title = "Prior predictive distribution", y = "", x = "") +
  theme_bw()

# get simulation numbers with issues
check = merge(df.results %>%
    group_by(sim_id) %>% summarise(rhat = max(rhat, na.rm = T)) %>%
    filter(rhat >= 1.05),
  df.backend %>% filter(n_divergent > 0), all = T)

# plot SBC with functions from the SBC package focusing on population-level parameters
df.results.b = df.results %>%
  filter(substr(variable, 1, 2) == "b_") %>%
  filter(!(sim_id %in% check$sim_id))
p1 = plot_ecdf_diff(df.results.b) + theme_bw() + theme(legend.position = "none") +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
```

```
p2 = plot_rank_hist(df.results.b, bins = 20) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
p3 = plot_sim_estimated(df.results.b, alpha = 0.5) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))

prior_sd = setNames(c(1, 1, 1, # intercept and diagnosis
                      0.5, 0.5, 0.5, # emotions
                      1, 1, 1, 1, 1, 1), # interactions
                    unique(df.results.b$variable))

p4 = plot_contraction(df.results.b, prior_sd = prior_sd) + theme_bw() +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3))

p = ggarrange(p0, p1, p2, p3, p4,
              labels = "AUTO", ncol = 1, nrow = 5,
              heights = c(1, 2, 2, 2, 2))
annotate_figure(p,
                top = text_grob("Prior predictive checks and SBC",
                face = "bold", size = 14))
```

Everything looks good with the wider priors, so we continue and run the model.

Posterior predictive checks

As the next step, we fit the model, check whether there are divergence or rhat issues, and then check whether the chains have converged.

```
# fit the final model
set.seed(1234)
m.err = brm(f.err,
            df.fab.full, prior = priors,
            iter = iter, warmup = warm,
            family = "bernoulli",
            backend = "cmdstanr", threads = threading(8),
            file = "m_err",
            save_pars = save_pars(all = TRUE)
            )
rstan::check_hmc_diagnostics(m.err$fit)
```

```
##
## Divergences:
```

```
## 0 of 8000 iterations ended with a divergence.
```

```
##
## Tree depth:
```

```
## 0 of 8000 iterations saturated the maximum tree depth of 10.
```

```
##
## Energy:
```

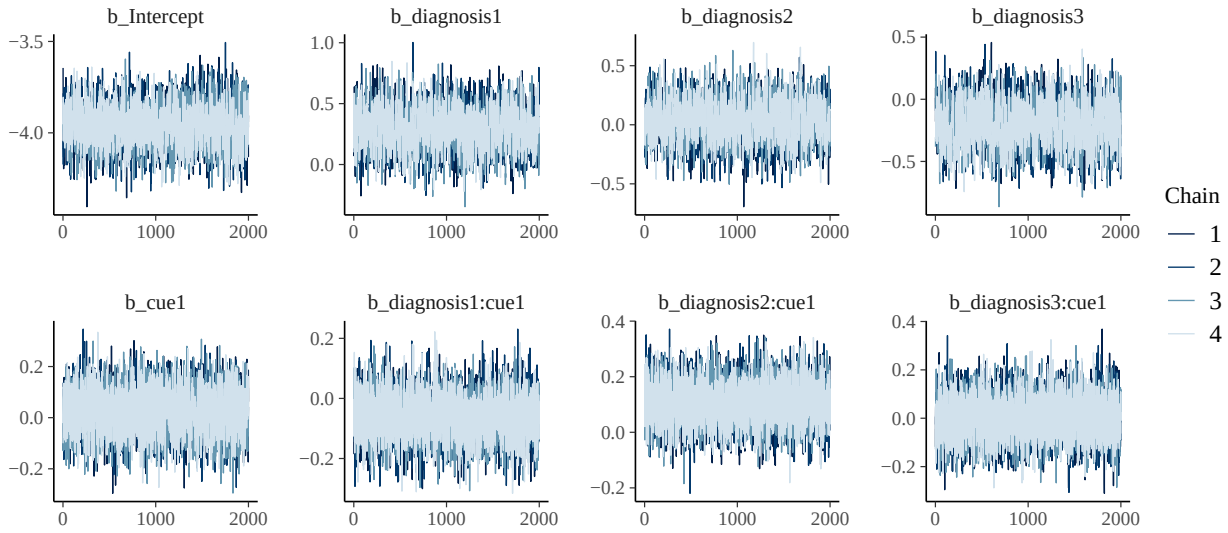
```
## E-BFMI indicated no pathological behavior.
```

