

```
##### 0 - safe choice A, 1 - risky choice B #####
library(rstan); rstan_options(javascript=FALSE)
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = T)

# Get list of files in 'data_2' folder with the pattern "riskytimed"
files <- dir(path = "data_2", pattern="riskytimed")

# Read all csv files in the list
data_list <- lapply(paste0("data_2/", files), read.table, header = TRUE, skip = 0,
fill = TRUE, sep= ";")

# Concatenate rows of all items in the list into a data frame
dat <- do.call("rbind", data_list)

# gamble characteristics
dat$eva = dat$oa1*dat$pa1+dat$oa2*dat$pa2 + dat$oa3*dat$pa3+dat$oa4*dat$pa4
dat$evb = dat$ob1*dat$pb1+dat$ob2*dat$pb2 + dat$ob3*dat$pb3+dat$ob4*dat$pb4
dat$evd = dat$evb - dat$eva
dat$sda = sqrt((dat$oa1-dat$eva)^2*dat$pa1 + (dat$oa2-dat$eva)^2*dat$pa2 + (dat$oa
3-dat$eva)^2*dat$pa3 + (dat$oa4-dat$eva)^2*dat$pa4)
dat$sdb = sqrt((dat$ob1-dat$evb)^2*dat$pb1 + (dat$ob2-dat$evb)^2*dat$pb2 + (dat$ob
3-dat$evb)^2*dat$pb3 + (dat$ob4-dat$evb)^2*dat$pb4)
dat$sdd = dat$sdb - dat$sda
dat$evdummy = ifelse(dat$evd>0,1,0)
```

```

# transform to +/- 1; safe - 1, risky +1
dat$cho <- ifelse(dat$choice==0,-1,ifelse(dat$choice==1,1,NA))

ids <- unique(dat$id)
for(j in 1:length(ids)){
  dat$tid[dat$id==ids[j]] <- j
}
tids <- unique(dat$tid)
# only control data
control_dat <- dat[dat$cond=="control",]
# remove fast RTs
rcontrol_dat <- control_dat[control_dat$rt>1,]

library(dplyr)

rcontrol_dat <- rcontrol_dat %>%
  rowwise() %>%
  mutate(
    oa_condition = sum(c_across(starts_with("oa")) == 0),
    ob_condition = sum(c_across(starts_with("ob")) == 0)
  ) %>%
  filter(
    (oa_condition == 2 & ob_condition == 0) |
    (oa_condition == 0 & ob_condition == 2)
  ) %>%
  mutate(
    oa_complex = ifelse(oa_condition == 2, -1, 1),
    chose_complex = ifelse((oa_complex == 1 & choice == 0) | (oa_complex == -1 & c
hoice == 1), 1, -1)
  )

```

```

oa = as.matrix(rcontrol_dat[, c("oa1", "oa2", "oa3", "oa4")])
ob = as.matrix(rcontrol_dat[, c("ob1", "ob2", "ob3", "ob4")])
pa = as.matrix(rcontrol_dat[, c("pa1", "pa2", "pa3", "pa4")])
pb = as.matrix(rcontrol_dat[, c("pb1", "pb2", "pb3", "pb4")])

```

```

dataList = list(cho = rcontrol_dat$chose_complex,rt = rcontrol_dat$rt, participan
t = rcontrol_dat$tid,N=nrow(rcontrol_dat), L = length(tids),starting_point=0.5,
  oa = as.matrix(rcontrol_dat[, c("oa1", "oa2", "oa3", "oa4")]),
  ob = as.matrix(rcontrol_dat[, c("ob1", "ob2", "ob3", "ob4")]),
  pa = as.matrix(rcontrol_dat[, c("pa1", "pa2", "pa3", "pa4")]),
  pb = as.matrix(rcontrol_dat[, c("pb1", "pb2", "pb3", "pb4")]),
  compindex = -rcontrol_dat$oa_complex
)

parameters = c("transf_mu_alpha","transf_mu_threshold","transf_mu_ndt", "transf_mu
_theta",'sd_threshold',"sd_alpha","sd_ndt", 'sd_theta', "alpha_sbj","threshold_sb
j","ndt_sbj",'theta_sbj',"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),
      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)

    )
  }

  return(initList)
}

