```
library(rstan); rstan_options(javascript=FALSE)
library(bayesplot)
library(dplyr)
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = T)

dat <- read.csv('final_data.csv')
```

```
dat <- dat %>%
  filter(skew != 'control')
dat <- dat %>%
  mutate(cho = ifelse(true_response == 'f', 1, -1))
```

```
ids <- unique(dat$Prolific_ID)
for(j in 1:length(ids)){
  dat$tid[dat$Prolific_ID==ids[j]] <- j
}
tids <- unique(dat$tid)

dat$rt <- as.numeric(dat$rt/1000)

dat <- dat %>%
  filter(test_part == 'cc' | test_part == 'ss')

dat <- dat %>%
  mutate(con = ifelse(test_part == "cc", 1, -1))
```

```
dat$P_A1 <- dat$P_A1 / 100
dat$P_A2 <- dat$P_A2 / 100
dat$P_B1 <- dat$P_B1 / 100
dat$P_B2 <- dat$P_B2 / 100
```

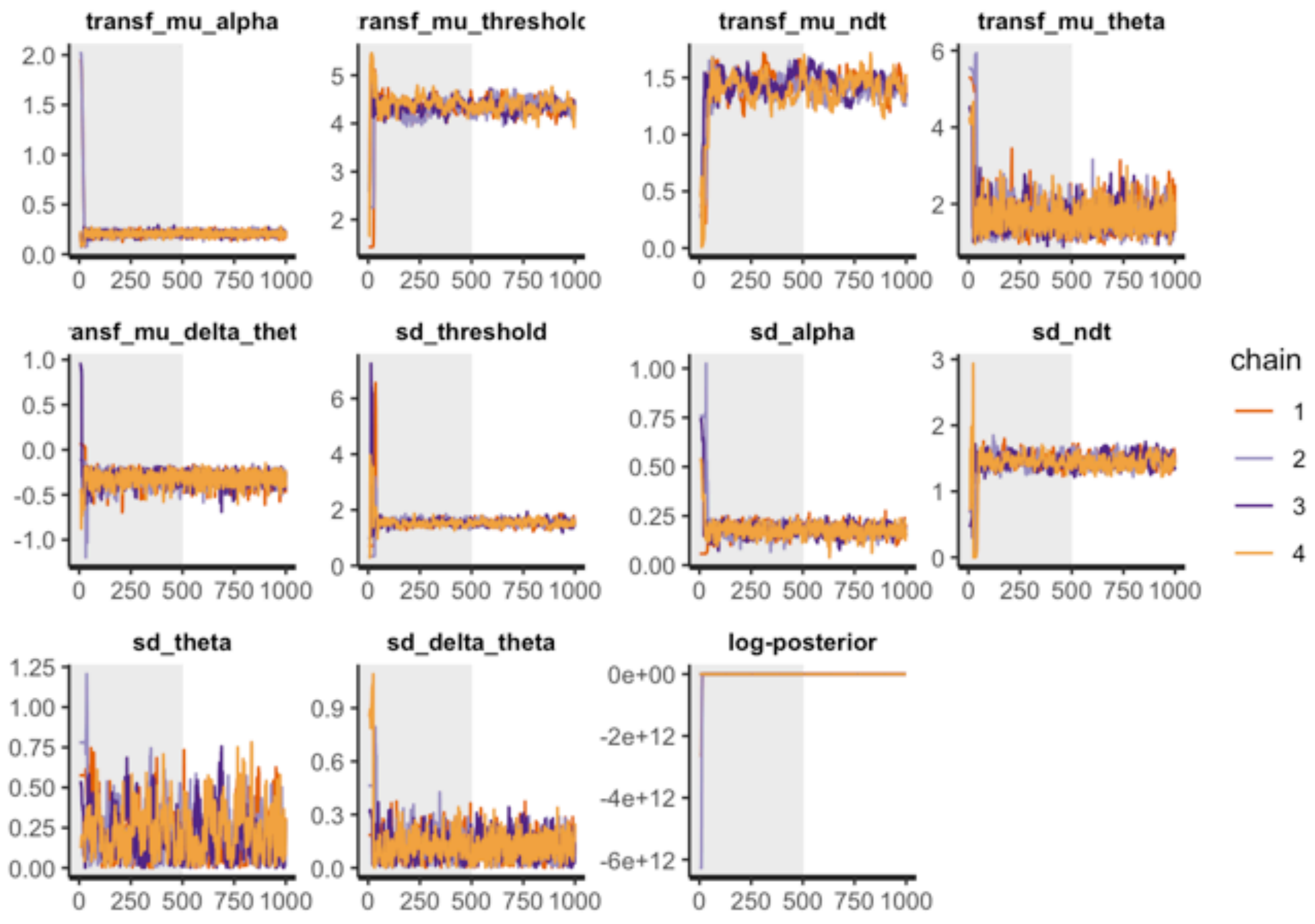
```
oa = as.matrix(dat[, c("O_A1", "O_A2")])
ob = as.matrix(dat[, c("O_B1", "O_B2")])
pa = as.matrix(dat[, c("P_A1", "P_A2")])
pb = as.matrix(dat[, c("P_B1", "P_B2")])
```

```
dataList  = list(cho = dat$cho,rt = dat$rt, participant = dat$tid,N=nrow(dat),  L
= length(tids),starting_point=0.5,
                 oa = as.matrix(dat[, c("O_A1", "O_A2")]),
                 ob = as.matrix(dat[, c("O_B1", "O_B2")]),
                 pa = as.matrix(dat[, c("P_A1", "P_A2")]),
                 pb = as.matrix(dat[, c("P_B1", "P_B2")]),
                 con =  dat$con
                 )

parameters = c("transf_mu_alpha","transf_mu_threshold","transf_mu_ndt", "transf_mu
_theta","transf_mu_delta_theta", 'sd_threshold',"sd_alpha","sd_ndt", 'sd_theta', '
sd_delta_theta', "alpha_sbj","threshold_sbj","ndt_sbj",'theta_sbj','delta_theta_sb
j', "log_lik")
```

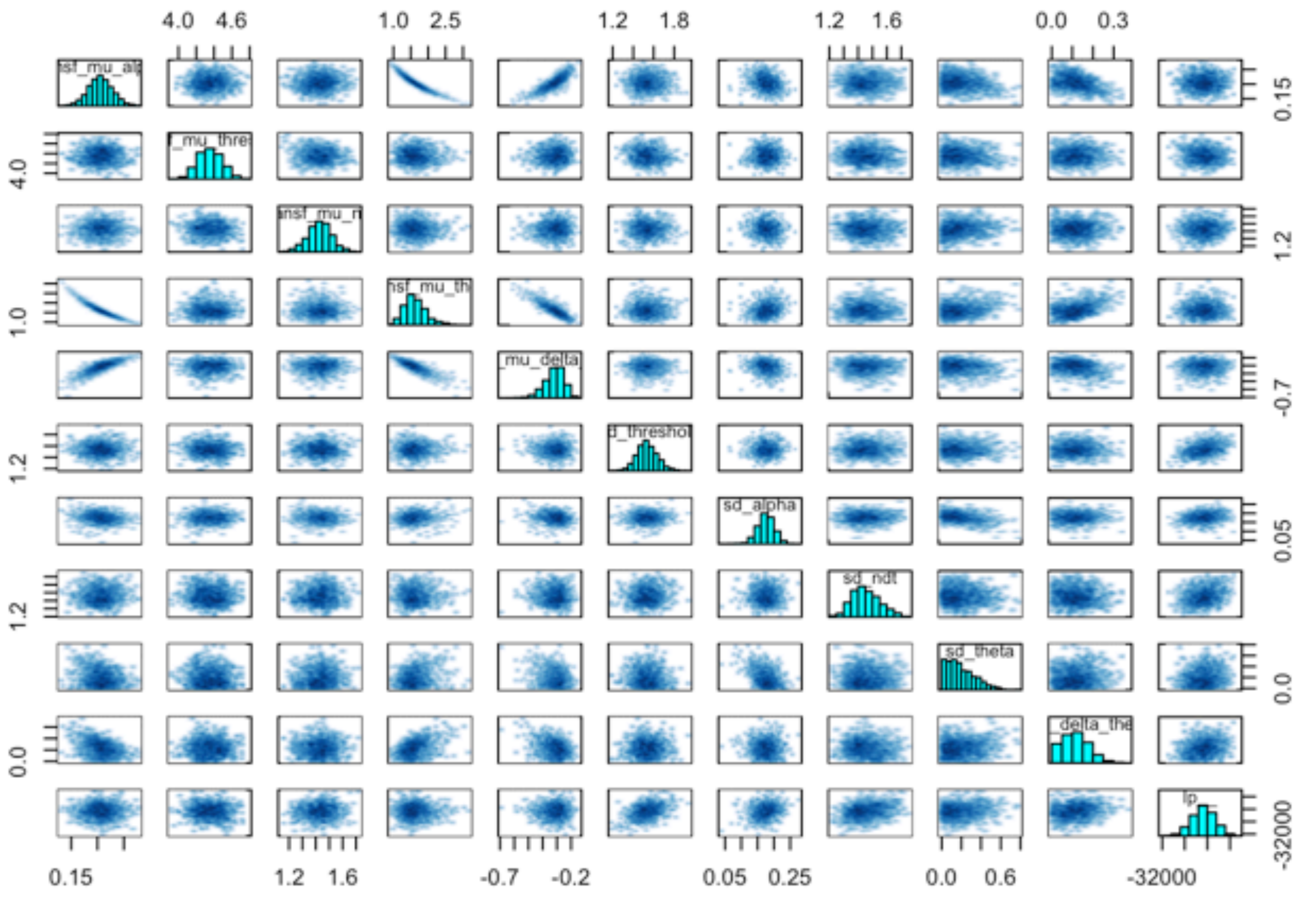
```