```
# check that rhats are below 1.01
sum(brms::rhat(m.err) >= 1.01, na.rm = T)
```

```
## [1] 0
```

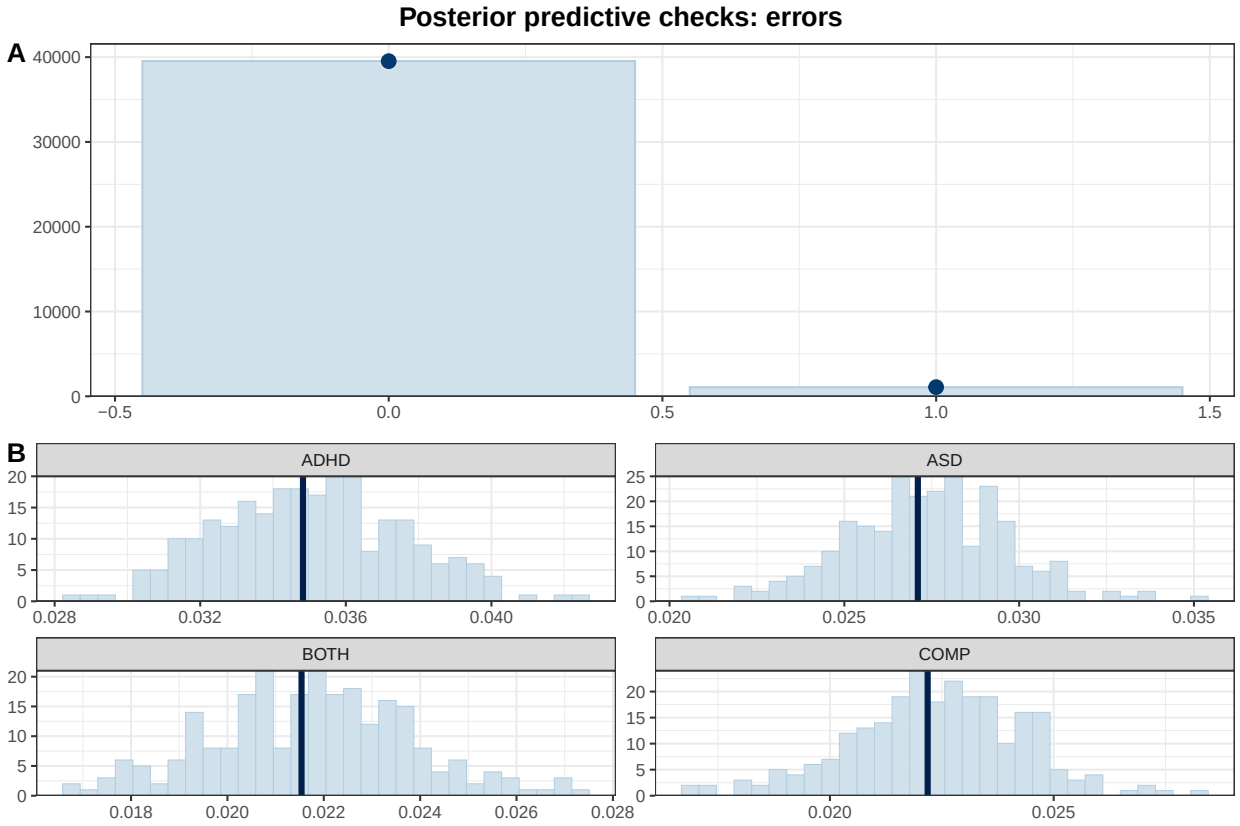
```
# check the trace plots
post.draws = as_draws_df(m.err)
mcmc_trace(post.draws, regex_pars = "^b_",
           facet_args = list(ncol = 4)) +
  scale_x_continuous(breaks=scales::pretty_breaks(n = 3)) +
  scale_y_continuous(breaks=scales::pretty_breaks(n = 3))
```