```

```
m <- stan_model("EU_Baseline ce.stan")
```

```
## hash mismatch so recompiling; make sure Stan code ends with a blank line
```

```
## Trying to compile a simple C file
```

```

## Running /usr/lib/R/bin/R CMD SHLIB foo.c
## using C compiler: 'gcc (Ubuntu 11.4.0-1ubuntu1~22.04) 11.4.0'
## gcc -I"/usr/share/R/include" -DNDEBUG -I"/usr/local/lib/R/site-library/Rcpp/include/" -I"/usr/local/lib/R/site-library/RcppEigen/include/" -I"/usr/local/lib/R/site-library/RcppEigen/include/unsupported" -I"/usr/local/lib/R/site-library/BH/include" -I"/usr/local/lib/R/site-library/StanHeaders/include/src/" -I"/usr/local/lib/R/site-library/StanHeaders/include/" -I"/usr/local/lib/R/site-library/RcppParallel/include/" -I"/usr/local/lib/R/site-library/rstan/include" -DEIGEN_NO_DEBUG -DBOOST_DISABLE_ASSERTS -DBOOST_PENDING_INTEGER_LOG2_HPP -DSTAN_THREADS -DDBOOST_NO_AUTO_PTR -include '/usr/local/lib/R/site-library/StanHeaders/include/stan/math/prim/mat/fun/Eigen.hpp' -D_REENTRANT -DRCPP_PARALLEL_USE_TBB=1 -fpic -g -O2 -ffile-prefix-map=/build/r-base-MHXHhT/r-base-4.3.1=. -fstack-protector-strong -Wformat -Werror=format-security -Wdate-time -D_FORTIFY_SOURCE=2 -c foo.c -o foo.o
## In file included from /usr/local/lib/R/site-library/RcppEigen/include/Eigen/Core:88,
##               from /usr/local/lib/R/site-library/RcppEigen/include/Eigen/Dense:1,
##               from /usr/local/lib/R/site-library/StanHeaders/include/stan/math/prim/mat/fun/Eigen.hpp:13,
##               from <command-line>:
## /usr/local/lib/R/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:628:1: error: unknown type name 'namespace'
## 628 | namespace Eigen {
##      | ^~~~~~
## /usr/local/lib/R/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:628:17: error: expected '=', ',', ';', 'asm' or '__attribute__' before '{' token
## 628 | namespace Eigen {
##      |           ^
## In file included from /usr/local/lib/R/site-library/RcppEigen/include/Eigen/Dense:1,
##               from /usr/local/lib/R/site-library/StanHeaders/include/stan/math/prim/mat/fun/Eigen.hpp:13,
##               from <command-line>:
## /usr/local/lib/R/site-library/RcppEigen/include/Eigen/Core:96:10: fatal error: complex: No such file or directory
## 96 | #include <complex>
##      |           ^~~~~~
## compilation terminated.
## make: *** [/usr/lib/R/etc/Makeconf:191: foo.o] Error 1

```

```
dsamples <- sampling(m,
  data=dataList,
  pars=parameters,
  iter=2000,
  chains=4,#If not specified, gives random inits
  init = initFunc(4),
  warmup = 1000, # Stands for burn-in; Default = iter/2
  seed = 12, # Setting seed; Default is random seed
  refresh = 0
)
```

```
## Warning: There were 58 divergent transitions after warmup. See
## https://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup
## to find out why this is a problem and how to eliminate them.
```

```
## Warning: There were 964 transitions after warmup that exceeded the maximum tree
depth. Increase max_treedepth above 10. See
## https://mc-stan.org/misc/warnings.html#maximum-treedepth-exceeded
```

