Homework 8 Solution

Math 315, Fall 2019

BSM Chapter 3 exercise 4

(a)

$$\begin{aligned}
p(\sigma_1^2|Y_1,\ldots,Y_n,\sigma_2^2,\ldots,\sigma_n^2,b) &\propto \prod_{i=1}^n f(y_i|\sigma_i^2)\prod_{i=1}^n \pi(\sigma_i^2|b)\cdot\pi(b)\\
&\propto f(Y_1|\sigma_1^2)\pi(\sigma_1^2|b)\\
&\propto \left(\sigma_1^2\right)^{-1/2}\exp\left[-\frac{Y_1^2}{2\sigma_1^2}\right]\cdot\left(\sigma_1^2\right)^{-a-1}\exp\left[-\frac{b}{\sigma_1^2}\right]\\
&= \left(\sigma_1^2\right)^{-(a+1/2)-1}\exp\left[-\frac{1}{\sigma_1^2}\left(\frac{Y_1^2}{2}+b\right)\right]
\end{aligned}$$

So $\sigma_1^2|\text{rest} \sim \text{InvGamma}\left(a+\frac{1}{2},\ \frac{Y_1^2}{2}+b\right)$.

$$\begin{aligned}
p(b|Y_1,\ldots,Y_n,\sigma_2^1,\ldots,\sigma_n^2) &\propto \prod_{i=1}^n f(y_i|\sigma_i^2)\prod_{i=1}^n \pi(\sigma_i^2|b)\cdot\pi(b)\\
&\propto \prod_{i=1}^n \pi(\sigma_i^2|b)\cdot\pi(b)\\
&\propto \left[\prod_{i=1}^n b^a\left(\sigma_i^2\right)^{-a-1}\exp\left(-\frac{b}{\sigma_i^2}\right)\right]\cdot\exp\left(-b\right)\\
&\propto b^{na}\exp\left[-b\left(1+\sum_{i=1}^n\frac{1}{\sigma_i^2}\right)\right]
\end{aligned}$$

So $b|\text{rest} \sim \text{Gamma}\left(na+1,\ 1+\sum_{i=1}^n \frac{1}{\sigma_i^2}\right)$.

(b) Write psuedocode for the Gibbs sampler

1. Set the initial values of the parameters. Here, it is reasonable to set $\sigma_i^{2^{(0)}} = Y_i^2$ (since $E(Y_i)=0$), and $b=1$. Other starting values could also be used.
2. For each $s=1,\ldots,S$ do the following
   - Draw each $\sigma_i^{2^{(s)}}$ from $\text{InvGamma}\left(a+\frac{1}{2},\ \frac{Y_i^2}{2}+b^{(s-1)}\right)$.
   - Draw $b^{(s)}$ from $\text{Gamma}\left(na+1,\ 1+\sum_{i=1}^n 1/\sigma_i^{2^{(s)}}\right)$