```
## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```



Again, we use the function brms::pp_check() with 250 draws to check whether the predicted data resembles the actual data as well as the ppc_stat_grouped function from the bayesplot package to check posterior fit for each diagnostic group separately. The model seems to be a good fit with the predicted data closely mirroring the real data.

```
# get posterior predictions
post.pred = posterior_predict(m.err, ndraws = nsim)

# check the fit of the predicted data compared to the real data
p1 = pp_check(m.err, ndraws = nsim, type = "bars") +
  theme_bw() + theme(legend.position = "none") + labs(y = "")

# distributions of means compared to the real values per group
p2 = ppc_stat_grouped(df.fab.full$error, post.pred, df.fab.full$diagnosis) +
  theme_bw() + theme(legend.position = "none")

p = ggarrange(p1, p2,
  nrow = 2, ncol = 1, labels = "AUTO")
annotate_figure(p,
                top = text_grob("Posterior predictive checks: errors",
                face = "bold", size = 14))
```



Our model fits the data very well.

Inferences

Now that we are convinced that we can trust our model, we have a look at its estimate and use the hypothesis function to perform explorative tests.

```
# print a summary
summary(m.err)
```

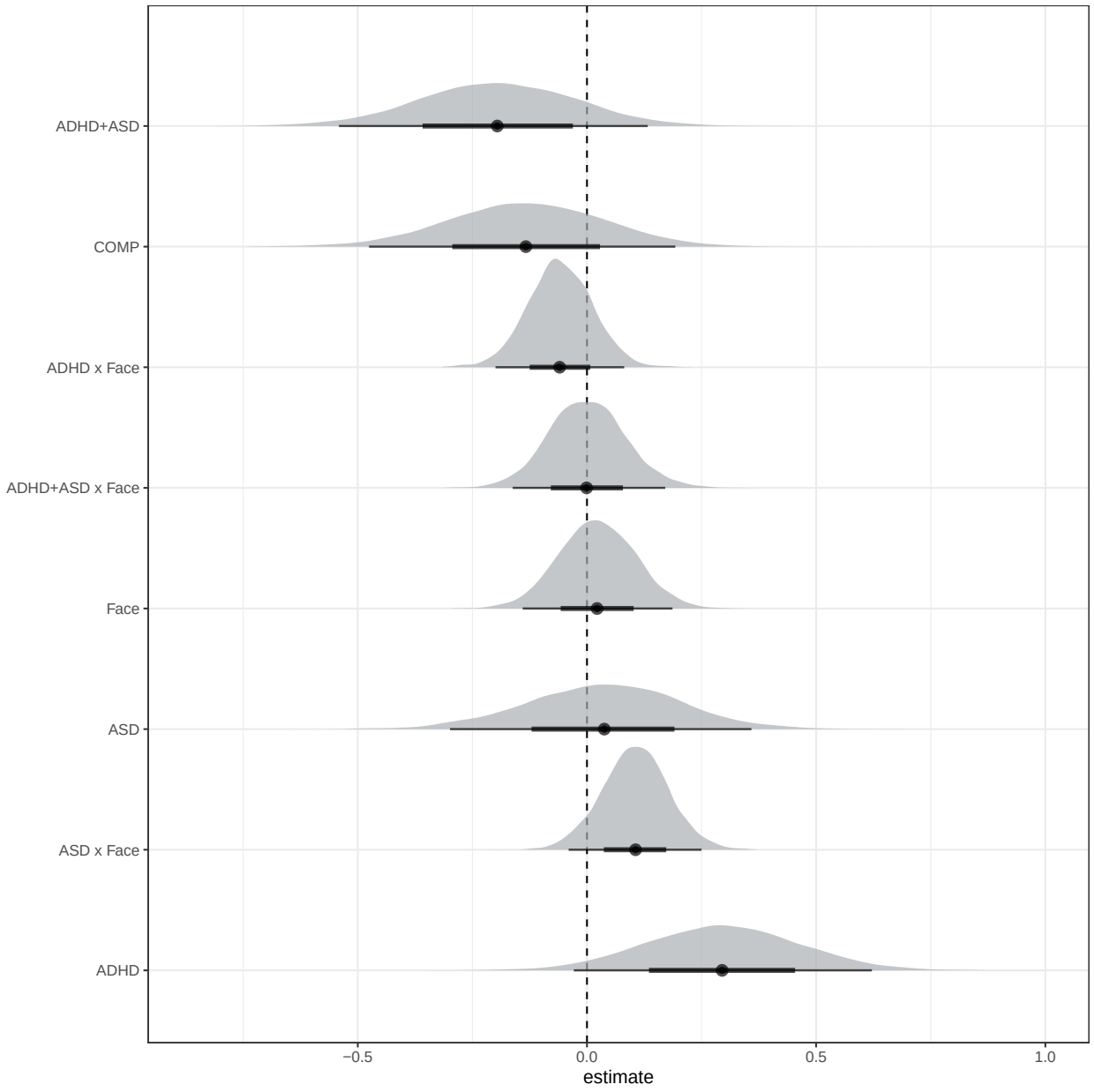
```
##  Family: bernoulli
##   Links: mu = logit
## Formula: error ~ diagnosis * cue + (cue | subID) + (diagnosis * cue | stm)
##    Data: df.fab.full (Number of observations: 40608)
##   Draws: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
##          total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~stm (Number of levels: 36)
##                                 Estimate Est.Error l-95% CI u-95% CI Rhat
## sd(Intercept)                       0.29      0.06     0.18     0.42 1.00
## sd(diagnosis1)                      0.11      0.07     0.01     0.25 1.00
## sd(diagnosis2)                      0.09      0.06     0.01     0.23 1.00
## sd(diagnosis3)                      0.10      0.07     0.00     0.26 1.00
## sd(cue1)                            0.41      0.07     0.30     0.55 1.00
## sd(diagnosis1:cue1)                 0.10      0.07     0.00     0.25 1.00
## sd(diagnosis2:cue1)                 0.08      0.06     0.00     0.22 1.00
## sd(diagnosis3:cue1)                 0.21      0.09     0.03     0.38 1.00
```

```
