Module 8: Introduction to Gibbs Sampling (Part II) with an Application to Missing Data

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Agenda

- Gibbs sampling (multi-stage sampler)
- Missing data application

Multi-stage Gibbs sampler

Assume d random variables, with joint pmf or pdf $p(v^1, \ldots, v^d)$.

At each iteration $(1, \ldots, M)$ of the algorithm, we sample from

$$
\begin{aligned}
v^1 &\mid v^2, v^3, \ldots, v^d \\
v^2 &\mid v^1, v^3, \ldots, v^d \\
&\vdots \\
v^d &\mid v^1, v^2, \ldots, v^{d-1}
\end{aligned}
$$

always using the most recent values of all the other variables.

The conditional distribution of a variable given all of the others is referred to as the *full conditional* in this context, and for brevity denoted $v^i \mid \cdots$.

Example: Censored data

In many real-world data sets, some of the data is either missing altogether or is partially obscured.

One way in which data can be partially obscured is by *censoring*, which means that we know a data point lies in some particular interval, but we do not observe it.

Medical data censoring

Suppose 6 patients participate in a cancer trial, however, patients 1, 2 and 4 leave the trial early.

Then we know when they leave the study, but we don't know information about them as the trial continues.

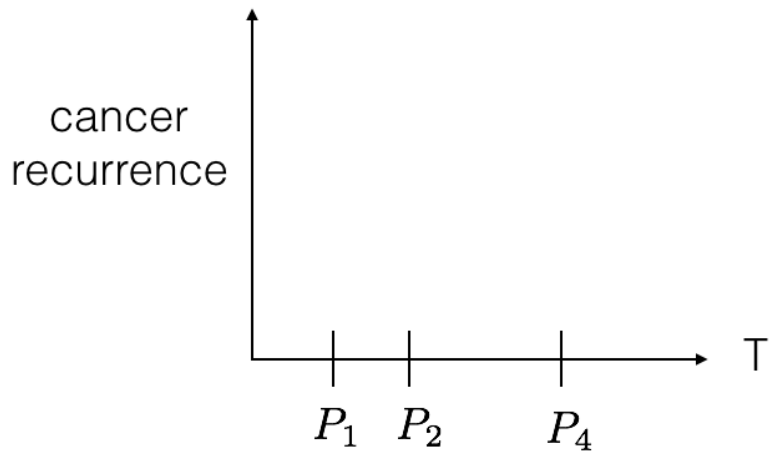


Figure 1: Example of censoring for medical data.

This is a certain type of missing data.

Heart Disease (Censoring) Example

- Researchers are studying the length of life (lifetime) following a particular medical intervention, such as a new surgical treatment for heart disease.
- The study consists of 12 patients.
- The number of years before death for each is

$$3.4, 2.9, 1.2+, 1.4, 3.2, 1.8, 4.6, 1.7+, 2.0+, 1.4+, 2.8, 0.6+$$

where the $+$ indicates that the patient was alive after x years, but the researchers lost contact with the patient after that point in time.

Model

$$X_i = \begin{cases} Z_i & \text{if } Z_i \leq c_i \\ c_i & \text{if } Z_i > c_i \end{cases} \tag{1}$$

$$Z_1, \ldots, Z_n | \theta \overset{iid}{\sim} \text{Gamma}(r, \theta) \tag{2}$$

$$\theta \sim \text{Gamma}(a, b) \tag{3}$$

where a, b, and r are known.

- c_i is the censoring time for patient i, which is fixed, but known only if censoring occurs.
- X_i is the observation
  - if the lifetime is less than c_i then we get to observe it ($X_i = Z_i$),
  - otherwise all we know is the lifetime is greater than c_i ($X_i = c_i$).
- θ is the parameter of interest—the rate parameter for the lifetime distribution.
- Z_i is the lifetime for patient i, however, this is not directly observed.

Posterior inference

Goal: find $p(\theta, z_{1:n}|x_{1:n})$?

1. Straightforward approaches that are in closed form do not work (think about these on your own). Instead we turn to Gibbs!

2. To sample from $p(\theta, z_{1:n}|x_{1:n})$, we cycle through each of the full conditional distributions,

$$
\begin{aligned}
\theta \mid z_{1:n}, x_{1:n} \\
z_1 \mid \theta, z_{2:n}, x_{1:n} \\
z_2 \mid \theta, z_1, z_{3:n}, x_{1:n} \\
\vdots \\
z_n \mid \theta, z_{1:n-1}, x_{1:n}
\end{aligned}
$$

sampling from each in turn, always conditioning on the most recent values of the other variables.

