

Half Title

Solution Manual
Introduction to Bayesian Data Modeling: A GUIDed
toolkit using R



Title Page

Solution Manual
Introduction to Bayesian Data Modeling: A GUIDed
toolkit using R

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To my parents, Nancy and Orlando.



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Foreword





Preface



Symbols

Symbol Description

| | | | |
|-----------|----------------------|---------------|---------------------|
| \neg | Negation symbol. | \mathcal{R} | The Real set. |
| \propto | Proportional symbol. | \emptyset | Empty set. |
| \perp | Independence symbol. | $\mathbb{1}$ | Indicator function. |



Part I

Foundations: Theory, simulation methods and programming



1

Basic formal concepts

Solutions of Exercises

1. *The court case: the blue or green cap*

A cab was involved in a hit and run accident at night. There are two cab companies in the town: blue and green. The former has 150 cabs, and the latter 850 cabs. A witness said that a blue cab was involved in the accident; the court tested his/her reliability under the same circumstances, and got that 80% of the times the witness correctly identified the color of the cab. *What is the probability that the color of the cab involved in the accident was blue given that the witness said it was blue?*

Answer

Set WB and WG equal to the events that the witness said the cab was blue and green, respectively. Set B and G equal to the events that the cabs are blue and green, respectively. We need to calculate $P(B|WB)$, then:

$$\begin{aligned} P(B|WB) &= \frac{P(B, WB)}{P(WB)} \\ &= \frac{P(WB|B) \times P(B)}{P(WB|B) \times P(B) + (1 - P(WB|B)) \times (1 - P(B))} \\ &= \frac{0.8 \times 0.15}{0.8 \times 0.15 + 0.2 \times 0.85} \\ &= 0.41 \end{aligned} \tag{1.1}$$

2. *The Monty Hall problem*

What is the probability of winning a car in the *Monty Hall problem* switching the decision if there are four doors, where there are three goats and one car? Solve this problem analytically and computationally. What if there are n doors, $n - 1$ goats and one car?

Answer

Let's name P_i the event *contestant picks door No. i* , H_i the event *host picks door No. i* , and C_i the event *car is behind door No. i* . Let's assume that the

contestant picked door number 1, and the host picked door number 3, then the contestant is interested in the probability of the event $P(C_i|H_3, P_1)$, $i = 2$ or 4 . Then, $P(H_3|C_3, P_1) = 0$, $P(H_3|C_2, P_1) = P(H_3|C_4, P_1) = 1/2$ and $P(H_3|C_1, P_1) = 1/3$. Then,

$$\begin{aligned}
 P(C_i|H_3, P_1) &= \frac{P(C_i, H_3, P_1)}{P(H_3, P_1)} \\
 &= \frac{P(H_3|C_i, P_1)P(C_i|P_1)P(P_1)}{P(H_3|P_1) \times P(P_1)} \\
 &= \frac{P(H_3|C_i, P_1)P(C_i)}{P(H_3|P_1)} \\
 &= \frac{1/2 \times 1/4}{1/3} \\
 &= \frac{3}{8},
 \end{aligned} \tag{1.2}$$

where the third equation uses the fact that C_i and P_i are independent events, and $P(H_3|P_1) = 1/3$ due to this depending just on P_1 (not on C_i).

Therefore, changing the initial decision increases the probability of getting the car from $1/4$ to $3/8$!

Let's check the case with n doors, and assume that the contestant picks the door No. 1, the car is behind the door No. n , and the host, who knows what is behind each door, opens any of the remaining $n - 2$ doors, where there is a goat. The contestant is interested in the probability of the event:

$$\begin{aligned}
 P(C_n|(H_2 \cup \dots \cup H_{n-1}) \cap P_1) &= \frac{P((H_2 \cup H_3 \cup \dots \cup H_{n-1})|C_n \cap P_1)P(C_n|P_1)P(P_1)}{P((H_2 \cup H_3 \cup \dots \cup H_{n-1})|P_1)P(P_1)} \\
 &= \frac{[P(H_2|C_n \cap P_1) + \dots + P(H_{n-1}|C_n \cap P_1)]P(C_n)}{P(H_2|P_1) + P(H_3|P_1) + \dots + P(H_{n-1}|P_1)} \\
 &= \frac{1 \times (\frac{1}{n})}{\frac{1}{n-1} + \frac{1}{n-1} + \dots + \frac{1}{n-1}} \\
 &= \left(\frac{1}{n}\right) \left(\frac{n-1}{n-2}\right).
 \end{aligned} \tag{1.3}$$

In general, the probability of winning the car changing the pick is $\frac{1}{n} \frac{n-1}{n-2}$, while the probability of winning given no change is $\frac{1}{n}$. Given that $\frac{1}{n} \frac{n-1}{n-2} > \frac{1}{n}$ for all $n \geq 3$, where the difference between both probabilities is $\frac{1}{n(n-2)}$. We observe that as the number of doors increases, the difference between the two probabilities becomes zero.

Let's see a code for the general setting,

R code. The Monty Hall Problem

```

1 set.seed(0101) # Set simulation seed
2 S <- 100000 # Simulations
3 Game <- function(opt = 3){
4   # opt: number of options. opt > 2
5   opts <- 1:opt
6   car <- sample(opts, 1) # car location
7   guess1 <- sample(opts, 1) # Initial guess
8   if(opt == 3 && car != guess1) {
9     host <- opts[-c(car, guess1)]
10    } else {
11    host <- sample(opts[-c(car, guess1)], 1)
12  }
13  win1 <- guess1 == car # Win given no change
14  if(opt == 3) {
15    guess2 <- opts[-c(host, guess1)]
16  } else {
17    guess2 <- sample(opts[-c(host, guess1)], 1)
18  }
19  win2 <- guess2 == car # Win given change
20  return(c(win1, win2))
21 }
22 #Win probabilities
23 Prob <- rowMeans(replicate(S, Game(opt = 4)))
24 #Winning probabilities no changing door
25 Prob[1]
26 0.25151
27 #Winning probabilities changing door
28 Prob[2]
29 0.37267

```

3. Solve the health insurance example using a Gamma prior in the rate parametrization, that is, $\pi(\lambda) = \frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \lambda^{\alpha_0-1} \exp\{-\lambda\beta_0\}$.

Answer

First, we get the posterior distribution,

$$\pi(\lambda|\mathbf{y}) = \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \lambda^{\alpha_0-1} e^{-\lambda\beta_0} \right) \left(\prod_{i=1}^N \frac{\lambda^{y_i} e^{-\lambda}}{y_i!} \right) \quad (1.4)$$

$$\begin{aligned}
&= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \lambda^{\alpha_0-1} e^{-\lambda\beta_0} \right) \left(\frac{\lambda^{\sum_{i=1}^N y_i} e^{-N\lambda}}{\prod_{i=1}^N y_i!} \right) \\
&= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \frac{1}{\prod_{i=1}^N y_i!} \right) \lambda^{\sum_{i=1}^N y_i + \alpha_0 - 1} e^{-\lambda(\beta_0 + N)} \\
&\propto \lambda^{\sum_{i=1}^N y_i + \alpha_0 - 1} e^{-\lambda(\beta_0 + N)}.
\end{aligned} \tag{1.5}$$

The last expression is the kernel of a Gamma distribution with parameters $\alpha_n = \sum_{i=1}^N y_i + \alpha_0$ and $\beta_n = \beta_0 + N$.

Given that $\int_0^\infty \pi(\lambda|\mathbf{y}) d\lambda = 1$, then the constant of proportionality in the last expression is $\Gamma(\alpha_n) / \beta_n^{\alpha_n}$. Therefore the posterior density function $\pi(\lambda|\mathbf{y})$ is $G(\alpha_n, \beta_n)$.

The posterior mean is

$$\begin{aligned}
E[\lambda|\mathbf{y}] &= \frac{\alpha_n}{\beta_n} \\
&= \frac{\sum_{i=1}^N y_i + \alpha_0}{\beta_0 + N} \\
&= \left(\frac{N}{\beta_0 + N} \right) \bar{y} + \left(\frac{\beta_0}{\beta_0 + N} \right) \frac{\alpha_0}{\beta_0} \\
&= w\bar{y} + (1-w) E[\lambda],
\end{aligned} \tag{1.6}$$

where $w = \frac{N}{\beta_0 + N}$, \bar{y} is the sample mean, and $E[\lambda] = \frac{\alpha_0}{\beta_0}$.

The posterior predictive distribution is given by

$$\begin{aligned}
\pi(Y_0|\mathbf{y}) &= \int_0^\infty \frac{\lambda^{y_0} e^{-\lambda}}{y_0!} \pi(\lambda|\mathbf{y}) d\lambda \\
&= \int_0^\infty \left(\frac{\lambda^{y_0} e^{-\lambda}}{y_0!} \right) \left(\frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n)} \lambda^{\alpha_n-1} e^{-\lambda\beta_n} \right) d\lambda \\
&= \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n) y_0!} \int_0^\infty \lambda^{y_0 + \alpha_n - 1} e^{-\lambda(1+\beta_n)} d\lambda \\
&= \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n) y_0!} \frac{\Gamma(y_0 + \alpha_n)}{(1 + \beta_n)^{y_0 + \alpha_n}} \\
&= \frac{\Gamma(y_0 + \alpha_n)}{\Gamma(\alpha_n) y_0!} \left(\frac{1}{1 + \beta_n} \right)^{y_0} \left(\frac{\beta_n}{1 + \beta_n} \right)^{\alpha_n}
\end{aligned} \tag{1.7}$$

$$\begin{aligned}
&= \frac{(y_0 + \alpha_n - 1)!}{(\alpha_n - 1)! y_0!} \left(\frac{1}{1 + \beta_n} \right)^{y_0} \left(\frac{\beta_n}{1 + \beta_n} \right)^{\alpha_n} \\
&= \binom{y_0 + \alpha_n - 1}{y_0} \left(\frac{1}{1 + \beta_n} \right)^{y_0} \left(\frac{\beta_n}{1 + \beta_n} \right)^{\alpha_n}.
\end{aligned}$$

Therefore $Y_0|y \sim NB(\alpha_n, p_n)$ where $p_n = \frac{1}{1+\beta_n}$.

To use empirical Bayes, we have the following setting

$$[\hat{\alpha}_0, \hat{\beta}_0] = \arg \max_{\alpha_0, \beta_0} \ln(p(\mathbf{y})),$$

where

$$\begin{aligned}
p(y) &= \int_0^\infty \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \lambda^{\alpha_0-1} e^{-\lambda \beta_0} \right) \left(\prod_{i=1}^N \frac{\lambda^{y_i} e^{-\lambda}}{y_i!} \right) d\lambda \quad (1.8) \\
&= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0) \prod_{i=1}^N y_i!} \right) \int_0^\infty \lambda^{\sum_{i=1}^N y_i + \alpha_0 - 1} e^{-\lambda(\beta_0 + N)} d\lambda \\
&= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0) \prod_{i=1}^N y_i!} \right) \left(\frac{\Gamma(\sum_{i=1}^N y_i + \alpha_0)}{(\beta_0 + N)^{\sum_{i=1}^N y_i + \alpha_0}} \right) \\
&= \frac{\Gamma(\sum_{i=1}^N y_i + \alpha_0)}{\Gamma(\alpha_0) \prod_{i=1}^N y_i!} \left(\frac{1}{\beta_0 + N} \right)^{\sum_{i=1}^N y_i} \left(\frac{\beta_0}{\beta_0 + N} \right)^{\alpha_0}.
\end{aligned}$$

*R code. Health insurance, predictive distribution
using vague hyperparameters*

```

1 set.seed(010101)
2 y <- c(0, 3, 2, 1, 0) # Data
3 N <- length(y)
4
5 # Predictive distribution
6 ProbBo <- function(y, a0, b0){
7   N <- length(y)
8   #sample size
9   aN <- a0 + sum(y)
10  # Posterior shape parameter
11  bN <- b0 + N
12  # Posterior scale parameter
13  p <- 1 / (bN + 1)
14  # Probability negative binomial density
15  Pr <- 1 - pbinom(0, size = aN, prob = (1 - p))
16  # Probability of visiting the Doctor
17  # Observe that in R there is a slightly
18  # different parametrization.
19  return(Pr)
20 }
21
22 # Using a vague prior:
23 a0 <- 0.001 # Prior shape parameter
24 b0 <- 0.001 # Prior scale parameter
25 PriMeanV <- a0 / b0 # Prior mean
26 PriVarV <- a0 / b0^2 # Prior variance
27 Pp <- ProbBo(y, a0 = 0.001, b0 = 0.001)
28 # This setting is vague prior information.
29 Pp
30 0.67

