

Supplementary materials

Comparison of face attention bias in adults with ASD, ADHD or double diagnosis ADHD+ASD

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Contents

1	Introduction	1
1.1	Some general settings	1
1.2	Package versions	1
1.3	General info	2
1.4	Preparation and group comparisons	2
2	Reaction times	8
2.1	Full model	8
2.2	Aggregated model	17
2.3	Plots	35
3	Explorative analysis of RTs considering number of saccades	36
4	Explorative analysis of subject-specific FAB	42
4.1	Overall RT, RADS and ASRS	42
4.2	Gender	47
4.3	FAB as percentage of total reaction time	48
5	Explorative analysis of errors	50
5.1	Simulation-based calibration	50
5.2	Posterior predictive checks	52
5.3	Inferences	54
5.4	Plots	60
6	Summary table	61
7	Preparation for eye-tracking analysis	62
8	Number of saccades towards face during trial	66
8.1	Specify the model	66
8.2	Simulation-based calibration	66
8.3	Prior predictive checks	67
8.4	Computational faithfulness and model sensitivity	68
8.5	Posterior predictive checks	71
8.6	Inferences	73
8.7	Plots	77
9	Latencies of target-elicited saccades	78
9.1	Full model	78
9.2	Aggregated model	85
10	Correlation with reaction times: number of saccades	97
11	Exploration: cue-elicited saccades	99
11.1	Posterior predictive checks	100
11.2	Inferences	102

11.3 Plots	105
12 Exploration: Latencies of cue-elicited saccades	106
12.1 Model	106
12.2 Inferences	109
12.3 Plots	112
13 Exploration: Dwell times starting within cue-elicited saccade window	113
13.1 Model	113
13.2 Inferences	116
13.3 Plots	119

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.

1.1 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)
```

1.2 Package versions

The following packages are used in this RMarkdown file:

```
## [1] "R version 4.5.1 (2025-06-13)"

## [1] "knitr version 1.50"
## [1] "ggplot2 version 3.5.2"
## [1] "brms version 2.22.0"
## [1] "designr version 0.1.13"
## [1] "bridgesampling version 1.1.2"
## [1] "tidyverse version 2.0.0"
## [1] "ggpubr version 0.6.1"
## [1] "vtable version 1.4.8"
## [1] "ggrain version 0.0.4"
## [1] "bayesplot version 1.13.0"
## [1] "SBC version 0.3.0.9000"
## [1] "rstatix version 0.7.2"
## [1] "flextable version 0.9.9"
## [1] "officer version 0.6.10"
## [1] "BayesFactor version 0.9.12.4.7"
```

```
## [1] "effectsize version 1.0.1"
## [1] "bayestestR version 0.16.1"
```

1.3 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 predictive checks and in some cases simplify the model by aggregating values to improve posterior fit.

1.4 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_cenraXX.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, change in diagnosis)
  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()

  # load the behavioral data and merge with group
  df.fab = merge(df.sub %>% select(subID, diagnosis,
                                      RAADS_total, ASRS_total, adhd.meds, gender),
                 readRDS(file = paste0(dt.path, '/df_FAB.RDS'))) %>%
    mutate_if(is.character, as.factor) %>%
    filter(!(subID %in% exc))
  df.exp = merge(df.sub %>% select(subID, diagnosis,
                                      RAADS_total, ASRS_total, adhd.meds, gender),
```

```

    readRDS(file = paste0(dt.expl0, '/df_FAB.RDS'))) %>%
  mutate_if(is.character, as.factor) %>%
  filter(!(subID %in% exc))

# 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.expl0, "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.numeric(subID)
  )
df.exp = df.exp %>%
  mutate(
    PID = subID,
    subID = as.factor(as.numeric(subID) + max(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)

# 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")

```

```

# we add this information to our demographics table
df.demo = data.frame(
  measurement = "Gender",
  ADHD         = sprintf("%.0f - %.0f - %.0f",
                        tb.gen["fem","ADHD"],
                        tb.gen["mal","ADHD"],
                        tb.gen["dan","ADHD"]),
  `ADHD+ASD`   = sprintf("%.0f - %.0f - %.0f",
                        tb.gen["fem","BOTH"],
                        tb.gen["mal","BOTH"],
                        tb.gen["dan","BOTH"]),
  ASD          = sprintf("%.0f - %.0f - %.0f",
                        tb.gen["fem","ASD"],
                        tb.gen["mal","ASD"],
                        tb.gen["dan","ASD"]),
  COMP         = sprintf("%.0f - %.0f - %.0f",
                        tb.gen["fem","COMP"],
                        tb.gen["mal","COMP"],
                        tb.gen["dan","COMP"]),
  bf.log       = ct.full@bayesFactor[["bf"]]
)

# then, we save some more gender information in a table in case we need it
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))

# convert the measures to long which we include in the participant table
df.sublng = df.sub %>%
  # rename some of the variables
  rename(
    "RADS-R" = "RAADS_total",
    "ASRS-v1.1" = "ASRS_total",
    "Age" = "age",
    "IQ estimate" = "iq",
    "Education" = "edu"
  ) %>%
  select(diagnosis, Age, `IQ estimate`, `ASRS-v1.1`, `RADS-R`, Education) %>%
  pivot_longer(cols = where(is.numeric)) %>%
  mutate_if(is.character, as.factor)

# initialise the data frame for posthoc tests
df.post = data.frame()

# now we loop through our measurements to create our demographics table
for (m in unique(df.sublng$name)) {
  # select the relevant part of df.sub
  df.rel = df.sublng %>% filter(name == m)
  # check which of the group's data is not normally distributed
  df.sht = df.rel %>%
    group_by(diagnosis) %>%
    shapiro_test(value) %>%
    filter(p < 0.05)
  # if more than zero is not normally distributed...
}

```

```

if (nrow(df.sht) > 0) {
  # rank transform the data
  df.rel = df.rel %>% ungroup() %>% mutate(value = rank(value))
}

# compute the ANOVA
aov = anovaBF(value ~ diagnosis, data = df.rel)
# get back the original, untransformed values
df.rel = df.sublng %>% filter(name == m)
# put all the information into the demographics table
df.demo = rbind(df.demo,
  data.frame(
    measurement = m,
    ADHD = sprintf("%.2f ±%.2f (%.0f to %.0f)",
      # ignore NAs because edu missing for one person
      mean(df.rel[df.rel$diagnosis == "ADHD",]$value, na.rm = T),
      sd(df.rel[df.rel$diagnosis == "ADHD",]$value, na.rm = T) /
        sqrt(sum(df.rel$diagnosis == "ADHD")),
      min(df.rel[df.rel$diagnosis == "ADHD",]$value, na.rm = T),
      max(df.rel[df.rel$diagnosis == "ADHD",]$value, na.rm = T)
    ),
    `ADHD+ASD` = sprintf("%.2f ±%.2f (%.0f to %.0f)",
      mean(df.rel[df.rel$diagnosis == "BOTH",]$value),
      sd(df.rel[df.rel$diagnosis == "BOTH",]$value) /
        sqrt(sum(df.rel$diagnosis == "BOTH")),
      min(df.rel[df.rel$diagnosis == "BOTH",]$value),
      max(df.rel[df.rel$diagnosis == "BOTH",]$value)
    ),
    ASD = sprintf("%.2f ±%.2f (%.0f to %.0f)",
      mean(df.rel[df.rel$diagnosis == "ASD",]$value),
      sd(df.rel[df.rel$diagnosis == "ASD",]$value) /
        sqrt(sum(df.rel$diagnosis == "ASD")),
      min(df.rel[df.rel$diagnosis == "ASD",]$value),
      max(df.rel[df.rel$diagnosis == "ASD",]$value)
    ),
    COMP = sprintf("%.2f ±%.2f (%.0f to %.0f)",
      mean(df.rel[df.rel$diagnosis == "COMP",]$value),
      sd(df.rel[df.rel$diagnosis == "COMP",]$value) /
        sqrt(sum(df.rel$diagnosis == "COMP")),
      min(df.rel[df.rel$diagnosis == "COMP",]$value),
      max(df.rel[df.rel$diagnosis == "COMP",]$value)
    ),
    bf.log = aov@bayesFactor[["bf"]]
  ))
}

# next, we want to check whether there are group differences
if (abs(exp(aov@bayesFactor$bf)) > 3) {
  # do the group comparisons
  aov.ADHDvASD = anovaBF(value ~ diagnosis,
    data = df.rel %>% filter(diagnosis %in% c("ADHD", "ASD")))
  aov.ADHDvBOTH = anovaBF(value ~ diagnosis,
    data = df.rel %>% filter(diagnosis %in% c("ADHD", "BOTH")))
  aov.ADHDvCOMP = anovaBF(value ~ diagnosis,
    data = df.rel %>% filter(diagnosis %in% c("ADHD", "COMP")))
  aov.ASDvBOTH = anovaBF(value ~ diagnosis,
    data = df.rel %>% filter(diagnosis %in% c("ASD", "BOTH")))
  aov.ASDvCOMP = anovaBF(value ~ diagnosis,
    data = df.rel %>% filter(diagnosis %in% c("ASD", "COMP")))
  aov.BOTHvCOMP = anovaBF(value ~ diagnosis,
    data = df.rel %>% filter(diagnosis %in% c("BOTH", "COMP")))
}

```

```

# put into the posthoc data frame
df.post = rbind(df.post,
  data.frame(
    measurement = m,
    ADHDvASD = aov.ADHDrvASD@bayesFactor[["bf"]],
    ADHDvBOTH = aov.ADHDrvBOTH@bayesFactor[["bf"]],
    ADHDvCOMP = aov.ADHDrvCOMP@bayesFactor[["bf"]],
    ASDvBOTH = aov.ASDvBOTH@bayesFactor[["bf"]],
    ASDvCOMP = aov.ASDvCOMP@bayesFactor[["bf"]],
    BOTHvCOMP = aov.BOTHvCOMP@bayesFactor[["bf"]]
  ))
}

}

# save the demographics and the posthoc table as word documents
read_docx() %>%
  body_add_table(df.demo %>% arrange(measurement) %>%
    mutate(bf.log =
      if_else(
        bf.log > log(3),
        sprintf("%.3f*", bf.log),
        sprintf("%.3f", bf.log)))) %>%
  print(target = "FAB_demo.docx")
read_docx() %>%
  body_add_table(df.post %>%
    mutate_if(is.numeric,
      ~ifelse(.>log(3), sprintf("%.3f*", .), sprintf("%.3f", .)))) %>%
  print(target = "FAB_post.docx")

# check how many of each group are above threshold for asrs and rads
tb.screen = xtabs(~ diagnosis + screening,
  data = df.sub %>%
    select(diagnosis, ASRS_screen, RAADS_total) %>%
    mutate(
      screening = case_when(
        ASRS_screen >= 4 & RAADS_total > 81 ~ "screenBOTH",
        ASRS_screen >= 4 & RAADS_total <= 81 ~ "screenADHD",
        ASRS_screen < 4 & RAADS_total <= 81 ~ "screenNone",
        ASRS_screen < 4 & RAADS_total > 81 ~ "screenASD"
      )
    ))
}

# save it all
save(df.fab, df.sac, df.exp, ct.full, ct.mf, df.exc, tb.screen,
  df.nosac, gen.desc, tb.gen, 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)
# as well as change in diagnosis
kable(df.exc)

```

diagnosis	n
ADHD	1

diagnosis	n
ASD	2
BOTH	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	23
BOTH	21	22
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 how many people are above threshold for clinical self assessment
kable(tb.screen)
```

	screenADHD	screenASD	screenBOTH	screenNone
ADHD	4	2	11	6
ASD	1	16	5	1
BOTH	0	8	14	0
COMP	1	3	0	20

```
# 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) -4.020544      0 Mon Jul 14 12:30:52 2025 30c72a3236db
# based on female and male participants only
ct.mf@bayesFactor
```

```
##                                bf error                  time          code
## Non-indep. (a=1) -2.43588      0 Mon Jul 14 12:30:52 2025 30c721d9416c5
```

```

# 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

```

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).

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.

2.1 Full model

2.1.1 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) )

# 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.

```

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

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

# compute one histogram per simulated data-set
binwidth = 20
breaks = seq(0, max(dvcfakemat, na.rm=T) + binwidth, binwidth)
histmat = matrix(NA, ncol = length(dat), nrow = length(breaks)-1)
for (i in 1:nrow(truePars)) {
  histmat[,i] = hist(dvcfakemat[,i], breaks = breaks, plot = F)$counts
}

```

```

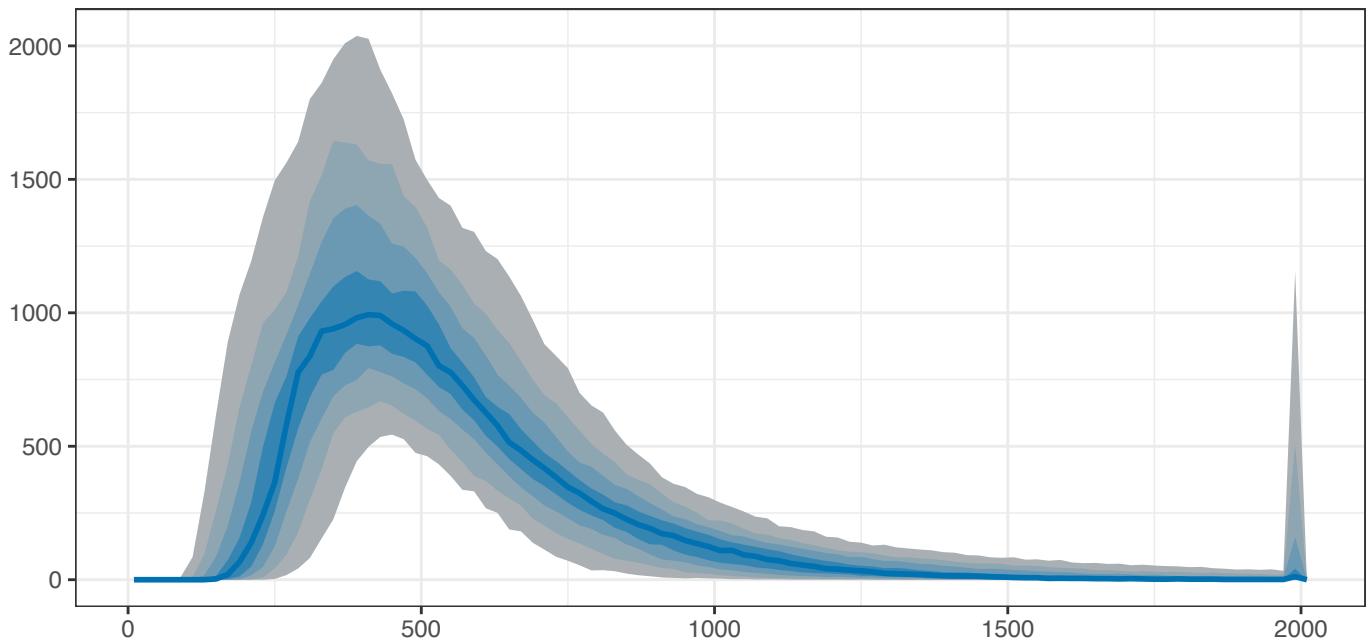
# for each bin, compute quantiles across histograms
probs = seq(0.1, 0.9, 0.1)
quantmat= as.data.frame(matrix(NA, nrow=dim(histmat)[1], ncol = length(probs)))
names(quantmat) = paste0("p", probs)
for (i in 1:dim(histmat)[1]) {
  quantmat[i,] = quantile(histmat[i,], p = probs)
}
quantmat$x = breaks[2:length(breaks)] - 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))

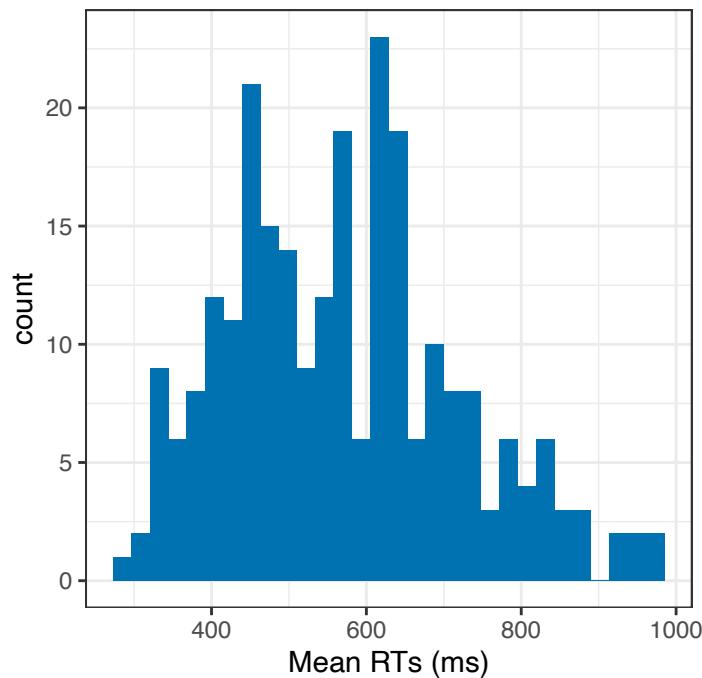
```

Prior predictive checks: reaction times

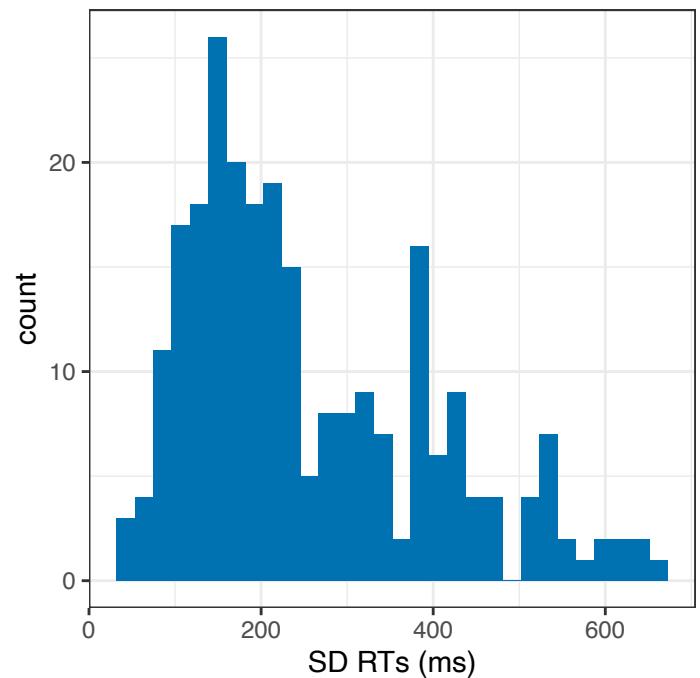
A Distribution of simulated discriminations



B Means of simulated RTs



C SDs of simulated RTs



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))
```

```

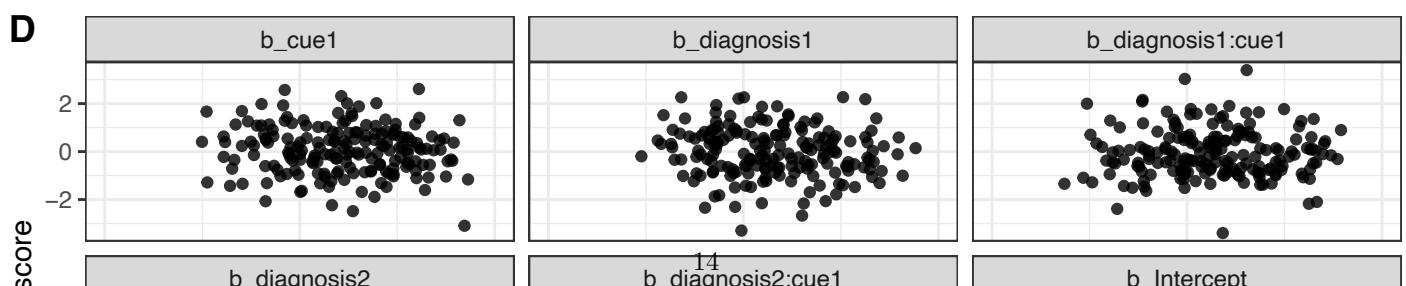
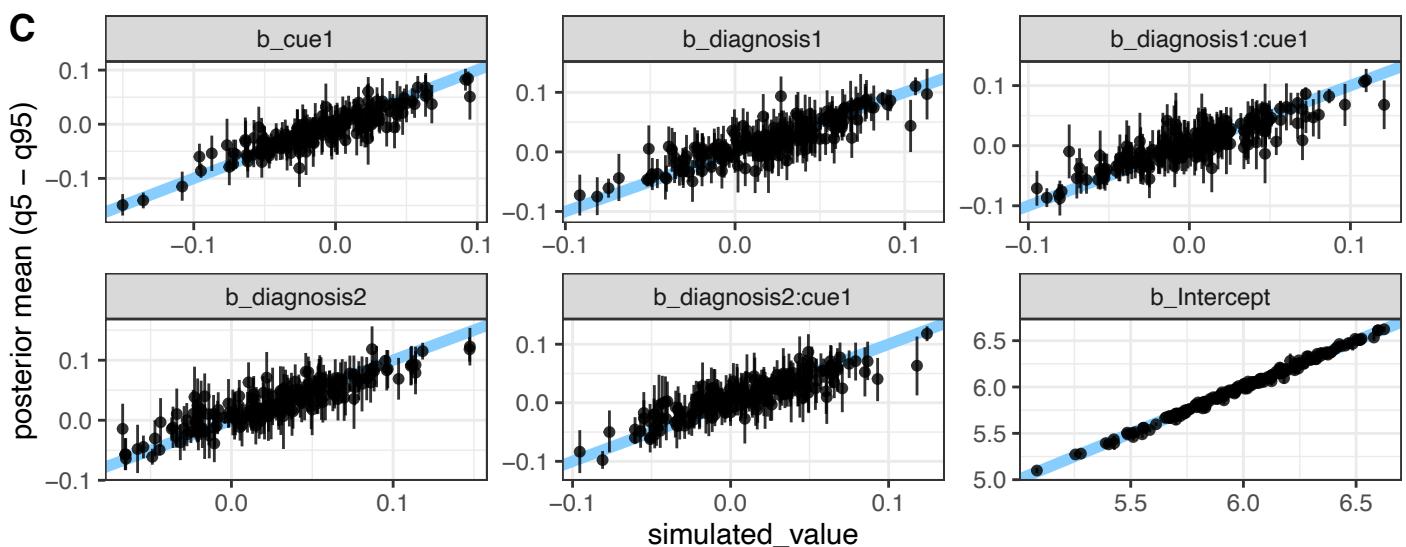
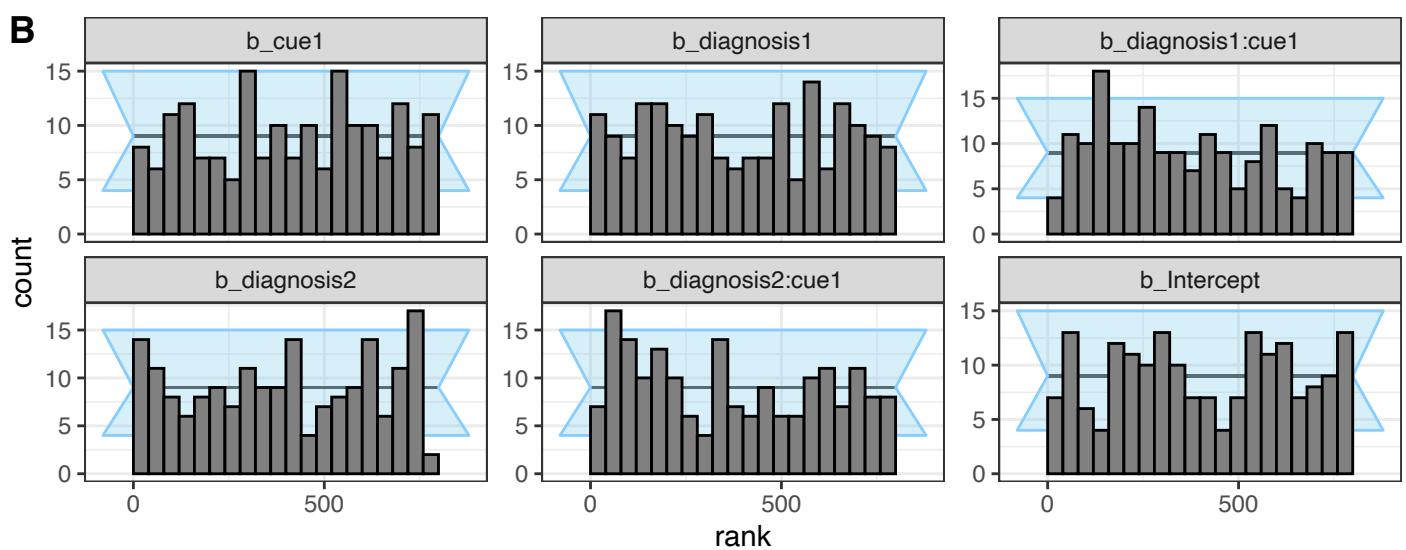
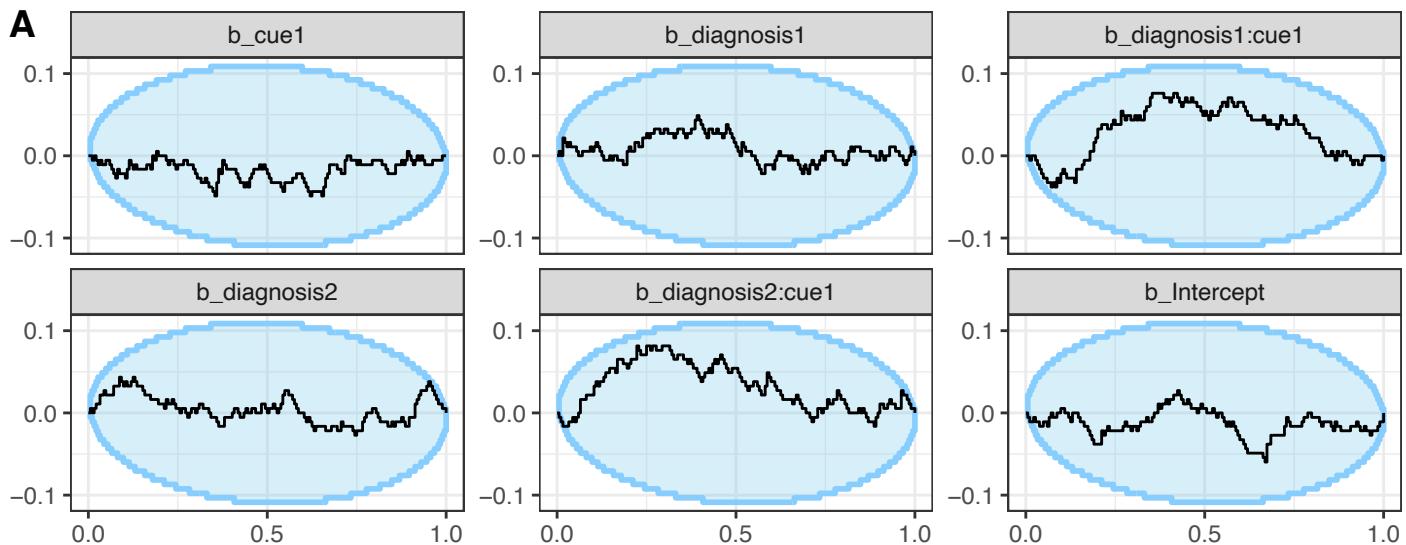
) %>%
filter(rhat >= 1.05 | mean_rank != rank),
df.backend %>% filter(n_divergent > 0), all = T)

# 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))

```

Computational faithfulness and model sensitivity



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.

2.1.2 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.

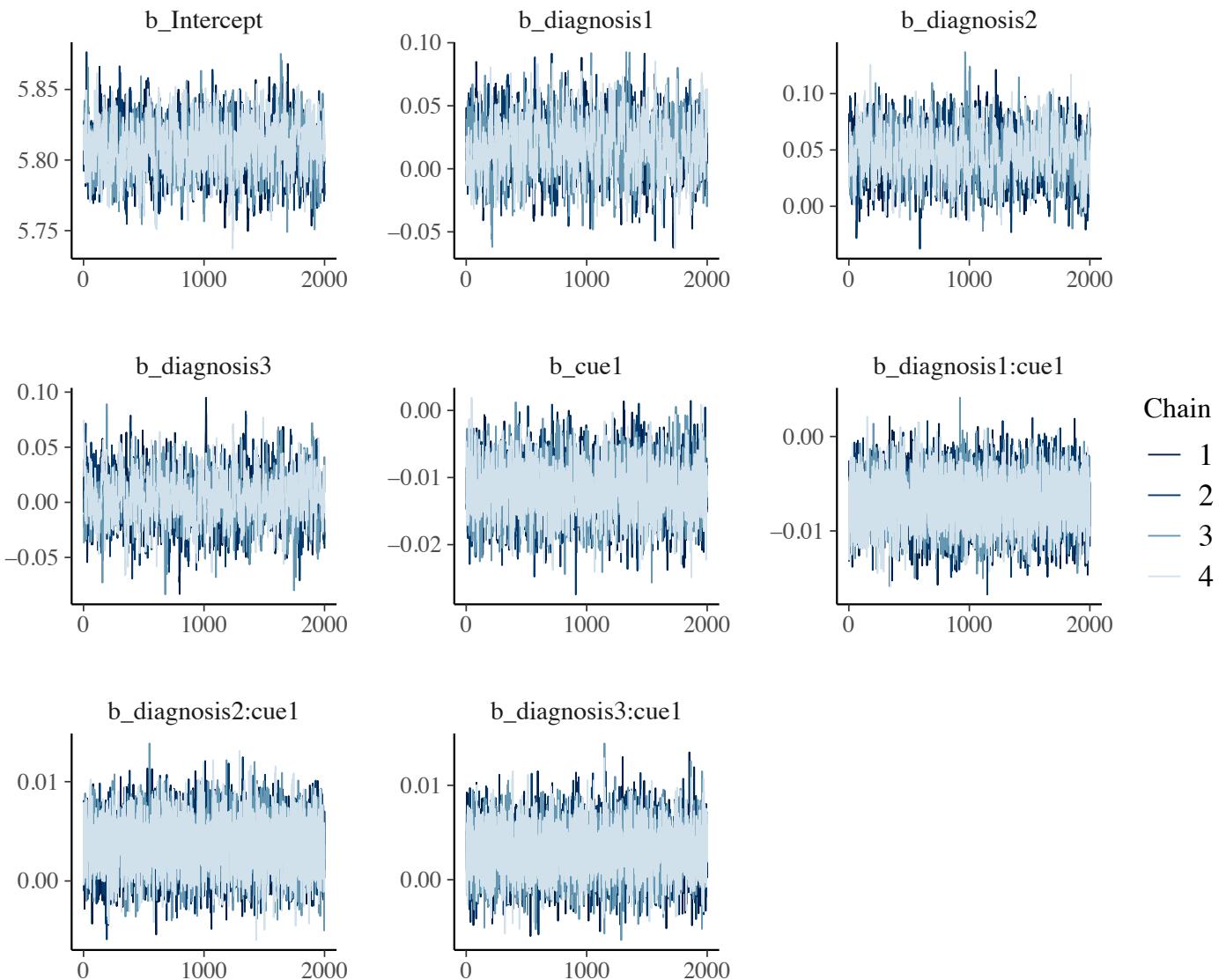
##
## Energy:
## E-BFMI indicated no pathological behavior.

# 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),]

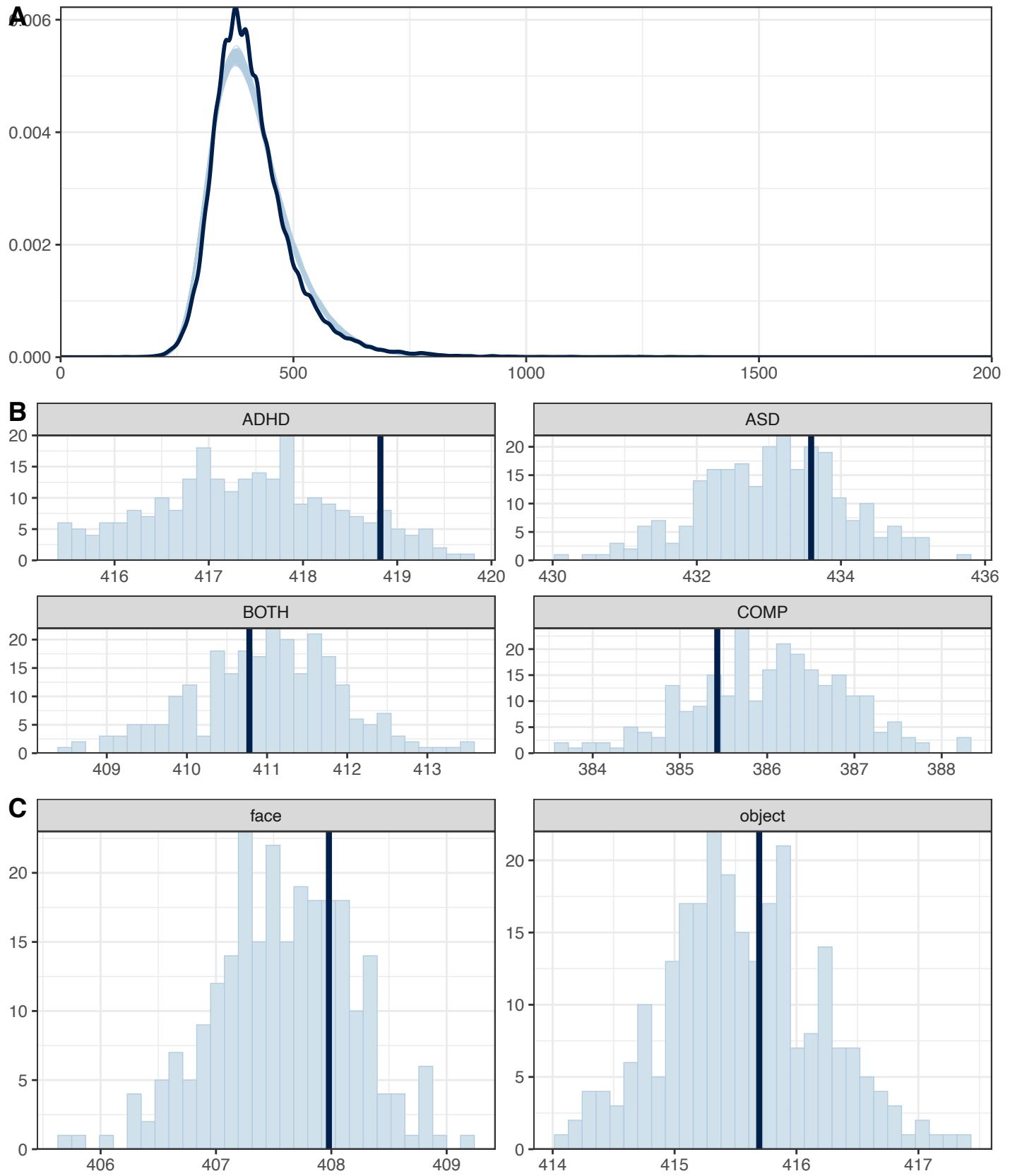
# distributions of means compared to the real values per group
p2 = ppc_stat_grouped(df.fab.na$rt.cor, post.pred, df.fab.na$diagnosis) +
  theme_bw() + theme(legend.position = "none")

# 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))
```

Posterior predictive checks: RTs



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.

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

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

summary(df.fab)
```

subID	diagnosis	stm	cue	rt.cor
1	ADHD:1656	1_10	face :3312	Min. :256.0
10	ASD :1656	1_11	object:3312	1st Qu.:364.0
11	BOTH:1584	1_12		Median :395.5
12	COMP:1728	1_7		Mean :407.4
13		1_8		3rd Qu.:436.1
14		1_9		Max. :919.0
(Other):6192		(Other):5520		

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

2.2.1 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
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) +

```

```

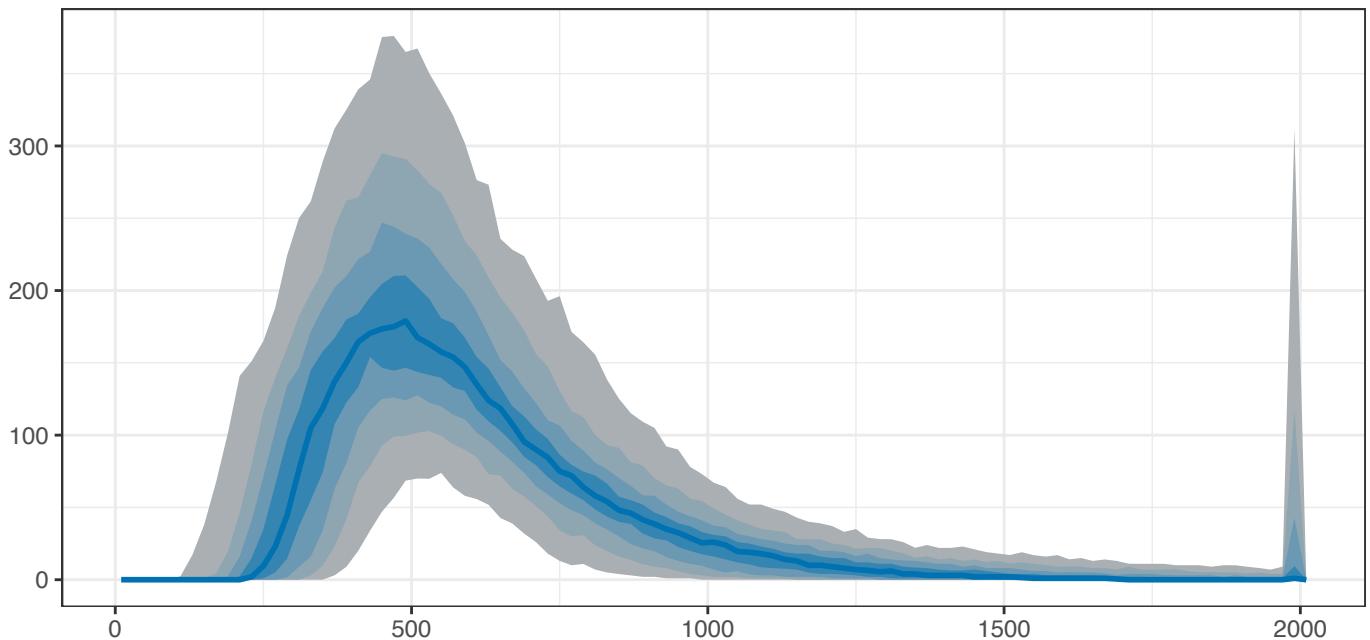
geom_line(aes(y = p0.5), colour = c_dark, linewidth = 1) +
  labs(title = "Distribution of simulated discriminations", y = "", x = "") +
  theme_bw()

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))

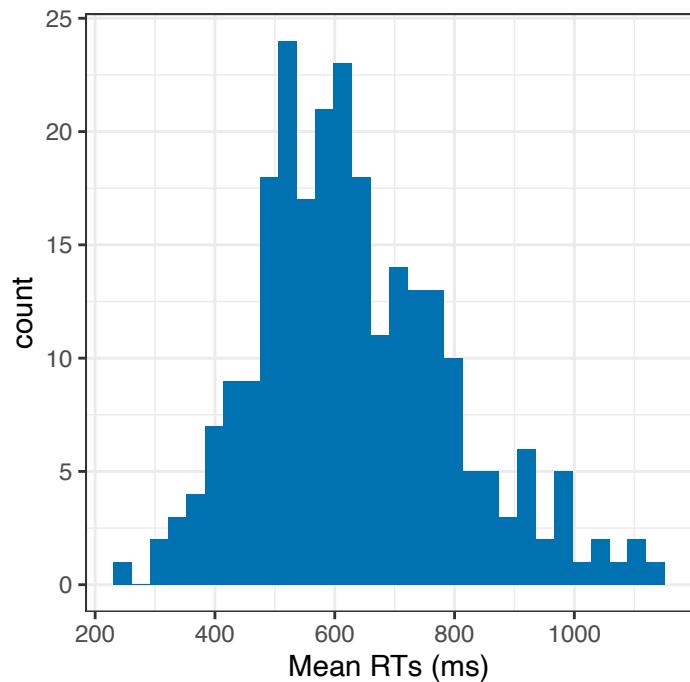
```

Prior predictive checks: reaction times

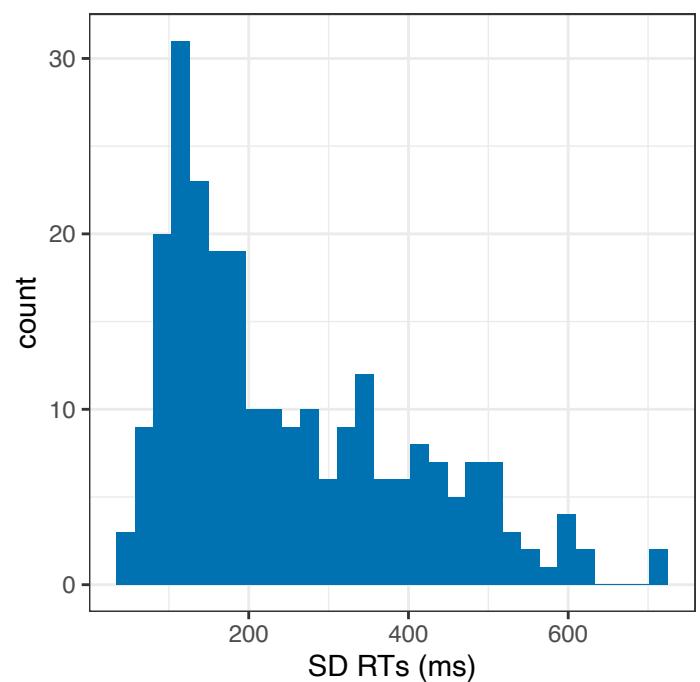
A Distribution of simulated discriminations



B Means of simulated RTs



C SDs of simulated RTs



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)
```

