

# S2: Analysis of FAB eye tracking data with brms

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## S2.1 Introduction

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

### Some general settings

```
# number of simulations
nsim = 250

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

### Package versions

```
## [1] "R version 4.4.3 (2025-02-28)"
## [1] "knitr version 1.46"
## [1] "ggplot2 version 3.5.1"
## [1] "brms version 2.21.0"
## [1] "tidyverse version 2.0.0"
## [1] "ggnetwork version 0.6.0"
## [1] "ggridges version 0.0.4"
## [1] "bayesplot version 1.11.1"
## [1] "SBC version 0.3.0.9000"
## [1] "rstatix version 0.7.2"
## [1] "logspline version 2.1.22"
## [1] "BayesFactor version 0.9.12.4.7"
## [1] "effectsize version 0.8.9"
## [1] "bayestestR version 0.15.0"
```

### Preparation

First, we load the eye tracking data and combine it with demographic information including the diagnostic status of the subjects. 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. We also load in the behavioural data again to be able to use reaction times for further correlational analyses.

```
# 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))

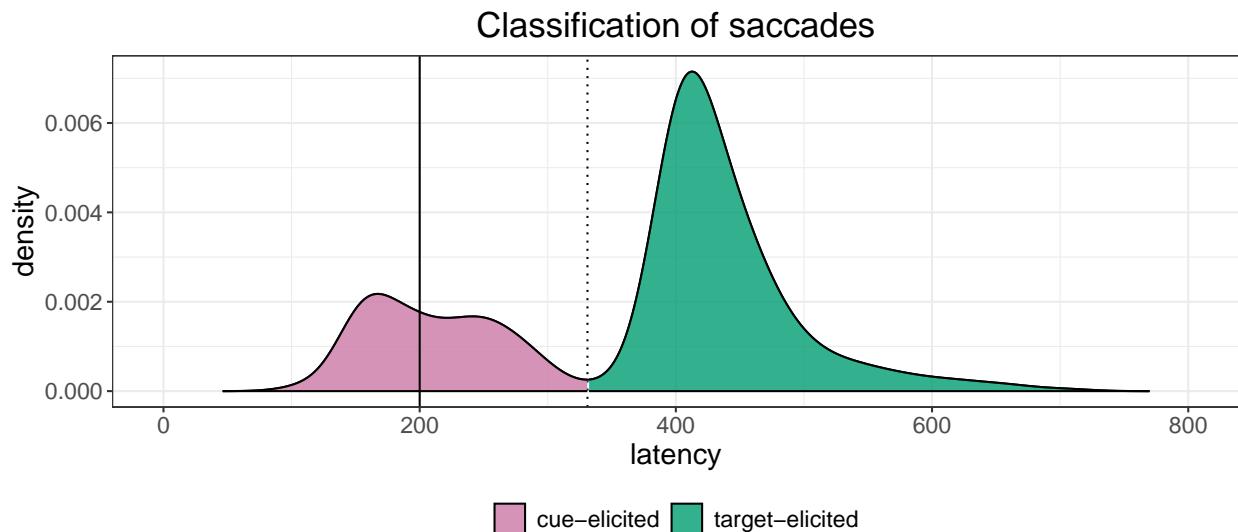
# find which point is the global minimum
lat.points = dd$y[points$minima]
idx = which.min(lat.points)

```

```

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())

```



```

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

```

## S2.2 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.

### 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

```

## 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.

## 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()

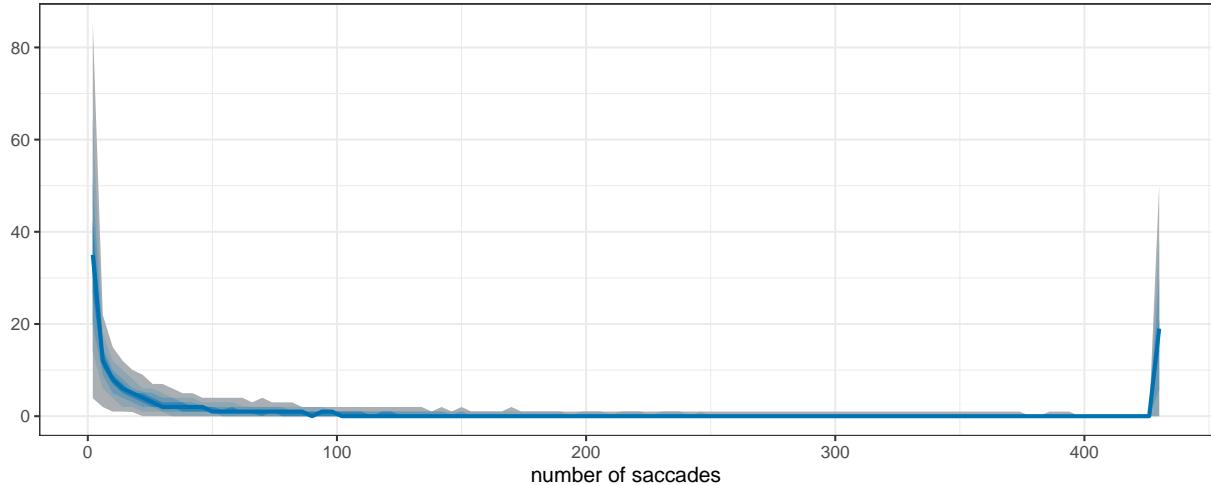
tmpM = apply(dvfakemath, 2, mean) # mean
tmpSD = apply(dvfakemath, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark) +
  labs(x = "Mean number of saccades", title = "Means of simulated data") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD number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

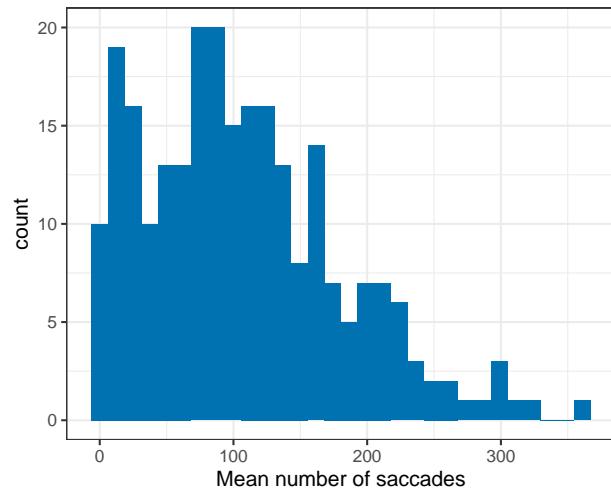
```

## Prior predictive checks

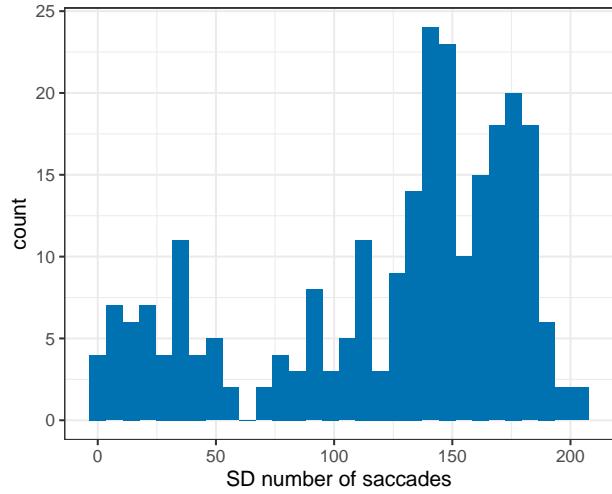
**A** Prior predictive distribution



**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.

## 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
```

