

Homework 6 Template, STA 360/602

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```
knitr::opts_chunk$set(cache=FALSE)
library(xtable)
# 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){
  # This function samples from a truncated gamma with
  # truncation (t, infty), shape a, and rate b
  p0 <- pgamma(t, shape = a, rate = b)
  x <- runif(1, min = p0, max = 1)
  y <- qgamma(x, shape = a, rate = b)
  return(y)
}
# Gibbs sampler for censored data
# Inputs:
# this function is a 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 parameters
# burnin is number of iterations to use as burnin
# Output: theta, z
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
r <- 10
a <- 1
b <- 1
# input data
```

```

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 <- 200
init.theta <- 1
init.missing <- rgamma(length(c), shape = r, rate = init.theta)
# run sampler
res <- sampleGibbs(z, c, n.iter, init.theta, init.missing, r, a, b)

```

In figure 1 and 2 we see traceplots for 200 iterations of the Gibbs sampler. It is difficult to tell whether or not the sampler has failed to converge, thus, we turn to running average plots.

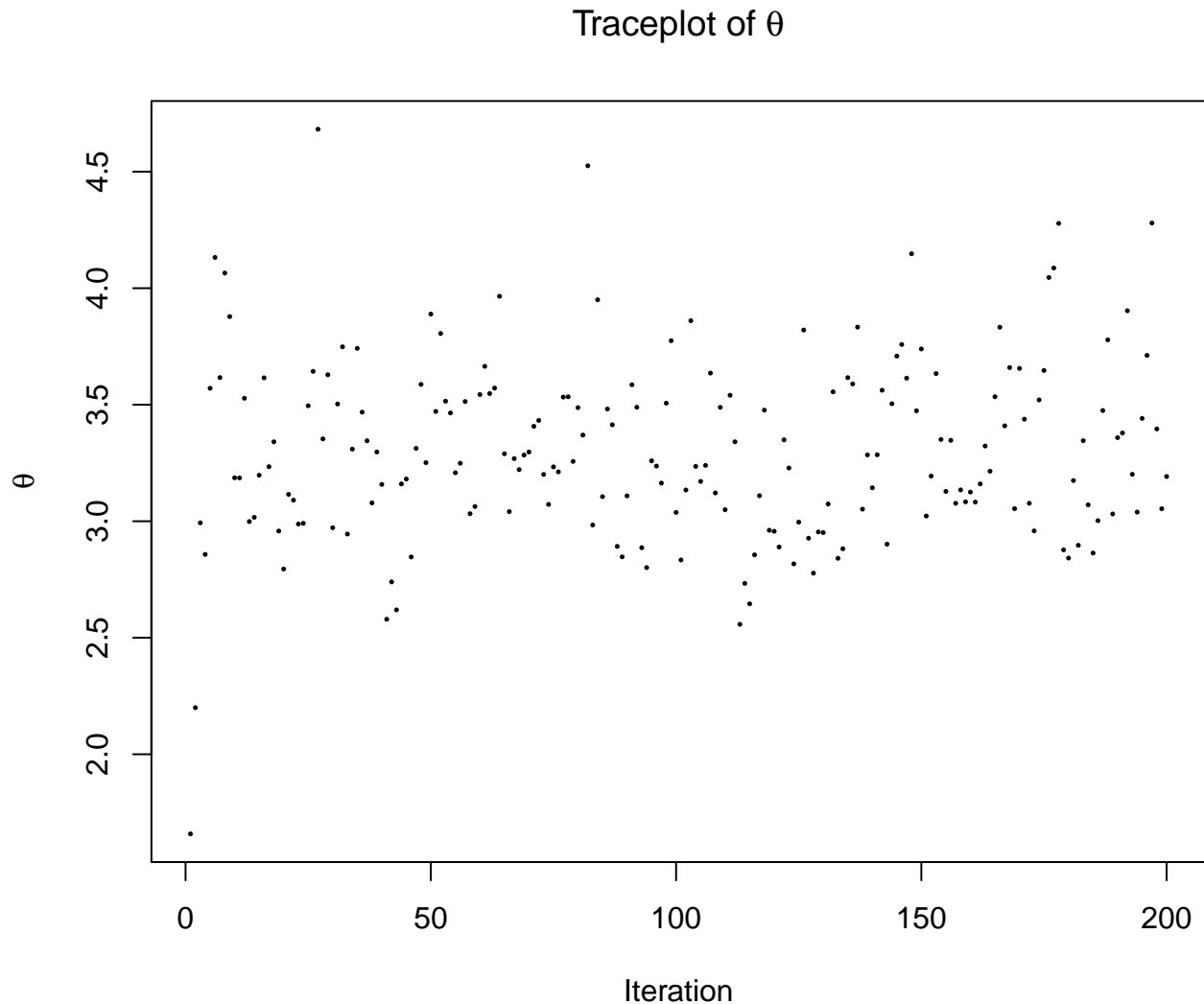


Figure 1: Traceplot of theta

In figures 3 and 4 we see running average plots for 200 iterations of the Gibbs sampler, where from all of these it is clear that after 200 iterations the sampler is having mixing issues, and should be run for long to check that “it has not failed to converge.”