Likelihood

Recall the model is:

$$X_i = \begin{cases} Z_i & \text{if } Z_i \leq c_i \\ c_i & \text{if } Z_i > c_i \end{cases} \tag{4}$$

$$Z_1, \ldots, Z_n | \theta \overset{iid}{\sim} \text{Gamma}(r, \theta) \tag{5}$$

$$\theta \sim \text{Gamma}(a, b) \tag{6}$$

The pdf associated with this random variable is rather strange, as it consists of two point masses: one at Z_i and one at c_i. The formula is

$$p(x_i|z_i) = \mathbf{1}(x_i = z_i)\mathbf{1}(z_i \leq c_i) + \mathbf{1}(x_i = c_i)\mathbf{1}(z_i > c_i).$$

.

Full conditionals

The full conditionals are easy to calculate. Let's start with $\theta|\cdots$

- Since $\theta \perp x_{1:n} \mid z_{1:n}$ (i.e., θ is conditionally independent of $x_{1:n}$ given $z_{1:n}$),

$$p(\theta|\cdots) = p(\theta|z_{1:n}, x_{1:n}) = p(\theta|z_{1:n}) \tag{7}$$

$$= \text{Gamma}\left(\theta \,\middle|\, a + nr,\ b + \textstyle\sum_{i=1}^{n} z_i\right) \tag{8}$$

  using the fact that the prior on θ is conjugate.

Full conditionals

Now we can easily find the full conditionals.

- Note that z_i is conditionally independent of z_j given θ for $i \neq j$.
- This implies that x_i is conditionally independent of x_j given z_i for $i \neq j$.

Now we have

$$\begin{aligned} p(z_i|z_{-i}, x_{1:n}, \theta) &= p(z_i|x_i, \theta) \\ &\underset{z_i}{\propto} p(z_i, x_i, \theta) \\ &= p(\theta)p(z_i|\theta)p(x_i|z_i, \theta) \\ &\underset{z_i}{\propto} p(z_i|\theta)p(x_i|z_i, \theta) \\ &= p(z_i|\theta)p(x_i|z_i). \end{aligned}$$

Full conditionals (continued)

There are now two cases to consider.

1. If $x_i \neq c_i$, then $p(z_i|\theta)p(x_i|z_i)$ is only non-zero when $z_i = x_i$.

   - The density devolves to a point mass at x_i.

2. If $x_i = c_i$, then the density becomes $p(x_i|z_i) = \mathbf{1}(z_i > c_i)$, so

$$p(z_i|\ldots) \propto p(z_i|\theta)\mathbf{1}(z_i > c_i),$$

   which is a truncated Gamma.

Sampling from the truncated Gamma

We sample from the truncated gamma using a modified version of the inverse CDF method.

For the censored values of Z_i we know c_i.

If we know θ (which we will in a Gibbs' sampler), we know the distribution of $Z_i|\theta \sim Gamma(r, \theta)$.

Let F be the CDF of this distribution.

Suppose we truncate this distribution to (c, ∞). The new CDF is

$$Y = P(Z_i < z) = \frac{F(z) - F(c)}{1 - F(c)}.$$

Therefore Y is a sample from the truncated Gamma.

Remark: when we implement the GS, we do not sample the observed values. We impute the censored values using the method just outlined.

Application to censored data

```
knitr::opts_chunk$set(cache=TRUE)
# Samples from a truncated gamma with
# truncation (t, infty), shape a, and rate b
# Input: t,a,b
# Output: truncated Gamma(a,b)
sampleTrunGamma <- function(t, a, b){
  p0 <- pgamma(t, shape = a, rate = b)
  # Use the modification of the inverse CD method
  x <- runif(1, min = p0, max = 1)
  y <- qgamma(x, shape = a, rate = b)
  return(y)
}
```

Application to censored data (continued)

```
# Gibbs sampler
# z is the fully observe data
# c is censored data
# n.iter is number of iterations
# init.theta and init.miss are initial values for sampler
# r,a, and b are fixed parameters
# burnin is number of iterations to use as burnin
sampleGibbs <-
  function(z, c, n.iter, init.theta, init.miss, r, a, b, burnin = 1){
  z.sum <- sum(z); m <- length(c); n <- length(z) + m
  miss.vals <- init.miss
  res <- matrix(NA, nrow = n.iter, ncol = 1 + m)
  for (i in 1:n.iter){
    var.sum <- z.sum + sum(miss.vals)
    theta <- rgamma(1, shape = a + n*r, rate = b + var.sum)
    miss.vals <- sapply(c, function(x) {sampleTrunGamma(x, r, theta)})
    res[i,] <- c(theta, miss.vals)
  }
  return(res[burnin:n.iter,])
}
```