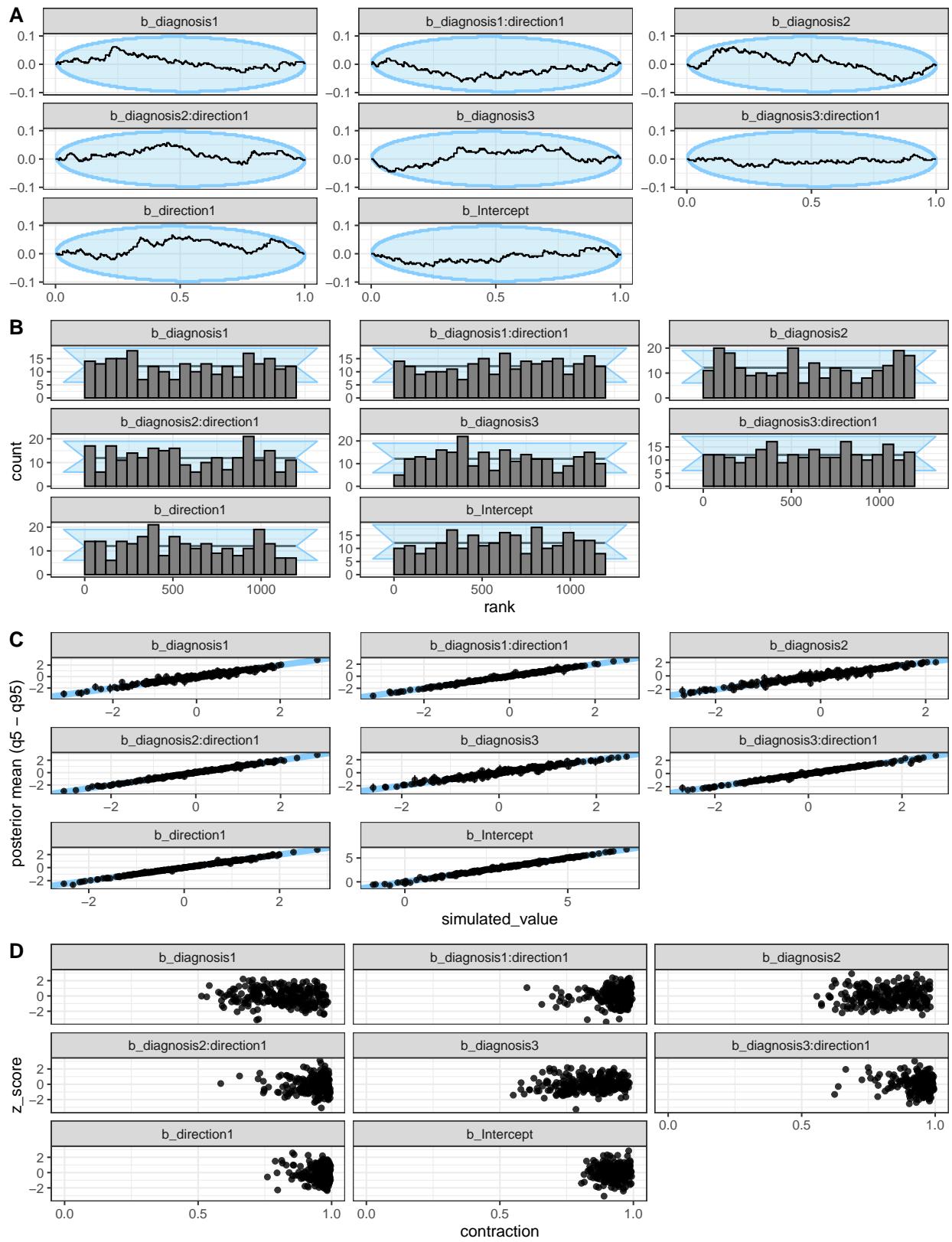
```

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.

## 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.

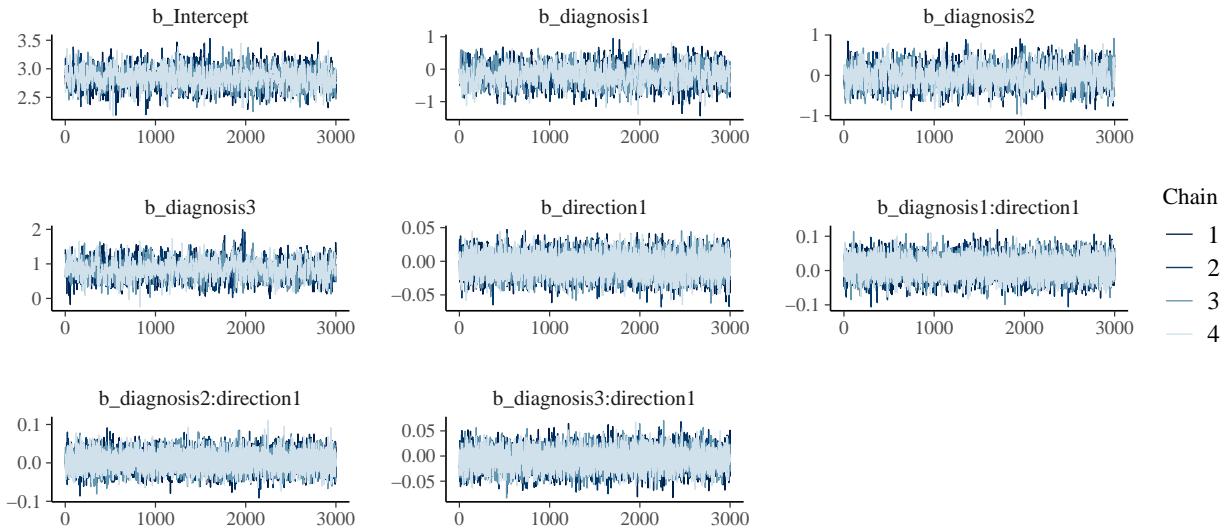
##
## Energy:
## E-BFMI indicated no pathological behavior.

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

## [1] 2

# 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.

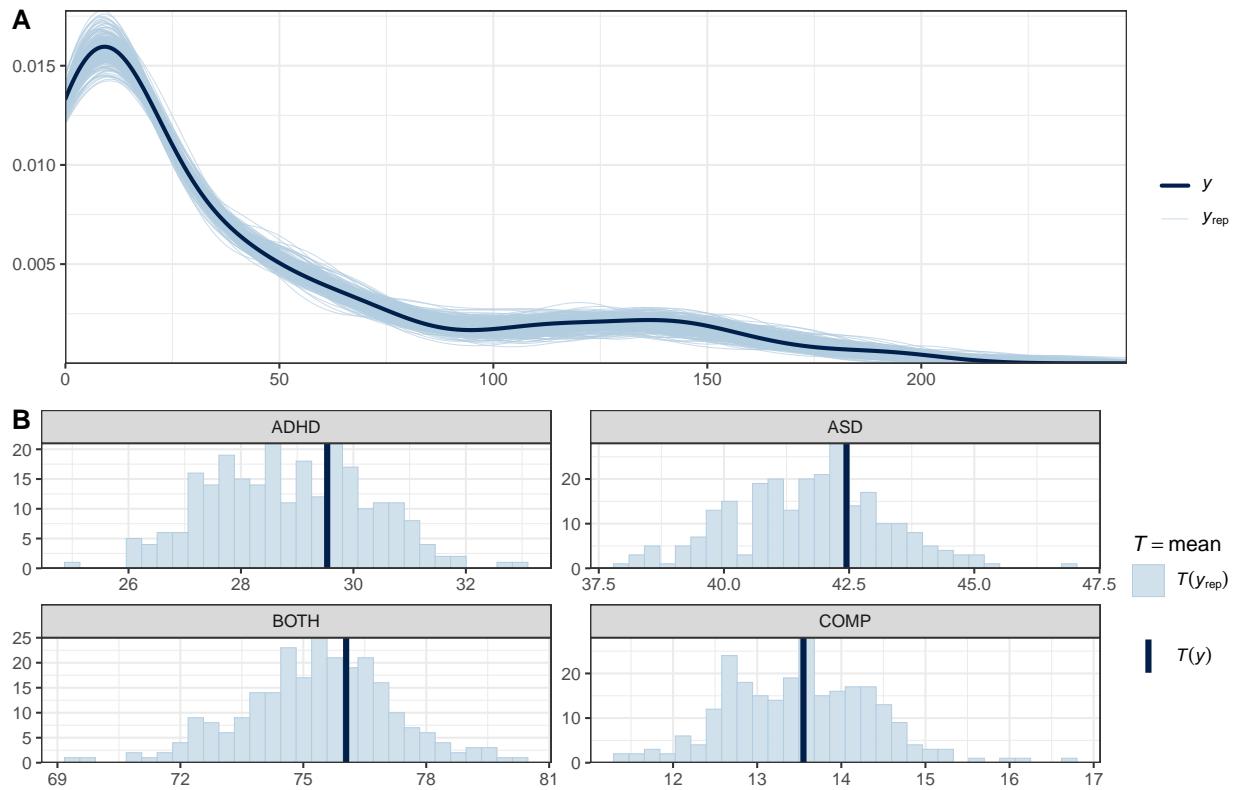
```
# get the posterior predictions
post.pred = posterior_predict(m.cnt, ndraws = nsim)

# 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.

## 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: 152)
## Draws: 4 chains, each with iter = 4500; warmup = 1500; thin = 1;
##         total post-warmup draws = 12000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 76)
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    1.39      0.13     1.16     1.67 1.00      1831     3498
##
## Regression Coefficients:
##                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                  2.84      0.17     2.52     3.17 1.01      1329
## diagnosis1                 -0.17      0.30    -0.75     0.42 1.00      1484
## diagnosis2                 -0.02      0.26    -0.52     0.49 1.00      1339
## diagnosis3                  0.84      0.26     0.33     1.35 1.01      1095
## direction1                 -0.01      0.02    -0.04     0.02 1.00      7632
```

```

## diagnosis1:direction1      0.01      0.03     -0.05      0.07 1.00      8711
## diagnosis2:direction1      0.01      0.02     -0.04      0.05 1.00      9149
## diagnosis3:direction1     -0.01      0.02     -0.05      0.03 1.00      7972
##                                     Tail_ESS
## Intercept                      2298
## diagnosis1                     2349
## diagnosis2                     2388
## diagnosis3                     2245
## direction1                     8645
## diagnosis1:direction1          8131
## diagnosis2:direction1          8479
## diagnosis3:direction1          8677
##
## 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
  )

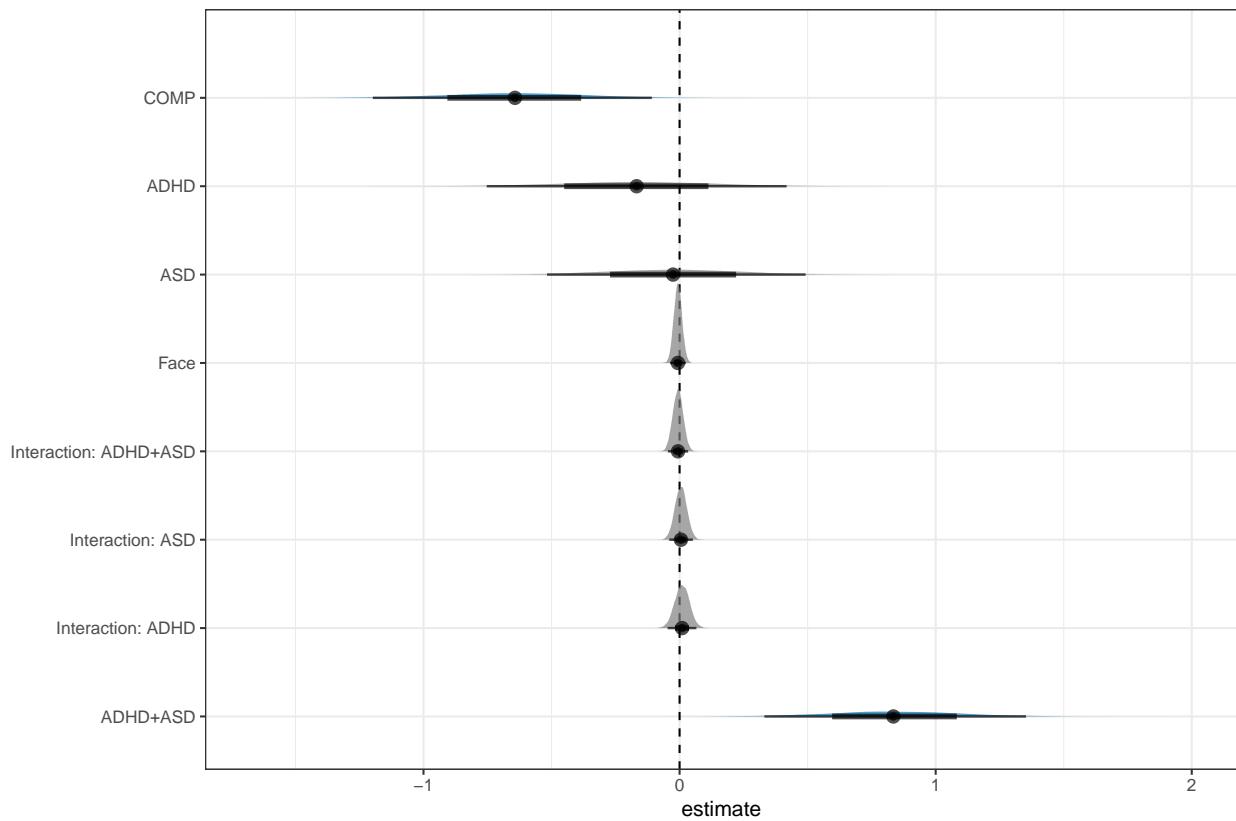
# plot the posterior distributions
df.m.cnt %>%
  select(starts_with("b_")) %>%
  pivot_longer(cols = starts_with("b_"), names_to = "coef", values_to = "estimate") %>%
  filter(coef != "b_Intercept") %>%
  mutate(
    coef = case_match(coef,
      "b_diagnosis1" ~ "ADHD",
      "b_diagnosis2" ~ "ASD",
      "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 1: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	21	3.9	11	14	29	45
object	21	3.9	11	14	30	44
FAB	0.32	0.58	-2	-0.86	1.4	3.2

```

## 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      0.51
##   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

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

```

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* = 36.31%). 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* = 33.99%).

