3.1 Markov Chain Monte Carlo (MCMC) Methods

Computation via conjugate analysis (Chapter 2) produces **closed-form results** (good) but is **limited in scope** to a fairly small set of models for which straightforward conjugate results are possible (bad); for example, there is **no conjugate prior** for \( (\mu, \sigma^2, \nu) \) in the NB10 \( t \) model.

This was a **severe limitation** for Bayesians for almost 250 years (from the 1750s to the 1980s).

Over the past 25 years or so the Bayesian community has “discovered” and developed an entirely new computing method, **Markov chain Monte Carlo (MCMC)** (“discovered” because the physicists first figured it out about 70 years ago: Metropolis and Ulam, 1949; Metropolis et al., 1953).

It became clear above that the **central Bayesian practical challenge** is the **computation of high-dimensional integrals**.

People working on the first atom bomb in World War II faced a **similar challenge**, and noticed that **digital computers** (which were then passing from theory (Turing 1943) to reality) offered an **entirely new approach** to solving the problem.
The idea (Metropolis and Ulam, 1949) was based on the observation that anything I want to know about a probability distribution can be learned to arbitrary accuracy by sampling from it.

Suppose, for example, that I’m interested in a posterior distribution \( p(\theta|y) \) that cannot be worked with (easily) in closed form, and initially (to keep things simple) think of \( \theta \) as a scalar (real number) rather than a vector.

Three things of direct interest to me about \( p(\theta|y) \) would be

- its low-order moments, including the **mean** \( \mu = E(\theta|y) \) and **standard deviation** \( \sigma = \sqrt{V(\theta|y)} \),
- its **shape** (basically I’d like to be able to trace out (an estimate of) the entire **density curve**), and
- one or more of its **quantiles** (e.g., to construct a 95% central posterior interval for \( \theta \) I need to know the **2.5% and 97.5% quantiles**, and sometimes the **posterior median** (the **50th percentile**) is of interest too).
Suppose I could take an arbitrarily large random sample from \( p(\theta|y) \), say \( \theta_1^*, \ldots, \theta_m^* \).

Then each of the above three aspects of \( p(\theta|y) \) can be estimated from the \( \theta^* \) sample:

- \( \hat{E}(\theta|y) = \bar{\theta}^* = \frac{1}{m} \sum_{j=1}^{m} \theta_j^* \), and \( \sqrt{\hat{V}(\theta|y)} = \sqrt{\frac{1}{m-1} \sum_{j=1}^{m} (\theta_j^* - \bar{\theta}^*)^2} \);

- the density curve can be estimated by a histogram or kernel density estimate; and

- percentiles can be estimated by counting how many of the \( \theta^* \) values fall below a series of specified points — e.g., to find an estimate of the 2.5% quantile I solve the equation

\[
\hat{F}_\theta(t) = \frac{1}{m} \sum_{j=1}^{m} I(\theta_j^* \leq t) = 0.025
\]

for \( t \), where \( I(A) \) is the indicator function (1 if \( A \) is true, otherwise 0).

These are called Monte Carlo estimates of the true summaries of \( p(\theta|y) \) (in
honor of the casinos) because they’re based on the controlled use of chance.

Theory shows that with large enough \( m \), each of the Monte Carlo (or simulation-based) estimates can be made arbitrarily close to the truth with arbitrarily high probability, under some reasonable assumptions about the nature of the random sampling.

One way to achieve this, of course, is to make the sampling IID (interesting, this is sufficient but not necessary — see below).

If, for example, \( \bar{\theta}^* = \frac{1}{m} \sum_{j=1}^{m} \theta_j^* \) is based on an IID sample of size \( m \) from \( p(\theta|y) \), I can use the frequentist fact that in repeated sampling \( V(\bar{\theta}^*) = \frac{\sigma^2}{m} \), where (as above) \( \sigma^2 \) is the variance of \( p(\theta|y) \), to construct a Monte Carlo standard error (MCSE) for \( \bar{\theta}^* \):

\[
\hat{SE}(\bar{\theta}^*) = \frac{\hat{\sigma}}{\sqrt{m}},
\]

where \( \hat{\sigma} \) is the sample SD of the \( \theta^* \) values.

This can be used, possibly after some preliminary experimentation, to decide on \( m \), the Monte Carlo sample size, which later will be called the
An IID Example

length of the monitoring run.

An IID example. Consider the posterior distribution

\[ p(\theta|y) = \text{Beta}(76.5, 353.5) \]

in the AMI mortality example in Part 2.

Theory says that the posterior mean of \( \theta \) in this example is

\[
\frac{76.5}{76.5+353.5} \approx 0.1779;
\]

let’s see how well the Monte Carlo method does in estimating this known truth.

Here’s an R function to construct Monte Carlo estimates of the posterior mean and MCSE values for these estimates.

```r
beta.sim <- function( m, alpha, beta, n.sim, seed ) {
  set.seed( seed )
  theta.out <- matrix( 0, n.sim, 2 )
  for ( i in 1:n.sim ) {
    theta.sample <- rbeta( m, alpha, beta )
    theta.out[ i, 1 ] <- mean( theta.sample )
    theta.out[ i, 2 ] <- sqrt( var( theta.sample ) / m )
  }
}
```
This function simulates, \(n \cdot \text{sim}\) times, the process of taking an IID sample of size \(m\) from the Beta(\(\alpha, \beta\)) distribution and calculating \(\bar{\theta}^*\) and \(\overline{SE}(\bar{\theta}^*)\).

```r
> m <- 100
> alpha <- 76.5
> beta <- 353.5
> n.sim <- 500
> seed <- c(6425451, 9626954)
> theta.out <- beta.sim(m, alpha, beta, n.sim, seed)
# This took about 0.2 second at 1.6 Unix GHz.
> theta.out[1:5,]
     [,1]      [,2]
[1,] 0.1756400 0.001854220
[2,] 0.1764806 0.001703780
[3,] 0.1781742 0.001979863
[4,] 0.1793588 0.002038532
[5,] 0.1781556 0.001596011
```
The $\bar{\theta}^*$ values fluctuate around the truth with a \textbf{give-or-take} of about 0.0018, which agrees well with the \textbf{theoretical SE} $\frac{\sigma}{\sqrt{m}} = \frac{0.0184}{\sqrt{100}} = 0.00184$ (the SD value 0.0184 comes from page 47 in Part 2).

```r
> theta.bar <- theta.out[, 1]
> qqnorm((theta.bar - mean(theta.bar)) / sd(theta.bar),
       xlab = "Quantiles of Standard Normal", main = "", pch = 20)
> abline(0, 1)
```

![Quantile-Quantile Plot](image-url)
IID Example (continued)

Each of the $\bar{\theta}^*$ values is the mean of $m = 100$ IID draws, so (by the CLT) the distribution of the random variable $\bar{\theta}^*$ should be closely approximated by a Gaussian, and you can see from the qqplot above that this is true.

```r
> truth <- alpha / ( alpha + beta )
> theta.bar.SE <- theta.out[, 2]
> sum( ( theta.bar - 1.96 * theta.bar.SE < truth ) *
> ( truth < theta.bar + 1.96 * theta.bar.SE ) ) / n.sim
> [1] 0.94
```

With this set of pseudo-random numbers, 94% of the nominal 95% Monte Carlo confidence intervals for the posterior mean included the truth.

Evidently frequentist ideas can be used to work out how big $m$ needs to be to have any desired Monte Carlo accuracy for $\bar{\theta}^*$ as an estimate of the posterior mean $E(\theta|y)$.

In practice, with $p(\theta|y)$ unknown, I would probably take an initial sample (in this case, of size $m = 100$) and look at the MCSE to decide how big $m$ really needs to be.
IID Example (continued)

Let’s say I ran the program with \( n\text{.sim} = 1 \) and \( m = 100 \) and got the following results:

\[
> \text{theta.bar} \leftarrow \text{beta.sim}(m, \alpha, \beta, 1, \text{seed})
\]

\[
> \text{theta.bar}
\]

\[
[,1] [,2]
[1,] 0.17564000 0.001854220
\]

(1) Suppose I wanted the MCSE of \( \bar{\theta}^* \) to be (say) \( \epsilon = 0.00005 \); then I could

solve the equation

\[
\frac{\hat{\sigma}}{\sqrt{m}} = \epsilon \quad \leftrightarrow \quad m = \frac{\hat{\sigma}^2}{\epsilon^2},
\]

which says (unhappily) that the required \( m \) goes up as the square of the posterior SD and as the inverse square of \( \epsilon \).

The program results above show that \( \frac{\hat{\sigma}}{\sqrt{100}} \doteq 0.001854220 \), from which

\( \hat{\sigma} \doteq 0.01854220 \), meaning that to get \( \epsilon = 0.00005 \) I need a sample of size

\[
\frac{0.01854220^2}{0.00005^2} \doteq 137,525 \doteq 138K.
\]
(2) Suppose instead that I wanted $\bar{\theta}^*$ to differ from the true posterior mean $\mu$ by no more than $\epsilon_1$ with Monte Carlo probability at least $(1 - \epsilon_2)$:

$$P(\lvert \bar{\theta}^* - \mu \rvert \leq \epsilon_1) \geq 1 - \epsilon_2,$$

where $P(\cdot)$ here is based on the (frequentist) Monte Carlo randomness inherent in $\bar{\theta}^*$.

I know from the CLT and the calculations above that in repeated sampling $\bar{\theta}^*$ is approximately Gaussian with mean $\mu$ and variance $\frac{\sigma^2}{m}$; this leads to the inequality

$$m \geq \frac{\sigma^2 \left[ \Phi^{-1}(1 - \frac{\epsilon_2}{2}) \right]^2}{\epsilon_1^2},$$

where $\Phi^{-1}(q)$ is the place on the standard normal curve where 100$q\%$ of the area is to the left of that place (the $q$th quantile of the standard Gaussian distribution).