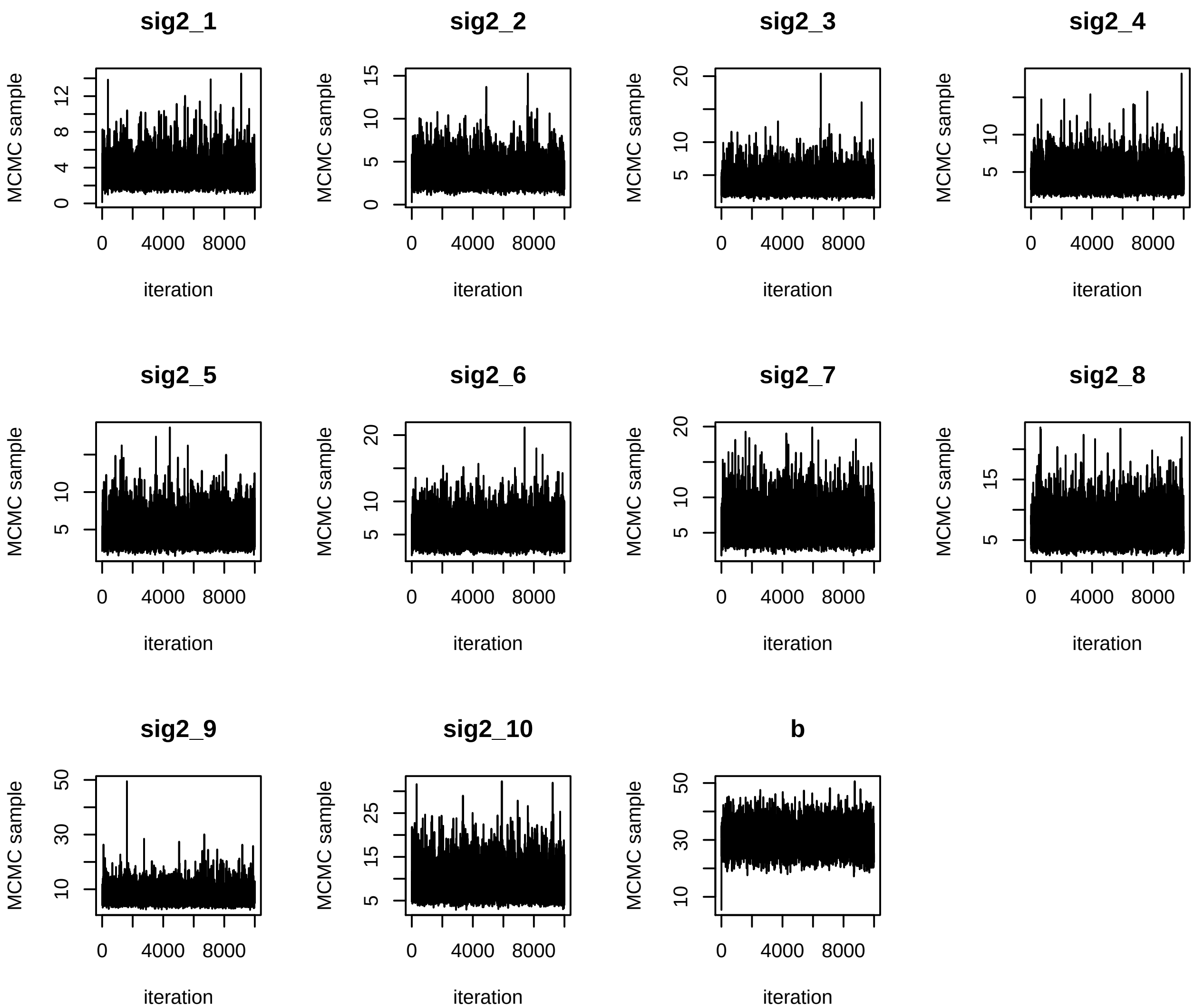
Note: Equivalently, you can sample $b^{(s)}$ first and then cycle through the σ_i^2.

(c) Write your own Gibbs sampler

```
# Data
y <- 1:10
n <- length(y)

# Prior specification
a <- 10

# Initial parameter values
s2i <- y^2
b   <- 1


# Create empty S x p matrix for MCMC draws
S                    <- 10000
mcmc.draws           <- matrix(NA, nrow = S, ncol = n + 1)


# Cycle through the full conditional distributions
for(i in 1:S) {
  # sample from each sigma^2_i | b, data
  sigma2 <- MCMCpack::rinvgamma(n, shape = a + 0.5, scale = y^2/2 + b)

  # sample from each b | sigma^2_i, data
  b <- rgamma(1, n * a + 1, 1 + sum(1 / sigma2))

  # Store the draws
  mcmc.draws[i, ] <- c(sigma2, b)
}
```

Before plotting the posterior distributions, we should assess convergence to see what draws are part of the burn-in period:

```
param_labels <- c(paste0("sig2_", 1:10), "b")
par(mfrow = c(3, 4))
for(i in 1:ncol(mcmc.draws)) {
  plot(x = 1:S, y = mcmc.draws[,i], xlab = "iteration", ylab = "MCMC sample",
       type = 'l', main = param_labels[i])
}
```

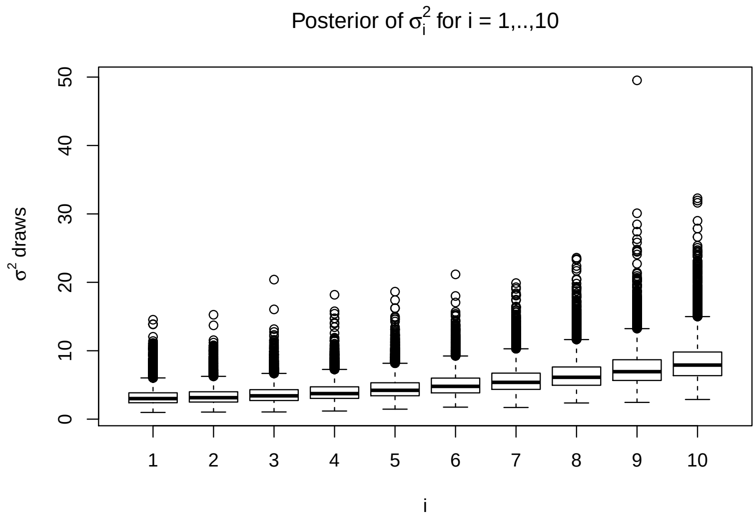


Overall, convergence appears to be very quick, so if we drop 100 iterations, we should safely be in the posterior distribution.

```
mcmc.draws <- mcmc.draws[-c(1:100),]
```

