The Metropolis Hastings algorithm, Part 2

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January 23, 2026

See here for a PDF version of this vignette.

Prerequisites

You should be familiar with the basics of the Metropolis-Hastings algorithm.

Introduction

In this vignette, we follow up on the original algorithm with a couple of points: (i) numerical issues that were glossed over, and (ii) a useful plot.

Avoiding numerical issues in the acceptance probability

The key to the M-H algorithm is computing the acceptance probability, which recall is given by

$$A = \min \left\{ 1, \frac{\pi(y) \, Q(x_t \mid y)}{\pi(x_t) \, Q(y \mid x_t)} \right\}.$$

In practice, both terms in the fraction may be very close to zero, so on a computer you should do this computation on the logarithmic scale before exponentiating, something like this:

$$\frac{\pi(y) \, Q(x_t \mid y)}{\pi(x_t) \, Q(y \mid x_t)} = \exp \left\{ \log \pi(y) - \log \pi(x_t) + \log Q(x_t \mid y) - \log Q(y \mid x_t) \right\}].$$

Furthermore, the log values in this expression should be computed directly, and not by computing them and then taking the log. For example, in our previous example we sampled from a target distribution, which was the exponential:

$$\pi(x) = e^{-x}, \quad x > 0.$$

Instead, we can directly compute $\log \pi(x) = -x$. The code we had in that previous example can therefore be written as follows:

```
log_target <- function (x)
  ifelse(x < 0,-Inf,-x)
x <- rep(0,10000)
x[1] <- 100
for (i in 2:10000) {
```

```
  current_x <- x[i-1]
  proposed_x <- current_x + rnorm(1)
  A <- exp(log_target(proposed_x) - log_target(current_x))
  u <- runif(1)
  if (u < A)
    x[i] <- proposed_x
  else
    x[i] <- current_x
}
```

An important and useful plot

In practice, MCMC is usually performed in high-dimensional space. It can therefore be really hard to visualize directly the values of the chain. A simple 1-d summary that is always available is the log-target density, $\log \pi(x)$. So you should usually plot a trace of this whenever you run an MCMC scheme:

```
plot(log_target(x),xlab = "time",ylab = "log target",
     main = "log-target value")
```

log–target value
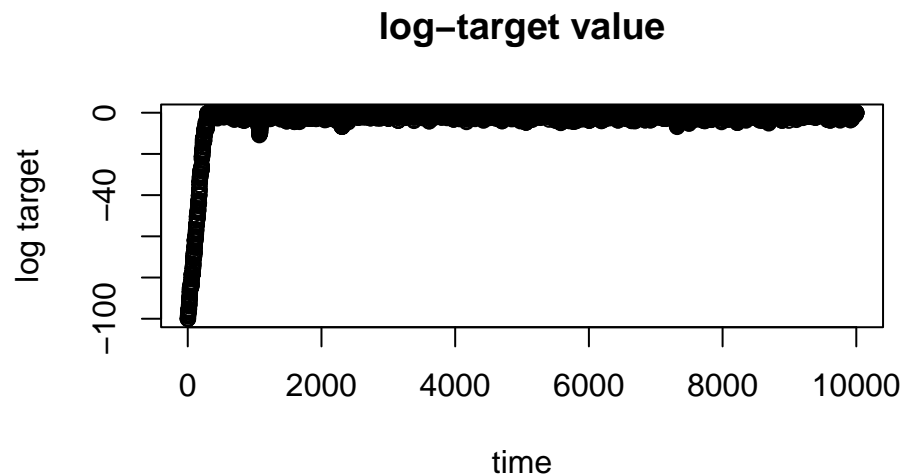
Here the plot shows "typical" behaviour of MCMC scheme: because the starting point was not close to the optimal of π, the chain initially makes large changes to find a part of the space where $\pi(x)$ is "large". Once it finds that part of the space, it starts to explore around the region where $\pi(x)$ is large.

Burn-in

The plot in the previous section immediately shows that there is an initial period of time where the Markov chain is unduly influenced by its starting position. In other words, during those iterations the Markov chain has not "converged" and those samples should not be considered to be samples

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from π. To address this, it is common to discard the first set of iterations of any chain; the iterations that are discarded are often called "burn-in".

Based on the plot, we might discard the first 1,000 iterations or so as "burn-in". Here are comparisons of the samples with and without burnin discarded:

```r
par(mfrow = c(1,2))
hist(x,xlab = "x",main = "burnin not discarded")
hist(x[-(1:1000)],xlab = "x",main = "burnin discarded")
```