(5) is like (3) except that the value of $m$ from (3) has to be multiplied by $\left[ \Phi^{-1}(1 - \frac{\epsilon_2}{2}) \right]^2$, which typically makes the required sample sizes even bigger.
A Closer Look at IID Sampling

For example, with $\epsilon_1 = 0.00005$ and $\epsilon_2 = 0.05$ — i.e., to have at least 95% Monte Carlo confidence that reporting the posterior mean as 0.1756 will be correct to about four significant figures — (5) says that I would need a monitoring run of at least $137,525(1.959964)^2 \div 528,296 \div 528K$.

This sounds like a long monitoring run but only takes about 2 seconds at 1.6 Unix GHz, yielding $\left[\hat{\theta}^*, \widehat{SE}(\hat{\theta}^*)\right] = (0.1779052, 0.00002)$, which compares favorably with the true value 0.1779070.

It’s evident from calculations like these that people often report simulation-based answers with numbers of significant figures far in excess of what’s justified by the actual accuracy of the Monte Carlo estimates.

A closer look at IID sampling. I was able to easily perform the above simulation study because R has a large variety of built-in functions like rbeta for pseudo-random-number generation.

How would I go about writing such functions myself?

There are a number of general-purpose methods for generating random numbers (I won’t attempt a survey here); the one we need to look closely at, to
Understand the algorithms that arise later in this part of the short course, is rejection sampling (von Neumann 1951), which is often one of the most computationally efficient ways to make IID draws from a distribution.

**Example.** Continuing the AMI mortality case study from Part 2, consider an alternative prior specification in which I’d like to put most (90%, say) of the prior mass in the interval (0.05, 0.50); calculations like those in Part 2 within the conjugate Beta family yield prior hyperparameter values of \((\alpha_0, \beta_0) = (2.0, 6.4)\) (this Beta distribution has prior mean and SD 0.24 and 0.14, respectively).

Suppose that the sample size \(n\) was smaller at 74, and \(s = 16\) AMI deaths were observed, so that the data mean was 0.216; the posterior is then

\[
\text{Beta}(\alpha_0 + s, \beta_0 + n - s) = \text{Beta}(18.0, 64.4).
\]

I’ll pretend for the sake of illustration of rejection sampling that I don’t know the formulas for the mean and SD of a Beta distribution, and suppose that I wanted to use IID Monte Carlo sampling from the \(\text{Beta}(\alpha_0 + s, \beta_0 + n - s)\) posterior to estimate the posterior mean.
Here’s von Neumann’s **basic idea**, which (as it turns out) works equally well for **scalar** or **vector** $\theta$: suppose the target density $p(\theta|y)$ is **difficult** to sample from, but you can find an integrable **envelope function** $G(\theta|y)$ such that

(a) $G$ **dominates** $p$ in the sense that $G(\theta|y) \geq p(\theta|y) \geq 0$ for all $\theta$ and

(b) the density $g$ obtained by normalizing $G$ — later to be called the **proposal distribution** — is easy and fast to sample from.

Then to get a **random draw** from $p$, make a draw $\theta^*$ from $g$ instead and **accept** or **reject** it according to an **acceptance probability** $\alpha_R(\theta^*|y)$; if you **reject** the draw, **repeat** this process until you accept.

von Neumann showed that the choice

$$\alpha_R(\theta^*|y) = \frac{p(\theta^*|y)}{G(\theta^*|y)}$$  (6)

**correctly** produces IID draws from $p$, and you can **intuitively** see that he’s right by the following argument.

Making a **draw** from the posterior distribution of interest is like choosing a
point at random (in two dimensions) under the density curve $p(\theta|y)$ in such a way that all possible points are equally likely, and then writing down its $\theta$ value.

If you instead draw from $G$ so that all points under $G$ are equally likely, to get correct draws from $p$ you’ll need to throw away any point that falls between $p$ and $G$, and this can be accomplished by accepting each sampled point $\theta^*$ with probability $\frac{p(\theta^*|y)}{G(\theta^*|y)}$, as von Neumann said.

A summary of this method is on the next page.

The figure two pages below demonstrates this method on the Beta(18.0, 64.4) density arising in the Beta-Bernoulli example above.

Rejection sampling permits considerable flexibility in the choice of envelope function; here, borrowing an idea from Gilks and Wild (1992), I’ve noted that the relevant Beta density is log concave (a real-valued function is log concave if its second derivative on the log scale is everywhere non-positive), meaning that it’s easy to construct an envelope on that scale in a piecewise linear fashion, by choosing points on the log density and constructing
Algorithm (rejection sampling). To make \( m \) draws at random from the density \( p(\theta|y) \) for scalar or vector \( \theta \), select an integrable envelope function \( G \) — which when normalized to integrate to 1 is the proposal distribution \( g \) — such that \( G(\theta|y) \geq p(\theta|y) \geq 0 \) for all \( \theta \); define the acceptance probability
\[
\alpha_{R}(\theta^{*}|y) = \frac{p(\theta^{*}|y)}{G(\theta^{*}|y)};
\]
and

Initialize \( t \leftarrow 0 \)

Repeat \{
    Sample \( \theta^{*} \sim g(\theta|y) \)
    Sample \( u \sim \text{Uniform}(0, 1) \)
    If \( u \leq \alpha_{R}(\theta^{*}|y) \) then
        \{ \( \theta_{t+1} \leftarrow \theta^{*}; \ t \leftarrow (t + 1) \) \}
\}
until \( t = m \).

Tangents to the curve at those points.

The simplest possible such envelope involves two line segments, one on either side of the mode.
The optimal choice of the tangent points would maximize the marginal probability of acceptance of a draw in the rejection algorithm, which can be shown to be
Rejection Sampling (continued)

\[
\left[ \int G(\theta) \, d\theta \right]^{-1} ;
\]

in other words, you should **minimize** the area under the (un-normalized) envelope function subject to the constraint that it **dominates** the target density \(p(\theta|y)\) (which makes eminently good sense).

Here this optimum turns out to be attained by locating the two tangent points at about 0.17 and 0.26, as in the figure above; the resulting acceptance probability of about 0.75 could clearly be **improved** by adding more tangents.

**Piecewise linear** envelope functions on the log scale are a **good choice** because the resulting envelope density on the raw scale is a piecewise set of **scaled exponential distributions** (see the bottom panel in the figure above), from which random samples can be taken easily and **quickly**.

A **preliminary** sample of \(m_0 = 500\) IID draws from the Beta(18.0, 64.4) distribution using the above rejection sampling method yields \(\hat{\theta}^* = 0.2197\) and \(\hat{\sigma} = 0.04505\), meaning that the posterior mean has already been estimated with an **MCSE** of only \(\frac{\hat{\sigma}}{\sqrt{m_0}} = 0.002\) even with just 500 draws.
Suppose, however, that — as in equation (4) above — I want $\bar{\theta}^*$ to differ from the true posterior mean $\mu$ by no more than some (perhaps even smaller) tolerance $\epsilon_1$ with Monte Carlo probability at least $(1 - \epsilon_2)$; then equation (5) tells me how long to monitor the simulation output.

For instance, to pin down three significant figures (sigfigs) in the posterior mean in this example with high Monte Carlo accuracy I might take $\epsilon_1 = 0.0005$ and $\epsilon_2 = 0.05$, which yields a recommended IID sample size of

$$\frac{(0.04505^2)(1.96)^2}{0.0005^2} \approx 31,200.$$

So I take another sample of 30,700 (which is virtually instantaneous at 1.6 Unix GHz) and merge it with the 500 draws I already have; this yields $\bar{\theta}^* = 0.21827$ and $\hat{\sigma} = 0.04528$, meaning that the MCSE of this estimate of $\mu$ is

$$\frac{0.04528}{\sqrt{31200}} \approx 0.00026.$$

I might announce that I think $E(\theta|y)$ is about 0.2183, give or take about 0.0003, which accords well with the true value 0.2184.

Of course, other aspects of $p(\theta|y)$ are equally easy to monitor; for example, if I want a Monte Carlo estimate of $p(\theta \leq q|y)$ for some $q$, as noted above I just work out the proportion of the sampled $\theta^*$ values that are no larger than $q$. 
Beyond Rejection Sampling

Or, even better, I recall that $P(A) = E[I(A)]$ for any event or proposition $A$, so to the Monte Carlo dataset (see page 35 below) consisting of 31,200 rows and one column (the $\theta^*_t$) I add a column monitoring the values of the derived variable which is 1 whenever $\theta^*_t \leq q$ and 0 otherwise; the mean of this derived variable is the Monte Carlo estimate of $p(\theta \leq q|y)$, and I can attach an MCSE to it in the same way I did with $\bar{\theta}^*$.  

By this approach, for instance, the Monte Carlo estimate of $p(\theta \leq 0.15|y)$ based on the 31,200 draws examined above comes out $\hat{p} = 0.0556$ with an MCSE of $0.0013$.

Percentiles are typically harder to pin down with equal Monte Carlo accuracy (in terms of sigfigs) than means or SDs, because the 0/1 scale on which they’re based is less information-rich than the $\theta^*$ scale itself; if I wanted an MCSE for $\hat{p}$ of 0.0001 I would need an IID sample of more than 5 million draws (which would still only take a few seconds at contemporary workstation speeds).

IID sampling is not necessary. Nothing in the Metropolis-Ulam idea of
Monte Carlo estimates of posterior summaries requires that these estimates be based on **IID samples from the posterior**.

This is lucky, because in practice it’s often difficult, particularly when $\theta$ is a **vector of high dimension** (say $k$), to figure out how to make such an IID sample, via rejection sampling or other methods (e.g., imagine trying to find an **envelope function** for $p(\theta|y)$ when $k$ is 10 or 100 or **1,000**).