Set parameter values

```
set.seed(5983)
# set parameter values and enter data
r <- 10
a <- 1
b <- 1
z <- c(3.4,2.9,1.4,3.2,1.8,4.6,2.8)
c <- c(1.2,1.7,2.0,1.4,0.6)
n.iter <- 100
init.theta <- 1
init.missing <-
  rgamma(length(c), shape = r, rate = init.theta)
```

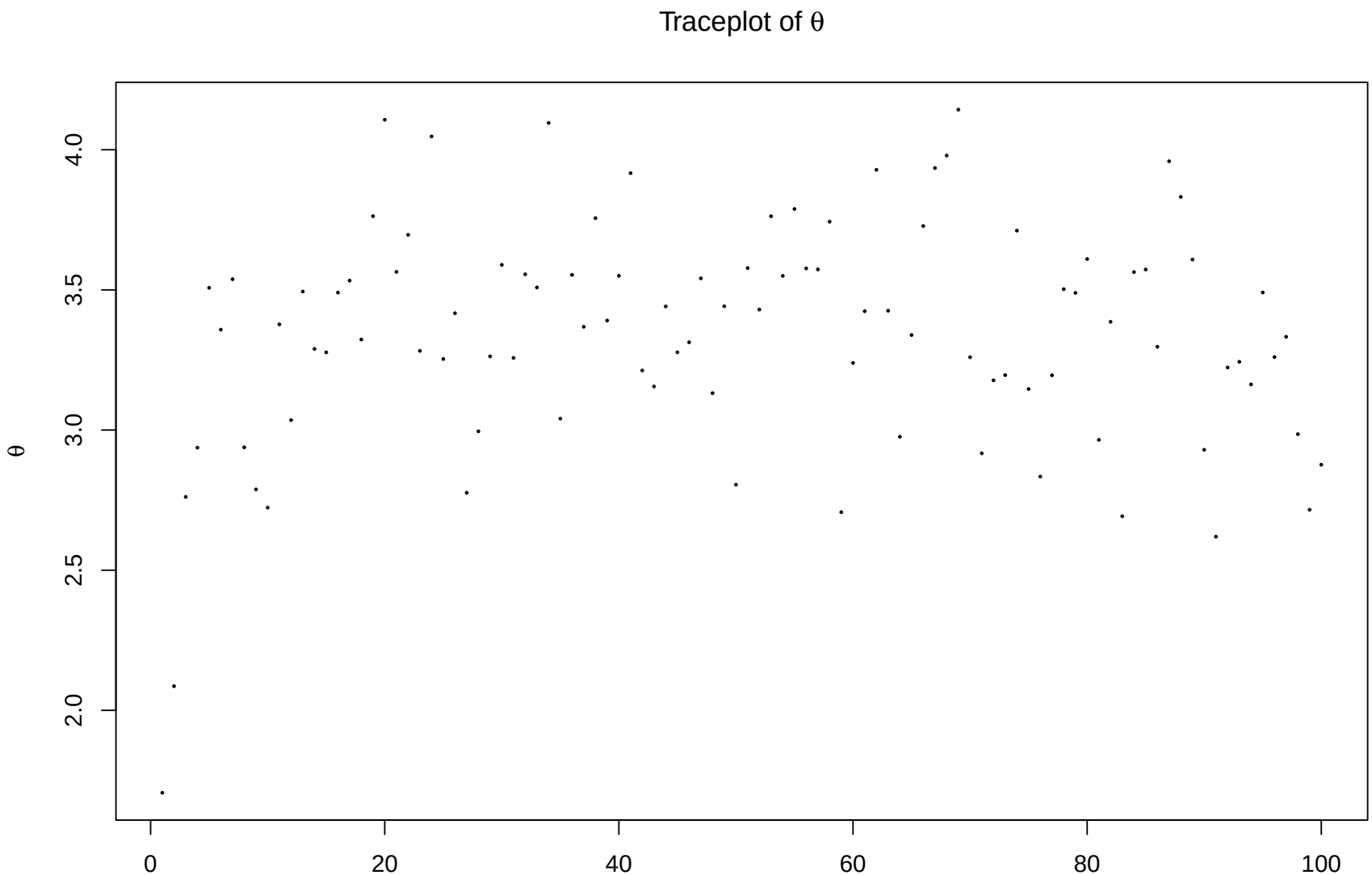
Run Gibbs sampler

```
res <- sampleGibbs(z, c, n.iter, init.theta, init.missing,
                   r, a, b)
```