```

*R code. Health insurance, predictive distribution
using empirical Bayes*

```

1 # Using Empirical Bayes
2 LogMgLik <- function(theta, y){
3   N <- length(y)
4   #sample size
5   a0 <- theta[1]
6   # prior shape hyperparameter
7   b0 <- theta[2]
8   # prior scale hyperparameter
9   aN <- sum(y) + a0
10  # posterior shape parameter
11  if(a0 <= 0 || b0 <= 0){
12    #Avoiding negative values
13    lnp <- -Inf
14  }else{lnp <- lgamma(aN) - sum(y)*log(b0+N) + a0*log(b0/(b0
15    +N)) - lgamma(a0)}
16    # log marginal likelihood
17    return(-lnp)
18  }
19  theta0 <- c(0.01, 0.01)
20  # Initial values
21  control <- list(maxit = 1000)
22  # Number of iterations in optimization
23  EmpBay <- optim(theta0, LogMgLik, method = "BFGS", control =
24    control, hessian = TRUE, y = y)
25  # Optimization
26  EmpBay$convergence
27  # Checking convergence
28  EmpBay$value # Maximum
29  a0EB <- EmpBay$par[1]
30  # Prior shape using empirical Bayes
31  a0EB
32  128.383
33  b0EB <- EmpBay$par[2]
34  # Prior scale using empirical Bayes
35  b0EB
36  106.801
37  PriMeanEB <- a0EB / b0EB
38  # Prior mean
39  PriVarEB <- a0EB / b0EB^2
40  # Prior variance
41  PpEB <- ProbBo(y, a0 = a0EB, b0 = b0EB)
42  # This setting is using empirical Bayes.
43  PpEB
44  0.69

```

4. Suppose that you are analyzing to buy a car insurance next year. To make

a better decision you want to know *what is the probability that you have a car claim next year?* You have the records of your car claims in the last 15 years, $\mathbf{y} = \{0, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 1, 0\}$.

Assume that this is a random sample from a data generating process (statistical model) that is Bernoulli, $Y_i \sim \text{Ber}(p)$, and your probabilistic prior beliefs about p are well described by a beta distribution with parameters α_0 and β_0 , $p \sim B(\alpha_0, \beta_0)$, then, you are interested in calculating the probability of a claim the next year $P(Y_0 = 1|\mathbf{y})$.

Solve this using an empirical Bayes approach and a non-informative approach where $\alpha_0 = \beta_0 = 1$ (uniform distribution).

Answer

The posterior distribution is given by

$$\begin{aligned} \pi(p|\mathbf{y}) &= \left[\frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0)\Gamma(\beta_0)} p^{\alpha_0-1} (1-p)^{\beta_0-1} \right] \left[\prod_{i=1}^N p^{y_i} (1-p)^{1-y_i} \right] \quad (1.9) \\ &= \frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0)\Gamma(\beta_0)} p^{\sum_{i=1}^N y_i + \alpha_0 - 1} (1-p)^{\beta_0 + N - \sum_{i=1}^N y_i - 1} \\ &\propto p^{\sum_{i=1}^N y_i + \alpha_0 - 1} (1-p)^{\beta_0 + N - \sum_{i=1}^N y_i - 1}. \end{aligned}$$

The last expression is the kernel of a Beta distribution with parameters $\alpha_n = \sum_{i=1}^N y_i + \alpha_0$ and $\beta_n = \beta_0 + N - \sum_{i=1}^N y_i$. Thus, the posterior mean is

$$\begin{aligned} E[p|\mathbf{y}] &= \frac{\alpha_n}{\alpha_n + \beta_n} \\ &= \frac{\sum_{i=1}^N y_i + \alpha_0}{\alpha_0 + \beta_0 + N} \quad (1.10) \\ &= \frac{N\bar{y}}{\alpha_0 + \beta_0 + N} + \frac{\alpha_0}{\alpha_0 + \beta_0 + N} \\ &= \frac{N}{\alpha_0 + \beta_0 + N} (\bar{y}) + \frac{\alpha_0 + \beta_0}{\alpha_0 + \beta_0 + N} \left(\frac{\alpha_0}{\alpha_0 + \beta_0} \right) \\ &= w(\bar{y}) + (1-w)E[p], \end{aligned}$$

where $w = \frac{N}{\alpha_0 + \beta_0 + N}$, \bar{y} is the sample mean, and $E[p] = \frac{\alpha_0}{\alpha_0 + \beta_0}$ is the prior mean.

The posterior predictive distribution of claim the next year is given by

$$\begin{aligned}
\pi(Y_0 = 1|\mathbf{y}) &= \int_0^1 P(Y_0 = 1|\mathbf{y}, p) \pi(p|\mathbf{y}) dp \\
&= \int_0^1 p \times \pi(p|\mathbf{y}) dp \\
&= \mathbb{E}[p|\mathbf{y}] \\
&= \frac{\alpha_n}{\alpha_n + \beta_n}.
\end{aligned} \tag{1.11}$$

To use empirical Bayes, we have the following setting

$$[\hat{\alpha}_0 \ \hat{\beta}_0] = \arg \max_{\alpha_0, \beta_0} \ln(p(\mathbf{y})),$$

where

$$\begin{aligned}
p(\mathbf{y}) &= \int_0^1 \left[\frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0) \Gamma(\beta_0)} p^{\alpha_0-1} (1-p)^{\beta_0-1} \right] \left[\prod_{i=1}^N (1-p)^{1-y_i} \right] dp \tag{1.12} \\
&= \frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0) \Gamma(\beta_0)} \int_0^1 p^{\sum_{i=1}^N y_i + \alpha_0 - 1} (1-p)^{\beta_0 + N - \sum_{i=1}^N y_i - 1} dp \\
&= \frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0) \Gamma(\beta_0)} \frac{\Gamma\left(\sum_{i=1}^N y_i + \alpha_0\right) \Gamma\left(\beta_0 + N - \sum_{i=1}^N y_i\right)}{\Gamma(\alpha_0 + \beta_0 + N)}.
\end{aligned}$$

*R code. Car claim, predictive distribution using
vague hyperparameters*

```

1 set.seed(010101)
2 y <- c(0, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 1, 0)
3 # Data
4 N <- length(y)
5 #require(TailRank)
6 # Predictive distribution
7 ProbBo <- function(y, a0, b0){
8   N <- length(y)
9   #sample size
10  aN <- a0 + sum(y)
11  # Posterior shape parameter
12  bN <- b0 + N - sum(y)
13  # Posterior scale parameter
14  pr <- aN / (aN + bN)
15  # Probability of a claim the next year
16  return(pr)
17 }
18 # Using a vague prior:
19 a0 <- 1 # Prior shape parameter
20 b0 <- 1 # Prior scale parameter
21 PriMeanV <- a0 / (a0 + b0)
22 # Prior mean
23 PriVarV <- (a0*b0) / (((a0+b0)^2)*(a0+b0+1))
24 # Prior variance
25 Pp <- ProbBo(y, a0 = 1, b0 = 1)
26 # This setting is defining vague prior information.
27 # The probability of a claim
28 Pp
29 0.47

```

R code. Car claim, predictive distribution using empirical Bayes

```

1 # Using Empirical Bayes
2 LogMgLik <- function(theta, y){
3   N <- length(y)
4   #sample size
5   a0 <- theta[1]
6   # prior shape hyperparameter
7   b0 <- theta[2]
8   # prior scale hyperparameter
9   aN <- sum(y) + a0
10  # posterior shape parameter
11  if(a0 <= 0 || b0 <= 0){
12    #Avoiding negative values
13    lnp <- -Inf
14  }else{lnp <- lgamma(a0+b0) + lgamma(aN) + lgamma(b0+N-sum(
15    y)) -lgamma(a0) - lgamma(b0) - lgamma(a0+b0+N)}
16  # log marginal likelihood
17  return(-lnp)
18 }
19 theta0 <- c(0.1, 0.1)
20 # Initial values
21 control <- list(maxit = 1000)
22 # Number of iterations in optimization
23 EmpBay <- optim(theta0, LogMgLik, method = "BFGS", control =
24   control, hessian = TRUE, y = y)
25 # Optimization
26 EmpBay$convergence
27 # Checking convergence
28 EmpBay$value # Maximum
29 a0EB <- EmpBay$par[1]
30 # Prior shape using empirical Bayes
31 b0EB <- EmpBay$par[2]
32 # Prior scale using empirical Bayes
33 PriMeanEB <- a0EB / (a0EB + b0EB)
34 # Prior mean
35 PriVarEB <- (a0EB*b0EB) / (((a0EB+b0EB)^2)*(a0EB+b0EB+1))
36 # Prior variance
37 PpEB <- ProbBo(y, a0 = a0EB, b0 = b0EB)
38 # This setting is using empirical Bayes.
39 PpEB
40 0.47

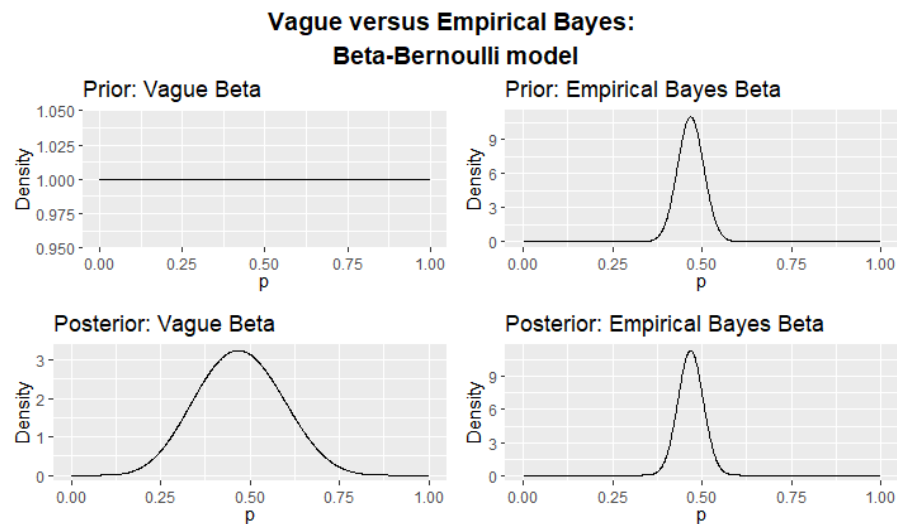
```

R code. Car claim, density plots

```

1 # Density figures
2 lambda <- seq(0.001, 1, 0.001)
3 # Values of lambda
4 VaguePrior <- dbeta(lambda, shape1 = a0, shape2 = b0)
5 EBPrior <- dbeta(lambda, shape1 = a0EB, shape2 = b0EB)
6 PosteriorV <- dbeta(lambda, shape1 = a0 + sum(y), shape2 =
  b0 + N - sum(y))
7 PosteriorEB <- dbeta(lambda, shape1 = a0EB + sum(y), shape2
  = b0EB + N - sum(y))
8 # Likelihood function
9 Likelihood <- function(theta, y){
10   LogL <- dbinom(y, 1, theta, log = TRUE)
11   # LogL <- dbern(y, theta)
12   Lik <- prod(exp(LogL))
13   return(Lik)
14 }
15 Liks <- sapply(lambda, function(par) {Likelihood(par, y = y)
  })
16 Sc <- max(PosteriorEB)/max(Liks)
17 #Scale for displaying in figure
18 LiksScale <- Liks * Sc
19 data <- data.frame(cbind(lambda, VaguePrior, EBPrior,
  PosteriorV, PosteriorEB, LiksScale))
20 #Data frame
21 require(ggplot2)
22 # Cool figures
23 require(latex2exp)
24 # LaTeX equations in figures
25 require(ggpubr)
26 # Multiple figures in one page
27 fig1 <- ggplot(data = data, aes(lambda, VaguePrior)) +
  geom_line() +
  xlab(TeX("$p$")) + ylab("Density") + ggtitle("Prior: Vague
  Beta")
28 fig2 <- ggplot(data = data, aes(lambda, EBPrior)) +
  geom_line() +
  xlab(TeX("$p$")) + ylab("Density") +
  ggtitle("Prior: Empirical Bayes Beta")
29 fig3 <- ggplot(data = data, aes(lambda, PosteriorV)) +
  geom_line() +
  xlab(TeX("$p$")) + ylab("Density") +
  ggtitle("Posterior: Vague Beta")
30 fig4 <- ggplot(data = data, aes(lambda, PosteriorEB)) +
  geom_line() +
  xlab(TeX("$p$")) + ylab("Density") +
  ggtitle("Posterior: Empirical Bayes Beta")
31 FIG <- ggarrange(fig1, fig2, fig3, fig4,
32 ncol = 2, nrow = 2)
33 annotate_figure(FIG,
34 top = text_grob("Vague versus Empirical Bayes: Beta-
  Bernoulli model", color = "black", face = "bold", size =
  14))

```

**FIGURE 1.1**

Vague versus Empirical Bayes: Bernoulli-Beta model.