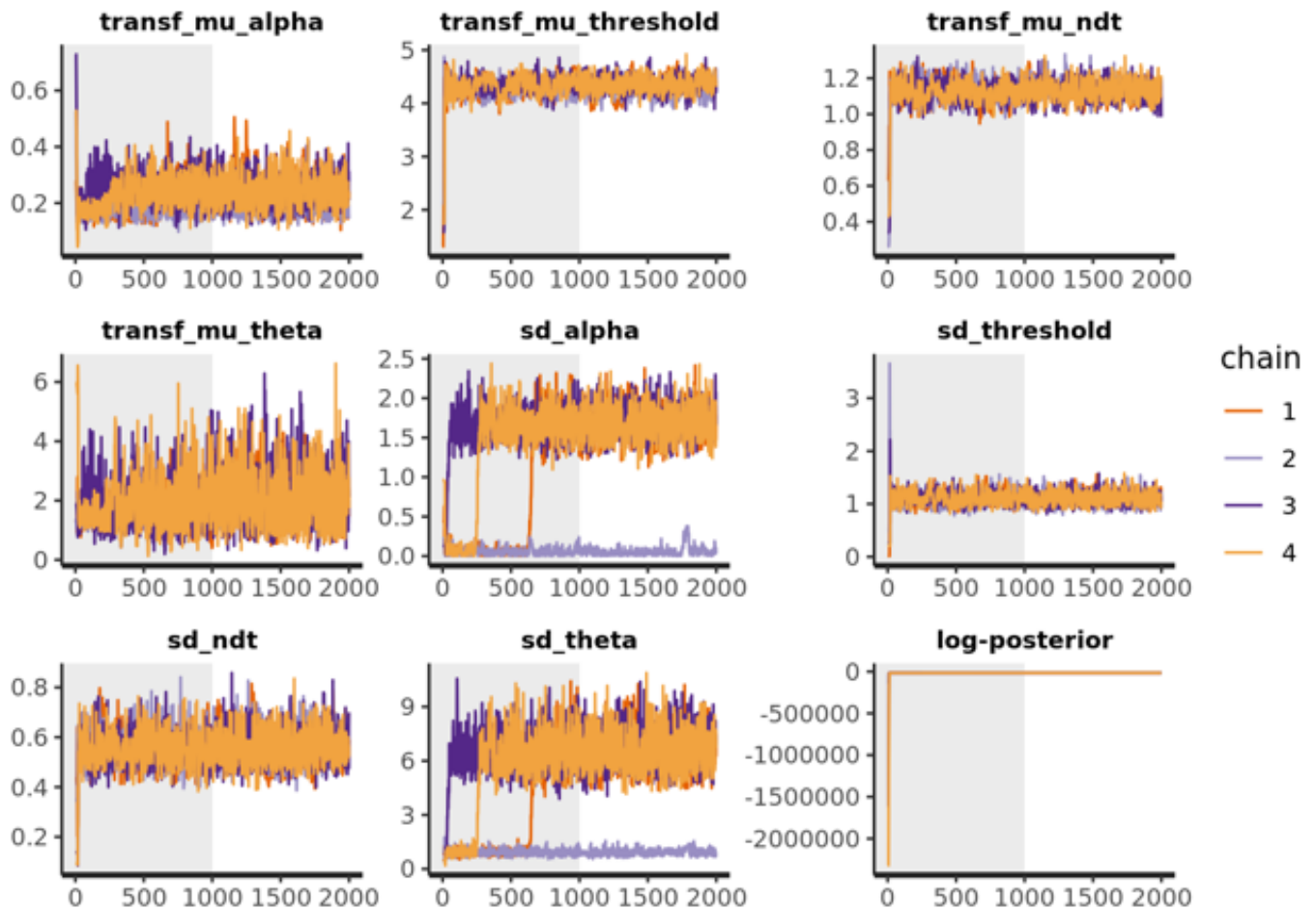
```
## Warning: Examine the pairs() plot to diagnose sampling problems
```

```
## Warning: The largest R-hat is 1.54, indicating chains have not mixed.
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#r-hat
```

```
## Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior mea
ns and medians may be unreliable.
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#bulk-ess
```