## Plots

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

```

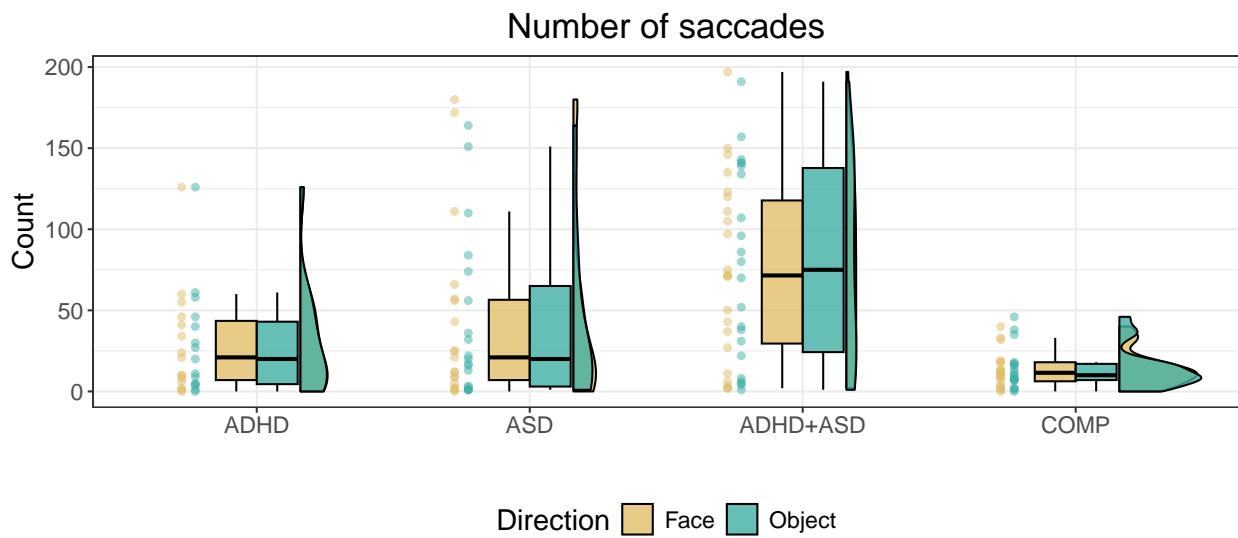
# rain cloud plot
df.cnt %>%
  mutate(
    diagnosis = recode(diagnosis, "BOTH" = "ADHD+ASD"),
    ...
  )

```

```

  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)

```

## S2.3 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.

## 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.

### 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.

### 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]]
}

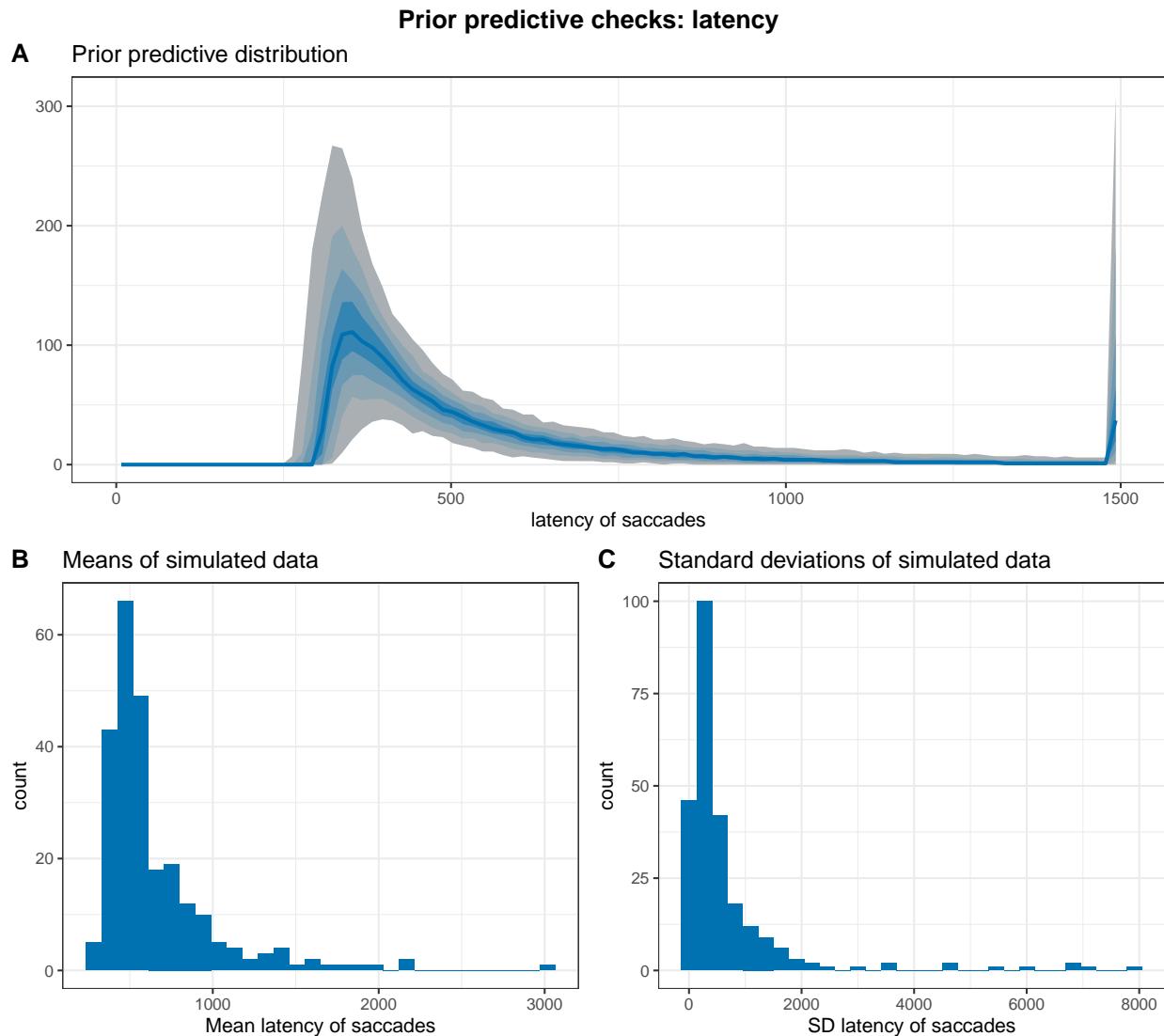
# set very large data points to a value of 1500
dvfakemath = dvfakemat;
dvfakemath[dvfakemath < 0] = 0
dvfakemath[dvfakemath > 1500] = 1500
# compute one histogram per simulated data-set
breaks = seq(0, 1500, length.out = 101)
binwidth = breaks[2] - breaks[1]
histmat = matrix(NA, ncol = nrow(truePars) + 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))

```



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.

### 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)

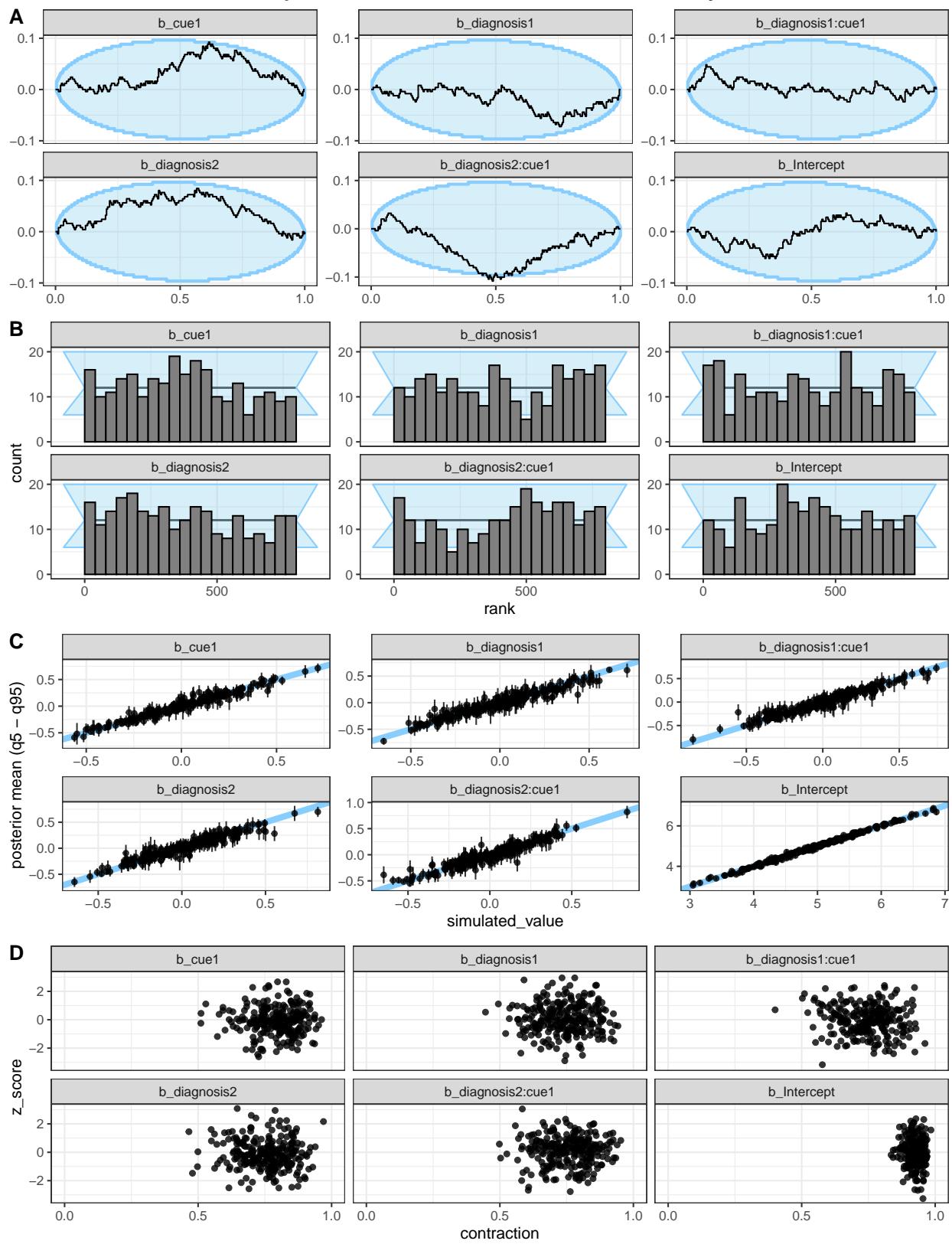
# plot SBC with functions from the SBC package focusing on population-level parameters

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.

## 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.

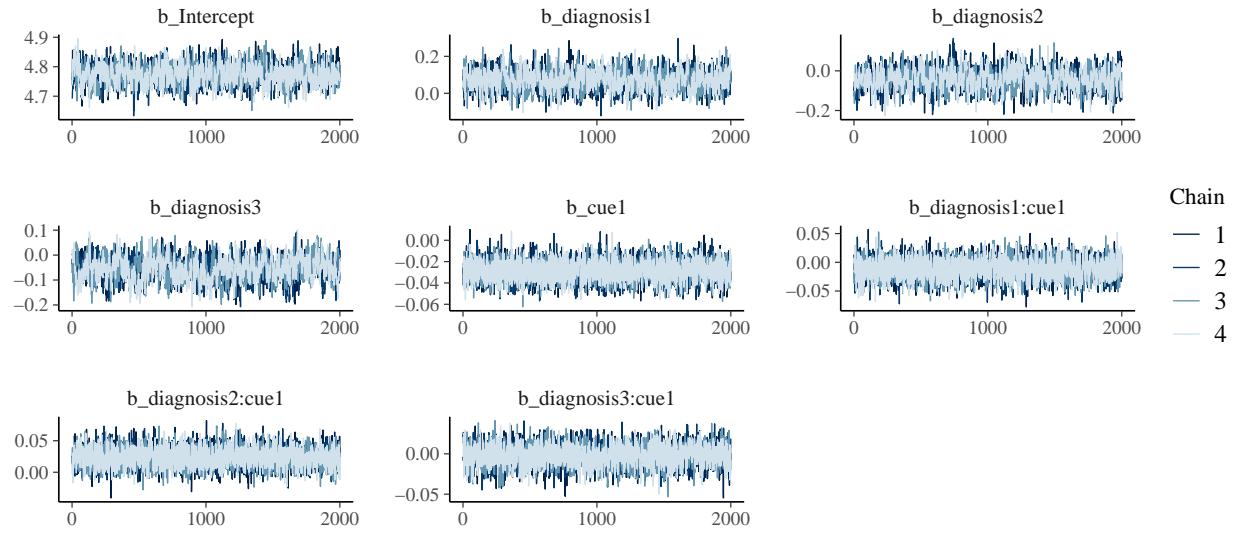
##
## Energy:
## E-BFMI indicated no pathological behavior.

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

## [1] 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 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.

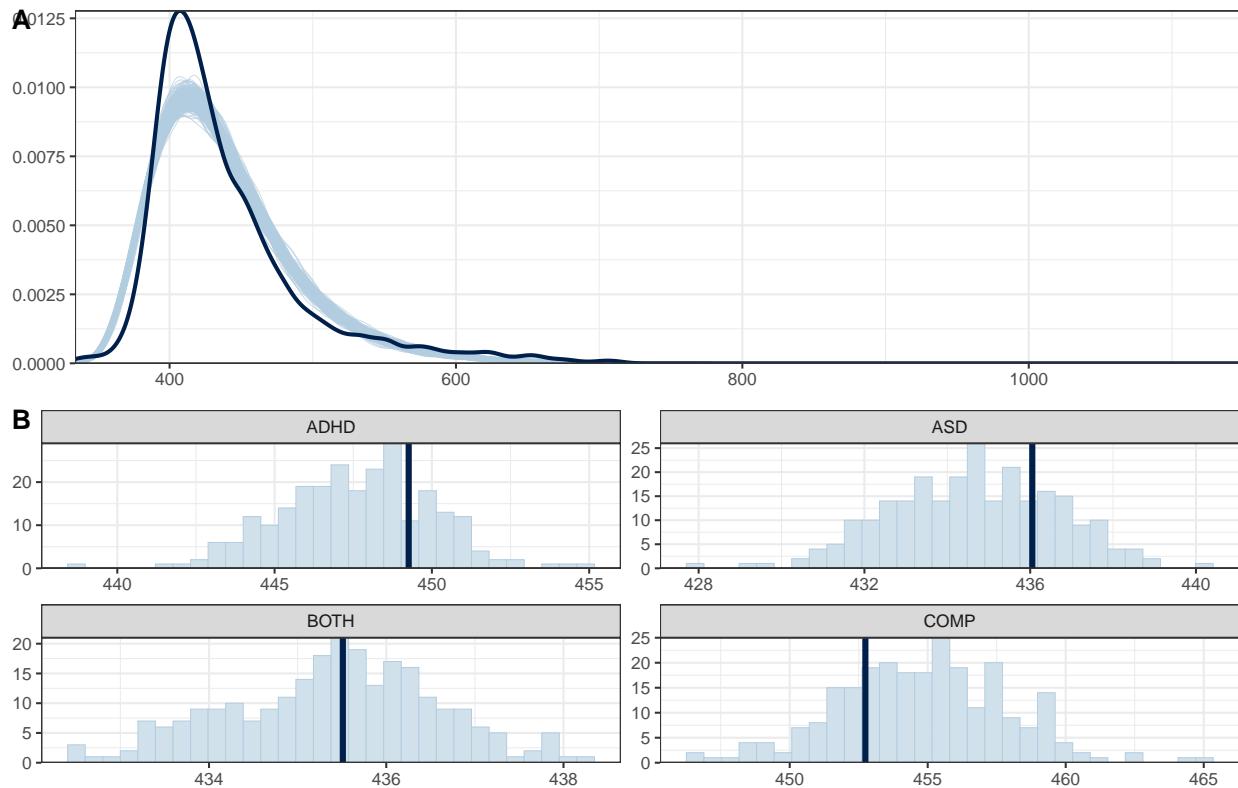
```
# get the posterior predictions
post.pred = posterior_predict(m.lat, ndraws = nsim)