initFunc <-function (i) {
  initList=list()
  for (ll in 1:i){
    initList[[ll]] = list(mu_alpha = runif(1,-1.4578,2.5413),
                          sd_alpha = runif(1,0,1),
                          mu_threshold = runif(1,-0.5, 2.5),
                          sd_threshold = runif(1,0,1),
                          mu_ndt = runif(1, -1.5, 0),
                          sd_ndt = runif(1, 0, 1),
                          mu_theta = runif(1,0, 6),
                          sd_theta = runif(1,0,1),
                          mu_delta_theta = runif(1, -1, 1),
                          sd_delta_theta = runif(1,0,1),
                          z_alpha = runif(length(tids),-0.1,0.1),
                          z_theta = runif(length(tids),-0.1,0.1),
                          z_threshold = runif(length(tids),-0.1,0.1),
                          z_ndt = runif(length(tids),-0.1,0.1),
                          z_delta_theta = runif(length(tids),-0.1,0.1)


    )
  }

  return(initList)
}
```

```
m <- stan_model("EU_Baseline.stan")
dsamples <- sampling(m,
                data=dataList,
                pars=parameters,
                iter=1000,
                chains=4,#If not specified, gives random inits
                init = initFunc(4),
                warmup = 500,  # Stands for burn-in; Default = iter/2
                seed = 12
                )
```

```
#"transf_mu_alpha","transf_mu_threshold","transf_mu_ndt", "transf_mu_theta","trans
f_mu_delta_theta", 'sd_threshold',"sd_alpha","sd_ndt", 'sd_theta', 'sd_delta_thet
a', "alpha_sbj","threshold_sbj","ndt_sbj",'theta_sbj','delta_theta_sbj', "log_lik"

rstan::traceplot(dsamples, pars=c("transf_mu_alpha","transf_mu_threshold","transf_