Thus it’s necessary to **relax** the assumption that $\theta_j^* \sim p(\theta|y)$, and to consider samples $\theta_1^*, \ldots, \theta_m^*$ that form a **time series**: a series of draws from $p(\theta|y)$ in which $\theta_j^*$ may **depend on** $\theta_j^*$, for $j' < j$.

In their pioneering paper Metropolis et al. (1953) allowed for **serial dependence** of the $\theta_j^*$ by combining von Neumann’s idea of rejection sampling (which had itself only been published a few years earlier in 1951) with concepts from **Markov chains**, a subject in the theory of **stochastic processes**.

Combining **Monte Carlo sampling** with **Markov chains** gives rise to the name now used for this technique for solving the Bayesian high-dimensional integration problem: **Markov chain Monte Carlo** (MCMC).
3.3 Brief Review of Markov Chains

**Markov chains.** A stochastic process is just a collection of random variables \( \{\theta_t^*, t \in T\} \) for some index set \( T \), usually meant to stand for time.

In practice \( T \) can be either discrete, e.g., \( \{0, 1, \ldots \} \), or continuous, e.g., \( [0, \infty) \).

Markov chains are a special kind of stochastic process that can either unfold in discrete or continuous time — I’ll talk here about discrete-time Markov chains, which is all you need for MCMC.

The possible values that a stochastic process can take on are collectively called the state space \( S \) of the process — in the simplest case \( S \) is real-valued and can also either be discrete or continuous.

Intuitively speaking, a Markov chain (e.g., Feller, 1968; Roberts, 1996; Gamerman, 1997) is a stochastic process evolving in time in such a way that the past and future states of the process are independent given the present state—in other words, to figure out where the chain is likely to go next you don’t need to pay attention to where it’s been, you just need to consider where it is now.
More formally, a stochastic process \( \{\theta_t^*, t \in T\} \), \( T = \{0, 1, \ldots\} \), with state space \( S \) is a **Markov chain** if, for any set \( A \in S \),

\[
P(\theta^*_{t+1} \in A | \theta^*_0, \ldots, \theta^*_t) = P(\theta^*_{t+1} \in A | \theta^*_t). \tag{8}
\]

The theory of Markov chains is **harder mathematically** if \( S \) is continuous (e.g., Tierney, 1996), which is what we need for MCMC with real-valued parameters, but **most of the main ideas emerge with discrete state spaces**, and I’ll assume discrete \( S \) in the intuitive discussion here.

**Example.** For a simple example of a **discrete-time Markov chain** with a **discrete state space**, imagine a **particle** that moves around on the integers \( \{\ldots, -2, -1, 0, 1, 2, \ldots\} \), starting at 0 (say).

Wherever it finds itself at time \( t \)—say at \( i \)—it **tosses a (3-sided) coin** and moves to \( (i - 1) \) with probability \( p_1 \), stays at \( i \) with probability \( p_2 \), and moves to \( (i + 1) \) with probability \( p_3 \), for some \( 0 < p_1, p_2, p_3 < 1 \) with \( p_1 + p_2 + p_3 = 1 \)—these are the **transition probabilities** for the process.

This is a **random walk** (on the integers), and it’s **clearly a Markov chain**.
Markov Chains (continued)

**Nice behavior.** The most *nicely-behaved* Markov chains satisfy three properties:

- They’re **irreducible**, which basically means that no matter where it starts the chain has to be able to reach any other state in a finite number of iterations with positive probability;

- They’re **aperiodic**, meaning that for all states $i$ the set of possible sojourn times, to get back to $i$ having just left it, can have no divisor bigger than 1 (this is a *technical* condition; periodic chains still have some nice properties, but the nicest chains are aperiodic).

- They’re **positive recurrent**, meaning that (a) for all states $i$, if the process starts at $i$ it will return to $i$ with probability 1, and (b) the expected length of waiting time til the first return to $i$ is finite.

Notice that this is a bit delicate: wherever the chain is now, we insist that it **must certainly come back here**, but we don’t expect to have to **wait forever** for this to happen.
The random walk defined above is clearly **irreducible** and **aperiodic**, but it may not be **positive recurrent** (depending on the $p_i$): it’s true that it has positive probability of returning to wherever it started, but (because $S$ is **unbounded**) this probability may not be 1, and on average you may have to wait forever for it to return.

We can fix this by **bounding** $S$: suppose instead that

$$S = \{-k, -(k-1), \ldots, -1, 0, 1, \ldots, k\},$$

keeping the same transition probabilities except **rejecting** any moves **outside the boundaries** of $S$.

This bounded random walk now satisfies **all three of the nice properties**.

**The value of nice behavior.** Imagine running the bounded random walk for a long time, and look at the **distribution** of the **states** it visits—over time this distribution should **settle down** (converge) to a kind of limiting, **steady-state** behavior.

This can be demonstrated by **simulation**, for instance in R, and using the **bounded random walk** as an example:
Markov Chains (continued)

```r
rw.sim <- function(k, p, theta.start, n.sim, seed) {
  set.seed(seed)
  theta <- rep(0, n.sim + 1)
  theta[1] <- theta.start
  for (i in 1:n.sim) {
    theta[i + 1] <- move(k, p, theta[i])
  }
  return(table(theta))
}
move <- function(k, p, theta) {
  repeat {
    increment <- sample(x = c(-1, 0, 1), size = 1, prob = p)
    theta.next <- theta + increment
    if (abs(theta.next) <= k) {
      return(theta.next)
      break
    }
  }
}
```

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```r
greco 171> R
R version 2.5.1 (2007-06-27)
Copyright (C) 2007 The R Foundation for Statistical Computing
> p <- c( 1, 1, 1 ) / 3
> k <- 5
> theta.start <- 0
> seed <- c( 6425451, 9626954 )
> rw.sim( k, p, theta.start, 10, seed )
theta
 0 1 2
5 5 1
> rw.sim( k, p, theta.start, 100, seed )
-2 -1  0  1  2  3  4  5
 7  9 16 17 23 14  8  7
> rw.sim( k, p, theta.start, 1000, seed )
-5 -4 -3 -2 -1  0  1  2  3  4  5
65 115 123 157 148 123 106  82  46  21  15
> rw.sim( k, p, theta.start, 10000, seed )
-5 -4 -3 -2 -1  0  1  2  3  4  5
581  877  941  976  959 1034 1009  982 1002  959  681
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Markov Chains (continued)

You can see that the distribution of where the chain has visited is **converging** to something close to **uniform** on \(-5, -4, \ldots, 4, 5\), except for the effects of the **boundaries**.

Letting \(q_1\) denote the **limiting** probability of being in one of the 9 **non-boundary** states \((-4, -3, \ldots, 3, 4)\) and \(q_2\) be the **long-run** probability of being in one of the 2 **boundary** states \((-5, 5)\), on grounds of **symmetry** you can guess that \(q_1\) and \(q_2\) should satisfy

\[
9q_1 + 2q_2 = 1 \quad \text{and} \quad q_1 = \frac{3}{2} q_2, \quad (9)
\]

from which \((q_1, q_2) = (\frac{3}{31}, \frac{2}{31}) \equiv (0.096774, 0.064516)\).

Based on the run of **1,000,001 iterations** above you would estimate these
probabilities \textit{empirically} as
\[
\left[ \frac{98535 + \ldots + 95703}{9(1000001)}, \frac{65273 + 63767}{2(1000001)} \right] \approx (0.096773, 0.064520).
\]

It should also be clear that the limiting distribution \textbf{does not depend} on the initial value of the chain:

\begin{verbatim}
> rw.sim( k, p, 5, 100000, seed )
-5  -4  -3  -2  -1   0   1   2   3   4   5
6515 9879 9876 9624 9374 9705 9959 9738 9678 9365 6288
\end{verbatim}

Of course, you get a \textbf{different limiting distribution} with a \textbf{different choice} of \((p_1, p_2, p_3)\):

\begin{verbatim}
> p <- c( 0.2, 0.3, 0.5 )
> rw.sim( k, p, 0, 10, seed )
0 1 2 3
1 3 4 3
> rw.sim( k, p, 0, 100, seed )
0 1 2 3 4 5
1 3 6 13 30 48
\end{verbatim}
Stationary distributions. A positive recurrent and aperiodic chain is called ergodic, and it turns out that such chains possess a unique stationary (or equilibrium, or invariant) distribution $\pi$, characterized by the relation

$$\pi(j) = \sum_i \pi(i) P_{ij}(t)$$  \hspace{1cm} (10)$$

for all states $j$ and times $t \geq 0$, where $P_{ij}(t) = P(\theta_t^* = j|\theta_{t-1}^* = i)$ is the transition matrix of the chain.
The MCMC Payoff

Informally, the stationary distribution characterizes the behavior that the chain will settle into after it’s been run for a long time, regardless of its initial state.

The point of all of this. Given a parameter vector $\theta$ and a data vector $y$, the Metropolis et al. (1953) idea is to simulate random draws from the posterior distribution $p(\theta|y)$, by constructing a Markov chain with the following four properties:

- It should have the same state space as $\theta$,
- It should be easy to simulate from,
- It should work equally well with an un-normalized $p(\theta|y)$, so that it’s not necessary to evaluate the normalizing constant, and
- Its equilibrium distribution should be $p(\theta|y)$.