# 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.

### 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.

#### 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.

### 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()

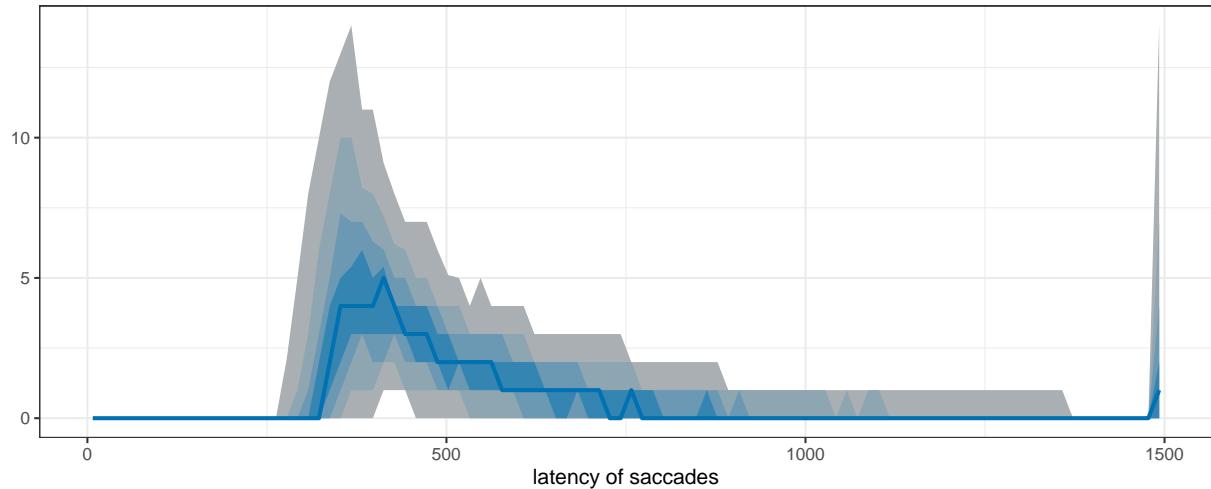
tmpM = apply(dvfakemat, 2, mean) # mean
tmpSD = apply(dvfakemat, 2, sd)
p2 = ggplot() +
  stat_bin(aes(x = tmpM), fill = c_dark) +
  labs(x = "Mean latency of saccades", title = "Means of simulated data") +
  theme_bw()
p3 = ggplot() +
  stat_bin(aes(x = tmpSD), fill = c_dark) +
  labs(x = "SD latency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

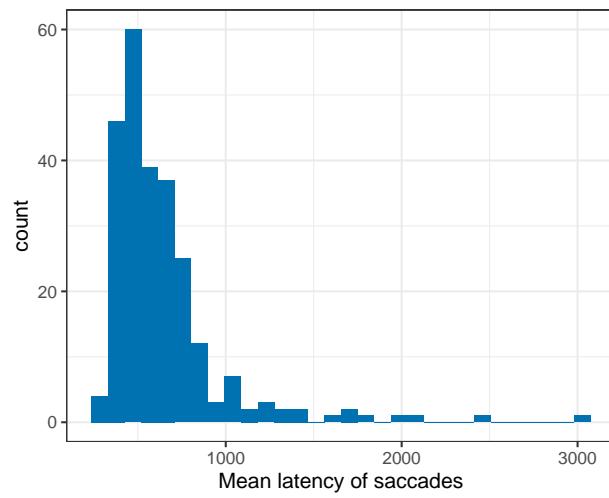
```

### Prior predictive checks: latency

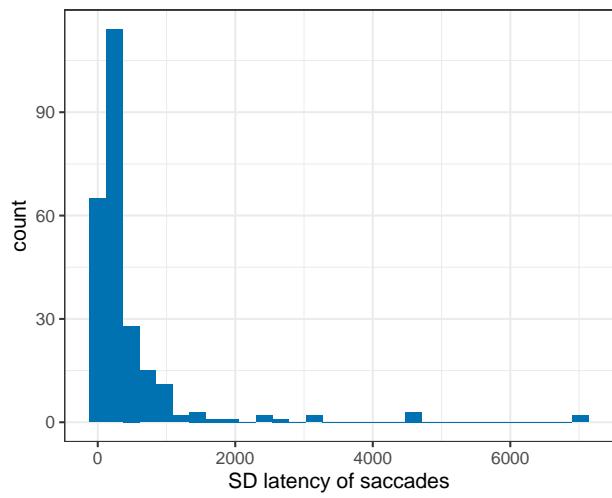
**A** Prior predictive distribution



**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.

### 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 %>%
```