*R code. Car claim, prior, likelihood and posterior
density plots*

```

1 # Prior, likelihood and posterior:
2 #Empirical Bayes Binomial-Beta model
3 dataNew <- data.frame(cbind(rep(lambda, 3),
4 c(EBPrior, PosteriorEB, Likelihood),
5 rep(1:3, each = 1000)))
6 #Data frame
7
8 colnames(dataNew) <- c("Lambda", "Density", "Factor")
9 dataNew$Factor <- factor(dataNew$Factor, levels=c("1", "3",
10 "2"), labels=c("Prior", "Likelihood", "Posterior"))
11
12 ggplot(data = dataNew, aes_string(x = "Lambda",
13 y = "Density", group = "Factor")) +
14 geom_line(aes(color = Factor)) +
15 xlab(TeX("$\\lambda$")) + ylab("Density") +
16 ggtitle("Prior, likelihood and posterior: Empirical Bayes
17 Poisson-Gamma model") +
18 guides(color=guide_legend(title="Information")) +
19 scale_color_manual(values = c("red", "yellow", "blue"))

```

**FIGURE 1.2**

Prior, likelihood and posterior: Bernoulli-Beta model.

R code. Car claim, predictive probabilities plots

```

1 # Predictive distributions
2 require(TailRank)
3 PredDen <- function(y, y0, a0, b0){
4   N <- length(y)
5   aN <- a0 + sum(y) # Posterior shape parameter
6   bN <- b0 + N - sum(y) # Posterior scale parameter
7   Pr <- aN/(aN+bN)
8   Probs <- dbinom(y0, 1, prob = Pr)
9   return(Probs)
10 }
11 y0 <- 0:1
12 PredVague <- PredDen(y = y, y0 = y0, a0 = a0, b0 = b0)
13 PredEB <- PredDen(y = y, y0 = y0, a0 = a0EB, b0 = b0EB)
14 dataPred <- as.data.frame(cbind(y0, PredVague, PredEB))
15 colnames(dataPred) <- c("y0", "PredictiveVague",
16   "PredictiveEB")
17 ggplot(data = dataPred) +
18   geom_point(aes(y0, PredictiveVague, color = "red")) +
19   xlab(TeX("$y_0$")) + ylab("Density") +
20   ggtitle("Predictive density: Vague and Empirical Bayes
21     priors") + geom_point(aes(y0, PredictiveEB, color = "
22     yellow")) +
23   guides(color = guide_legend(title="Prior")) +
24   scale_color_manual(labels = c("Vague", "Empirical Bayes"),
25     values = c("red", "yellow")) +
26   scale_x_continuous(breaks=seq(0,1,by=1))

```

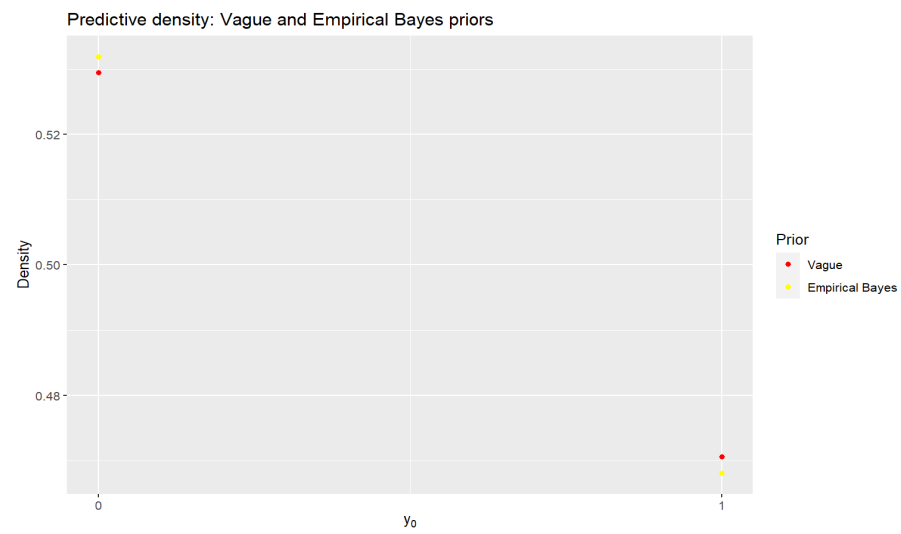


FIGURE 1.3
Predictive probabilities: Bernoulli-Beta model.

R code. Car claim, Bayesian model average

```

1 # Posterior odds: Vague vs Empirical Bayes
2 P012 <- exp(-LogMgLik(c(a0EB, b0EB), y = y))/exp(-LogMgLik(c
  (a0, b0), y = y))
3 PostProMEM <- P012/(1 + P012)
4 # Posterior model probability Empirical Bayes
5 PostProMEM
6 0.757
7 PostProbMV <- 1 - PostProMEM
8 # Posterior model probability vague prior
9 PostProbMV
10 0.242
11 # Bayesian model average (BMA)
12 PostMeanEB <- (a0EB + sum(y)) / (a0EB + b0EB + N)
13 # Posterior mean Empirical Bayes
14 PostMeanV <- (a0 + sum(y)) / (a0 + b0 + N)
15 # Posterior mean vague priors
16 BMAMean <- PostProMEM * PostMeanEB + PostProbMV * PostMeanV
17 # BMA posterior mean
18 PostVarEB <- (a0EB + sum(y))*(b0EB + N - sum(y)) / ((a0EB +
  b0EB + N)^2*(a0EB + b0EB + N - 1))
19 # Posterior variance Empirical Bayes
20 PostVarV <- (a0 + sum(y))*(b0 + N - sum(y)) / ((a0 + b0 + N)
  ^2*(a0 + b0 + N - 1))
21 # Posterior variance vague prior
22 BMAVar <- PostProMEM * PostVarEB + PostProbMV * PostVarV +
  PostProMEM * (PostMeanEB - BMAMean)^2 + PostProbMV * (
  PostMeanV - BMAMean)^2
23 # BMA posterior variance
24 # BMA: Predictive
25 BMAPred <- PostProMEM * PredEB + PostProbMV * PredVague
26 dataPredBMA <- as.data.frame(cbind(y0, BMAPred))
27 colnames(dataPredBMA) <- c("y0", "PredictiveBMA")
28 ggplot(data = dataPredBMA) +
29   geom_point(aes(y0, PredictiveBMA, color = "red")) +
30   xlab(TeX("$y_0$")) + ylab("Density") +
31   ggtitle("Predictive density: BMA") +
32   guides(color = guide_legend(title="BMA")) +
33   scale_color_manual(labels = c("Probability"), values = c("
  red")) + scale_x_continuous(breaks=seq(0,1,by=1))

```


R code. Car claim, Bayesian updating plots

```

1 # Bayesian updating
2 BayUp <- function(y, lambda, a0, b0){
3   N <- length(y)
4   aN <- a0 + sum(y)
5   # Posterior shape parameter
6   bN <- b0 + N - sum(y)
7   # Posterior scale parameter
8   p <- dbeta(lambda, shape1 = aN, shape2 = bN)
9   # Posterior density
10  return(list(Post = p, a0New = aN, b0New = bN))
11 }
12 PostUp <- NULL
13 for(i in 1:N){
14   if(i == 1){
15     PostUpi <- BayUp(y[i], lambda, a0 = 1, b0 = 1)}
16   else{
17     PostUpi <- BayUp(y[i], lambda,
18       a0 = PostUpi$a0New, b0 = PostUpi$b0New)
19   }
20   PostUp <- cbind(PostUp, PostUpi$Post)
21 }
22 DataUp <- data.frame(cbind(rep(lambda, 15), c(PostUp), rep
23   (1:15, each = 1000))) #Data frame
24 colnames(DataUp) <- c("Lambda", "Density", "Factor")
25 DataUp$Factor <- factor(DataUp$Factor, levels=c("1","2","3",
26   "4","5","6","7","8","9","10","11","12","13","14","15"),
27   labels=c("Iter_1","Iter_2","Iter_3","Iter_4","Iter_5",
28     "Iter_6","Iter_7","Iter_8","Iter_9","Iter_10","Iter_11",
29     "Iter_12","Iter_13","Iter_14","Iter_15"))
30 ggplot(data = DataUp, aes_string(x = "Lambda",
31   y = "Density", group = "Factor")) +
32   geom_line(aes(color = Factor)) +
33   xlab(TeX("$p$")) + ylab("Density") +
34   ggtitle("Bayesian updating:
35   Beta-Binomial model with vague prior") +
36   guides(color=guide_legend(title="Update"))

```

5. Show that given the loss function, $L(\theta, a) = |\theta - a|$, then the optimal decision rule minimizing the risk function, $a^*(\mathbf{y})$, is the median.

Answer

$\int_{\Theta} |\theta - a| \pi(\theta|\mathbf{y}) d\theta = \int_{-\infty}^a (a - \theta) \pi(\theta|\mathbf{y}) d\theta + \int_a^{\infty} (\theta - a) \pi(\theta|\mathbf{y}) d\theta$. Differentiating with respect to a , and equating to zero,

$$\int_{-\infty}^a \pi(\theta|\mathbf{y}) d\theta = \int_a^{\infty} \pi(\theta|\mathbf{y}) d\theta, \quad (1.13)$$

**FIGURE 1.4**

Predictive probabilities: Bernoulli-Beta Bayesian model average.

**FIGURE 1.5**

Predictive probabilities: Bernoulli-Beta Bayesian model updating.

then,

$$2 \int_{-\infty}^a \pi(\theta|\mathbf{y}) d\theta = \int_{-\infty}^{\infty} \pi(\theta|\mathbf{y}) d\theta = 1, \quad (1.14)$$

that is, $a^*(\mathbf{y})$ is the median.



2

Conceptual differences of the Bayesian and Frequentist approaches

Solutions of Exercises

1. Jeffreys-Lindley's paradox

The **Jeffreys-Lindley's paradox** [10, 15] is an apparent disagreement between the Bayesian and Frequentist frameworks to a hypothesis testing situation.

In particular, assume that in a city 49,581 boys and 48,870 girls have been born in 20 years. Assume that the male births is distributed Binomial with probability θ . We want to test the null hypothesis H_0 . $\theta = 0.5$ versus H_1 . $\theta \neq 0.5$.

- Show that the posterior model probability for the model under the null is approximately 0.95. Assume $\pi(H_0) = \pi(H_1) = 0.5$, and $\pi(\theta)$ equal to $U(0, 1)$ under H_1 .
- Show that the p -value for this hypothesis test is equal to 0.023 using the normal approximation, $Y \sim N(N \times \theta, N \times \theta \times (1 - \theta))$.

Answer

- The marginal likelihood under the null hypothesis is $p(y|H_0) = \binom{n}{y} \theta^y (1 - \theta)^{n-y} \approx 1.95 \times 10^{-4}$ given $\theta = 0.5$ under H_0 , $N = 49,581 + 48,870$ and $y = 49,581$. On the other hand, the marginal likelihood under the alternative hypothesis is

$$\begin{aligned}
p(y|H_1) &= \int_0^1 \binom{n}{y} \theta^y (1-\theta)^{n-y} d\theta \\
&= \binom{n}{y} B(y+1, n-k+1) \\
&= \frac{\Gamma(N+1)}{\Gamma(y+1)\Gamma(n-y+1)} \frac{\Gamma(y+1)\Gamma(N-y+1)}{\Gamma(N+2)} \\
&= \frac{N!}{(N+1)!} \\
&= \frac{1}{N+1} \\
&\approx 1.016 \times 10^{-5}.
\end{aligned}$$

Then, $PO_{01} = \frac{1.95 \times 10^{-4}}{1.016 \times 10^{-5}} = 19.19$, this implies that the posterior model probability under the null hypothesis is $\pi(H_0|y) = \frac{19.19}{1+19.19} = 0.95$.

