

Monte-Carlo sampling

Homework #8

Due Tuesday, Mar 17, 2026

Contents

Homework	1
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Homework

Preliminary Information

This homework set gives you practice working with Monte Carlo sampling as a more sophisticated way of estimating Bayesian posterior probability distributions than the quadratic approximation that we have been using with the `quap` function. For Monte Carlo sampling, we use the `ulam` function, which we have read about in Chapters 9–11. For these homework exercises, you will need the `cmdstanr` package for R and the `cmdstan` tool installed. See the Tools page on the course web site for detailed instructions on installing `cmdstanr` and `cmdstan`, and please come to my office hours for help if you can't get these tools to work.

Homework Exercises:

Self-study: Work these exercises, but do not turn them in.

- Exercises 9E3–9E6
- Exercises 11E1–11E3

Turn in: Work these exercises and turn them in.

- Exercises 9M1–9M2
- Exercises 11M3–11M4 and 11M7

Notes on Homework:

You can download a PDF copy of the exercises from chapters 9–11 of *Statistical Rethinking* from <https://ees5891.jgilligan.org/>

Exercise 9M2 For exercise 9M2, the question is ambiguous, about whether you should use the original `dexp(1)` or the `dunif(0, 1)` from 9M1 as the prior for sigma. Use `dexp(1)` and only change the prior for `b` from the `m9.1` in the book.

Exercises 9M1–9M2 For comparing the results, you should both look at the `precis` of the models and also plot the densities of the posteriors.

To easily plot the densities of the posteriors for one model, do the following (assume the model from the book is `m9.1`, and the models from the exercises are `ex9m1` and `ex9m2`).

This is equivalent to the code from the textbook for `m9.1`:

```
library(cmdstanr)
library(rethinking)
library(tidyverse)

data(rugged)
d <- rugged %>% mutate(log_gdp = log(rgdppc_2000))

dd <- d %>% filter(complete.cases(rgdppc_2000)) %>%
  mutate(
    log_gdp_std = log_gdp / mean(log_gdp),
    rugged_std = rugged / max(rugged),
    cid = ifelse(cont_africa == 1, 1, 2)
  )

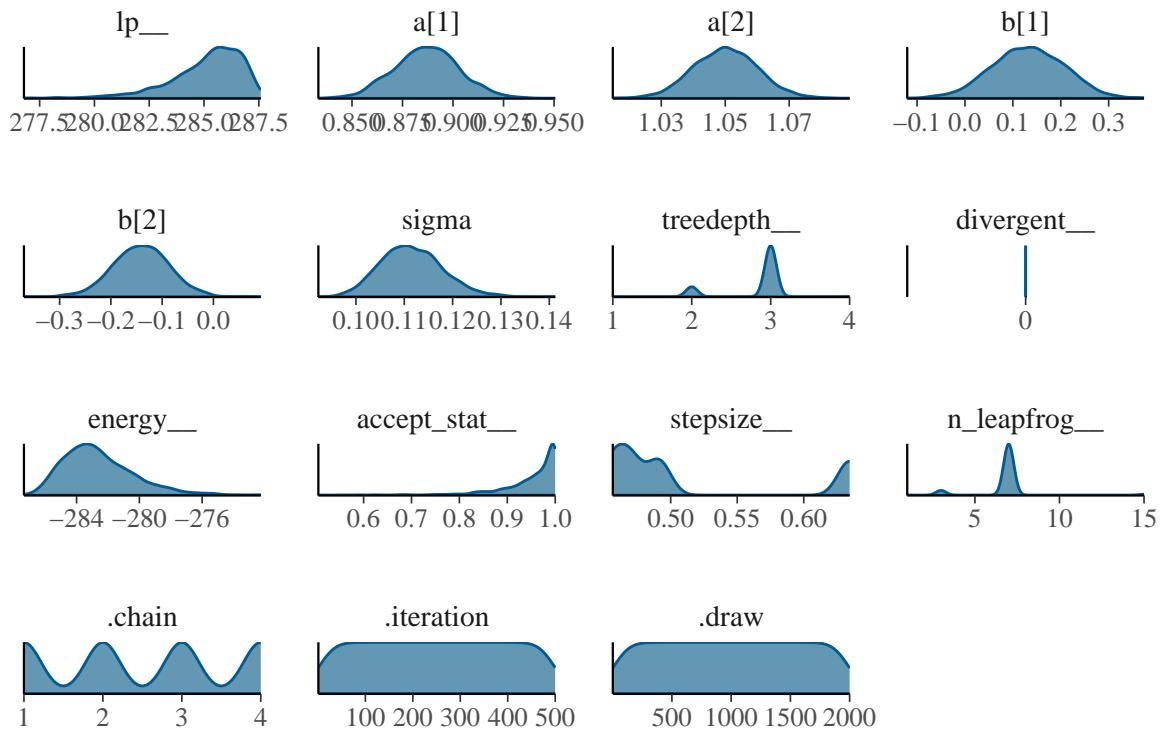
dat_slim <- dd %>% select(log_gdp_std, rugged_std, cid) %>%
  mutate(cid = as.integer(cid))

m9.1 <- ulam(
  alist(
    log_gdp_std ~ dnorm(mu, sigma),
    mu <- a[cid] + b[cid] * (rugged_std - 0.215) ,
    a[cid] ~ dnorm(1, 0.1),
    b[cid] ~ dnorm(0, 0.3),
    sigma ~ dexp(1)
  ), data=dat_slim, chains = 4, cores = 4, cmdstan = TRUE)
```