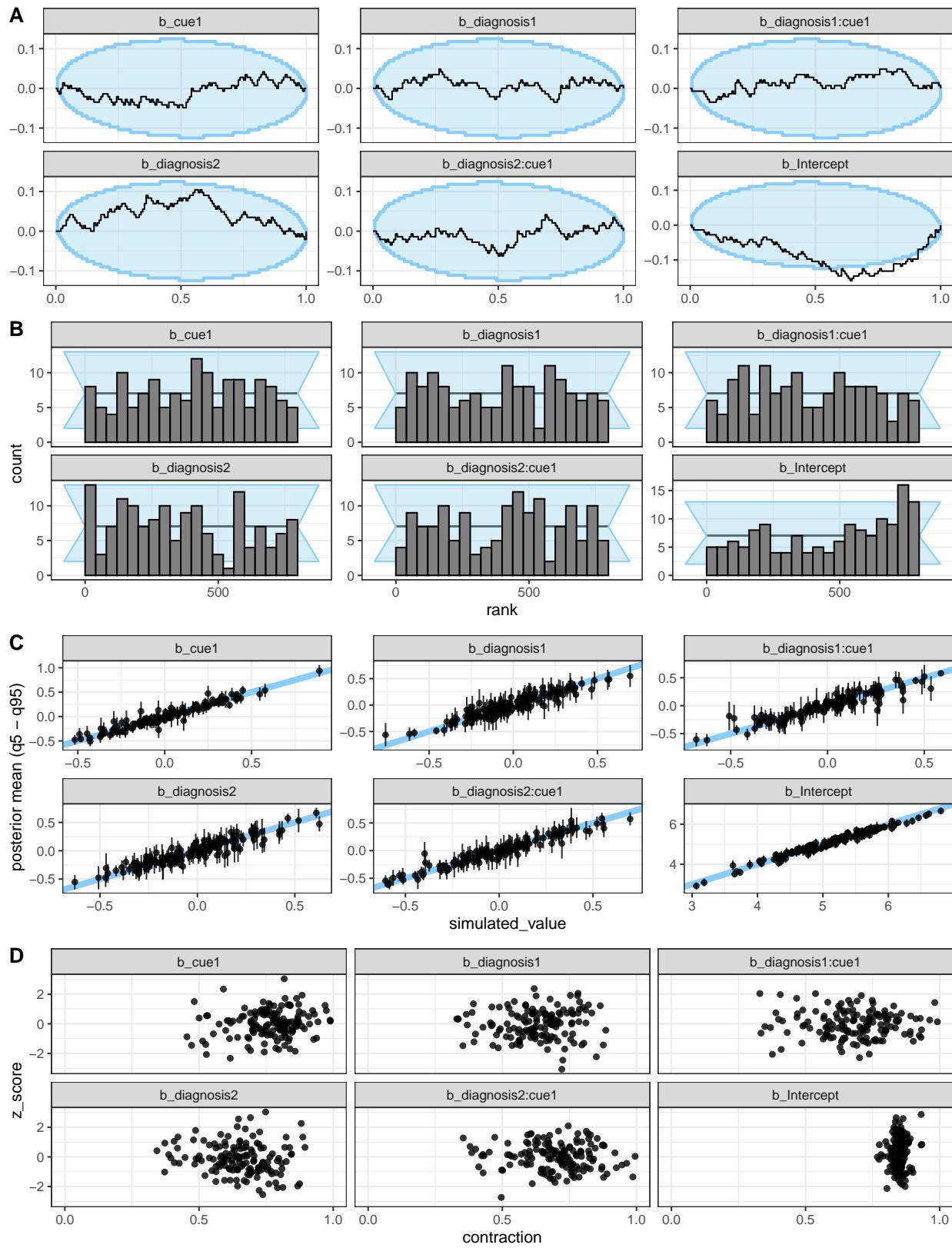
```

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.

## 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.

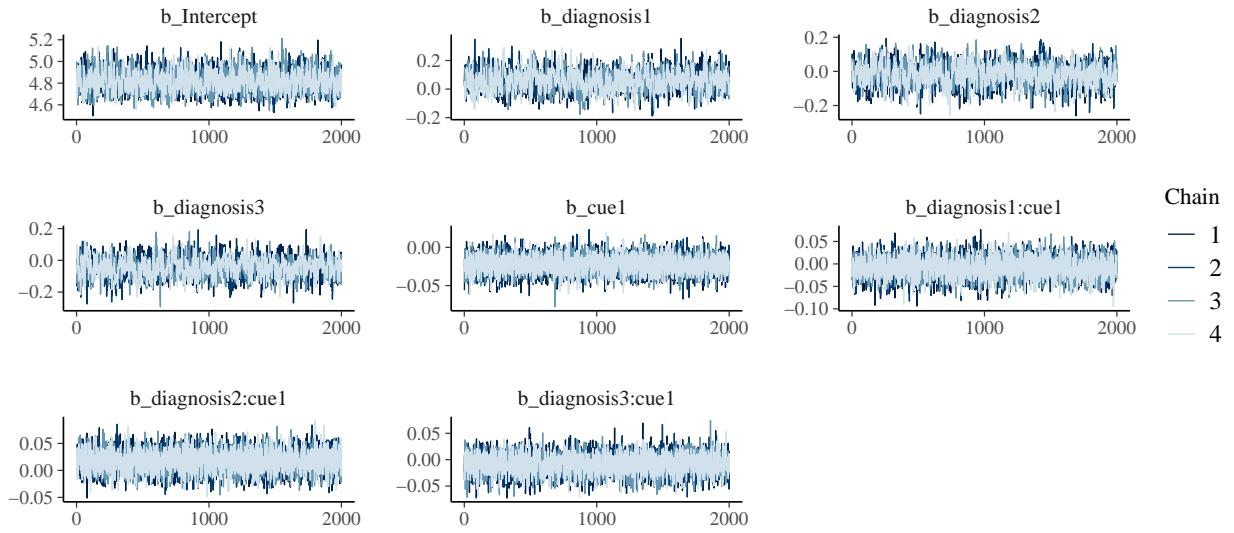
##
## Energy:
## E-BFMI indicated no pathological behavior.

# 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.

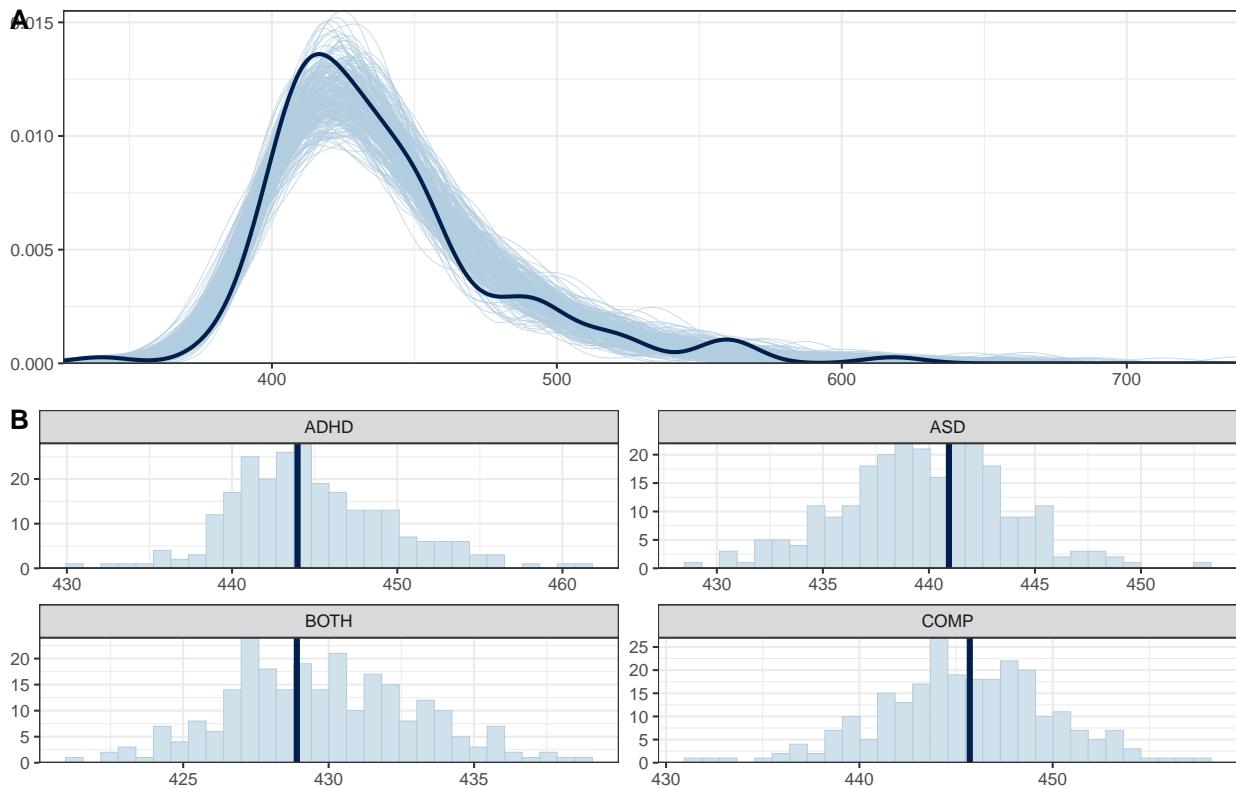
```
# get the posterior predictions
post.pred = posterior_predict(m.lat, ndraws = nsim)

# 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.

### 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
```

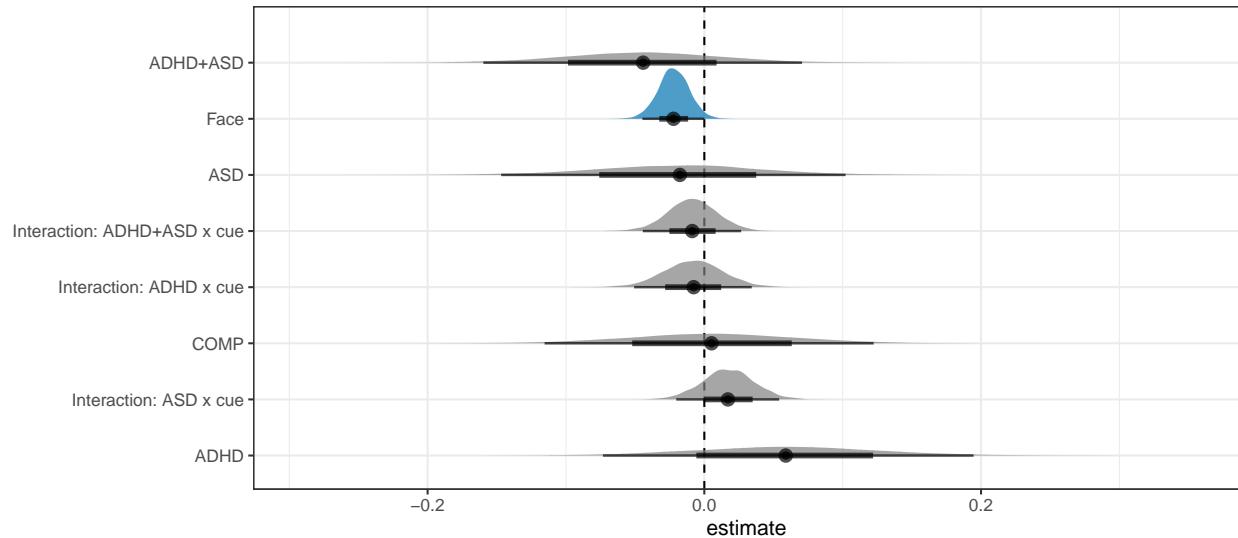
```
summary(m.lat)
```