- Under the null hypothesis,

$$\begin{aligned}
p &= 2 \int_{49,581}^{\infty} (2\pi\sigma^2)^{-1/2} \exp\left\{-\frac{1}{2\sigma^2}(y-\mu)^2\right\} dy \\
&= 0.0235,
\end{aligned}$$

where $\mu = N \times \theta = 49,225.5$, and $\sigma^2 = N \times \theta \times (1-\theta) = 24,612.75$ under the null hypothesis ($\theta = 0.5$).

Observe that the posterior model probability supports the null hypothesis, whereas the p-value implies rejection of the null hypothesis using a 5% significance level.

Observe that actually this is not a paradox, as we are answering two different questions. The Bayes factor is comparing two models ($\theta = 0.5$ versus $\theta \sim U(0,1)$), whereas the p-value is checking the compatibility between $\theta = 0.5$ and the sample information. Despite that $\theta = 0.5$ is not compatible with sample information, it is better than the models assuming $\theta \sim U(0,1)$ as most of these values of θ are far away from the sample mean. Thus, the model under the null is a bad description of the data, but it is better than the model under the alternative hypothesis.¹

¹Observe that there are at least another two issues in this example. First, the prior under the alternative is non-informative, this implies problems for Bayes factors, and second, the prior under the alternative is positive at $\theta = 0.5$, which is the null ([12] propose non-local prior densities in Bayesian hypothesis tests to tackle these issues).

2. We want to test $H_0: \mu = \mu_0$ vs $H_1: \mu \neq \mu_0$ given $y_i \stackrel{iid}{\sim} N(\mu, \sigma^2)$.

Assume $\pi(H_0) = \pi(H_1) = 0.5$, and $\pi(\mu, \sigma) \propto 1/\sigma$ under the alternative hypothesis.

Show that

$$p(\mathbf{y}|\mathcal{M}_1) = \frac{\pi^{-N/2}}{2} \Gamma(N/2) 2^{N/2} \left(\frac{1}{\alpha_n \hat{\sigma}^2} \right)^{N/2} \left(\frac{N}{\alpha_n \hat{\sigma}^2} \right)^{-1/2} \frac{\Gamma(1/2) \Gamma(\alpha_n/2)}{\Gamma((\alpha_n+1)/2)} \text{ and}$$

$$p(\mathbf{y}|\mathcal{M}_0) = (2\pi)^{-N/2} \left[\frac{2}{\Gamma(N/2)} \left(\frac{N}{2} \frac{\sum_{i=1}^N (y_i - \mu_0)^2}{N} \right)^{N/2} \right]^{-1}. \text{ Then,}$$

$$PO_{01} = \frac{p(\mathbf{y}|\mathcal{M}_0)}{p(\mathbf{y}|\mathcal{M}_1)}$$

$$= \frac{\Gamma((\alpha_n + 1)/2)}{\Gamma(1/2) \Gamma(\alpha_n/2)} (\alpha_n \hat{\sigma}^2 / N)^{-1/2} \left[1 + \frac{(\mu_0 - \bar{y})^2}{\alpha_n \hat{\sigma}^2 / N} \right]^{-\left(\frac{\alpha_n + 1}{2}\right)},$$

where $\alpha_N = N - 1$ and $\hat{\sigma}^2 = \frac{\sum_{i=1}^N (y_i - \bar{y})^2}{N - 1}$.

Find the relationship between the posterior odds and the classical test statistic for the null hypothesis.

Answer

$$\begin{aligned} p(\mathbf{y}|\mathcal{M}_1) &= \int_{-\infty}^{\infty} \int_0^{\infty} (2\pi)^{-N/2} \sigma^{-N} \exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^N (y_i - \mu)^2 \right\} \frac{1}{\sigma} d\sigma d\mu \\ &= (2\pi)^{-N/2} \int_{-\infty}^{\infty} \int_0^{\infty} \sigma^{-(N+1)} \exp \left\{ -\frac{N}{2\sigma^2} \frac{\sum_{i=1}^N (y_i - \mu)^2}{N} \right\} d\sigma d\mu \\ &= (2\pi)^{-N/2} \frac{\Gamma(N/2)}{2} 2^{N/2} \int_{-\infty}^{\infty} \left[\sum_{i=1}^N (y_i - \mu)^2 \right]^{-N/2} d\mu \\ &= (2\pi)^{-N/2} \frac{\Gamma(N/2)}{2} 2^{N/2} \int_{-\infty}^{\infty} \left[\sum_{i=1}^N [(y_i - \bar{y}) - (\mu - \bar{y})]^2 \right]^{-N/2} d\mu \\ &= (2\pi)^{-N/2} \frac{\Gamma(N/2)}{2} 2^{N/2} \int_{-\infty}^{\infty} [\alpha_n \hat{\sigma}^2 + N(\mu - \bar{y})^2]^{-N/2} d\mu \\ &= (2\pi)^{-N/2} \frac{\Gamma(N/2)}{2} 2^{N/2} \left(\frac{\alpha_n \hat{\sigma}^2}{\alpha_n \hat{\sigma}^2} \right)^{-N/2} \int_{-\infty}^{\infty} [\alpha_n \hat{\sigma}^2 + N(\mu - \bar{y})^2]^{-N/2} d\mu \\ &= (2\pi)^{-N/2} \frac{\Gamma(N/2)}{2} 2^{N/2} (\alpha_n \hat{\sigma}^2)^{-N/2} \int_{-\infty}^{\infty} \left[1 + \frac{N(\mu - \bar{y})^2}{\alpha_n \hat{\sigma}^2} \right]^{-N/2} d\mu \\ &= \frac{\pi^{-N/2}}{2} \Gamma(N/2) 2^{N/2} \left(\frac{1}{\alpha_n \hat{\sigma}^2} \right)^{N/2} \left(\frac{N}{\alpha_n \hat{\sigma}^2} \right)^{-1/2} \frac{\Gamma(1/2) \Gamma(\alpha_n/2)}{\Gamma((\alpha_n + 1)/2)}. \end{aligned}$$

The third line takes into account that the integral in the second line is the kernel of an inverted-gamma distribution, and the last line takes into account that the integral in the previous line is the kernel of a student's t distribution [34].

$$\begin{aligned}
p(\mathbf{y}|\mathcal{M}_0) &= \int_0^\infty (2\pi)^{-N/2} \sigma^{-N} \exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^N (y_i - \mu_0)^2 \right\} \frac{1}{\sigma} d\sigma \\
&= (2\pi)^{-N/2} \int_0^\infty \sigma^{-(N+1)} \exp \left\{ -\frac{N}{2\sigma^2} \frac{\sum_{i=1}^N (y_i - \mu_0)^2}{N} \right\} d\sigma \\
&= (2\pi)^{-N/2} \left[\frac{2}{\Gamma(N/2)} \left(\frac{N}{2} \frac{\sum_{i=1}^N (y_i - \mu_0)^2}{N} \right)^{N/2} \right]^{-1}.
\end{aligned}$$

The third line takes into account that the integral in the second line is the kernel of an inverted-gamma distribution [34].

Given these results is easy to get PO_{01} .

In addition,

$$\begin{aligned}
PO_{01} &= \frac{\Gamma((\alpha_n + 1)/2)}{\Gamma(1/2)\Gamma(\alpha_N/2)} (\alpha_n \hat{\sigma}^2/N)^{-1/2} \left[1 + \frac{(\mu_0 - \bar{y})^2}{\alpha_n \hat{\sigma}^2/N} \right]^{-\left(\frac{\alpha_n+1}{2}\right)} \\
&= \frac{\Gamma((\alpha_n + 1)/2)}{\Gamma(1/2)\Gamma(\alpha_N/2)} (\alpha_n \hat{\sigma}^2/N)^{-1/2} \left[1 + \frac{1}{\alpha_n} \left(\frac{\mu_0 - \bar{y}}{\hat{\sigma}/\sqrt{N}} \right)^2 \right]^{-\left(\frac{\alpha_n+1}{2}\right)} \\
&= \frac{\Gamma((\alpha_n + 1)/2)}{\Gamma(1/2)\Gamma(\alpha_N/2)} (\alpha_n \hat{\sigma}^2/N)^{-1/2} \left[1 + \frac{1}{\alpha_n} t^2 \right]^{-\left(\frac{\alpha_n+1}{2}\right)},
\end{aligned}$$

where $t = \frac{\bar{y} - \mu_0}{\hat{\sigma}/\sqrt{N}}$ is the classical statistical test. Then, as t increases then the PO_{01} decreases, both indicating support against the null hypothesis H_0 . $\mu = \mu_0$. However, there are other terms affecting the posterior odds, then, there is no necessary agreement between the classical test statistic and the posterior odds.

3. Math test continues

Using the setting of the **Example: Math test** in subsection 2.6.1 in the book, test H_0 . $\mu = \mu_0$ vs H_1 . $\mu \neq \mu_0$ where $\mu_0 = \{100, 100.5, 101, 101.5, 102\}$.

- What is the p -value for these hypothesis tests?
- Find the posterior model probability of the null model for each μ_0 .

Answer

R code. Example: Math test

```

1 N <- 50 # Sample size
2 y_bar <- 102 # Sample mean
3 s2 <- 10 # Sample variance
4 alpha <- N - 1
5 serror <- (s2/N)^0.5
6 y.H0 <- c(100, 100.5, 101, 101.5, 102)
7 test <- (y.H0 - y_bar)/serror
8 pval <- 2*pt(test, alpha)
9 pval
10 0.0000459 0.0015431 0.0299338 0.2690040 1
11 # p-values
12 P001 <- (gamma(N/2)*((N-1)*serror^2)^(-0.5)*(1+test^2/alpha)
13         ^(-N/2))/(gamma(1/2)*gamma((N-1)/2))
14 P001/(1+P001)
15 0.0001705 0.0050345 0.0725330 0.3210223 0.4702050
16 # Posterior model probability of the null hypothesis.

```



3

Cornerstone models: Conjugate families

Solutions of Exercises

1. Write in the canonical form the distribution of the Bernoulli example, and find the mean and variance of the sufficient statistic.

Answer

Given $p(\mathbf{y}|\theta) = (1-\theta)^N \exp \left\{ \sum_{i=1}^N y_i \log \left(\frac{\theta}{1-\theta} \right) \right\}$ where $\eta = \log \frac{\theta}{1-\theta}$ which implies $\theta = \frac{\exp(\eta)}{1+\exp(\eta)}$, then $p(\mathbf{y}|\theta) = \exp \left\{ \sum_{i=1}^N y_i \eta - N \log(1 + \exp(\eta)) \right\}$. Thus $B(\eta) = N \log(1 + \exp(\eta))$, $\nabla(B(\eta)) = N \frac{\exp(\eta)}{1+\exp(\eta)} = N\theta$ and $\nabla^2(B(\eta)) = N \left\{ \frac{\exp(\eta)(1+\exp(\eta))}{(1+\exp(\eta))^2} - \frac{\exp(\eta)\exp(\eta)}{(1+\exp(\eta))^2} \right\} = N\theta(1-\theta)$.

2. Given a random sample $\mathbf{y} = [y_1, y_2, \dots, y_N]^\top$ from N binomial experiments each having known size n_i and same unknown probability θ . Show that $p(\mathbf{y}|\theta)$ is in the exponential family, and find the posterior distribution, the marginal likelihood and the predictive distribution of the binomial-beta model assuming the number of trials is known.

Answer

The density function is

$$\begin{aligned} p(\mathbf{y}|\theta) &= \prod_{i=1}^N \binom{n_i}{y_i} \theta^{y_i} (1-\theta)^{n_i-y_i} \\ &= \prod_{i=1}^N \binom{n_i}{y_i} \theta^{\sum_{i=1}^N y_i} (1-\theta)^{\sum_{i=1}^N n_i - \sum_{i=1}^N y_i} \\ &= \prod_{i=1}^N \binom{n_i}{y_i} \exp \left\{ \sum_{i=1}^N y_i \log \left(\frac{\theta}{1-\theta} \right) + \sum_{i=1}^N n_i \log(1-\theta) \right\} \\ &= \prod_{i=1}^N \binom{n_i}{y_i} (1-\theta)^{\sum_{i=1}^N n_i} \exp \left\{ \sum_{i=1}^N y_i \log \left(\frac{\theta}{1-\theta} \right) \right\}, \end{aligned}$$

Observe that $\sum_{i=1}^N n_i$ is the total sample size of Bernoulli experiments.

