Plotting MCMC draws using the bayesplot package

Jonah Gabry

2019-05-22

Introduction

This vignette focuses on plotting parameter estimates from MCMC draws. MCMC diagnostic plots are covered in the separate vignette *Visual MCMC diagnostics*, and graphical posterior predictive model checking is covered in the vignette *Graphical posterior predictive checks*.

Setup

In addition to **bayesplot** we'll load the following packages:

- **ggplot2**, in case we want to customize the ggplot objects created by **bayesplot**
- **rstanarm**, for fitting the example models used throughout the vignette

```
library("bayesplot")
library("ggplot2")
library("rstanarm")
```

Example model

The **bayesplot** package provides various plotting functions for visualizing Markov chain Monte Carlo (MCMC) draws from the posterior distribution of the parameters of a Bayesian model.

In this vignette we'll use draws obtained using the `stan_glm` function in the **rstanarm** package (Gabry and Goodrich, 2017), but MCMC draws from using any package can be used with the functions in the **bayesplot** package. See, for example, **brms**, which, like **rstanarm**, calls the **rstan** package internally to use Stan's MCMC sampler.

```
head(mtcars) # see help("mtcars")
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```
# linear regression model using stan_glm
# using '~ .' to include all variables
fit <- stan_glm(mpg ~ ., data = mtcars, seed = 1111)
print(fit)
```

```
stan_glm
 family:       gaussian [identity]
 formula:      mpg ~ .
 observations: 32
 predictors:   11
------
            Median MAD_SD
(Intercept) 12.6   20.1  
cyl         -0.1    1.1  
disp         0.0    0.0  
hp           0.0    0.0  
drat         0.8    1.7  
wt          -3.7    1.9  
qsec         0.8    0.8  
vs           0.3    2.1  
am           2.5    2.1  
gear         0.6    1.6  
carb        -0.2    0.9  

Auxiliary parameter(s):
      Median MAD_SD
sigma 2.7    0.4   

------
* For help interpreting the printed output see ?print.stanreg
* For info on the priors used see ?prior_summary.stanreg
```

To use the posterior draws with the functions in the **bayesplot** package we'll extract them from the fitted model object:

```
posterior <- as.array(fit)
dim(posterior)
```

```
[1] 1000    4   12
```

```r
dimnames(posterior)
```

```
$iterations
NULL

$chains
[1] "chain:1" "chain:2" "chain:3" "chain:4"

$parameters
 [1] "(Intercept)" "cyl"         "disp"        "hp"          "drat"       
 [6] "wt"          "qsec"        "vs"          "am"          "gear"       
[11] "carb"        "sigma"      
```

We've used `as.array` above (as opposed to `as.matrix`) because it keeps the Markov chains separate (`stan_glm` runs four chains by default). Most of the plots don't actually need the chains to be separate, but for a few of the plots we make in this vignette we'll want to show the chains individually.

Posterior uncertainty intervals

For models fit using MCMC we can compute posterior uncertainty intervals (sometimes called "credible intervals") in various ways. **bayesplot** currently provides plots of central intervals based on quantiles, although additional options may be provided in future releases (e.g., HDIs, which can be useful in particular cases).

Documentation:

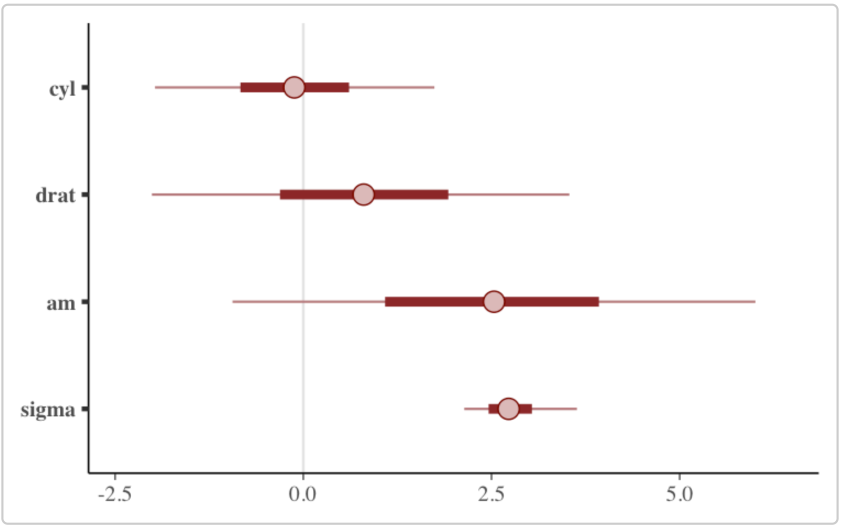
- `help("MCMC-intervals")`
- mc-stan.org/bayesplot/reference/MCMC-intervals