```

# get running averages
run.avg <- apply(res, 2, cumsum)/(1:n.iter)

```

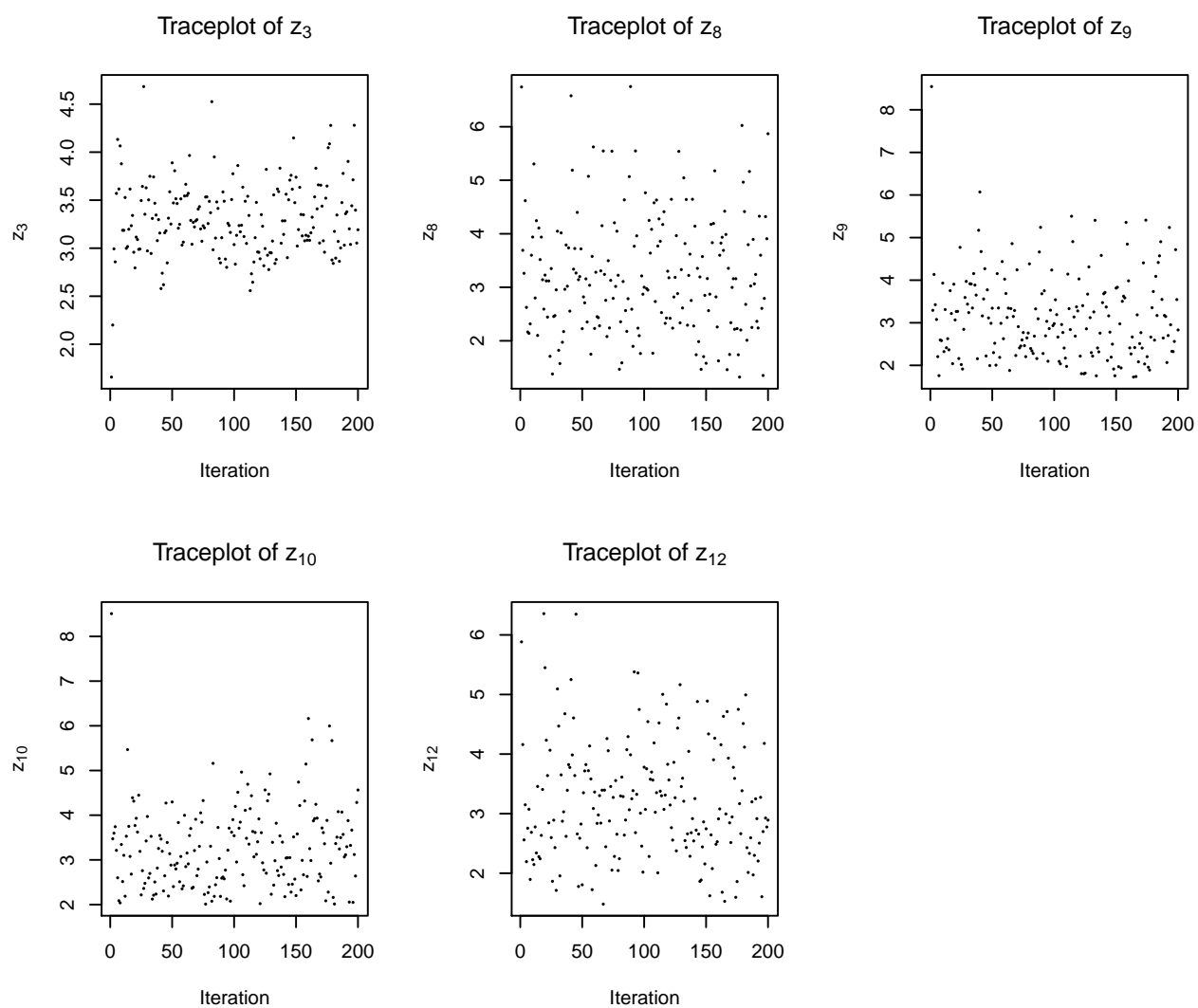


Figure 2: Traceplot of $z_3, z_8, z_9, z_{10}, z_{12}$.