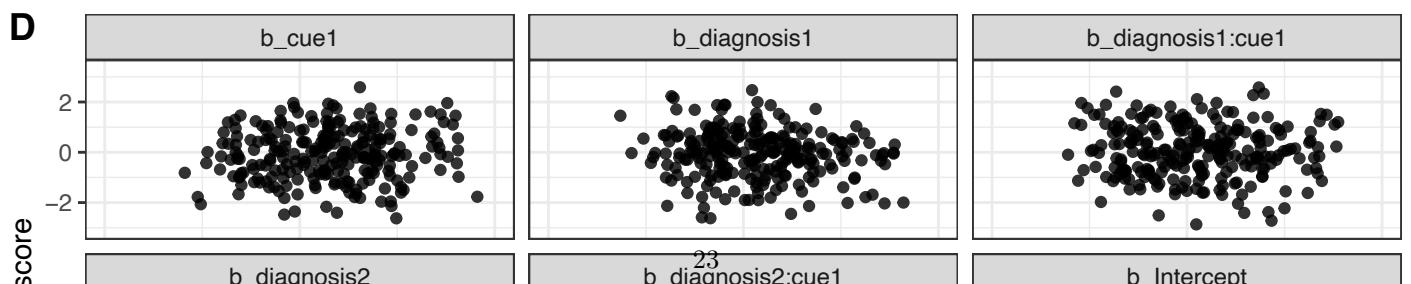
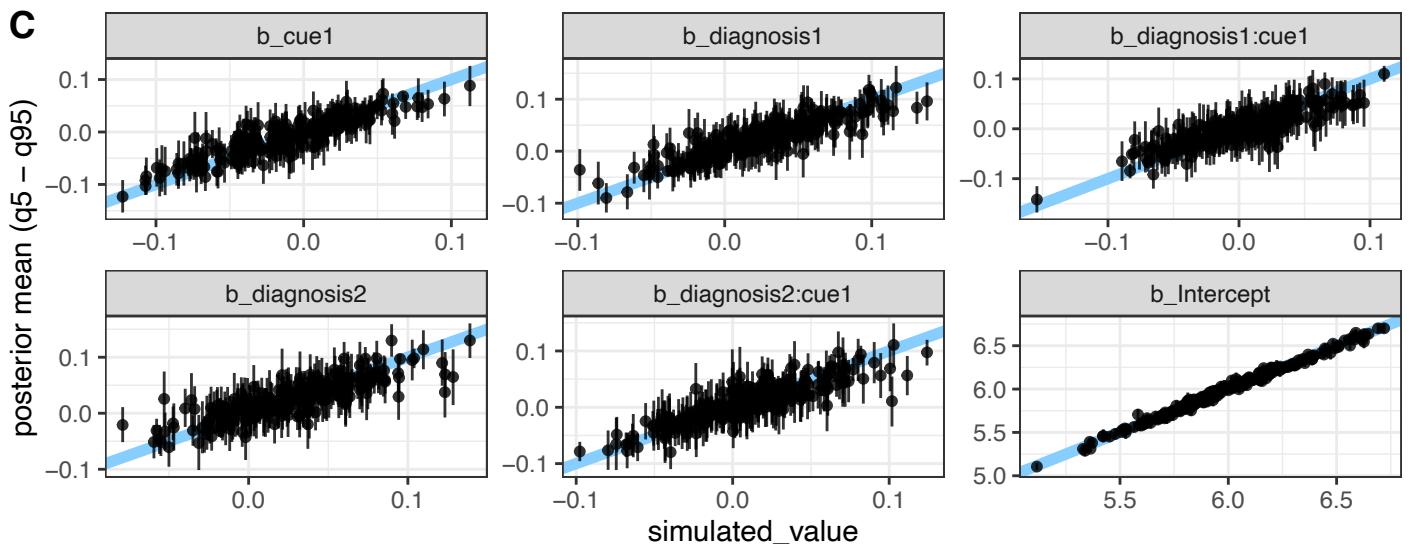
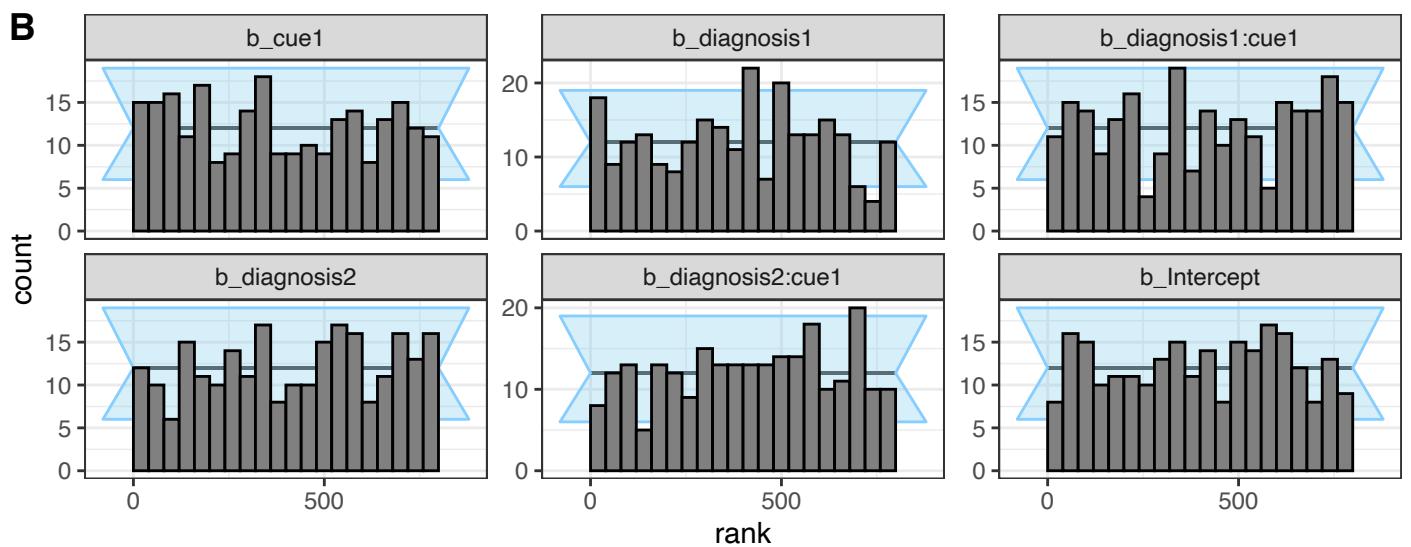
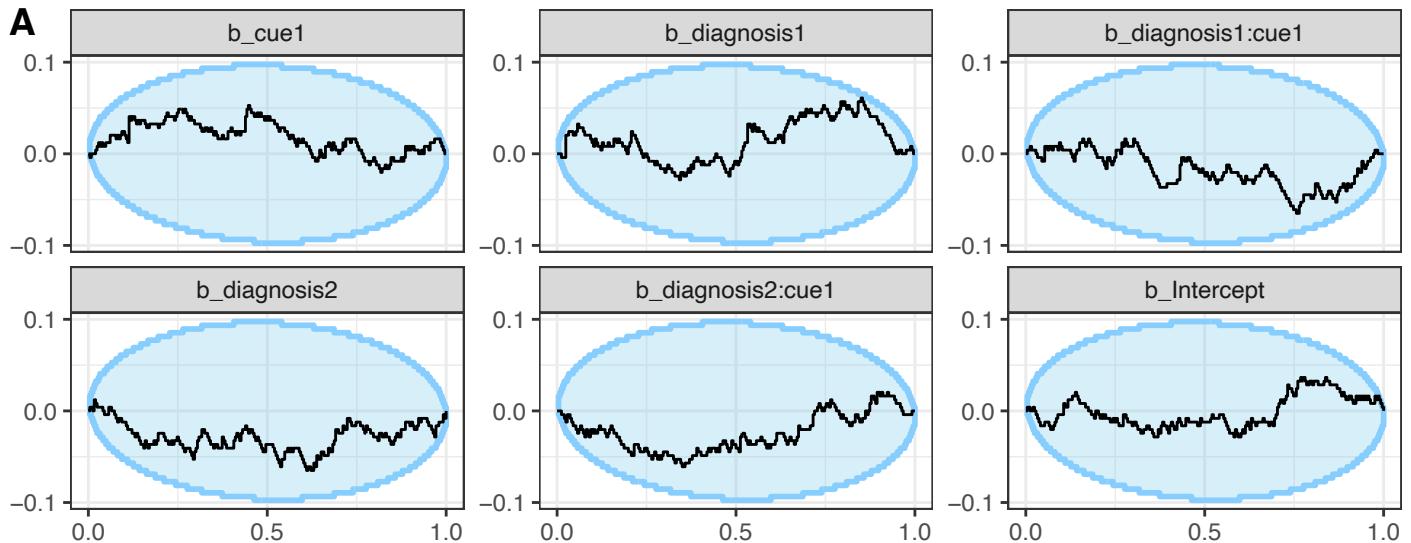
```

# 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))

```

Computational faithfulness and model sensitivity



Rank histograms, 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.

2.2.2 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.

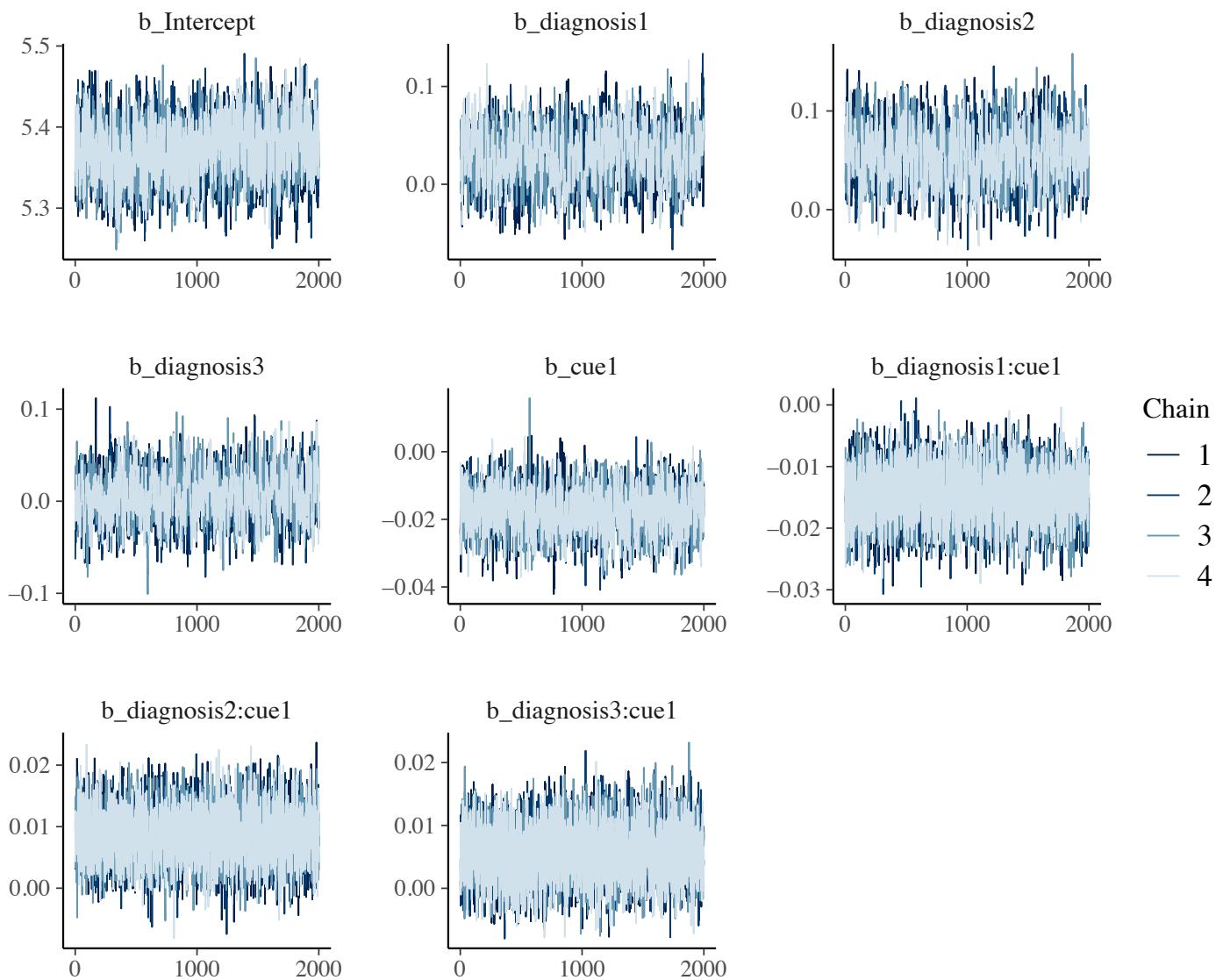
## 
## Energy:
## E-BFMI indicated no pathological behavior.

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

## [1] 49

# 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)

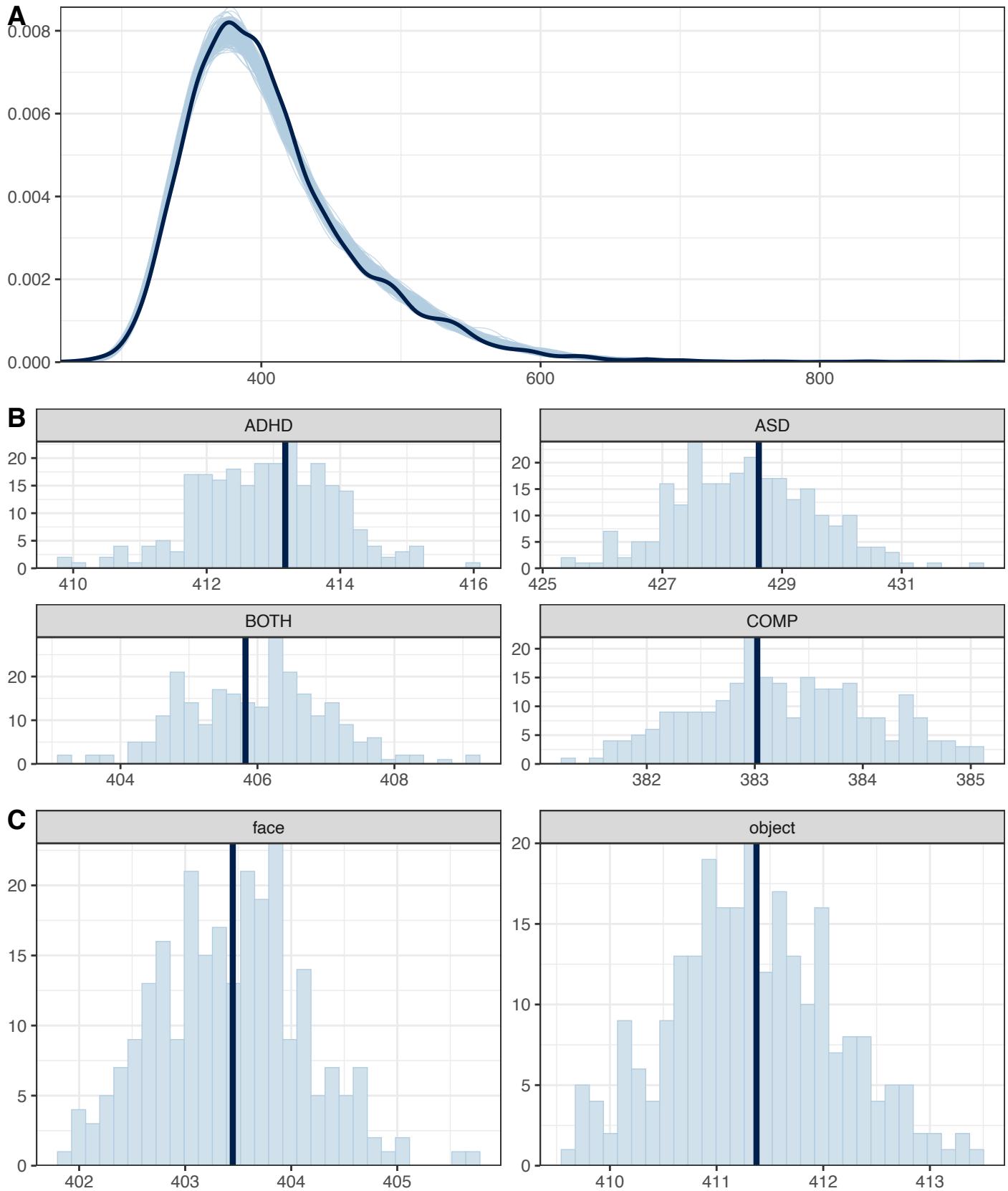
# check the fit of the predicted data compared to the real data
p1 = pp_check(m.fab, ndraws = nsim) +
  theme_bw() + theme(legend.position = "none")

# 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))
```

Posterior predictive checks: RTs



This model fits our data much better.

2.2.3 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: 6624)
## 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    0.04 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)                0.01     0.00    0.00    0.01 1.00
## cor(Intercept,cue1)                -0.30    0.15   -0.58    0.02 1.00
## cor(Intercept,diagnosis1)          -0.12    0.27   -0.60    0.43 1.00
## cor(cue1,diagnosis1)               0.01    0.26   -0.51    0.51 1.00
## cor(Intercept,diagnosis2)          -0.09    0.29   -0.63    0.49 1.00
## cor(cue1,diagnosis2)               -0.03    0.29   -0.58    0.53 1.00
## cor(diagnosis1,diagnosis2)        -0.01    0.30   -0.59    0.57 1.00
## cor(Intercept,diagnosis3)          0.07    0.28   -0.48    0.60 1.00
## cor(cue1,diagnosis3)               0.17    0.27   -0.39    0.65 1.00
## cor(diagnosis1,diagnosis3)        -0.13    0.31   -0.69    0.48 1.00
## cor(diagnosis2,diagnosis3)        -0.07    0.30   -0.63    0.53 1.00
## cor(Intercept,cue1:diagnosis1)    0.03    0.28   -0.51    0.56 1.00
## cor(cue1,cue1:diagnosis1)        -0.05    0.28   -0.57    0.49 1.00
## cor(diagnosis1,cue1:diagnosis1)   -0.00    0.30   -0.57    0.57 1.00
## cor(diagnosis2,cue1:diagnosis1)   0.00    0.30   -0.57    0.57 1.00
## cor(diagnosis3,cue1:diagnosis1)   -0.03    0.30   -0.61    0.56 1.00
## cor(Intercept,cue1:diagnosis2)    -0.16    0.29   -0.67    0.44 1.00
## cor(cue1,cue1:diagnosis2)        -0.05    0.28   -0.58    0.51 1.00
## cor(diagnosis1,cue1:diagnosis2)   0.04    0.30   -0.54    0.61 1.00
## cor(diagnosis2,cue1:diagnosis2)   0.04    0.31   -0.56    0.60 1.00
## cor(diagnosis3,cue1:diagnosis2)   -0.05    0.30   -0.60    0.53 1.00
## cor(cue1:diagnosis1,cue1:diagnosis2) -0.07    0.31   -0.64    0.52 1.00
## cor(Intercept,cue1:diagnosis3)    -0.12    0.28   -0.63    0.46 1.00
## cor(cue1,cue1:diagnosis3)        -0.16    0.28   -0.64    0.43 1.00
## cor(diagnosis1,cue1:diagnosis3)   0.05    0.30   -0.52    0.61 1.00
## cor(diagnosis2,cue1:diagnosis3)   0.07    0.30   -0.52    0.62 1.00
## cor(diagnosis3,cue1:diagnosis3)   -0.02    0.29   -0.58    0.55 1.00
## cor(cue1:diagnosis1,cue1:diagnosis3) -0.08    0.30   -0.65    0.52 1.00
## cor(cue1:diagnosis2,cue1:diagnosis3) -0.01    0.30   -0.57    0.56 1.00
##                                         Bulk_ESS Tail_ESS
## sd(Intercept)                      2724     4317
## sd(cue1)                           2215     3985
## sd(diagnosis1)                     2240     3682
## sd(diagnosis2)                     4108     3660
## sd(diagnosis3)                     3017     4012
## sd(cue1:diagnosis1)                3368     4350
## sd(cue1:diagnosis2)                3580     3611
## sd(cue1:diagnosis3)                2788     3253
## cor(Intercept,cue1)                1852     3479
## cor(Intercept,diagnosis1)          11906    5652

```

```

## cor(cue1,diagnosis1)           13168    5256
## cor(Intercept,diagnosis2)      15076    5534
## cor(cue1,diagnosis2)           13876    5843
## cor(diagnosis1,diagnosis2)     9969     6171
## cor(Intercept,diagnosis3)      12876    5591
## cor(cue1,diagnosis3)           12089    6067
## cor(diagnosis1,diagnosis3)     7225     6300
## cor(diagnosis2,diagnosis3)     6838     6402
## cor(Intercept,cue1:diagnosis1) 13820    5873
## cor(cue1,cue1:diagnosis1)      14433    6204
## cor(diagnosis1,cue1:diagnosis1) 8323     6155
## cor(diagnosis2,cue1:diagnosis1) 7080     6710
## cor(diagnosis3,cue1:diagnosis1) 7663     6743
## cor(Intercept,cue1:diagnosis2) 12437    5566
## cor(cue1,cue1:diagnosis2)      15034    6271
## cor(diagnosis1,cue1:diagnosis2) 9124     6070
## cor(diagnosis2,cue1:diagnosis2) 7129     6208
## cor(diagnosis3,cue1:diagnosis2) 6894     6281
## cor(cue1:diagnosis1,cue1:diagnosis2) 6020     6368
## cor(Intercept,cue1:diagnosis3) 10944    5628
## cor(cue1,cue1:diagnosis3)      11833    5556
## cor(diagnosis1,cue1:diagnosis3) 8457     6691
## cor(diagnosis2,cue1:diagnosis3) 7239     6504
## cor(diagnosis3,cue1:diagnosis3) 7829     6571
## cor(cue1:diagnosis1,cue1:diagnosis3) 6017     6727
## cor(cue1:diagnosis2,cue1:diagnosis3) 6320     6748
##
## ~subID (Number of levels: 92)
##                                     Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)                 0.21     0.02    0.18   0.25 1.00    992    1981
## sd(cue1)                      0.02     0.00    0.01   0.02 1.00   4100    4812
## cor(Intercept,cue1)          -0.04     0.14   -0.31   0.25 1.00   6863    6208
##
## Regression Coefficients:
##                                     Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept                     5.37     0.03    5.30   5.44 1.01   1112    2284
## diagnosis1                   0.03     0.03   -0.02   0.08 1.00    875    1591
## diagnosis2                   0.06     0.03    0.00   0.11 1.00   853    1715
## diagnosis3                   0.01     0.03   -0.04   0.06 1.00   997    1817
## cue1                          -0.02    0.01   -0.03  -0.01 1.00   2008    3129
## diagnosis1:cue1              -0.01    0.00   -0.02  -0.01 1.00   7114    6917
## diagnosis2:cue1              0.01     0.00    0.00   0.02 1.00   6998    6946
## diagnosis3:cue1              0.01     0.00   -0.00   0.01 1.00   7086    6813
##
## Further Distributional Parameters:
##                                     Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma                         0.13     0.00    0.13   0.14 1.00   5353    5447
## ndt                           185.27    5.48   174.05 195.53 1.00   5293    5409
##
## 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,

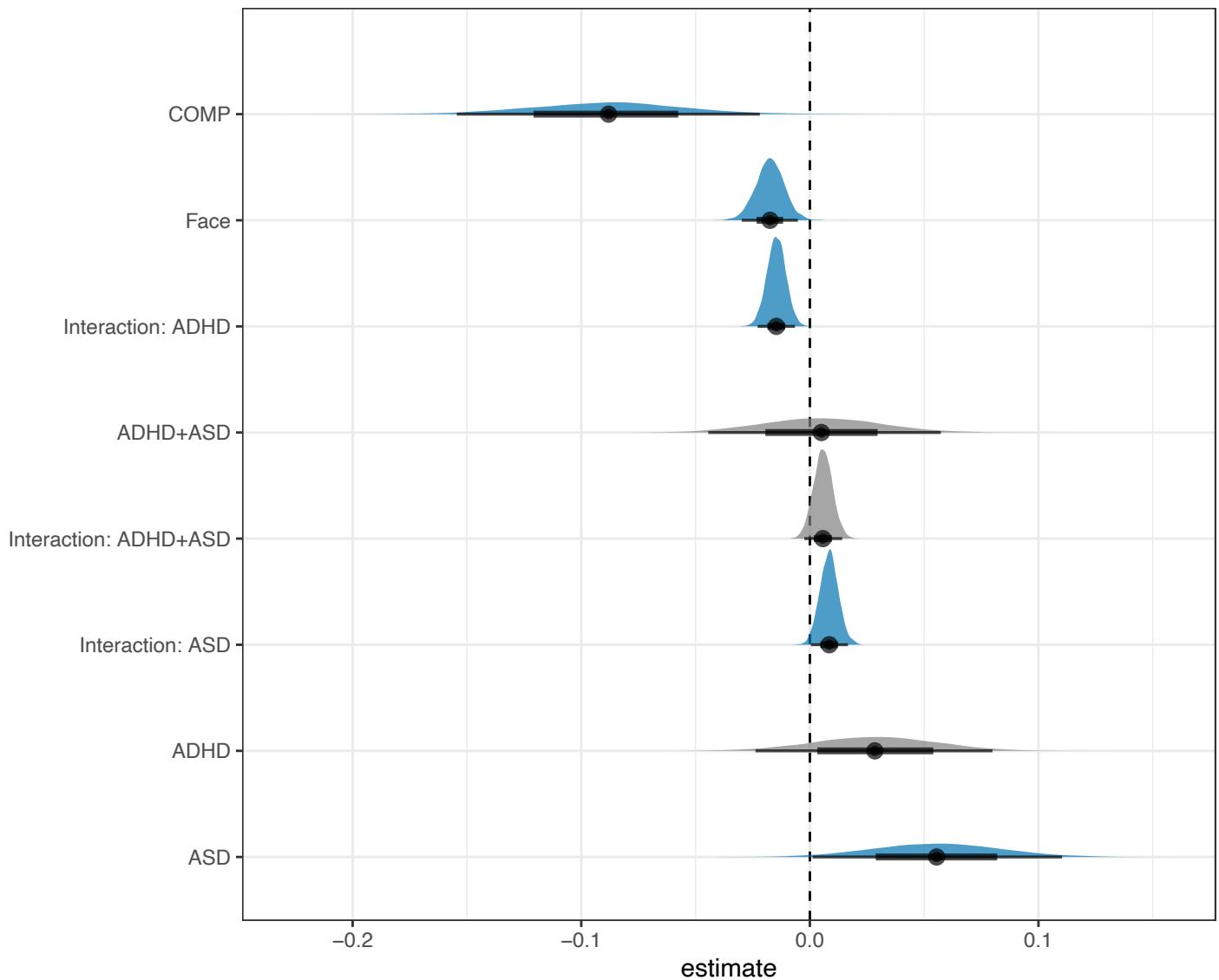
```

```

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, not_credible)) +
  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      66.8
##   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     -0.03      100.27
##   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    -0.23    -0.06    189.48
##   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.

# 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     7.02
##   Post.Prob Star
## 1      0.88
## ---
## '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    65.12
##   Post.Prob Star
## 1      0.98      *
## ---
## '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    379.95      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       7.89
##   Post.Prob Star
## 1           0.89
## ---
## '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      16.94
##   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.

# 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      1141.86
##   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    -0.01    570.43
##   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     0.01      0.01    -0.02     0.03     1.95
##   Post.Prob Star
## 1          0.66
## ---
## '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     0.02     3.37
##   Post.Prob Star
## 1          0.77
## ---
## '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.

# E9: face in COMP versus face in ADHD
e9 = hypothesis(m.fab,
                 "0 < 2*diagnosis1 + diagnosis2 + diagnosis3 +
                  2*diagnosis1:cue1 + diagnosis2:cue1 + diagnosis3:cue1",
                 alpha = 0.025)
e9

## Hypothesis Tests for class b:
##                               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis1... < 0     -0.1       0.05     -0.2        0     44.45
##   Post.Prob Star
## 1          0.98      *

```

```

## ---
## '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.

# E10: object in COMP versus object in ADHD
e10 = hypothesis(m.fab,
                  "0 < 2*diagnosis1 + diagnosis2 + diagnosis3 -
                   (2*diagnosis1:cue1 + diagnosis2:cue1 + diagnosis3:cue1)",
                  alpha = 0.025)
e10

## Hypothesis Tests for class b:
##                               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*diagnosis1... < 0     -0.13      0.05    -0.23    -0.03     189.48
##   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.

# E11: E10 > E9
e11 = hypothesis(m.fab,
                  "2*diagnosis1 + diagnosis2 + diagnosis3 -
                   (2*diagnosis1:cue1 + diagnosis2:cue1 + diagnosis3:cue1) >
                   2*diagnosis1 + diagnosis2 + diagnosis3 +
                   (2*diagnosis1:cue1 + diagnosis2:cue1 + diagnosis3:cue1)",
                  alpha = 0.025)
e11

## Hypothesis Tests for class b:
##                               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (2*diagnosis1+dia... > 0     0.03      0.01      0     0.06     65.12
##   Post.Prob Star
## 1      0.98      *
## ---
## '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

st(df.ms,
  summ = c('mean(x)', 'sd(x)', 'min(x)', 'pctile(x)[2.5]',
           'pctile(x)[97.5]', 'max(x)'))

# calculate our difference columns
df.ms = df.ms %>%

```

Table 5: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
ADHD_face	402	7.6	378	387	416	428
ADHD_object	416	8.2	388	399	432	446
COMP_face	381	8	352	365	396	414
COMP_object	387	8.5	360	371	404	421
ASD_face	413	8.1	384	397	429	447
ASD_object	417	8.3	387	401	433	448
BOTH_face	401	7.5	377	387	415	438
BOTH_object	406	7.8	383	391	421	446

Table 6: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	399	4.8	380	390	408	418
object	407	5.2	390	397	417	425
FAB	7.6	2.7	-6.5	1.9	13	18
ADHDvCOMP_face	21	10	-20	-0.37	40	62
ADHDvCOMP_object	29	11	-12	6.3	49	74
diff_ADHDvCOMP	7.6	3	-3.3	1.5	13	18

```

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
)

st(df.ms %>%
  mutate(
    face = rowMeans(select(., matches(".*_face"))), na.rm = T),
    object = rowMeans(select(., matches(".*_object"))), na.rm = T),
    ADHDvCOMP_face = ADHD_face - COMP_face,
    ADHDvCOMP_object = ADHD_object - COMP_object,
    diff_ADHDvCOMP = ADHDvCOMP_object - ADHDvCOMP_face
) %>% select(face, object, FAB, ADHDvCOMP_face, ADHDvCOMP_object, diff_ADHDvCOMP),
  summarise_all(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, -0.03], *posterior probability* = 99.01%; COMP - ASD: *estimate* = -0.14 [-0.23, -0.06], *posterior probability* = 99.48%). The model predicts that participants in the comparison group react 24.74ms [4.15, 45.24] faster than the participants in the ADHD group and 30.78ms [8.27, 52.27] faster than autistic participants. Additionally, the model predicts that the participants in the comparison group react 19.54ms [-0.89, 40.35] faster than adults

in the ADHD+ASD group.

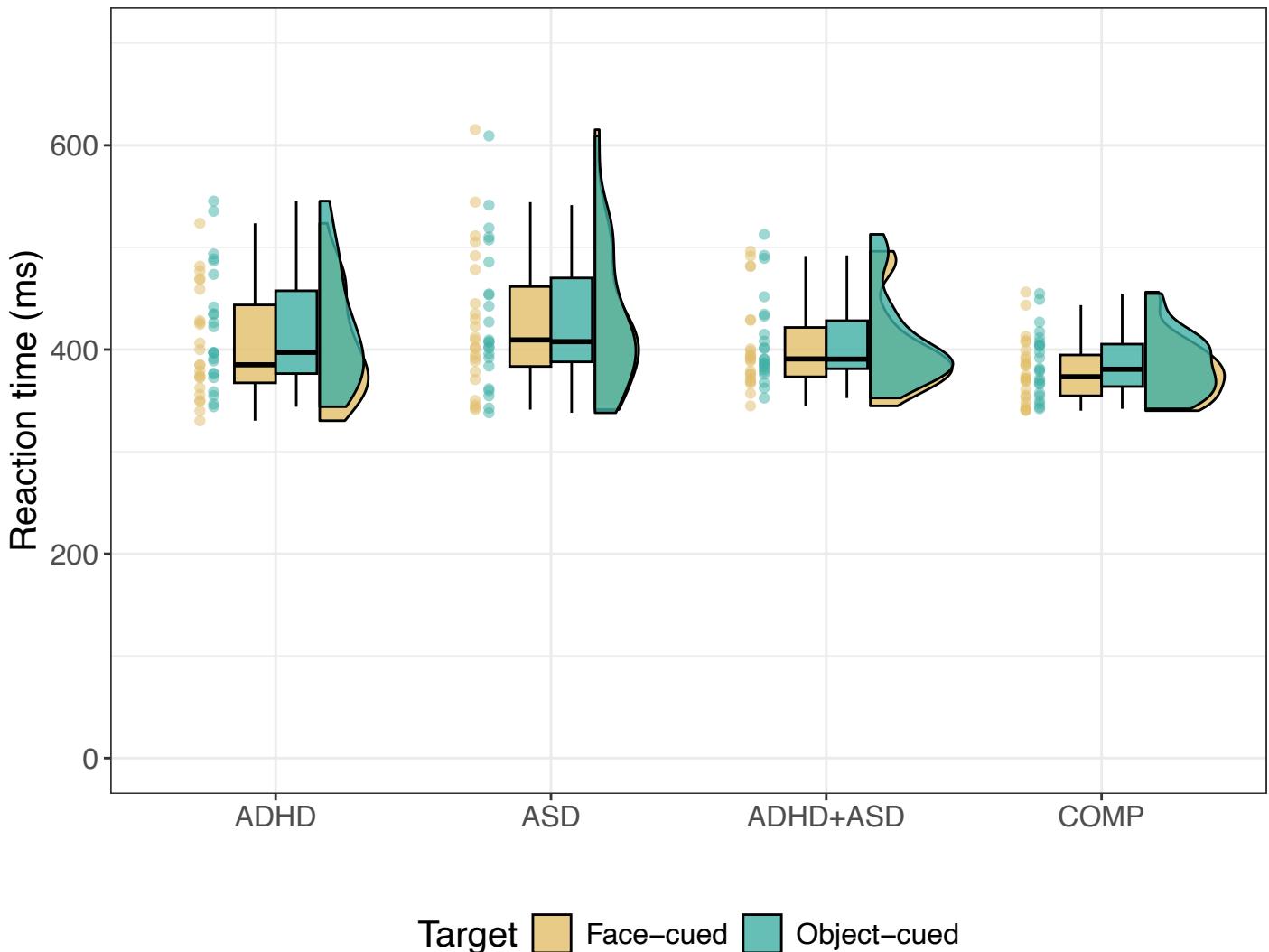
Our Bayesian linear mixed model with the median of correct reaction times as the outcome and diagnostic status, cue (face or object) and their interaction confirmed a face attention bias in our comparison group: COMP participants reacted faster in response to targets appearing on the side of the face compared to targets appearing on the side of the object (*estimate* = -0.03 [-0.06, -0.01], *posterior probability* = 98.52%). FAB was not credibly decreased in ASD participants compared to COMP participants (*estimate* = -0.02 [-0.04, 0.01], *posterior probability* = 87.52%). However, FAB was credibly higher in the ADHD than the COMP group (*estimate* = 0.03 [0, 0.06], *posterior probability* = 98.49%). Specifically, predicted reaction times based on the model estimate a FAB of 6.77ms [0.78, 12.98] in the COMP group, 14.35ms [7.89, 20.93] in the ADHD group, 4.13ms [-2.58, 10.82] in the ASD group as well as 5.12ms [-1.21, 11.46] 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* = 99.74%) 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* = 88.75%) and the ADHD+ASD group (*estimate* = -0.02 [-0.05, 0.01], *posterior probability* = 94.42%).

Exploration regarding comparison between ADHD and COMP on face and object separately:

- Face: *estimate* = -0.1 [-0.2, 0], *posterior probability* = 97.8%
- Object: *estimate* = -0.13 [-0.23, -0.03], *posterior probability* = 99.48%
- Object(ADHD-COMP) > Face(ADHD-COMP): *estimate* = 0.03 [0, 0.06], *posterior probability* = 98.49%

2.3 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"),
    Target      = recode(cue, "face" = "Face-cued", "object" = "Object-cued")
  ) %>%
  ggplot(aes(diagnosis, rt.cor, fill = Target, colour = Target)) + #
  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 = "",
       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))
```



Target Face-cued Object-cued

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

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

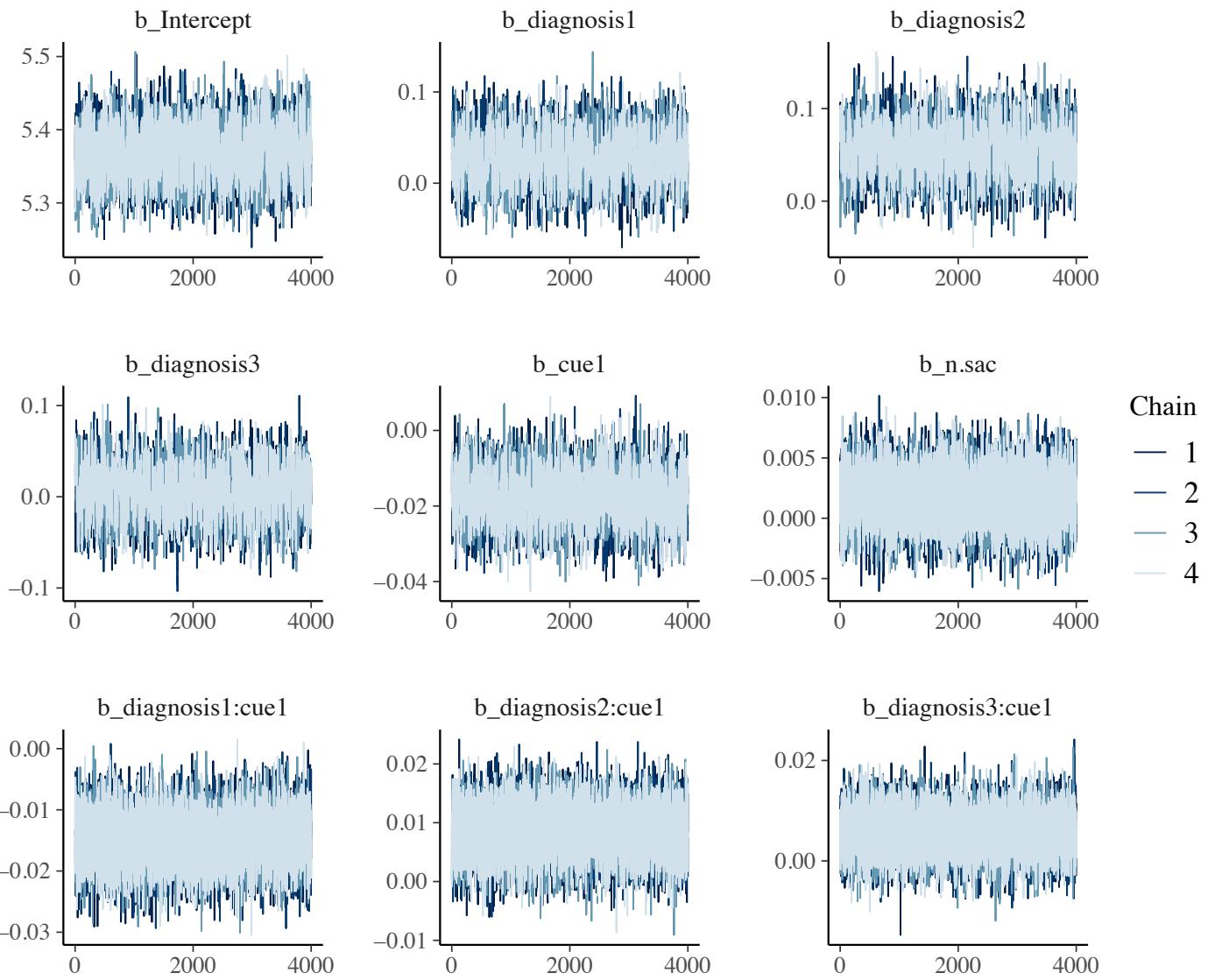
# run the model > more iterations due to some suboptimal rhats in the first try
set.seed(1357)
m.rtsac = brm(rt.cor ~ diagnosis * cue + n.sac + (cue | subID) + (cue * diagnosis | stm),
               df.sac.fab, prior = priors,
               family = shifted_lognormal,
               iter = iter*2, 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")