---

mcmc_intervals, mcmc_areas

Central posterior uncertainty intervals can be plotted using the `mcmc_intervals` function.

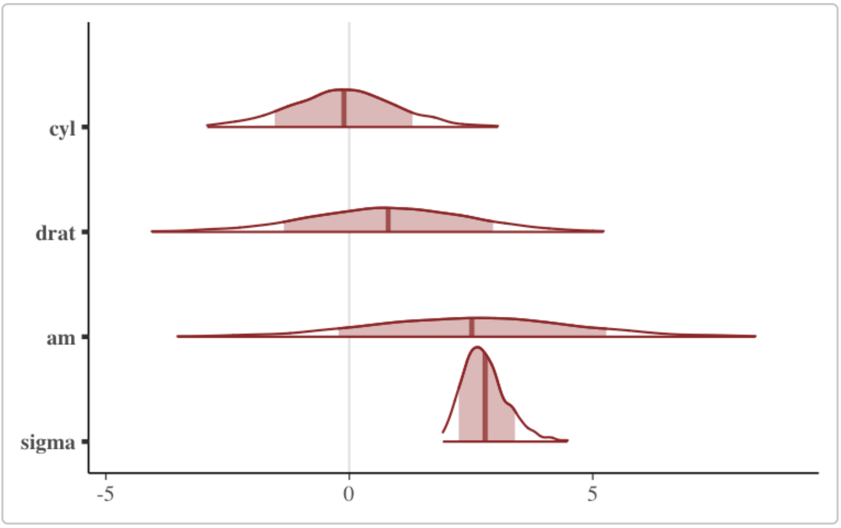
```r
color_scheme_set("red")
mcmc_intervals(posterior, pars = c("cyl", "drat", "am", "sigma"))
```



The default is to show 50% intervals (the thick segments) and 90% intervals (the thinner outer lines). These defaults can be changed using the `prob` and `prob_outer` arguments, respectively. The points in the above plot are posterior medians. The `point_est` argument can be used to select posterior means instead or to omit the point estimates.

To show the uncertainty intervals as shaded areas under the estimated posterior density curves we can use the `mcmc_areas` function.

```
mcmc_areas(
  posterior,
  pars = c("cyl", "drat", "am", "sigma"),
  prob = 0.8, # 80% intervals
  prob_outer = 0.99, # 99%
  point_est = "mean"
)
```



Univariate marginal posterior distributions

bayesplot provides functions for looking at histograms or kernel density estimates of marginal posterior distributions, either with all Markov chains combined or with the chains separate.

Documentation:

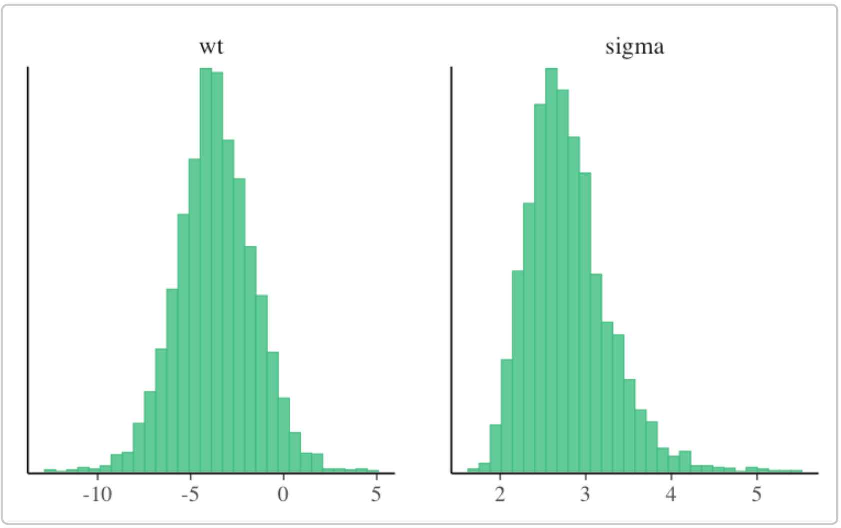
- `help("MCMC-distributions")`
- mc-stan.org/bayesplot/reference/MCMC-distributions

---

mcmc_hist

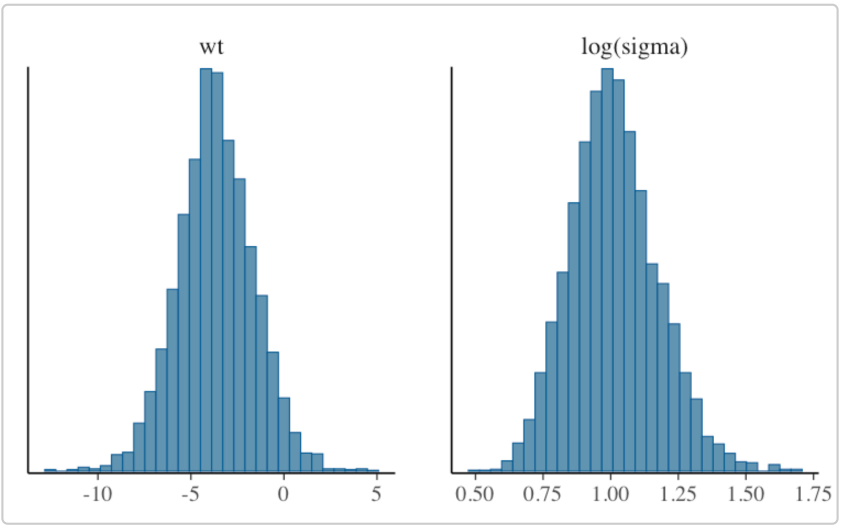
The `mcmc_hist` function plots marginal posterior distributions (combining all chains):

```
color_scheme_set("green")
mcmc_hist(posterior, pars = c("wt", "sigma"))
```



If we want to plot `log(sigma)` rather than `sigma` we can either transform the draws in advance or use the `transformations` argument.

```
color_scheme_set("blue")
mcmc_hist(posterior, pars = c("wt", "sigma"),
          transformations = list("sigma" = "log"))
```

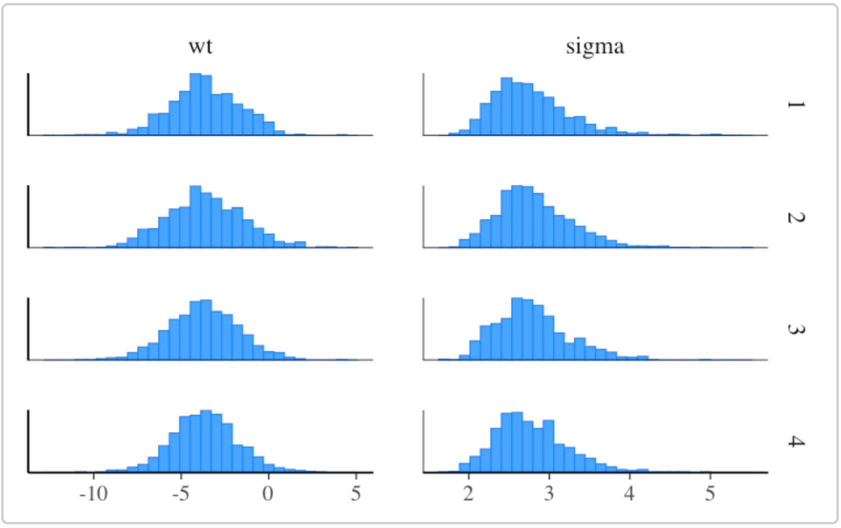


Most of the other functions for plotting MCMC draws also have a `transformations` argument.

mcmc_hist_by_chain

To view separate histograms of each of the four Markov chains we can use `mcmc_hist_by_chain`, which plots each chain in a separate facet in the plot.