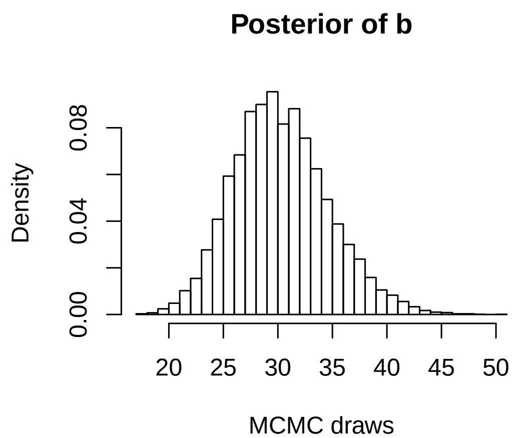
Now, let's plot the marginal distribution of each paramter. For the σ_i^2, side-by-side boxplots will allow us to compare key quantiles. We should, of course, draw histograms/density plots as well to check that each distribution is unimodal, since boxplots obscure the modality.

```
boxplot(mcmc.draws[, 1:10], xlab = "i", ylab = bquote(~sigma^2 ~draws),
        main = bquote("Posterior of" ~sigma[i]^2 ~"for i = 1,..,10"))
```



A histogram of the posterior for b is shown below:

```
hist(mcmc.draws[,11], freq = FALSE, xlab = "MCMC draws", main = bquote("Posterior of b"), breaks = 30)
```



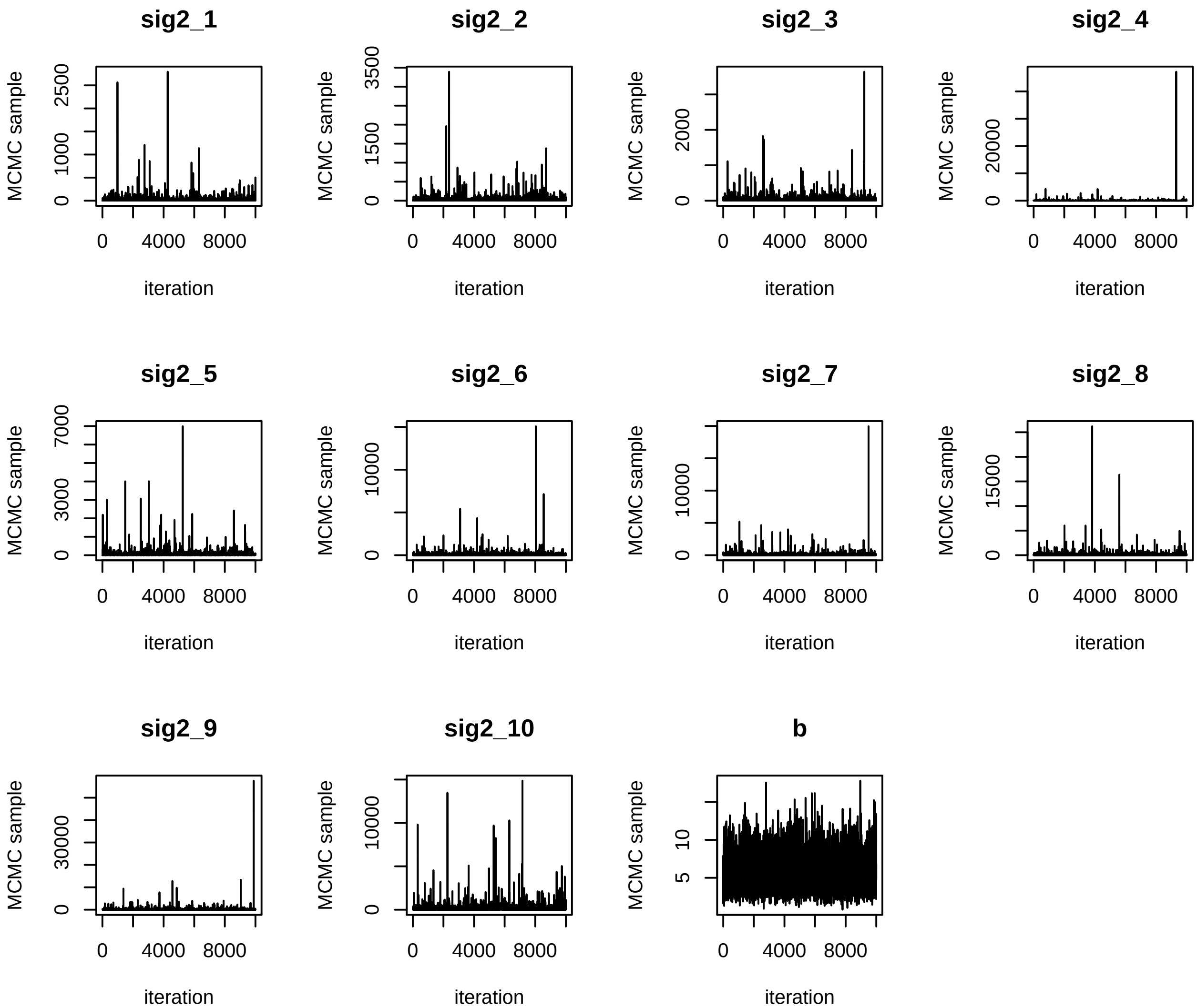
(d) Repeat the analysis with a = 1

```
# Data
y <- 1:10
n <- length(y)

# Prior specification
a <- 1

# Initial parameter values
s2i <- y^2
b   <- 1


# Create empty S x p matrix for MCMC draws
S                    <- 10000
mcmc.draws2          <- matrix(NA, nrow = S, ncol = n + 1)
```

```
# Cycle through the full conditional distributions
for(i in 1:S) {
  # sample from each sigma^2_i | b, data
  sigma2 <- MCMCpack::rinvgamma(n, shape = a + 0.5, scale = y^2/2 + b)

  # sample from each b | sigma^2_i, data
  b <- rgamma(1, n * a + 1, 1 + sum(1 / sigma2))

  # Store the draws
  mcmc.draws2[i, ] <- c(sigma2, b)
}
```