```
## Family: shifted_lognormal
## Links: mu = identity; sigma = identity; ndt = identity
## Formula: lat ~ diagnosis * cue + (1 | subID)
## Data: df.lat.agg (Number of observations: 144)
## Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
##         total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 76)
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.30      0.04     0.23     0.39 1.00     1606     2660
## 
## Regression Coefficients:
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept        4.82      0.09     4.65     5.01 1.00     1883     2993
## diagnosis1       0.06      0.07    -0.07     0.19 1.00     1046     1940
## diagnosis2      -0.02      0.06    -0.15     0.10 1.00     1153     1948
## diagnosis3      -0.04      0.06    -0.16     0.07 1.00     1042     2027
## cue1            -0.02      0.01    -0.04    -0.00 1.00      7366     5787
```

```

## diagnosis1:cue1    -0.01      0.02     -0.05      0.03 1.00      5985      5124
## diagnosis2:cue1     0.02      0.02     -0.02      0.05 1.00      7074      5703
## diagnosis3:cue1    -0.01      0.02     -0.04      0.03 1.00      6622      5519
##
## 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      2514      3608
## ndt       309.30     10.65   284.58   325.59 1.00      2173      2914
##
## 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 = c_light)) +
  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      0.1     -0.17     0.18      0.9
##   Post.Prob Star
## 1      0.47
## ---
## '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      39.4      0.98
##   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 2: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	232	4.7	217	222	241	252
object	238	4.9	222	228	247	262
FAB	5.6	2.8	-5.9	-0.27	11	17

```

)
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

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

vtable::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* = 47.24%). 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* = 97.52%). Specifically, the model predicted a 5.56ms [0.01, 11.18] shorter latency of for saccades produced towards a face-cued compared to an object-cued target.

## Plots

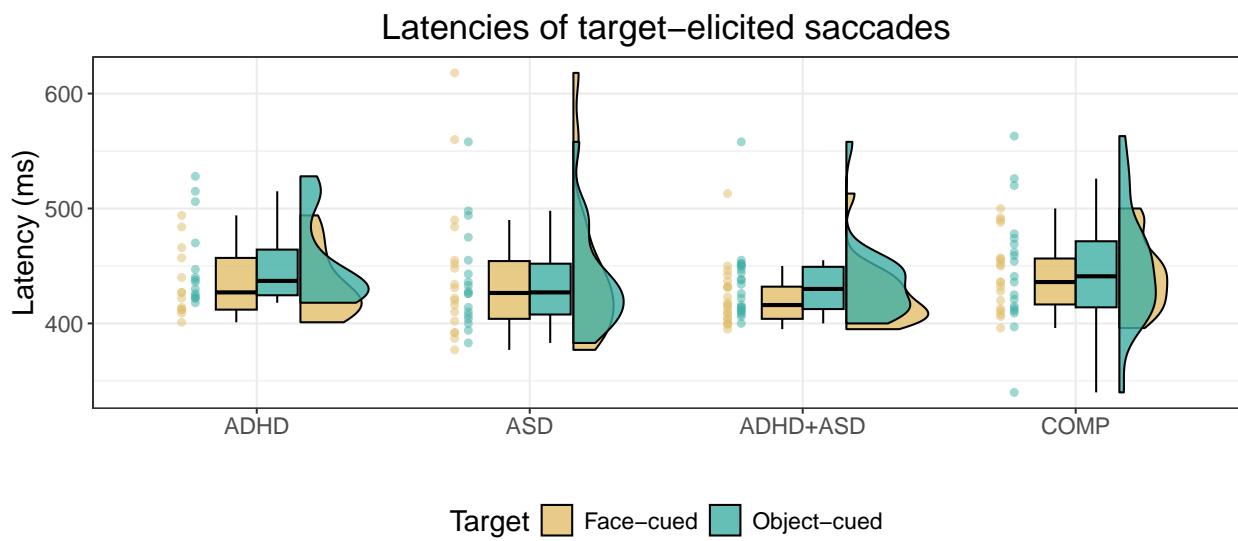
```

# 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_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_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))

```



```

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

```

## S2.4 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")

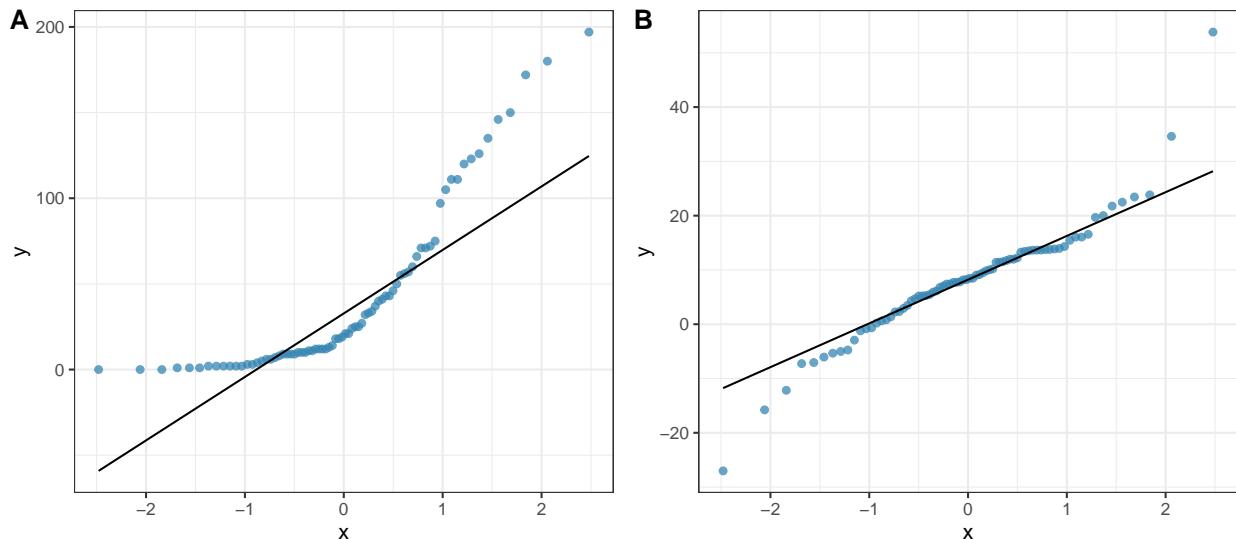
# check the distribution plot > not normally distributed
p1 = ggplot(df.diff, aes(sample = n.sac)) +
  stat_qq(alpha = 0.75, colour = c_mid_highlight) +
  stat_qq_line() +
  theme_bw()

```

```

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")

```



```

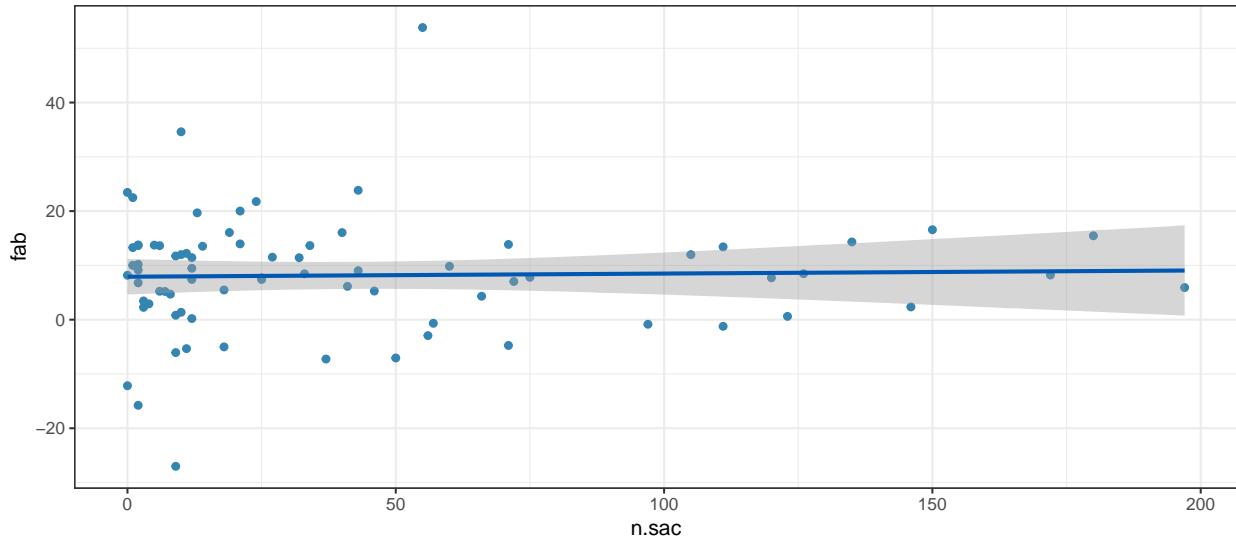
# do a Bayesian Spearman correlation: https://osf.io/j5wud
source("./helpers/rankBasedCommonFunctions.R")
source("./helpers/spearmanSampler.R")

# 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 ( $\log(BF) = -1.98$ ).

## S2.5 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. ([!ADD]) 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

```

## 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.

```

```

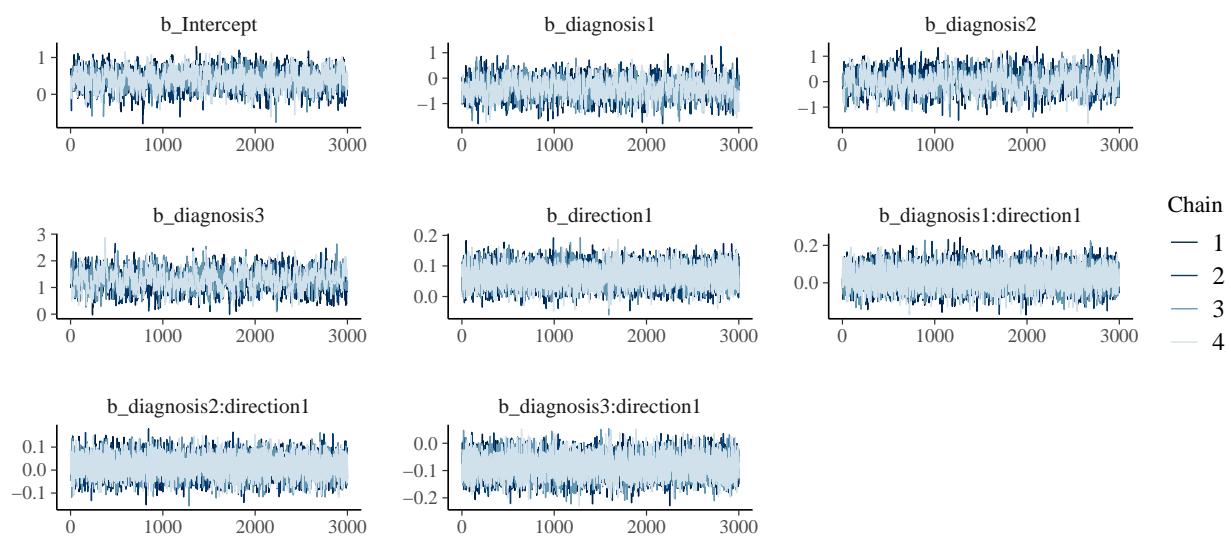
# check that rhats are below 1.01
sum(brms::rhat(m.cnt) >= 1.01, na.rm = T)