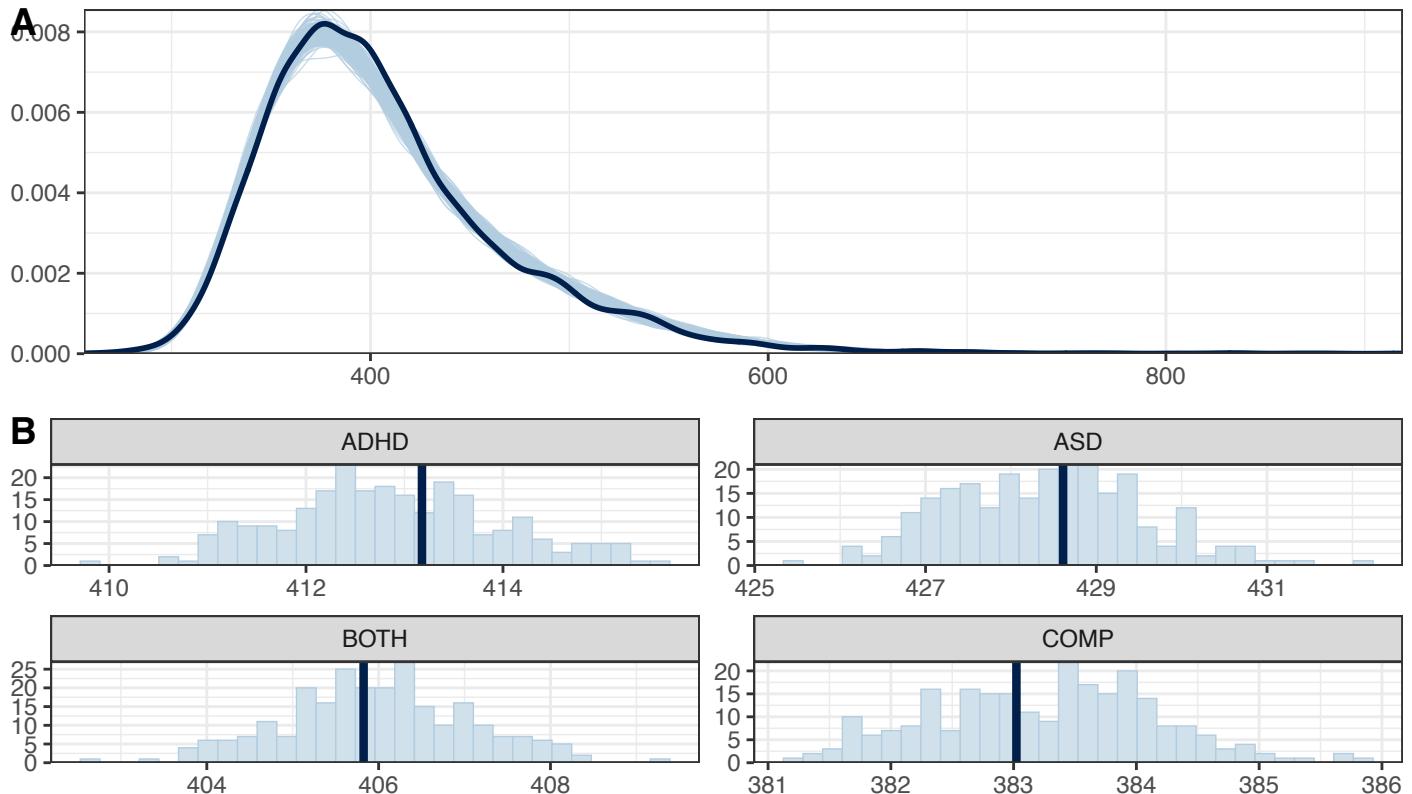
df.sac.fab = df.sac.fab %>% drop_na()

# 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))

```

Posterior predictive checks: RTs of trials with saccade covariate



```
# 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: 6624)
##   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 1-95% 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    0.04 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)                0.01     0.00    0.00    0.01 1.00
## cor(Intercept,cue1)                -0.31    0.15   -0.58    0.01 1.00
## cor(Intercept,diagnosis1)           -0.12    0.26   -0.59    0.42 1.00
## cor(cue1,diagnosis1)                0.01    0.26   -0.50    0.50 1.00
## cor(Intercept,diagnosis2)           -0.09    0.29   -0.62    0.50 1.00
## cor(cue1,diagnosis2)                0.04    0.29   -0.58    0.54 1.00
## cor(diagnosis1,diagnosis2)          -0.01    0.30   -0.58    0.57 1.00
## cor(Intercept,diagnosis3)           0.07    0.28   -0.48    0.58 1.00
## cor(cue1,diagnosis3)                0.17    0.28   -0.41    0.65 1.00
## cor(diagnosis1,diagnosis3)          -0.13    0.31   -0.68    0.49 1.00
## cor(diagnosis2,diagnosis3)          -0.07    0.30   -0.63    0.53 1.00
## cor(Intercept,cue1:diagnosis1)      0.03    0.29   -0.52    0.58 1.00
## cor(cue1,cue1:diagnosis1)          -0.04    0.28   -0.58    0.51 1.00
```

```

## cor(diagnosis1,cue1:diagnosis1)      0.00    0.30   -0.57    0.57 1.00
## cor(diagnosis2,cue1:diagnosis1)      0.01    0.30   -0.57    0.58 1.00
## cor(diagnosis3,cue1:diagnosis1)     -0.02    0.30   -0.59    0.56 1.00
## cor(Intercept,cue1:diagnosis2)     -0.16    0.29   -0.67    0.44 1.00
## cor(cue1,cue1:diagnosis2)        -0.05    0.28   -0.57    0.51 1.00
## cor(diagnosis1,cue1:diagnosis2)      0.03    0.30   -0.54    0.59 1.00
## cor(diagnosis2,cue1:diagnosis2)      0.04    0.30   -0.55    0.61 1.00
## cor(diagnosis3,cue1:diagnosis2)     -0.05    0.30   -0.60    0.54 1.00
## cor(cue1:diagnosis1,cue1:diagnosis2) -0.07    0.31   -0.64    0.54 1.00
## cor(Intercept,cue1:diagnosis3)     -0.12    0.28   -0.62    0.45 1.00
## cor(cue1,cue1:diagnosis3)        -0.16    0.27   -0.65    0.40 1.00
## cor(diagnosis1,cue1:diagnosis3)      0.06    0.30   -0.53    0.61 1.00
## cor(diagnosis2,cue1:diagnosis3)      0.07    0.30   -0.53    0.62 1.00
## cor(diagnosis3,cue1:diagnosis3)     -0.01    0.30   -0.58    0.56 1.00
## cor(cue1:diagnosis1,cue1:diagnosis3) -0.08    0.31   -0.64    0.53 1.00
## cor(cue1:diagnosis2,cue1:diagnosis3) -0.01    0.30   -0.57    0.56 1.00
##                                         Bulk_ESS Tail_ESS
## sd(Intercept)                      5517    9259
## sd(cue1)                           4842    9387
## sd(diagnosis1)                     4157    5899
## sd(diagnosis2)                     8220    8076
## sd(diagnosis3)                     5643    7912
## sd(cue1:diagnosis1)                6971    8262
## sd(cue1:diagnosis2)                7929    7331
## sd(cue1:diagnosis3)                6451    7329
## cor(Intercept,cue1)                 3458    6962
## cor(Intercept,diagnosis1)          23743   11429
## cor(cue1,diagnosis1)               25498   12290
## cor(Intercept,diagnosis2)          30347   12059
## cor(cue1,diagnosis2)               30653   12458
## cor(diagnosis1,diagnosis2)         22011   11736
## cor(Intercept,diagnosis3)          26342   11764
## cor(cue1,diagnosis3)               24760   11835
## cor(diagnosis1,diagnosis3)         13936   12640
## cor(diagnosis2,diagnosis3)         14508   13143
## cor(Intercept,cue1:diagnosis1)     28278   11416
## cor(cue1,cue1:diagnosis1)          30576   12352
## cor(diagnosis1,cue1:diagnosis1)    18194   13379
## cor(diagnosis2,cue1:diagnosis1)    15612   12785
## cor(diagnosis3,cue1:diagnosis1)    14525   13518
## cor(Intercept,cue1:diagnosis2)     25666   11945
## cor(cue1,cue1:diagnosis2)          28313   11313
## cor(diagnosis1,cue1:diagnosis2)    20782   12759
## cor(diagnosis2,cue1:diagnosis2)    16363   13241
## cor(diagnosis3,cue1:diagnosis2)    15503   13335
## cor(cue1:diagnosis1,cue1:diagnosis2) 12375   13060
## cor(Intercept,cue1:diagnosis3)     25460   11935
## cor(cue1,cue1:diagnosis3)          23560   12516
## cor(diagnosis1,cue1:diagnosis3)    19594   12131
## cor(diagnosis2,cue1:diagnosis3)    14364   13359
## cor(diagnosis3,cue1:diagnosis3)    14322   12731
## cor(cue1:diagnosis1,cue1:diagnosis3) 12229   13830
## cor(cue1:diagnosis2,cue1:diagnosis3) 12440   13054
##
## ~subID (Number of levels: 92)
##                                         Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)                  0.21      0.02    0.18    0.25 1.00    2454    4627
## sd(cue1)                      0.02      0.00    0.01    0.02 1.00    7352   10575
## cor(Intercept,cue1)           -0.03      0.14   -0.31    0.25 1.00   16266   13844
## 
```

```

## Regression Coefficients:
##             Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      5.37     0.03   5.30   5.44 1.00    2078    4770
## diagnosis1     0.03     0.03  -0.02   0.08 1.00    1902    3867
## diagnosis2     0.06     0.03   0.00   0.11 1.00    1892    3726
## diagnosis3     0.01     0.03  -0.05   0.06 1.00    1860    3959
## cue1        -0.02     0.01  -0.03  -0.01 1.00    3932    6920
## n.sac        0.00     0.00  -0.00   0.01 1.00    33237   11017
## diagnosis1:cue1 -0.01     0.00  -0.02  -0.01 1.00    14772   13354
## diagnosis2:cue1  0.01     0.00   0.00   0.02 1.00    14556   12851
## diagnosis3:cue1  0.01     0.00  -0.00   0.01 1.00    14891   12256
##
## Further Distributional Parameters:
##             Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma       0.13     0.00   0.13   0.14 1.00    10674   11494
## ndt        185.49    5.47 174.29 195.80 1.00    10487   10634
##
## 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    65.39
## Post.Prob Star
## 1      0.98    *
## ---
## '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     0.05    -0.2    -0.04    109.34
## 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.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     -0.15     0.05    -0.23   -0.06    469.59
## 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      7.9
##   Post.Prob Star
## 1      0.89
## ---
## '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     75.56
##   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.

4 Explorative analysis of subject-specific FAB

4.1 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, gender) %>%
  # 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, gender) %>%
  # calculate the mean FAB per person
  summarise(
    fab      = mean(fab),
    overall = mean(overall)

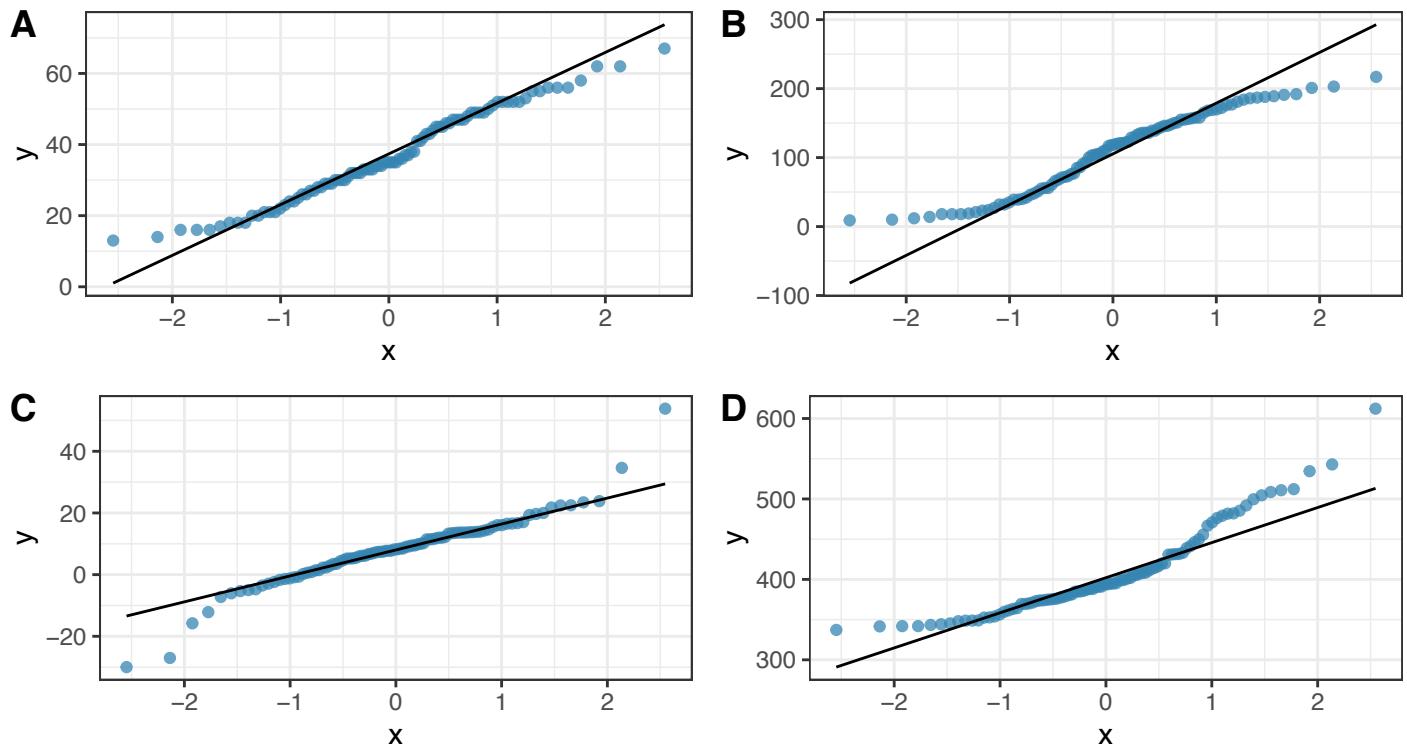
```

```

) %>% ungroup() %>%
select(subID, diagnosis, overall, fab, ASRS_total, RAADS_total, adhd.meds, gender)

# 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: $\log(BF) = -1.72$) or ADHD (ASRS: $\log(BF) = -1.57$). 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 ($\log(BF) = -1.3$).

```

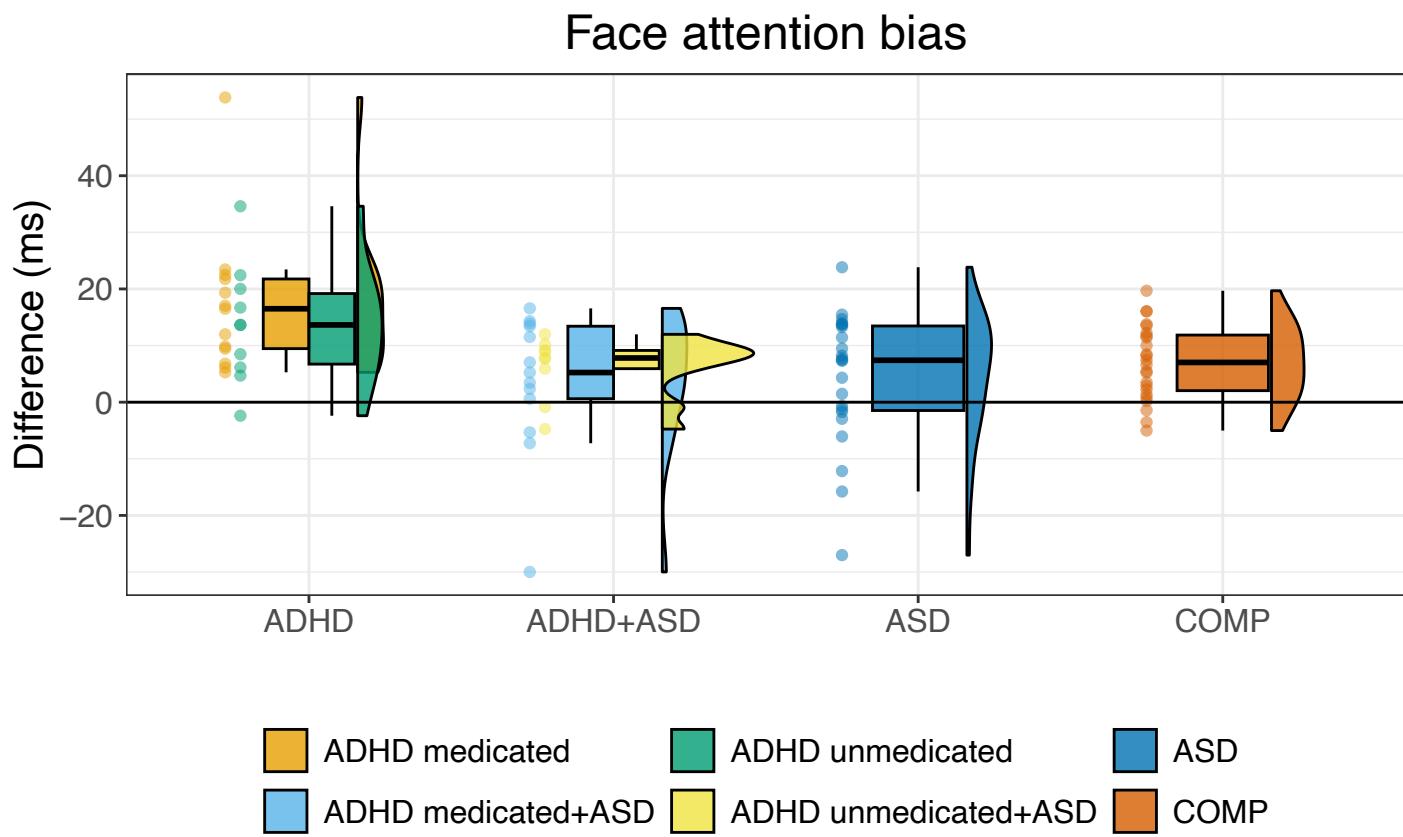
# focus on the FAB effect
df.que %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD"),
    diagnosis = factor(diagnosis, levels = c("ADHD", "ADHD+ASD", "ASD", "COMP")),
    diagnosis_med = as.factor(case_when(
      adhd.meds & diagnosis == "ADHD" ~ "ADHD medicated",
      adhd.meds & 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_dodgejudge(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_dodgegenudge(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.svg",
       units = "mm",
       width  = 170,
       height = 100,
       dpi    = 300)

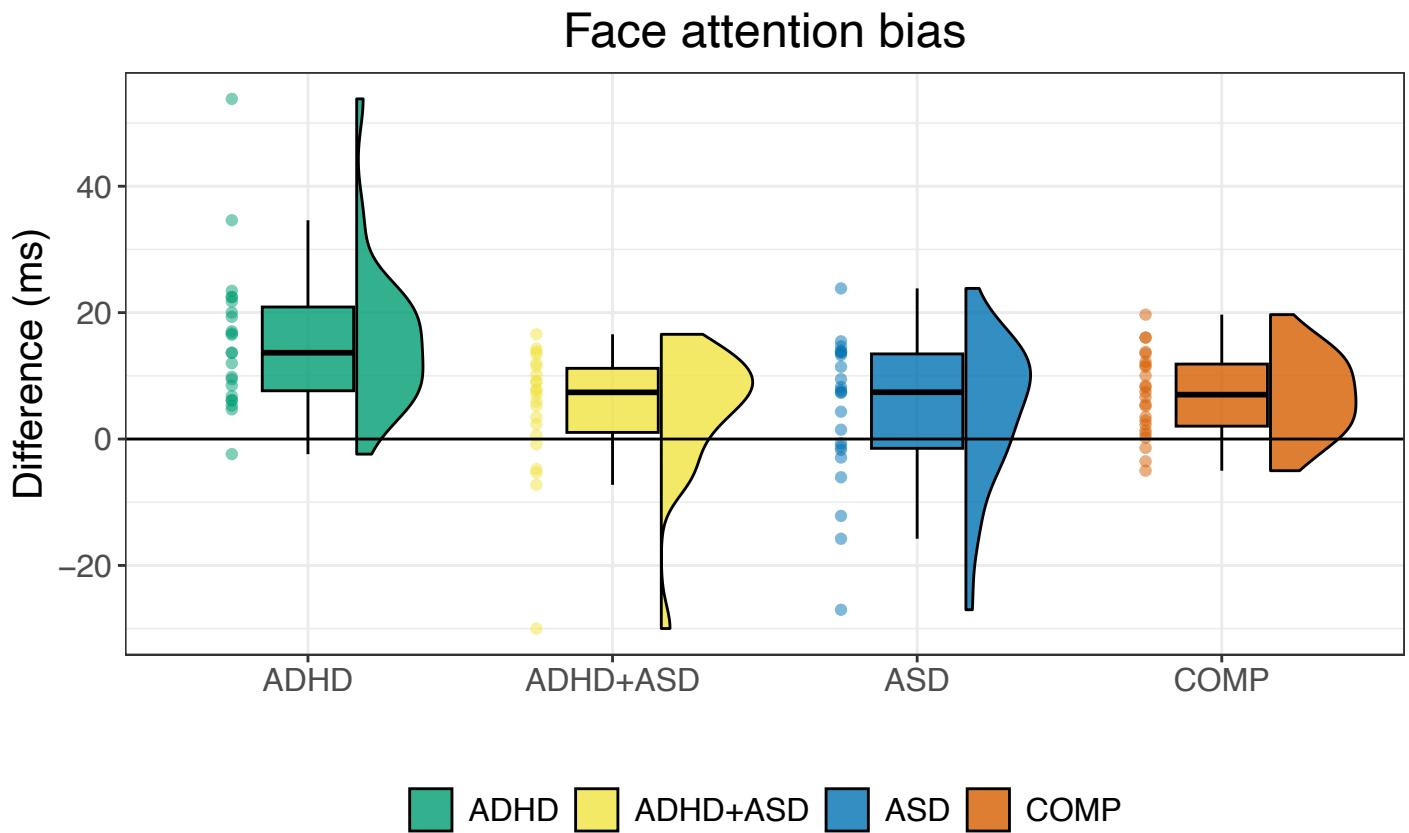
# focus on the FAB effect
df.que %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD"),
    diagnosis = factor(diagnosis, levels = c("ADHD", "ADHD+ASD", "ASD", "COMP")))
  ) %>%
  ggplot(aes(diagnosis, fab, fill = diagnosis, colour = diagnosis)) +
  geom_rain(rain.side = 'r',
            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[c(3, 4, 5, 6)]) +
  scale_color_manual(values = custom.col[c(3, 4, 5, 6)]) +
  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())

```



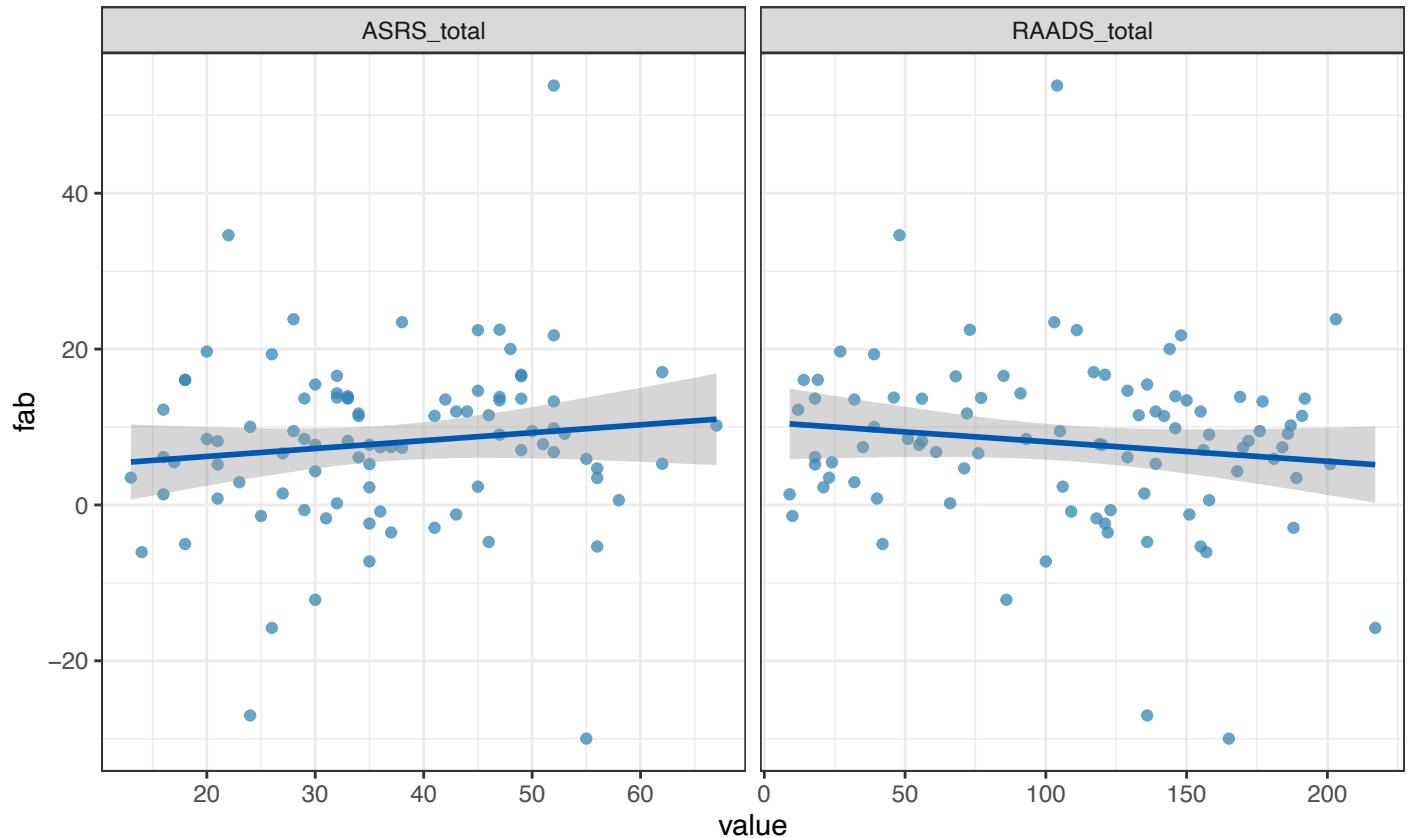
```

ggsave("Fig4_FAB_new.svg",
  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()
```



4.2 Gender

```
df.que %>%
  mutate(fab = fab > 0) %>%
  group_by(diagnosis, gender, fab) %>% count()

## # A tibble: 16 x 4
## # Groups:   diagnosis, gender, fab [16]
##   diagnosis gender fab      n
##   <fct>     <fct>  <lgl> <int>
## 1 ADHD       dan    TRUE     2
## 2 ADHD       fem    TRUE     9
## 3 ADHD       mal    FALSE    1
## 4 ADHD       mal    TRUE    11
## 5 ASD        fem   FALSE    4
## 6 ASD        fem   TRUE     8
## 7 ASD        mal   FALSE    4
## 8 ASD        mal   TRUE     7
## 9 BOTH       dan   TRUE     3
## 10 BOTH      fem   FALSE    4
## 11 BOTH      fem   TRUE     8
## 12 BOTH      mal   FALSE    1
## 13 BOTH      mal   TRUE     6
## 14 COMP      fem   TRUE    11
## 15 COMP      mal   FALSE    3
## 16 COMP      mal   TRUE    10

aov.gen = anovaBF(fab ~ gender * diagnosis, data = df.que %>% filter(gender != "dan"))
aov.gen@bayesFactor
```

```

##                                bf      error
## diagnosis                  2.817692 4.331993e-05
## gender                     -1.063725 1.768721e-04
## diagnosis + gender        1.520020 8.329957e-03
## diagnosis + gender + diag 0.334665 5.046557e-02
##                                         time      code
## diagnosis                   Sun Jul 27 19:04:51 2025 7c174f1227a2
## gender                      Sun Jul 27 19:04:51 2025 7c1730e8253c
## diagnosis + gender         Sun Jul 27 19:04:51 2025 7c1799184c7
## diagnosis + gender + diag Sun Jul 27 19:04:51 2025 7c1769af49a1

```

4.3 FAB as percentage of total reaction time

Since ADHD participants took longer on both cues, we want to make sure that the effect of FAB is actually increased and not just larger because they take longer to response.

```

df.fab.wide = df.fab %>%
  pivot_wider(names_from = cue, values_from = rt.cor) %>%
  mutate(fab.perc = (object - face)*100/(object + face))

# set weakly informed priors
priors = c(
  prior(normal(0, 0.50), class = Intercept),
  prior(normal(1.0, 1.00), class = sd),
  prior(lkj(2), class = cor),
  prior(normal(0, 1.00), class = b),
  prior(normal(0, 10.00), class = sigma)
)

m.fab.perc = brm(fab.perc ~ diagnosis + (1 | subID) + (diagnosis | stm) ,
  df.fab.wide, prior = priors,
  iter = iter, warmup = warm,
  backend = "cmdstanr", threads = threading(8),
  file = "m_fab_perc",
  seed = 222
)
rstan::check_hmc_diagnostics(m.fab.perc$fit)

## 
## Divergences:
## 
## Tree depth:
## 
## Energy:
# check that rhats are below 1.01
sum(brms::rhat(m.fab.perc) >= 1.01, na.rm = T)

## [1] 0
# print the summary
summary(m.fab.perc)

## Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: fab.perc ~ diagnosis + (1 | subID) + (diagnosis | stm)
## Data: df.fab.wide (Number of observations: 3312)
## 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 1-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)                 1.76     0.23    1.36    2.26 1.00   2060
## sd(diagnosis1)                0.31     0.21    0.01    0.77 1.00   2613
## sd(diagnosis2)                0.23     0.17    0.01    0.61 1.00   3534
## sd(diagnosis3)                0.28     0.19    0.01    0.70 1.00   2822
## cor(Intercept,diagnosis1)    -0.01     0.33   -0.65    0.62 1.00  10018
## cor(Intercept,diagnosis2)    -0.02     0.35   -0.66    0.67 1.00   9300
## cor(diagnosis1,diagnosis2)   -0.13     0.39   -0.79    0.65 1.00   6174
## cor(Intercept,diagnosis3)    -0.15     0.34   -0.73    0.55 1.00  10128
## cor(diagnosis1,diagnosis3)   -0.18     0.39   -0.82    0.61 1.00   5590
## cor(diagnosis2,diagnosis3)   -0.04     0.38   -0.72    0.69 1.00   6798
##                                     Tail_ESS
## sd(Intercept)                  3624
## sd(diagnosis1)                 3600
## sd(diagnosis2)                 4671
## sd(diagnosis3)                 3202
## cor(Intercept,diagnosis1)      5916
## cor(Intercept,diagnosis2)      5607
## cor(diagnosis1,diagnosis2)     5105
## cor(Intercept,diagnosis3)      5843
## cor(diagnosis1,diagnosis3)     5480
## cor(diagnosis2,diagnosis3)     6634
##
## ~subID (Number of levels: 92)
##                                     Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)          0.82     0.13    0.57    1.09 1.00   3053    4447
##
## Regression Coefficients:
##                                     Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept           0.67     0.27    0.13    1.20 1.00   1793    3242
## diagnosis1          0.80     0.21    0.36    1.22 1.00   4831    5036
## diagnosis2         -0.42     0.21   -0.83    0.01 1.00   5698    4716
## diagnosis3          -0.31    0.22   -0.74    0.11 1.00   4893    4773
##
## Further Distributional Parameters:
##                                     Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma              5.09     0.07    4.97    5.23 1.00   10076   5423
##
## 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).

# FAB in ADHD > FAB in COMP
hypothesis(m.fab.perc, "diagnosis1 > - diagnosis1 - diagnosis2 - diagnosis3")

## Hypothesis Tests for class b:
##                                     Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (diagnosis1)-(-di... > 0     0.87      0.36    0.28    1.46      124
## 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.

# print an overview
kable(df.fab.wide %>% group_by(diagnosis, subID) %>%
      summarise(fab.perc = mean(fab.perc)) %>%
      group_by(diagnosis) %>%

```

```

summarise(
  fab.perc.avg = mean(fab.perc),
  fab.perc.se  = sd(fab.perc)/sqrt(n())
) %>% arrange(desc(fab.perc.avg))

```

diagnosis	fab.perc.avg	fab.perc.se
ADHD	1.8046277	0.2552834
COMP	0.8870717	0.1772152
BOTH	0.6075702	0.2310650
ASD	0.5096168	0.3028107

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.

5.1 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
10	face	216
10	object	216
11	face	216
11	object	216

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

stm	cue	diagnosis	n
1_10	face	ADHD	138
1_10	face	ASD	138
1_10	face	BOTH	132
1_10	face	COMP	144
1_10	object	ADHD	138
1_10	object	ASD	138

```

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), max_rank = min(max_rank)) %>%
  filter(rhat >= 1.05 | max_rank != max(max_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 = 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(rep(1, length(unique(df.results.b$variable))), # all same SD
                     unique(df.results.b$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.

5.2 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.

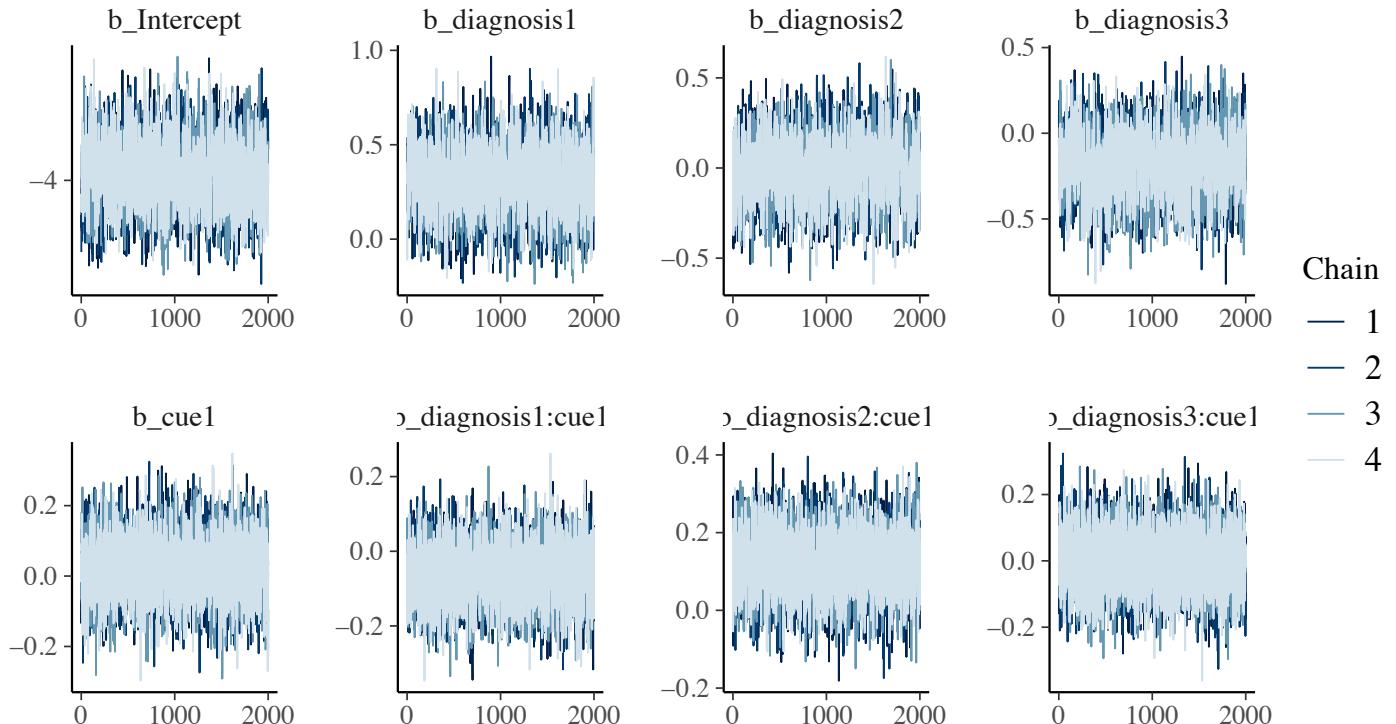
# check that rhats are below 1.01
sum(brms::rhat(m.err) >= 1.01, na.rm = T)

## [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.

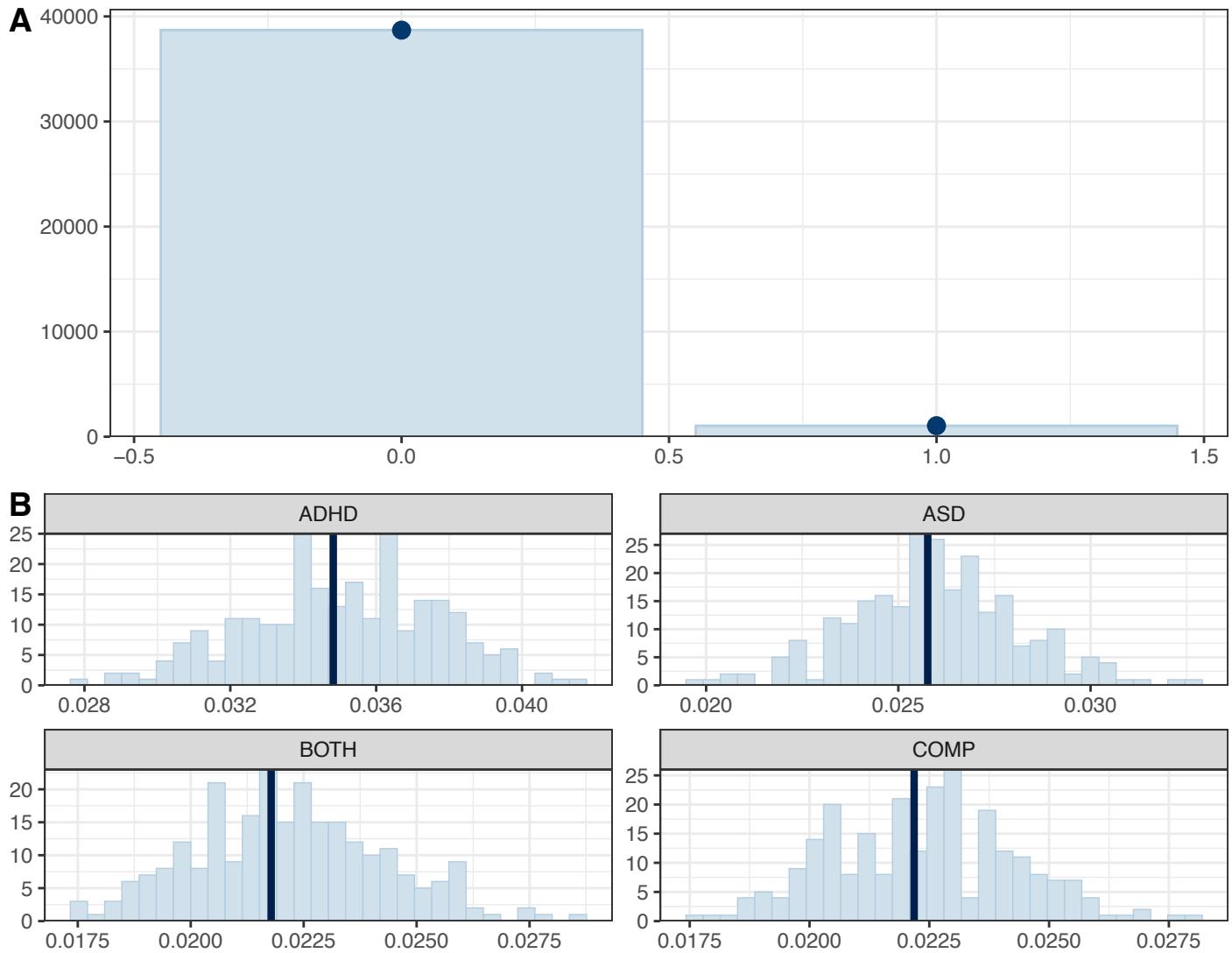
```
# get posterior predictions
post.pred = posterior_predict(m.err, ndraws = nsim)