## cor(Intercept,diagnosis1)                -0.14      0.28    -0.64     0.43 1.00
## cor(Intercept,diagnosis2)                 0.14      0.29    -0.47     0.66 1.00
## cor(diagnosis1,diagnosis2)               -0.08      0.30    -0.64     0.51 1.00
## cor(Intercept,diagnosis3)                 0.06      0.29    -0.51     0.60 1.00
## cor(diagnosis1,diagnosis3)               -0.02      0.30    -0.60     0.56 1.00
## cor(diagnosis2,diagnosis3)               -0.07      0.31    -0.62     0.55 1.00
## cor(Intercept,cue1)                      -0.14      0.20    -0.51     0.25 1.00
## cor(diagnosis1,cue1)                      0.07      0.28    -0.47     0.60 1.01
## cor(diagnosis2,cue1)                      0.14      0.29    -0.46     0.65 1.00
## cor(diagnosis3,cue1)                     -0.01      0.28    -0.54     0.54 1.00
## cor(Intercept,diagnosis1:cue1)           -0.09      0.29    -0.62     0.49 1.00
## cor(diagnosis1,diagnosis1:cue1)           0.01      0.29    -0.55     0.58 1.00
## cor(diagnosis2,diagnosis1:cue1)          -0.01      0.30    -0.59     0.57 1.00
## cor(diagnosis3,diagnosis1:cue1)          -0.02      0.30    -0.57     0.56 1.00
## cor(cue1,diagnosis1:cue1)                -0.03      0.28    -0.57     0.54 1.00
## cor(Intercept,diagnosis2:cue1)           -0.09      0.29    -0.63     0.49 1.00
## cor(diagnosis1,diagnosis2:cue1)           0.06      0.30    -0.53     0.62 1.00
## cor(diagnosis2,diagnosis2:cue1)          -0.03      0.30    -0.58     0.56 1.00
## cor(diagnosis3,diagnosis2:cue1)           0.04      0.30    -0.55     0.61 1.00
## cor(cue1,diagnosis2:cue1)                -0.00      0.29    -0.57     0.54 1.00
## cor(diagnosis1:cue1,diagnosis2:cue1)     -0.06      0.31    -0.63     0.54 1.00
## cor(Intercept,diagnosis3:cue1)           -0.17      0.25    -0.64     0.35 1.00
## cor(diagnosis1,diagnosis3:cue1)          -0.01      0.29    -0.57     0.55 1.00
## cor(diagnosis2,diagnosis3:cue1)          -0.00      0.30    -0.57     0.57 1.00
## cor(diagnosis3,diagnosis3:cue1)           0.03      0.30    -0.54     0.59 1.00
## cor(cue1,diagnosis3:cue1)                 0.16      0.25    -0.34     0.62 1.00
## cor(diagnosis1:cue1,diagnosis3:cue1)      0.02      0.29    -0.53     0.58 1.00
## cor(diagnosis2:cue1,diagnosis3:cue1)     -0.00      0.30    -0.56     0.56 1.00
##                                       Bulk_ESS Tail_ESS
## sd(Intercept)                             3331     5105
## sd(diagnosis1)                            2577     2934
## sd(diagnosis2)                            2917     3935
## sd(diagnosis3)                            2595     3064
## sd(cue1)                                  4182     5911
## sd(diagnosis1:cue1)                       