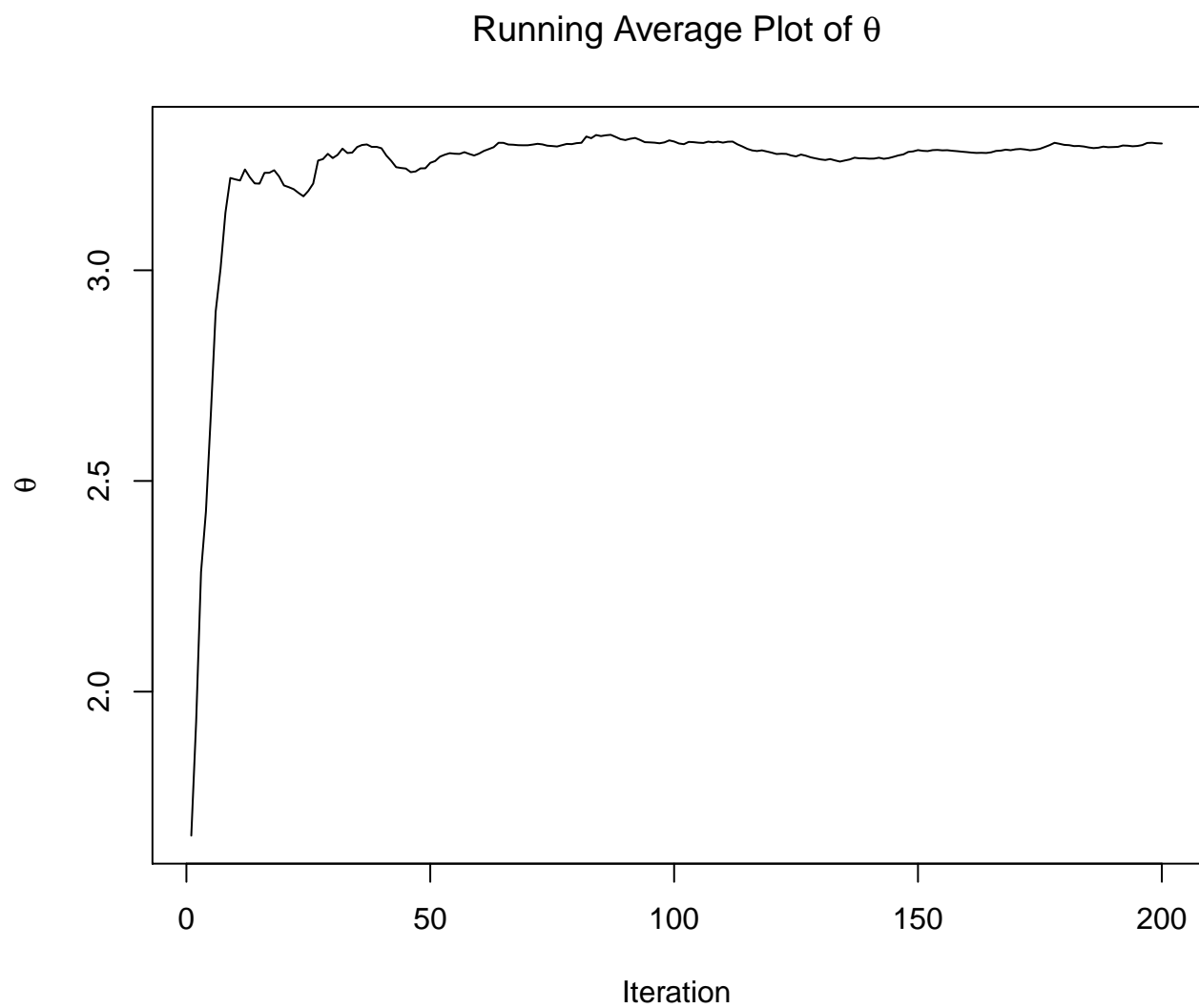


Figure 3: Running average plot of theta