Using Theorem 1 in Chapter 4, the prior distribution is

$$\begin{aligned}\pi(\theta) &\propto (1-\theta)^{B_0} \exp \left\{ a_0 \log \left(\frac{\theta}{1-\theta} \right) \right\} \\ &= \theta^{a_0} (1-\theta)^{B_0-a_0} \\ &= \theta^{\alpha_0-1} (1-\theta)^{\beta_0-1},\end{aligned}$$

where $\alpha_0 = a_0 + 1$ and $\beta_0 = B_0 - a_0 + 1$. This is the kernel of a beta distribution. Thus, the posterior distribution is

$$\begin{aligned}\pi(\theta|\mathbf{y}) &\propto \theta^{\alpha_0-1} (1-\theta)^{\beta_0-1} \times \theta^{\sum_{i=1}^N y_i} (1-\theta)^{\sum_{i=1}^N n_i - \sum_{i=1}^N y_i} \\ &= \theta^{\alpha_0 + \sum_{i=1}^N y_i - 1} (1-\theta)^{\beta_0 + \sum_{i=1}^N n_i - \sum_{i=1}^N y_i - 1} \\ &= \theta^{\alpha_n-1} (1-\theta)^{\beta_n-1},\end{aligned}$$

where $\alpha_n = \alpha_0 + \sum_{i=1}^N y_i$ and $\beta_n = \beta_0 + \sum_{i=1}^N n_i - \sum_{i=1}^N y_i$.

The marginal likelihood is

$$\begin{aligned}p(\mathbf{y}) &= \int_0^1 \frac{\theta^{\alpha_0-1} (1-\theta)^{\beta_0-1}}{B(\alpha_0, \beta_0)} \times \prod_{i=1}^N \binom{n_i}{y_i} \theta^{\sum_{i=1}^N y_i} (1-\theta)^{\sum_{i=1}^N n_i - \sum_{i=1}^N y_i} d\theta \\ &= \frac{\prod_{i=1}^N \binom{n_i}{y_i}}{B(\alpha_0, \beta_0)} \int_0^1 \theta^{\alpha_0 + \sum_{i=1}^N y_i - 1} (1-\theta)^{\beta_0 + \sum_{i=1}^N n_i - \sum_{i=1}^N y_i - 1} d\theta \\ &= \frac{\prod_{i=1}^N \binom{n_i}{y_i} B(\alpha_n, \beta_n)}{B(\alpha_0, \beta_0)}.\end{aligned}$$

The third line due to having the kernel of a Beta distribution.

Finally, the predictive distribution is

$$\begin{aligned}p(Y_0|\mathbf{y}) &= \int_0^1 \binom{n_{y_0}}{y_0} \theta^{y_0} (1-\theta)^{n_{y_0}-y_0} \frac{\theta^{\alpha_n-1} (1-\theta)^{\beta_n-1}}{B(\alpha_n, \beta_n)} d\theta \\ &= \frac{\binom{n_{y_0}}{y_0}}{B(\alpha_n, \beta_n)} \int_0^1 \theta^{\alpha_n+y_0-1} (1-\theta)^{\beta_n+n_{y_0}-y_0-1} d\theta \\ &= \binom{n_{y_0}}{y_0} \frac{B(\alpha_n+y_0, \beta_n+n_{y_0}-y_0)}{B(\alpha_n, \beta_n)},\end{aligned}$$

where n_{y_0} is the known size associated with y_0 , and the last line due to having the kernel of a beta distribution. The predictive is a *beta-binomial distribution*.

3. Given a random sample $\mathbf{y} = [y_1, y_2, \dots, y_N]^\top$ from a *exponential distribution*. Show that $p(\mathbf{y}|\lambda)$ is in the exponential family, and find the posterior distribution, marginal likelihood and predictive distribution of the exponential-gamma model.

Answer

We see that the exponential distribution belongs to the exponential family as $p(\mathbf{y}|\lambda) = \prod_{i=1}^N \lambda \exp(-\lambda y_i) = \lambda^N \exp(-\lambda \sum_{i=1}^N y_i)$.

Using the gamma distribution in the rate parametrization, we see that $\pi(\lambda|\mathbf{y}) \propto \lambda^{\alpha_0-1} \exp(-\lambda\beta_0) \times \lambda^N \exp(-\lambda \sum_{i=1}^N y_i) = \lambda^{\alpha_0+N-1} \exp(-\lambda(\beta_0 + \sum_{i=1}^N y_i))$. This is the kernel of a gamma distribution, that is, $\lambda|\mathbf{y} \sim G(\alpha_n, \beta_n)$ where $\alpha_n = \alpha_0 + N$ and $\beta_n = \beta_0 + \sum_{i=1}^N y_i$.

The marginal likelihood is

$$\begin{aligned} p(\mathbf{y}) &= \int_0^\infty \lambda^N \exp\left\{-\lambda \sum_{i=1}^N y_i\right\} \lambda^{\alpha_0-1} \exp\{-\beta_0 \lambda\} \frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} d\lambda \\ &= \frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \int_0^\infty \lambda^{\alpha_0+N-1} \exp\left\{-\lambda \left(\beta_0 + \sum_{i=1}^N y_i\right)\right\} d\lambda \\ &= \frac{\beta_0^{\alpha_0} \Gamma(\alpha_n)}{\Gamma(\alpha_0) \beta_n^{\alpha_n}}. \end{aligned}$$

Finally, the predictive distribution is

$$\begin{aligned} p(Y_0|\mathbf{y}) &= \int_0^\infty \lambda \exp\{-\lambda y_0\} \lambda^{\alpha_n-1} \exp\{-\beta_n \lambda\} \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n)} d\lambda \\ &= \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n)} \int_0^\infty \lambda^{\alpha_n+1-1} \exp\{-\lambda(\beta_n + y_0)\} d\lambda \\ &= \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n)} \times \frac{\Gamma(\alpha_n + 1)}{(\beta_n + y_0)^{\alpha_n+1}} \\ &= \frac{\alpha_n \beta_n^{\alpha_n}}{(\beta_n + y_0)^{\alpha_n+1}}. \end{aligned}$$

This is a *Lomax distribution*.

4. Given $\mathbf{y} \sim N_N(\boldsymbol{\mu}, \boldsymbol{\Sigma})$, that is, a *multivariate normal distribution* show that $p(\mathbf{y}|\boldsymbol{\mu}, \boldsymbol{\Sigma})$ is in the exponential family.

Answer

$$\begin{aligned}
p(\mathbf{y}|\boldsymbol{\mu}, \boldsymbol{\Sigma}) &= (2\pi)^{-N/2} |\boldsymbol{\Sigma}|^{-1/2} \exp \left\{ -\frac{1}{2} (\mathbf{y} - \boldsymbol{\mu})^\top \boldsymbol{\Sigma}^{-1} (\mathbf{y} - \boldsymbol{\mu}) \right\} \\
&= (2\pi)^{-N/2} \exp \left\{ -\frac{1}{2} (\mathbf{y}^\top \boldsymbol{\Sigma}^{-1} \mathbf{y} - 2\mathbf{y}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \boldsymbol{\mu}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \log(|\boldsymbol{\Sigma}|)) \right\} \\
&= (2\pi)^{-N/2} \exp \left\{ -\frac{1}{2} (tr \{ \mathbf{y}^\top \boldsymbol{\Sigma}^{-1} \mathbf{y} \} - 2\mathbf{y}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \boldsymbol{\mu}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \log(|\boldsymbol{\Sigma}|)) \right\} \\
&= (2\pi)^{-N/2} \exp \left\{ -\frac{1}{2} (vec(\mathbf{y}\mathbf{y}^\top)^\top vec(\boldsymbol{\Sigma}^{-1}) - 2\mathbf{y}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \boldsymbol{\mu}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \log(|\boldsymbol{\Sigma}|)) \right\},
\end{aligned}$$

where tr and vec are the trace and vectorization operators, respectively.

Then, $h(\mathbf{y}) = (2\pi)^{-N/2}$, $\eta(\boldsymbol{\mu}, \boldsymbol{\Sigma}) = [\boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} \quad vec(\boldsymbol{\Sigma}^{-1})]$, $T(\mathbf{y}) = [\mathbf{y} \quad \frac{1}{2} vec(\mathbf{y}\mathbf{y}^\top)]$ and $C(\boldsymbol{\mu}, \boldsymbol{\Sigma}) = \exp \left\{ -\frac{1}{2N} (\boldsymbol{\mu}^\top \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu} + \log(|\boldsymbol{\Sigma}|)) \right\}$.

5. Find the marginal likelihood in the normal/inverse-Wishart model.

Answer

$$\begin{aligned}
p(\mathbf{Y}) &= \int_{\mathcal{R}^p} \int_{\mathcal{S}} (2\pi)^{-pN/2} |\boldsymbol{\Sigma}|^{-N/2} \exp \left\{ -\frac{1}{2} tr[(\mathbf{S} + N(\boldsymbol{\mu} - \hat{\boldsymbol{\mu}})(\boldsymbol{\mu} - \hat{\boldsymbol{\mu}})^\top) \boldsymbol{\Sigma}^{-1}] \right\} \\
&\quad \times (2\pi)^{-p/2} \beta_0^{p/2} |\boldsymbol{\Sigma}|^{-1/2} \exp \left\{ -\frac{\beta_0}{2} tr[(\boldsymbol{\mu} - \boldsymbol{\mu}_0)(\boldsymbol{\mu} - \boldsymbol{\mu}_0)^\top \boldsymbol{\Sigma}^{-1}] \right\} \\
&\quad \times |\boldsymbol{\Sigma}|^{-(\alpha_0 + p + 1)/2} \frac{2^{-\alpha_0 p/2} |\boldsymbol{\Psi}_0|^{\alpha_0/2}}{\Gamma_p(\alpha_0/2)} \exp \left\{ -\frac{1}{2} tr(\boldsymbol{\Psi}_0 \boldsymbol{\Sigma}^{-1}) \right\} d\boldsymbol{\Sigma} d\boldsymbol{\mu} \\
&= \frac{(2\pi)^{-frac{1}{2}(pN+p)} |\boldsymbol{\Psi}_0|^{\alpha_0/2} \beta_0^{p/2} 2^{-\alpha_0 p/2}}{\Gamma_p(\alpha_0/2)} \int_{\mathcal{R}^p} \int_{\mathcal{S}} |\boldsymbol{\Sigma}|^{-\frac{1}{2}(N+1+\alpha_0+p+1)} \\
&\quad \times \exp \left\{ -\frac{1}{2} tr[(\mathbf{S} + N(\boldsymbol{\mu} - \hat{\boldsymbol{\mu}})(\boldsymbol{\mu} - \hat{\boldsymbol{\mu}})^\top + \beta_0(\boldsymbol{\mu} - \boldsymbol{\mu}_0)(\boldsymbol{\mu} - \boldsymbol{\mu}_0)^\top + \boldsymbol{\Psi}_0) \boldsymbol{\Sigma}^{-1}] \right\} d\boldsymbol{\Sigma} d\boldsymbol{\mu}.
\end{aligned}$$

We have in the integral the kernel of an Inverse-Wishart distribution, then

$$\begin{aligned}
p(\mathbf{Y}) &= \frac{\Gamma_p\left(\frac{N+1+\alpha_0}{2}\right) |\Psi_0|^{\alpha_0/2} \beta_0^{p/2}}{\Gamma_p(\alpha_0/2) \pi^{p(N+1)/2}} \\
&\quad \times \int_{\mathcal{R}^p} |\mathbf{S} + \Psi_0 + (N + \beta_0)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \\
&\quad + N\beta_0/(N + \beta_0)(\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}_0)(\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}_0)^\top| d\boldsymbol{\mu} \\
&= \frac{\Gamma_p\left(\frac{N+1+\alpha_0}{2}\right) |\Psi_0|^{\alpha_0/2} \beta_0^{p/2}}{\Gamma_p(\alpha_0/2) \pi^{p(N+1)/2}} \\
&\quad \times \int_{\mathcal{R}^p} |\Psi_n| |1 + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n) \Psi_n^{-1}(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top|^{-\frac{1}{2}(\alpha_n+1)} d\boldsymbol{\mu} \\
&= \frac{\Gamma_p\left(\frac{\alpha_n+1}{2}\right) |\Psi_0|^{\alpha_0/2} \beta_0^{p/2}}{\Gamma_p(\alpha_0/2) \pi^{p(N+1)/2}} |\Psi_n|^{-\frac{1}{2}(\alpha_n+1)} \\
&\quad \times \int_{\mathcal{R}^p} [1 + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \Psi_n^{-1}(\boldsymbol{\mu} - \boldsymbol{\mu}_n)]^{-\frac{1}{2}(\alpha_n+1)} d\boldsymbol{\mu}.
\end{aligned}$$

