MCMC examples

```r
library(MCMCglmm)   ## older, Gibbs-sampling
library(brms)        ## newest, lme4-like syntax, very flexible, compiled
library(rstanarm)   ## lme4-like syntax, pre-compiled
library(lme4)        ## to get data
options(brms.backend = "cmdstanr")
library(broom.mixed)  ## 'tidy'
library(tidybayes)   ## convenience functions for getting MCMC output in 'tidy' format
library(bayesplot)
library(bayestestR)   ## diagnostics
library(ggplot2); theme_set(theme_bw())
library(shinystan)   ## diagnostics for Stan in a Shiny window
library(tidyverse)   ## general-purpose manipulations
```

- a little more on priors:
    - parameter-expanded priors: $y_j|\mu,\xi_j \sim N(\mu + \alpha\sigma_j, \sigma_j^2)$, $\sigma_j \sim N(0, \sigma_\xi^2)$; $\alpha \sim N(\alpha_0, \sigma_\alpha)$, $\sigma_\alpha \sim$ inverse-Gamma(ν)

```r
df(v/alpha.V, df1 = 1, df2 = nu, ncp = (alpha.mu^2)/alpha.V)
2 * dt(sqrt(v)/sqrt(alpha.V), df = nu, ncp = alpha.mu/sqrt(alpha.V))
```

… always set `alpha.mu=0`, can set `V = 1` (or `diag()` in more complex cases) wlog; `sqrt(alpha.V)` (scale) and `nu` are the only relevant parameters

effective sample size

- number of samples, corrected for autocorrelation
- ESS may be > sample size! (e.g. *antithetic sampling*)
- efficiency of a sampler is not (samples/time), but (effective samples/time)
- effective sample size >1000 for both tail and bulk quantities (Vehtari et al. 2021)

Bayesian workflow

Gelman et al. (2020)
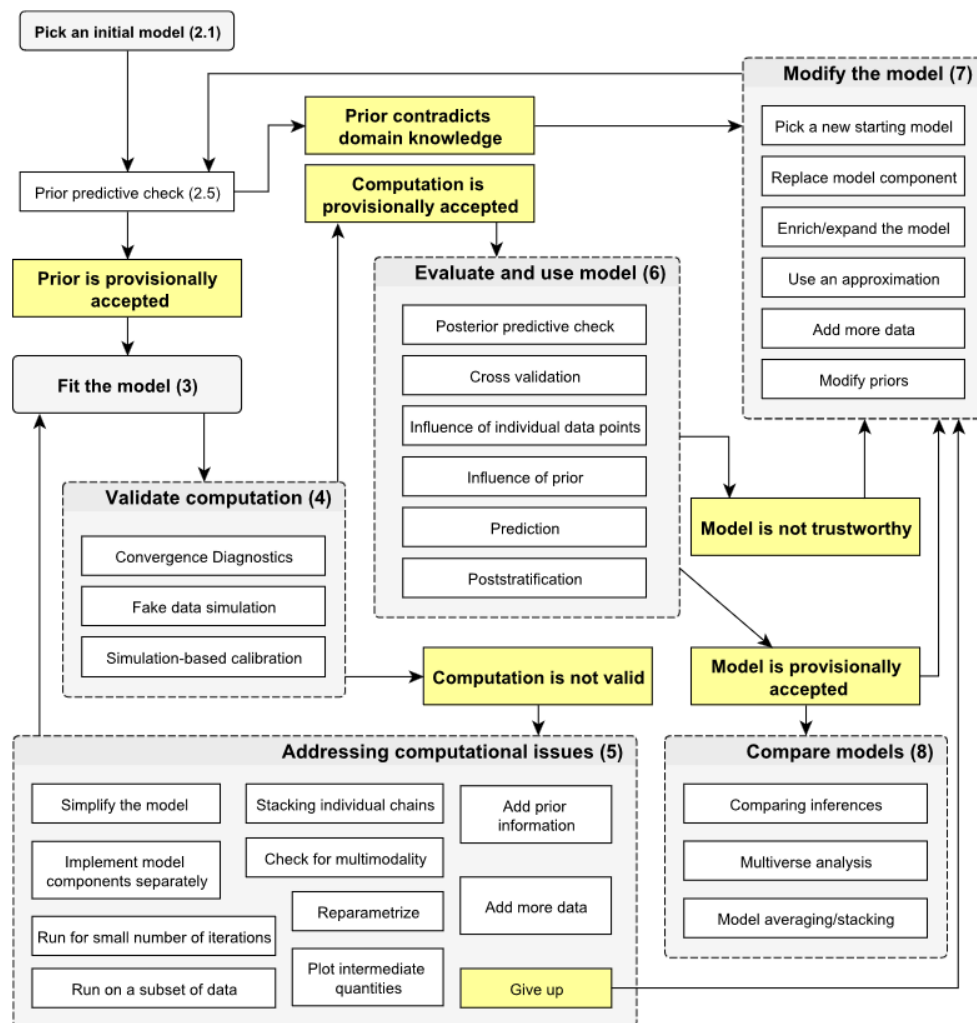
simulation-based calibration