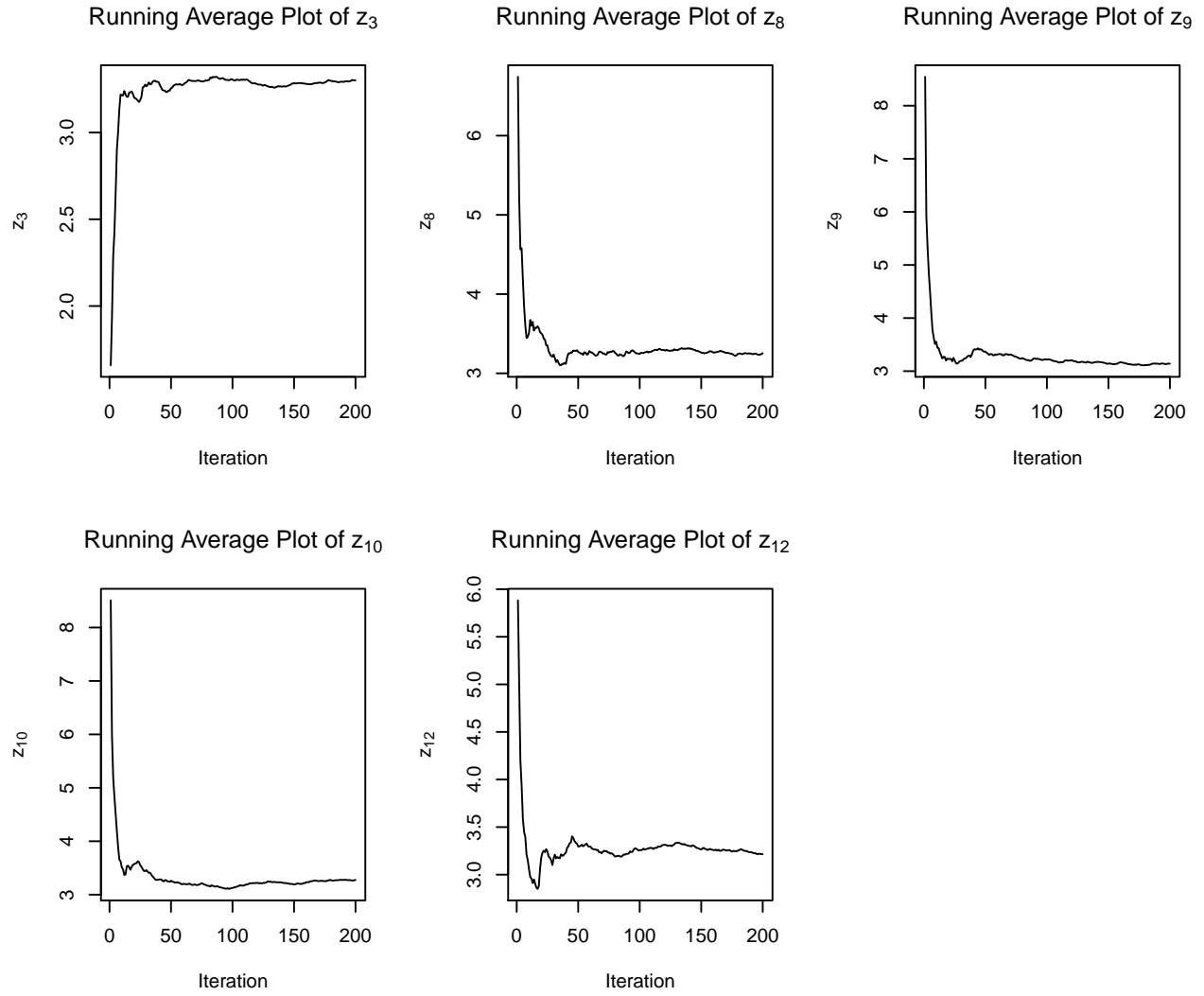


Figure 4: Running average plots of $z_3, z_8, z_9, z_{10}, z_{12}$.