The last equality uses the definition of Ψ_n , β_n and α_n , and the Sylvester's determinant theorem. Observe that we have the kernel of a multivariate t distribution. Then,

$$\begin{aligned}
p(\mathbf{Y}) &= \frac{\Gamma_p\left(\frac{\alpha_n+1}{2}\right) |\Psi_0|^{\alpha_0/2} \beta_0^{p/2}}{\Gamma_p(\alpha_0/2) \pi^{p(N+1)/2}} |\Psi_n|^{-\frac{1}{2}(\alpha_n+1)} \\
&\quad \times \int_{\mathcal{R}^p} \left[1 + \frac{1}{\alpha_n + 1 - p} (\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \left(\frac{\Psi_n}{\beta_n(\alpha_n + 1 - p)} \right)^{-1} (\boldsymbol{\mu} - \boldsymbol{\mu}_n) \right]^{-\frac{1}{2}(\alpha_n+1-p+p)} d\boldsymbol{\mu} \\
&= \frac{\Gamma_p\left(\frac{\alpha_n+1}{2}\right) \Gamma_p\left(\frac{\alpha_n+1-p}{2}\right) |\Psi_0|^{\alpha_0/2} \beta_0^{p/2} (\alpha_n + 1 - p)^{p/2} \pi^{p/2} |\Psi_n|^{-\frac{1}{2}(\alpha_n+1)}}{\Gamma_p(\alpha_0/2) \pi^{p(N+1)/2} \Gamma_p\left(\frac{\alpha_n+1-p+p}{2}\right) \left(\frac{\Psi_n}{\alpha_n+1-p} \right)^{-1/2}} \\
&= \frac{\Gamma_p\left(\frac{v_n}{2}\right) |\Psi_0|^{\alpha_0/2}}{\Gamma_p\left(\frac{\alpha_0}{2}\right) |\Psi_n|^{\alpha_n/2}} \left(\frac{\beta_0}{\beta_n} \right)^{p/2} (2\pi)^{-Np/2},
\end{aligned}$$

where $v_n = \alpha_n + 1 - p$.

6. Find the posterior predictive distribution in the normal/inverse-Wishart model, and show that $\mathbf{Y}_0 | \mathbf{Y} \sim T_{N_0, M}(\alpha_n - M + 1, \mathbf{X}_0 \mathbf{B}_n, \mathbf{I}_{N_0} + \mathbf{X}_0 \mathbf{V}_n \mathbf{X}_0^\top, \Psi_n)$ in the multivariate regression linear model.

Answer

$$\begin{aligned}
p(\mathbf{Y}_0|\mathbf{Y}) &\propto \int_{\mathcal{R}^p} \int_S |\Sigma|^{-1/2} \exp \left\{ -\frac{1}{2} \text{tr}[(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top \Sigma^{-1}] \right\} \\
&\quad \times |\Sigma|^{-1/2} \exp \left\{ -\frac{\beta_n}{2} \text{tr}[(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \Sigma^{-1}] \right\} \\
&\quad \times |\Sigma|^{-(\alpha_n + p + 1)/2} \exp \left\{ -\frac{1}{2} \text{tr}(\Psi_n \Sigma^{-1}) \right\} d\Sigma d\boldsymbol{\mu} \\
&\propto \int_{\mathcal{R}^p} |(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top + (\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top + \Psi_n|^{-(\alpha_n + 2)/2} d\boldsymbol{\mu}.
\end{aligned}$$

The last equality uses that there is the kernel of an Inverse Wishart distribution.

Taking into account that

$$\begin{aligned}
(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top + (\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top &= (1 + \beta_n) \left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n \boldsymbol{\mu}_n)}{1 + \beta_n} \right) \left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n \boldsymbol{\mu}_n)}{1 + \beta_n} \right)^\top \\
&\quad + \frac{\beta_n}{1 + \beta_n} (\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top.
\end{aligned}$$

Then,

$$\begin{aligned}
p(\mathbf{Y}_0|\mathbf{Y}) &\propto \int_{\mathcal{R}^p} |(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top + (\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top + \Psi_n|^{-(\alpha_n + 2)/2} d\boldsymbol{\mu} \\
&= \int_{\mathcal{R}^p} \left| (1 + \beta_n) \left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n \boldsymbol{\mu}_n)}{1 + \beta_n} \right) \left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n \boldsymbol{\mu}_n)}{1 + \beta_n} \right)^\top \right. \\
&\quad \left. + \frac{\beta_n}{1 + \beta_n} (\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top + \Psi_n \right|^{-(\alpha_n + 2)/2} d\boldsymbol{\mu} \\
&= \int_{\mathcal{R}^p} \left| \underbrace{\Psi_n + \frac{\beta_n}{1 + \beta_n} (\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top}_{\Lambda_n} \right| \\
&\quad \left| 1 + (1 + \beta_n) \left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n \boldsymbol{\mu}_n)}{1 + \beta_n} \right)^\top \frac{1}{\alpha_n + 2 - p} \left(\frac{\Lambda_n}{\alpha_n + 2 - p} \right)^{-1} \left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n \boldsymbol{\mu}_n)}{1 + \beta_n} \right) \right|^{-(\alpha_n + 2 - p + p)/2} d\boldsymbol{\mu} \\
&\propto \left| \Psi_n + \frac{\beta_n}{1 + \beta_n} (\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top \right|^{-(\alpha_n + 2)/2} \\
&\quad \times \left| \Psi_n + \frac{\beta_n}{1 + \beta_n} (\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top \right|^{1/2} \\
&= \left| \Psi_n + \frac{\beta_n}{1 + \beta_n} (\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top \right|^{-(\alpha_n + 1)/2} \\
&\propto \left[1 + (\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top \frac{1}{\alpha_n + 1 - p} \left(\frac{\Psi_n (1 + \beta_n)}{(\alpha_n + 1 - p) \beta_n} \right)^{-1} (\mathbf{y}_0 - \boldsymbol{\mu}_n) \right]^{-(\alpha_n + 1 - p + p)}.
\end{aligned}$$

The second equality and last line use the Sylvester's determinant theorem, and the second equality uses that there is the kernel of a multivariate t distribution.

Then, we have that the predictive distribution is a multivariate t distribution centered at $\boldsymbol{\mu}_n$, $\alpha_n + 1 - p$ degrees of freedom, and scale matrix $\frac{\boldsymbol{\Psi}_n(1+\beta_n)}{(\alpha_n+1-p)\beta_n}$.

To show the second statement, let's start by the definition of the predictive density to show that $\mathbf{Y}_0|\mathbf{Y} \sim T_{N_0,M}(\alpha_n - M + 1, \mathbf{X}_0\mathbf{B}_n, \mathbf{I}_{N_0} + \mathbf{X}_0\mathbf{V}_n\mathbf{X}_0^\top, \boldsymbol{\Psi}_n)$.

$$\begin{aligned} \pi(\mathbf{Y}_0|\mathbf{Y}) &\propto \int_{\mathcal{S}} \int_{\mathcal{B}} \left\{ |\boldsymbol{\Sigma}|^{-N_0/2} \exp \left\{ -\frac{1}{2} \text{tr}[(\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B})^\top (\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}) \boldsymbol{\Sigma}^{-1}] \right\} \right. \\ &\quad \times |\boldsymbol{\Sigma}|^{-K/2} \exp \left\{ -\frac{1}{2} \text{tr}[(\mathbf{B} - \mathbf{B}_n)^\top \mathbf{V}_n^{-1} (\mathbf{B} - \mathbf{B}_n) \boldsymbol{\Sigma}^{-1}] \right\} \\ &\quad \times |\boldsymbol{\Sigma}|^{-(\alpha_n+M+1)/2} \exp \left\{ -\frac{1}{2} \text{tr}[\boldsymbol{\Psi}_n \boldsymbol{\Sigma}^{-1}] \right\} \Big\} d\mathbf{B} d\boldsymbol{\Sigma} \\ &= \int_{\mathcal{S}} \int_{\mathcal{B}} \left\{ |\boldsymbol{\Sigma}|^{-(N_0+K+\alpha_n+M+1)/2} \exp \left\{ -\frac{1}{2} \text{tr} [((\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B})^\top (\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}) \right. \right. \\ &\quad \left. \left. + (\mathbf{B} - \mathbf{B}_n)^\top \mathbf{V}_n^{-1} (\mathbf{B} - \mathbf{B}_n) + \boldsymbol{\Psi}_n) \boldsymbol{\Sigma}^{-1}] \right\} \right\} d\mathbf{B} d\boldsymbol{\Sigma}. \end{aligned}$$

Setting $\mathbf{M} = (\mathbf{X}_0^\top \mathbf{X}_0 + \mathbf{V}_n^{-1})$, and $\mathbf{B}_* = \mathbf{M}^{-1}(\mathbf{V}_n \mathbf{B}_n + \mathbf{X}_0^\top \mathbf{Y}_0)$, we have that $(\mathbf{B} - \mathbf{B}_*)^\top \mathbf{M} (\mathbf{B} - \mathbf{B}_*) + \mathbf{B}_n^\top \mathbf{V}_n^{-1} \mathbf{B}_n + \mathbf{Y}_0^\top \mathbf{Y}_0 - \mathbf{B}_*^\top \mathbf{M} \mathbf{B}_* = (\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B})^\top (\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}) + (\mathbf{B} - \mathbf{B}_n)^\top \mathbf{V}_n^{-1} (\mathbf{B} - \mathbf{B}_n)$. Then,

$$\begin{aligned} \pi(\mathbf{Y}_0|\mathbf{Y}) &\propto \int_{\mathcal{S}} |\boldsymbol{\Sigma}|^{-(N_0+K+\alpha_n+M+1)/2} \\ &\quad \times \exp \left\{ -\frac{1}{2} \text{tr}[(\boldsymbol{\Psi}_n + \mathbf{B}_n^\top \mathbf{V}_n^{-1} \mathbf{B}_n + \mathbf{Y}_0^\top \mathbf{Y}_0 - \mathbf{B}_*^\top \mathbf{M} \mathbf{B}_*) \boldsymbol{\Sigma}^{-1}] \right\} \\ &\quad \times \int_{\mathcal{B}} \exp \left\{ -\frac{1}{2} \text{tr}[(\mathbf{B} - \mathbf{B}_*)^\top \mathbf{M} (\mathbf{B} - \mathbf{B}_*) \boldsymbol{\Sigma}^{-1}] \right\} d\mathbf{B} d\boldsymbol{\Sigma}. \end{aligned}$$

The latter is the kernel of a matrix normal distribution, thus

$$\begin{aligned} \pi(\mathbf{Y}_0|\mathbf{Y}) &\propto \int_{\mathcal{S}} |\boldsymbol{\Sigma}|^{-(N_0+\alpha_n+M+1)/2} \\ &\quad \times \exp \left\{ -\frac{1}{2} \text{tr}[(\boldsymbol{\Psi}_n + \mathbf{B}_n^\top \mathbf{V}_n^{-1} \mathbf{B}_n + \mathbf{Y}_0^\top \mathbf{Y}_0 - \mathbf{B}_*^\top \mathbf{M} \mathbf{B}_*) \boldsymbol{\Sigma}^{-1}] \right\} d\boldsymbol{\Sigma} \end{aligned}$$

This is the kernel of an inverse-Wishart distribution, then

$$\pi(\mathbf{Y}_0|\mathbf{Y}) \propto |\boldsymbol{\Psi}_n + \mathbf{B}_n^\top \mathbf{V}_n^{-1} \mathbf{B}_n + \mathbf{Y}_0^\top \mathbf{Y}_0 - \mathbf{B}_*^\top \mathbf{M} \mathbf{B}_*|^{-(N_0+\alpha_n)/2}.$$