If you can do this, you can run the Markov chain for a long time, generating a huge sample from the posterior, and then use simple descriptive summaries (means, SDs, correlations, histograms or kernel density estimates) to extract any features of the posterior you want.
The Ergodic Theorem

The mathematical fact that underpins this strategy is the ergodic theorem: if the Markov chain \( \{\theta_t^*\} \) is ergodic and \( f \) is any real-valued function for which
\[
E_\pi |f(\theta)| \text{ is finite, then with probability 1 as } m \to \infty
\]
\[
\frac{1}{m} \sum_{t=1}^{m} f(\theta_t^*) \to E_\pi [f(\theta)] = \sum_i f(i) \pi(i),
\]
(11)
in which the right side is just the expectation of \( f(\theta) \) under the stationary distribution \( \pi \).

In plain English this means that — as long as the stationary distribution is \( p(\theta|y) \) — you can learn (to arbitrary accuracy) about things like posterior means, SDs, and so on just by waiting for stationarity to kick in and monitoring thereafter for a long enough period.

Of course, as Roberts (1996) notes, the theorem is silent on the two key practical questions it raises: how long you have to wait for stationarity, and how long to monitor after that.

A third practical issue is what to use for the initial value \( \theta_0^* \): intuitively the
The Monte Carlo and MCMC Datasets

closer $\theta_0^*$ is to the center of $p(\theta|y)$ the less time you should have to wait for stationarity.

The standard way to deal with waiting for stationarity is to (a) run the chain from a good starting value $\theta_0^*$ for $b$ iterations, until equilibrium has been reached, and (b) discard this initial burn-in period.

All of this motivates the topic of MCMC diagnostics, which are intended to answer the following questions:

- What should I use for the initial value $\theta_0^*$?

- How do I know when I’ve reached equilibrium? (This is equivalent to asking how big $b$ should be.)

- Once I’ve reached equilibrium, how big should $m$ be, i.e., how long should I monitor the chain to get posterior summaries with decent accuracy?

The Monte Carlo and MCMC datasets. The basis of the Monte Carlo approach to obtaining numerical approximations to posterior summaries like means and SDs is the (weak) Law of Large Numbers: with IID sampling
the Monte Carlo estimates of the true summaries of \( p(\theta|y) \) are consistent, meaning that they can be made arbitrarily close to the truth with arbitrarily high probability as the number of monitoring iterations \( m \to \infty \).

Before we look at how Metropolis et al. attempted to achieve the same goal with a non-IID Monte Carlo approach, let’s look at the practical consequences of switching from IID to Markovian sampling.

Running the IID rejection sampler on the AMI mortality example above for a total of \( m \) monitoring iterations would produce something that might be called the Monte Carlo (MC) dataset, with one row for each iteration and one column for each monitored quantity; in that example it might look like the table on the next page (MCSEs in parenthesis).

Running the Metropolis sampler on the same example would produce something that might be called the MCMC dataset.

It would have a similar structure as far as the columns are concerned, but the rows would be divided into three phases:

- Iteration 0 would be the value(s) used to initialize the Markov chain;
The MC and MCMC Data Sets

The MC Data Set:

<table>
<thead>
<tr>
<th>Iteration</th>
<th>$\theta$</th>
<th>$I(\theta \leq 0.15)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>$\theta_1^* = 0.244$</td>
<td>$I_1^* = 0$</td>
</tr>
<tr>
<td>2</td>
<td>$\theta_2^* = 0.137$</td>
<td>$I_2^* = 1$</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>$m = 31, 200$</td>
<td>$\theta_m^* = 0.320$</td>
<td>$I_m^* = 0$</td>
</tr>
<tr>
<td>Mean</td>
<td>0.2183 (0.003)</td>
<td>0.0556 (0.0013)</td>
</tr>
<tr>
<td>SD</td>
<td>0.04528</td>
<td>—</td>
</tr>
<tr>
<td>Density</td>
<td>(like the bottom Trace plot on page 17)</td>
<td>—</td>
</tr>
</tbody>
</table>

- Iterations 1 through $b$ would be the **burn-in** period, during which the chain reaches its **equilibrium** or **stationary** distribution (as mentioned above, iterations 0 through $b$ are generally **discarded**); and

- Iterations $(b + 1)$ through $(b + m)$ would be the **monitoring** run, on which **summaries** of the posterior (means, SDs, density traces, ...) will be based.
A Metropolis Example \((k = 1)\)

Here’s an example that can serve as the basis of a fairly general strategy for Metropolis sampling when the unknown \(\theta\) is a vector of real numbers of length \(k \geq 1\); I’ll first give details in a situation with \(k = 1\), and then we’ll look at how to generalize this to \(k > 1\).

**Example:** The setup is one-sample Gaussian data with known \(\mu\), unknown \(\theta = \sigma^2\), and little information about \(\theta\) external to the data set \(y = (y_1, \ldots, y_n)\):

\[
\begin{align*}
\sigma^2 & \sim \text{diffuse} \\
(y_i|\sigma^2) & \stackrel{\text{IID}}{\sim} N(\mu, \sigma^2) \quad (i = 1, \ldots, n).
\end{align*}
\]  

The joint sampling distribution is

\[
p(y|\sigma^2) = \prod_{i=1}^{n} \frac{1}{\sigma \sqrt{2\pi}} \exp \left[ -\frac{1}{2\sigma^2} (y_i - \mu)^2 \right] \\
= c(\sigma^2)^{-\frac{n}{2}} \exp \left[ -\frac{1}{2\sigma^2} \sum_{i=1}^{n} (y_i - \mu)^2 \right].
\]  

(13)
In homework 3 you showed that the MLE for $\sigma^2$ in this model is

$$\hat{\sigma}^2 = \frac{1}{n} \sum_{i=1}^{n} (y_i - \mu)^2,$$ \hspace{1cm} (14)

so that the joint sampling distribution can also be written as

$$p(y|\sigma^2) = c (\sigma^2)^{-\frac{n}{2}} \exp\left[-\frac{n}{2} \frac{\hat{\sigma}^2}{\sigma^2}\right];$$ \hspace{1cm} (15)

in the alternative parameterization $\theta = \sigma^2$ this is

$$p(y|\theta) = c \theta^{-\frac{n}{2}} \exp\left[-\frac{n}{2} \frac{\hat{\sigma}^2}{\theta}\right].$$ \hspace{1cm} (16)

Now Metropolis sampling is based on a symmetric proposal distribution, and $\theta$ lives on the positive part of the real line; if you use a symmetric proposal distribution on $\theta$, you’ll have to reject any proposed moves below 0, and this can be Monte-Carlo inefficient.

An easy way to solve this problem is to propose moves not on $\theta$ but on a transformed version of $\theta$ that lives on the whole real line; the obvious candidate is $\lambda = \log \theta$, so that $\theta = e^\lambda$. 


Need the Prior on the Transformed Parameter

In this parameterization the sampling distribution (16) is

\[ p(y|\lambda) = c e^{-\frac{n\lambda}{2}} \exp\left[-\frac{n \hat{\sigma}^2}{2 e^\lambda}\right] \]  

(17)

(just substitute \( e^\lambda \) everywhere you see \( \theta \)), so that the likelihood function in terms of \( \lambda \) is also

\[ l(\lambda|y) = c e^{-\frac{n\lambda}{2}} \exp\left[-\frac{n \hat{\sigma}^2}{2 e^\lambda}\right] ; \]  

(18)

thus the log likelihood in this parameterization is

\[ ll(\lambda|y) = c - \frac{n \lambda}{2} - \frac{n \hat{\sigma}^2}{2 e^\lambda} . \]  

(19)

From Bayes’s Theorem,

\[ \log p(\lambda|y) = c + \log p(\lambda) + ll(\lambda|y) , \]  

(20)

so to define the log posterior analytically we need to work out the prior for \( \lambda \) that’s implied (from the change of variables formula) by a suitably-chosen diffuse prior for \( \theta \).
Need the Change-of-Variables Formula For the Prior

In homework 3 I mentioned that a **popular diffuse prior** for \( \theta = \sigma^2 \) in this setup is the **improper prior**

\[
p(\theta) = c \theta^{-1};
\]  

(21)

let’s see what this **corresponds to** as a prior on \( \lambda = \log \theta \).

A **quick way** to use the **change-of-variables formula** is through the expression

\[
p(\theta) |d\theta| = p(\lambda) |d\lambda|, \quad \text{from which} \quad p(\lambda) = p(\theta) \left| \frac{d\theta}{d\lambda} \right|.
\]  

(22)

Now **in this case** \( \theta = e^\lambda \), so that \( \left| \frac{d\theta}{d\lambda} \right| = e^\lambda \), and (in terms of \( \lambda \))

\[
p(\theta) = c \theta^{-1} = c (e^\lambda)^{-1} = c e^{-\lambda}, \quad \text{so that}
\]

\[
p(\lambda) = c \theta^{-1} e^\lambda = c e^{-\lambda} e^\lambda = c.
\]  

(23)

Thus we see why this is a **popular diffuse prior** for \( \theta = \sigma^2 \): it corresponds to the **(improper) uniform prior** on \((-\infty, \infty)\) for \( \lambda = \log \theta \) (which is a **natural choice for diffuseness** on the log \( \theta \) scale).
Random-Walk Metropolis, With a Tuning Constant

Now I’m ready to think about what to use for my symmetric proposal distribution \( g(\theta^*|\theta_t, y) \). which tells me how to sample a value \( \theta^* \) as a possible place for the Markov chain to go next, given that it’s currently at \( \theta_t \); symmetry here means that \( g(\theta^*|\theta_t, y) = g(\theta_t|\theta^*, y) \).

A choice that’s simultaneously simple and reasonably Monte-Carlo efficient is what people call random-walk Metropolis: I’ll center the proposal distribution at where I am now \((\theta_t)\), and then make a draw from a distribution that’s symmetric about that point.

Metropolis et al. (1953) used the uniform distribution \( U(\theta_t - c, \theta_t + c) \); these days people tend to use a Gaussian distribution \( N(\theta_t, \sigma_*^2) \); in both cases \( c \) and \( \sigma_* \) are tuning constants, which we can choose to optimize the Monte Carlo efficiency of the resulting Metropolis sampler.