## [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)

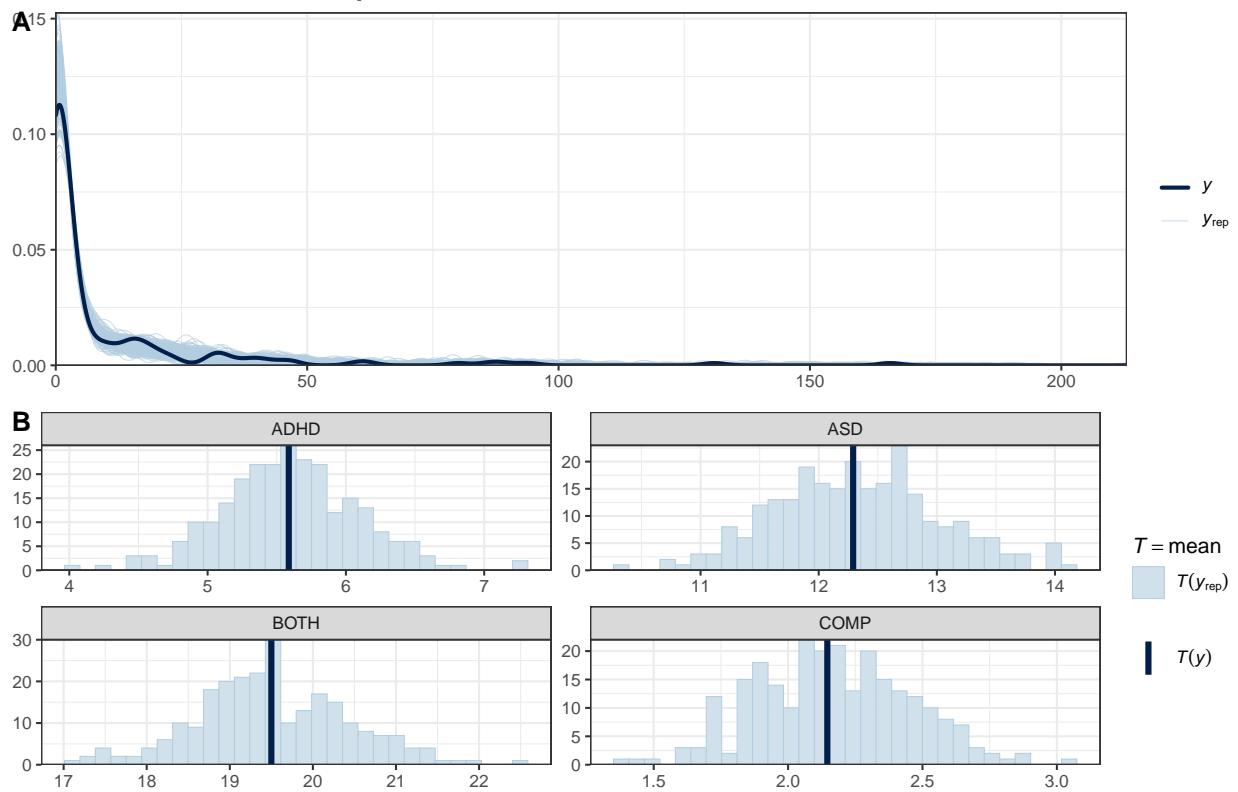
# check the fit of the predicted data compared to the real data
p1 = pp_check(m.cnt, ndraws = nsim) +
  theme_bw()

# 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.

## 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: 188)
## Draws: 4 chains, each with iter = 4500; warmup = 1500; thin = 1;
##         total post-warmup draws = 12000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 94)
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    2.12      0.21     1.74     2.57 1.00     1657     3655
##
## Regression Coefficients:
##                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                  0.40      0.25    -0.10     0.87 1.00     1145
## diagnosis1                 -0.40      0.38    -1.15     0.34 1.00     1375
## diagnosis2                 -0.00      0.38    -0.76     0.76 1.01     1059
## diagnosis3                  1.28      0.37     0.57     1.99 1.01      930
## direction1                  0.07      0.03     0.01     0.13 1.00     7479
```

```

## diagnosis1:direction1      0.03      0.06     -0.08      0.14  1.00    11802
## diagnosis2:direction1      0.02      0.04     -0.07      0.10  1.00    9058
## diagnosis3:direction1     -0.08      0.04     -0.16     -0.01  1.00    8418
##                                     Tail_ESS
## Intercept                      2593
## diagnosis1                     2504
## diagnosis2                     2057
## diagnosis3                     2244
## direction1                     9326
## diagnosis1:direction1          7984
## diagnosis2:direction1          8944
## diagnosis3:direction1          8315
##
## 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
  )

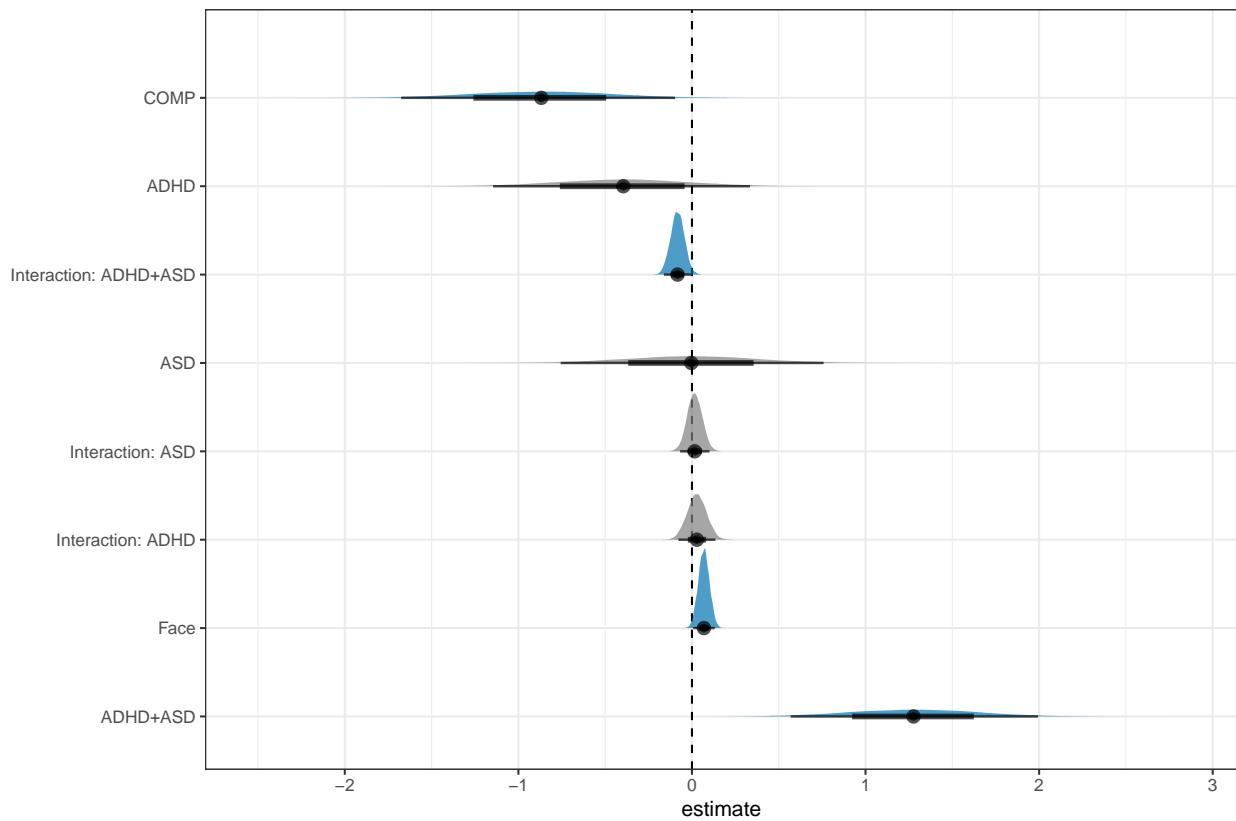
# plot the posterior distributions
df.m.cnt %>%
  select(starts_with("b_")) %>%
  pivot_longer(cols = starts_with("b_"), names_to = "coef", values_to = "estimate") %>%
  filter(coef != "b_Intercept") %>%
  mutate(
    coef = case_match(coef,
      "b_diagnosis1" ~ "ADHD",
      "b_diagnosis2" ~ "ASD",
      "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    -0.26    -0.01     67.57
##   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(

```

Table 3: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	2.4	0.73	0.63	1.3	4	8.7
object	2.3	0.72	0.56	1.2	3.8	8.8
FAB	-0.12	0.14	-0.77	-0.42	0.14	0.77

```

        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

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

```

On average, participants produced cue-elicited saccades on 4.55%  $\pm$  1.04 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 [-0.26, -0.01], *posterior probability* = 98.54%).

## Plots

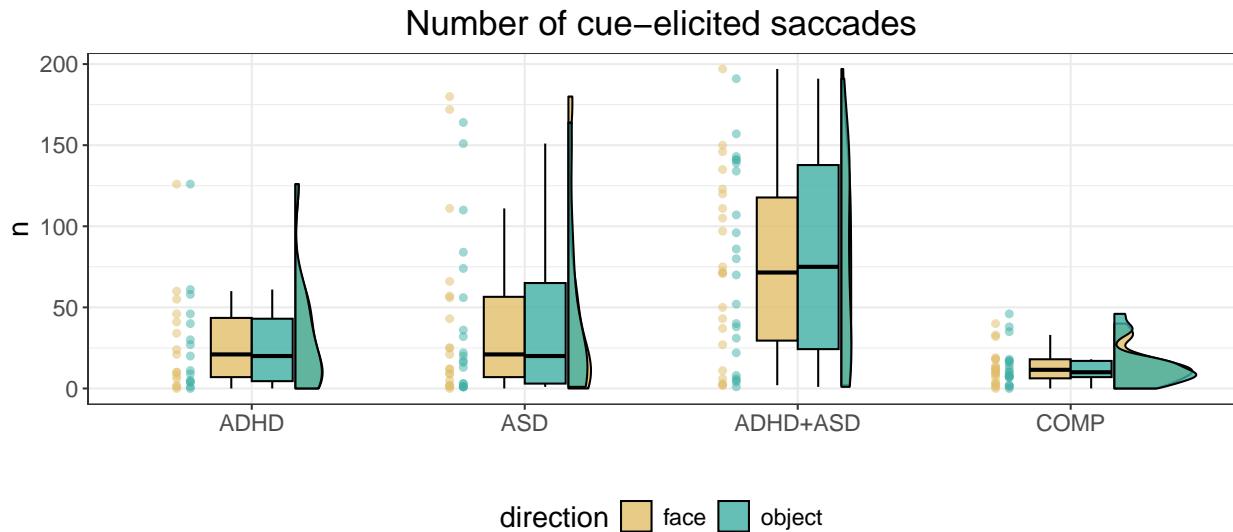
As a last step, we can plot our data.