Setting $\mathbf{C}^{-1} = \mathbf{I}_{N_0} + \mathbf{X}_0 \mathbf{V}_n \mathbf{X}_0^\top$ such that $\mathbf{C} = \mathbf{I}_{N_0} - \mathbf{X}_0 (\mathbf{X}_0^\top \mathbf{X}_0 + \mathbf{V}_n^{-1})^{-1} \mathbf{X}_0^\top$ (see footnote 4 in Chapter 4), then $\mathbf{B}_n^\top \mathbf{V}_n^{-1} \mathbf{B}_n + \mathbf{Y}_0^\top \mathbf{Y}_0 - \mathbf{B}_*^\top \mathbf{M} \mathbf{B}_* = (\mathbf{Y}_0 - \mathbf{X}_0 \mathbf{B}_n)^\top \mathbf{C} (\mathbf{Y}_0 - \mathbf{X}_0 \mathbf{B}_n)$. This is done following exactly same procedure as deducing the predictive distribution in the linear regression model in the book. Thus,

$$\begin{aligned} \pi(\mathbf{Y}_0 | \mathbf{Y}) &\propto |\boldsymbol{\Psi}_n + (\mathbf{Y}_0 - \mathbf{X}_0 \mathbf{B}_n)^\top \mathbf{C} (\mathbf{Y}_0 - \mathbf{X}_0 \mathbf{B}_n)|^{-(N_0 + \alpha_n)/2} \\ &\propto |\mathbf{I}_{N_0} + \mathbf{C} (\mathbf{Y}_0 - \mathbf{X}_0 \mathbf{B}_n) \boldsymbol{\Psi}^{-1} (\mathbf{Y}_0 - \mathbf{X}_0 \mathbf{B}_n)^\top|^{-(\alpha_n + 1 - M + N_0 + M - 1)/2}. \end{aligned}$$

The second proportionality follows from the Sylvester's theorem. Observe that this is the kernel of a matrix t distribution with $\alpha_n + 1 - M$ degrees of freedom, location $\mathbf{X}_0 \mathbf{B}_n$ and scale matrices $\boldsymbol{\Psi}_n$ and $\mathbf{C}^{-1} = \mathbf{I}_{N_0} + \mathbf{X}_0 \mathbf{V}_n \mathbf{X}_0^\top$.

7. Show that $\delta_n = \delta_0 + (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})^\top (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}) + (\hat{\boldsymbol{\beta}} - \boldsymbol{\beta}_0)^\top ((\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{B}_0)^{-1} (\hat{\boldsymbol{\beta}} - \boldsymbol{\beta}_0)$ in the linear regression model, and that $\boldsymbol{\Psi}_n = \boldsymbol{\Psi}_0 + \mathbf{S} + (\hat{\mathbf{B}} - \mathbf{B}_0)^\top \mathbf{V}_n (\hat{\mathbf{B}} - \mathbf{B}_0)$ in the linear multivariate regression model.

Answer

Taking into account that

$$\begin{aligned} \delta^* &= \delta_0 + \mathbf{y}^\top \mathbf{y} + \boldsymbol{\beta}_0^\top \mathbf{B}_0^{-1} \boldsymbol{\beta}_0 - \boldsymbol{\beta}_n^\top \mathbf{B}_n^{-1} \boldsymbol{\beta}_n \\ &= \delta_0 + \mathbf{y}^\top \mathbf{y} + \boldsymbol{\beta}_0^\top \mathbf{B}_0^{-1} \boldsymbol{\beta}_0 - (\mathbf{B}_0^{-1} \boldsymbol{\beta}_0 + \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}})^\top \mathbf{B}_n (\mathbf{B}_0^{-1} \boldsymbol{\beta}_0 + \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}}) \\ &= \delta_0 + \mathbf{y}^\top \mathbf{y} - \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \mathbf{B}_n \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}} - 2\hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \mathbf{B}_n \mathbf{B}_0^{-1} \boldsymbol{\beta}_0 + \boldsymbol{\beta}_0^\top (\mathbf{B}_0^{-1} - \mathbf{B}_0^{-1} \mathbf{B}_n \mathbf{B}_0^{-1}) \boldsymbol{\beta}_0 \\ &\quad - \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}} \\ &= \delta_0 + \mathbf{y}^\top \mathbf{y} - \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\beta}}^\top (\mathbf{X}^\top \mathbf{X} - \mathbf{X}^\top \mathbf{X} \mathbf{B}_n \mathbf{X}^\top \mathbf{X}) \hat{\boldsymbol{\beta}} \\ &\quad - 2\hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \mathbf{B}_n \mathbf{B}_0^{-1} \boldsymbol{\beta}_0 + \boldsymbol{\beta}_0^\top (\mathbf{B}_0^{-1} - \mathbf{B}_0^{-1} \mathbf{B}_n \mathbf{B}_0^{-1}) \boldsymbol{\beta}_0. \end{aligned}$$

Observe that

$$\begin{aligned} (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})^\top (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}) &= \mathbf{y}^\top \mathbf{y} - 2\hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{y} + \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}} \\ &= \mathbf{y}^\top \mathbf{y} - 2\hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top (\mathbf{X}\hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\mu}}) + \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}} \\ &= \mathbf{y}^\top \mathbf{y} - \hat{\boldsymbol{\beta}}^\top \mathbf{X}^\top \mathbf{X} \hat{\boldsymbol{\beta}}, \end{aligned}$$

where $\mathbf{y} = \mathbf{X}\hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\mu}}$, and $\mathbf{X}^\top \hat{\boldsymbol{\mu}} = 0$.

The following matrix identities are useful [29]:

$$(\mathbf{D} + \mathbf{E})^{-1} = \mathbf{D}^{-1} - \mathbf{D}^{-1} (\mathbf{D}^{-1} + \mathbf{E}^{-1})^{-1} \mathbf{D}^{-1},$$

and

$$(\mathbf{D} + \mathbf{E})^{-1} = \mathbf{D}^{-1} (\mathbf{E}^{-1} + \mathbf{D}^{-1}) \mathbf{E}^{-1}.$$

Using these identities,

$$\begin{aligned} [(\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{B}_0]^{-1} &= \mathbf{X}^\top \mathbf{X} - \mathbf{X}^\top \mathbf{X}(\mathbf{X}^\top \mathbf{X} + \mathbf{B}_0^{-1})^{-1} \mathbf{X}^\top \mathbf{X} \\ &= \mathbf{B}_0^{-1} - \mathbf{B}_0^{-1}(\mathbf{X}^\top \mathbf{X} + \mathbf{B}_0^{-1})^{-1} \mathbf{B}_0^{-1} \\ &= \mathbf{X}^\top \mathbf{X}(\mathbf{X}^\top \mathbf{X} + \mathbf{B}_0^{-1})^{-1} \mathbf{B}_0^{-1}. \end{aligned}$$

Then,

$$\begin{aligned} \delta^* &= \delta_0 + (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})^\top (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}) + \hat{\boldsymbol{\beta}}^\top [(\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{B}_0]^{-1} \hat{\boldsymbol{\beta}} \\ &\quad - 2\hat{\boldsymbol{\beta}}^\top [(\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{B}_0]^{-1} \boldsymbol{\beta}_0 + \boldsymbol{\beta}_0^\top [(\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{B}_0]^{-1} \boldsymbol{\beta}_0 \\ &= \delta_0 + (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})^\top (\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}) \\ &\quad + (\hat{\boldsymbol{\beta}} - \boldsymbol{\beta}_0)^\top [(\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{B}_0]^{-1} (\hat{\boldsymbol{\beta}} - \boldsymbol{\beta}_0). \end{aligned}$$

In a similar way for the second part,

$$\begin{aligned} (\mathbf{V}_0 + (\mathbf{X}^\top \mathbf{X})^{-1})^{-1} &= \mathbf{V}_0^{-1} - \mathbf{V}_0^{-1}(\mathbf{V}_0^{-1} + \mathbf{X}^\top \mathbf{X})^{-1} \mathbf{V}_0^{-1} \\ &= \mathbf{X}^\top \mathbf{X} - \mathbf{X}^\top \mathbf{X}(\mathbf{V}_0^{-1} + \mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{X} \\ &= \mathbf{X}^\top \mathbf{X}((\mathbf{X}^\top \mathbf{X})^{-1} + \mathbf{V}_0)^{-1} \mathbf{V}_0^{-1}, \end{aligned}$$

we use these results and some algebra to show that $\mathbf{B}_0^\top \mathbf{V}_0^{-1} \mathbf{B}_0 + \hat{\mathbf{B}}^\top \mathbf{X}^\top \mathbf{X} \hat{\mathbf{B}} - \mathbf{B}_n^\top \mathbf{V}_n^{-1} \mathbf{B}_n = (\hat{\mathbf{B}} - \mathbf{B}_0)^\top \mathbf{V}_n (\hat{\mathbf{B}} - \mathbf{B}_0)$ taking into account that $\mathbf{V}_n = (\mathbf{V}_0^{-1} + \mathbf{X}^\top \mathbf{X})^{-1}$ and $\hat{\mathbf{B}} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{Y}$.

8. Show that in the linear regression model $\boldsymbol{\beta}_n^\top (\mathbf{B}_n^{-1} - \mathbf{B}_n^{-1} \mathbf{M}^{-1} \mathbf{B}_n^{-1}) \boldsymbol{\beta}_n = \boldsymbol{\beta}_{**}^\top \mathbf{C} \boldsymbol{\beta}_{**}$ and $\boldsymbol{\beta}_{**} = \mathbf{X}_0 \boldsymbol{\beta}_n$.

Answer

Taking into account that $(\mathbf{A} + \mathbf{B})^{-1} = \mathbf{A}^{-1} - \mathbf{A}^{-1}(\mathbf{A}^{-1} + \mathbf{B}^{-1})^{-1} \mathbf{A}^{-1}$ [29], then we observe that $(\mathbf{B}_n^{-1} - \mathbf{B}_n^{-1} \mathbf{M}^{-1} \mathbf{B}_n^{-1}) = (\mathbf{B}_n + (\mathbf{X}_0^\top \mathbf{X}_0)^{-1})^{-1}$, where $(\mathbf{B}_n + (\mathbf{X}_0^\top \mathbf{X}_0)^{-1})^{-1} = \mathbf{X}_0^\top \mathbf{X}_0 - \mathbf{X}_0^\top \mathbf{X}_0 (\mathbf{B}_n^{-1} + \mathbf{X}_0^\top \mathbf{X}_0)^{-1} \mathbf{X}_0^\top \mathbf{X}_0 = \mathbf{X}_0^\top \mathbf{X}_0 - \mathbf{X}_0^\top \mathbf{X}_0 \mathbf{M}^{-1} \mathbf{X}_0^\top \mathbf{X}_0$, thus

$$\begin{aligned} \boldsymbol{\beta}_n^\top (\mathbf{B}_n^{-1} - \mathbf{B}_n^{-1} \mathbf{M}^{-1} \mathbf{B}_n^{-1}) \boldsymbol{\beta}_n &= \boldsymbol{\beta}_n^\top (\mathbf{X}_0^\top \mathbf{X}_0 - \mathbf{X}_0^\top \mathbf{X}_0 \mathbf{M}^{-1} \mathbf{X}_0^\top \mathbf{X}_0) \boldsymbol{\beta}_n \\ &= \boldsymbol{\beta}_n^\top \mathbf{X}_0^\top (\mathbf{I}_{N_0} - \mathbf{X}_0 \mathbf{M}^{-1} \mathbf{X}_0^\top) \mathbf{X}_0 \boldsymbol{\beta}_n \\ &= \boldsymbol{\beta}_n^\top \mathbf{X}_0^\top \mathbf{C} \mathbf{X}_0 \boldsymbol{\beta}_n \\ &= \boldsymbol{\beta}_{**}^\top \mathbf{C} \boldsymbol{\beta}_{**}. \end{aligned}$$

Let's show that $\boldsymbol{\beta}_{**} = \mathbf{X}_0 \boldsymbol{\beta}_n$,

$$\begin{aligned}
\beta_{**} &= \mathbf{C}^{-1} \mathbf{X}_0 \mathbf{M}^{-1} \mathbf{B}_n^{-1} \beta_n \\
&= (\mathbf{I}_{N_0} + \mathbf{X}_0 \mathbf{B}_n \mathbf{X}_0^\top) \mathbf{X}_0 \mathbf{M}^{-1} \mathbf{B}_n^{-1} \beta_n \\
&= (\mathbf{I}_{N_0} + \mathbf{X}_0 \mathbf{B}_n \mathbf{X}_0^\top) \mathbf{X}_0 (\mathbf{B}_n - \mathbf{B}_n ((\mathbf{X}_0^\top \mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1} \mathbf{B}_n) \mathbf{B}_n^{-1} \beta_n \\
&= (\mathbf{I}_{N_0} + \mathbf{X}_0 \mathbf{B}_n \mathbf{X}_0^\top) (\mathbf{X}_0 \beta_n - \mathbf{X}_0 \mathbf{B}_n ((\mathbf{X}_0^\top \mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1} \beta_n) \\
&= \mathbf{X}_0 \beta_n - \mathbf{X}_0 \mathbf{B}_n ((\mathbf{X}_0^\top \mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1} \beta_n + \mathbf{X}_0 \mathbf{B}_n \mathbf{X}_0^\top \mathbf{X}_0 \beta_n \\
&\quad - \mathbf{X}_0 \mathbf{B}_n \mathbf{X}_0^\top \mathbf{X}_0 \mathbf{B}_n ((\mathbf{X}_0^\top \mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1} \beta_n \\
&= \mathbf{X}_0 \beta_n - \mathbf{X}_0 \mathbf{B}_n [((\mathbf{X}_0^\top \mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1} - \mathbf{X}_0^\top \mathbf{X}_0 + \mathbf{X}_0^\top \mathbf{X}_0 \mathbf{B}_n ((\mathbf{X}_0^\top \mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1}] \beta_n.
\end{aligned}$$

Using that $(\mathbf{A} + \mathbf{B})^{-1} = \mathbf{A}^{-1} - \mathbf{A}^{-1} \mathbf{B} (\mathbf{A} + \mathbf{B})^{-1}$, we observe that the expression in brackets is equal to $\mathbf{0}$, then we have the result.