Talts et al. (2020)

default priors/prior predictive simulations:

- `rstanarm` default priors: https://cran.r-project.org/web/packages/rstanarm/vignettes/priors.html

Using the good old `sleepstudy` example:

```r
priorpred <- stan_lmer(Reaction ~ Days + (Days|Subject),
                       prior_PD = TRUE, data = sleepstudy, chains = 1,
                       seed = 101,
                       refresh = 0)
```

```r
prior_summary(priorpred)
```

```
Priors for model 'priorpred'
------
Intercept (after predictors centered)
  Specified prior:
    ~ normal(location = 299, scale = 2.5)
  Adjusted prior:
    ~ normal(location = 299, scale = 141)

Coefficients
  Specified prior:
    ~ normal(location = 0, scale = 2.5)
  Adjusted prior:
    ~ normal(location = 0, scale = 49)

Auxiliary (sigma)
  Specified prior:
    ~ exponential(rate = 1)
  Adjusted prior:
    ~ exponential(rate = 0.018)

Covariance
 ~ decov(reg. = 1, conc. = 1, shape = 1, scale = 1)
------
See help('prior_summary.stanreg') for more details
```
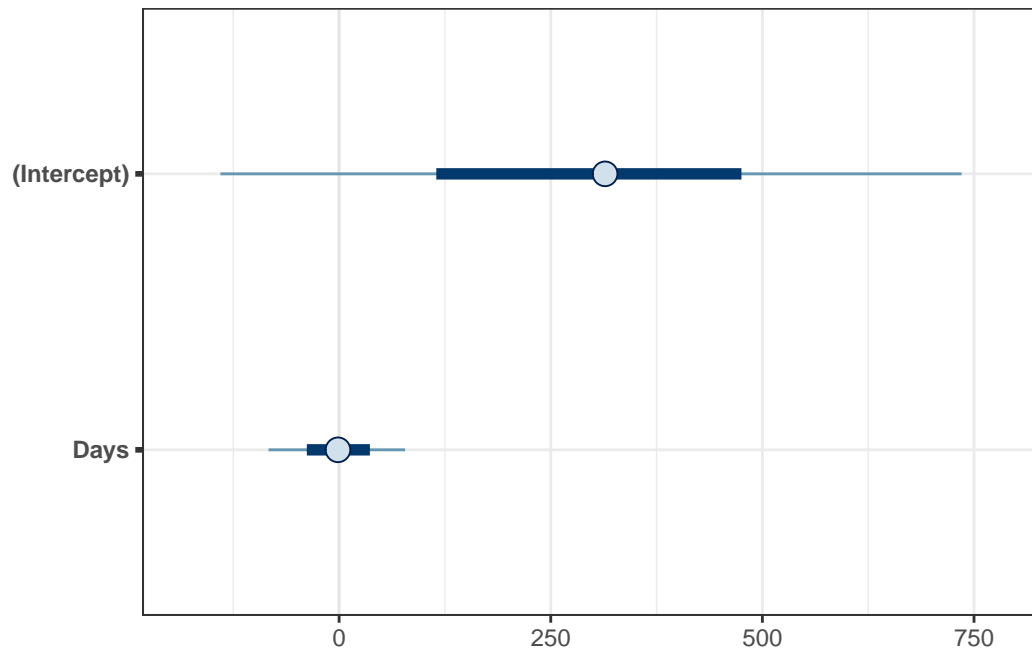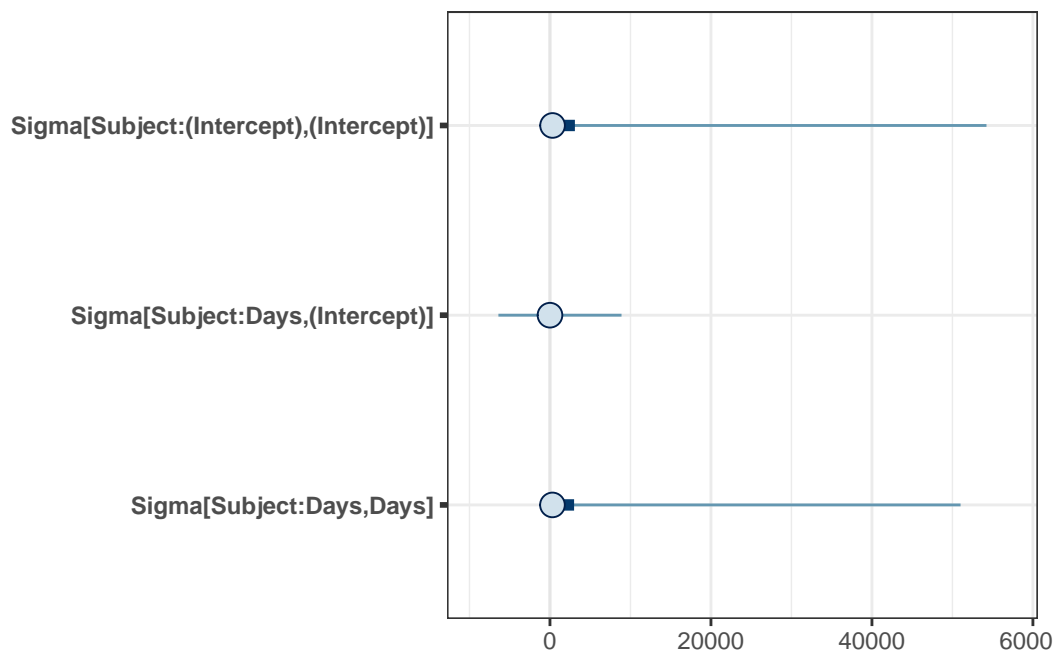
```r
plot(priorpred, pars = c("(Intercept)", "Days"))
```

```
plot(priorpred, regex_pars = "Sigma")
```