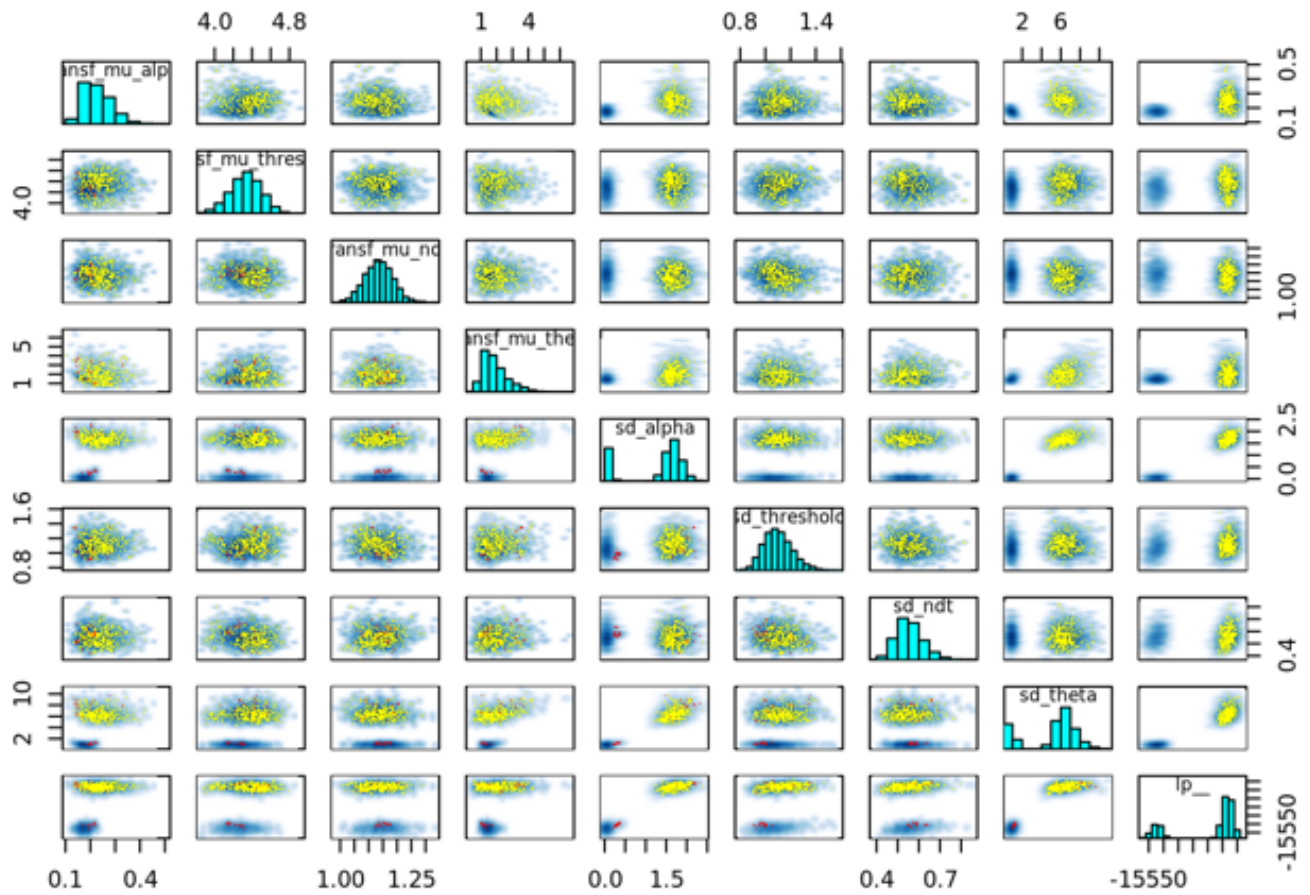
```
## Warning: Tail Effective Samples Size (ESS) is too low, indicating posterior var
iances and tail quantiles may be unreliable.
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#tail-ess
```

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



```
pairs(dsamples, pars = c( "transf_mu_alpha","transf_mu_threshold","transf_mu_ndt",
"transf_mu_theta", "sd_alpha","sd_threshold","sd_ndt",'sd_theta', "lp__"))
```

```
## Warning in par(usr): argument 1 does not name a graphical parameter
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```