# 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))
```

Posterior predictive checks: errors



Our model fits the data very well.

5.3 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: 39744)
## 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)                      0.27     0.06    0.17    0.40 1.00
## sd(diagnosis1)                     0.10     0.06    0.00    0.23 1.00
## sd(diagnosis2)                     0.08     0.06    0.00    0.21 1.00
## sd(diagnosis3)                     0.10     0.07    0.00    0.26 1.00
## sd(cue1)                           0.41     0.07    0.29    0.56 1.00
## sd(diagnosis1:cue1)                0.10     0.07    0.00    0.24 1.00
## sd(diagnosis2:cue1)                0.10     0.07    0.01    0.25 1.00
## sd(diagnosis3:cue1)                0.20     0.09    0.03    0.38 1.00
## cor(Intercept,diagnosis1)          -0.09    0.28   -0.61    0.49 1.00
## cor(Intercept,diagnosis2)          0.10     0.29   -0.49    0.64 1.00
## cor(diagnosis1,diagnosis2)         -0.03    0.30   -0.60    0.55 1.00
## cor(Intercept,diagnosis3)          0.07     0.29   -0.51    0.60 1.00
## cor(diagnosis1,diagnosis3)         -0.01    0.30   -0.57    0.55 1.00
## cor(diagnosis2,diagnosis3)         -0.05    0.31   -0.62    0.55 1.00
## cor(Intercept,cue1)                -0.15    0.20   -0.53    0.26 1.00
## cor(diagnosis1,cue1)               0.09     0.28   -0.48    0.60 1.01
## cor(diagnosis2,cue1)               0.10     0.30   -0.50    0.64 1.00
## cor(diagnosis3,cue1)               -0.01    0.28   -0.55    0.54 1.00
## cor(Intercept,diagnosis1:cue1)     -0.08    0.30   -0.62    0.51 1.00
## cor(diagnosis1,diagnosis1:cue1)    0.01     0.31   -0.58    0.60 1.00
## cor(diagnosis2,diagnosis1:cue1)    -0.00    0.30   -0.58    0.57 1.00
## cor(diagnosis3,diagnosis1:cue1)    -0.03    0.30   -0.61    0.55 1.00
## cor(cue1,diagnosis1:cue1)          -0.01    0.29   -0.56    0.54 1.00
## cor(Intercept,diagnosis2:cue1)     -0.12    0.29   -0.65    0.46 1.00
## cor(diagnosis1,diagnosis2:cue1)    0.07     0.30   -0.52    0.63 1.00
## cor(diagnosis2,diagnosis2:cue1)    -0.03    0.30   -0.60    0.56 1.00
## cor(diagnosis3,diagnosis2:cue1)    0.06     0.30   -0.54    0.63 1.00
## cor(cue1,diagnosis2:cue1)          0.04     0.28   -0.52    0.57 1.00
## cor(diagnosis1:cue1,diagnosis2:cue1) -0.06    0.30   -0.62    0.53 1.00
## cor(Intercept,diagnosis3:cue1)     -0.18    0.26   -0.65    0.35 1.00
## cor(diagnosis1,diagnosis3:cue1)    -0.03    0.29   -0.58    0.54 1.00
## cor(diagnosis2,diagnosis3:cue1)    -0.01    0.30   -0.58    0.57 1.00
## cor(diagnosis3,diagnosis3:cue1)    0.01     0.30   -0.56    0.59 1.00
## cor(cue1,diagnosis3:cue1)          0.14     0.24   -0.36    0.59 1.00
## cor(diagnosis1:cue1,diagnosis3:cue1) 0.02     0.29   -0.54    0.58 1.00
## cor(diagnosis2:cue1,diagnosis3:cue1) 0.00     0.29   -0.55    0.57 1.00
##                                         Bulk_ESS Tail_ESS
## sd(Intercept)                      3180      4943
## sd(diagnosis1)                     3037      3160
## sd(diagnosis2)                     4164      3892
## sd(diagnosis3)                     2639      3595
## sd(cue1)                           4461      5351
## sd(diagnosis1:cue1)                2894      3630
## sd(diagnosis2:cue1)                3559      3888
## sd(diagnosis3:cue1)                3044      2652
## cor(Intercept,diagnosis1)          11464     6131
## cor(Intercept,diagnosis2)          12676     5841

```

```

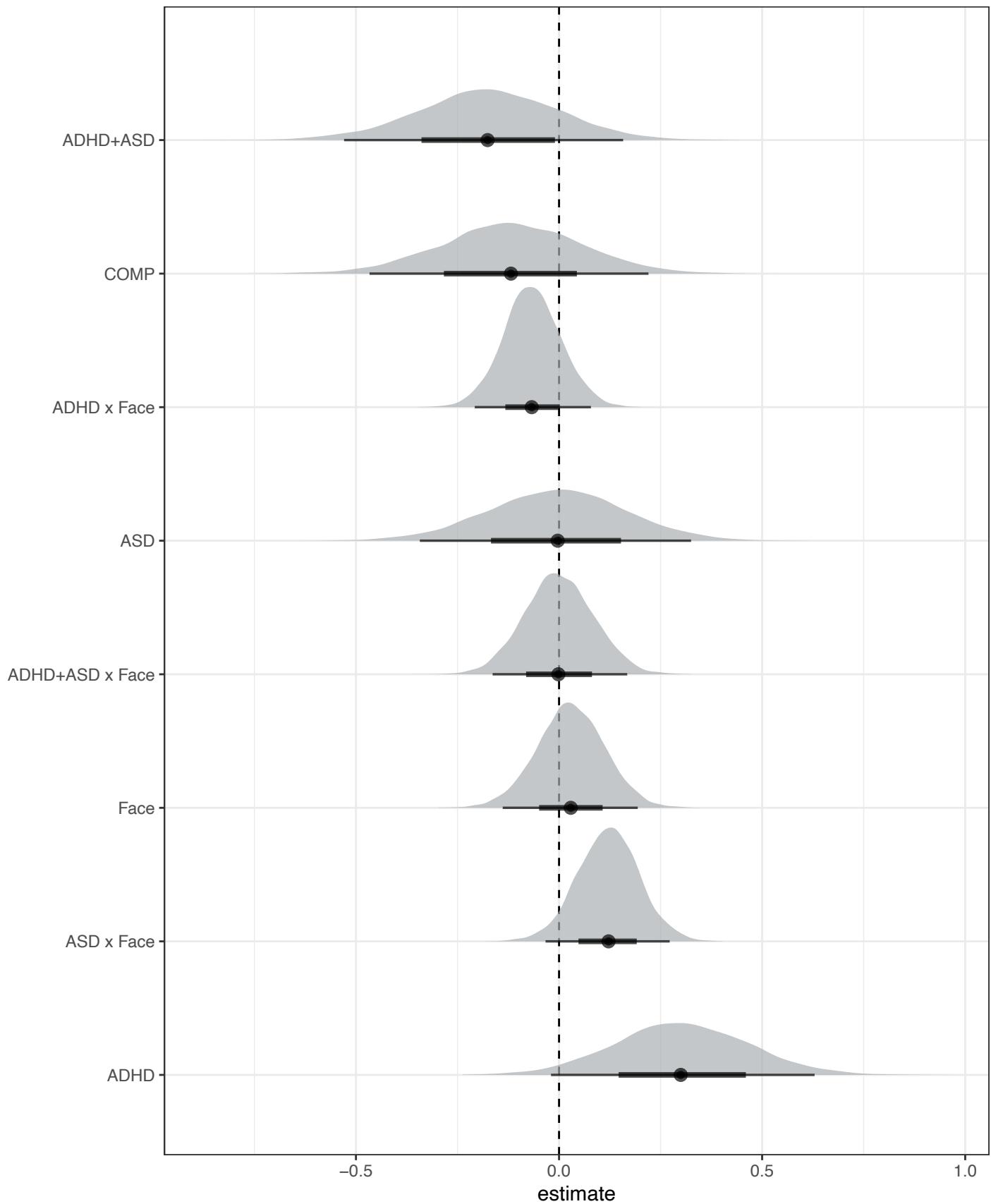
## cor(diagnosis1,diagnosis2)      10568    5984
## cor(Intercept,diagnosis3)      10830    5808
## cor(diagnosis1,diagnosis3)      9519     6325
## cor(diagnosis2,diagnosis3)      7752     6125
## cor(Intercept,cue1)            3418     4852
## cor(diagnosis1,cue1)           1314     2330
## cor(diagnosis2,cue1)           1175     2265
## cor(diagnosis3,cue1)           1698     3942
## cor(Intercept,diagnosis1:cue1) 11169     6189
## cor(diagnosis1,diagnosis1:cue1) 8951     6180
## cor(diagnosis2,diagnosis1:cue1) 7464     6489
## cor(diagnosis3,diagnosis1:cue1) 6554     6153
## cor(cue1,diagnosis1:cue1)       11797    6838
## cor(Intercept,diagnosis2:cue1) 11154     5917
## cor(diagnosis1,diagnosis2:cue1) 8485     6081
## cor(diagnosis2,diagnosis2:cue1) 7835     6775
## cor(diagnosis3,diagnosis2:cue1) 6929     6569
## cor(cue1,diagnosis2:cue1)       11365    6347
## cor(diagnosis1:cue1,diagnosis2:cue1) 5844     5975
## cor(Intercept,diagnosis3:cue1) 8037     6164
## cor(diagnosis1,diagnosis3:cue1) 5547     5893
## cor(diagnosis2,diagnosis3:cue1) 4725     5764
## cor(diagnosis3,diagnosis3:cue1) 5023     5485
## cor(cue1,diagnosis3:cue1)       8883     6422
## cor(diagnosis1:cue1,diagnosis3:cue1) 6098     6517
## cor(diagnosis2:cue1,diagnosis3:cue1) 5441     6221
##
## ~subID (Number of levels: 92)
##                               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)             0.86     0.09    0.71   1.05 1.00   2188    3544
## sd(cue1)                 0.21     0.07    0.05   0.33 1.00   1189    635
## cor(Intercept,cue1)      0.11     0.23   -0.37   0.54 1.00   5792    4821
##
## Regression Coefficients:
##                               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept                  -3.97     0.11   -4.19   -3.74 1.00   2326    3451
## diagnosis1                  0.30     0.16   -0.02   0.63 1.00   2064    3624
## diagnosis2                 -0.01     0.17   -0.34   0.33 1.00   2008    3333
## diagnosis3                 -0.18     0.17   -0.53   0.16 1.00   2022    3971
## cue1                        0.03     0.08   -0.14   0.19 1.00   4801    5423
## diagnosis1:cue1            -0.07     0.07   -0.21   0.08 1.00   7398    6505
## diagnosis2:cue1            0.12     0.08   -0.03   0.27 1.00   6430    6252
## diagnosis3:cue1            -0.00     0.09   -0.16   0.17 1.00   6506    5913
##
## 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).
# 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     -0.42      0.27    -0.96     0.11     15.7
```

```

## 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     -0.11      0.28    -0.68     0.44      1.92
## Post.Prob Star
## 1      0.66
## ---
## '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      0.29     -0.5      0.62      1.42
## 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     -0.06      0.17    -0.39     0.28      1.79      0.64
## 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.

# 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,

```

Table 10: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
ADHD_face	0.025	0.0054	0.011	0.015	0.036	0.05
ADHD_object	0.026	0.0057	0.012	0.016	0.039	0.057
COMP_face	0.017	0.0039	0.0064	0.0098	0.025	0.037
COMP_object	0.017	0.004	0.0065	0.01	0.026	0.038
ASD_face	0.022	0.0049	0.008	0.013	0.032	0.05
ASD_object	0.016	0.0037	0.0066	0.0098	0.024	0.037
BOTH_face	0.016	0.004	0.0061	0.0095	0.025	0.04
BOTH_object	0.016	0.0039	0.0056	0.009	0.024	0.036

Table 11: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	0.02	0.0027	0.012	0.015	0.025	0.032
object	0.019	0.0027	0.01	0.014	0.024	0.032
FAB	-0.00094	0.0032	-0.014	-0.0073	0.0052	0.013

```

    re_formula = NA))
colnames(df.ms) = df.new$condition

st(df.ms,
  summ = c('mean(x)', 'sd(x)', 'min(x)', 'pctile(x)[2.5]',
           'pctile(x)[97.5]', 'max(x)'))

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)'))

```

Accuracies were generally high, with a total of 2.61% 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).

5.4 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) +

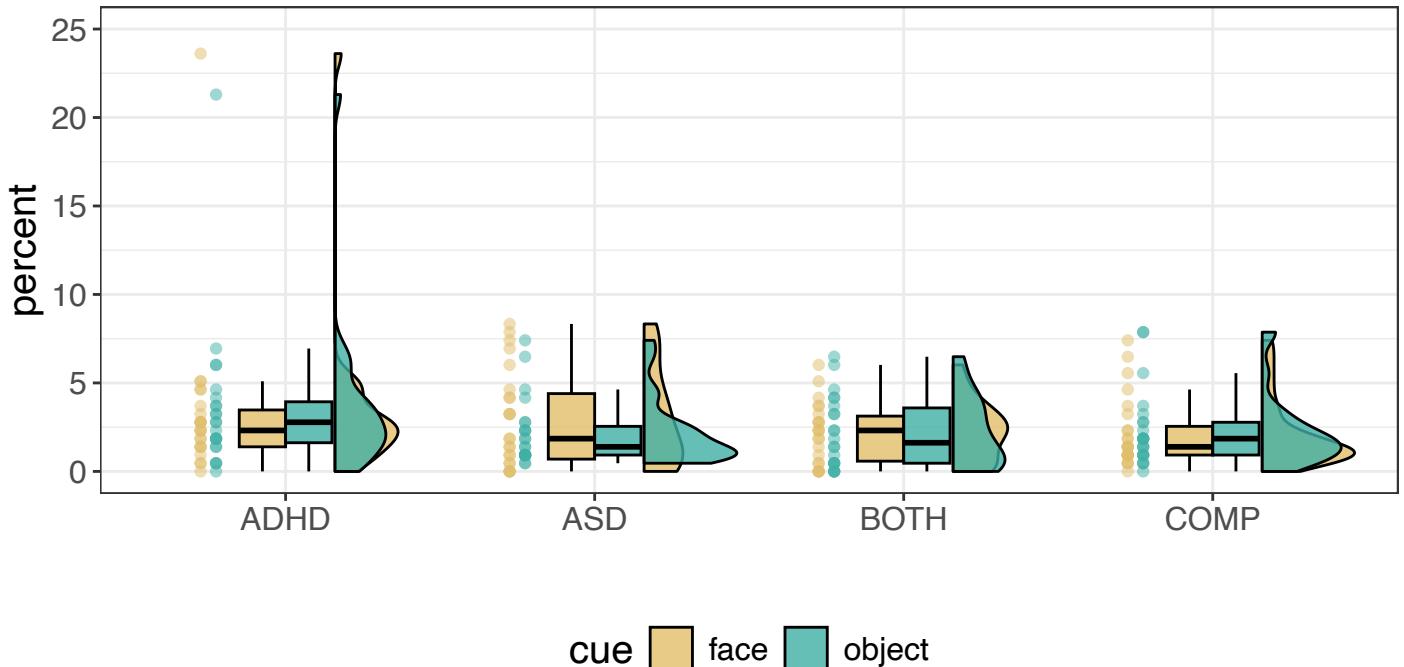
```

```

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))

```

Mean error rates



6 Summary table

```

# get grand average of accuracies and reaction times
df.agg = rbind(
  df.fab.full %>%
    group_by(subID, diagnosis, cue) %>%
    summarise(error = 100*mean(error, na.rm = T)) %>%
    group_by(diagnosis, cue) %>%
    summarise(mean = mean(error, na.rm = T), se = sd(error, na.rm = T)/sqrt(n())) %>%
    mutate(measure = "accuracy") %>%
    mutate(
      value = sprintf("%.2f ±%.2f", mean, se)
    ) %>% select(measure, diagnosis, cue, value) %>%
    pivot_wider(names_from = c(diagnosis, cue), values_from = value),
  df.fab.full %>%
    group_by(subID, diagnosis, cue) %>%
    summarise(rt.cor = mean(rt.cor, na.rm = T)) %>%
    group_by(diagnosis, cue) %>%
    summarise(mean = mean(rt.cor, na.rm = T), se = sd(rt.cor, na.rm = T)/sqrt(n())) %>%
    mutate(measure = "rt.cor") %>%
    mutate(
      value = sprintf("%.0f ±%.0f", mean, se)
    ) %>% select(measure, diagnosis, cue, value) %>%
    pivot_wider(names_from = c(diagnosis, cue), values_from = value))

read_docx() %>%

```

```
body_add_table(df.agg) %>%
print(target = "FAB_tbl2.docx")
```

7 Preparation for eye-tracking analysis

First, we reload the data. Second, we preprocess the latencies of the saccades and divide them into saccades elicited by the cues and saccades elicited by the target. To do so, we use the knowledge that latencies below 100ms are extremely unlikely and use the global minimum in the density function.

```
# number of simulations
nsim = 250

# set the seed
set.seed(2468)

# load the data
load("FAB_data.RData")

# combine both behavioural datasets
df.fab = rbind(df.fab, df.exp)
df.fab$diagnosis = factor(df.fab$diagnosis,
                           levels = c("ADHD", "ASD", "BOTH", "COMP"))

# compute subject specific FAB
df.fab.agg = df.fab %>%
  group_by(subID, diagnosis, stm, cue) %>%
  # 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
  ) %>% group_by(subID, diagnosis) %>%
  # calculate the mean FAB per person
  summarise(
    fab = mean(fab)
  ) %>% ungroup()

# remove participants without any data
df.sac = df.sac %>% filter(!is.na(lat)) %>% ungroup() %>%
  # remove unbelievably short and extremely long saccades
  filter(lat <= quantile(lat, probs = 0.99) &
         lat > 100) %>%
  # recode so that it is more consistent
  mutate(
    direction = if_else(dir_face, "face", "object")
  )

# divide into cue and target saccades
criticalpoints = function(density, threshold = 1){
  up   = sapply(1:threshold, function(n) c(density$y[-(seq(n))], rep(NA, n)))
  down = sapply(-1:-threshold,
                function(n) c(rep(NA, abs(n)),
                             density$y[-seq(length(density$y),
                                           length(density$y) - abs(n) + 1)]))
  a    = cbind(density$y, up, down)
  minima = round(density$x[which(apply(a, 1, min) == a[,1])])
```

```

maxima = round(density$x[which(apply(a, 1, max) == a[,1])])
return(list(minima = minima, maxima = maxima))
}

points = criticalpoints(density(df.sac$lat))

# get the density of the latencies
dd = with(density(df.sac$lat), data.frame(x,y))

# find which point is the global minimum
lat.points = dd$y[points$minima]
idx = which.min(lat.points)

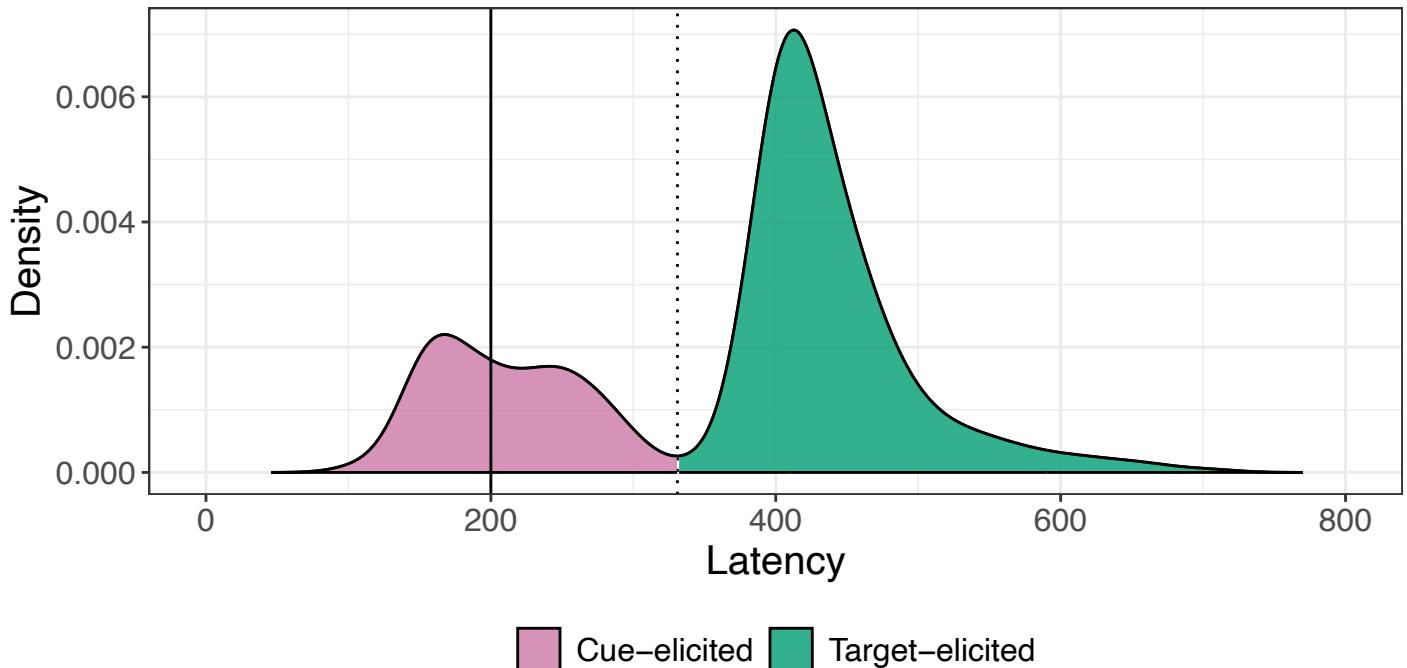
# print the latency
points$minima[idx]

## [1] 331

# plot it all
ggplot(dd, aes(x = x, y = y)) +
  geom_line() +
  geom_vline(xintercept = points$minima[idx], linetype=3) +
  geom_ribbon(data = subset(dd, x <= points$minima[idx]),
              aes(ymax = y, fill = "cue-elicited"), ymin = 0,
              colour = "black", alpha = .8) +
  geom_ribbon(data = subset(dd, x >= points$minima[idx]),
              aes(ymax = y, fill = "target-elicited"), ymin = 0,
              colour = "black", alpha = .8) +
  scale_fill_manual(name = "test",
                    values = c("cue-elicited" = custom.col[7], "target-elicited" = custom.col[3]),
                    labels = c("Cue-elicited", "Target-elicited")) +
  geom_vline(xintercept = 200) +
  labs(title = "Classification of saccades", x = "Latency", y = "Density") +
  xlim(0, 800) +
  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())

```

Classification of saccades



```
ggsave("Fig2_densLatency.svg",
       units = "mm",
       width = 170,
       height = 100,
       dpi    = 300)
```

The graph above shows the density of the latencies with zero on the x-axis being the onset of the cue. After 200ms, the cue disappears and the target is presented on the screen (solid line). We can see that there is a minimum about 130ms after the target appears (dotted line). We can assume that saccades produced before this were in response to the cue (pink) and saccades after were in response to the target (green). Therefore, we divide the saccades accordingly. Then, we aggregate the data per subject and cue. Last, we set all predictors to sum contrasts.

```
# summarise overall saccade count based on direction: whole trial
df.cnt = df.sac %>%
  group_by(subID, direction) %>%
  summarise(
    n.sac = n()
  )

# add a zero if no saccades were produced
subID      = rep(as.character(unique(df.sac$subID)),
                 each = length(unique(df.sac$direction)))
direction = rep(as.character(unique(df.sac$direction)),
               times = length(unique(df.sac$subID)))
df.cnt = merge(df.cnt, data.frame(subID, direction), all = T) %>%
  mutate(
    n.sac = if_else(is.na(n.sac), 0, n.sac)
  ) %>%
# merge with behavioural data
  merge(., df.fab.agg) %>%
  mutate_if(is.character, as.factor)

# code whether or not cue associated saccade occurred and capture latencies
df.cue = merge(df.fab,
               df.sac %>% filter(lat <= points$minima[idx] & sac_trl == 1),
               all = T) %>%
  select(subID, diagnosis, trl, stm, cue, rt.cor, acc, direction, lat) %>%
```

```

  mutate(
    sac = if_else(is.na(direction), 0, 1)
  ) %>%
  mutate_if(is.character, as.factor)

# preprocess target latencies
df.lat = df.sac %>%
  # only keep latencies associated with target
  filter(lat > points$minima[idx]) %>%
  # only keep the first target saccade latency of each trial
  group_by(subID, diagnosis, trl, cue) %>%
  filter(sac_trl == min(sac_trl)) %>%
  merge(., df.fab) %>%
  mutate_if(is.character, as.factor)

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

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

contrasts(df.lat$diagnosis) = contr.sum(4)
contrasts(df.lat$diagnosis)

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

contrasts(df.cue$direction) = contr.sum(2)
contrasts(df.cue$direction)

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

contrasts(df.cue$diagnosis) = contr.sum(4)
contrasts(df.cue$diagnosis)

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

contrasts(df.cnt$direction) = contr.sum(2)
contrasts(df.cnt$direction)

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

contrasts(df.cnt$diagnosis) = contr.sum(4)
contrasts(df.cnt$diagnosis)

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

```

8 Number of saccades towards face during trial

First, we are going to assess the saccades that are produced in the direction of the face throughout the full trial: cue and target presentation. Based on Entzmann et al. (2021), we hypothesised that COMP participants produce more saccades towards the face than towards the object cues during the trials.

8.1 Specify the model

Since we are counting the number of saccades, we use a poisson distribution for our model. We add an group-level intercept for each subject, and assess the influence of the predictors diagnostic status and whether the saccade was directed towards the side of the face or object as well as the interaction. We set our priors very wide because we do not have strong prior assumptions apart from people producing fewer saccades than there are trials.

```
code = "CNT"

# set the formula
f.cnt = brms::bf(n.sac ~ diagnosis * direction + (1 | subID))

# set priors based on study design
priors = c(
  prior(normal(3, 1.5), class = Intercept),
  prior(normal(0, 1.0), class = sd),
  prior(normal(0, 1.0), class = b)
)

# set number of iterations and warmup for models
iter = 4500
warm = 1500
```

8.2 Simulation-based calibration

```
# 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
  set.seed(2468)
  gen = SBC_generator_brms(f.cnt, data = df.cnt, prior = priors,
    thin = 50, warmup = 10000, refresh = 2000,
    generate_lp = TRUE, family = poisson(), init = 0.1)
  bck = SBC_backend_brms_from_generator(gen, chains = 4, thin = 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 only 0 models had divergent samples. This suggests that this model performs well.

8.3 Prior predictive checks

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

```
# get the true values
truePars = dat[["variables"]]

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

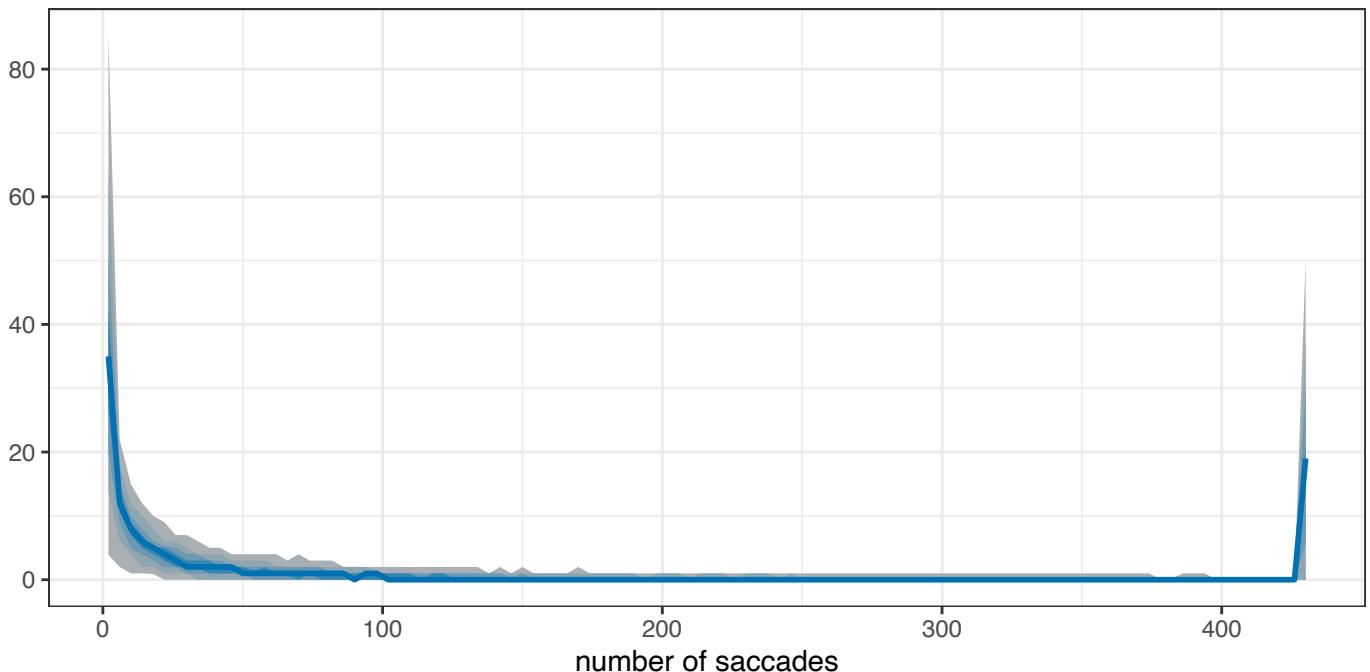
# set very large data points to a value of 432
dvfakemath = dvfakemat;
dvfakemath[dvfakemath > 432] = 432
# compute one histogram per simulated data-set
breaks = seq(0, max(dvfakemath, na.rm=T), length.out = 100)
binwidth = round(breaks[2] - breaks[1])
breaks = seq(0, max(dvfakemath, na.rm=T), binwidth)
histmat = matrix(NA, ncol = nrow(truePars) + binwidth, nrow = length(breaks)-1)
for (i in 1:nrow(truePars)) {
  histmat[,i] = hist(dvfakemath[,i], breaks = breaks, plot = F)$counts
}
# for each bin, compute quantiles across histograms
probs = seq(0.1, 0.9, 0.1)
quantmat= as.data.frame(matrix(NA, nrow=dim(histmat)[1], ncol = length(probs)))
names(quantmat) = paste0("p", probs)
for (i in 1:dim(histmat)[1]) {
  quantmat[i,] = quantile(histmat[i,], p = probs, na.rm = T)
}
quantmat$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 = "Prior predictive distribution", y = "", x = "number of saccades") +
  theme_bw()

tmpM = apply(dvfakemath, 2, mean) # mean
tmpSD = apply(dvfakemath, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark) +
  labs(x = "Mean number of saccades", title = "Means of simulated data") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD number of saccades", title = "Standard deviations of simulated data") +
  theme_bw()

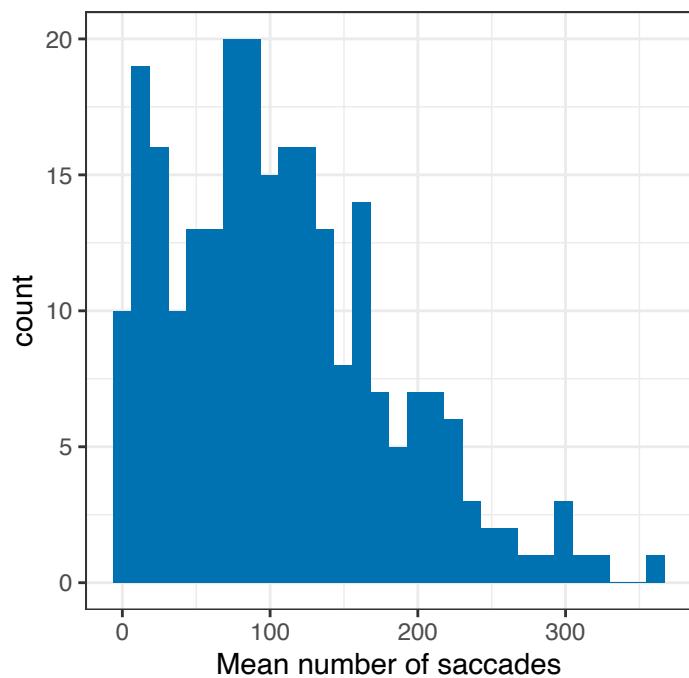
p = ggarrange(p1,
  ggarrange(p2, p3, ncol = 2, labels = c("B", "C")),
  nrow = 2, labels = "A")
annotate_figure(p, top = text_grob("Prior predictive checks", face = "bold", size = 14))
```

Prior predictive checks

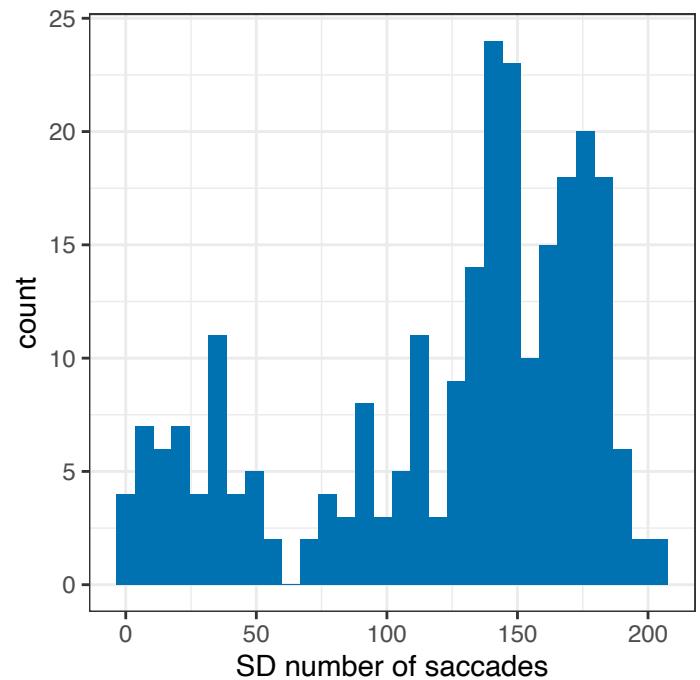
A Prior predictive distribution



B Means of simulated data



C Standard deviations of simulated data



Since our priors were set very wide, we do get wide prior predictive distributions. We accept this and continue with our checks.

8.4 Computational faithfulness and model sensitivity

```
# get simulation numbers with issues
des_rank = max(df.results$max_rank)
check = merge(df.results %>%
  group_by(sim_id) %>%
  summarise(
    rhat = max(rhat, na.rm = T),
    mean_rank = max(max_rank)
  ) %>%
```

```

filter(rhat >= 1.05 | mean_rank < des_rank),
df.backend %>% filter(n_divergent > 0), all = T)

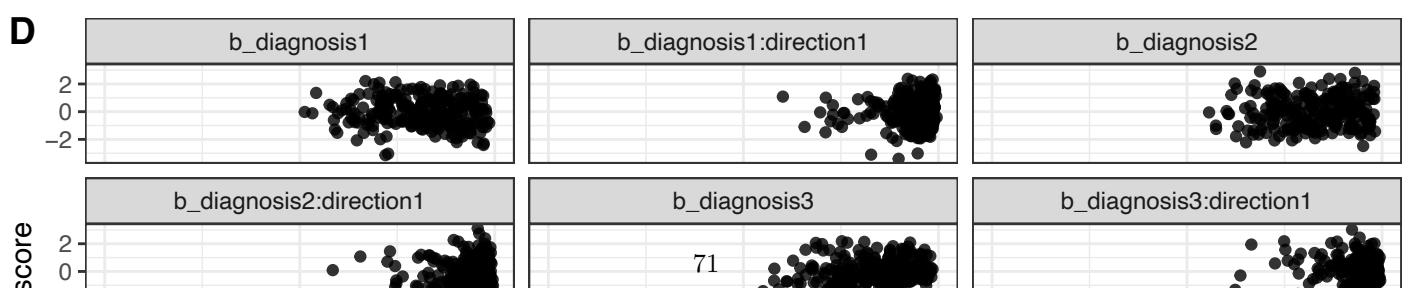
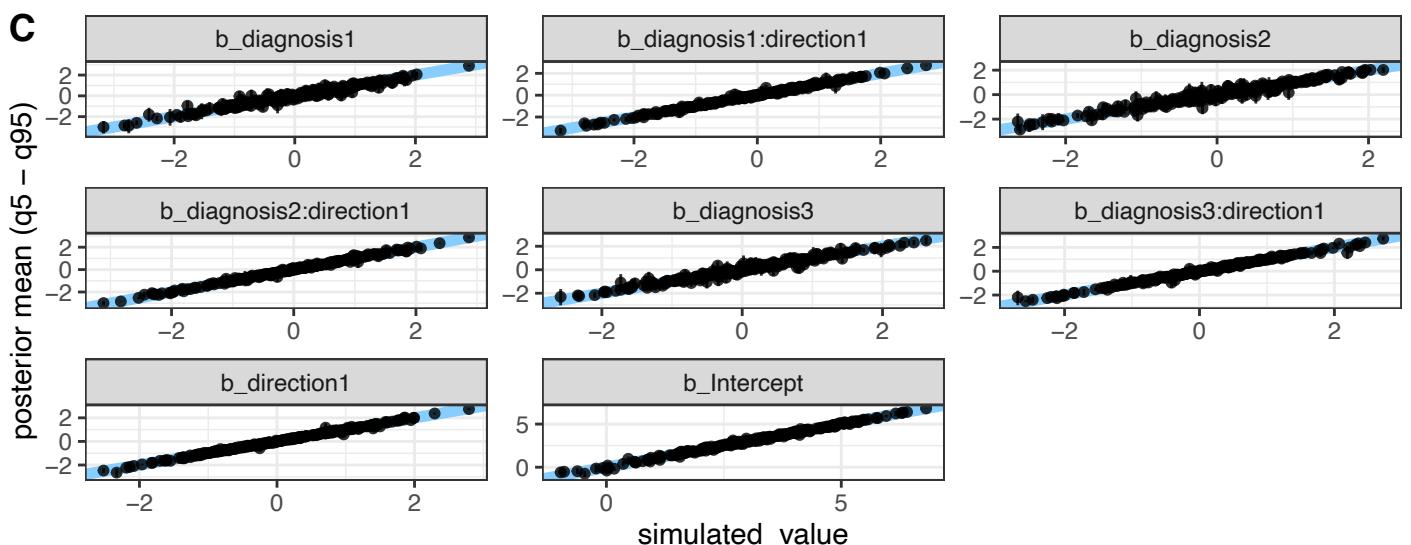
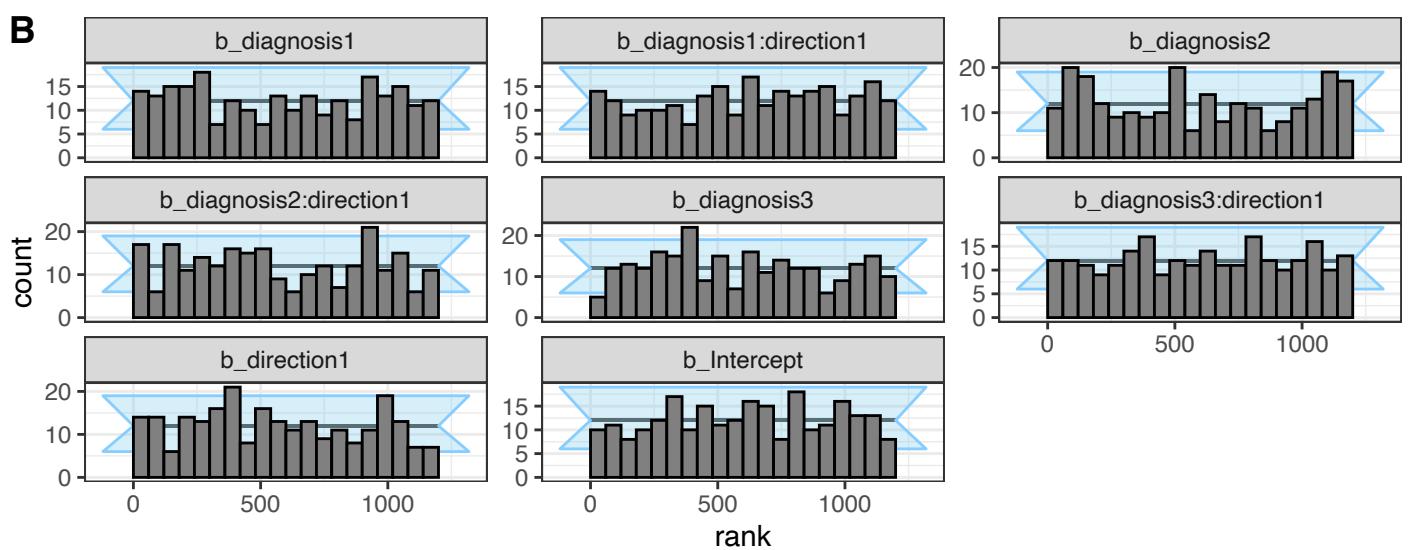
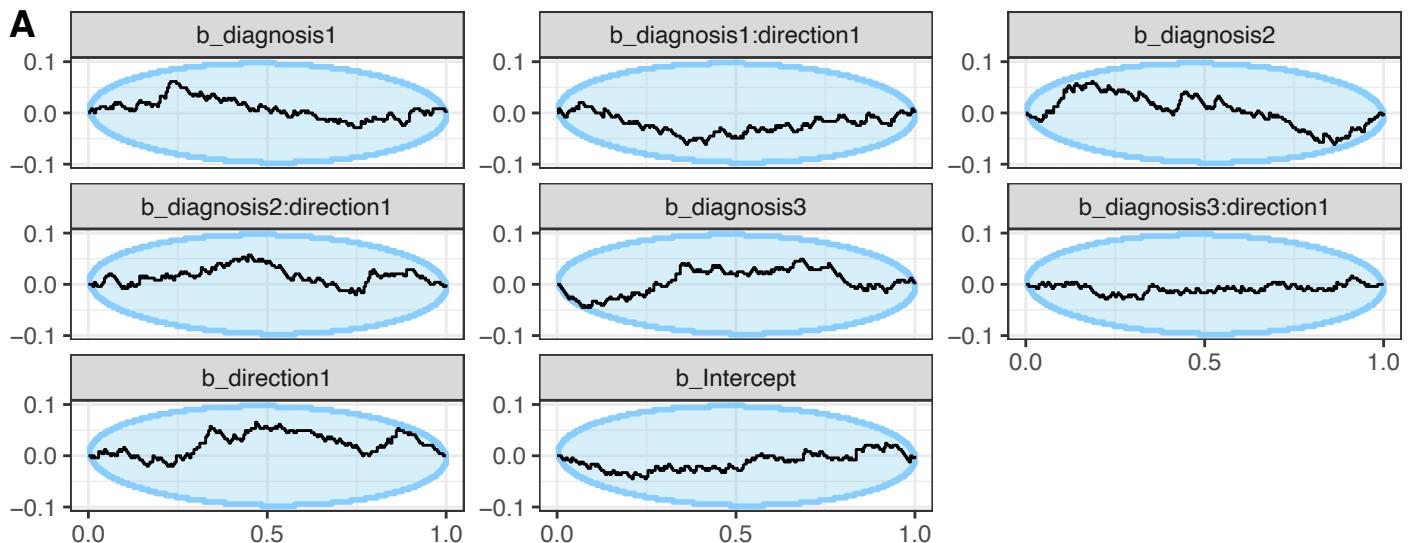
# plot SBC with functions from the SBC package focusing on population-level parameters

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

```

Computational faithfulness and model sensitivity



All of this looks good. Despite our wide priors, the contraction shows a bit of a distribution which increases our trust that the wide priors are appropriate.