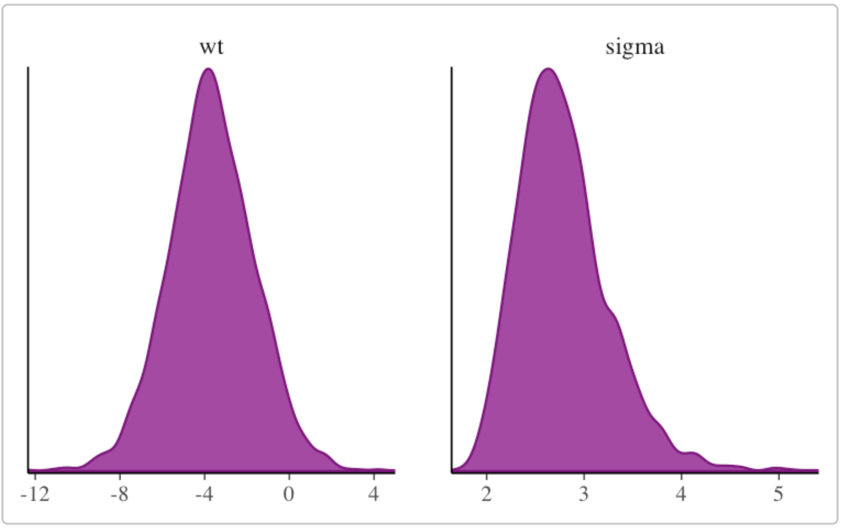
```
color_scheme_set("brightblue")
mcmc_hist_by_chain(posterior, pars = c("wt", "sigma"))
```



mcmc_dens

The `mcmc_dens` function is similar to `mcmc_hist` but plots kernel density estimates instead of histograms.

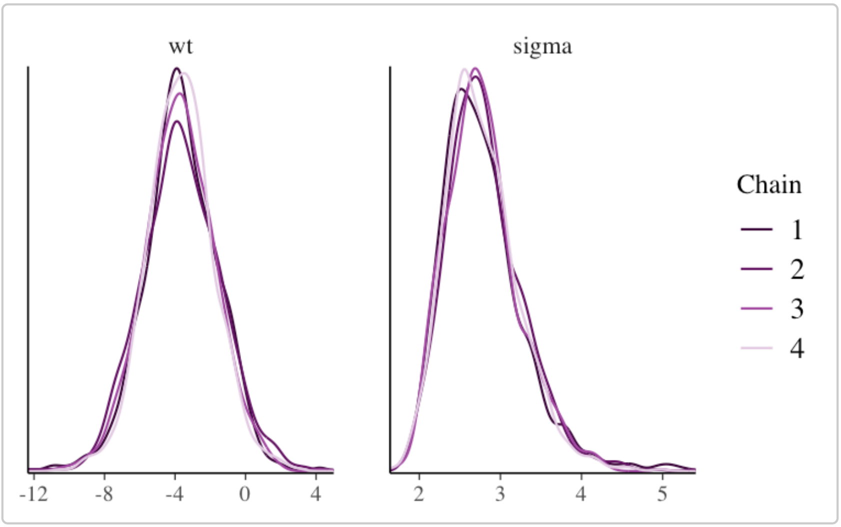
```
color_scheme_set("purple")
mcmc_dens(posterior, pars = c("wt", "sigma"))
```



mcmc_dens_overlay

Like `mcmc_hist_by_chain`, the `mcmc_dens_overlay` function separates the Markov chains. But instead of plotting each chain individually, the density estimates are overlaid.

