

Penguin workflow

Nicole Cruz

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Packages

```
library(tidyverse)  # Graphs mit ggplot()
library(knitr)      # Tables mit kable()
library(ggokabeito) # colorblind friendly colors
library(brms)       # Hierarchical Bayesian models
library(rstan)      # Interface to Stan
library(shinystan)  # Model output graphs
library(bayesplot)  # Model output graphs

# General settings
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = TRUE)
options(contrasts = c("contr.equalprior_pairs", "contr.poly"))
set.seed(1234) # For reproducibility

output1 <- capture.output(m1 <- brm(flipper_len ~ 1,
                                   data = penguins,
                                   family = gaussian(),
                                   sample_prior = TRUE,
                                   warmup = 1000,
                                   iter = 4000, # to later compute BFs
                                   chains = 4,
                                   cores = 4,
                                   save_pars = save_pars(all = TRUE), # to later compute BFs
                                   control = list(adapt_delta = 0.99,
                                                  max_treedepth = 12))
                                   )

summary(m1, waic = TRUE)

## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: flipper_len ~ 1
## Data: penguins (Number of observations: 342)
## Draws: 4 chains, each with iter = 4000; warmup = 1000; thin = 1;
## total post-warmup draws = 12000
##
## Regression Coefficients:
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept 200.89 0.78 199.36 202.41 1.00 6223 5451
##
## Further Distributional Parameters:
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma 14.10 0.54 13.07 15.19 1.00 6016 5806
##
```

```

## Draws were sampled using sampling(NUTS). 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(m1)
# m1$fit
default_prior(m1)

##           prior      class coef group resp dpar nlpar lb ub  source
## student_t(3, 197, 16.3) Intercept                                default
## student_t(3, 0, 16.3)    sigma                                0    default

output2 <- capture.output(m2 <- brm(flipper_len ~ bill_len,
                                   data = penguins,
                                   family = gaussian(),
                                   sample_prior = TRUE,
                                   warmup = 1000,
                                   iter = 4000, # to later compute BFs
                                   chains = 4,
                                   cores = 4,
                                   save_pars = save_pars(all = TRUE), # to later compute BFs
                                   control = list(adapt_delta = 0.99,
                                                  max_treedepth = 12))
                                   )

output3 <- capture.output(m3 <- brm(flipper_len ~ bill_len + bill_dep,
                                   data = penguins,
                                   family = gaussian(),
                                   sample_prior = TRUE,
                                   warmup = 1000,
                                   iter = 4000, # to later compute BFs
                                   chains = 4,
                                   cores = 4,
                                   save_pars = save_pars(all = TRUE), # to later compute BFs
                                   control = list(adapt_delta = 0.99,
                                                  max_treedepth = 12))
                                   )

mcmc_areas(m3, prob = 0.95
           , pars = c("b_bill_len", "b_bill_dep", "sigma"))

mar1 <- bridge_sampler(m1, silent = T)
mar2 <- bridge_sampler(m2, silent = T)
mar3 <- bridge_sampler(m3, silent = T)
bf_12 <- bayes_factor(mar1, mar2)
bf_23 <- bayes_factor(mar2, mar3)
bf_13 <- bayes_factor(mar1, mar3)

```

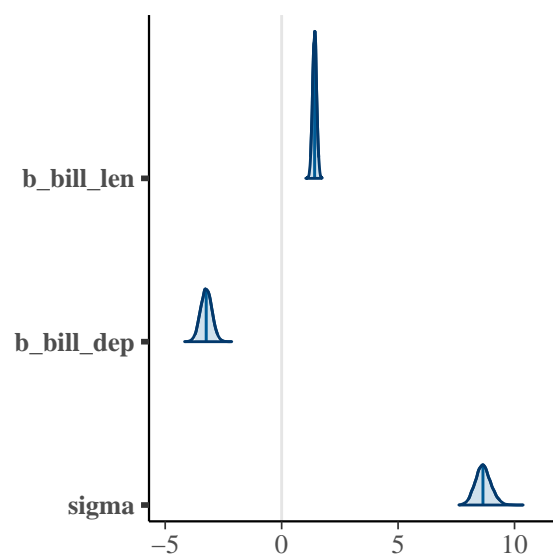


Figure 1: Posterior parameter distributions to complement the Bayes factor.