```
print(dsamples, pars = c("transf_mu_alpha", "transf_mu_threshold", "transf_mu_ndt", "
transf_mu_theta", "sd_alpha", "sd_threshold", "sd_ndt", "sd_theta", "lp__"))
```

```
## Inference for Stan model: EU_Baseline ce.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##               mean se_mean      sd      2.5%      25%      50%
## transf_mu_alpha      0.23      0.02    0.06      0.14      0.18      0.22
## transf_mu_threshold    4.33      0.02    0.16      4.00      4.23      4.34
## transf_mu_ndt          1.14      0.00    0.05      1.04      1.10      1.14
## transf_mu_theta        1.90      0.11    0.81      0.78      1.33      1.72
## sd_alpha              1.28      0.50    0.72      0.01      0.93      1.60
## sd_threshold           1.10      0.01    0.11      0.91      1.02      1.09
## sd_ndt                 0.56      0.00    0.06      0.45      0.51      0.55
## sd_theta               5.14      1.74    2.58      0.74      3.43      6.04
## lp__                  -15342.50    74.22 106.01 -15545.66 -15379.56 -15288.99
##               75%      97.5% n_eff Rhat
## transf_mu_alpha      0.26      0.35      7 1.20
## transf_mu_threshold    4.44      4.64     61 1.09
## transf_mu_ndt          1.17      1.24    200 1.01
## transf_mu_theta        2.32      3.89     54 1.06
## sd_alpha              1.76      2.06      2 4.60
## sd_threshold           1.17      1.35    199 1.02
## sd_ndt                 0.59      0.70    417 1.00
## sd_theta               6.85      8.68      2 3.16
## lp__                  -15274.71 -15253.71      2 7.07
##
## Samples were drawn using NUTS(diag_e) at Thu Nov  2 05:19:21 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(bayesplot)
```