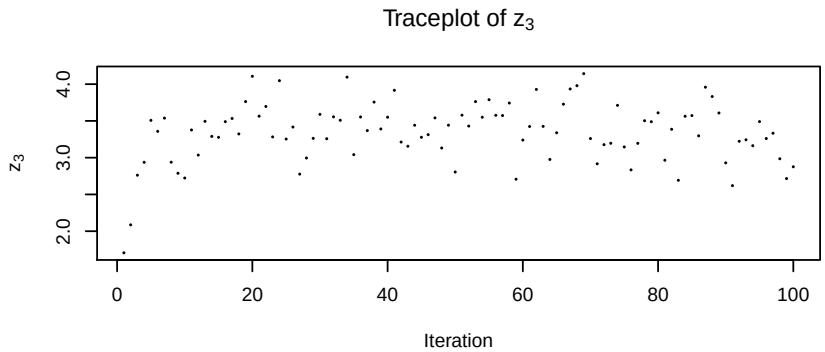
Let's first look at some diagnostics — trace plots and runnning average plots.

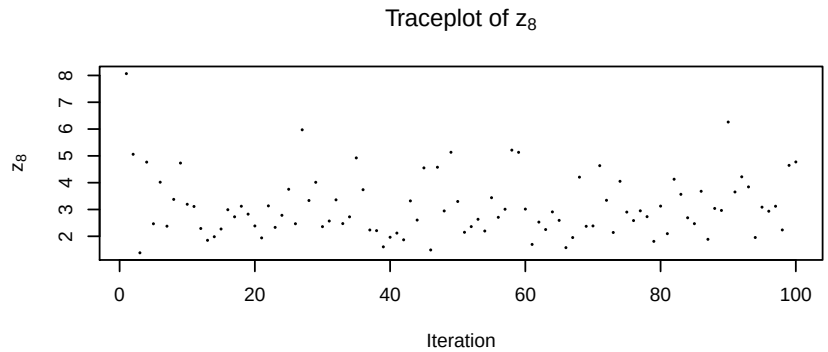
Traceplot of θ

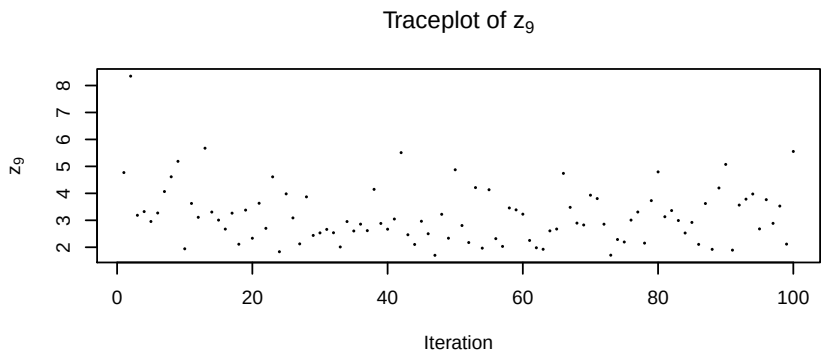
```
plot(1:n.iter, res[,1], pch = 16, cex = .35,
     xlab = "Iteration", ylab = expression(theta),
     main = expression(paste("Traceplot of ", theta)))
```