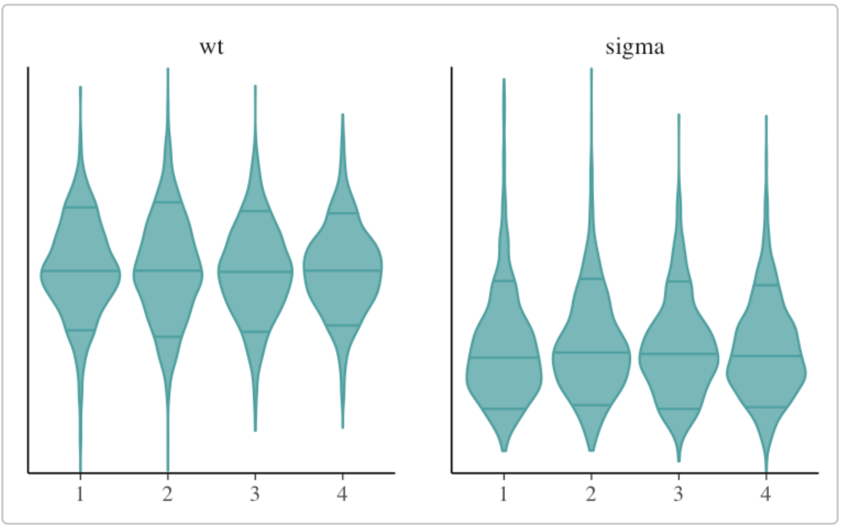
```
mcmc_dens_overlay(posterior, pars = c("wt", "sigma"))
```



mcmc_violin

The `mcmc_violin` function plots the density estimates of each chain as violins and draws horizontal line segments at user-specified quantiles.

```
color_scheme_set("teal")
mcmc_violin(posterior, pars = c("wt", "sigma"), probs = c(0.1, 0.5, 0.9))
```



Bivariate plots

Various functions are available for plotting bivariate marginal posterior distributions. Some of these functions also take optional arguments for adding MCMC diagnostic information to the plots. That additional functionality is discussed in the separate *Visual MCMC diagnostics* vignette.

Documentation:

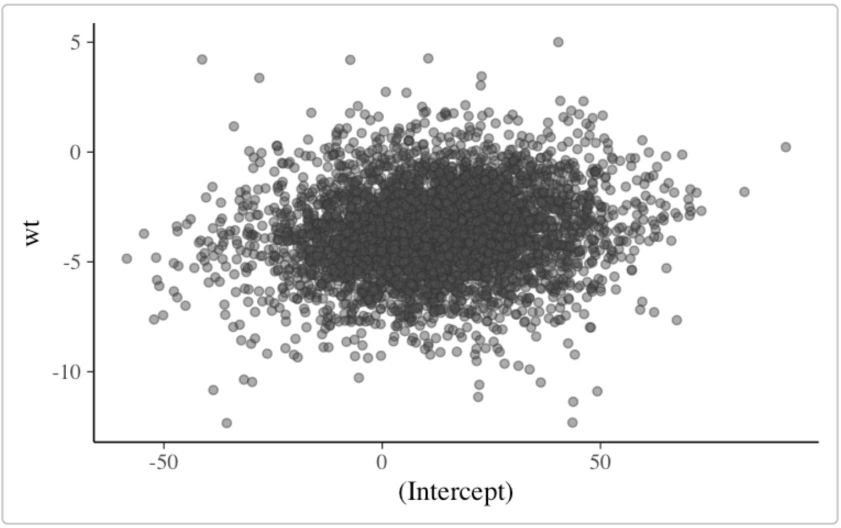
- `help("MCMC-scatterplots")`
- mc-stan.org/bayesplot/reference/MCMC-scatterplots

---

mcmc_scatter

The `mcmc_scatter` function creates a simple scatterplot of two parameters.

