

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

```
dat <- read.csv('final_data.csv')
dat <- dat %>%
  filter(skew != 'control')
```

```
ids <- unique(dat$subject)
for(j in 1:length(ids)){
  dat$tid[dat$subject==ids[j]] <- j
}
tids <- unique(dat$tid)
dat$rt <- as.numeric(dat$rt/1000)

dat <- dat %>%
  filter(test_part == 'cc' | test_part == 'ss',
         rt >= 1,
         subject != '4ld6kjtr',
         subject != 'm73bj2hn')

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, # Setting seed; Default is random seed
  refresh = 0
)

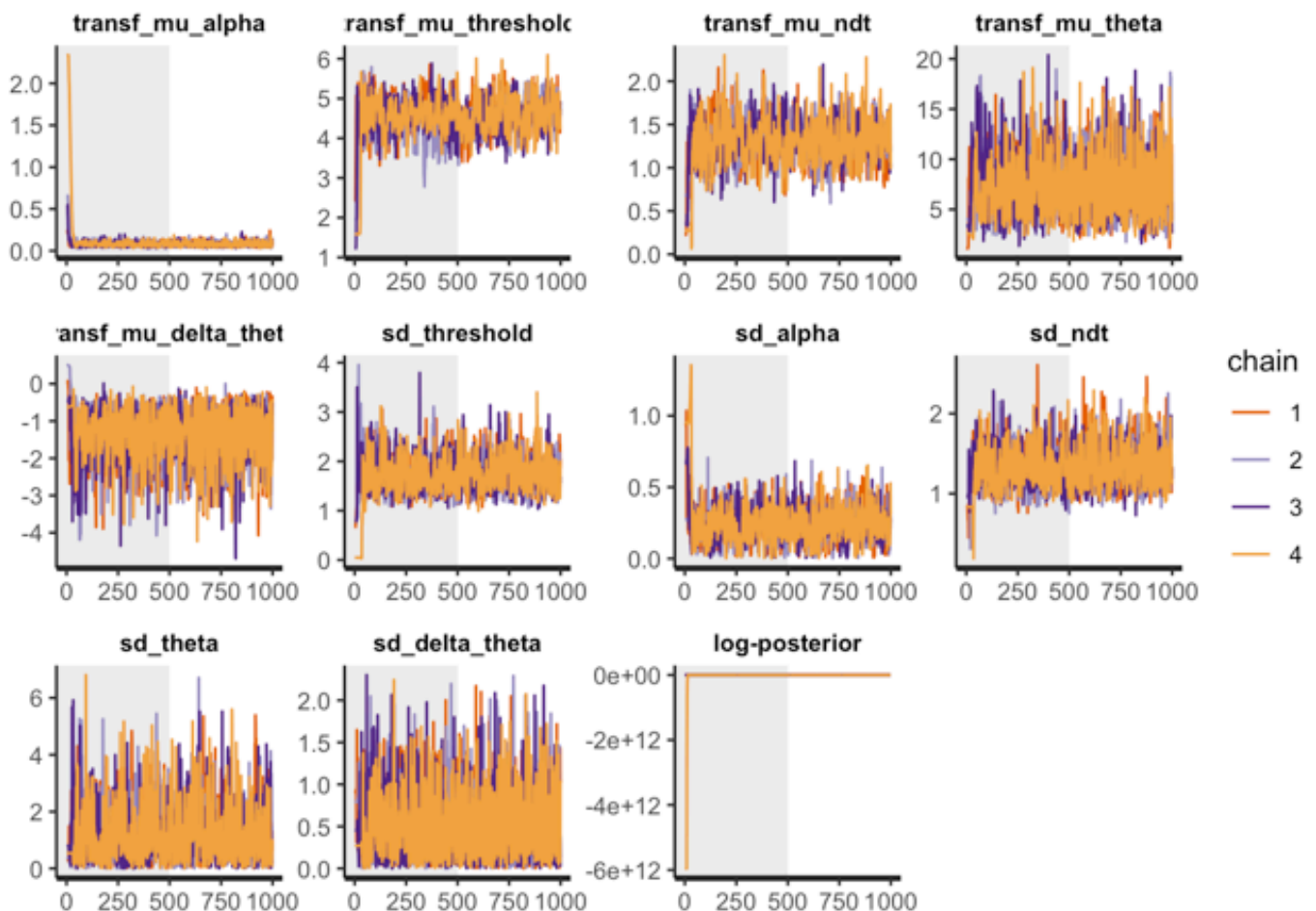
```

```

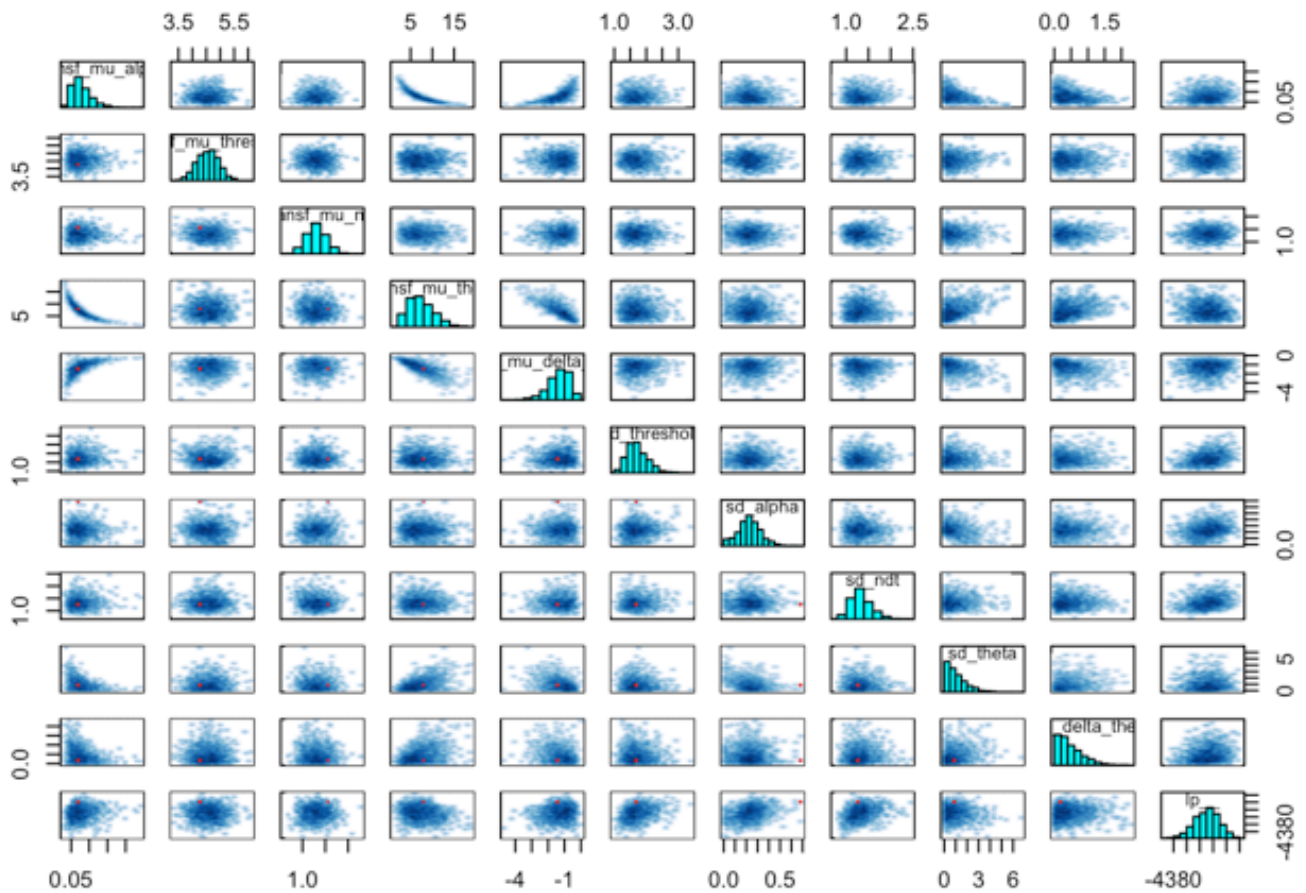
#"transf_mu_alpha", "transf_mu_threshold", "transf_mu_ndt", "transf_mu_theta", "transf_mu_delta_theta", 'sd_threshold', "sd_alpha", "sd_ndt", 'sd_theta', 'sd_delta_theta', "alpha_sbj", "threshold_sbj", "ndt_sbj", 'theta_sbj', 'delta_theta_sbj', "log_lik"

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: EU_Baseline.
## 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%	75%
transf_mu_alpha	0.08	0.00	0.03	0.04	0.06	0.07	0.09
transf_mu_threshold	4.55	0.02	0.40	3.78	4.27	4.56	4.83
transf_mu_ndt	1.30	0.01	0.22	0.89	1.15	1.30	1.45