3358     4107
## sd(diagnosis2:cue1)                       3994     3354
## sd(diagnosis3:cue1)                       2482     2203
## cor(Intercept,diagnosis1)                 8818     5766
## cor(Intercept,diagnosis2)                 8891     5504
## cor(diagnosis1,diagnosis2)                6537     5896
## cor(Intercept,diagnosis3)                 9817     6004
## cor(diagnosis1,diagnosis3)                9427     6365
## cor(diagnosis2,diagnosis3)                6602     6202
## cor(Intercept,cue1)                       3286     4640
## cor(diagnosis1,cue1)                      1136     2520
## cor(diagnosis2,cue1)                      1059     1781
## cor(diagnosis3,cue1)                      1240     2554
## cor(Intercept,diagnosis1:cue1)            9979     5965
## cor(diagnosis1,diagnosis1:cue1)           8566     6095
## cor(diagnosis2,diagnosis1:cue1)           7508     5399
## cor(diagnosis3,diagnosis1:cue1)           6392     5813
## cor(cue1,diagnosis1:cue1)                10897     6192
## cor(Intercept,diagnosis2:cue1)           10303     6064
## cor(diagnosis1,diagnosis2:cue1)           8178     6098
```

```
## cor(diagnosis2,diagnosis2:cue1)          7641     6144
## cor(diagnosis3,diagnosis2:cue1)          7422     6547
## cor(cue1,diagnosis2:cue1)                9720     6039
## cor(diagnosis1:cue1,diagnosis2:cue1)     6110     6005
## cor(Intercept,diagnosis3:cue1)           6693     5359
## cor(diagnosis1,diagnosis3:cue1)          4803     5384
## cor(diagnosis2,diagnosis3:cue1)          4253     5924
## cor(diagnosis3,diagnosis3:cue1)          3807     5235
## cor(cue1,diagnosis3:cue1)                9371     6338
## cor(diagnosis1:cue1,diagnosis3:cue1)     4578     6707
## cor(diagnosis2:cue1,diagnosis3:cue1)     5120     6589
##
## ~subID (Number of levels: 94)
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)           0.86      0.08     0.70     1.03 1.00     2082     4075
## sd(cue1)                0.20      0.06     0.06     0.32 1.00     1735     1440
## cor(Intercept,cue1)     0.09      0.23    -0.37     0.53 1.00     5194     4798
##
## Regression Coefficients:
##                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept          -3.96      0.11    -4.17    -3.74 1.01     1638     3633
## diagnosis1          0.30      0.17    -0.03     0.62 1.00     1674     3067
## diagnosis2          0.04      0.17    -0.30     0.36 1.00     1635     2955
## diagnosis3         -0.20      0.17    -0.54     0.13 1.00     1604     2827
## cue1                0.02      0.08    -0.14     0.19 1.00     4409     5756
## diagnosis1:cue1    -0.06      0.07    -0.20     0.08 1.00     5509     5863
## diagnosis2:cue1     0.11      0.07    -0.04     0.25 1.00     5505     6178
## diagnosis3:cue1     0.00      0.08    -0.16     0.17 1.00     5826     5175
##
## Draws were sampled using sample(hmc). 