mu_ndt", "transf_mu_theta","transf_mu_delta_theta", 'sd_threshold',"sd_alpha","sd_
ndt", 'sd_theta', 'sd_delta_theta', "lp__"), inc_warmup = TRUE, nrow = 3)
```



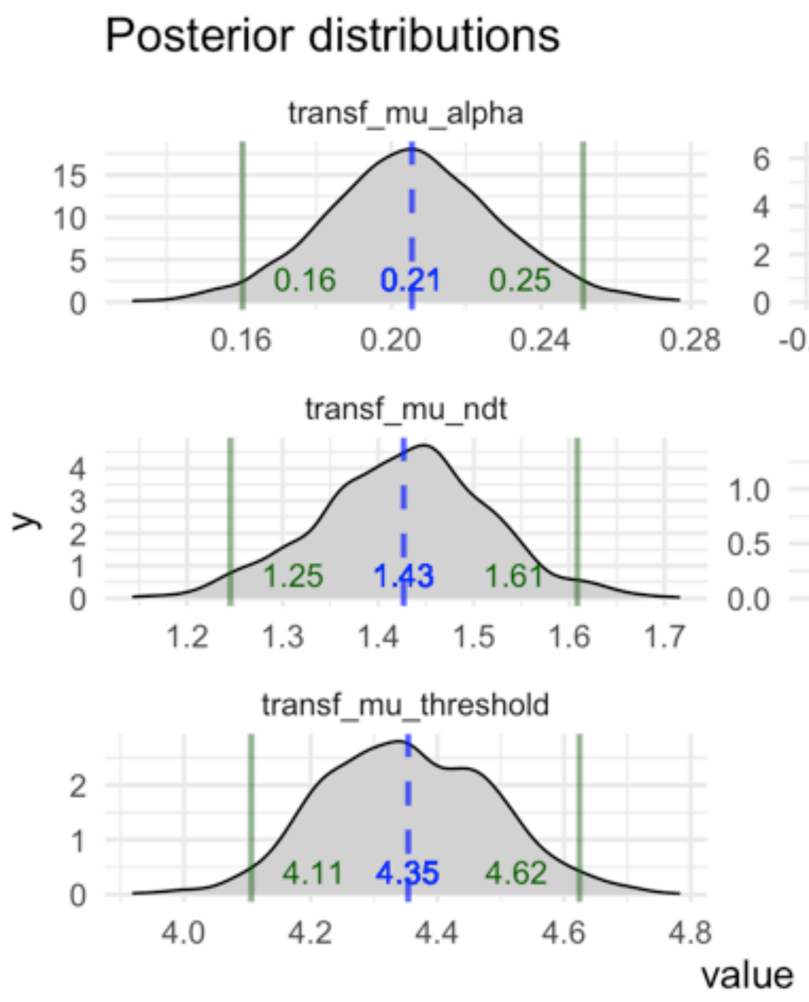
```
pairs(dsamples, pars = c("transf_mu_alpha","transf_mu_threshold","transf_mu_ndt",
"transf_mu_theta","transf_mu_delta_theta", 'sd_threshold',"sd_alpha","sd_ndt", 'sd
_theta', 'sd_delta_theta', "lp__"))
```



```
print(dsamples, pars = c("transf_mu_alpha","transf_mu_threshold","transf_mu_ndt",
"transf_mu_theta","transf_mu_delta_theta", 'sd_threshold',"sd_alpha","sd_ndt", 'sd
_theta', 'sd_delta_theta', "lp__"))
```

```
## Inference for Stan model: anon_model.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##                            mean se_mean    sd      2.5%       25%       50%
## transf_mu_alpha            0.21    0.00  0.02      0.16      0.19      0.21
## transf_mu_threshold        4.35    0.01  0.13      4.11      4.26      4.35
## transf_mu_ndt              1.43    0.01  0.09      1.25      1.37      1.43
## transf_mu_theta            1.63    0.01  0.32      1.11      1.41      1.59
## transf_mu_delta_theta     -0.32    0.00  0.07     -0.48     -0.36     -0.31
## sd_threshold               1.54    0.01  0.10      1.34      1.47      1.53
## sd_alpha                   0.18    0.00  0.03      0.12      0.16      0.18
## sd_ndt                     1.46    0.01  0.10      1.29      1.39      1.45
## sd_theta                   0.20    0.01  0.15      0.01      0.09      0.17
## sd_delta_theta             0.12    0.00  0.06      0.01      0.07      0.11
## lp__                  -31908.85    