Let’s call \( \sigma_* \) the proposal distribution standard deviation (PDSD); with that convention I’m ready to write R code to implement the algorithm.

I’ll need a driver function that does the sampling and generates the MCMC data set; this will depend on a function that calculates
the **acceptance probabilities**; this will in turn depend on a **function** to calculate the **log posterior**; and this will finally depend on functions to calculate the log prior and log likelihood.

```r
metropolis.example <- function( y, mu, sigma.star, sigma2.0, M, B ) {
  n <- length( y )
  sigma2.hat <- sum( ( y - mu )^2 ) / n
  lambda.hat <- log( sigma2.hat )
  mcmc.data.set <- matrix( NA, M + B + 1, 2 )
  mcmc.data.set[1,] <- c( log(sigma2.0), sigma2.0 )
  acceptance.count <- 0
  for( i in 2:( M + B + 1 ) ) {
    lambda.current <- mcmc.data.set[ i - 1, 1 ]
    lambda.star <- rnorm( 1, lambda.current, sigma.star )
    u <- runif( 1 )
    if ( u <= acceptance.probability( lambda.star, lambda.current, lambda.hat, n ) ) {
      mcmc.data.set[ i, 1 ] <- lambda.star
      mcmc.data.set[ i, 2 ] <- exp( lambda.star )
      acceptance.count <- acceptance.count + 1
    }
  }
}
```
else {
    mcmc.data.set[ i, 1 ] <- lambda.current
    mcmc.data.set[ i, 2 ] <- exp( lambda.current )
}
if ( ( i %% 1000 ) == 0 ) print( i )

print( acceptance.rate <- acceptance.count / ( M + B ) )
return( mcmc.data.set )

acceptance.probability <- function( lambda.star, lambda.current, lambda.hat, n ) {
    return( exp( log.posterior( lambda.star, lambda.hat, n ) - log.posterior( lambda.current, lambda.hat, n ) ) )
}

log.posterior <- function( lambda, lambda.hat, n ) {
    return( log.prior( lambda ) + log.likelihood( lambda, lambda.hat, n ) )
}
log.likelihood <- function( lambda, lambda.hat, n ) {
    return( -lambda * n / 2 - n * exp( lambda.hat ) /
            ( 2 * exp( lambda ) ) )
}

log.prior <- function( lambda ) {
    return( 0 )
}

Let’s run this code on the NB10 data, (for illustration) taking \( \mu \) to be the sample mean \( \bar{y} \):

\[
        406., 409., 400., 408., 404., 401., 404., 408., 406., 408., 406., 401.,
        406., 398., 406., 403., 404. )
\]
Choosing the PDSD

```r
print( mu <- mean(y) )
[1] 404.59
print( sigma2.0 <- var(y) )
[1] 41.8201
M <- 100000
B <- 500
```

Now I need to choose a **PDSD** \( \sigma_* \): if I know something about the **scale** of the **posterior** I’m sampling from — e.g., if I’ve computed \( \hat{\sigma}(\hat{\theta}_{MLE}) \) — I can use this to set the **initial PDSD** intelligently (it’s been shown that with \( k = 1 \) the **optimal PDSD** when the posterior is **approximately** Gaussian is \( \sigma_* = 2.4 \sigma_\theta \), where \( \sigma_\theta \) is the **posterior SD** for \( \theta \)), but if I don’t know about the **scale** of \( p(\theta|y) \) I can use **trial and error** and **tune the sampler** to have a **good acceptance rate** (it’s also been shown that with \( k = 1 \) the **optimal acceptance rate** is about 44%).

I’ll start **out** with \( \sigma_* = 1.0 \) and see what the **acceptance rate** is:

```r
sigma.star <- 1
mcmc.data.set.1 <- metropolis.example( y, mu, sigma.star, sigma2.0, M, B )
[1] 0.1747861
```
Blocky Output: PDSD Too Big (Acceptance Rate Too Low)

This took about **26 sec** at **1.6 Unix GHz** and produced the following posterior summaries:

```r
mean(mcmc.data.set.1[, 2])
[1] 42.19285
sd(mcmc.data.set.1[, 2])
[1] 6.038515
plot(1:100, mcmc.data.set.1[1:100, 2], type='l',
     xlab = 'Iteration Number', ylab = 'Draws From p(\sigma^2 | y)')
```

This output is **blocky**: the PDSD is **too big** and the acceptance rate is **too low**.
Demonstrating the Validity of the Sampler

In this problem we know the right answer for the posterior —
\( (\sigma^2|y) \sim \chi^{-2}(n, \hat{\sigma}^2) \) — so we can use this to demonstrate the validity of the Metropolis sampler:

```r
rsichi2 <- function(n, nu, s2) {
  return(nu * s2 / rchisq(n, nu))
}
n <- 100
print(sigma2.hat <- (n - 1) * var(y) / n)
[1] 41.4019
direct.simulation <- rsichi2(100000, 100, 41.4019)
n * sigma2.hat / (n - 2)
[1] 42.24684
qqplot(mcmc.data.set.1[,2], backup, xlab = 'MCMC Draws',
  ylab = 'Scaled Inverse Chi Square Draws')
abline(0, 1)
```

The MCMC posterior mean is correct up to Monte-Carlo noise in the third significant figure, and the qqplot shows that we’re sampling from the right distribution:
(The discrepancy in the right tail is just Monte-Carlo noise, as you can verify by (a) sampling twice with the rchisq function, (b) making a qqplot of the resulting two samples, and (c) repeating (a) and (b) a few times.)
Sticky Output: PDSD Too Small (Acceptance Rate Too Big)

For illustration, here’s what happens with a Metropolis sampler when the PDSD is too small:

```
sigma.star <- 0.05
mcmc.data.set.2 <- metropolis.example( y, mu, sigma.star, sigma2.0, M, B )
[1] 0.8869552
plot( 1:100, mcmc.data.set.2[ 1:100, 2 ], type = 'l',
   xlab = 'Iteration Number', ylab = 'Draws From p(\sigma^2 | y)' )
```

Now the acceptance rate is too high, and the sampler output is sticky:
Optimized Random-Walk Metropolis Sampler

We can use the result mentioned above to optimize this process: using a random-walk Metropolis sampler with a Gaussian proposal distribution and an approximately Gaussian target distribution, to get the optimal acceptance rate of about 44% the PDSD (on the scale on which the moves are made, which here is the log(θ) scale) should be about 2.4 times bigger than the posterior SD:

\[ 2.4 \times \text{sd}( \text{mcmc.data.set.1[,1]} ) \]

\[
\begin{array}{l}
\text{sigma.star} <- 0.34 \\
\text{mcmc.data.set.3} <- \text{metropolis.example( y, mu, sigma.star, sigma2.0, M, B )} \\
\text{plot( 1:100, mcmc.data.set.3[1:100,2], type = 'l',} \\
\text{ xlab = 'Iteration Number', ylab = 'Draws From p( sigma^2 | y )'})
\end{array}
\]

The resulting time series (on the next page) is the best we can do in this class of Metropolis samplers for this problem; as MCMC output goes, this plot actually shows pretty good mixing of the Markov chain (there are relatively few flat spots, and the output is not as sticky as it was with \( \sigma_* = 0.05 \)).
A useful graphical diagnostic for each monitored quantity $\theta_j$ in $\theta = (\theta_1, \ldots, \theta_k)$ is a picture that might be called an MCMC 4–plot, containing

(a) a time series plot of the $\theta_j^*$ values;
(b) a density trace of the $\theta_j^*$ output, which is an estimate of $p(\theta_j|y)$;
(c) a plot of the autocorrelation function (ACF) of the $\theta_j^*$ values; and
(d) a plot of the **partial autocorrelation function** (PACF) of the $\theta_j^*$ output (see the **portrait version** of chapter 3 of the lecture notes for details on the **ACF** and **PACF**).

Here’s some R code for the **MCMC 4–plot** for the **output** of the **sampler** with $\sigma_*=1.0$:

```r
par( mfrow = c( 2, 2 ) )
plot( 1:( M + B + 1 ), mcmc.data.set.1[, 2 ], type = 'l',
    xlab = 'Iteration Number', ylab = 'Draws from p ( sigma^2 | y )',
    main = 'sigma.star = 1.0' )
plot( density( mcmc.data.set.1[, 2 ], adjust = 2 ), xlab = 'sigma^2',
    ylab = 'Density', main = '' )
acf( mcmc.data.set.1[, 2 ], main = '' )
pacf( mcmc.data.set.1[, 2 ], main = '' )
```

The **plots** on the next page **reveal** the following:

- the **time series plot** exhibits **stationarity**;
- the **density trace** looks like You would **expect** it to, for a **posterior** distribution for a **variance**;
the \textbf{PACF} diagnoses this \textbf{output} as that of an \textit{AR$_1$} process with a first-order autocorrelation of about $\hat{\rho}_1 \doteq 0.8$, and

- this is \textbf{consistent} with the \textbf{behavior} of the \textbf{ACF}.
Poor Mixing Shows Up in the 4–Plot

\[
\text{sigma.star} = 0.05
\]

With \( \sigma_* = 0.05 \) the **mixing** is even worse than with \( \sigma_* = 1.0 \): the **first-order autocorrelation** is now about \( \hat{\rho}_1 \approx 0.95 \).
Even with the best-possible $\sigma_* \doteq 0.34$ (for this random-walk Metropolis sampler with a Gaussian proposal distribution on log $\theta$), the first-order autocorrelation is still about $\hat{\rho}_1 \doteq 0.6$. 