transf_mu_theta	7.41	0.10	2.92	2.81	5.25	6.97	9.31
transf_mu_delta_theta	-1.36	0.02	0.66	-2.97	-1.75	-1.28	-0.88
sd_threshold	1.72	0.02	0.33	1.20	1.49	1.67	1.92
sd_alpha	0.23	0.00	0.11	0.02	0.17	0.23	0.29
sd_ndt	1.34	0.01	0.24	0.96	1.17	1.31	1.47
sd_theta	1.11	0.04	0.94	0.04	0.41	0.87	1.56
sd_delta_theta	0.49	0.01	0.39	0.01	0.19	0.39	0.70
lp__	-4354.83	0.46	9.35	-4374.30	-4361.21	-4354.26	-4348.10

```
##
##          97.5% n_eff Rhat
## transf_mu_alpha      0.14   736 1.00
## transf_mu_threshold   5.34   264 1.01
## transf_mu_ndt        1.73   339 1.01
## transf_mu_theta     13.69   825 1.00
## transf_mu_delta_theta -0.36   882 1.00
## sd_threshold         2.50   427 1.02
## sd_alpha            0.45   488 1.00
## sd_ndt             1.88   607 1.00
## sd_theta            3.55   540 1.01
## sd_delta_theta       1.46  1248 1.00
## lp__              -4337.90   408 1.02
##
## Samples were drawn using NUTS(diag_e) at Wed Nov 29 14:05:14 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).
```

```
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_mu_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", size = 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