8.5 Posterior predictive checks

As the next step, we fit the model and check whether the chains have converged, which they seem to have. We then perform posterior predictive checks on the model using the bayesplot package.

```
# fit the model
set.seed(2468)
m.cnt = brm(f.cnt,
             df.cnt, prior = priors,
             iter = iter, warmup = warm,
             backend = "cmdstanr", threads = threading(8),
             file = "m_cnt-face",
             family = "poisson",
             save_pars = save_pars(all = TRUE)
)
rstan::check_hmc_diagnostics(m.cnt$fit)

##
## Divergences:
## 0 of 12000 iterations ended with a divergence.

##
## Tree depth:
## 0 of 12000 iterations saturated the maximum tree depth of 10.

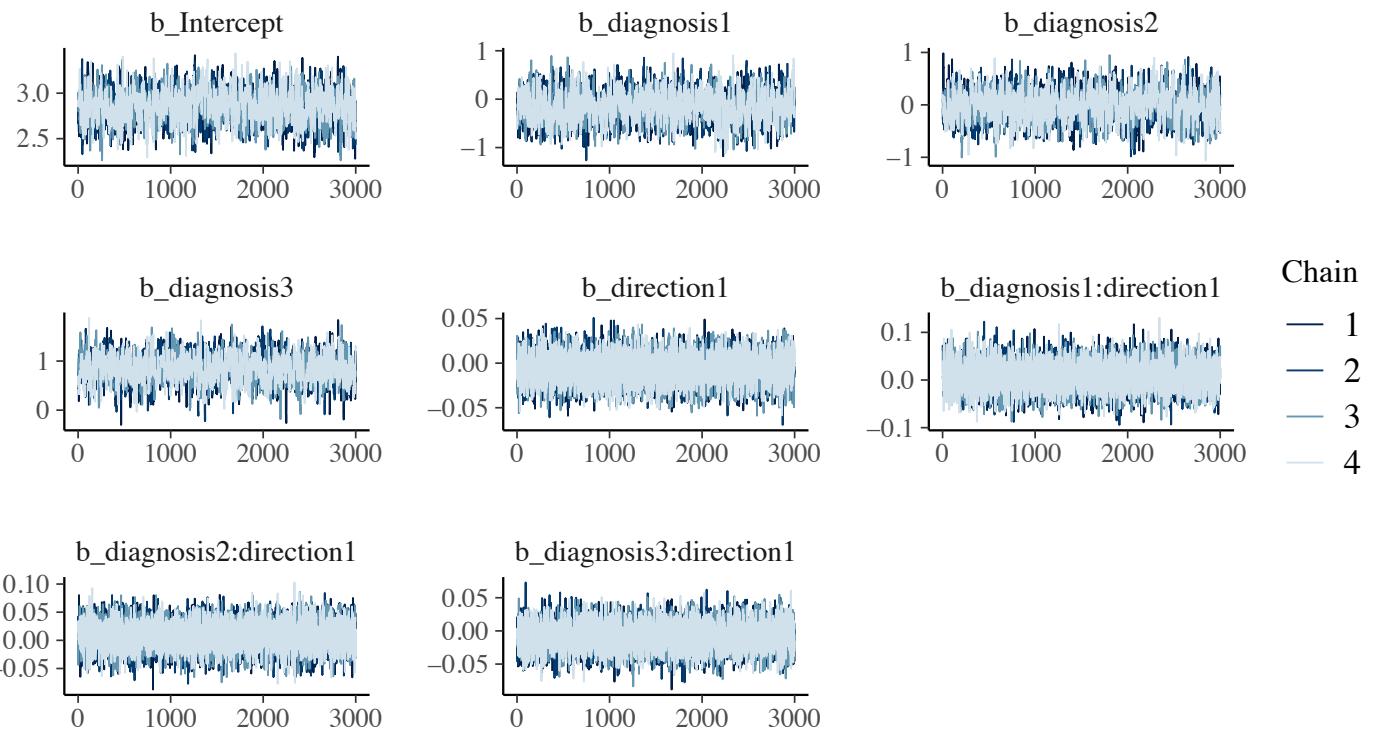
##
## Energy:
## E-BFMI indicated no pathological behavior.

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

## [1] 0

# check the trace plots
post.draws = as_draws_df(m.cnt)
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 divergent samples and no rhats that are higher or equal to 1.01. Therefore, we go ahead and perform our posterior predictive checks.

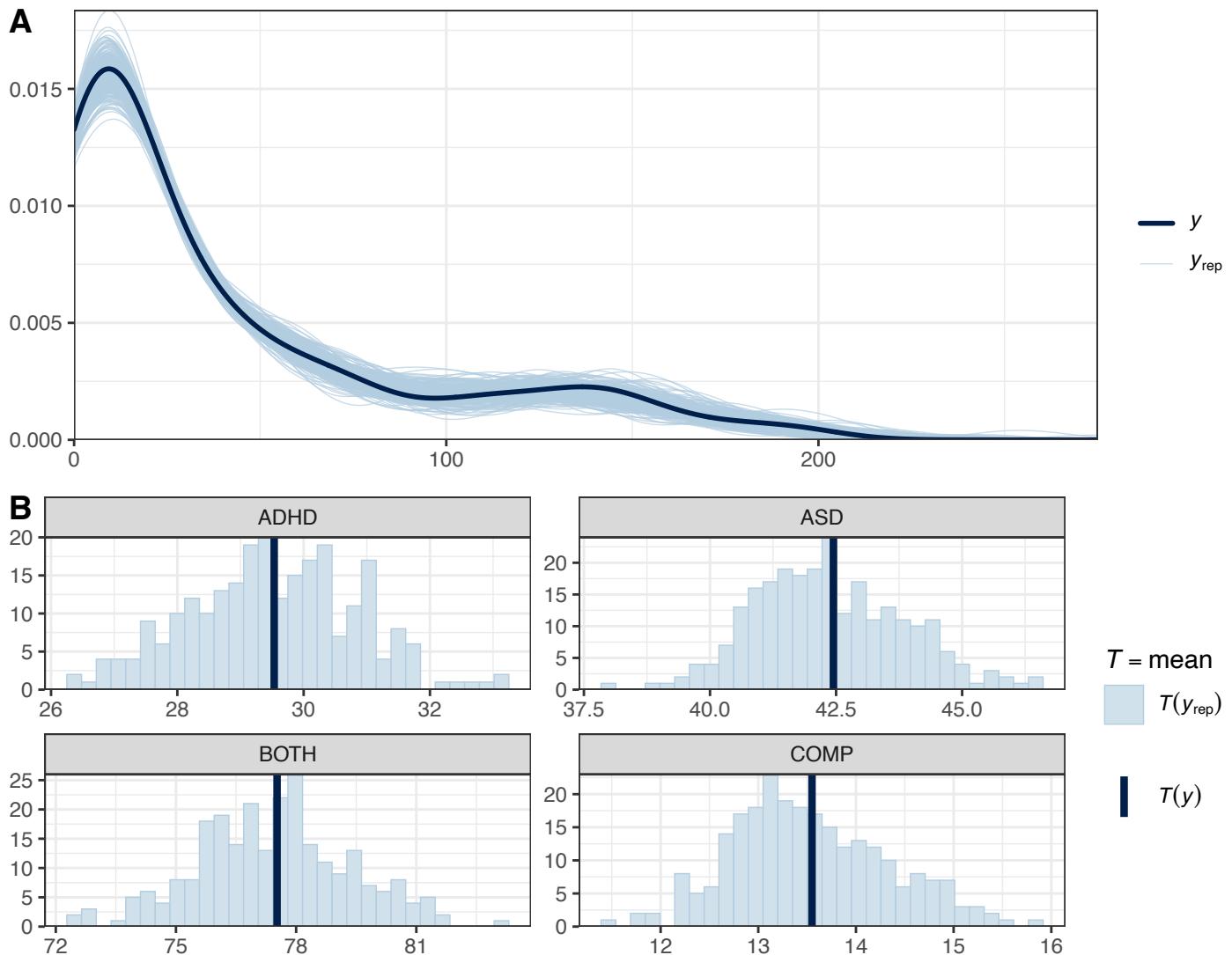
```
# get the posterior predictions
post.pred = posterior_predict(m.cnt, ndraws = nsim)

# check the fit of the predicted data compared to the real data
p1 = pp_check(m.cnt, ndraws = nsim) +
  theme_bw()

# distributions of means and sds compared to the real values per group
p2 = ppc_stat_grouped(df.cnt$n.sac, post.pred, df.cnt$diagnosis) +
  theme_bw()

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

Posterior predictive checks: number of saccades towards face



The predictions based on the model capture the data well. This further increases our trust in the model.

8.6 Inferences

Now that we are convinced that we can trust our model, we have a look at the model and its estimates.

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

## Family: poisson
## Links: mu = log
## Formula: n.sac ~ diagnosis * direction + (1 | subID)
## Data: df.cnt (Number of observations: 150)
## Draws: 4 chains, each with iter = 4500; warmup = 1500; thin = 1;
##         total post-warmup draws = 12000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 75)
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     1.40      0.13     1.18     1.68 1.00     1641     3249
##
## Regression Coefficients:
##                         Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                  2.86      0.17     2.52     3.19 1.00     1307
## diagnosis1                 -0.15      0.30    -0.73     0.43 1.00     1381
```

```

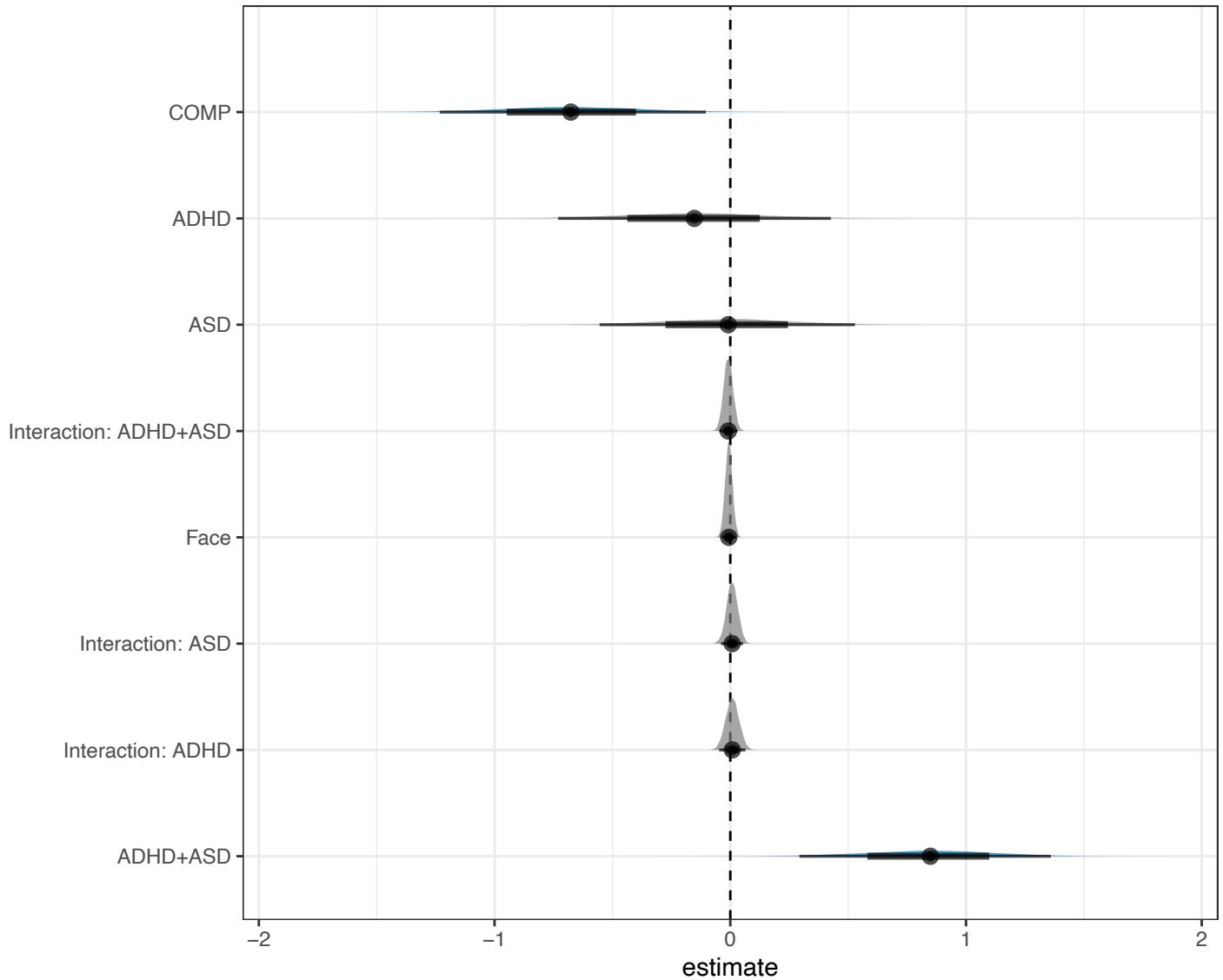
## diagnosis2      -0.01    0.27   -0.55    0.53 1.00    1119
## diagnosis3      0.84    0.27    0.29    1.36 1.00    1112
## direction1     -0.01    0.02   -0.04    0.02 1.00    7199
## diagnosis1:direction1  0.01    0.03   -0.05    0.06 1.00    8978
## diagnosis2:direction1  0.01    0.02   -0.04    0.05 1.00    8923
## diagnosis3:direction1  -0.01   0.02   -0.05    0.03 1.00    8022
##                           Tail_ESS
## Intercept            2576
## diagnosis1           2640
## diagnosis2           2341
## diagnosis3           1912
## direction1          7950
## diagnosis1:direction1  7990
## diagnosis2:direction1  8625
## diagnosis3:direction1  8414
##
## 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.cnt = as_draws_df(m.cnt) %>%
  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.cnt %>%
  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_direction1" ~ "Face",
      "b_diagnosis1:direction1" ~ "Interaction: ADHD",
      "b_diagnosis2:direction1" ~ "Interaction: ASD",
      "b_diagnosis3:direction1" ~ "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")
```



```
# H2a: COMP: face > object
h2a = hypothesis(m.cnt,
                 "0 < 2*(direction1 - diagnosis1:direction1 -
                 diagnosis2:direction1 - diagnosis3:direction1)")
h2a

## Hypothesis Tests for class b:
##                               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*(direction... < 0      0.03       0.09     -0.11      0.17      0.57
##   Post.Prob Star
## 1      0.36
## ---
## '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.

# explore general FAB
e1 = hypothesis(m.cnt, "0 < 2*direction1",
                alpha = 0.025)
e1
```

Table 12: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
COMP_face	9.2	3.1	2.7	4.4	16	31
COMP_object	9.5	3.2	2.5	4.5	17	30
ADHD_face	16	5.8	3.6	7.2	29	54
ADHD_object	16	5.8	4	7.1	29	55
ASD_face	18	6	5.4	8.8	31	61
ASD_object	18	6	5.3	8.8	31	62
BOTH_face	42	13	8.8	21	70	134
BOTH_object	43	13	9.8	21	73	136

Table 13: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	21	4	11	14	30	44
object	22	4.1	11	15	30	44
FAB	0.35	0.59	-2.8	-0.81	1.5	3

```

## Hypothesis Tests for class b:
##                               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*direction1) < 0      0.01       0.03    -0.05     0.07      0.52
##   Post.Prob Star
## 1      0.34
## ---
## '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
df.new = df.cnt %>%
  select(diagnosis, direction) %>%
  distinct() %>%
  mutate(
    condition = paste(diagnosis, direction, sep = "_")
  )
df.ms = as.data.frame(
  fitted(m.cnt, summary = F,
         newdata = df.new %>% select(diagnosis, direction),
         re_formula = NA))
colnames(df.ms) = df.new$condition

st(df.ms,
  summ = c('mean(x)', 'sd(x)', 'min(x)', 'pctile(x)[2.5]',
           'pctile(x)[97.5]', 'max(x)'))

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)'))
)

```

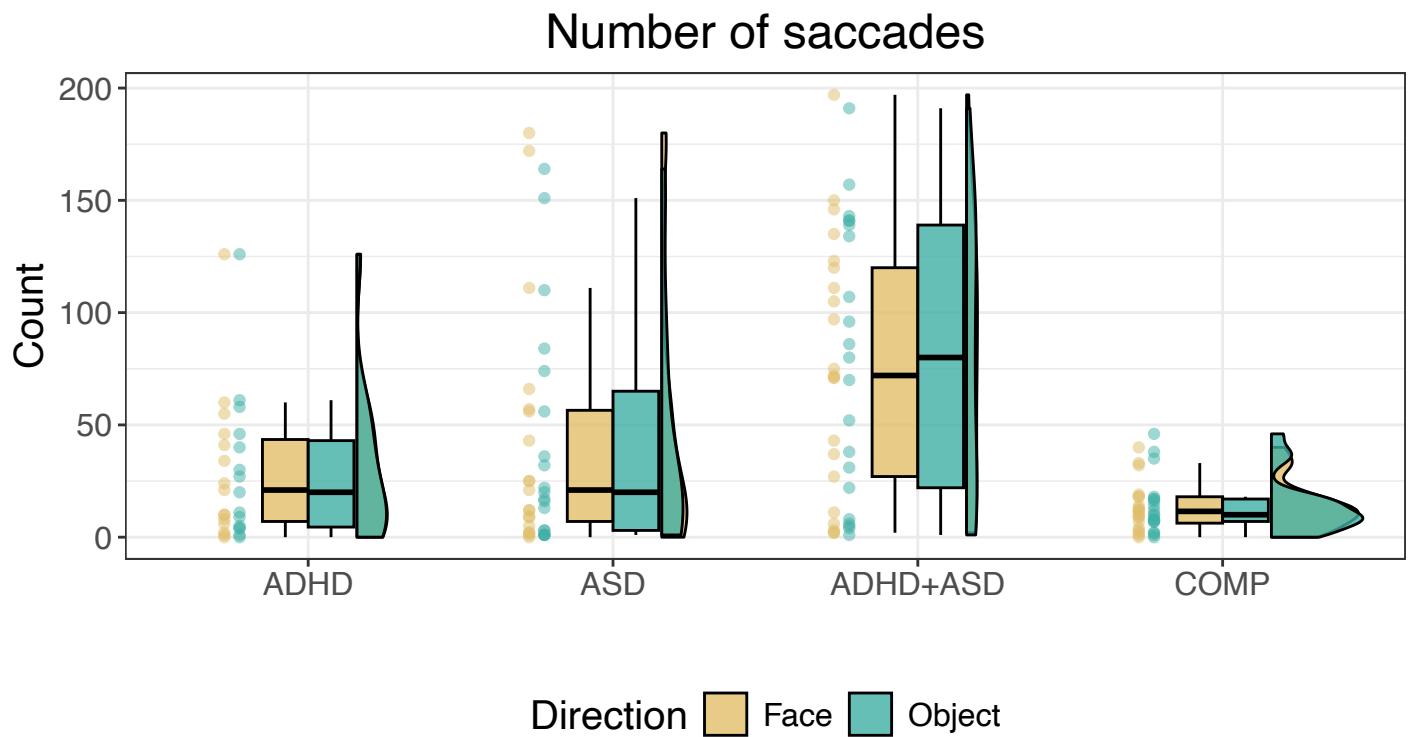
Our hypothesis regarding the number of saccades towards face or object cues was not confirmed: there was no credible difference in our COMP group (*estimate* = 0.03 [-0.11, 0.17], *posterior probability* = 36.33%). Exploration of FAB effect

regardless of the group similarly indicates no FAB in the form of a larger number of saccades produced towards the faces over the whole trial (*estimate* = 0.01 [-0.05, 0.07], *posterior probability* = 34.08%).

8.7 Plots

As a next step, we can now finally plot our data.

```
# rain cloud plot
df.cnt %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD"),
    Direction = recode(direction, "face" = "Face", "object" = "Object")
  ) %>%
  ggplot(aes(diagnosis, n.sac, fill = Direction, colour = Direction)) +
  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_dodgegenudge(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_dodgegenudge(x = -0.25, width = 0.1))) +
  scale_fill_manual(values = custom.col2) +
  scale_color_manual(values = custom.col2) +
  labs(title = "Number of saccades", x = "", y = "Count") +
  theme_bw() +
  theme(legend.position = "bottom",
    plot.title = element_text(hjust = 0.5),
    legend.direction = "horizontal",
    text = element_text(size = 15))
```



```
ggsave("Fig5_nrSac.svg",
  units = "mm",
  width = 170,
  height = 100,
  dpi = 300)
```

9 Latencies of target-elicited saccades

Next, we focus on the latencies of the saccades that are produced during the presentation of the targets to assess whether cue type, diagnostic group or their interaction influence latencies. We hypothesised that ASD participants show an increased latency compared to COMP participants when producing saccades towards targets appearing at the location of a face.

9.1 Full model

We start with the model containing all latencies of saccades produced during the target presentation. We choose a shifted lognormal distribution because saccade latencies below 100ms are very unlikely. Additionally, latencies are determined based on the onset of the cue presentation (200ms). The SBC was run on three groups.

9.1.1 Setting up and assessing the model

```
code = "LAT"

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

# set weakly informative priors
priors = c(
  prior(normal(5,     0.75), class = Intercept),
  prior(normal(0,     0.25), class = sd),
  prior(normal(0,     0.25), class = b),
  prior(normal(0.5,   0.50), class = sigma),
  prior(normal(350, 50.00), class = ndt), # threshold between target and cue saccades
  prior(lkj(2),           class = cor)
)

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

if (file.exists(file.path(cache_dir, paste0("df_res_", code, ".rds")))) {
  # load in the results of the SBC
  df.results = readRDS(file.path(cache_dir, paste0("df_res_", code, ".rds")))
  df.backend = readRDS(file = file.path(cache_dir, paste0("df_div_", code, ".rds")))
  dat       = readRDS(file = file.path(cache_dir, paste0("dat_", code, ".rds")))
} else {
  # create the data and the results
  set.seed(2468)
  gen = SBC_generator_brms(f.lat, data = df.lat, prior = priors,
                           family = "shifted_lognormal",
                           thin = 50, warmup = 10000, refresh = 2000,
                           generate_lp = TRUE)
  dat = generate_datasets(gen, nsim)
  saveRDS(dat, file = file.path(cache_dir, paste0("dat_", code, ".rds")))
  backend = SBC_backend_brms_from_generator(gen, chains = 4, thin = 1,
                                              warmup = 1000, iter = 3000)
  results = compute_SBC(dat, backend,
                        cache_mode      = "results",
                        cache_location = file.path(cache_dir, paste0("res_", code)))
  saveRDS(results$stats,
          file = file.path(cache_dir, paste0("df_res_", code, ".rds")))
  saveRDS(results$backend_diagnostics,
          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 0 of 250 simulations had at least one parameter that had an rhat of at least 1.05 and only 1 model had divergent samples (mean number of samples of the simulations with divergent samples: 1). This suggests that this model performs well.

9.1.2 Prior predictive checks

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

```
# get the true values
truePars = dat[["variables"]]

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

# set very large data points to a value of 1500
dvcakemH = dvcakem;
dvcakemH[dvcakemH < 0] = 0
dvcakemH[dvcakemH > 1500] = 1500
# compute one histogram per simulated data-set
breaks = seq(0, 1500, length.out = 101)
binwidth = breaks[2] - breaks[1]
histmat = matrix(NA, ncol = nrow(truePars) + binwidth, nrow = length(breaks)-1)
for (i in 1:nrow(truePars)) {
  histmat[,i] = hist(dvcakemH[,i], breaks = breaks, plot = F)$counts
}
# for each bin, compute quantiles across histograms
probs = seq(0.1, 0.9, 0.1)
quantmat = as.data.frame(matrix(NA, nrow=dim(histmat)[1], ncol = length(probs)))
names(quantmat) = paste0("p", probs)
for (i in 1:dim(histmat)[1]) {
  quantmat[i,] = quantile(histmat[i,], p = probs, na.rm = T)
}
quantmat$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 = "Prior predictive distribution", y = "", x = "latency of saccades") +
  theme_bw()

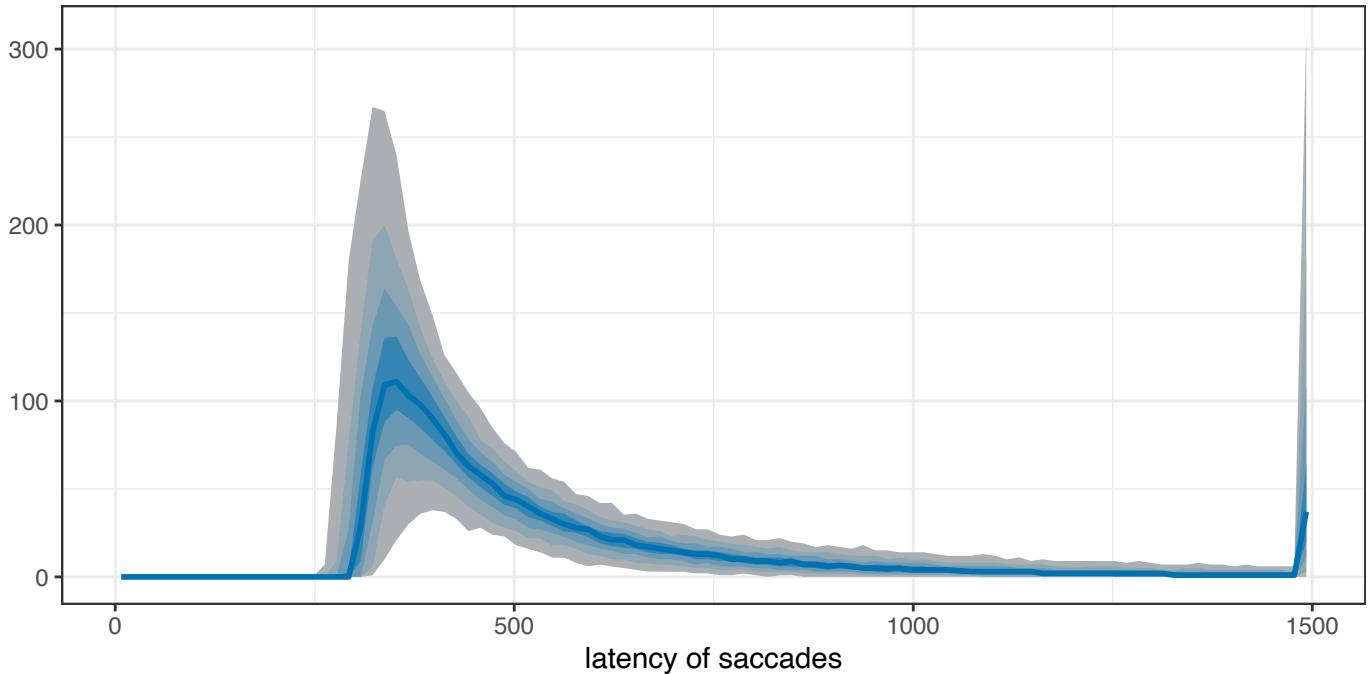
tmpM = apply(dvcakem, 2, mean) # mean
tmpSD = apply(dvcakem, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark) +
  labs(x = "Mean latency of saccades", title = "Means of simulated data") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD latency of saccades", title = "Standard deviations of simulated data") +
  theme_bw()

p = ggarrange(p1,
  ggarrange(p2, p3, ncol = 2, labels = c("B", "C")),
  nrow = 2, labels = "A")
annotate_figure(p,
```

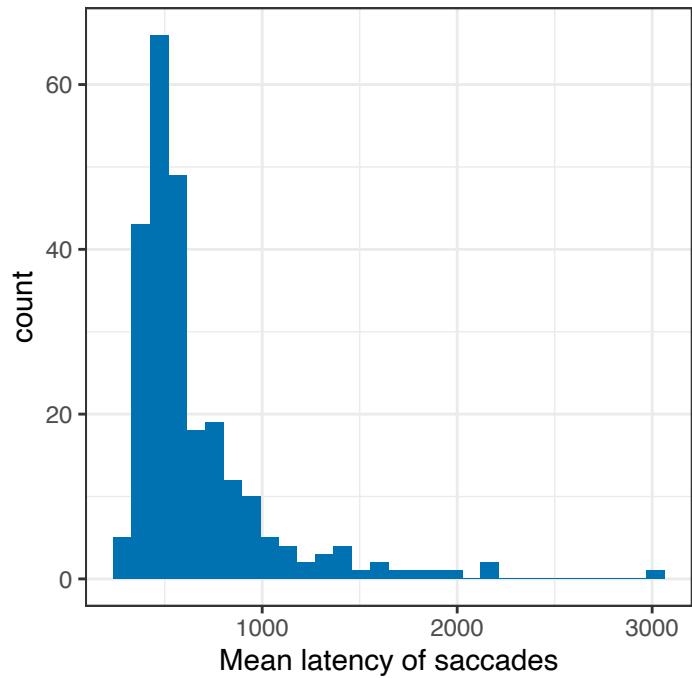
```
top = text_grob("Prior predictive checks: latency",
face = "bold", size = 14))
```

Prior predictive checks: latency

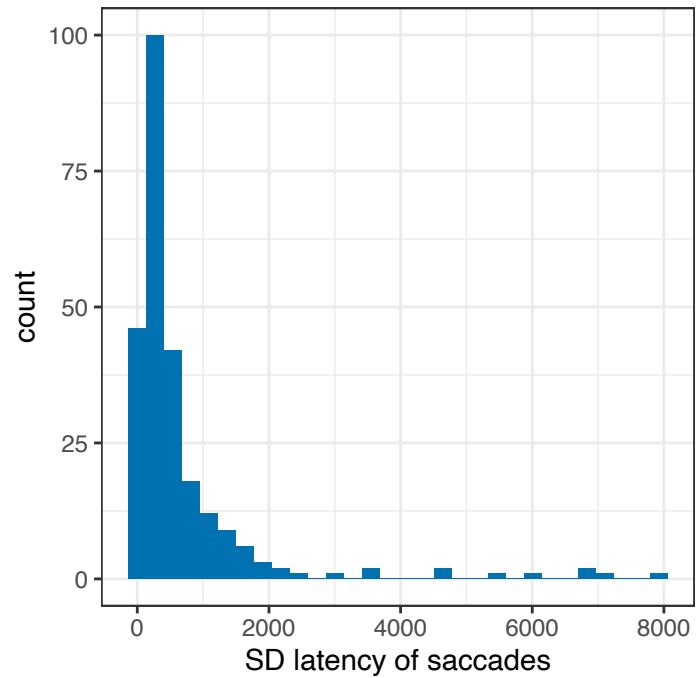
A Prior predictive distribution



B Means of simulated data



C Standard deviations of simulated data



First, we assess whether the simulated values fit our expectations of the distribution of the data. Previous literature has found that saccade latencies are around 200ms with few saccades being produced faster than 100ms. If we add 200ms from the cue presentation, this means we expect most latencies to be above 300ms and centered around 400ms. Our simulated datasets seem to capture this well.

9.1.3 Computational faithfulness and model sensitivity

```

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

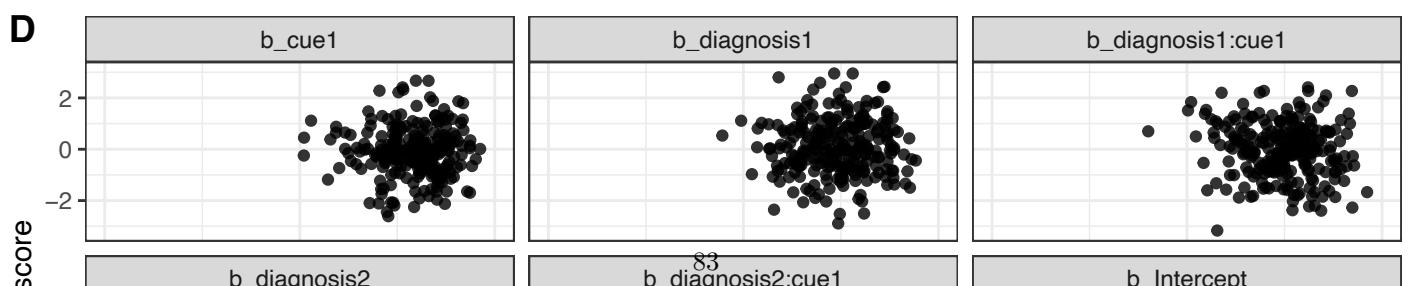
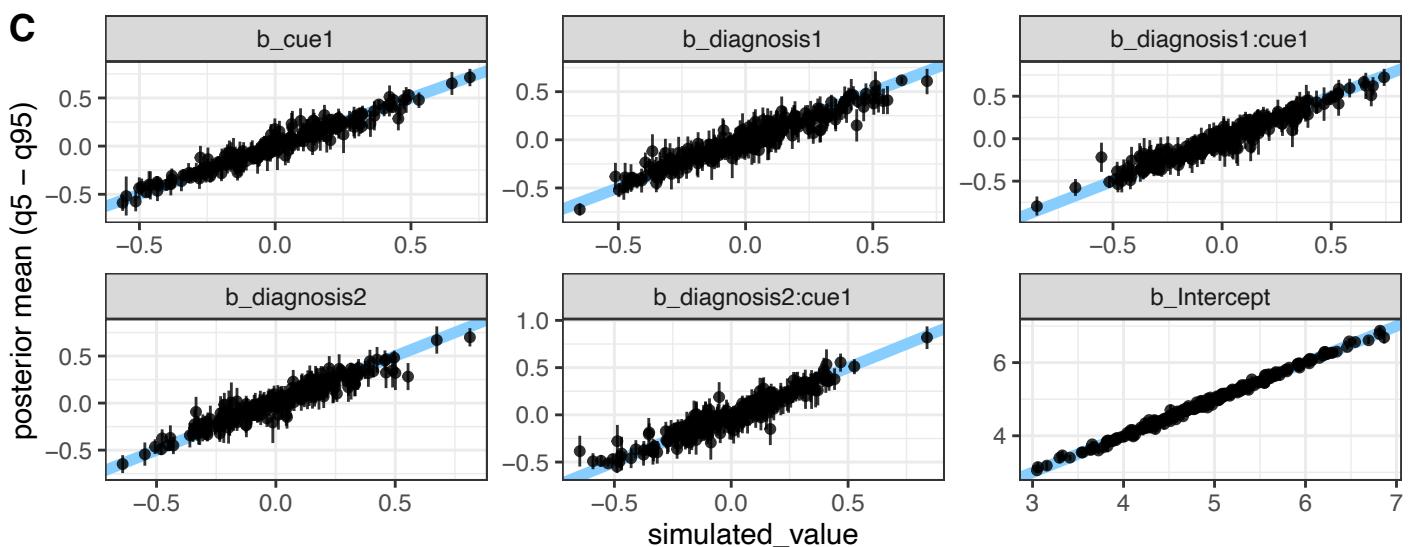
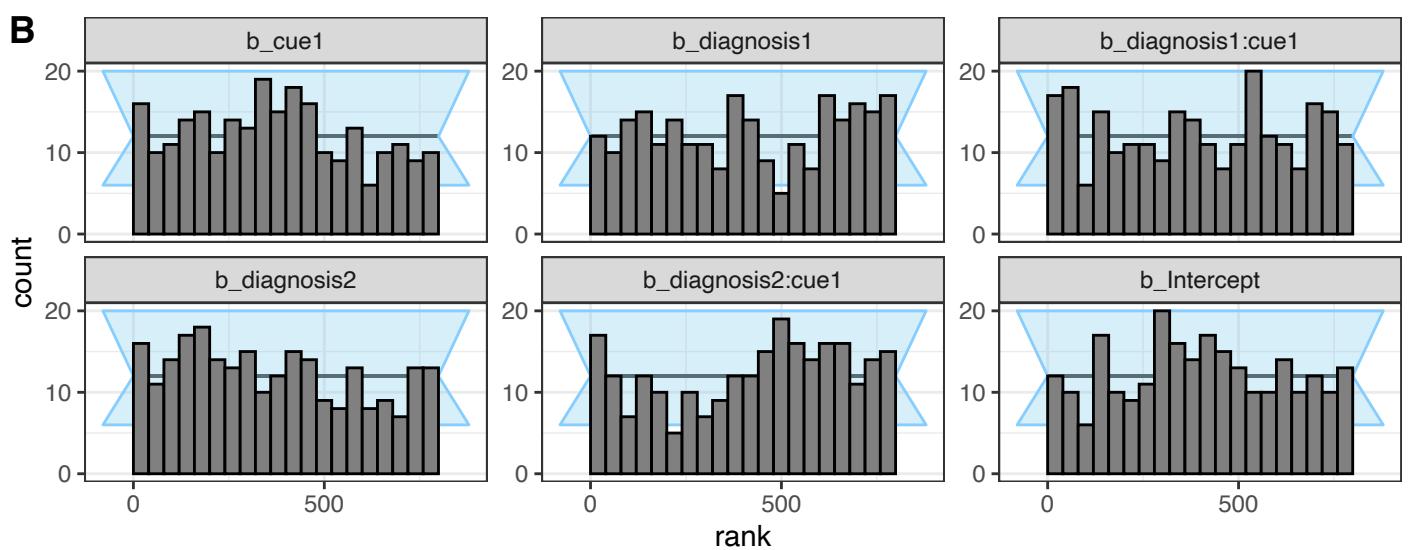
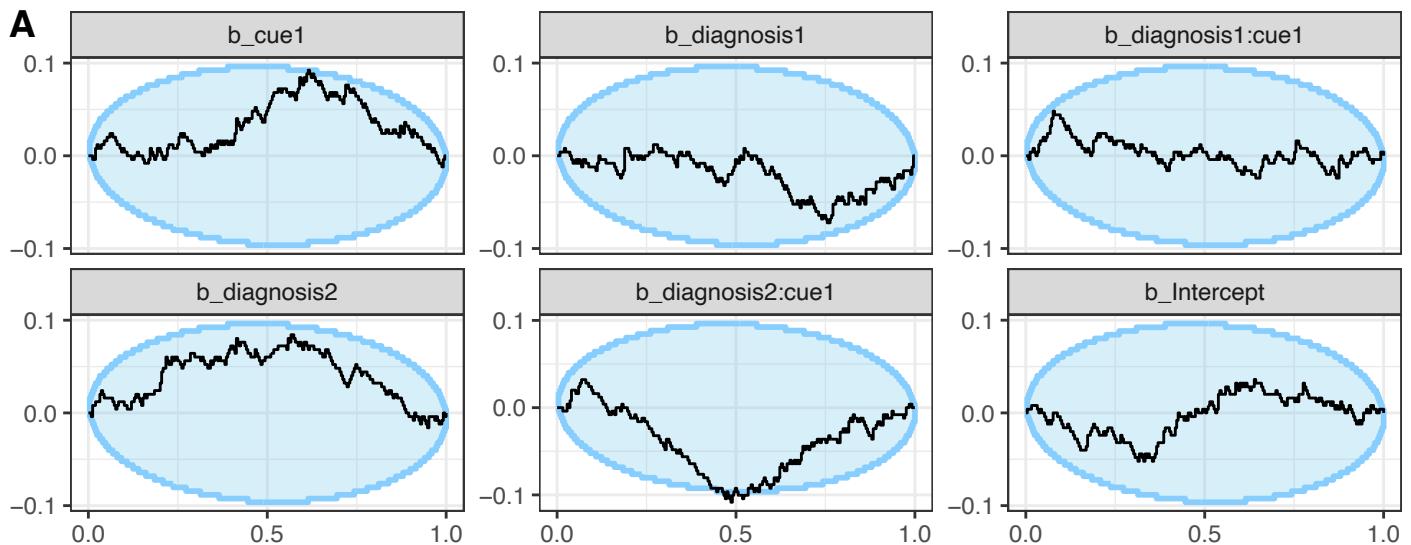
# plot SBC with functions from the SBC package focusing on population-level parameters

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

```

Computational faithfulness and model sensitivity



All looks acceptable here.