Even the Optimal Sampler Has $\hat{\rho}_1 \doteq 0.6$
With **commands** like the following for **all three output series** —

```r
print( rho.1 <- acf( mcmc.data.set.1[, 2], plot = F )$acf[ 2 ] )
print( posterior.mean.1 <- mean( mcmc.data.set.1[, 2] ) )
print( posterior.sd.1 <- sd( mcmc.data.set.1[, 2] ) )
print( MCSE.1 <- ( posterior.sd.1 / sqrt( M ) ) *
    sqrt( ( 1 + rho.1 ) / ( 1 - rho.1 ) ) )
print( correct.posterior.mean <- sigma2.hat * n / ( n - 2 ) )
print( correct.posterior.sd <- sigma2.hat * sqrt( 2 * n^2 /
    ( ( n - 2 )^2 * ( n - 4 ) ) ) )
```

— you can **make** the following **table**:

<table>
<thead>
<tr>
<th>PDSD</th>
<th>Acceptance Rate</th>
<th>Posterior Mean</th>
<th>MCSE of Posterior Mean</th>
<th>Posterior SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.05</td>
<td>0.89</td>
<td>42.3</td>
<td>0.124</td>
<td>6.09</td>
</tr>
<tr>
<td>0.34</td>
<td>0.44</td>
<td>42.2</td>
<td>0.041</td>
<td>6.10</td>
</tr>
<tr>
<td>1.00</td>
<td>0.18</td>
<td>42.2</td>
<td>0.055</td>
<td>6.04</td>
</tr>
</tbody>
</table>

The **correct** posterior mean and **SD** are **42.25** and **6.097** (respectively).
Gibbs Sampling

Note that the MCSE for $\sigma_*=0.05$ is $\frac{0.124}{0.041} = 3.05$ times bigger than for $\sigma_*=0.34$, so that the $\sigma_*=0.05$ sampler would require $3.05^2 = 9.3$ times more monitoring iterations to get the same accuracy.

As discussed in the portrait version of chapter 3 of these lecture notes, when the goal is summarization (via MCMC) of a posterior distribution $p(\theta_1, \ldots, \theta_k|y)$ for $k > 1$, you have a fair amount of flexibility: you can update all the components of $\theta$ simultaneously with a $k$-dimensional proposal distribution, or you can update them one at a time (single-scan MCMC), or you can block-update some of them simultaneously and others one at a time (the basic rule is: always use the most recent version of anything that’s not currently being updated).

Gibbs sampling is a special case of Metropolis-Hastings sampling in which (a) the proposal distribution for $\theta_j$ is the full-conditional distribution $p(\theta_j|\theta_{-j}, y)$ and (b) with this choice you accept all proposed moves; let’s see an example in action.
Gibbs Sampling in the Gaussian Model

**Gibbs sampling example.** In the Gaussian sampling model with both parameters unknown, we saw in Chapter 2 that the conjugate model was (for \( i = 1, \ldots, n \))

\[
\begin{align*}
\sigma^2 & \sim \text{SI-}\chi^2(\nu_0, \sigma_0^2) \\
(\mu|\sigma^2) & \sim N\left(\mu_0, \frac{\sigma^2}{\kappa_0}\right) \\
(y_i|\mu, \sigma^2) & \overset{\text{IID}}{\sim} N(\mu, \sigma^2),
\end{align*}
\]

and the full conditionals for this model were shown (in the portrait version of Chapter 3) to be

\[
\begin{align*}
(\mu|\sigma^2, y) & \sim N\left(\frac{\kappa_0 \mu_0 + n \bar{y}}{\kappa_0 + n}, \frac{\sigma^2}{\kappa_0 + n}\right) \quad \text{and} \\
(\sigma^2|\mu, y) & \sim \text{SI-}\chi^2\left(\nu_0 + 1 + n, \frac{\nu_0 \sigma_0^2 + \kappa_0 (\mu - \mu_0)^2 + n s_\mu^2}{\nu_0 + 1 + n}\right),
\end{align*}
\]

in which \( \bar{y} = \frac{1}{n} \sum_{i=1}^{n} y_i \) and \( s_\mu^2 = \frac{1}{n} \sum_{i=1}^{n} (y_i - \mu)^2 \).
We already know (Chapter 2) that the correct marginal posteriors for $\mu$ and $\sigma^2$ and the correct posterior predictive distribution for the next observation are

$$
(\sigma^2|y) \sim \text{SI-}\chi^2(\nu_n, \sigma_n^2),
$$

$$
(\mu|y) \sim t_{\nu_n}\left(\mu_n, \frac{\sigma_n^2}{\kappa_n}\right), \quad \text{and} \quad (26)
$$

$$
(y_{n+1}|y) \sim t_{\nu_n}\left(\mu_n, \frac{\kappa_n + 1}{\kappa_n} \sigma_n^2\right), \quad \text{in which}
$$

$$
\nu_n = \nu_0 + n,
$$

$$
\sigma_n^2 = \frac{1}{\nu_n} \left[\nu_0 \sigma_0^2 + (n - 1)s^2 + \frac{\kappa_0 n}{\kappa_0 + n}(\bar{y} - \mu_0)^2\right],
$$

$$
\mu_n = \frac{\kappa_0}{\kappa_0 + n} \mu_0 + \frac{n}{\kappa_0 + n} \bar{y}, \quad \text{and} \quad (27)
$$

$$
\kappa_n = \kappa_0 + n,
$$

with $s^2 = \frac{1}{n-1} \sum_{i=1}^{n} (y_i - \bar{y})^2$ as the usual sample variance.

Here’s some R code to implement the Gibbs sampler in this problem:
gibbs.example <- function( y, nu.0, sigma2.0, mu.0, kappa.0, mu.initial, 
                     sigma2.initial, M, B, seed ) {
    set.seed( seed )
    n <- length( y )
    y.bar <- mean( y )
    mcmc.data.set <- matrix( NA, M + B + 1, 4 )
    mcmc.data.set[ 1, ] <- c( mu.initial, sigma2.initial, 
                                sqrt( sigma2.initial ), mu.initial )
    for ( i in 2:( M + B + 1 ) ) {
        mu.star <- rnorm( 1, ( kappa.0 * mu.0 + n * y.bar ) / ( kappa.0 + n ), 
                          sqrt( mcmc.data.set[ i - 1, 2 ] / ( kappa.0 + n ) ) )
        s2.mu.star <- sum( ( y - mu.star )^2 ) / n
        sigma2.star <- rsichi2( 1, nu.0 + 1 + n, ( nu.0 * sigma2.0 + 
                                   kappa.0 * ( mu.star - mu.0 )^2 + n * s2.mu.star ) / 
                                   ( nu.0 + 1 + n ) )
        y.star <- rnorm( 1, mu.star, sqrt( sigma2.star ) )
        mcmc.data.set[ i, ] <- c( mu.star, sigma2.star, 
                                    sqrt( sigma2.star ), y.star )
        if ( ( i %% 1000 ) == 0 ) print( i )
    }
Simulating From the Posterior Predictive Distribution

```r
return( mcmc.data.set )
}
rsichi2 <- function( n, nu, s2 ) {
  return( nu * s2 / rchisq( n, nu ) )
}
```

There are **three new things** about this code in relation to the previous random-walk-Metropolis example: (a) **sampling** from the full-conditional distributions (Gibbs); (b) **monitoring** a function of \( \theta = (\mu, \sigma^2) \) (in this case, \( \sigma = \sqrt{\sigma^2} \)); and (c) **sampling** from the **posterior predictive distribution** \( p(y_{n+1}|y) \) (we could have done (b) and (c) in the same way in the previous example; I just **forgot** to do so), which You’ll **recall** has the form

\[
p(y_{n+1}|y) = \int p(y_{n+1}|\theta) p(\theta|y) \, d\theta. \tag{28}
\]

Equation (28) represents \( p(y_{n+1}|y) \) **hierarchically** as a mixture of \( p(y_{n+1}|\theta) \) weighted by \( p(\theta|y) \); back in Chapter 2 we agreed that to **make** a random draw \( y^*_n \) from such a mixture you just have to (i) draw \( \theta \) from \( p(\theta|y) \), obtaining \( \theta^* \), and then (ii) draw \( y_{n+1} \) from \( p(y_{n+1}|\theta^*) \).
Testing the Code

But that’s **exactly** what the line

```r
y.star <- rnorm( 1, mu.star, sqrt( sigma2.star ) )
```

does, to fill in a **draw** $y^*_{n+1}$ from $p(y_{n+1}|y)$ in each row of the MCMC data set.