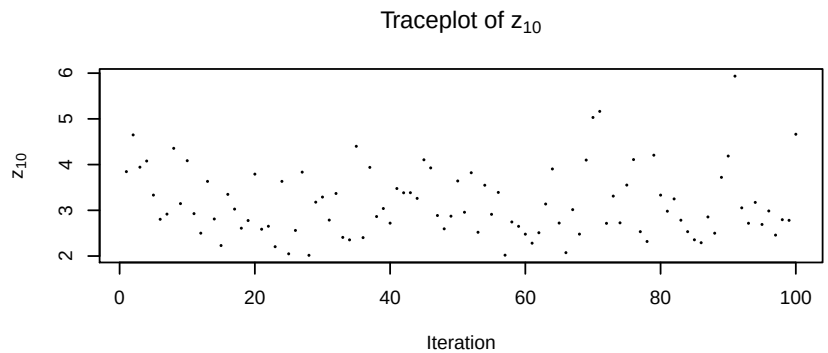


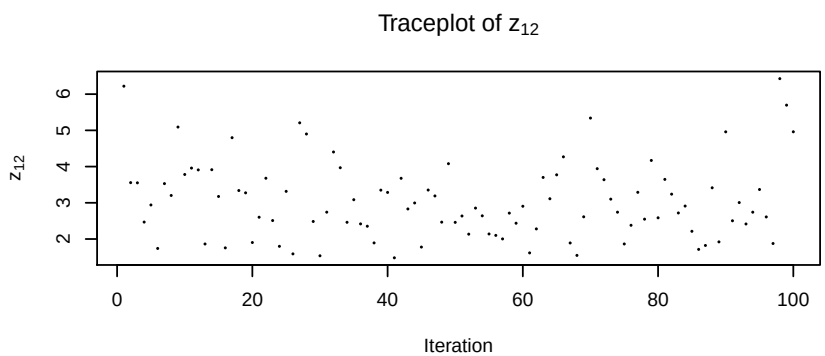
Traceplot of censored observations



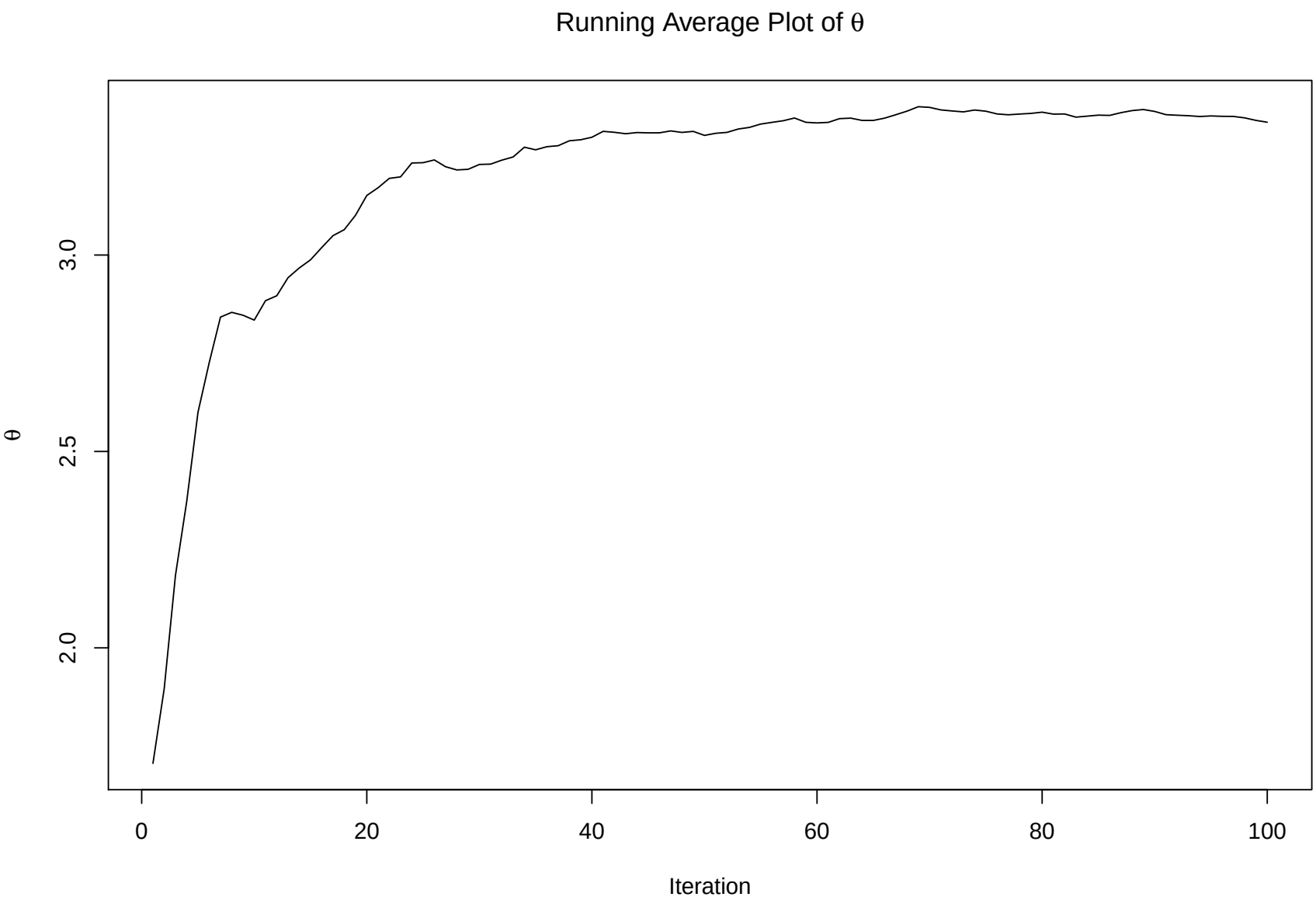




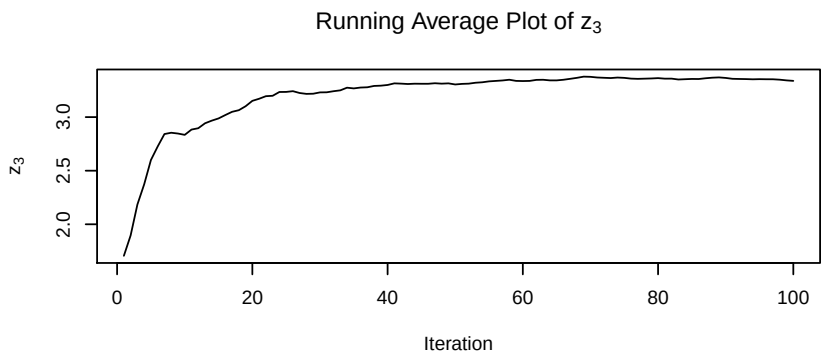


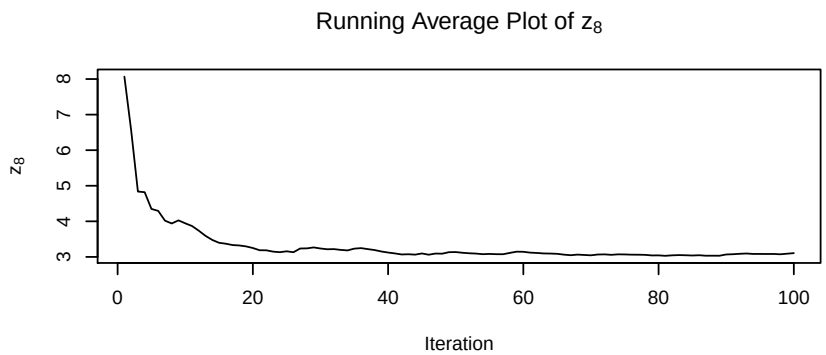


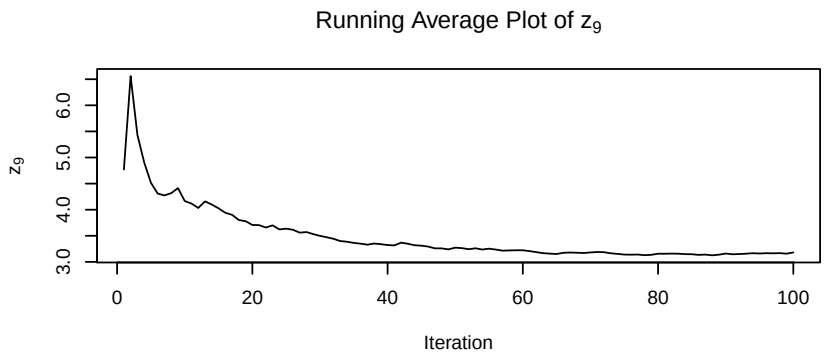
Running average plots

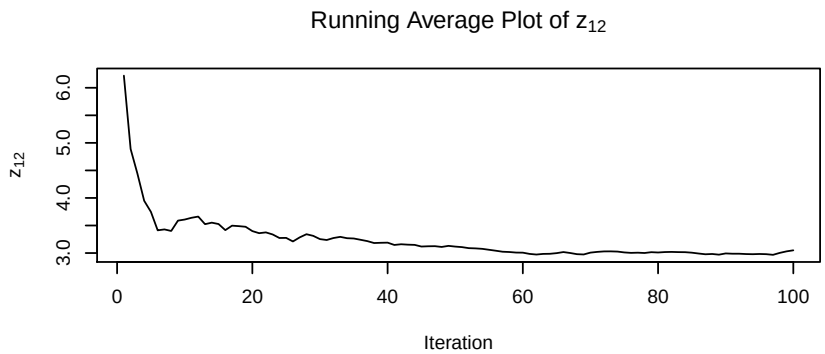


Running average plots