9.1.4 Posterior predictive checks

As the next step, we fit the model and check whether the chains have converged, which they seem to have. We then perform posterior predictive checks on the model using the bayesplot package.

```
# fit the maximal model
set.seed(2587)
m.lat = brm(f.lat,
             df.lat, prior = priors,
             iter = iter, warmup = warm,
             backend = "cmdstanr", threads = threading(8),
             family = "shifted_lognormal",
             file = "m_lat",
             save_pars = save_pars(all = TRUE)
            )
rstan::check_hmc_diagnostics(m.lat$fit)

## 
## Divergences:
## 0 of 8000 iterations ended with a divergence.

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

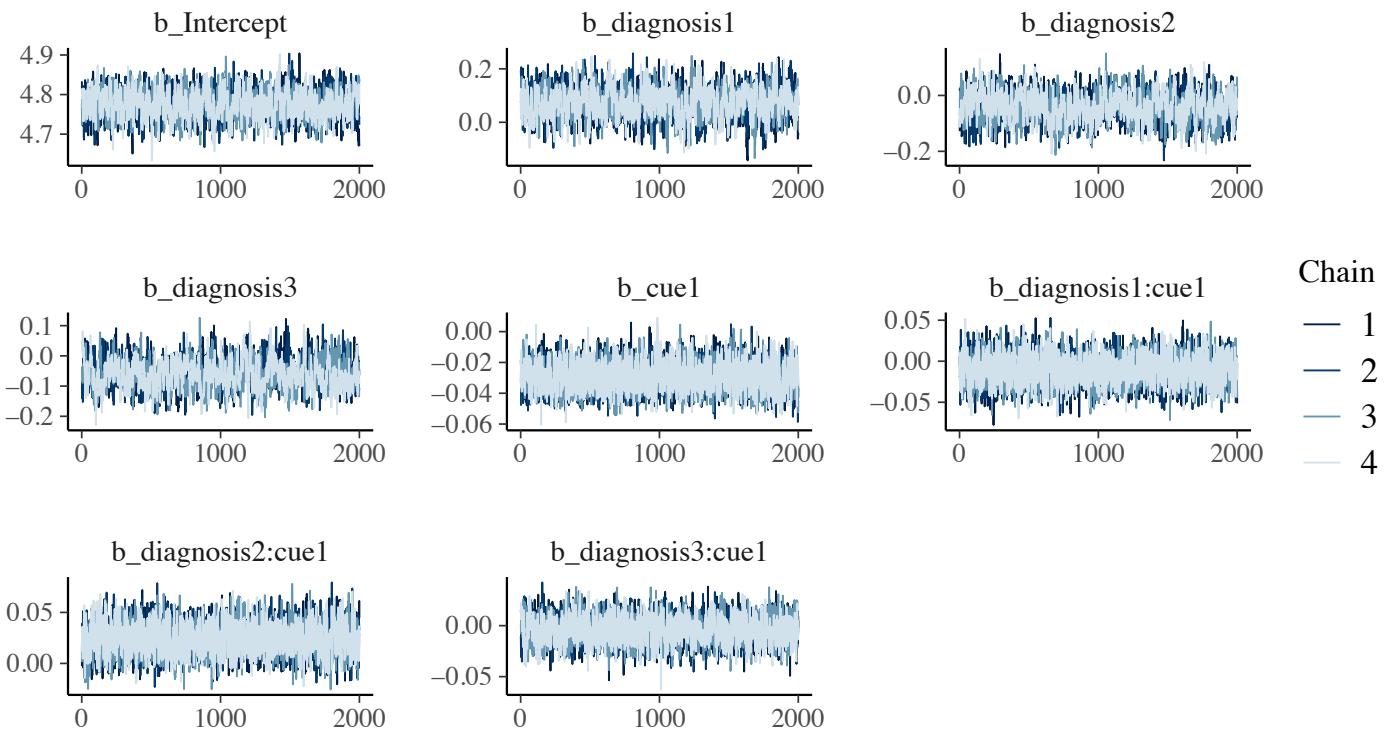
## 
## Energy:
## E-BFMI indicated no pathological behavior.

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

## [1] 5

# check the trace plots
post.draws = as_draws_df(m.lat)
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.
```



The model does not have any divergent transitions nor high rhats. The trace plots also look good, therefore, we move on to the posterior predictive checks.

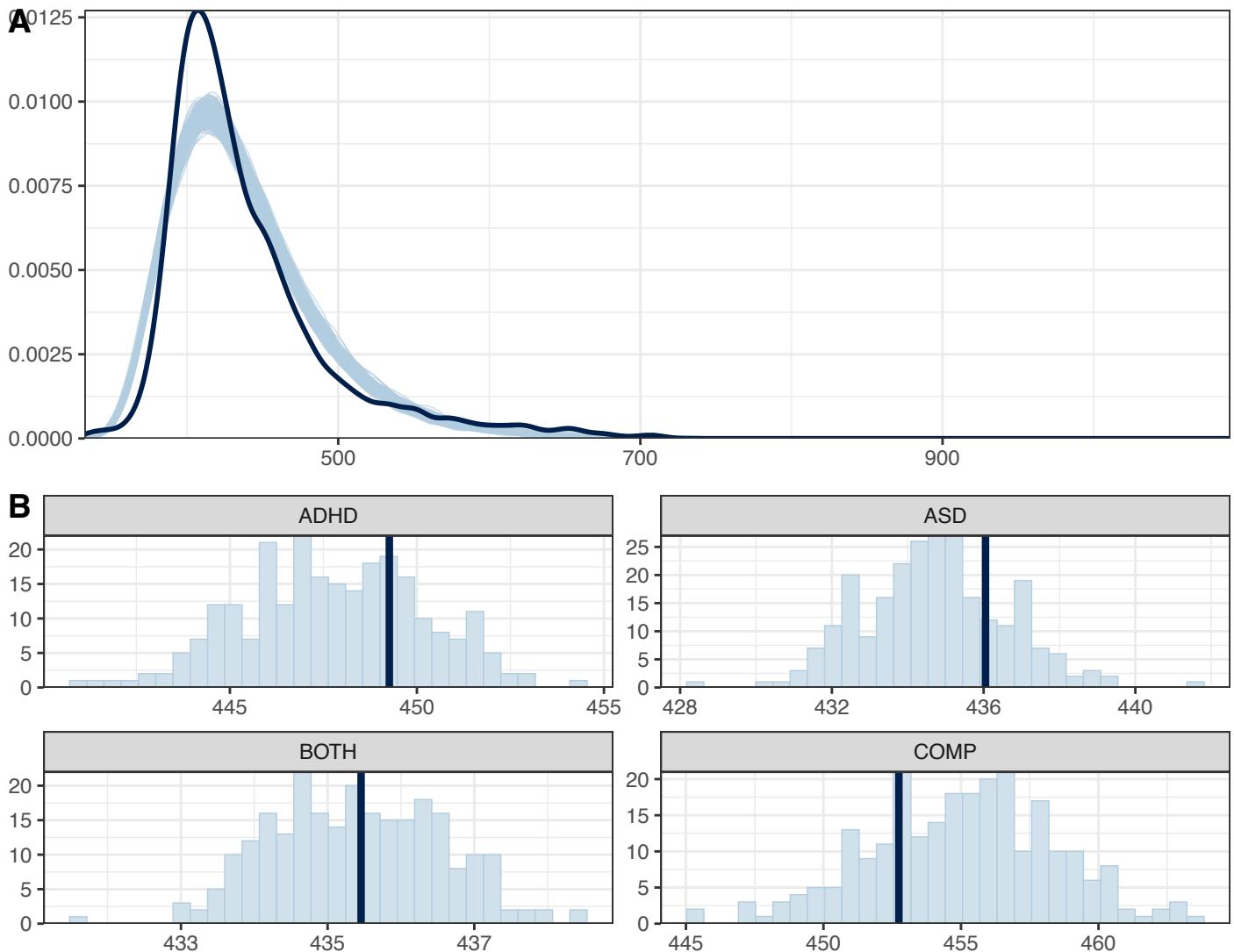
```
# get the posterior predictions
post.pred = posterior_predict(m.lat, ndraws = nsim)

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

# distributions of means and sds compared to the real values per group
p2 = ppc_stat_grouped(df.lat$lat, post.pred, df.lat$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: latency",
  face = "bold", size = 14))
```

Posterior predictive checks: latency



The simulated data based on the model does not fit our data very well: it is wider and seems to underestimate latencies for COMP while overestimating for ADHD and ASD with the dark blue line showing the mean of the actual dataset and the light blue bars showing the distribution of the predicted data.

9.2 Aggregated model

Since we want to base our inferences on the estimates, we go back to the drawing board and aggregate our data to see whether this resolves these issues.

9.2.1 Setting up and assessing the model

```
code = "LAT_agg"

# aggregate the data
df.lat.agg = df.lat %>%
  group_by(subID, cue, diagnosis) %>%
  summarise(lat = median(lat, na.rm = T))

# set the formula
f.lat = brms::bf(lat ~ diagnosis * cue + (1 | subID) )

# set weakly informative priors
priors = priors %>% filter(class != "cor")
```

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

Again, we ran the SBC based on the three original, preregistered groups.

```
if (file.exists(file.path(cache_dir, paste0("df_res_", code, ".rds")))) {
  # load in the results of the SBC
  df.results = readRDS(file.path(cache_dir, paste0("df_res_", code, ".rds")))
  df.backend = readRDS(file = file.path(cache_dir, paste0("df_div_", code, ".rds")))
  dat       = readRDS(file = file.path(cache_dir, paste0("dat_", code, ".rds")))
} else {
  # create the data and the results
  set.seed(2468)
  gen = SBC_generator_brms(f.lat, data = df.lat.agg, prior = priors,
                           family = "shifted_lognormal",
                           thin = 50, warmup = 10000, refresh = 2000,
                           generate_lp = TRUE)
  dat = generate_datasets(gen, nsim)
  saveRDS(dat, file = file.path(cache_dir, paste0("dat_", code, ".rds")))
  backend = SBC_backend_brms_from_generator(gen, chains = 4, thin = 1,
                                              warmup = 1000, iter = 3000)
  results = compute_SBC(dat, backend,
                        cache_mode      = "results",
                        cache_location = file.path(cache_dir, paste0("res_", code)))
  saveRDS(results$stats,
          file = file.path(cache_dir, paste0("df_res_", code, ".rds")))
  saveRDS(results$backend_diagnostics,
          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 1 of 250 simulations had at least one parameter that had an rhat of at least 1.05, but 105 models had divergent samples (mean number of samples of the simulations with divergent samples: 7.21). This is something to look out for in the final model.

9.2.2 Prior predictive checks

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

```
# get the true values
truePars = dat[["variables"]]

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

# set very large data points to a value of 1500
dvfakemath = dvfakemat;
dvfakemath[dvfakemath < 0] = 0
dvfakemath[dvfakemath > 1500] = 1500
# compute one histogram per simulated data-set
breaks = seq(0, 1500, length.out = 101)
binwidth = breaks[2] - breaks[1]
histmat = matrix(NA, ncol = nrow(truePars) + binwidth, nrow = length(breaks)-1)
for (i in 1:nrow(truePars)) {
  histmat[,i] = hist(dvfakemath[,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, na.rm = T)
}
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 = "Prior predictive distribution", y = "", x = "latency of saccades") +
  theme_bw()

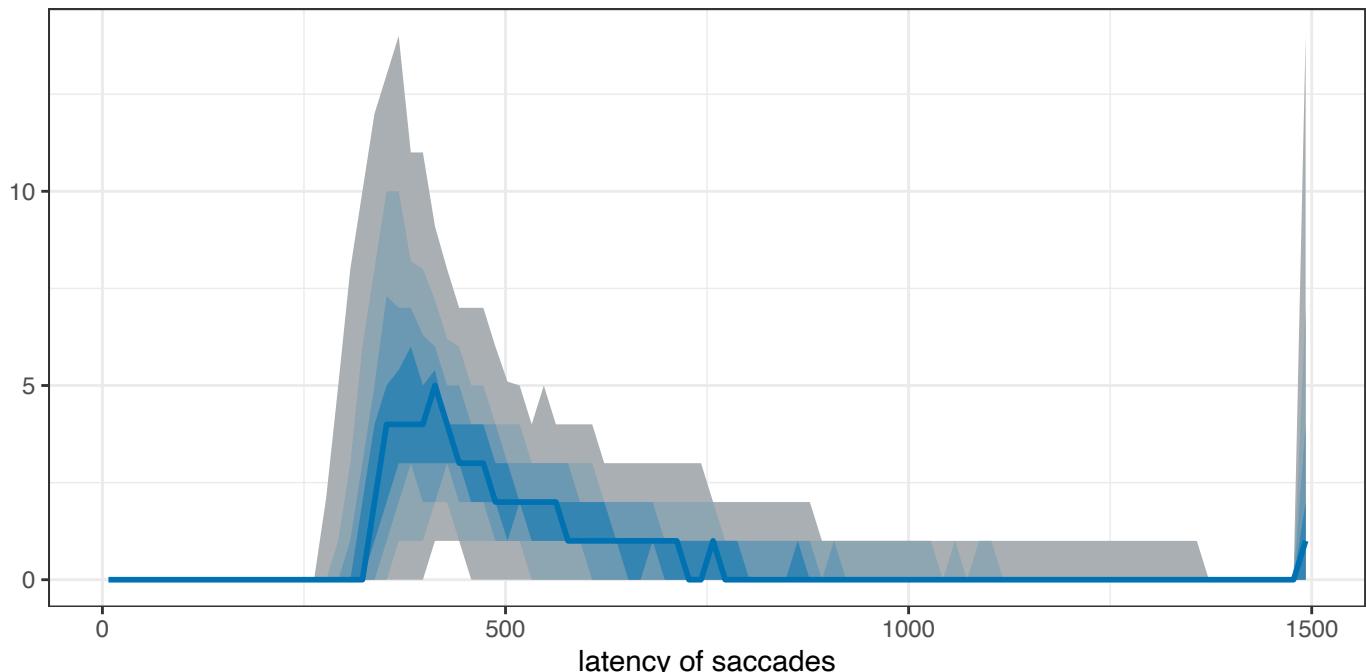
tmpM = apply(dvfakemat, 2, mean) # mean
tmpSD = apply(dvfakemat, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark) +
  labs(x = "Mean latency of saccades", title = "Means of simulated data") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD latency of saccades", title = "Standard deviations of simulated data") +
  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: latency",
  face = "bold", size = 14))

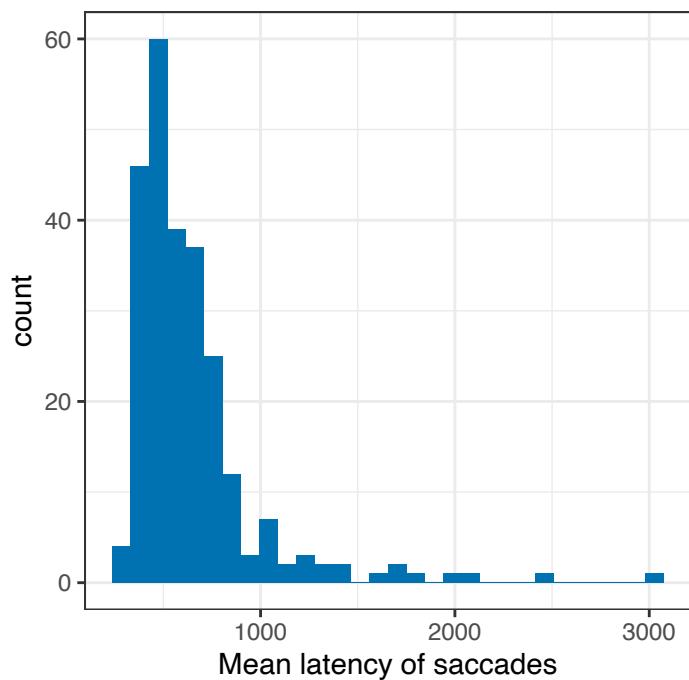
```

Prior predictive checks: latency

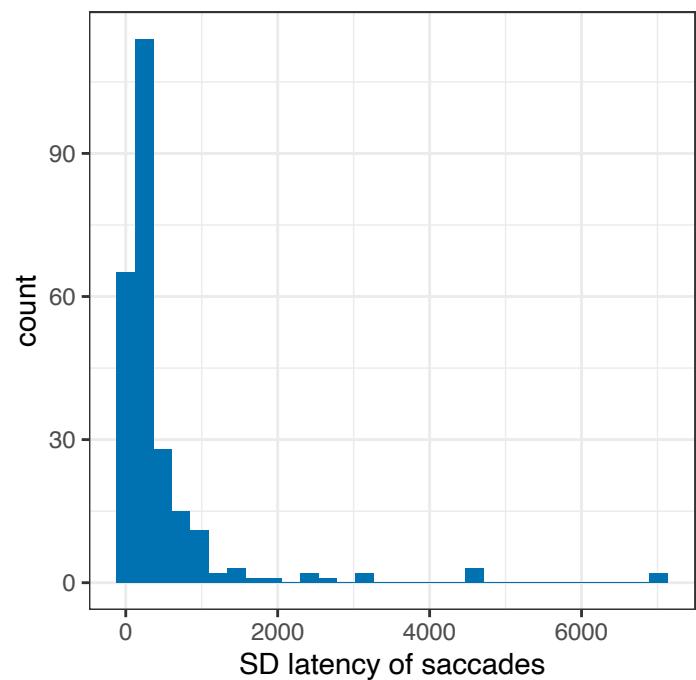
A Prior predictive distribution



B Means of simulated data



C Standard deviations of simulated data



Again, our simulated datasets seem to capture well what we know about saccade latencies.

9.2.3 Computational faithfulness and model sensitivity

```
# get simulation numbers with issues
des_rank = max(df.results$max_rank)
check = merge(df.results %>%
  group_by(sim_id) %>%
  summarise(
    rhat = max(rhat, na.rm = T),
    mean_rank = max(max_rank)
  ) %>%
```

```

filter(rhat >= 1.05 | mean_rank < des_rank),
df.backend %>% filter(n_divergent > 0), all = T)

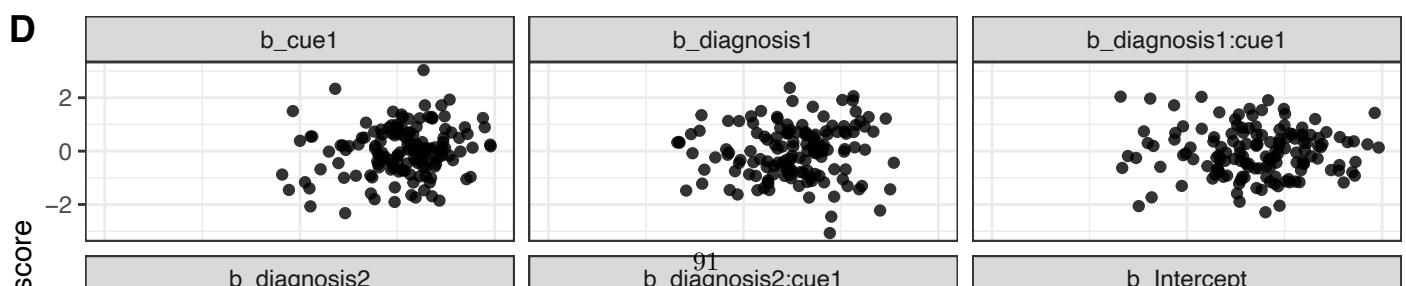
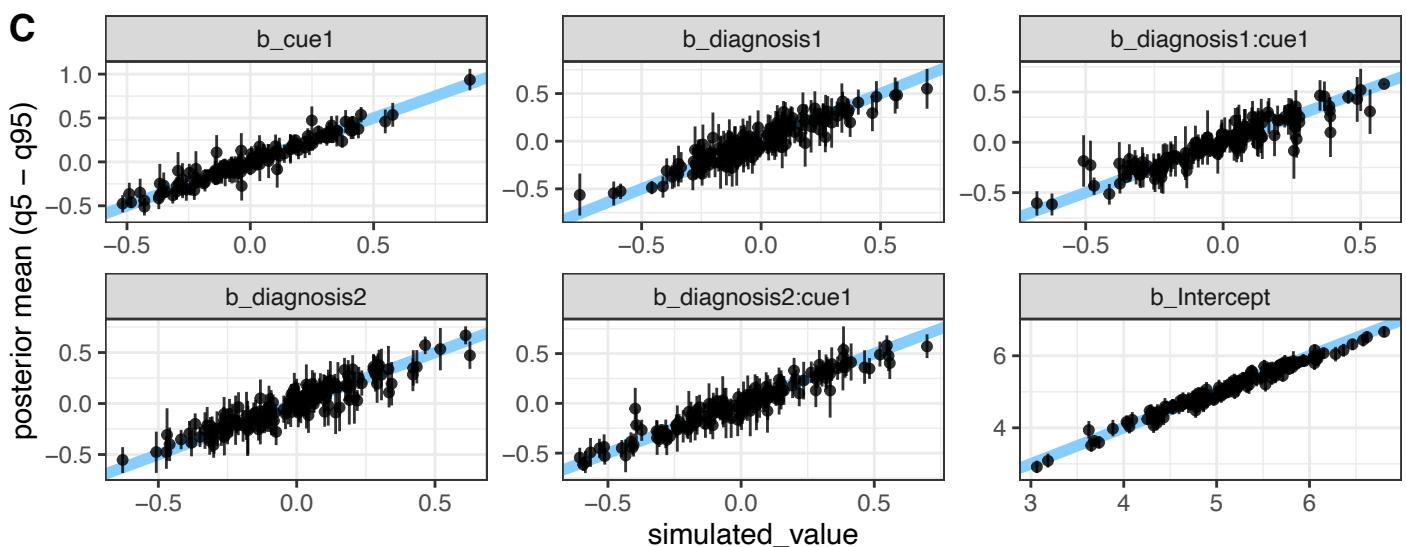
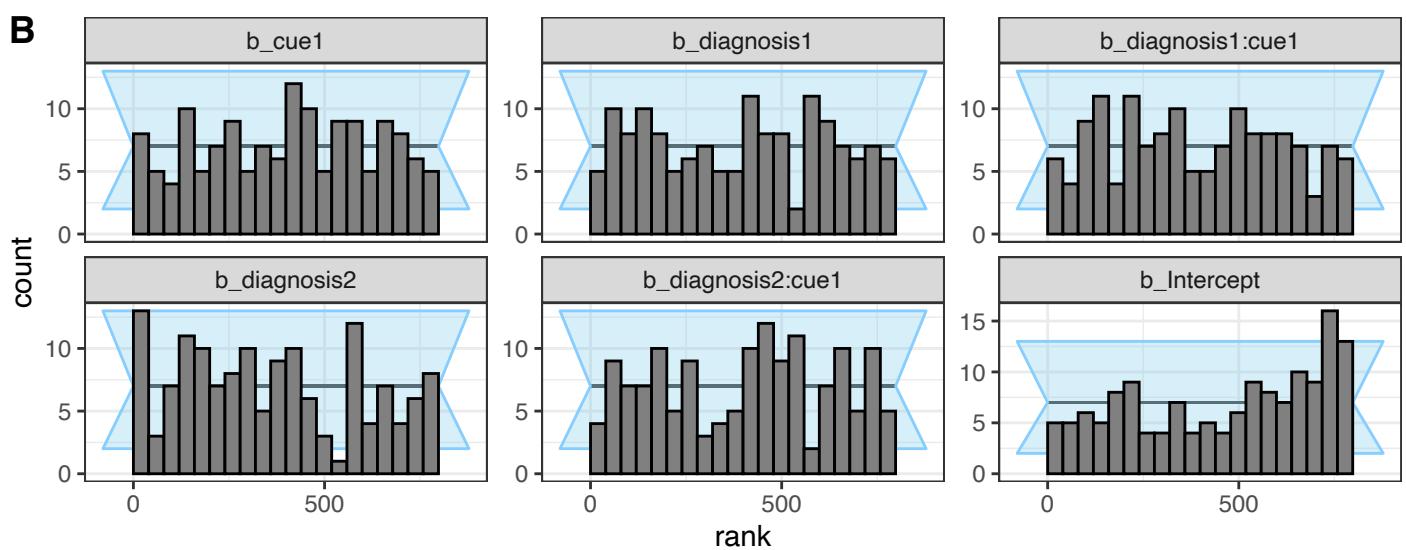
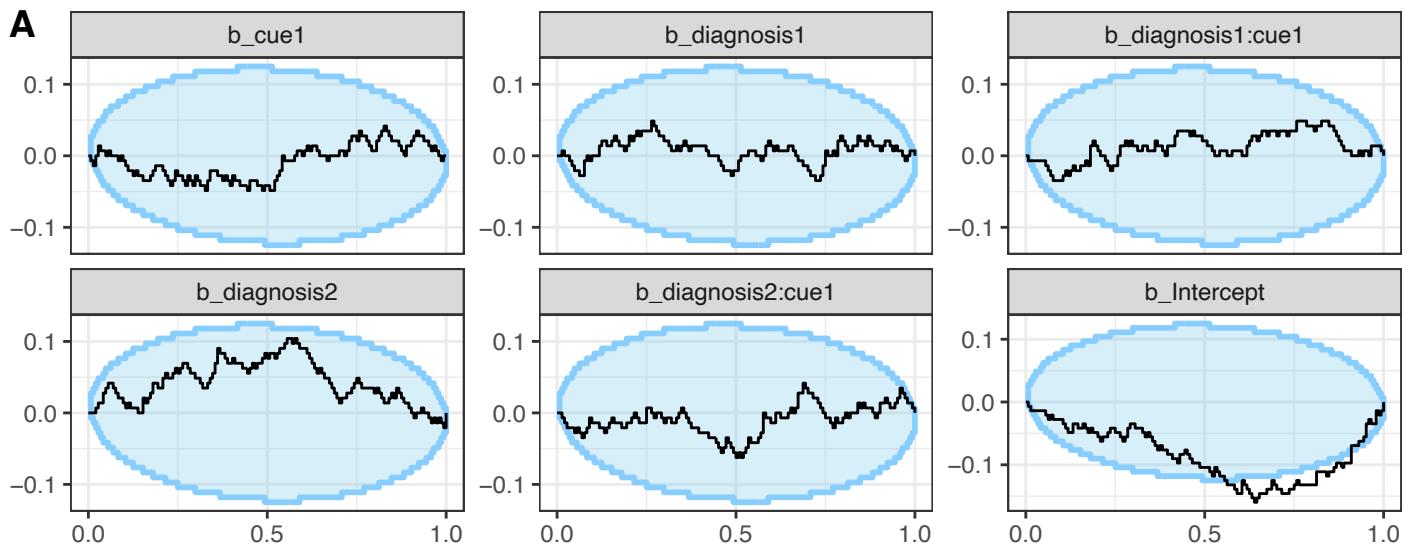
# plot SBC with functions from the SBC package focusing on population-level parameters

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

```

Computational faithfulness and model sensitivity



The intercept looks slightly off here, the model could have a slight tendency to underestimate it.

9.2.4 Posterior predictive checks

As the next step, we fit the model and check whether the chains have converged, which they seem to have. We then perform posterior predictive checks on the model using the bayesplot package.

```
# fit the maximal model
set.seed(7799)
m.lat = brm(f.lat,
             df.lat.agg, prior = priors,
             iter = iter, warmup = warm,
             backend = "cmdstanr", threads = threading(8),
             family = "shifted_lognormal",
             file = "m_lat_agg",
             save_pars = save_pars(all = TRUE)
            )
rstan::check_hmc_diagnostics(m.lat$fit)

## 
## Divergences:
## 0 of 8000 iterations ended with a divergence.

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

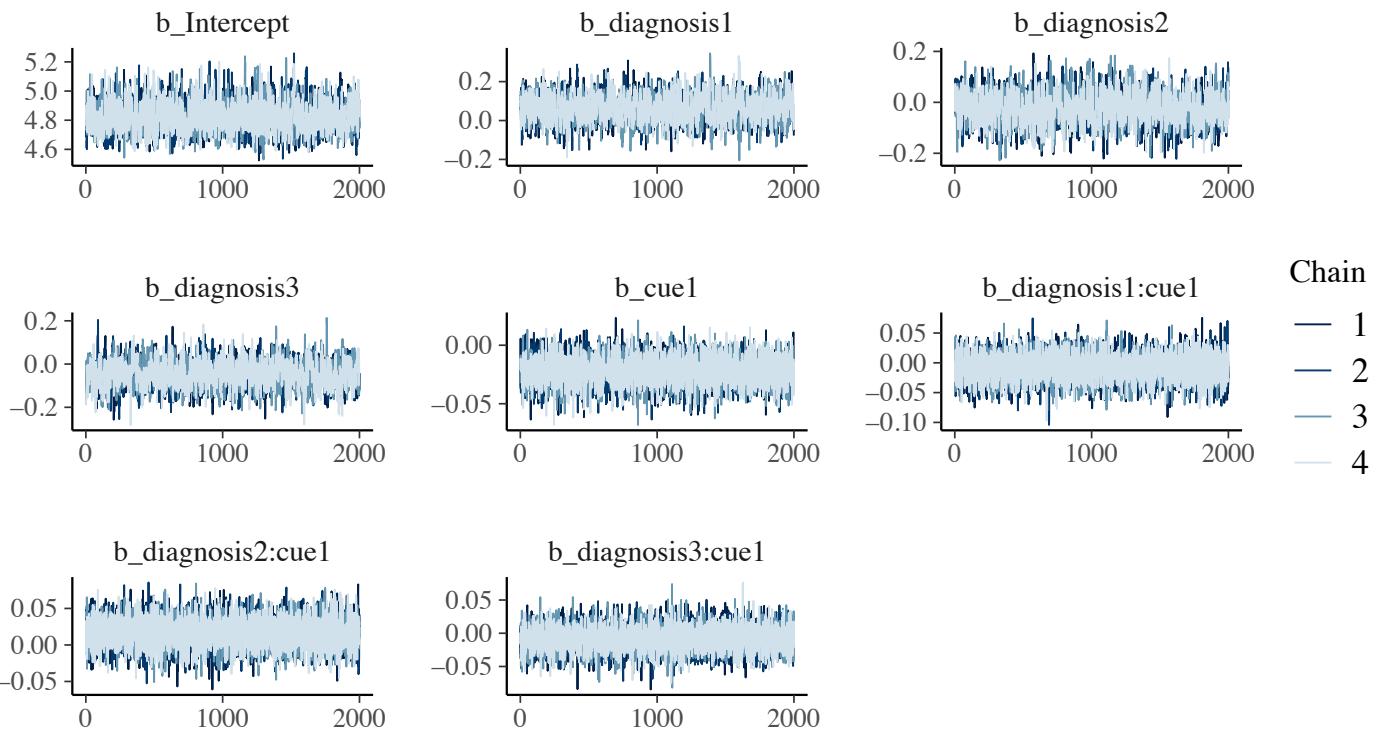
## 
## Energy:
## E-BFMI indicated no pathological behavior.

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

## [1] 0

# check the trace plots
post.draws = as_draws_df(m.lat)
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.
```



The final model does not exhibit any divergence issues or suboptimal rhats.

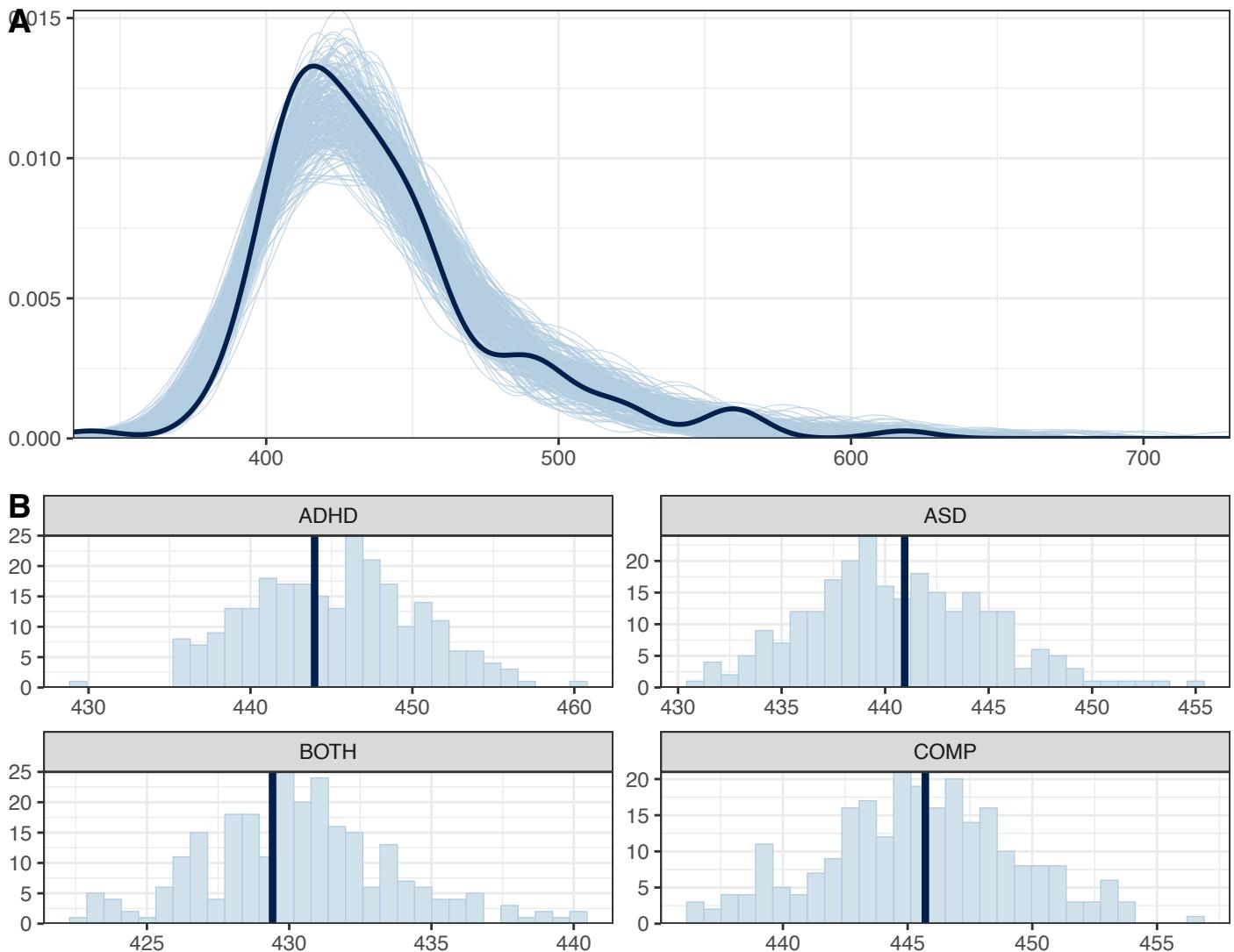
```
# get the posterior predictions
post.pred = posterior_predict(m.lat, ndraws = nsim)

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

# distributions of means and sds compared to the real values per group
p2 = ppc_stat_grouped(df.lat.agg$lat, post.pred, df.lat.agg$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: latency",
  face = "bold", size = 14))
```

Posterior predictive checks: latency



This looks much better with the simulated data based on the model capturing our actual data well.

9.2.5 Inferences

Now that we are convinced that we can trust our model, we have a look at the model and its estimates.

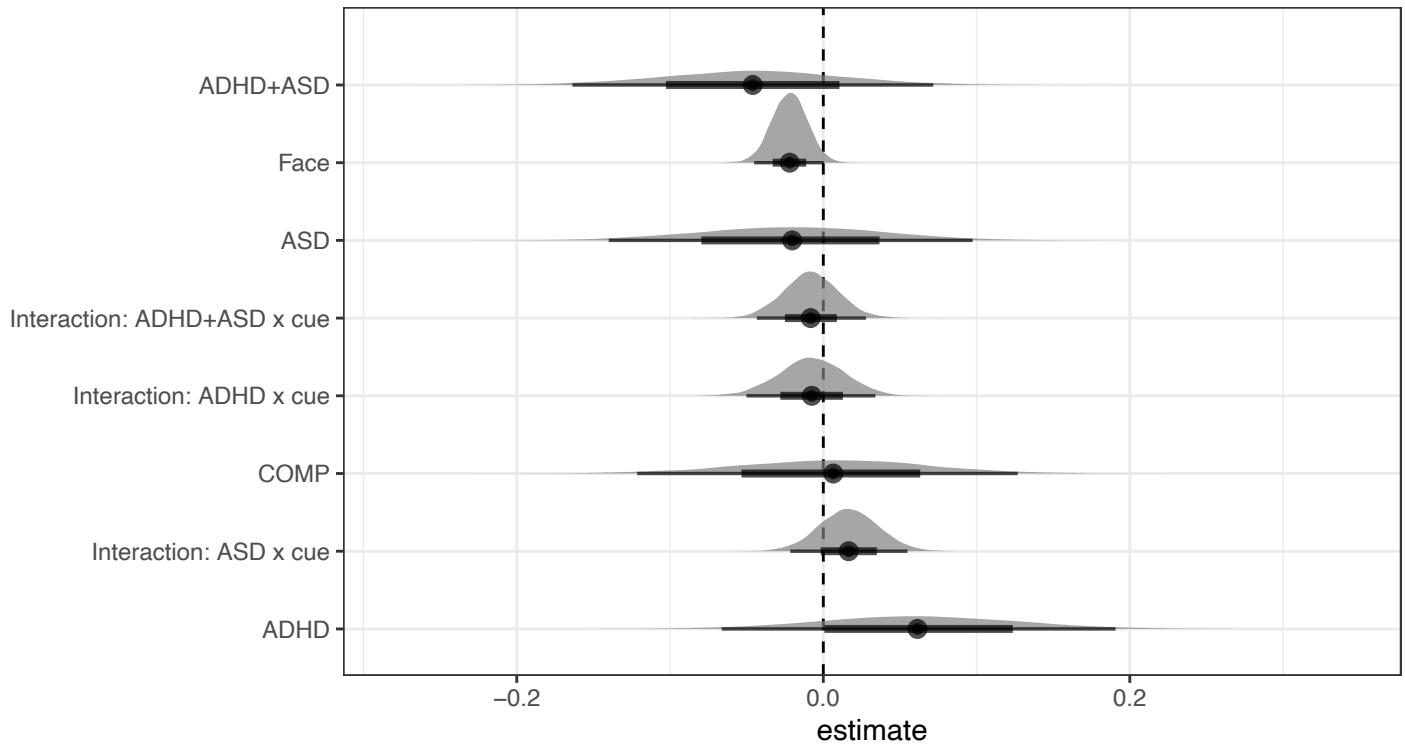
```
# print a summary
summary(m.lat)