```
## This is bayesplot version 1.10.0
```

```
## - Online documentation and vignettes at mc-stan.org/bayesplot
```

```
## - bayesplot theme set to bayesplot::theme_default()
```

```
## * Does _not_ affect other ggplot2 plots
```

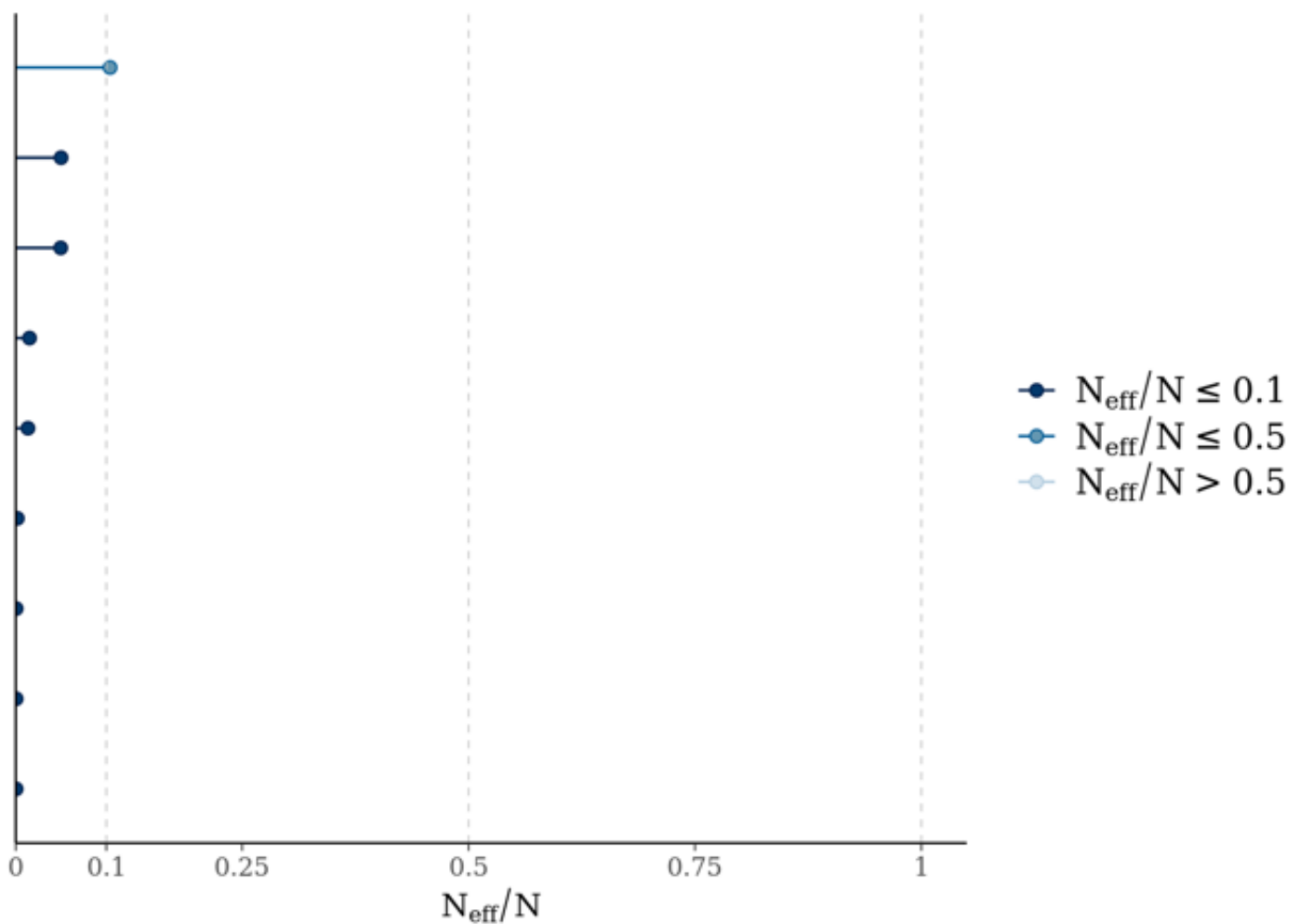
```
## * See ?bayesplot_theme_set for details on theme setting
```



```
ratios_cp <- neff_ratio(dsamples, pars = c("transf_mu_alpha", "transf_mu_theta", "transf_mu_threshold", "transf_mu_ndt", 'sd_threshold', "sd_alpha", "sd_ndt", 'sd_theta', "lp__"))
df_ratios_cp <- as.data.frame(ratios_cp)
print(df_ratios_cp)
```

```
##              ratios_cp
## transf_mu_alpha    0.0018557653
## transf_mu_theta    0.0135325650
## transf_mu_threshold 0.0152909831
## transf_mu_ndt      0.0500787593
## sd_threshold       0.0497232045
## sd_alpha           0.0005233804
## sd_ndt             0.1042280005
## sd_theta           0.0005520569
## lp__               0.0005099871
```

```
mcmc_neff(ratios_cp, size = 2)
```



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

```
## — Attaching core tidyverse packages ————— tidyverse 2.0.0 —
—
## ✓ forcats    1.0.0      ✓ stringr    1.5.0
## ✓ lubridate  1.9.2      ✓ tibble     3.2.1
## ✓ purrr      1.0.1      ✓ tidyr      1.3.0
## ✓ readr      2.1.4
## — Conflicts ————— tidyverse_conflicts() —
—
## ✖ tidyr::extract() masks rstan::extract()
## ✖ dplyr::filter()  masks stats::filter()
## ✖ dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
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_theta", "transf_mu_threshold",
               "transf_mu_ndt")
```

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

```
## Warning: Using an external vector in selections was deprecated in tidysselect 1.
1.0.
## i Please use `all_of()` or `any_of()` instead.
##   # Was:
##   data %>% select(parameters)
##
##   # Now:
##   data %>% select(all_of(parameters))
##
## See <https://tidysselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```

# 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")

```

```

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

```

```
print(p)
```

```
## Warning: The `guide` argument in `scale_*()` cannot be `FALSE`. This was deprecated in
## ggplot2 3.3.4.
## i Please use "none" instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

Posterior distributions