```

# 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_dodge_nudge(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_dodge_nudge(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))
```



## S2.6 Exploration: Latencies of cue-elicited saccades

### 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_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.

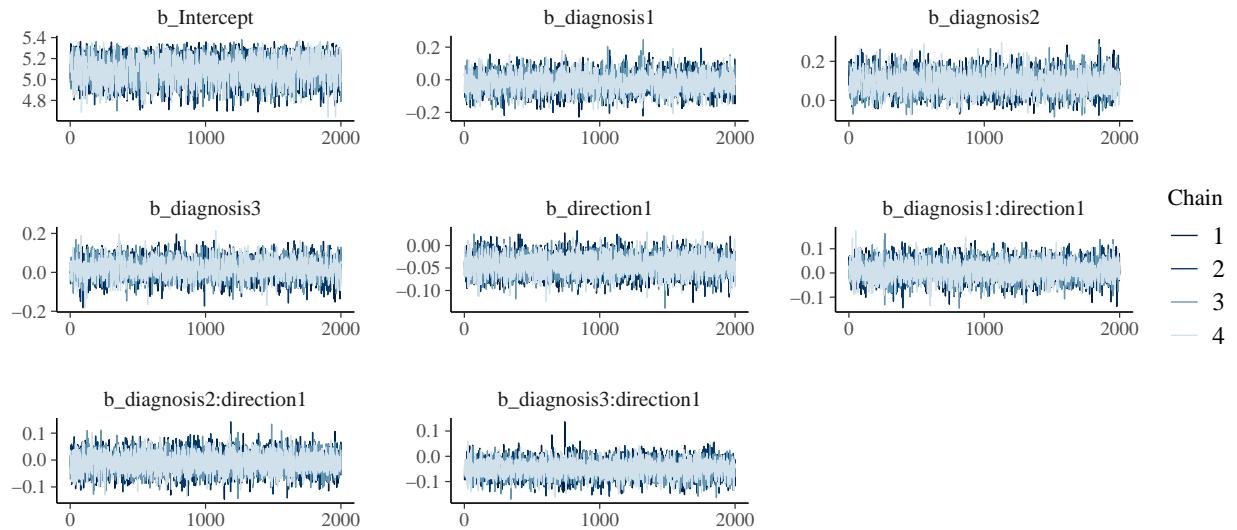
# check that rhats are below 1.01
sum(brms::rhat(m.lat) >= 1.01, na.rm = T)

## [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.

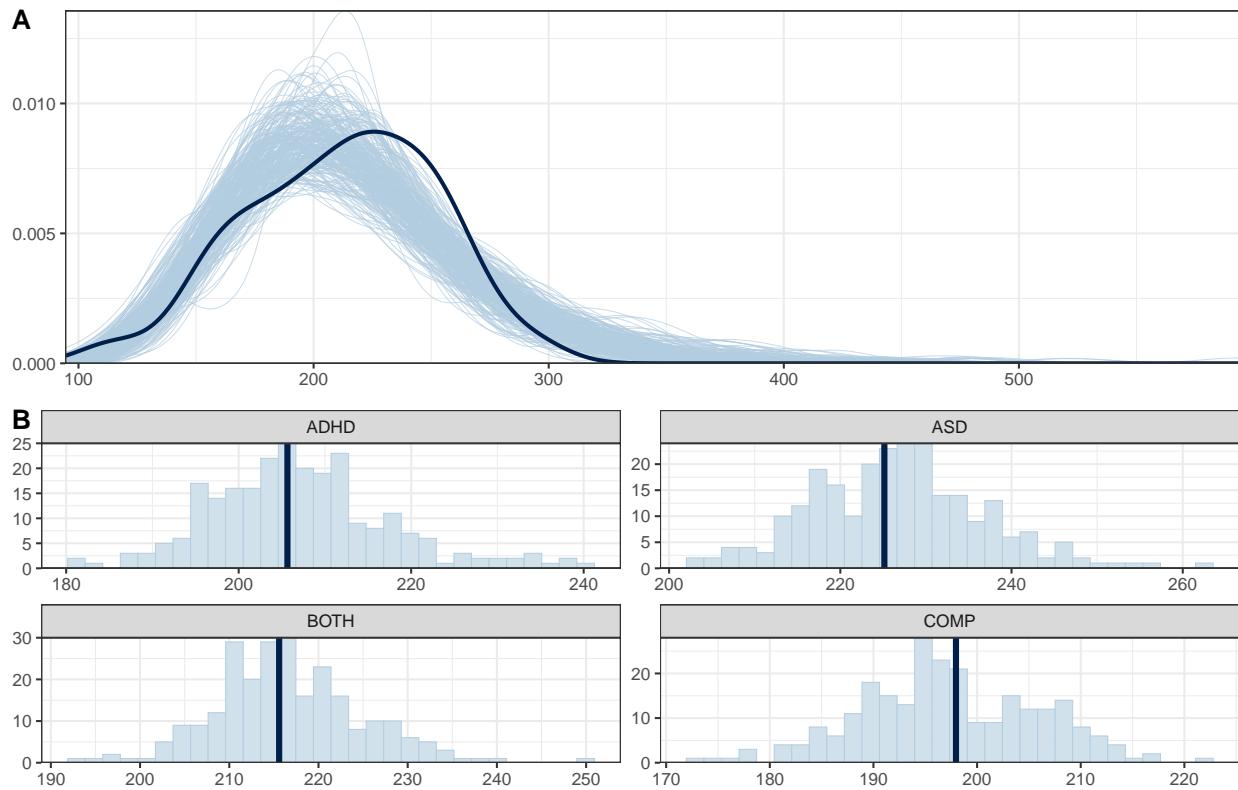
```
# get the posterior predictions
post.pred = posterior_predict(m.lat, ndraws = nsim)

# 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.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.

## 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: 115)
## Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;
##         total post-warmup draws = 8000
##
## Multilevel Hyperparameters:
## ~subID (Number of levels: 64)
##             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.17      0.05     0.06     0.28 1.00     1249     1635
##
## Regression Coefficients:
##                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                  5.09      0.12     4.85     5.31 1.00     3116
## diagnosis1                 -0.02      0.05    -0.13     0.09 1.00     4137
## diagnosis2                  0.09      0.05    -0.01     0.19 1.00     4364
## diagnosis3                  0.02      0.05    -0.07     0.11 1.00     3717
## direction1                 -0.04      0.02    -0.09    -0.00 1.00     7486
```

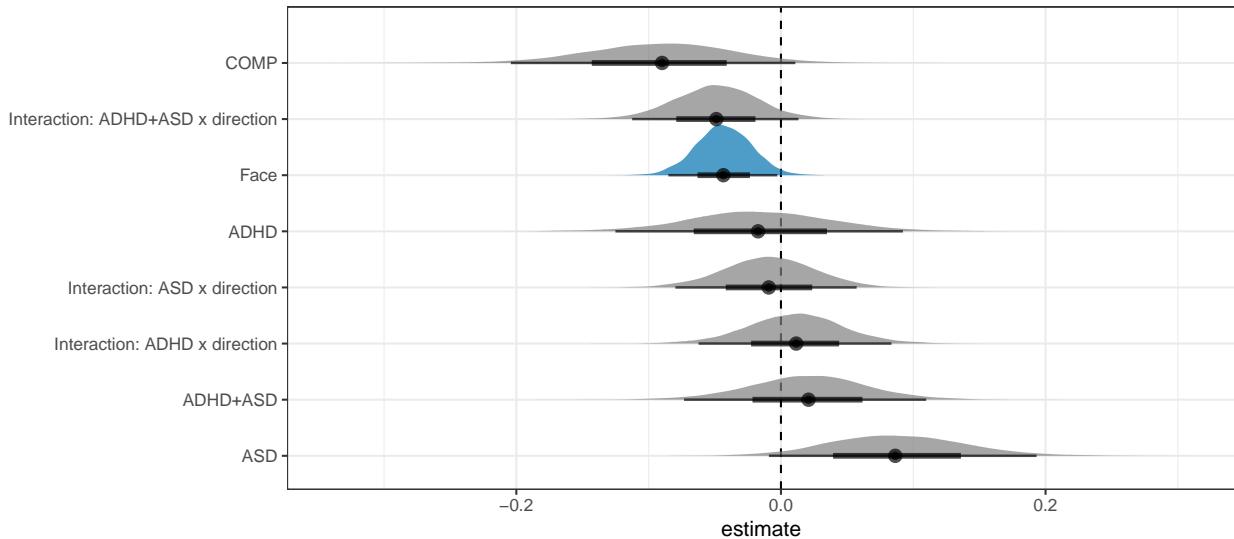
```

## diagnosis1:direction1      0.01      0.04     -0.06      0.08 1.00      7694
## diagnosis2:direction1    -0.01      0.03     -0.08      0.06 1.00      7773
## diagnosis3:direction1    -0.05      0.03     -0.11      0.01 1.00      8254
##                                     Tail_ESS
## Intercept                      3595
## diagnosis1                     4184
## diagnosis2                     4666
## diagnosis3                     5104
## direction1                     5756
## diagnosis1:direction1        5542
## diagnosis2:direction1        5688
## diagnosis3:direction1        5502
##
## Further Distributional Parameters:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma       0.20      0.04     0.14      0.29 1.00      1699      3667
## ndt        41.05     18.32     5.21     74.26 1.00      3142      3479
##
## 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, c_light)) +
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     0.09      0.04     0.01     0.17      53.42
##   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
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

# 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 4: Summary Statistics

Variable	Mean	Sd	Min	Pctile[2.5]	Pctile[97.5]	Max
face	201	6	179	190	213	225
object	216	6.3	193	204	229	241
FAB	15	6.8	-9.7	0.9	27	41

```
)
vtable::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* = 0.09 [0.01, 0.17], *posterior probability* = 98.16%). This model predicted that if a cue-induced saccade was produced towards the face, the latency was 14.92ms [1.41, 27.87] shorter than if a saccade was produced towards the object cue.

## 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_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 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))
```

### Latencies of cue-elicited saccades