## Family: shifted_lognormal
## Links: mu = identity; sigma = identity; ndt = identity
## Formula: lat ~ diagnosis * cue + (1 | subID)
## Data: df.lat.agg (Number of observations: 142)
## Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
##         total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 75)
##             Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.30      0.04     0.22     0.40 1.00     1256     1927
## 
## Regression Coefficients:
##             Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept       4.82      0.10     4.65     5.04 1.00     1496     2392
## diagnosis1      0.06      0.07    -0.07     0.19 1.00     1253     2101
```

```

## diagnosis2      -0.02      0.06     -0.14      0.10 1.00      988    2165
## diagnosis3      -0.05      0.06     -0.16      0.07 1.01     1003    1867
## cue1            -0.02      0.01     -0.05      0.00 1.00     8491    5794
## diagnosis1:cue1 -0.01      0.02     -0.05      0.03 1.00     5273    5549
## diagnosis2:cue1  0.02      0.02     -0.02      0.05 1.00     5909    5217
## diagnosis3:cue1 -0.01      0.02     -0.04      0.03 1.00     6645    5798
##
## Further Distributional Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.13      0.02      0.10      0.16 1.00     2521    3666
## ndt       308.93     11.12    281.81    325.98 1.00     1724    2856
##
## 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).
# plot the posterior distributions
as_draws_df(m.lat) %>%
  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") %>%
  filter(coef != "b_Intercept") %>%
  mutate(
    coef = case_match(coef,
      "b_cue1" ~ "Face",
      "b_diagnosis1" ~ "ADHD",
      "b_diagnosis2" ~ "ASD",
      "b_diagnosis3" ~ "ADHD+ASD",
      "b_COMP" ~ "COMP",
      "b_diagnosis1:cue1" ~ "Interaction: ADHD x cue",
      "b_diagnosis2:cue1" ~ "Interaction: ASD x cue",
      "b_diagnosis3:cue1" ~ "Interaction: ADHD+ASD x cue"
    ),
    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, not_credible)) +
  theme(legend.position = "none")

```



```

# H2b: ASD(face) > COMP(face)
h2b = hypothesis(m.lat,
                 "0 < diagnosis1 + diagnosis3 + 2*diagnosis2 +
                 diagnosis1:cue1 + diagnosis3:cue1 + 2*diagnosis2:cue1")
h2b

## Hypothesis Tests for class b:
##          Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(diagnosis1+d... < 0      0.01      0.11     -0.17      0.18      0.85
## Post.Prob Star
## 1      0.46
## ---
## '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.
# explore: overall faster towards face-cued targets
e = hypothesis(m.lat, "0 > 2*cue1", alpha = 0.025)
e

## Hypothesis Tests for class b:
##          Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio Post.Prob
## 1 (0)-(2*cue1) > 0      0.04      0.02        0      0.09     36.74      0.97
## 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.
# extract predicted differences
df.new = df.lat %>%
  select(diagnosis, cue) %>%
  distinct() %>%
  mutate(
    condition = paste(diagnosis, cue, sep = "_"))

```

Table 14: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
COMP_face	433	9.2	401	415	451	474
COMP_object	439	9.6	408	420	458	478
ADHD_face	439	11	405	419	460	490
ADHD_object	447	11	409	425	470	501
ASD_face	432	9.1	397	414	450	470
ASD_object	433	9.3	398	415	452	470
BOTH_face	426	8.1	400	410	442	461
BOTH_object	433	8.5	405	417	450	474

Table 15: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	233	4.9	214	223	242	253
object	238	5.1	220	228	248	257
FAB	5.6	2.9	-6	-0.36	11	16

```

)
df.ms = as.data.frame(
  fitted(m.lat, summary = F,
         newdata = df.new %>% select(diagnosis, cue),
         re_formula = NA))
colnames(df.ms) = df.new$condition

st(df.ms,
  summ = c('mean(x)', 'sd(x)', 'min(x)', 'pctile(x)[2.5]',
           'pctile(x)[97.5]', 'max(x)'))

# calculate our difference columns
df.ms = df.ms %>%
  mutate(
    e = rowMeans(select(., matches(".*_object"))), na.rm = T) -
    rowMeans(select(., matches(".*_face"))), na.rm = T)
)

st(df.ms %>%
  mutate(
    # get the face and object latencies -200, so they start with target onset
    face = rowMeans(select(., matches(".*_face"))), na.rm = T) - 200,
    object = rowMeans(select(., matches(".*_object"))), na.rm = T) - 200,
    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)'))
)

```

Our hypothesis that target-elicited saccades towards the faces have a longer latency in ASD than COMP adults was not confirmed by the data (*estimate* = 0.01 [-0.17, 0.18], *posterior probability* = 45.93%). Our exploration revealed that that latencies of target-elicited saccades were faster in response to face-cued compared to object-cued targets regardless of the diagnostic group (*estimate* = 0.04 [0, 0.09], *posterior probability* = 97.35%). Specifically, the model predicted a 5.55ms [-0.1, 11.1] shorter latency of for saccades produced towards a face-cued compared to an object-cued target.

9.2.6 Plots

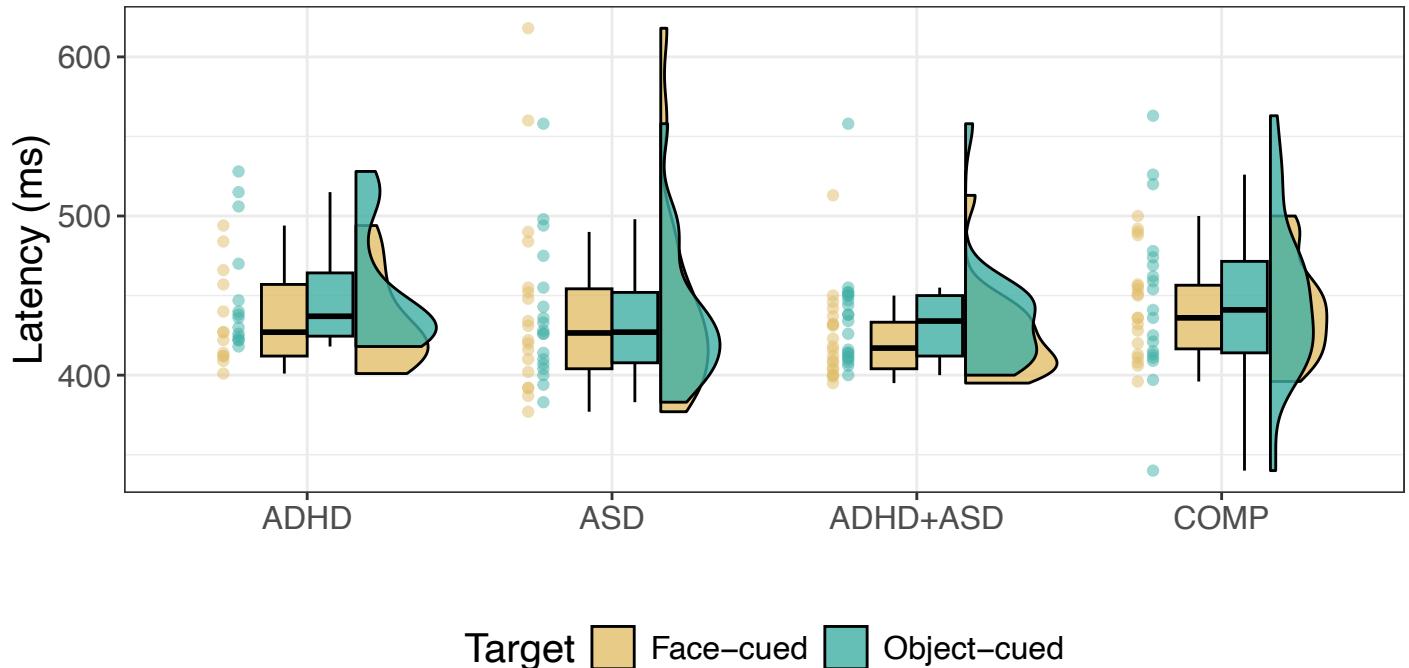
```
# rain cloud plot for the
df.lat.agg %>%
```

```

mutate(
  diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD"),
  Target      = recode(cue, "face" = "Face-cued", "object" = "Object-cued")
) %>%
ggplot(aes(diagnosis, lat, fill = Target, colour = Target)) +
  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))) +
  scale_fill_manual(values = custom.col2) +
  scale_color_manual(values = custom.col2) +
  labs(title = "Latencies of target-elicited saccades", x = "", y = "Latency (ms)") +
  theme_bw() +
  theme(legend.position = "bottom",
    plot.title = element_text(hjust = 0.5),
    legend.direction = "horizontal",
    text = element_text(size = 15))

```

Latencies of target–elicited saccades



Target Face-cued Object-cued

```

ggsave("Fig6_latSac.svg",
  units = "mm",
  width  = 170,
  height = 100,
  dpi    = 300)

```

10 Correlation with reaction times: number of saccades

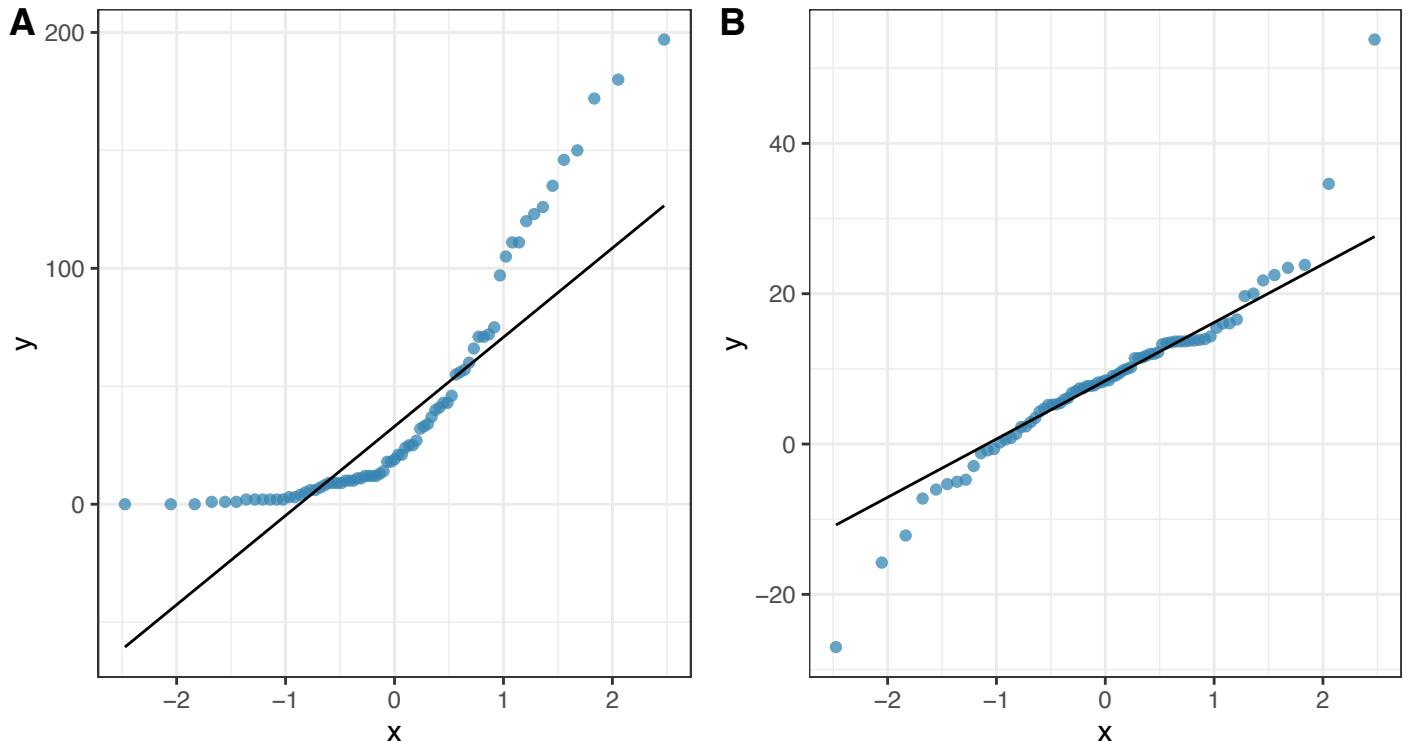
Last, we hypothesised that the FAB effect on reaction times may be associated with saccades produced towards the face. To investigate this, we use a Bayesian Spearman correlation as both FAB effect and number of saccades are not normally distributed.

```

# only keep saccades towards faces
df.diff = df.cnt %>% filter(direction == "face")

# check the distribution plot > not normally distributed
p1 = ggplot(df.diff, aes(sample = n.sac)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()
p2 = ggplot(df.diff, aes(sample = fab)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()
ggarrange(p1, p2,
           nrow = 1, ncol = 2, labels = "AUTO")

```



```

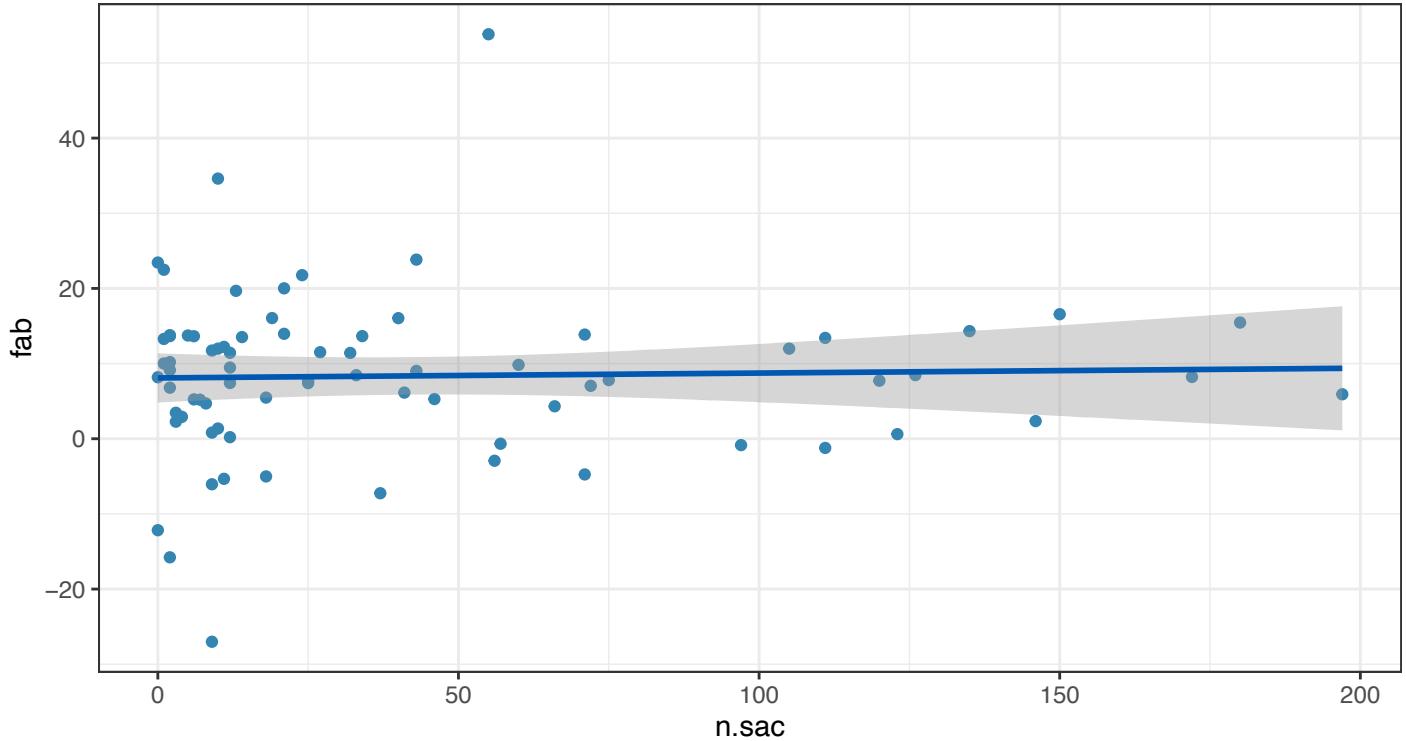
# do a Bayesian Spearman correlation: https://osf.io/j5wud
source("./helpers/rankBasedCommonFunctions.R")
source("./helpers/spearmanSampler.R")

# Default beta prior width is set to a = b = 1 for the sampler
if (file.exists("rho_CNT.rds")) {
  rhoSamples.cnt = readRDS("rho_CNT.rds")
} else {
  set.seed(1597)
  rhoSamples.cnt =
    spearmanGibbsSampler(xVals = df.diff$n.sac,
                          yVals = df.diff$fab,
                          nSamples = 5e3)
  saveRDS(rhoSamples.cnt, file = "rho_CNT.rds")
}

# give the posterior samples for rho to the function below to compute BF01
cor.bf = computeBayesFactorOneZero(rhoSamples.cnt$rhoSamples,
                                   whichTest = "Spearman",
                                   priorParameter = 1)

```

```
# visualise it
ggplot(data = df.diff, aes(x = n.sac, y = fab)) +
  geom_point(colour = c_mid_highlight) +
  geom_smooth(method = "lm",
              formula = y ~ x,
              geom = "smooth", colour = c_dark_highlight) +
  theme_bw()
```



Furthermore, we assessed the relationship between FAB and number of saccades produced towards the face on the participant level (see supplementary materials S2.4). We used a Bayesian Spearman correlation due to both values not being normally distributed. This model revealed no association between number of saccades and face attention bias, in fact there was moderate evidence against an association between the number of saccades and face attention bias ($\log(BF) = -1.95$).

11 Exploration: cue-elicited saccades

Additionally to our hypotheses, we also explored any effects of diagnostic status, cue type and their interaction on whether a saccade was produced during the presentation of the cues to assess the findings of increased saccade frequency towards faces by Pereira et al. (2020) in our data. Since these are again count data, we will use a Poisson and then compare the overall descriptives and effects to Pereira and colleague's results. Pereira found about 6% of trials contained cue-elicited saccades which translates to an intercept of 3. Therefore, we can use the same priors and SBC as in our Poisson investigating numbers of saccades in general.

```
# aggregate to counts
df.cnt.cue = df.cue %>%
  group_by(subID, diagnosis) %>%
  summarise(
    face = sum(direction == "face", na.rm = T),
    object = sum(direction == "object", na.rm = T)
  ) %>%
  pivot_longer(cols = c(face, object), names_to = "direction", values_to = "n.sac") %>%
  mutate_if(is.character, as.factor)

# aggregate for descriptives over both conditions
df.cnt.cue.agg = df.cnt.cue %>% group_by(subID, diagnosis) %>%
  summarise(n.sac = sum(n.sac))
```

```

# set the contrasts
contrasts(df.cnt.cue$direction) = contr.sum(2)
contrasts(df.cnt.cue$direction)

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

contrasts(df.cnt.cue$diagnosis) = contr.sum(4)
contrasts(df.cnt.cue$diagnosis)

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

# set the same formula
f.cnt = brms::bf(n.sac ~ diagnosis * direction + (1 | subID))

# set priors based on study design
priors = c(
  prior(normal(3, 1.5), class = Intercept),
  prior(normal(0, 1.0), class = sd),
  prior(normal(0, 1.0), class = b)
)

# set number of iterations and warmup for models
iter = 4500
warm = 1500

```

11.1 Posterior predictive checks

As the next step, we fit the model and check whether the chains have converged, which they seem to have. We then perform posterior predictive checks on the model using the bayesplot package.

```

# fit the model
set.seed(4682)
m.cnt = brm(f.cnt,
             df.cnt.cue, prior = priors,
             iter = iter, warmup = warm,
             backend = "cmdstanr", threads = threading(8),
             file = "m_cnt-cue",
             family = "poisson",
             save_pars = save_pars(all = TRUE)
            )
rstan::check_hmc_diagnostics(m.cnt$fit)

##
## Divergences:
## 0 of 12000 iterations ended with a divergence.

##
## Tree depth:
## 0 of 12000 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.cnt) >= 1.01, na.rm = T)

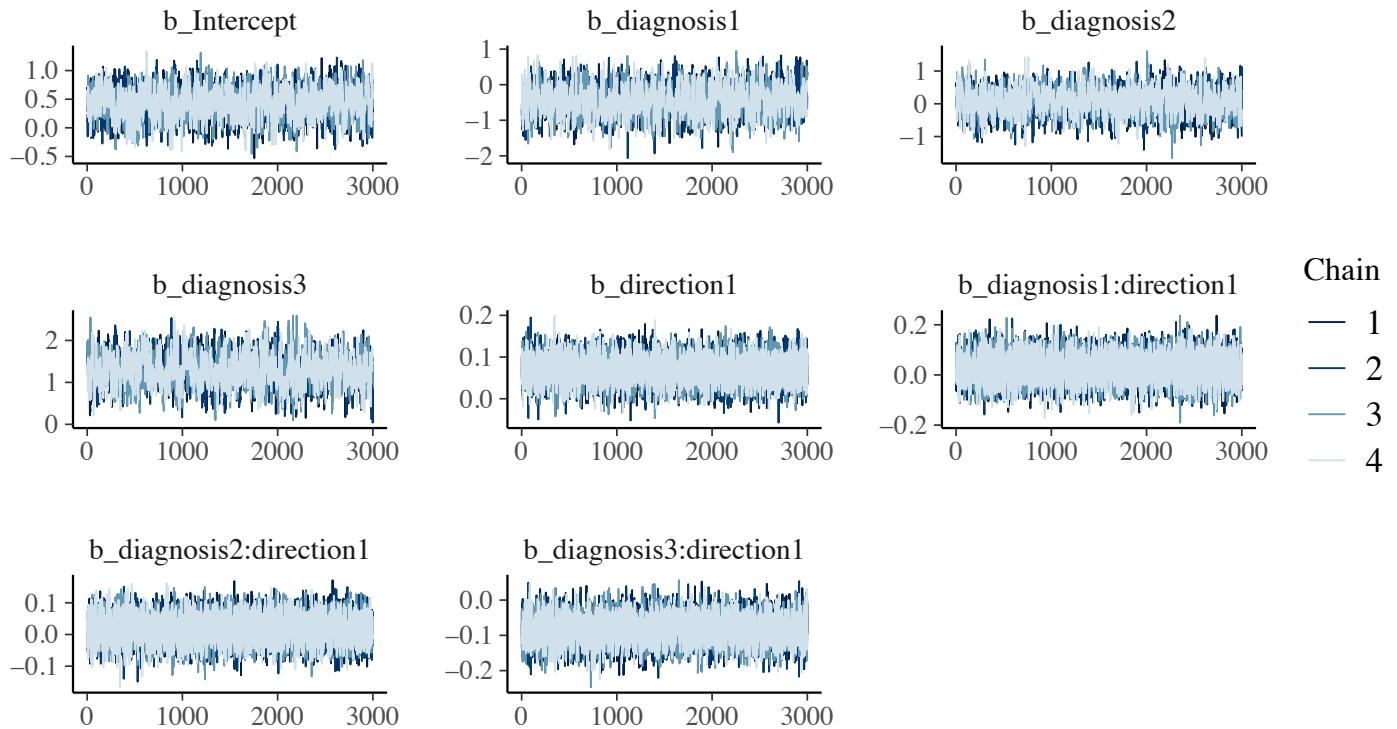
```

```

## [1] 0
# check the trace plots
post.draws = as_draws_df(m.cnt)
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 divergent samples and no rhats that are higher or equal to 1.01. Therefore, we go ahead and perform our posterior predictive checks.

```

# get the posterior predictions
post.pred = posterior_predict(m.cnt, ndraws = nsim)

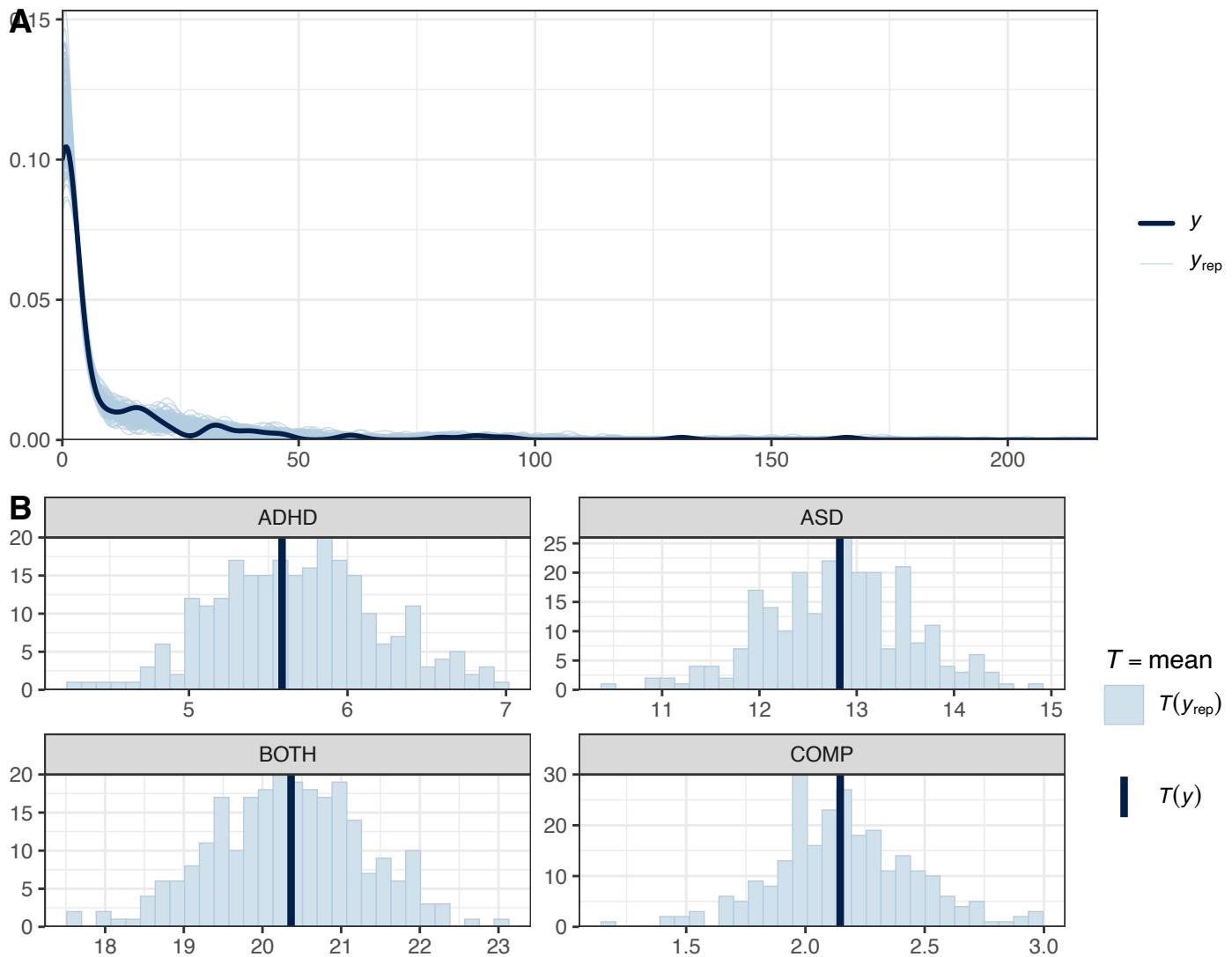
# check the fit of the predicted data compared to the real data
p1 = pp_check(m.cnt, ndraws = nsim) +
  theme_bw()

# distributions of means and sds compared to the real values per group
p2 = ppc_stat_grouped(df.cnt.cue$n.sac, post.pred, df.cnt.cue$diagnosis) +
  theme_bw()

p = ggarrange(p1, p2,
              nrow = 2, ncol = 1, labels = "AUTO")
annotate_figure(p,
               top = text_grob("Posterior predictive checks: number of cue-elicited saccades",
                               face = "bold", size = 14))

```

Posterior predictive checks: number of cue-elicited saccades



The predictions based on the model capture the data well. This further increases our trust in the model.

11.2 Inferences

Now that we are convinced that we can trust our model, we have a look at the model and its estimates.

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

## Family: poisson
## Links: mu = log
## Formula: n.sac ~ diagnosis * direction + (1 | subID)
## Data: df.cnt.cue (Number of observations: 184)
## Draws: 4 chains, each with iter = 4500; warmup = 1500; thin = 1;
##         total post-warmup draws = 12000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 92)
##             Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    2.08      0.21     1.71     2.52 1.00     1777    4082
## 
## Regression Coefficients:
##                         Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                  0.45      0.25    -0.06     0.92 1.00     1456
## diagnosis1                 -0.43      0.39   -1.21     0.35 1.00     1635
```

```

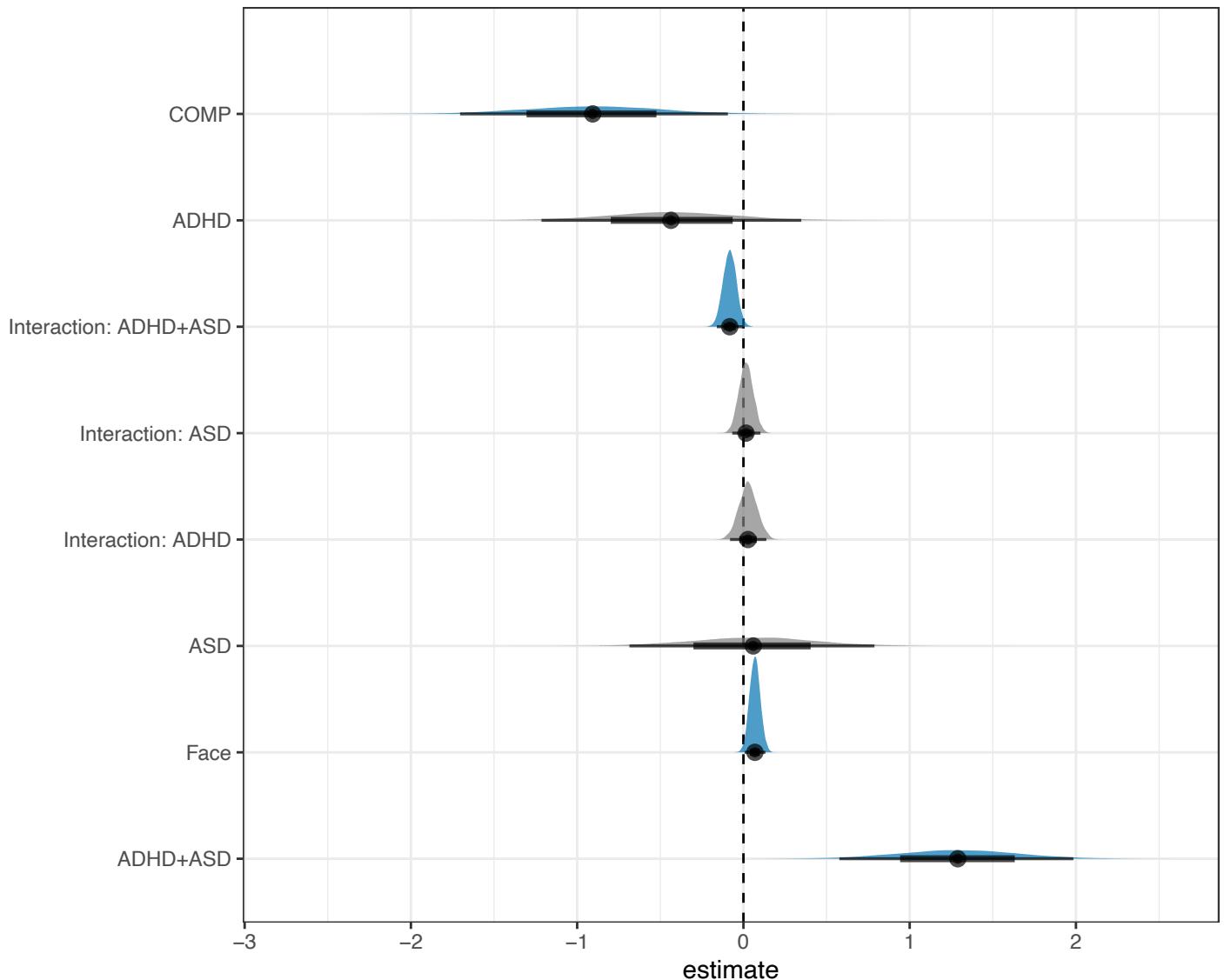
## diagnosis2          0.05    0.37   -0.69    0.79 1.01    1456
## diagnosis3          1.29    0.36    0.58    1.98 1.00    1063
## direction1          0.07    0.03    0.01    0.13 1.00    6981
## diagnosis1:direction1  0.03    0.06   -0.08    0.14 1.00   11505
## diagnosis2:direction1  0.02    0.04   -0.07    0.10 1.00    9677
## diagnosis3:direction1 -0.08    0.04   -0.16   -0.01 1.00    7276
##                               Tail_ESS
## Intercept                2652
## diagnosis1                 2945
## diagnosis2                 2552
## diagnosis3                 2189
## direction1                  8164
## diagnosis1:direction1      9294
## diagnosis2:direction1      9112
## diagnosis3:direction1      8565
##
## 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.cnt = as_draws_df(m.cnt) %>%
  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.cnt %>%
  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_direction1" ~ "Face",
      "b_diagnosis1:direction1" ~ "Interaction: ADHD",
      "b_diagnosis2:direction1" ~ "Interaction: ASD",
      "b_diagnosis3:direction1" ~ "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")
```



```
# face > object
e = hypothesis(m.cnt, "0 < 2*(direction1)",
               alpha = 0.025)
e

## Hypothesis Tests for class b:
##          Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*(direction1)) < 0     -0.14      0.06    -0.27    -0.02     68.36
##   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.

# extract predicted differences
df.new = df.cnt.cue %>% ungroup() %>%
  select(diagnosis, direction) %>%
  distinct() %>%
  mutate(
    condition = paste(diagnosis, direction, sep = "_")
```

Table 16: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
ADHD_face	1.3	0.63	0.17	0.41	2.7	6.3
ADHD_object	1	0.52	0.12	0.34	2.3	5.4
COMP_face	0.79	0.41	0.093	0.25	1.7	4.4
COMP_object	0.64	0.33	0.074	0.2	1.4	3.6
ASD_face	2	0.9	0.21	0.71	4	9.9
ASD_object	1.7	0.76	0.2	0.59	3.4	8.4
BOTH_face	6.1	2.7	1.2	2.3	12	26
BOTH_object	6.3	2.8	1.3	2.4	13	29

Table 17: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	2.5	0.77	0.77	1.3	4.3	7.5
object	2.4	0.76	0.75	1.2	4.2	8
FAB	-0.13	0.14	-0.84	-0.44	0.14	0.66

```

)
df.ms = as.data.frame(
  fitted(m.cnt, summary = F,
         newdata = df.new %>% select(diagnosis, direction),
         re_formula = NA))
colnames(df.ms) = df.new$condition

st(df.ms,
  summ = c('mean(x)', 'sd(x)', 'min(x)', 'pctile(x)[2.5]',
           'pctile(x)[97.5]', 'max(x)'))

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)'))
)

```

On average, participants produced cue-elicited saccades on 4.64% \pm 1.06 of the trials. However, the range was very wide, with some participants producing none and others producing them on 68.75% of the trials. Regardless of group, credibly more cue-elicited saccades were produced towards face compared to object cues (*estimate* = -0.14 [-0.27, -0.02], *posterior probability* = 98.56%).

11.3 Plots

As a last step, we can plot our data.

```

# rain cloud plot
df.cnt %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD")
  ) %>%
  ggplot(aes(diagnosis, n.sac, fill = direction, colour = direction)) + #
  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(

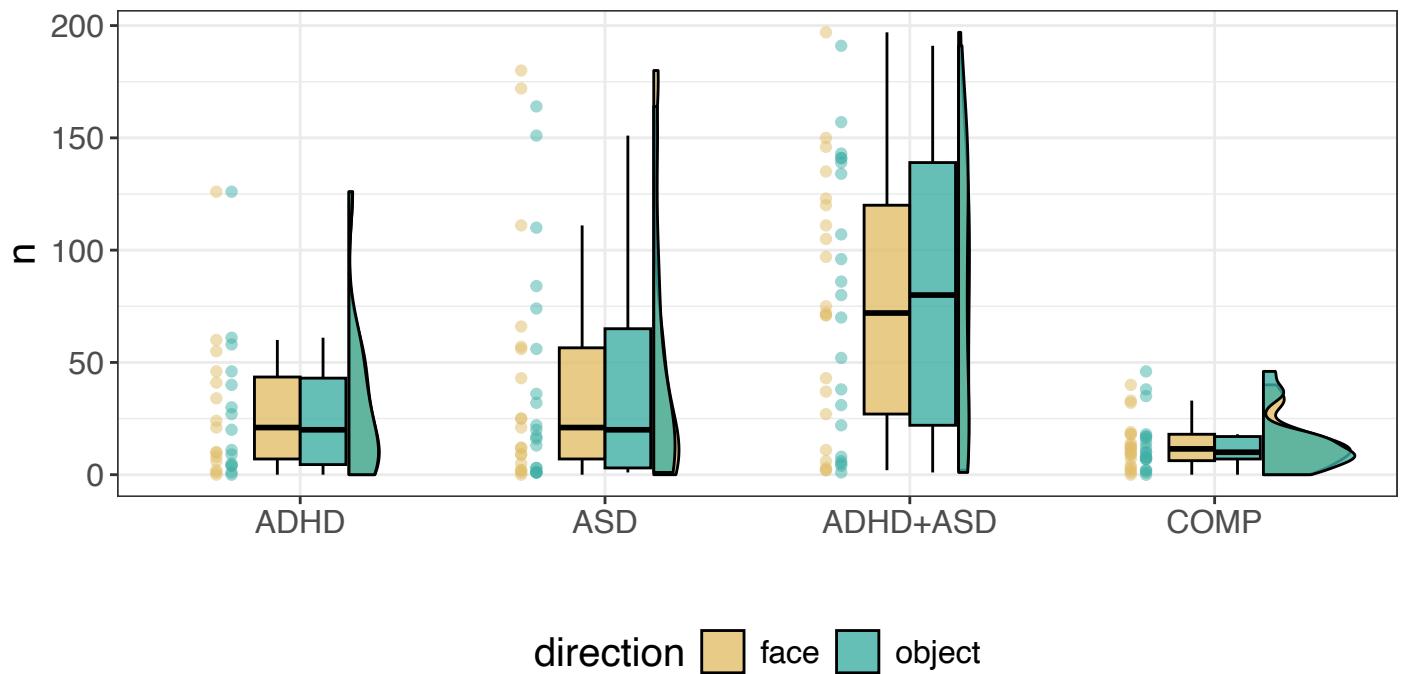
```

```

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))) +
  scale_fill_manual(values = custom.col2) +
  scale_color_manual(values = custom.col2) +
  labs(title = "Number of cue-elicited saccades", x = "", y = "n") +
  theme_bw() +
  theme(legend.position = "bottom",
        plot.title = element_text(hjust = 0.5),
        legend.direction = "horizontal",
        text = element_text(size = 15))

```

Number of cue-elicited saccades



direction face object

12 Exploration: Latencies of cue-elicited saccades

12.1 Model

We assume that the SBC for the hypothesis-guided latency analysis holds for this. We only need to slightly adjust the prior for the shift. This analysis only includes participants who performed cue-elicited saccades.