Figures 5 and 6 do not provide meaningful inference at this point since the sampler has not been run long enough.

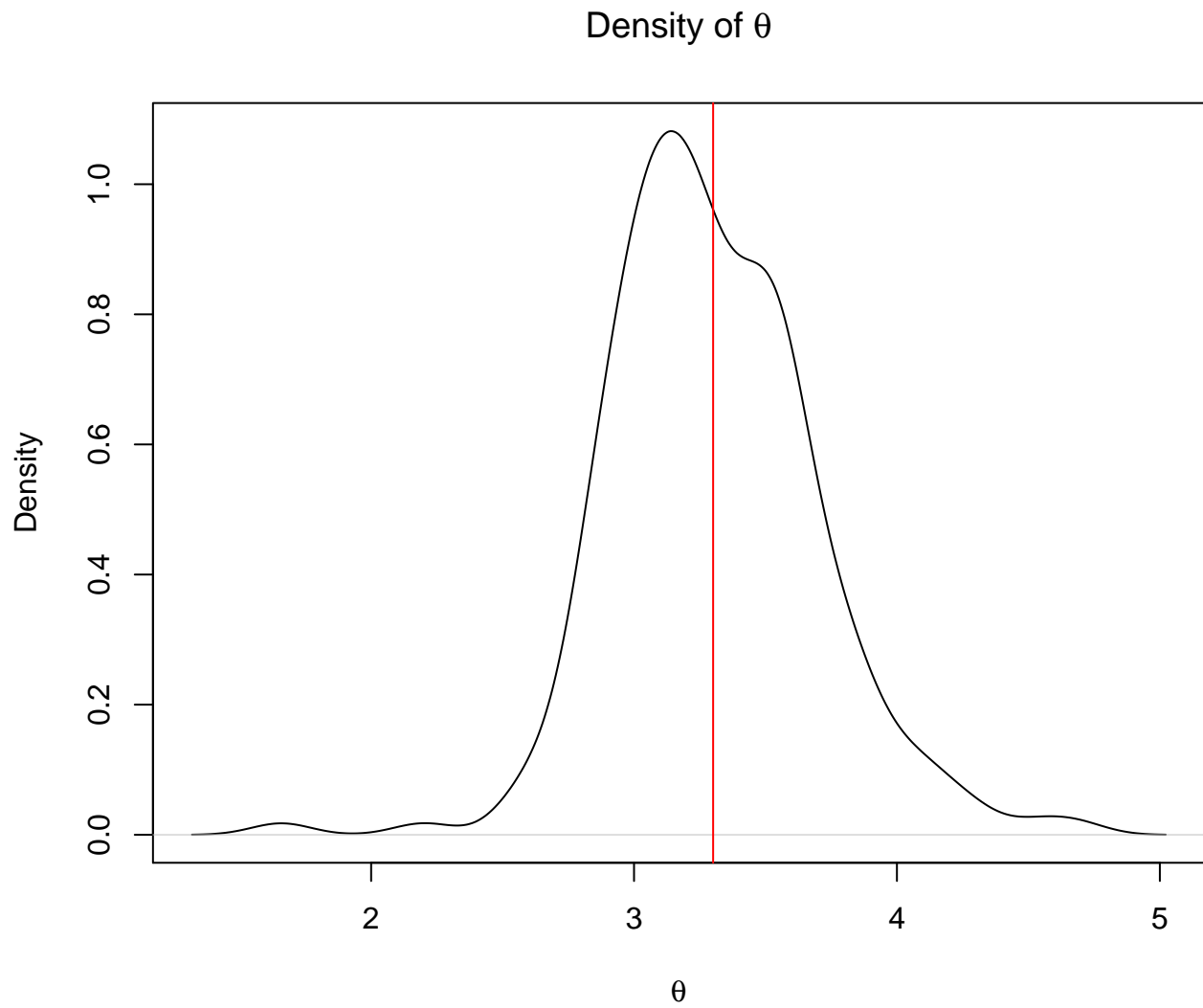