4

```
stanfit <- stan_lmer(Reaction ~ Days + (Days|Subject),
                     data = sleepstudy, chains = 4)


print(bayestestR::diagnostic_posterior(stanfit),      digits = 4)
```
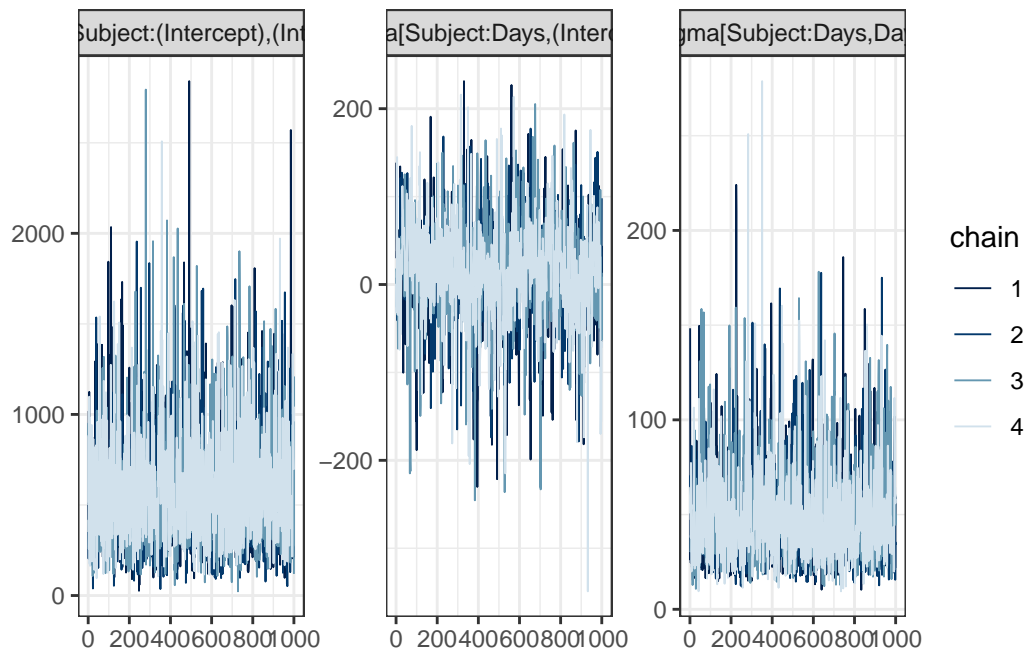
```
     Parameter  Rhat  ESS     MCSE
1  (Intercept) 1.001 1765 0.15964
38        Days 1.002 1315 0.04827
```
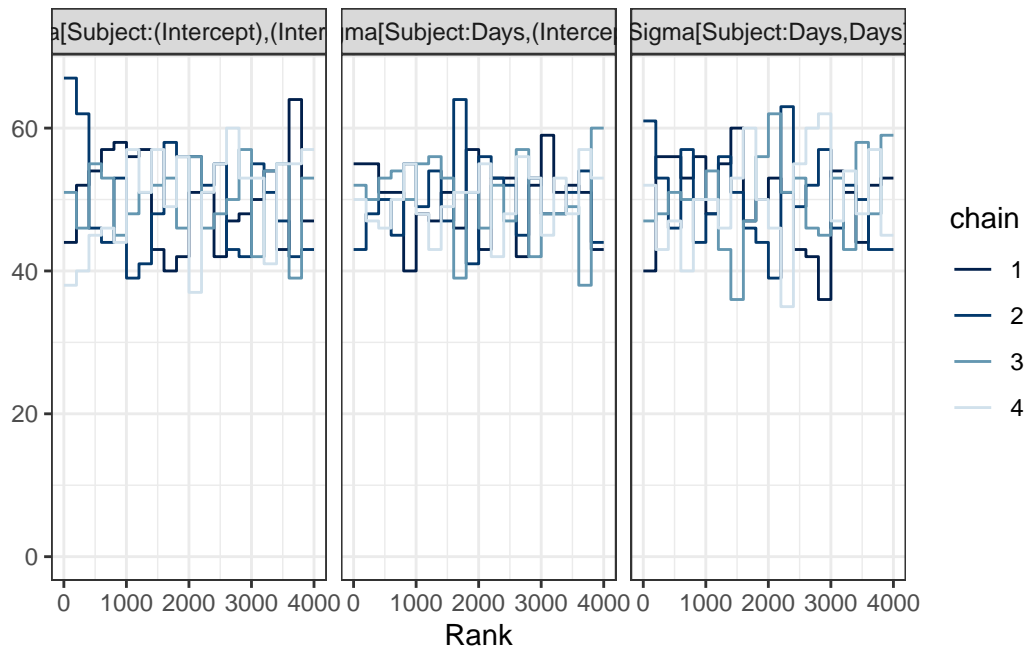
```
launch_shinystan(stanfit)
```

```
mcmc_trace(stanfit, regex_pars= "Sigma")
```



```
mcmc_rank_overlay(stanfit, regex_pars= "Sigma")
```