1.48 25.58 -31958.35 -31926.02 -31908.06
##                             75%     97.5% n_eff Rhat
## transf_mu_alpha            0.22      0.25  1091 1.00
## transf_mu_threshold        4.45      4.62    93 1.02
## transf_mu_ndt              1.49      1.61    68 1.03
## transf_mu_theta            1.81      2.41   944 1.00
## transf_mu_delta_theta     -0.27     -0.20  1058 1.00
## sd_threshold               1.60      1.75   209 1.00
## sd_alpha                   0.19      0.22   318 1.01
## sd_ndt                     1.52      1.66   171 1.03
## sd_theta                   0.29      0.54   130 1.04
## sd_delta_theta             0.16      0.25   384 1.01
## lp__                  -31891.29 -31860.18   298 1.00
##
## Samples were drawn using NUTS(diag_e) at Thu Dec 21 05:29:49 2023.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```r
library(ggplot2)
library(tidyverse) # for the gather function

samples_matrix <- as.matrix(dsamples)
means <- colMeans(samples_matrix)
hpd_interval <- t(apply(samples_matrix, 2, function(x) quantile(x, probs=c(0.025,
0.975))))




parameters <- c("transf_mu_alpha","transf_mu_threshold","transf_mu_ndt", "transf_m
u_theta","transf_mu_delta_theta")

# Reshape data to a long format
df_long <- as.data.frame(samples_matrix) %>%
  gather(key = "parameter", value = "value", parameters)

# Convert hpd_interval to a data frame and name the columns
hpd_interval_sub <- hpd_interval[parameters, ]
hpd_df <- as.data.frame(hpd_interval_sub)
colnames(hpd_df) <- c("lower", "upper")
rownames(hpd_df) <- parameters
hpd_df$parameter <- rownames(hpd_df)



# Aesthetic enhancements
theme_set(theme_minimal(base_size = 14)) # Set the default theme