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).
```

```r
# plot the posterior distributions
as_draws_df(m.err) %>%
  select(starts_with("b_")) %>%
  mutate(
    b_COMP     = - b_diagnosis1 - b_diagnosis2 - b_diagnosis3
  ) %>%
  pivot_longer(cols = starts_with("b_"), names_to = "coef", values_to = "estimate") %>%
  subset(!startsWith(coef, "b_Int")) %>%
  mutate(
    coef = substr(coef, 3, nchar(coef)),
    coef = str_replace_all(coef, ":", " x "),
    coef = str_replace_all(coef, "diagnosis1", "ADHD"),
    coef = str_replace_all(coef, "diagnosis2", "ASD"),
    coef = str_replace_all(coef, "diagnosis3", "ADHD+ASD"),
    coef = str_replace_all(coef, "cue1", "Face"),
    coef = fct_reorder(coef, desc(estimate))
  ) %>%
  group_by(coef) %>%
  mutate(
    cred = case_when(
      (mean(estimate) < 0 & quantile(estimate, probs = 0.975) < 0) |
```

```
      (mean(estimate) > 0 & quantile(estimate, probs = 0.025) > 0) ~ "credible",
    T ~ "not credible"
  )
) %>% ungroup() %>%
ggplot(aes(x = estimate, y = coef, fill = cred)) +
geom_vline(xintercept = 0, linetype = 'dashed') +
ggdist::stat_halfeye(alpha = 0.7) + ylab(NULL) + theme_bw() +
scale_fill_manual(values = c(c_light, c_dark)) + theme(legend.position = "none")
```




```
# COMP < ADHD
e1 = hypothesis(m.err, "0 < 2*diagnosis1 + diagnosis2 + diagnosis3", alpha = 0.025)
e1
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis1... < 0    -0.43      0.27    -0.98      0.1      16.78
##   Post.Prob Star
## 1      0.94
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# COMP < ASD
e2 = hypothesis(m.err, "0 < 2*diagnosis2 + diagnosis1 + diagnosis3", alpha = 0.025)
e2
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis2... < 0    -0.17      0.28    -0.72     0.37       2.71
##   Post.Prob Star
## 1      0.73
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# COMP < BOTH
e3 = hypothesis(m.err, "0 > 2*diagnosis3 + diagnosis1 + diagnosis2", alpha = 0.025)
e3
```

```
## Hypothesis Tests for class b:
##                 Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis3... > 0     0.06      0.28    -0.49     0.62       1.43
##   Post.Prob Star
## 1      0.59
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