- MCMC diagnostics

    - trace plots, improved trace plots
    - R-hat Vehtari et al. (2021)
    - divergences (HMC only)

See http://bbolker.github.io/bbmisc/bayes/examples.html

doing stuff with the results

```r
tidy(stanfit, effects=c("fixed", "ran_pars"), conf.int = TRUE)
```

```
# A tibble: 6 x 6
  term                         estimate std.error conf.low conf.high group
  <chr>                           <dbl>     <dbl>    <dbl>     <dbl> <chr>
1 (Intercept)                    251.        6.34   240.      262.   <NA>
2 Days                            10.5       1.65     7.52     13.2  <NA>
3 sd_(Intercept).Subject          23.8      NA       NA        NA    Subject
4 sd_Days.Subject                  6.94     NA       NA        NA    Subject
5 cor_(Intercept).Days.Subject     0.0806   NA       NA        NA    Subject
6 sd_Observation.Residual         26.0      NA       NA        NA    Residual
```

6

¿¿ why don't we get confidence intervals ?? Do it by hand …

```
(as_draws(stanfit)
    |> tidyr::pivot_longer(everything())
    |> group_by(name)
    |> summarise(estimate = median(value),
                 lwr = quantile(value, 0.025),
                 upr = quantile(value, 0.975))
    |> filter(!stringr::str_detect(name, "^b\\["))
)
```

```
# A tibble: 9 x 4
  name                                     estimate    lwr     upr
  <chr>                                       <dbl>  <dbl>   <dbl>
1 (Intercept)                                  251.   238.    265.
2 .chain                                        2.5     1       4
3 .draw                                        2000.   101.   3900.
4 .iteration                                    500.   26.0    975.
5 Days                                          10.5   6.86    13.8
6 Sigma[Subject:(Intercept),(Intercept)]        510.   156.   1295.
7 Sigma[Subject:Days,(Intercept)]               16.0 -106.     112.
8 Sigma[Subject:Days,Days]                      42.9   18.1    108.
9 sigma                                         26.0   23.2    29.4
```

```
form1 <- Reaction ~ Days + (Days|Subject)
get_prior(form1, sleepstudy)
```

```
                       prior      class      coef   group resp dpar nlpar lb ub
                       (flat)         b
                       (flat)         b      Days
                       lkj(1)       cor
                       lkj(1)       cor            Subject
 student_t(3, 288.7, 59.3) Intercept
    student_t(3, 0, 59.3)        sd                                         0
    student_t(3, 0, 59.3)        sd            Subject                      0
    student_t(3, 0, 59.3)        sd       Days Subject                      0
    student_t(3, 0, 59.3)       sd Intercept Subject                       0
    student_t(3, 0, 59.3)     sigma                                        0
      source
     default
```

```
(vectorized)
     default
(vectorized)
     default
     default
(vectorized)
(vectorized)
(vectorized)
     default
```

```r
b_prior <- c(set_prior("normal(200, 50)", "Intercept"),
            set_prior("normal(0, 10)", "b"),
            set_prior("normal(0, 1)", "sigma")
            )
```

```r
b <- brm(form1, sleepstudy,
        prior = b_prior,
        seed = 101,                  ## reproducibility
        sample_prior = 'only',    ## for prior predictive sim
        chains = 1, iter = 500,   ## very short sample for convenience
        silent = 2, refresh = 0   ## be vewy vewy quiet ...
        )
p_df <- sleepstudy |> add_predicted_draws(b)
```

'spaghetti plot' of prior preds

```r
gg0 <- ggplot(p_df,aes(Days, .prediction, group=interaction(Subject,.draw))) +
        geom_line(alpha = 0.1)
```

```r
b_prior4 <- c(set_prior("normal(200, 5)", "Intercept"),
            set_prior("normal(0, 2)", "b"),
            set_prior("normal(0, 1)", "sd"),
            set_prior("normal(0, 1)", "sigma")
            )
cc <-capture.output(
    b_reg <- brm(form1, sleepstudy,
            prior = b_prior4,
            seed = 101,
            init = 0,
            control = list(adapt_delta = 0.95)
```

```
                )
    )
```

Start sampling

Chain 1 Informational Message: The current Metropolis proposal is about to be rejected becau:

Chain 1 Exception: normal_id_glm_lpdf: Scale vector is inf, but must be positive finite! (in

Chain 1 If this warning occurs sporadically, such as for highly constrained variable types l:

Chain 1 but if this warning occurs often then your model may be either severely ill-condition

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```

From the Stan forums:

> This is common and not a problem, the algorithm explores a large range of values
> in the warm-up phase and often triggers numerical problems that go away.

```r
print(bayestestR::diagnostic_posterior(b_reg),       digits = 4)
```

```
    Parameter   Rhat  ESS    MCSE
1      b_Days 1.0002 3744 0.01764
2 b_Intercept 0.9997 3297 0.05154
```

```
## debug(MCMCglmm:::priorformat)
m <- MCMCglmm(Reaction ~ Days, random = ~us(1+Days):Subject,
              data = sleepstudy,
              verbose=FALSE,
              prior = list(G=list(G1=list(V=diag(2), nu = 0.1))))
broom.mixed::tidy(m)
```

```
# A tibble: 6 x 5
  effect    group    term                    estimate std.error
  <chr>     <chr>    <chr>                        <dbl>     <dbl>
1 fixed     <NA>     (Intercept)                  252.       6.65
2 fixed     <NA>     Days                          10.5      1.61
3 ran_pars  Subject  var__(Intercept)             508.     357.
4 ran_pars  Subject  cov__(Intercept).Days         49.1     63.5
5 ran_pars  Subject  var__Days                     33.3     19.9
6 ran_pars  Residual var__Observation            700.      98.6
```

```
try(MCMCglmm(Reaction ~ Days, random = ~us(1+Days):Subject,
             data = sleepstudy,
             verbose=FALSE,
             prior = list(G=list(G1=list(V=diag(2), nu = 0.1,
                                 alpha.mu = 0, alpha.V = diag(2))))))
```

```
Error in priorformat(if (NOpriorG) { :
  alpha.mu is the wrong length for some prior$G/prior$R elements
```

```
m2 <- MCMCglmm(Reaction ~ Days, random = ~us(1+Days):Subject,
               data = sleepstudy,
               verbose=FALSE,
               prior = list(G=list(G1=list(V=diag(2), nu = 0.1,
                                   alpha.mu = rep(0,2),
                                   alpha.V = diag(2)))))
```

```
lattice::xyplot(m2$VCV)
```
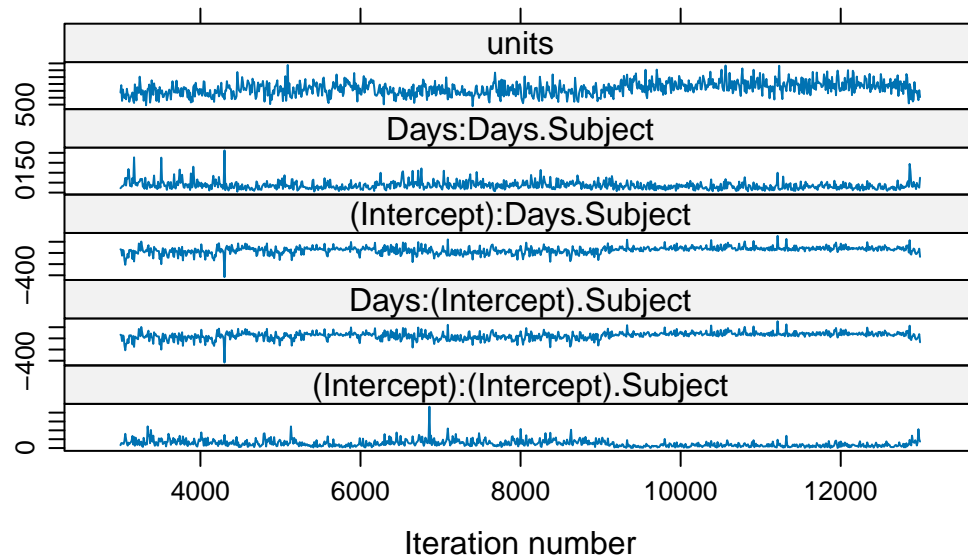
Run longer (and thin)? Strengthen prior?

to do

- sort out `cmdstanr` make stuff
- test silencing of `brms` messages
- improve `tidy` for `rstanarm`
- better ways to get draws
- prior pred sims for `MCMCglmm`? (examples of parameter-expansion)
- SBC examples?
- figure out compilation caching for `brms`?
- contact Hadfield about `MCMCglmm` tweaks

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