custom_palette <- c("density_fill" = "lightgray",
                    "mean_line" = "blue",
                    "hpd_line" = "darkgreen")

# Add text labels for mean, lower, and upper HPD values
df_long <- df_long %>%
  group_by(parameter) %>%
  mutate(mean = means[parameter])

hpd_df <- hpd_df %>%
  mutate(mid = (lower + upper) / 2)

p <- ggplot(df_long, aes(x = value)) +
  geom_density(aes(fill = "density_fill")) +
  scale_fill_manual(values = custom_palette, guide = FALSE) +
  geom_vline(aes(xintercept = mean, color = "mean_line"), linetype = "dashed", siz
e = 1, alpha = 0.7) +
  geom_text(data = df_long, aes(x = mean, y = 0, label = round(mean, 2)), vjust =
-0.5, hjust = 0.5, size = 4, color = custom_palette["mean_line"]) +
  geom_vline(data = hpd_df, aes(xintercept = lower, color = "hpd_line"), linetype
= "solid", size = 1, alpha = 0.5) +
  geom_text(data = hpd_df, aes(x = lower, y = 0, label = round(lower, 2)), vjust =
-0.5, hjust = -0.5, size = 4, color = custom_palette["hpd_line"]) +
  geom_vline(data = hpd_df, aes(xintercept = upper, color = "hpd_line"), linetype
= "solid", size = 1, alpha = 0.5) +
  geom_text(data = hpd_df, aes(x = upper, y = 0, label = round(upper, 2)), vjust =
-0.5, hjust = 1.5, size = 4, color = custom_palette["hpd_line"]) +
  facet_wrap(~ parameter, scales = "free", ncol = 2) +
  scale_color_manual(values = custom_palette, guide = FALSE) +
  labs(title = "Posterior distributions")

print(p)
```


Posterior distributions
transf_mu_alpha
0.16
0.21
0.25
transf_mu_delta_theta
-0.48
-0.32
-0.2
transf_mu_ndt
1.25
1.43
1.61
transf_mu_theta
1.11
1.63
2.41
transf_mu_threshold
4.11
4.35
4.62
y
value