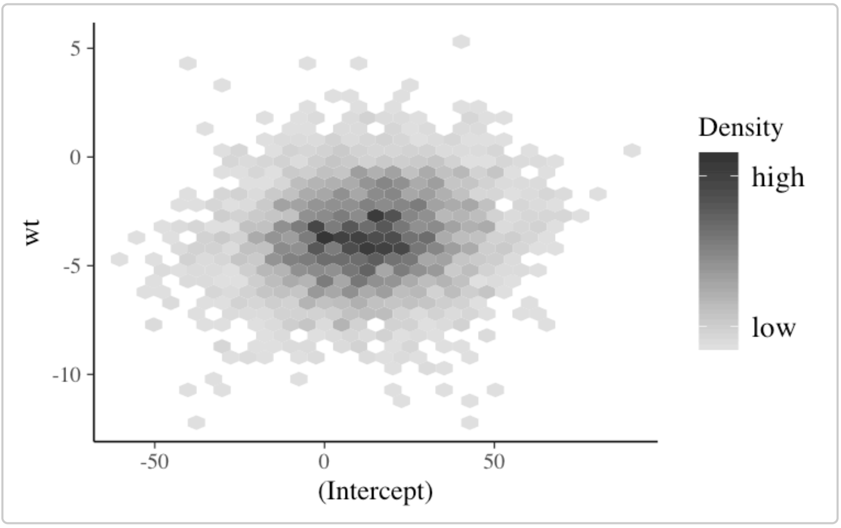
```
color_scheme_set("gray")
mcmc_scatter(posterior, pars = c("(Intercept)", "wt"),
             size = 1.5, alpha = 0.5)
```



mcmc_hex

The `mcmc_hex` function creates a similar plot but using hexagonal binning, which can be useful to avoid overplotting.

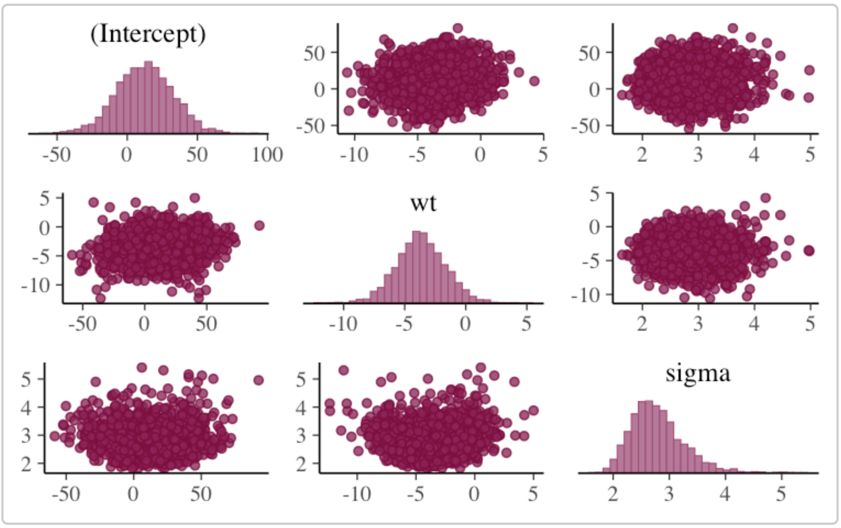
```r
# requires hexbin package
if (requireNamespace("hexbin", quietly = TRUE)) {
  mcmc_hex(posterior, pars = c("(Intercept)", "wt"))
}
```



mcmc_pairs

In addition to `mcmc_scatter` and `mcmc_hex`, **bayesplot** now provides an `mcmc_pairs` function for creating pairs plots with more than two parameters.

```r
color_scheme_set("pink")
mcmc_pairs(posterior, pars = c("(Intercept)", "wt", "sigma"),
           off_diag_args = list(size = 1.5))
```



The univariate marginal posteriors are shown along the diagonal as histograms, but this can be changed to densities by setting `diag_fun="dens"`. Bivariate plots are displayed above and below the diagonal as scatterplots, but it is also possible to use hex plots by setting `off_diag_fun="hex"`. By default, `mcmc_pairs` shows some of the Markov chains (half, if an even number of chains) above the diagonal and the others below. There are many more options for controlling how the draws should be split between the plots above and below the diagonal (see the documentation for the `condition` argument), but they are more useful when MCMC diagnostic information is included. This is discussed in the *Visual MCMC diagnostics* vignette.