To **test this code** I generated a little **artificial data set**, made the **following choices** for the **prior** and other inputs to the **driver function**, and ran it:

```r
print( sort( signif( rnorm( 10, 50, 5 ), 3 ) ) )
# 42.1 44.0 44.7 48.9 48.9 52.5 54.0 55.4 58.2 59.0
y <- c( 42.1, 44.0, 44.7, 48.9, 48.9, 52.5, 54.0, 55.4, 58.2, 59.0 )
mean( y )
# 50.77
sd( y )
# 5.987403
nu.0 <- 10
sigma2.0 <- 15
mu.0 <- 90
kappa.0 <- 10
mu.initial <- 70
```
Checking the Results

\[
sigma2.initial \leftarrow 20
\]
\[
M \leftarrow 99999
\]
\[
B \leftarrow 0
\]
\[
\text{seed} \leftarrow \text{c( 123456, 654321 )}
\]
\[
mcmc.data.set.1 \leftarrow \text{gibbs.example( y, nu.0, sigma2.0, mu.0, kappa.0, mu.initial, sigma2.initial, M, B, seed )}
\]

This took about **20 seconds** at **1.6 Unix GHz**; to **check the results** I can **simulate draws** from the **correct marginal posterior distributions** for \( \mu \) and \( \sigma^2 \) and the **correct posterior predictive distribution** for \( y_{n+1} \), and **compare** with the **MCMC output**:

\[
\text{print( n <- length( y ) )}
# 10
\]
\[
\text{print( nu.n <- nu.0 + n )}
# 20
\]
\[
\text{print( y.bar <- mean( y ) )}
# 50.77
\]
\[
\text{print( s2 <- var( y ) )}
# 35.849
\]
print( sigma2.n <- ( nu.0 * sigma2.0 + ( n - 1 ) * s2 + kappa.0 * n * 
    ( y.bar - mu.0 )^2 / ( kappa.0 + n ) ) / nu.n )
# 408.3803
print( mu.n <- ( kappa.0 * mu.0 + n * y.bar ) / ( kappa.0 + n ) )
# 70.385
print( kappa.n <- kappa.0 + n )
# 20
sigma2.benchmark <- rsichi2(M+B+1, nu.n, sigma2.n)
qqplot( mcmc.data.set.1[, 2], sigma2.benchmark,
    xlab = 'MCMC output for sigma^2', ylab = 'Benchmark output for sigma^2' )
abline( 0, 1 )
rscaled.t <- function( n, mu, sigma2, nu ) {
    return( sqrt( sigma2 ) * rt( n, nu ) + mu )
}
mu.benchmark <- rscaled.t( M + B + 1, mu.n, sigma2.n / kappa.n, nu.n)
qqplot( mcmc.data.set.1[, 1], mu.benchmark,
    xlab = 'MCMC output for mu', ylab = 'Benchmark output for mu' )
abline( 0, 1 )
y.next.benchmark <- rscaled.t( M + B + 1, mu.n, ( kappa.n + 1 ) * 
    sigma2.n / kappa.n, nu.n )
Checking the Results (continued)

\[
\text{qqplot( mcmc.data.set.1[,4], y.next.benchmark,}
\text{ xlab = 'MCMC output for y.next', ylab = 'Benchmark output for y.next')}
\text{abline( 0, 1 )}
\]
All of these plots (on pages 64-66) look great.
So now we can **begin looking** at the MCMC 4-plots:
In this problem Gibbs sampling $\neq$ IID sampling.
MCMC 4–Plot for $\sigma^2$

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MCMC 4–Plot for $\sigma$

- **Draws from $p(\sigma|y)$**

- **Density**

- **ACF**

- **Partial ACF**
With the hierarchical sampling method, the draws from $p(y_{n+1}|y)$ are always IID.
**Numerical Posterior Summaries**

With **commands** like those on page 55 you can readily produce the following **numerical posterior summaries**:

<table>
<thead>
<tr>
<th>Unknown</th>
<th>Posterior Mean</th>
<th>MCSE of Posterior Mean</th>
<th>Posterior SD</th>
<th>Quantiles 2.5%</th>
<th>Quantiles 97.5%</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mu$</td>
<td>70.37</td>
<td>0.015</td>
<td>4.766</td>
<td>60.89</td>
<td>79.82</td>
</tr>
<tr>
<td>$\sigma^2$</td>
<td>453.8</td>
<td>0.509</td>
<td>161.1</td>
<td>238.4</td>
<td>856.8</td>
</tr>
<tr>
<td>$\sigma$</td>
<td>21.01</td>
<td>0.011</td>
<td>3.541</td>
<td>15.44</td>
<td>29.27</td>
</tr>
<tr>
<td>$y_{n+1}$</td>
<td>70.30</td>
<td>0.069</td>
<td>21.79</td>
<td>27.41</td>
<td>113.3</td>
</tr>
</tbody>
</table>

You can see that

(a) **100,000 monitoring iterations** (about **20 seconds** of CPU time) has achieved **about 4 significant figures** worth of accuracy in the **posterior means** (and therefore **roughly the same order of magnitude** of accuracy for the **other summaries**), and

(b) (as usual) the **posterior uncertainty** about the **next observation** is **substantially bigger** than the **uncertainty** about the **mean** of the **process**.
We’re now ready to do **MCMC sampling** in the **NB10 case study**, for which the **model** is (for \( i = 1, \ldots, n \))

\[
\begin{align*}
(\mu, \sigma^2, \nu) & \sim p(\mu, \sigma^2, \nu) \\
(y_i | \mu, \sigma^2, \nu) & \overset{\text{IID}}{\sim} t_\nu(\mu, \sigma^2).
\end{align*}
\]

(29)

The **sampling distribution/likelihood function** in this model is

\[
p(y | \mu, \sigma^2, \nu) = \prod_{i=1}^{n} \frac{\Gamma \left(\frac{\nu+1}{2}\right)}{\Gamma \left(\frac{\nu}{2}\right) \sqrt{\pi \nu \sigma^2}} \left[ 1 + \frac{(y_i - \mu)^2}{\nu \sigma^2} \right]^{-\frac{\nu+1}{2}} = \]

\[
l(\mu, \sigma^2, \nu | y) = c \frac{\left[ \Gamma \left(\frac{\nu+1}{2}\right) \right]^n}{\left[ \Gamma \left(\frac{\nu}{2}\right) \right]^n} \nu^{-\frac{n}{2}} (\sigma^2)^{-\frac{n}{2}} \left\{ \prod_{i=1}^{n} \left[ 1 + \frac{(y_i - \mu)^2}{\nu \sigma^2} \right] \right\}^{-\frac{\nu+1}{2}};
\]

this leads to the **log likelihood function**

\[
ll(\mu, \sigma^2, \nu | y) = n \log \Gamma \left(\frac{\nu+1}{2}\right) - n \log \Gamma \left(\frac{\nu}{2}\right) - \frac{n}{2} \log \nu - \frac{n}{2} \log \sigma^2 - \]

\[
\left(\frac{\nu + 1}{2}\right) \sum_{i=1}^{n} \log \left[ 1 + \frac{(y_i - \mu)^2}{\nu \sigma^2} \right].
\]

(31)
Generic Random-Walk Metropolis

Gibbs sampling would be no fun in this model; it turns out that a good generic MCMC approach is single-scan random-walk Metropolis with Gaussian proposal distributions on each of the components of the vector \( \theta \) of unknowns, after all components have been transformed to live on the entire real line.

So define \( \eta = \log \sigma^2 \) and \( \gamma = \log \nu \), so that \( \theta = (\mu, \eta, \gamma) \) with \( \sigma^2 = e^\eta \) and \( \nu = e^\gamma \); in this parameterization the log likelihood function is

\[
ll(\mu, \eta, \gamma|y) = n \log \Gamma \left( \frac{e^\gamma + 1}{2} \right) - n \log \Gamma \left( \frac{e^\gamma}{2} \right) - \frac{n}{2} \gamma - \frac{n}{2} \eta - \left( \frac{e^\gamma + 1}{2} \right) \sum_{i=1}^{n} \log \left[ 1 + \frac{(y_i - \mu)^2}{e^{\gamma+\eta}} \right].
\]

(32)

If context implies a diffuse prior on \((\mu, \sigma^2, \nu)\) — as it does in the NB10 case study — then a reasonable place to start would be with the improper prior defined by \( \log p(\mu) = \log p(\eta) = \log p(\gamma) = 0 \); we can then do sensitivity analysis to see how much this particular diffuse prior choice affects the posterior.
Exploring the Log Likelihood

Before we launch into the MCMC, let’s take a bit of time to explore the log likelihood surface, first in R and then in Maple.

log.likelihood <- function( theta, y ) {
    n <- length( y )
    mu <- theta[ 1 ]
    eta <- theta[ 2 ]
    gamma <- theta[ 3 ]
    return( n * lgamma( ( exp( gamma ) + 1 ) / 2 ) / 2 ) - n *
            lgamma( exp( gamma ) / 2 ) - n * gamma / 2 - n * eta / 2 -
            ( ( exp( gamma ) + 1 ) / 2 ) * sum( log( 1 + ( y - mu )^2 /
            exp( gamma + eta ) ) )
}

R has a built-in function called optim that’s good at minimizing scalar functions of vector arguments without having to supply derivative information; however, the function I give it to optimize should depend only on \( \theta \) (not on \( \theta \) and \( y \)), and to use it I need to minimize minus the log likelihood, so I’ll define \( y \) as a variable in the workspace (rather than passing it into the function as an
Finding the MLE Vector

argument) and rewrite the function a bit:

```r
        403., 407., 402., 401., 399., 400., 401., 405., 402., 408., 399., 399.,
        ...
        406., 398., 406., 403., 404. )
minus.log.likelihood.for.optim <- function( theta ) {
  n <- length( y )
  mu <- theta[ 1 ]
  eta <- theta[ 2 ]
  gamma <- theta[ 3 ]
  log.likelihood <- n * lgamma((exp(gamma)+1)/2) - n *
    lgamma(exp(gamma)/2) - n * gamma/2 - n * eta/2 -
    ((exp(gamma)+1)/2)*sum(log(1+(y-mu)^2/exp(gamma+eta))
    exp(gamma+eta))
  return( -log.likelihood )
}
```
optim requires a vector of starting values for its optimization search: I’ll start \( \mu \) off at the sample mean of the \( y \) values (which should not be far from the MLE for \( \mu \) in the \( t \) model); I’ll start \( \eta = \log \sigma^2 \) off at the log of the sample variance of the \( y \) values (\( \sigma^2 \) is not quite the variance of \( y_i \) in this model, but it’s not far off); and for \( \nu \), I’ll remember that Churchill Eisenhart (an old NBS hand) once said that all measurement processes are approximately \( t_8 \) and start \( \gamma = \log \nu \) off at log 8:

\[
\text{print( mle <- optim( c(mean(y),log(var(y)),log(8)),}
\text{minus.log.likelihood.for.optim, hessian = T ))}
\]