This code will plot the posterior probability densities:

```
library(tidybayes)
library(tidybayes.rethinking)
library(bayesplot)

draws <- tidy_draws(m9.1)
mcmc_dens(draws)
```



If you have two models, `foo` and `bar`, you can compare the posteriors of a parameter like `sigma` using code like this, from the textbook:

```
post_foo <- extract.samples(foo)
post_bar <- extract.samples(bar)

dens(post_foo$sigma, lwd = 1)
dens(post_bar$sigma, lwd = 1, col = rangi2, add = TRUE)
```

Alternately, you can do the same thing using the tidyverse dialect:

```
foo_draws <- tidy_draws(foo) %>% mutate(model = "foo")
bar_draws <- tidy_draws(bar) %>% mutate(model = "bar")

bind_rows(foo_draws, bar_draws) %>%
  ggplot(aes(x = sigma, color = model, fill = model)) +
  geom_density(size = 1, alpha = 0.3)
```

The first two lines extract the Monte-Carlo samples of the posterior for each model, and add a label `model` to indicate which model they came from. Then I use `ggplot` to plot the posterior density of `sigma`, from each model, where the color of the line and the fill inside the density plot indicate which model is which.

The argument `size = 1` tells R how thick to make the line, and `alpha = 0.3` sets the transparency of the fills (1 = completely opaque and 0 = completely transparent)

If you want to make a single plot that shows comparisons of all the parameters for both models, the code gets a bit more complicated:

```
foo_draws <- tidy_draws(foo) %>%
  gather_draws(a[i], b[i], sigma) %>%
  mutate(model = "foo")
bar_draws <- tidy_draws(bar) %>%
```

```

gather_draws(a[i], b[i], sigma) %>%
  mutate(model = "bar")

bind_rows(foo_draws, bar_draws) %>%
  mutate(.variable = ifelse(is.na(i), .variable,
    str_c(.variable, "[", i, "]")) %>%
  ggplot(aes(x = .value, col = model, fill = model)) +
  geom_density(alpha = 0.3) + labs(x = NULL, y = NULL) +
  facet_wrap(~.variable, scales = "free")

```

Exercises 11E1–11E3 To check yourself, for 11E1 the log-odds is -0.619, for 11E2 the probability is 0.961, and for 11E3 the proportional change in the odds is 5.47

Exercise 11M7 For 11M7, I recommend using the following code to compare the precises of the two models (`m11.4` is the `ulam` model on page 330, and `m11.4q` is the `quap` version model that you should write for this exercise). This code prints the two precises side-by-side with each row representing a different parameter.

```

pr <- precis( m11.4 , 2 )[,1:4]
prq <- precis( m11.4q , 2 )
round( cbind( pr , prq ) , 2 )

```

Then for parameters that are really different in the two models (differences of more than 0.1 in the means or the 5.5% or 94.5% levels), make a density plot comparing the posteriors of the two models. You can use the code from my notes (above) for exercises 9M1 and 9M2 to do this. Think about what important differences you see in the posteriors from the two models, and what I've been emphasizing in class about the differences between the `quap` and Monte-Carlo methods for estimating posteriors.

You can also use the code, above, in the notes for 9M1 and 9M2, to make a single plot comparing the posteriors of all the parameters for both models. Then you can make a single comparison plot for any of the parameters that show significant differences between the `quap` and `ulam` models.

At the minimum, be sure to look carefully at `a[2]`.