Trace plots

Trace plots are time series plots of Markov chains. In this vignette we show the standard trace plots that **bayesplot** can make. For models fit using any Stan interface (or Hamiltonian Monte Carlo in general), the *Visual MCMC diagnostics* vignette provides an example of also adding information about divergences to trace plots.

Documentation:

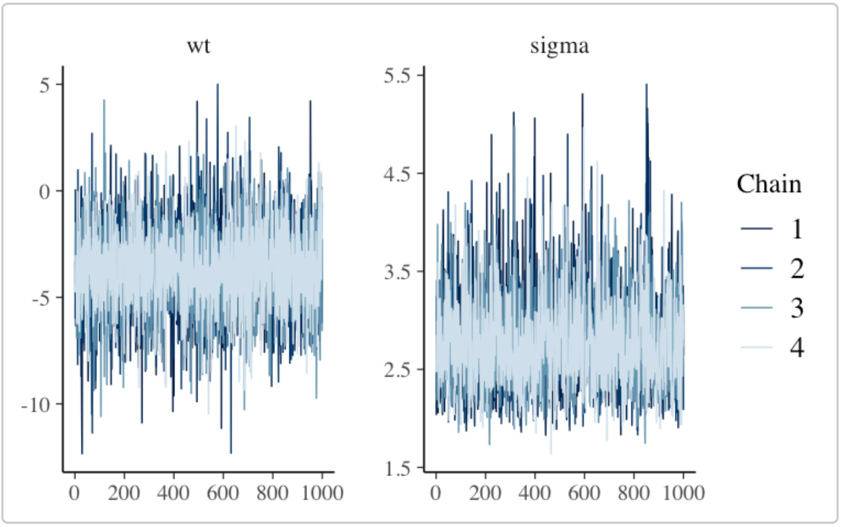
- `help("MCMC-traces")`
- mc-stan.org/bayesplot/reference/MCMC-traces

---

mcmc_trace

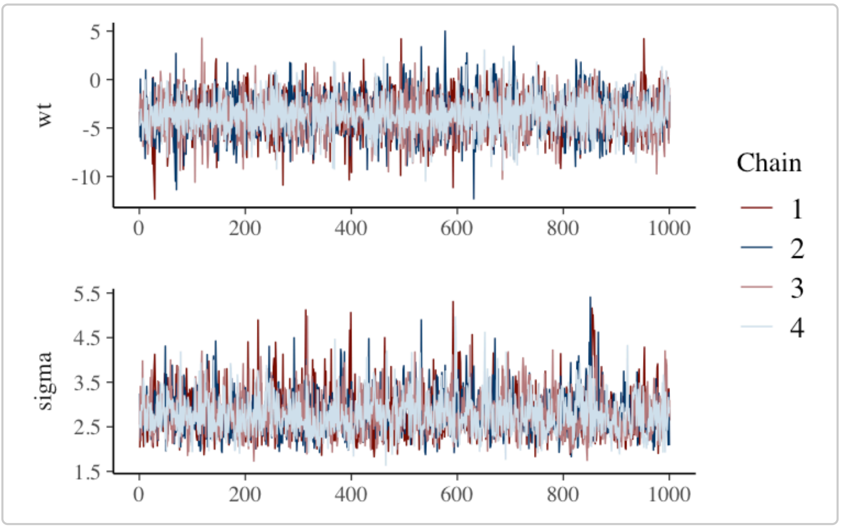
The `mcmc_trace` function creates standard trace plots:

```
color_scheme_set("blue")
mcmc_trace(posterior, pars = c("wt", "sigma"))
```



If it's hard to see the difference between the chains we can change to a mixed color scheme, for example:

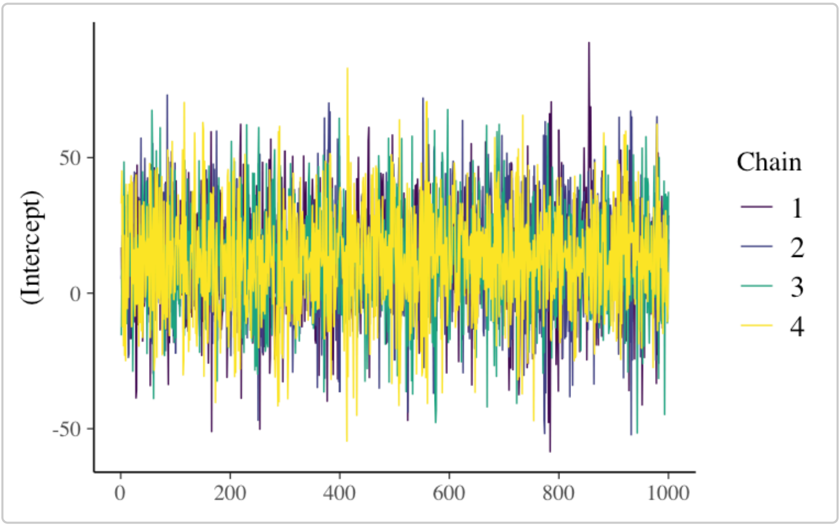
```
color_scheme_set("mix-blue-red")
mcmc_trace(posterior, pars = c("wt", "sigma"),
           facet_args = list(ncol = 1, strip.position = "left"))
```



The code above also illustrates the use of the `facet_args` argument, which is a list of parameters passed to `facet_wrap` in **ggplot2**. Specifying `ncol=1` means the trace plots will be stacked in a single column rather than placed side by side, and `strip.position="left"` moves the facet labels to the y-axis (instead of above each facet).

The `"viridis"` color scheme is also useful for trace plots because it is comprised of very distinct colors:

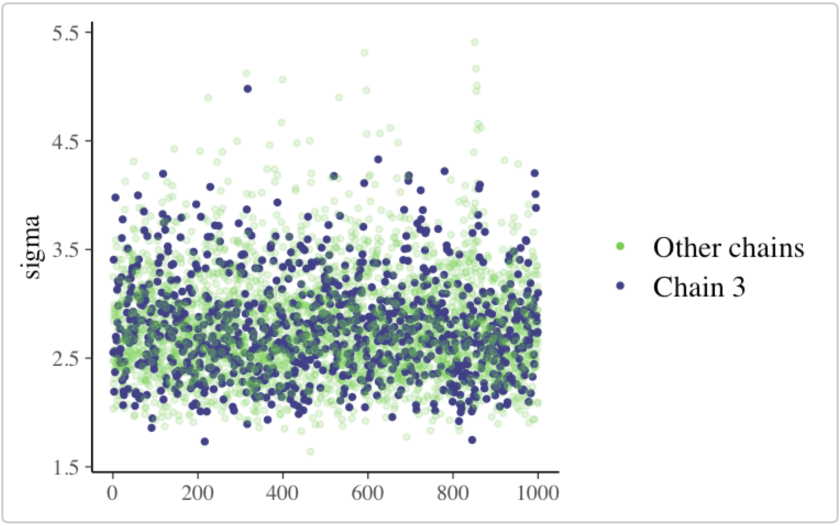
```
color_scheme_set("viridis")
mcmc_trace(posterior, pars = "(Intercept)")
```



mcmc_trace_highlight

The `mcmc_trace_highlight` function uses points instead of lines and reduces the opacity of all but a single chain (which is specified using the `highlight` argument).

```
mcmc_trace_highlight(posterior, pars = "sigma", highlight = 3)
```



References

Gabry, J., and Goodrich, B. (2017). rstanarm: Bayesian Applied Regression Modeling via Stan. R package version 2.15.3. https://mc-stan.org/rstanarm, https://CRAN.R-project.org/package=rstanarm

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. :10.1111/rssa.12378. (journal version, arXiv preprint, code on GitHub)

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., and Rubin, D. B. (2013). *Bayesian Data Analysis*. Chapman & Hall/CRC Press, London, third edition.

Stan Development Team. (2017). *Stan Modeling Language Users Guide and Reference Manual*.

https://mc-stan.org/users/documentation/