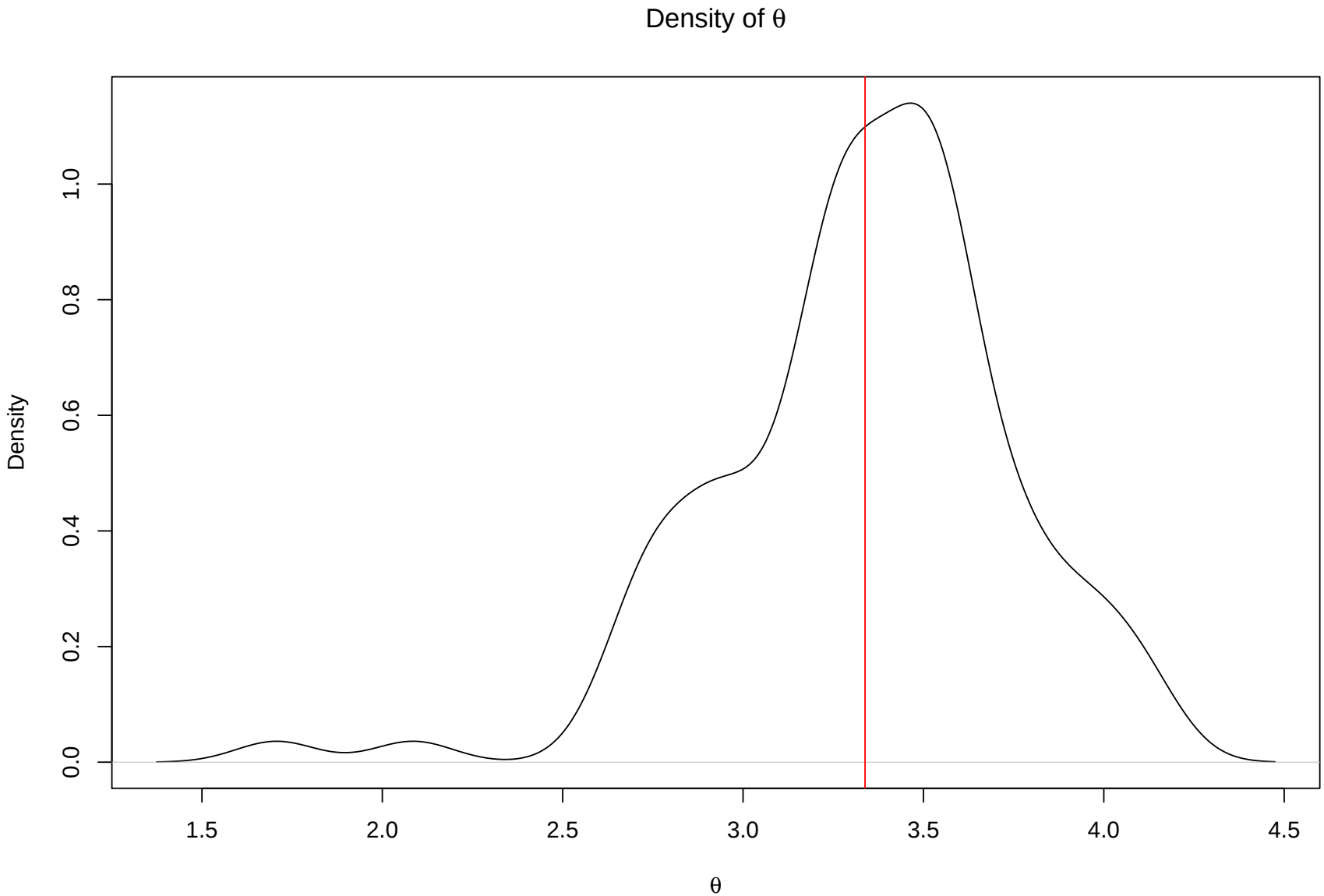




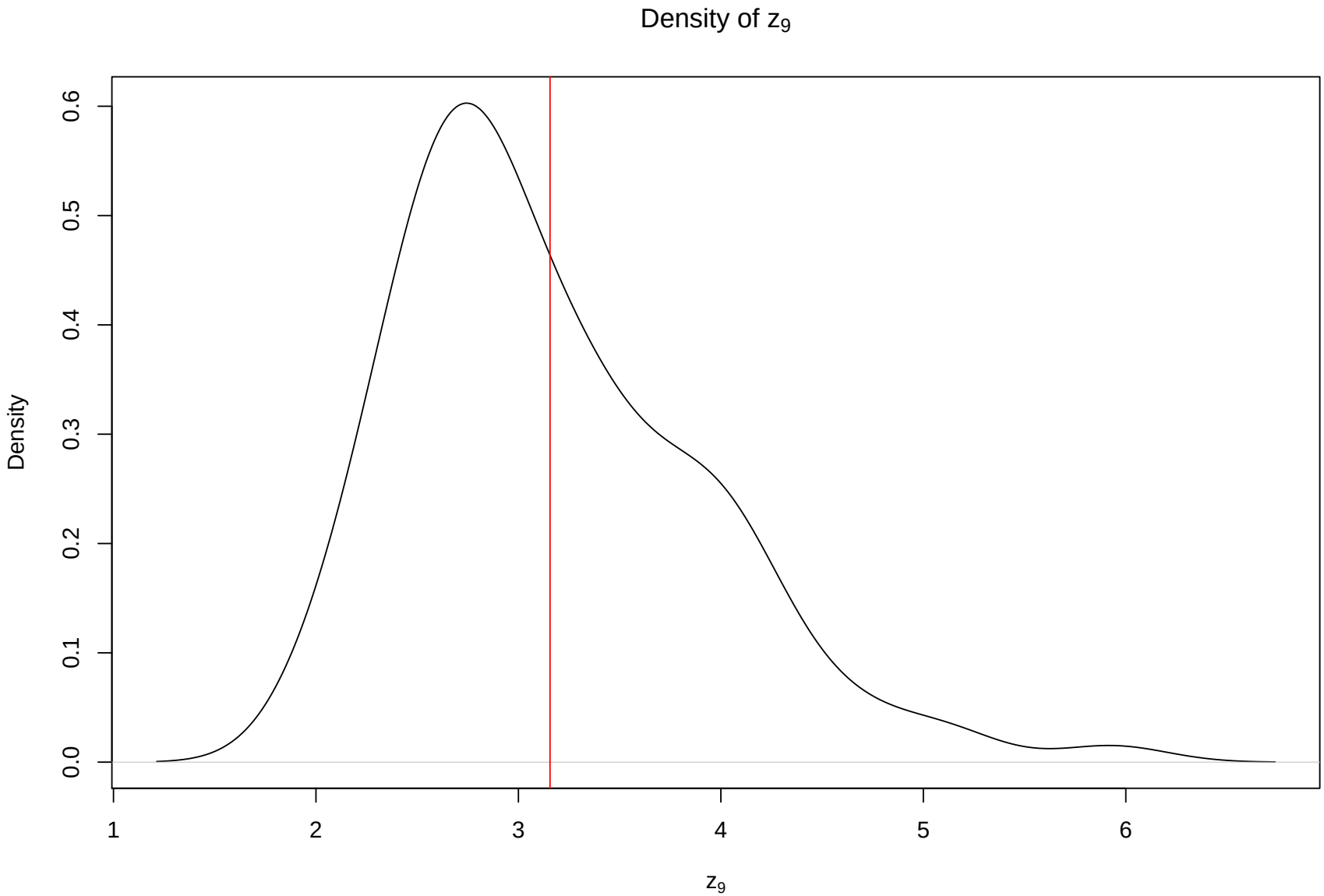




The estimated density of θ



The estimated density of z_9



Homework 8

Using the data and functions given to you (posted to Sakai with Homework 8), investigate the following questions:

1. Write code to produce traceplots and running average plots for the censored values for 200 iterations. Do these diagnostic plots suggest that you have run the sampler long enough? Explain.
2. Now run the chain for 10,000 iterations and update your diagnostic plots (traceplots and running average plots). Report your findings for both traceplots and the running average plots for θ and the censored values. Do these diagnostic plots suggest that you have run the sampler long enough? Explain.
3. Give plots of the estimated density of $\theta \mid \cdots$ and $z_9 \mid \cdots$. Be sure to give brief explanations of your results and findings. (Present plots for 10,000 iterations).
4. Finally, let's suppose that $r = 10, a = 1, b = 100$. Does your posterior change? What about when $r = 10, a = 10, b = 1$? (Use 10,000 iterations for the Gibbs sampler).