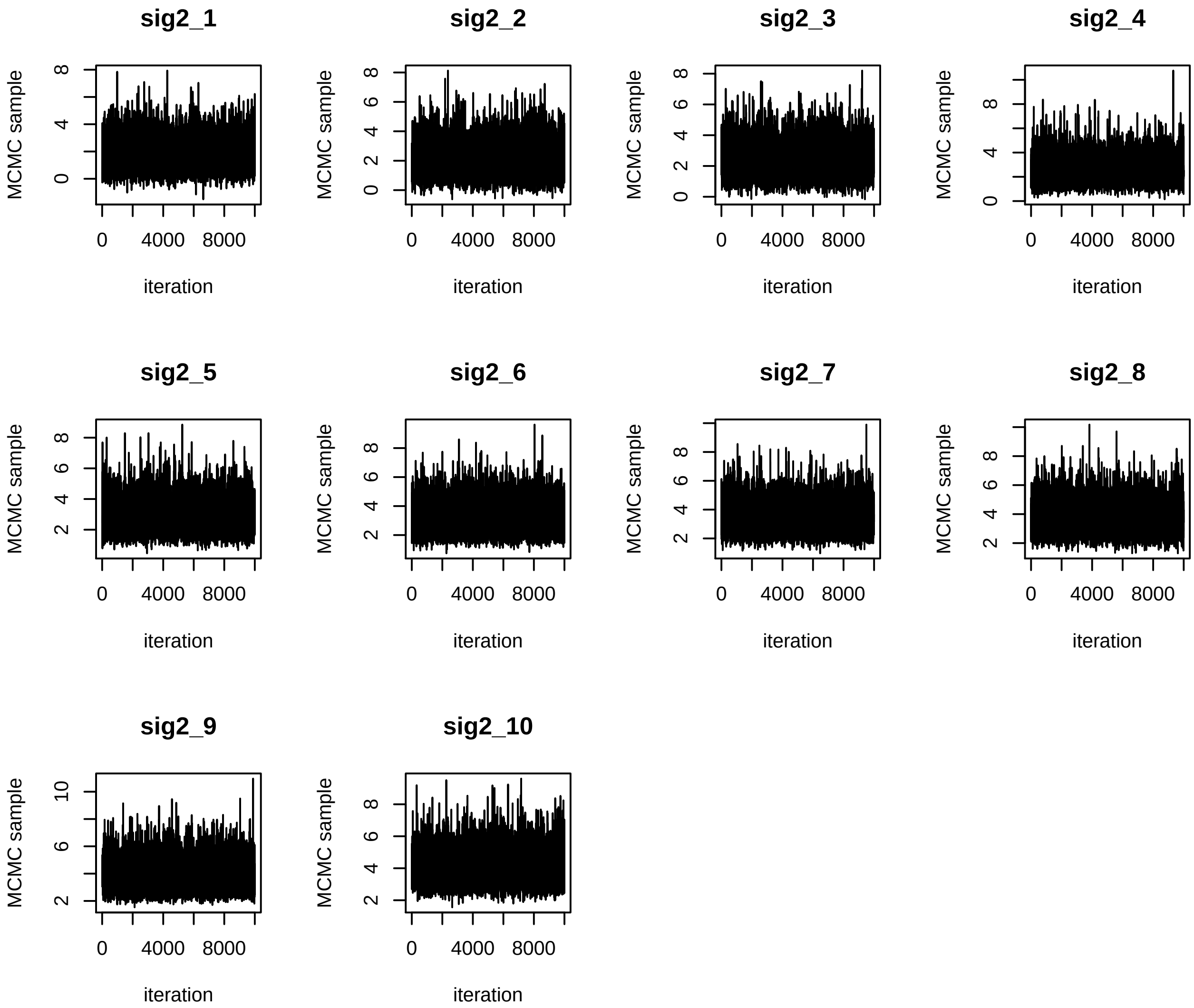
Again, let's assess the convergence of the chain:

```
param_labels <- c(paste0("sig2_", 1:10), "b")
par(mfrow = c(3, 4))
for(i in 1:ncol(mcmc.draws)) {
  plot(x = 1:S, y = mcmc.draws2[,i], xlab = "iteration", ylab = "MCMC sample", type = 'l', main = param_
}
```