```
# explore differences between cues
e4 = hypothesis(m.err, "0 > 2*cue1", alpha = 0.025)
e4
```

```
## Hypothesis Tests for class b:
##         Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob
## 1 (0)-(2*cue1) > 0    -0.04      0.17    -0.37     0.28       0.66       0.4
##   Star
## 1
## ---
## 'CI': 95%-CI for one-sided and 97.5%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 97.5%;
## for two-sided hypotheses, the value tested against lies outside the 97.5%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

Table 9: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	0.02	0.0027	0.012	0.015	0.025	0.031
object	0.019	0.0027	0.012	0.014	0.025	0.03
FAB	-0.00077	0.0032	-0.013	-0.0075	0.0052	0.012

```
# extract predicted differences
df.new = df.fab.full %>%
  select(diagnosis, cue) %>%
  mutate(
    condition = paste0(diagnosis, '_', cue)
  ) %>%
  distinct()
df.ms = as.data.frame(
  fitted(m.err, summary = F,
               newdata = df.new,
               re_formula = NA))
colnames(df.ms) = df.new$condition

vtable::st(df.ms %>%
  mutate(
    face   = rowMeans(select(., matches(".*_face")), na.rm = T),
    object = rowMeans(select(., matches(".*_object")), na.rm = T),
    FAB    = object - face
  ) %>% select(face, object, FAB),
  summ = c('mean(x)','sd(x)','min(x)','pctile(x)[2.5]','pctile(x)[97.5]','max(x)'))
```

```
# print grand average of accuracies
kable(df.fab.full %>%
        group_by(subID, diagnosis, cue) %>%
        summarise(error = 100*mean(error, na.rm = T)) %>%
        group_by(diagnosis, cue) %>%
        summarise(error_rates = mean(error, na.rm = T), se = sd(error, na.rm = T)/sqrt(n())))
```

diagnosis	cue	error_rates	se
ADHD	face	3.381642	0.9681639
ADHD	object	3.582931	0.8948533
ASD	face	3.067130	0.5572113
ASD	object	2.353395	0.4132575
BOTH	face	2.153784	0.3500122
BOTH	object	2.153784	0.4112214
COMP	face	2.160494	0.4092448
COMP	object	2.276235	0.4307397

Accuracies were generally high, with a total of 2.64% inaccurate responses across diagnostic groups. The explorative analysis of the error rates revealed no credible differences between any of the diagnostic groups and no credible difference between cues (see supplementary materials).

Plots

```
# overall accuracies
df.fab.full %>%
        group_by(subID, diagnosis, cue) %>%
        summarise(error = 100*mean(error, na.rm = T)) %>%
  ggplot(aes(diagnosis, error, fill = cue, colour = cue)) + #
  geom_rain(rain.side = 'r',
boxplot.args = list(color = "black", outlier.shape = NA, show_guide = FALSE, alpha = .8),
violin.args = list(color = "black", outlier.shape = NA, alpha = .8),
boxplot.args.pos = list(
  position = ggpp::position_dodgenudge(x = 0, width = 0.3), width = 0.3
),
point.args = list(show_guide = FALSE, alpha = .5),
violin.args.pos = list(
  width = 0.6, position = position_nudge(x = 0.16)),
point.args.pos = list(position = ggpp::position_dodgenudge(x = -0.25, width = 0.1))) +
  ylim(0, 25) +
  scale_fill_manual(values = custom.col2) +
  scale_color_manual(values = custom.col2) +
  labs(title = "Mean error rates", x = "", y = "percent") +
  theme_bw() +
  theme(legend.position = "bottom",
        plot.title = element_text(hjust = 0.5),
        legend.direction = "horizontal",
        text = element_text(size = 15))
```