```

# preprocess cue latencies
df.lat.cue = df.cue %>%
  filter(!is.na(direction)) %>%
  group_by(subID, direction, diagnosis) %>%
  summarise(lat = median(lat, na.rm = T)) %>%
  mutate_if(is.character, as.factor)

# set the formula
f.lat = brms::bf(lat ~ diagnosis * direction + (1 | subID) )

# set weakly informative priors
priors = c(
  prior(normal(5,      0.75), class = Intercept),
  prior(normal(0,      0.25), class = sd),

```

```

prior(normal(0,      0.25), class = b),
prior(normal(0.5,   0.50), class = sigma),
prior(normal(150, 50.00), class = ndt) # this is the only prior that differs
)

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

# set the contrasts
contrasts(df.lat.cue$direction) = contr.sum(2)
contrasts(df.lat.cue$direction)

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

contrasts(df.lat.cue$diagnosis) = contr.sum(4)
contrasts(df.lat.cue$diagnosis)

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

# fit the maximal model
set.seed(7799)
m.lat = brm(f.lat,
             df.lat.cue, prior = priors,
             iter = iter, warmup = warm,
             backend = "cmdstanr", threads = threading(8),
             family = "shifted_lognormal",
             file = "m_lat-cue_ags",
             save_pars = save_pars(all = TRUE)
            )
rstan::check_hmc_diagnostics(m.lat$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.lat) >= 1.01, na.rm = T)

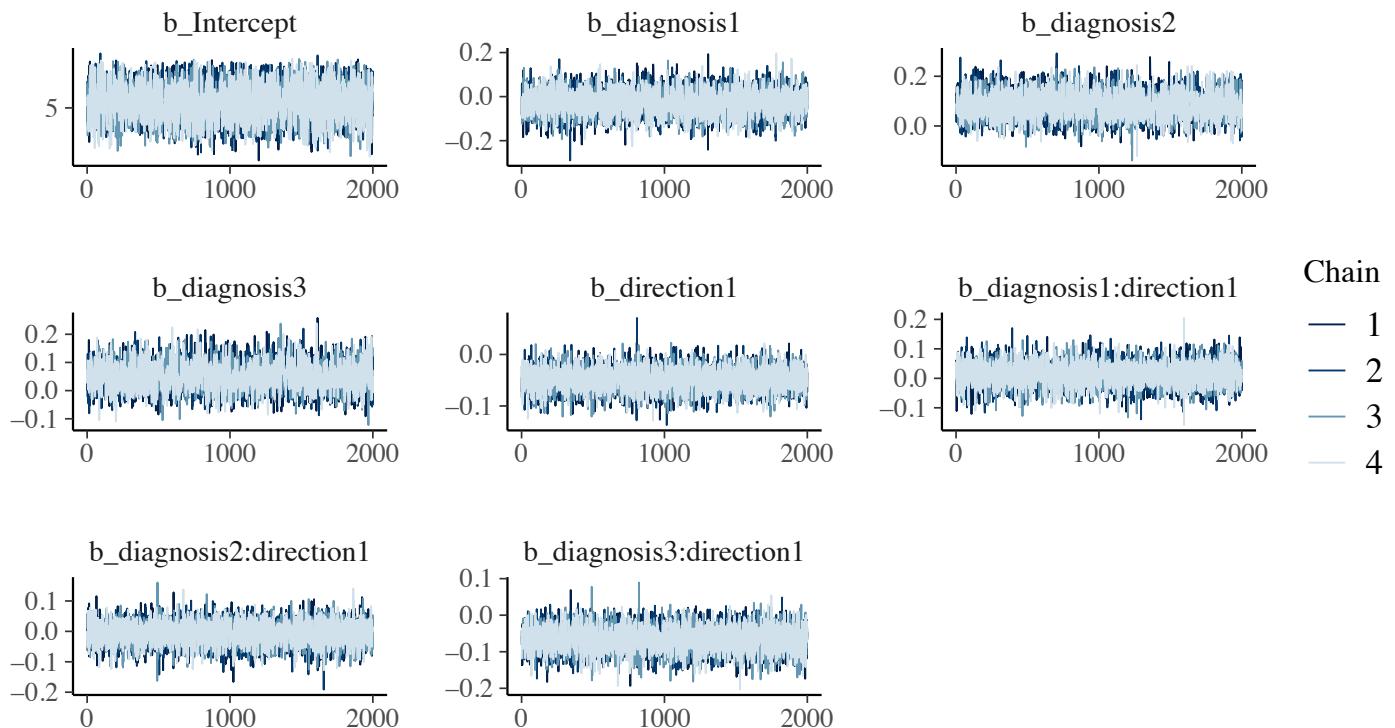
## [1] 0

# check the trace plots
post.draws = as_draws_df(m.lat)
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.
```



The final model does not exhibit any divergence issues or suboptimal rhats.

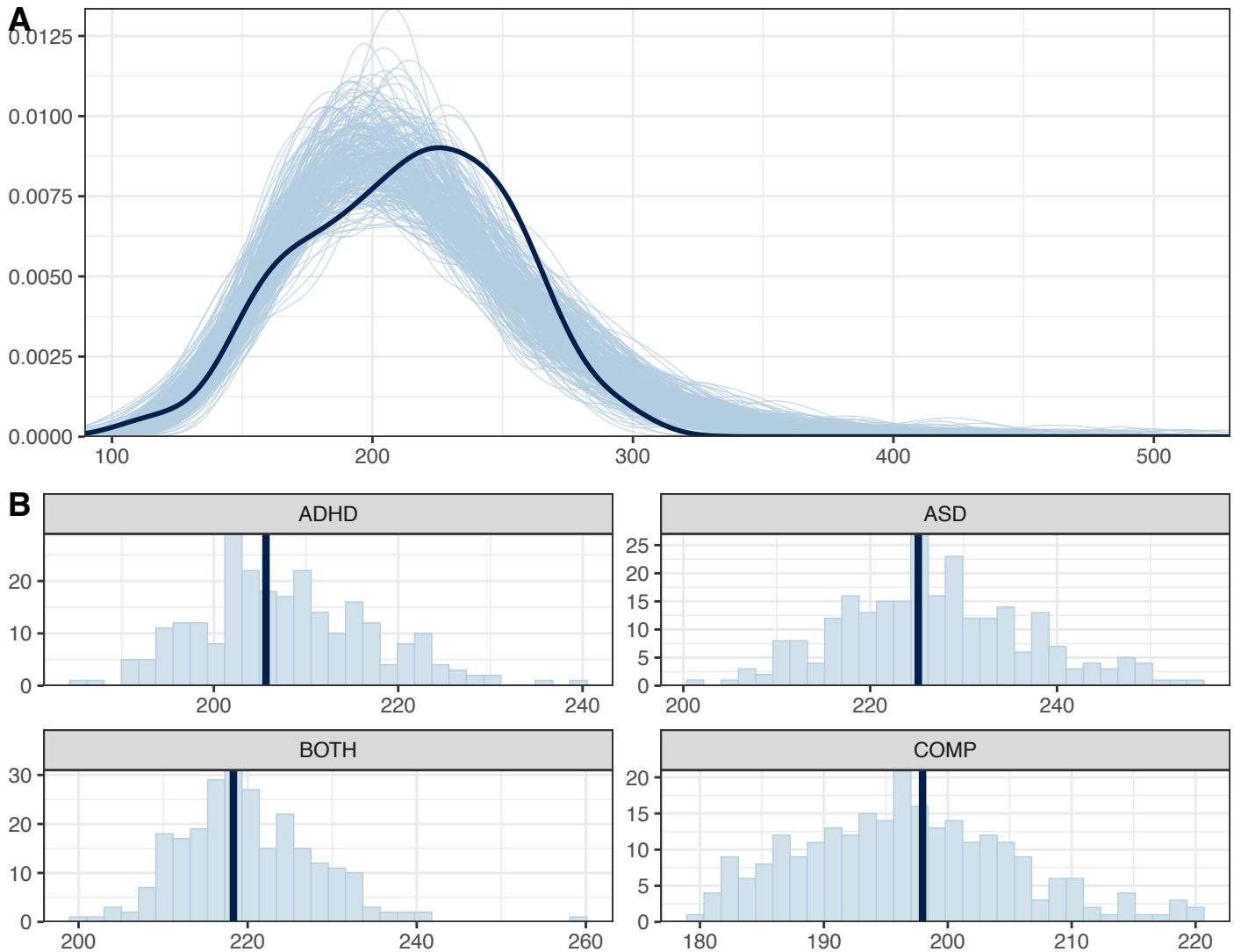
```
# get the posterior predictions
post.pred = posterior_predict(m.lat, ndraws = nsim)

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

# distributions of means and sds compared to the real values per group
p2 = ppc_stat_grouped(df.lat.cue$lat, post.pred, df.lat.cue$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: latency cues",
                               face = "bold", size = 14))
```

Posterior predictive checks: latency cues



This looks good.

12.2 Inferences

Now that we are convinced that we can trust our model, we have a look at the model and its estimates.

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

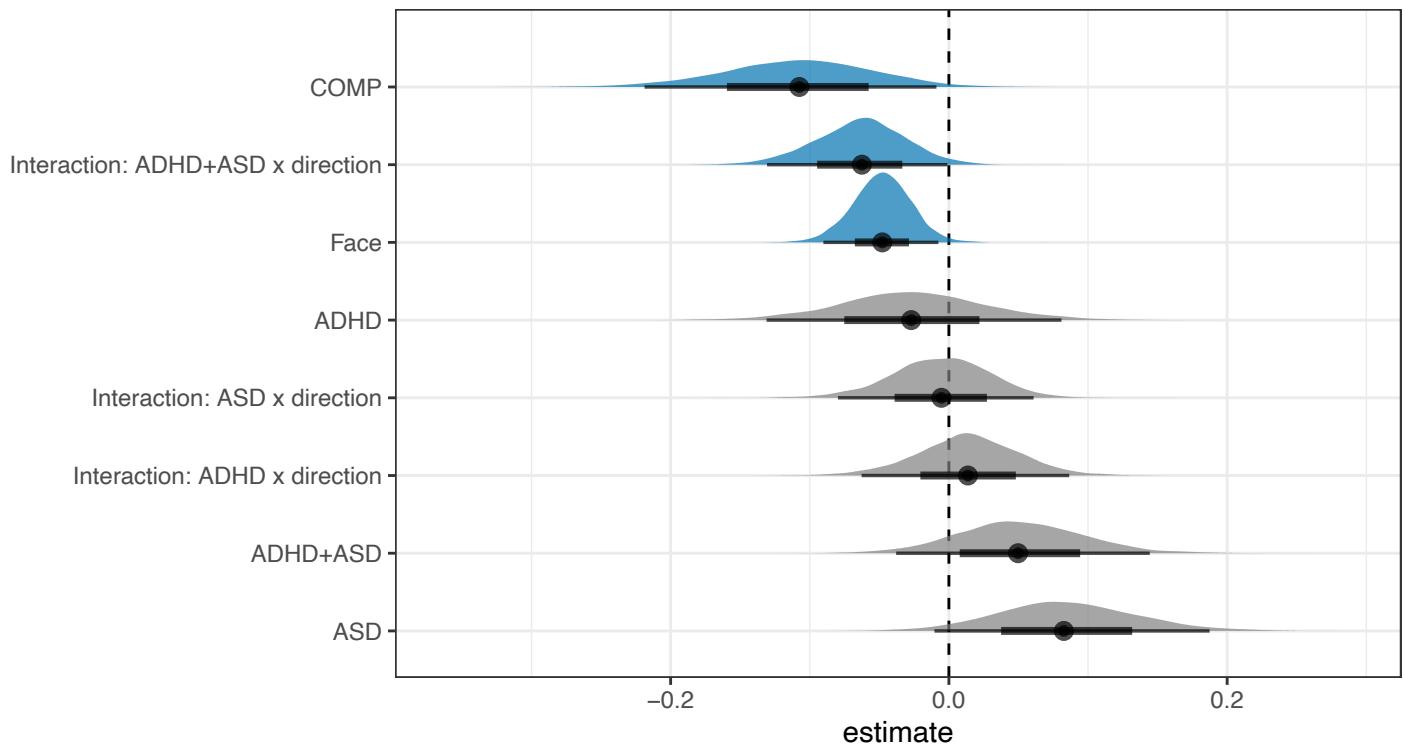
## Family: shifted_lognormal
##   Links: mu = identity; sigma = identity; ndt = identity
## Formula: lat ~ diagnosis * direction + (1 | subID)
##   Data: df.lat.cue (Number of observations: 114)
##   Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
##          total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 63)
##                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)      0.16      0.05     0.05     0.25 1.01     1185    1095
## 
## Regression Coefficients:
##                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept             5.05      0.13     4.80     5.29 1.00     3536
## diagnosis1        -0.03      0.05    -0.13     0.08 1.00     4200
```

```

## diagnosis2          0.08    0.05   -0.01    0.19 1.00    4853
## diagnosis3          0.05    0.05   -0.04    0.14 1.00    3921
## direction1         -0.05    0.02   -0.09   -0.01 1.00    8019
## diagnosis1:direction1  0.01    0.04   -0.06    0.09 1.00    8175
## diagnosis2:direction1  -0.01    0.04   -0.08    0.06 1.00    8286
## diagnosis3:direction1  -0.06    0.03   -0.13   -0.00 1.00    7929
##                           Tail_ESS
## Intercept              3811
## diagnosis1             4340
## diagnosis2             5316
## diagnosis3             4582
## direction1              5722
## diagnosis1:direction1  5645
## diagnosis2:direction1  4819
## diagnosis3:direction1  5779
##
## Further Distributional Parameters:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.21      0.04     0.15     0.30 1.00    2247    3746
## ndt       49.00     18.65     9.25    81.18 1.00    3620    3566
##
## 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).

# plot the posterior distributions
as_draws_df(m.lat) %>%
  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") %>%
  filter(coef != "b_Intercept") %>%
  mutate(
    coef = case_match(coef,
      "b_direction1" ~ "Face",
      "b_diagnosis1" ~ "ADHD",
      "b_diagnosis2" ~ "ASD",
      "b_diagnosis3" ~ "ADHD+ASD",
      "b_COMP" ~ "COMP",
      "b_diagnosis1:direction1" ~ "Interaction: ADHD x direction",
      "b_diagnosis2:direction1" ~ "Interaction: ASD x direction",
      "b_diagnosis3:direction1" ~ "Interaction: ADHD+ASD x direction"
    ),
    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, not_credible)) +
  theme(legend.position = "none")

```



```
# explore: faster towards faces
e = hypothesis(m.lat, "0 > 2*direction1", alpha = 0.025)
e
```

```
## Hypothesis Tests for class b:
##                               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (0)-(2*direction1) > 0      0.1       0.04     0.02     0.18      86.91
##   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.
```

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

st(df.ms,
  summ = c('mean(x)', 'sd(x)', 'min(x)', 'pctile(x)[2.5]',
           'pctile(x)[97.5]', 'max(x)'))
```

```
# calculate our difference columns
df.ms = df.ms %>%
  mutate(
    e = rowMeans(select(., matches(".*_object")), na.rm = T) -
      rowMeans(select(., matches(".*_face")), na.rm = T)
```

Table 18: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
COMP_face	194	11	162	174	215	243
COMP_object	192	10	155	172	213	236
ADHD_face	200	11	166	179	222	266
ADHD_object	211	13	163	187	236	281
ASD_face	214	12	171	191	237	265
ASD_object	233	12	194	209	258	286
BOTH_face	200	9	168	182	218	240
BOTH_object	237	11	201	215	260	291

Table 19: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	202	5.5	182	191	213	227
object	218	5.9	199	207	230	242
FAB	16	6.5	-18	2.7	29	40

)

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

A similar effect was found when exploring the latencies of cue-induced saccade, with participants producing saccades towards face cues faster than saccades towards object cues, independent of group (*estimate* = 0.1 [0.02, 0.18], *posterior probability* = 98.86%). This model predicted that if a cue-induced saccade was produced towards the face, the latency was 16.2ms [3.21, 29.02] shorter than if a saccade was produced towards the object cue.

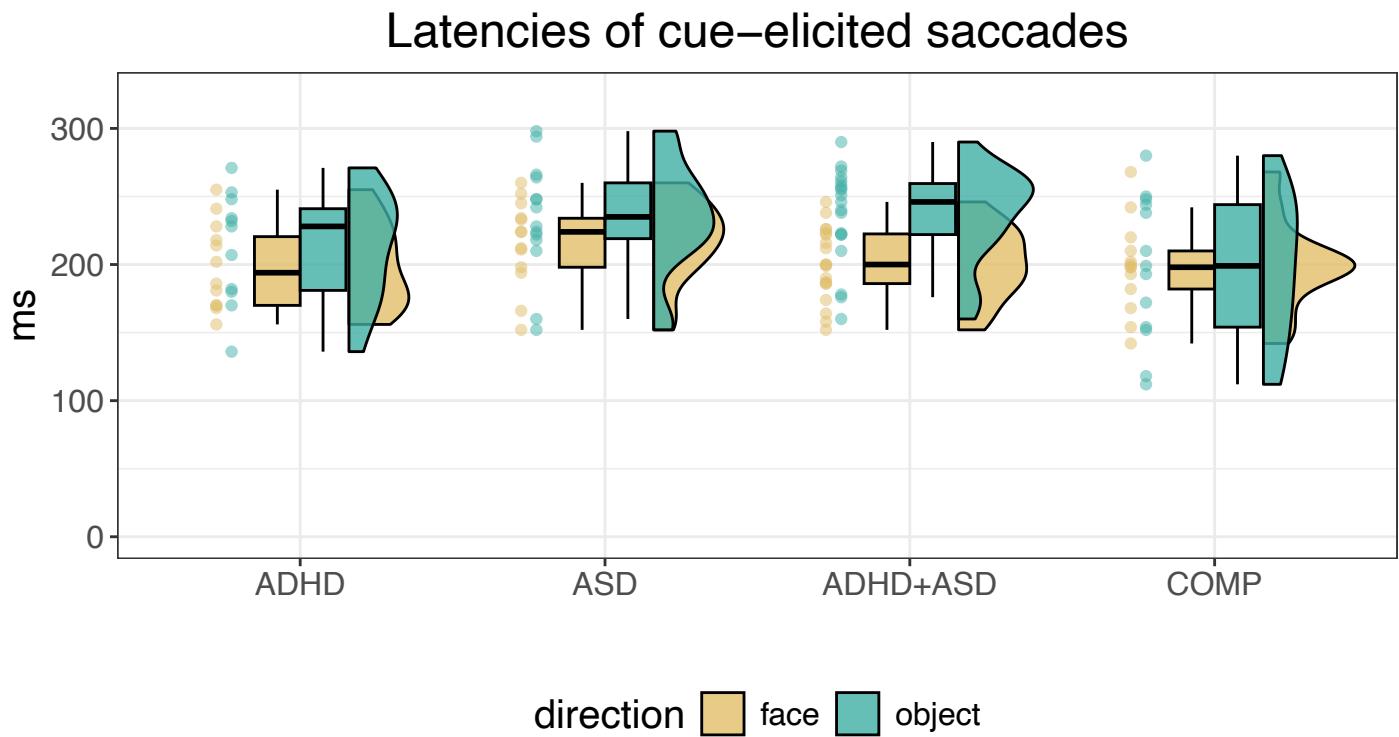
12.3 Plots

```
# rain cloud plot for the
df.lat.cue %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD")
  ) %>%
  ggplot(aes(diagnosis, lat, fill = direction, colour = direction)) +
  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_dodgegenudge(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_dodgegenudge(x = -0.25, width = 0.1))) +
  scale_fill_manual(values = custom.col2) +
  scale_color_manual(values = custom.col2) +
  labs(title = "Latencies of cue-elicited saccades", x = "", y = "ms") +
  theme_bw() +
```

```

ylim(0, 325) +
theme(legend.position = "bottom",
      plot.title = element_text(hjust = 0.5),
      legend.direction = "horizontal",
      text = element_text(size = 15))

```



13 Exploration: Dwell times starting within cue-elicited saccade window

13.1 Model

We assume that the SBC from the reaction time lognormal model holds here, although we slightly widen the Intercept because we have less prior knowledge.

```

# read in the preprocessed data
df.fix = readRDS("FAB_ET_fix.rds")

# set the formula
f.fix = brms::bf(duration ~ diagnosis * ROI * onTar +
                   (ROI * onTar | subID) + (ROI * onTar | subID))

# set weakly informative priors
priors = c(
  # general priors based on SBV
  prior(normal(6, 0.6), class = Intercept),
  prior(normal(0, 0.5), class = sigma),
  prior(normal(0, 0.1), class = sd),
  prior(lkj(2), class = cor),
  prior(normal(0, 0.04), class = b),
  # shift
  prior(normal(200, 100), class = ndt)
)

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

```

```

# set the contrasts
contrasts(df.fix$ROI) = contr.sum(2)
contrasts(df.fix$ROI)

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

contrasts(df.fix$onTar) = contr.sum(2)
contrasts(df.fix$onTar)

##      [,1]
## FALSE    1
## TRUE    -1

contrasts(df.fix$diagnosis) = contr.sum(4)
contrasts(df.fix$diagnosis)

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

# fit the maximal model
set.seed(5599)
m.fix = brm(f.fix,
             df.fix, prior = priors,
             iter = iter, warmup = warm,
             backend = "cmdstanr", threads = threading(8),
             family = "shifted_lognormal",
             file = "m_fix",
             save_pars = save_pars(all = TRUE)
            )
rstan::check_hmc_diagnostics(m.fix$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.

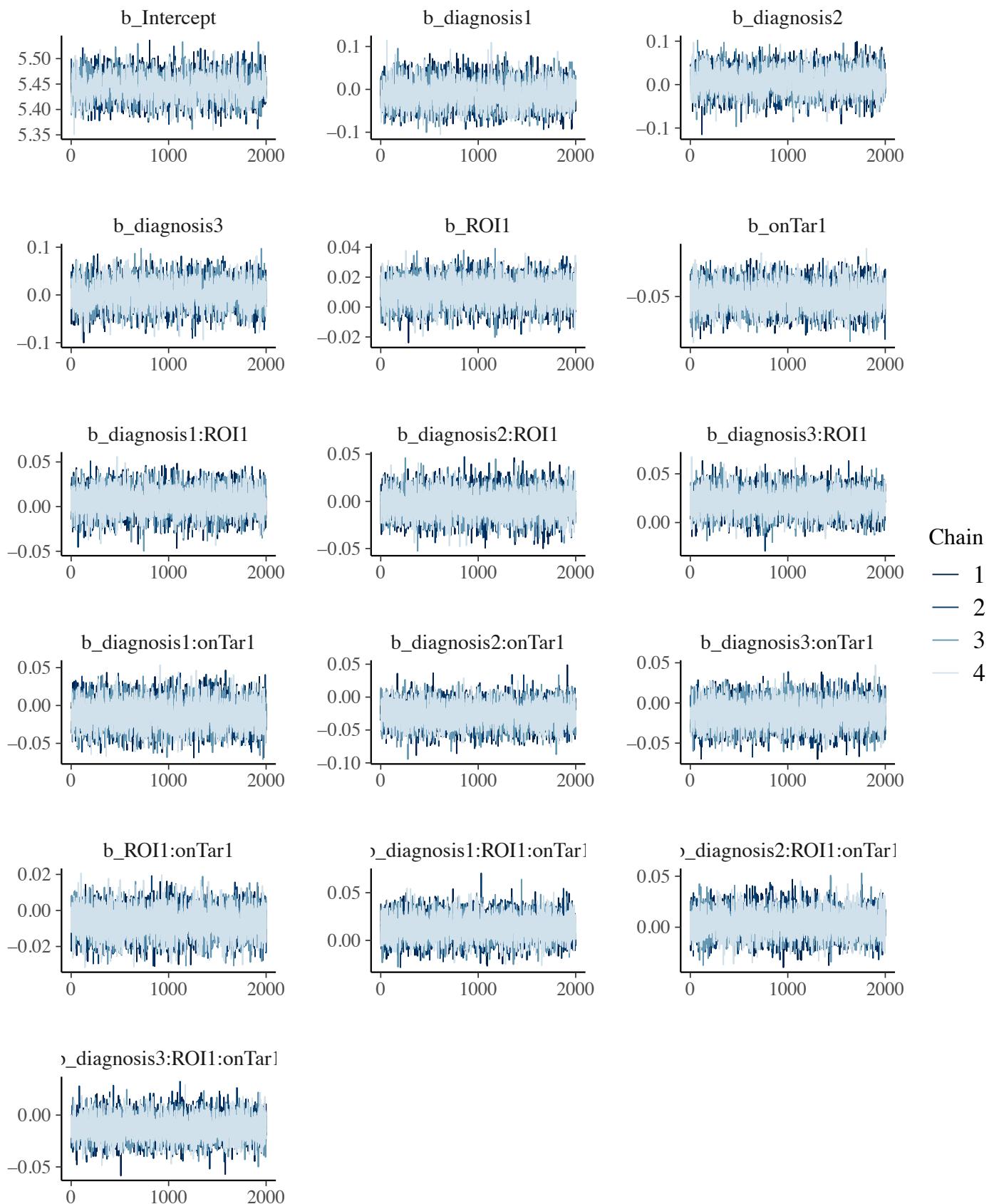
# check that rhats are below 1.01
sum(brms::rhat(m.fix) >= 1.01, na.rm = T)

## [1] 0

# check the trace plots
post.draws = as_draws_df(m.fix)
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.

```



The final model does not exhibit any divergence issues or suboptimal rhats.

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

# check the fit of the predicted data compared to the real data
p1 = pp_check(m.fix, ndraws = nsim) +
```

```

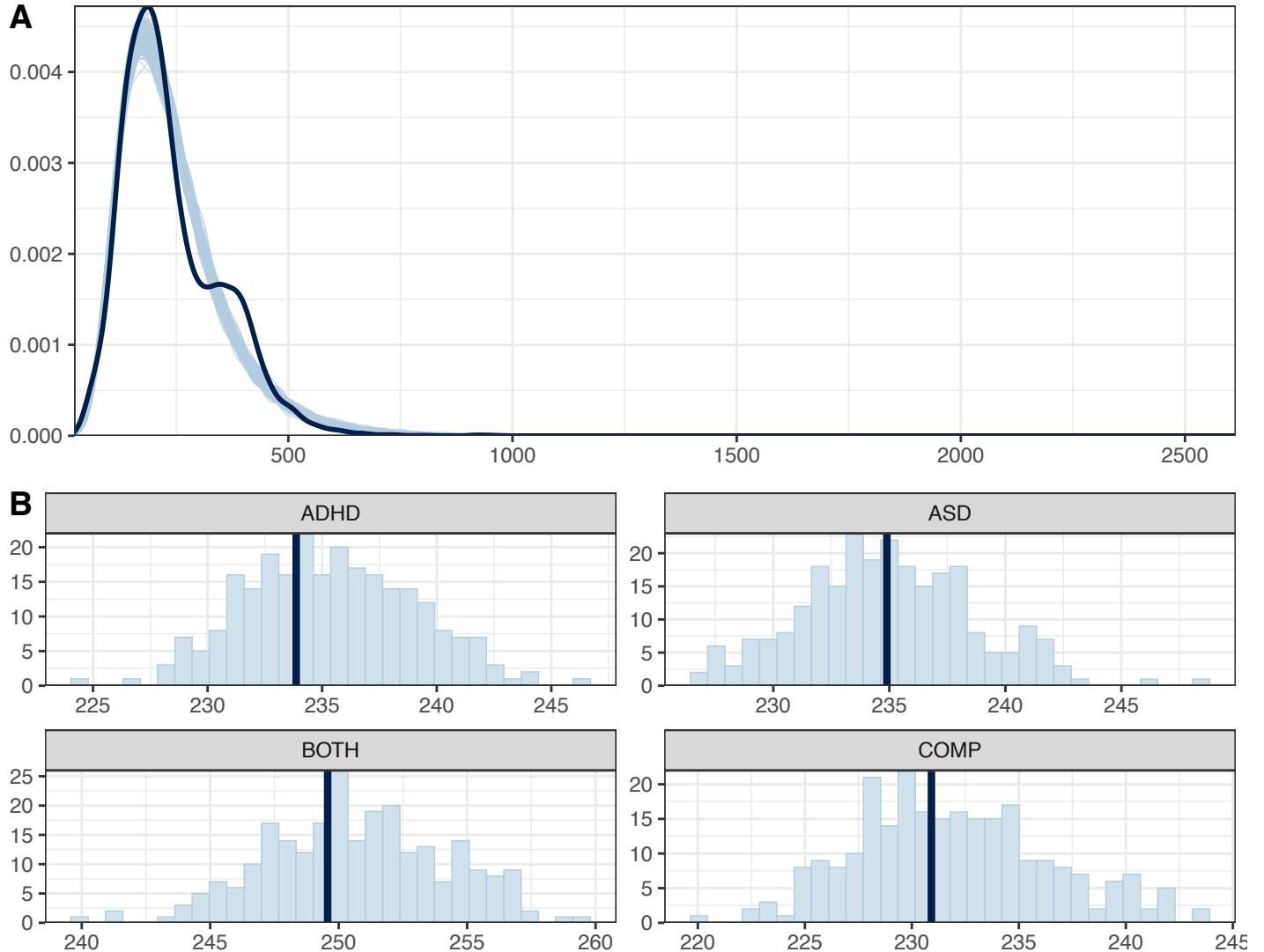
theme_bw() + theme(legend.position = "none")

# distributions of means and sds compared to the real values per group
p2 = ppc_stat_grouped(df.fix$duration, post.pred, df.fix$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: dwell times",
                                face = "bold", size = 14))

```

Posterior predictive checks: dwell times



This looks good.

13.2 Inferences

Now that we are convinced that we can trust our model, we have a look at the model and its estimates.

```

# print a summary
summary(m.fix)

## Family: shifted_lognormal
## Links: mu = identity; sigma = identity; ndt = identity
## Formula: duration ~ diagnosis * ROI * onTar + (ROI * onTar | subID) + (ROI * onTar | subID)
## Data: df.fix (Number of observations: 5654)

```

```

##   Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
##         total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 78)
##                               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)                0.18     0.02    0.15    0.22 1.00    2868
## sd(ROI1)                     0.04     0.01    0.02    0.06 1.00    2493
## sd(onTar1)                   0.07     0.01    0.05    0.09 1.00    4102
## sd(ROI1:onTar1)              0.03     0.01    0.00    0.05 1.00    2060
## cor(Intercept,ROI1)          -0.27     0.18   -0.61    0.10 1.00    8370
## cor(Intercept,onTar1)        0.19     0.15   -0.10    0.48 1.00    6500
## cor(ROI1,onTar1)             0.16     0.23   -0.29    0.59 1.01    1589
## cor(Intercept,ROI1:onTar1)   -0.20     0.24   -0.63    0.29 1.00   10173
## cor(ROI1,ROI1:onTar1)        -0.13     0.31   -0.68    0.52 1.00    5599
## cor(onTar1,ROI1:onTar1)      -0.39     0.26   -0.81    0.21 1.00    6749
##                               Tail_ESS
## sd(Intercept)                 4641
## sd(ROI1)                      2354
## sd(onTar1)                     5403
## sd(ROI1:onTar1)                2393
## cor(Intercept,ROI1)            6171
## cor(Intercept,onTar1)          6519
## cor(ROI1,onTar1)               3200
## cor(Intercept,ROI1:onTar1)     5528
## cor(ROI1,ROI1:onTar1)          5340
## cor(onTar1,ROI1:onTar1)        5340
##
## Regression Coefficients:
##                               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                    5.44     0.02    5.40    5.49 1.00    2092
## diagnosis1                  -0.01     0.03   -0.06    0.05 1.00    3909
## diagnosis2                   0.01     0.03   -0.04    0.06 1.00    4609
## diagnosis3                   0.00     0.03   -0.05    0.05 1.00    3235
## ROI1                         0.01     0.01   -0.01    0.03 1.00    8684
## onTar1                        -0.05     0.01   -0.07   -0.03 1.00    7288
## diagnosis1:ROI1              0.01     0.01   -0.02    0.03 1.00    9240
## diagnosis2:ROI1              -0.00     0.01   -0.03    0.02 1.00   10154
## diagnosis3:ROI1              0.02     0.01   -0.00    0.04 1.00    8498
## diagnosis1:onTar1             -0.01     0.02   -0.04    0.02 1.00    7463
## diagnosis2:onTar1             -0.03     0.02   -0.06    0.01 1.00    8029
## diagnosis3:onTar1             -0.01     0.02   -0.04    0.02 1.00    7224
## ROI1:onTar1                  -0.01     0.01   -0.02    0.01 1.00   10894
## diagnosis1:ROI1:onTar1       0.01     0.01   -0.01    0.04 1.00   11287
## diagnosis2:ROI1:onTar1       0.00     0.01   -0.02    0.03 1.00   11456
## diagnosis3:ROI1:onTar1       -0.01     0.01   -0.03    0.01 1.00    9056
##                               Tail_ESS
## Intercept                     3278
## diagnosis1                     5389
## diagnosis2                     5491
## diagnosis3                     4788
## ROI1                          7010
## onTar1                         5965
## diagnosis1:ROI1                6664
## diagnosis2:ROI1                6835
## diagnosis3:ROI1                6945
## diagnosis1:onTar1               6303
## diagnosis2:onTar1               6500
## diagnosis3:onTar1               6376
## ROI1:onTar1                     6985

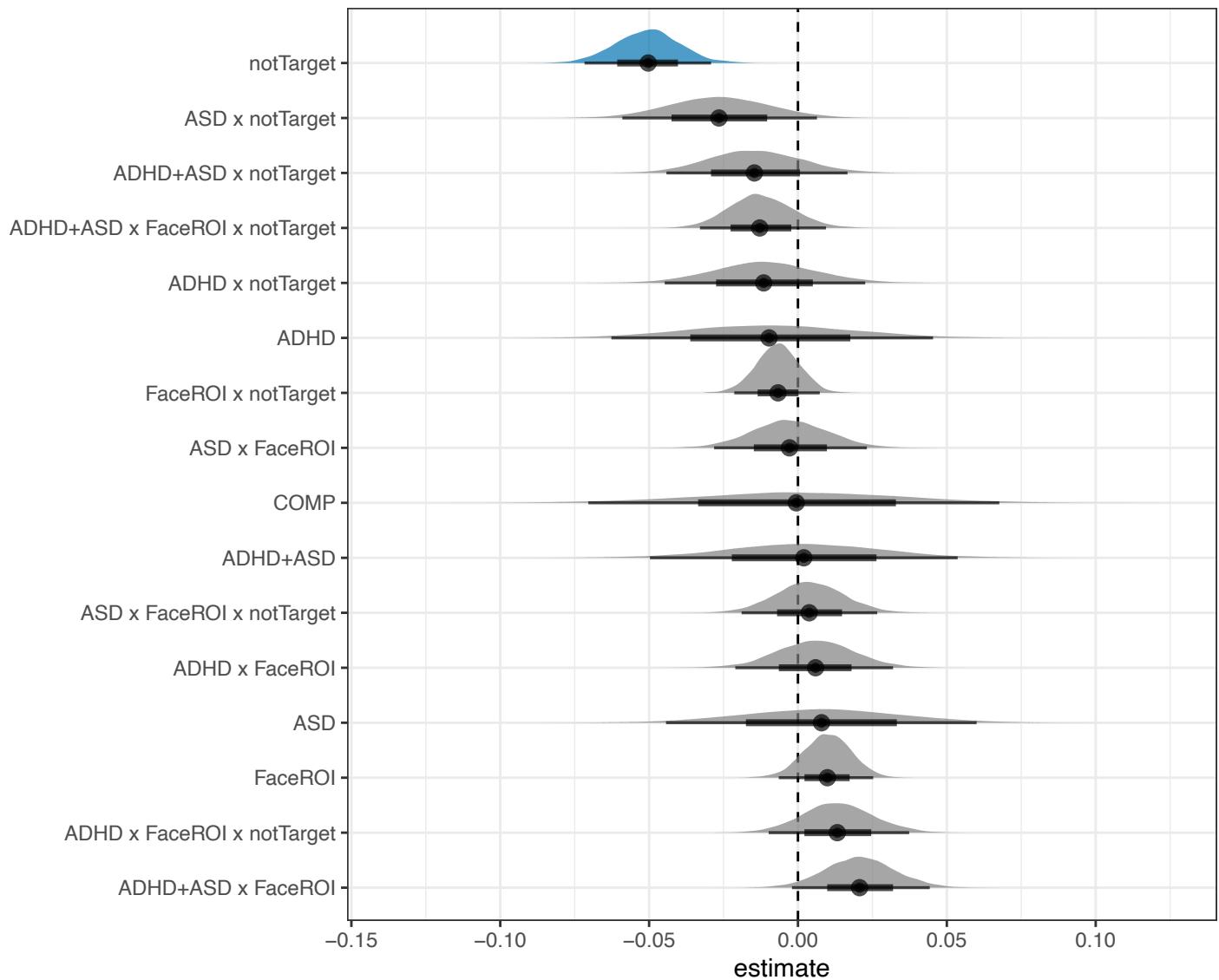
```

```

## diagnosis1:ROI1:onTar1      6701
## diagnosis2:ROI1:onTar1      6876
## diagnosis3:ROI1:onTar1      6098
##
## Further Distributional Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.41      0.00    0.40    0.42 1.00    13572    6037
## ndt       0.59      0.58    0.01    2.15 1.00     8922    4640
##
## 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).

# plot the posterior distributions
as_draws_df(m.fix) %>%
  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") %>%
  filter(coef != "b_Intercept") %>%
  mutate(
    coef = substr(coef, 3, nchar(coef)),
    coef = str_replace_all(coef, ":", " x "),
    coef = str_replace_all(coef, "ROI1", "FaceROI"),
    coef = str_replace_all(coef, "onTar1", "notTarget"),
    coef = str_replace_all(coef, "diagnosis1", "ADHD"),
    coef = str_replace_all(coef, "diagnosis2", "ASD"),
    coef = str_replace_all(coef, "diagnosis3", "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, not_credible)) +
  theme(legend.position = "none")

```



13.3 Plots

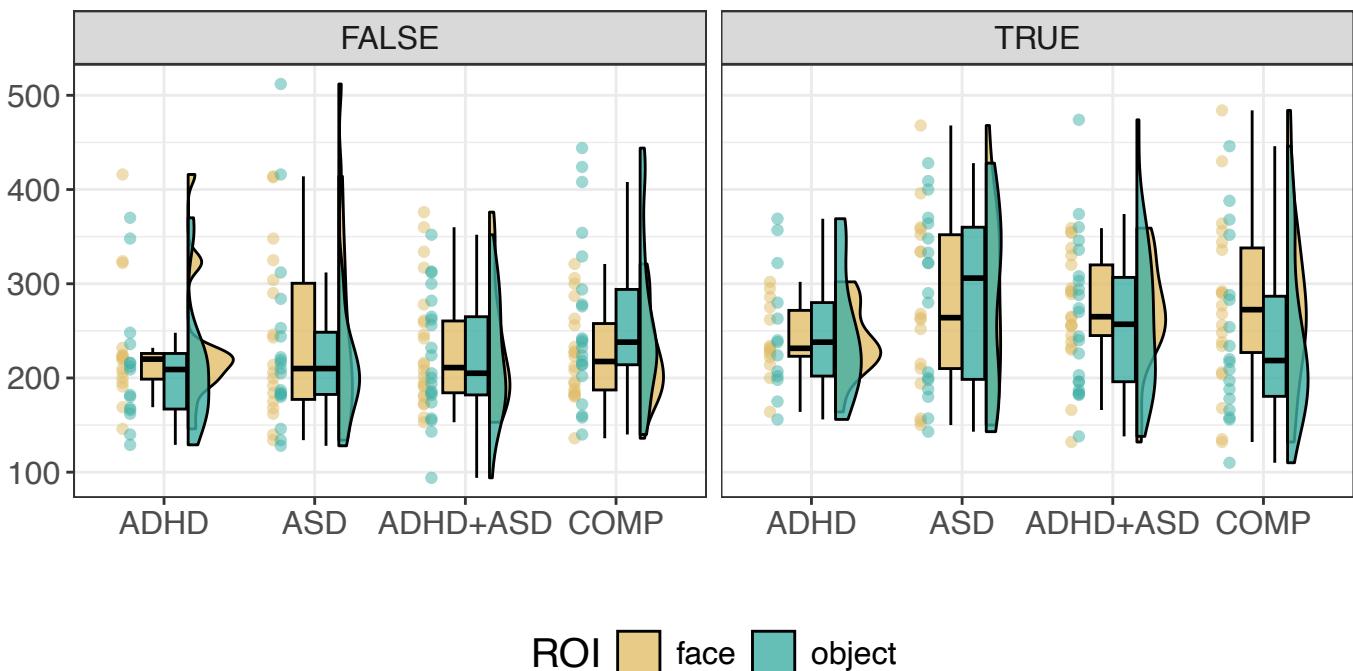
```
# rain cloud plot for the
df.fix %>%
  group_by(subID, diagnosis, ROI, onTar) %>%
  summarise(
    duration = median(duration, na.rm = T)
  ) %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD")
  ) %>%
  ggplot(aes(diagnosis, duration, fill = ROI, colour = ROI)) + #
  geom_rain(rain.side = '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_dodgegenudge(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_dodgegenudge(x = -0.25, width = 0.1))) +
  scale_fill_manual(values = custom.col2) +
```

```

scale_color_manual(values = custom.col2) +
  labs(title = "Dwell times starting during cue-elicited saccades", x = "", y = "") +
  theme_bw() +
  facet_wrap(. ~ onTar) +
  theme(legend.position = "bottom",
        plot.title = element_text(hjust = 0.5),
        legend.direction = "horizontal",
        text = element_text(size = 15))

```

Dwell times starting during cue-elicited saccades



ROI face object