$par
[1] 404.278968 2.617090 1.101340
$value
[1] 250.8514
$counts
function gradient
106 NA
The MLE and the Hessian Matrix

$\text{convergence}$

[1] 0

$\text{message}$

NULL

$\text{hessian}$

<table>
<thead>
<tr>
<th></th>
<th>[1]</th>
<th>[2]</th>
<th>[3]</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1,]</td>
<td>4.7201671</td>
<td>-0.3438449</td>
<td>-0.3419223</td>
</tr>
<tr>
<td>[2,]</td>
<td>-0.3438449</td>
<td>26.5910742</td>
<td>-10.9292142</td>
</tr>
<tr>
<td>[3,]</td>
<td>-0.3419223</td>
<td>-10.9292142</td>
<td>16.7254706</td>
</tr>
</tbody>
</table>

This output means that (a) convergence was successful ($\text{convergence} = 0$) after 106 function evaluations; (b) the maximum log likelihood value was $-250.8512$, attained at the MLE vector $(\hat{\mu}, \hat{\eta}, \hat{\gamma}) = (404.3, 2.617, 1.101)$; and (c) the Hessian of minus the log likelihood at the MLE is the $\text{hessian}$ matrix above.

optim may be sensitive to the quality of its starting values:

optim( c( 0, 0, 0 ), minus.log.likelihood.for.optim, hessian = T )

$\text{par}$

An Example of Failure to Converge

The documentation says that “convergence = 10 indicates degeneracy of the Nelder-Mead simplex,” and of course nothing in any of this guarantees that it has found the global minimum (even with the good starting values I gave it earlier).
You’ll recall that in repeated sampling the large-sample distribution of the MLE vector $\hat{\theta}$ is approximately $N_k(\theta, \hat{\Sigma})$ with $k = 3$ in this example and $\hat{\Sigma} = \hat{I}^{-1}$, where $\hat{I}$ is minus the Hessian matrix of the log likelihood function evaluated at $\hat{\theta}$ (which equals the Hessian matrix of minus the log likelihood at the same point); so to get $\hat{\Sigma}$ I just have to invert the Hessian:

```
print( Sigma.theta.hat <- solve( mle$hessian ) )
```

```
[,1] [,2] [,3]
[1,] 0.212918550 0.006210111 0.00841072
[2,] 0.006210111 0.051596574 0.03384260
[3,] 0.008410719 0.033842598 0.08207535
```

So this means that an approximate 99.7% interval estimate for component $j$ of $\theta$ is $\hat{\theta}_j \pm 3\sqrt{\hat{\Sigma}_{jj}}$, where $\hat{\Sigma}_{ij}$ is the $(i, j)$ element of $\hat{\Sigma}$; thus, according to the likelihood approach, $\mu$ is likely to be in the interval $404.3 \pm 3\sqrt{0.2129} = (402.9, 405.7)$, and similarly the 99.7% intervals for $\eta$ and $\gamma$ are approximately $(1.936, 3.298)$ and $(0.2415, 1.960)$, respectively.
Exploring the Log Likelihood Surface in R

Armed with this information we can explore the log likelihood surface near its maximum, by holding one component of $\theta$ constant at its MLE and making 3d-perspective and contour plots as a function of the other two components:

```r
theta.hat <- c( 404.278968, 2.617090, 1.101340 )
n.grid <- 30
mu.grid <- seq( 402.9, 405.7, length = n.grid )
eta.grid <- seq( 1.936, 3.298, length = n.grid )
gamma.grid <- seq( 0.2415, 1.960, length = n.grid )
mu.eta.log.likelihood.grid <- array(data=NA,dim=c(n.grid,n.grid))
for (i in 1:n.grid)
  for (j in 1:n.grid)
    mu.eta.log.likelihood.grid[i,j] <- log.likelihood(c(mu.grid[i],
      eta.grid[j], theta.hat[3]), y )
persp(mu.grid, eta.grid, mu.eta.log.likelihood.grid, xlab = 'mu',
      ylab = 'eta', zlab = 'Log Likelihood', axes = T,
      ticktype = 'detailed', theta = -30, phi = 15 )
```

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The Log Likelihood Surface in \((\mu, \eta)\) (3D-Perspective Plot)

This looks **pleasingly bivariate normal** in \(\mu\) and \(\eta\), with a well-defined (global) maximum.
The Log Likelihood Surface in the posterior

\[ \eta \] and \( \mu \) will be uncorrelated in the posterior.

\[
\text{mu}
\]
\[
\eta
\]

\[ -258 \]
\[ -259 \]
\[ -260 \]
\[ -261 \]
\[ -262 \]
\[ -263 \]

403.0 403.5 404.0 404.5 405.0 405.5

2.0 2.2 2.4 2.6 2.8 3.0 3.2

\[
Ylab = \text{etan}
\]
\[
contour( \text{mu.grid, eta.grid, mu.eta.log.likelihood.grid, xlab=, ylab=}
\]

The Log Likelihood Surface in (\( \mu, \eta \)) (Contour Plot)
The Log Likelihood Surface in \((\mu, \gamma)\)

**Similar code** produces the plots for \((\mu, \gamma)\) and \((\eta, \gamma)\); here’s the code for \((\mu, \gamma)\):

```r
mu.gamma.log.likelihood.grid <- array(data = NA, dim = c(n.grid, n.grid))

for (i in 1:n.grid) {
  for (j in 1:n.grid) {
    mu.gamma.log.likelihood.grid[i, j] <- log.likelihood(c(mu.grid[i], theta.hat[2], gamma.grid[j]), y)
  }
}

persp(mu.grid, gamma.grid, mu.gamma.log.likelihood.grid, xlab = 'mu', ylab = 'gamma', zlab = 'Log Likelihood', axes = T, ticktype = 'detailed', theta = -30, phi = 15)

contour(mu.grid, gamma.grid, mu.gamma.log.likelihood.grid, xlab = 'mu', ylab = 'gamma')
```

Bayesian Statistics 3a: Simulation-Based Computation
The Log Likelihood Surface in \((\mu, \gamma)\) (3D-Perspective Plot)
The Log Likelihood Surface in $(\mu, \gamma)$ (Contour Plot)

$\mu$ and $\gamma$ will also be uncorrelated in the posterior.
The Log Likelihood Surface in \((\eta, \gamma)\) (3D-Perspective Plot)
The Log Likelihood Surface in \((\eta, \gamma)\) (Contour Plot)

But \(\eta\) and \(\gamma\) will be \textbf{positively correlated} in the \textbf{posterior}.
By the Bernsteïn-von Mises Theorem we expect the posterior distribution with a diffuse prior to be approximately \( \theta | y \sim N_k(\hat{\theta}, \hat{\Sigma}) \), so we know that the posterior SDs of the components of \( \theta \) are approximately \((\sqrt{0.2129}, \sqrt{0.05160}, \sqrt{0.08208}) \div (0.4614, 0.2272, 0.2865)\); this can help us tune the proposal distribution SDs (PDSDs).

If things behave the same way for \( k = 3 \) as they do for \( k = 1 \), we could get acceptance rates of about 44\% using PDSDs

\[
2.4(0.4614, 0.2272, 0.2865) \div 1.11, 0.545, 0.689); \text{ let's see what happens.}
\]

Here’s some quite general R code to do single-scan random-walk Metropolis sampling — you can use this driver function, the acceptance probability function and the log posterior function without change in any other problem, and you’ll just have to write new code for the log likelihood, log prior and predictive sampling distribution for your specific situation:

(see the entry on the course web page for this code and output from it)
Running the code on the course web page with $M = 100,000$ monitoring iterations, you get the following numerical posterior summaries, in which I’ve tried not to overstate the significant figures:

<table>
<thead>
<tr>
<th>unknown</th>
<th>mean (mcse)</th>
<th>sd</th>
<th>2.5%</th>
<th>97.5%</th>
</tr>
</thead>
<tbody>
<tr>
<td>mu</td>
<td>404.3 (0.005)</td>
<td>0.446</td>
<td>403.4</td>
<td>405.2</td>
</tr>
<tr>
<td>sigma</td>
<td>3.77 (0.005)</td>
<td>0.428</td>
<td>2.99</td>
<td>4.68</td>
</tr>
<tr>
<td>nu</td>
<td>3.2 (0.012)</td>
<td>1.0</td>
<td>1.8</td>
<td>5.7</td>
</tr>
<tr>
<td>y.next</td>
<td>404.3 (0.022)</td>
<td>6.9</td>
<td>394.9</td>
<td>416.6</td>
</tr>
</tbody>
</table>

With 100,000 monitoring iterations, we’ve achieved 4–figure accuracy with the posterior mean and interval estimate for $\mu$ but only 2–figure accuracy for the summaries about $\nu$ (this turns out to be a hard parameter to pin down).

The posterior SD for $\mu$, the only parameter directly comparable across the Gaussian and $t$ models for the NB10 data, came out 0.45 from the $t$ modeling, versus 0.65 with the Gaussian, i.e., the interval estimate for $\mu$. 
from the (incorrect) Gaussian model is about 40% wider that that from the (much better-fitting) t model.

**NB** Moving from the Gaussian to the t model involves a net increase in model uncertainty, because when you assume the Gaussian you’re in effect saying that you know the t degrees of freedom are ∞, whereas with the t model you’re treating ν as unknown.

And yet, even though there’s been an increase in model uncertainty, the inferential uncertainty about μ has gone down.

This is relatively rare — usually when model uncertainty increases so does inferential uncertainty (Draper 1995, 2011) — and arises in this case because of two things: (a) the t model fits better than the Gaussian, and (b) the Gaussian is actually a conservative model to assume as far as inferential accuracy for location parameters is concerned: it turns out that among all symmetric unimodal densities the Gaussian has minimal Fisher information for location (this is related to the maximum-entropy property of the Gaussian).