Figure 5: Estimated posterior density of theta

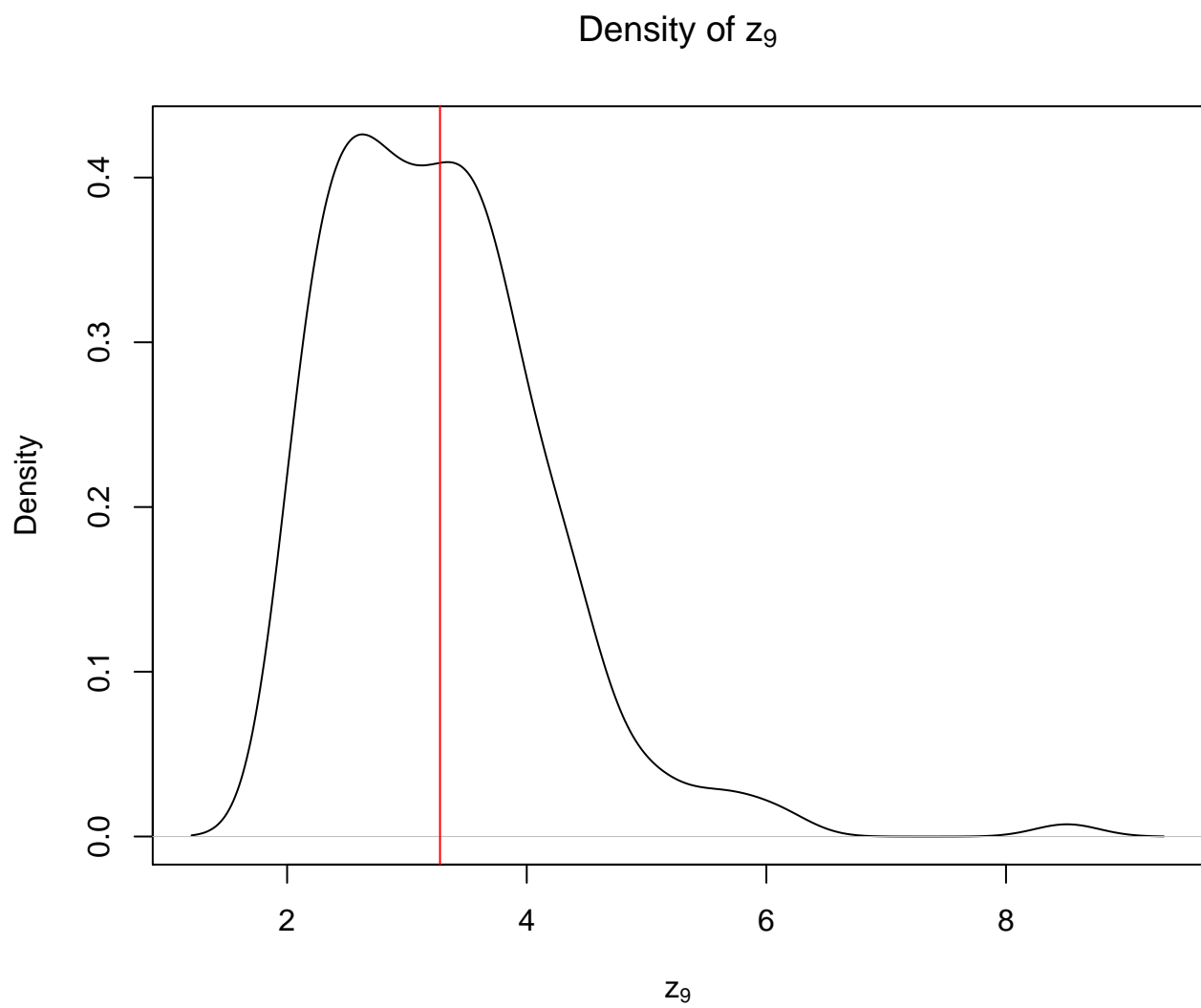


Figure 6: Estimated posterior density of z_9 (posterior mean in red).