Our chain converges for b very quickly, but it's very hard to assess convergence for the variances due to their volatility. To remedy this, we can log-transform the y-axis, which reveals convergence seem fine.

```
par(mfrow = c(3, 4))
for(i in 1:10) {
  plot(x = 1:S, y = log(mcmc.draws2[,i]), xlab = "iteration", ylab = "MCMC sample", type = 'l', main = p
}
```

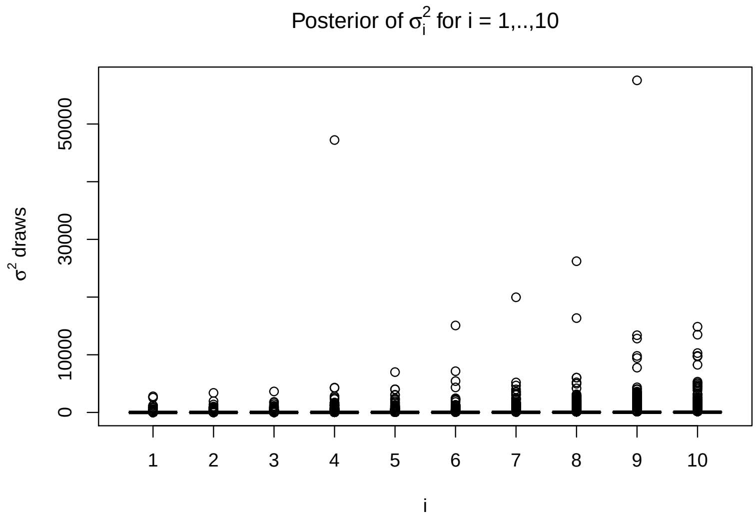


For now, let's assume that we've hit the stationary distribution in the first 200 iterations:

```
mcmc.draws2 <- mcmc.draws2[-c(1:200),]
```

Now, let's plot the marginal distribution of each paramter. For the σ_i^2, side-by-side boxplots will allow us to compare key quantiles. We should, of course, draw histograms/density plots as well to check that each distribution is unimodal, since boxplots obscure the modality.

```
boxplot(mcmc.draws2[, 1:10], xlab = "i", ylab = bquote(~sigma^2 ~draws), main = bquote("Posterior of" ~s
```



A histogram of the posterior for b is shown below:

```
hist(mcmc.draws2[,11], freq = FALSE, xlab = "MCMC draws", main = bquote("Posterior of b"), breaks = 30)
```