9. Show that $(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}}) = \mathbf{S} + (\mathbf{B} - \hat{\mathbf{B}})^\top \mathbf{X}^\top \mathbf{X} (\mathbf{B} - \hat{\mathbf{B}})$ where $\mathbf{S} = (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})$, $\hat{\mathbf{B}} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{Y}$ in the multivariate regression model.

Answer

$$\begin{aligned}
(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}}) &= (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}} + \mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B})^\top (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}} + \mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B}) \\
&= (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}}) + 2(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B}) \\
&\quad + (\mathbf{X}\mathbf{B} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{X}\mathbf{B} - \mathbf{X}\hat{\mathbf{B}}) \\
&= \mathbf{S} + (\mathbf{B} - \hat{\mathbf{B}})^\top \mathbf{X}^\top \mathbf{X} (\mathbf{B} - \hat{\mathbf{B}}),
\end{aligned}$$

given that $(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top (\mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B}) = \hat{\mathbf{U}}^\top \mathbf{X} (\hat{\mathbf{B}} - \mathbf{B})$, using that $\hat{\mathbf{B}} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{Y}$ which implies $\mathbf{X}^\top \mathbf{X}\hat{\mathbf{B}} = \mathbf{X}^\top \mathbf{Y} = \mathbf{X}^\top \mathbf{X}\hat{\mathbf{B}} + \mathbf{X}^\top \hat{\mathbf{U}}$, then $\mathbf{X}^\top \hat{\mathbf{U}} = \mathbf{0}$.

10. What is the probability that the Sun will rise tomorrow?

This is the most famous Richard Price's example developed in the Appendix of the Bayes' theorem paper [3]. Here, we implicitly use *Laplace's Rule of Succession* to solve this question. In particular, if we were a priori uncertain about the probability the Sun will rise on a specified day, we can assume a prior uniform distribution over (0,1), that is, a beta (1,1) distribution. Then, what is the probability that the Sun will rise tomorrow?

Answer

This exercise is an application of the Bernoulli-beta model. Thus, the likelihood is given by a binomial distribution where the probability of success is θ , $p(\mathbf{y}|\theta) \propto \theta^{\sum_{i=1}^N y_i} (1-\theta)^{N-\sum_{i=1}^N y_i}$. In addition, the prior distribution is beta, that is, $\pi(\theta) \propto \theta^{\alpha_0-1} (1-\theta)^{\beta_0-1}$, where $\alpha_0 = \beta_0 = 1$. Then, the predictive distribution that the sun will rise tomorrow is $p(Y_0 = 1|\mathbf{y}) = \frac{1+S}{2+N}$, where $S = \sum_{i=1}^N y_i$ is the number of successes (the Sun rise). $\frac{1+S}{2+N}$ is known

as the *Laplace's Rule of Succession* that was introduced by Laplace in the 18th century in the course of treating the sunrise problem.

11. Using information from Public Policy Polling in September 27th-28th for the 2016 presidential five-way race in USA, there are 411, 373 and 149 sampled people supporting Hillary Clinton, Donald Trump and other, respectively.
 - Find the posterior probability of the percentage difference of people supporting Hillary versus Trump according to this data using a non-informative prior, that is, $\alpha_0 = [1 \ 1 \ 1]$ in the multinomial-Dirichlet model. What is the probability of having more supporters of Hillary vs Trump?
 - What is the probability that sampling one hundred independent individuals 44, 40 and 16 support Hillary, Trump and other, respectively?

Answer

R code. Multinomial-Dirichlet model: Polling 2016 USA presidential race

```

1 set.seed(010101)
2 # Multinomial-Dirichlet example:
3 # Polling 2016 USA presidential race
4 y <- c(411, 373, 149)
5 # Clinton, Trump, Other
6 # Public Policy Polling September 27-28,
7 # 2016 five-way race
8 alpha0 <- rep(1, 3)
9 # Hyperparameters: non-informative distribution
10 alphan <- alpha0 + y
11 S <- 100000
12 # Sample draws of posterior
13 thetas <- MCMCpack::rdirichlet(S, alphan)
14 colnames(thetas) <- c("Clinton", "Trump", "Other")
15 head(thetas)
16      Clinton      Trump      Other
17 [1,] 0.4211346 0.4188607 0.1600046
18 [2,] 0.4244207 0.4224523 0.1531270
19 [3,] 0.4349268 0.3843953 0.1806779
20 [4,] 0.4533499 0.4005530 0.1460972
21 [5,] 0.4381799 0.3968502 0.1649699
22 [6,] 0.4436852 0.3971321 0.1591827
23 dif <- thetas[,1] - thetas[,2]
24 # Difference of shares Hillary vs Trump
25 data <- data.frame(dif)
26 names(data) <- c("Difference")
27 library(ggplot2)
28 p <- ggplot(data) +
29   geom_histogram(aes(x = Difference), binwidth = 0.01) +
30   geom_vline(xintercept=0.0, lwd=1, colour="red") +
31   ggtitle("Percentage difference Clinton vs Trump 2016
32     presidential race") + xlab("Percentage Difference") +
33     ylab("")
34 difmcmc <- coda::mcmc(dif)
35 # Declaring a MCMC object
36 summary(difmcmc)
37
38 Iterations = 1:1e+05
39 Thinning interval = 1
40 Number of chains = 1
41 Sample size per chain = 1e+05
42
43 1. Empirical mean and standard deviation for each
44 variable, plus standard error of the mean:
45
46      Mean          SD      Naive SE Time-series SE
47 4.062e-02  2.996e-02  9.474e-05  9.474e-05
48
49 2. Quantiles for each variable:
50
51      2.5%      25%      50%      75%      97.5%
52 -0.01817  0.02033  0.04058  0.06089  0.09923
53
54 CW <- mean(difmcmc>0)
55 CW
56 0.91339

```



FIGURE 3.1

Percentage difference: Hillary Clinton vs Donald Trump, five-way race.

There is a 95% probability that the percentage difference between Hillary and Trump according to this poll is (-1.8%, 9.9%). The probability of Hillary having more supporters is 91.3%

***R code. Multinomial-Dirichlet model: Polling 2016
USA presidential race***

```

1 # Predictive distribution by simulation
2 y0 <- c(44, 40, 16)
3 Pred <- apply(thetas, 1, function(p) {rmultinom(1, size =
4   sum(y0), prob = p)})
5 sum(sapply(1:S, function(s) {sum(Pred[,s] == y0) == 3}))/S
6 # Predictive distribution by analytical expression
7 PredY0 <- function(y0){
8   n <- sum(y0)
9   Res1 <- sum(sapply(1:length(y), function(l){lgamma(alphan[
10    l]+y0[l]) - lgamma(alphan[l])-lfactorial(y0[l]))}))
11   Res <- lfactorial(n)+lgamma(sum(alphan))-lgamma(sum(alphan
12    )+n) + Res1
13   return(exp(Res))
14 }
15 PredY0(y0)
16 0.00850

```

The probability that from one hundred random selected people 44 support Hillary, 40 support Trump and 16 support other candidate is 0.85%.

12. Math test example continues

You have a random sample of math scores of size $N = 50$ from a normal distribution, $Y_i \sim N(\mu, \sigma^2)$. The sample mean and variance are equal to 102 and 10, respectively. Using the normal-normal/inverse-gamma model where $\mu_0 = 100$, $\beta_0 = 1$, $\alpha_0 = \delta_0 = 0.001$

- Get 95% confidence and credible intervals for μ .
- What is the posterior probability that $\mu > 103$?

Answer

R code. Math test example continues

```

1 set.seed(010101)
2 N <- 50
3 # Sample size
4 muhat <- 102
5 # Sample mean
6 sig2hat <- 10
7 # Sample variance
8 # Hyperparameters
9 mu0 <- 100
10 beta0 <- 1
11 delta0 <- 0.001
12 alpha0 <- 0.001
13 S <- 100000
14 # Posterior draws
15 alphan <- alpha0 + N
16 deltan <- sig2hat*(N - 1) + delta0 + beta0*N/(beta0 + N)*(
    muhat - mu0)^2
17 sig2Post <- invgamma::rinvgamma(S, shape = alphan, rate =
    deltan)
18 summary(sig2Post)
19 betan <- beta0 + N
20 mun <- (beta0*mu0 + N*muhat)/betan
21 muPost_t <- ((deltan/(alphan*betan))^0.5)*rt(S, alphan) +
    mun
22 c1 <- rgb(173,216,230,max = 255, alpha = 50, names = "lt.
    blue")
23 c2 <- rgb(255,192,203, max = 255, alpha = 50, names = "lt.
    pink")
24 hist(muPost_t, main = "Histogram: Posterior mean", xlab = "
    Posterior mean", col = c1)
25 muPost_tq <- quantile(muPost_t, c(0.025, 0.5, 0.975))
26 muPost_tq
27 2.5%      50%      97.5%
28 101.0837 101.9608 102.8435
29 PmuPost_tcutoff <- mean(muPost_t > cutoff)
30 PmuPost_tcutoff
31 0.01087

```

Figure 3.2 shows the posterior distribution of the mean.

We have that the 95% credible interval is (101.08, 102.84), and the probability of having a value greater than 103 is 1.09%.

13. Demand of electricity example continues

Set c_0 such that maximizes the marginal likelihood in the specifications with and without electricity price in the example of demand of electricity

**FIGURE 3.2**

Histogram of the posterior distribution of the mean

(empirical Bayes). Then, calculate the Bayes factor, and conclude if there is evidence supporting the inclusion of the price of electricity in the demand equation.

Answer

R code. Demand of electricity

```

1 rm(list = ls())
2 set.seed(010101)
3 # Electricity demand
4 DataUt <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/Utilities.csv",
    sep = ",", header = TRUE, quote = "")
5 DataUtEst <- DataUt %>%
6 filter(Electricity != 0)
7 attach(DataUtEst)
8 # Dependent variable: Monthly consumption (kWh) in log
9 Y <- log(Electricity)
10 N <- length(Y)
11 # Regressors quantity including intercept
12 X <- cbind(LnPriceElect, IndSocio1, IndSocio2, Altitude,
    Nrooms, HouseholdMem, Children, Lnincome, 1)
13 # Regressor without price
14 Xnew <- cbind(IndSocio1, IndSocio2, Altitude, Nrooms,
    HouseholdMem, Children, Lnincome, 1)
15 # Log marginal function (multiply by -1 due to minimization)
16 LogMarLikLM <- function(X, c0){
17   k <- dim(X)[2]
18   N <- dim(X)[1]
19   # Hyperparameters
20   B0 <- c0*diag(k)
21   b0 <- rep(0, k)
22   # Posterior parameters
23   bhat <- solve(t(X)%*%X)%*%t(X)%*%Y
24   # Force this matrix to be symmetric
25   Bn <- as.matrix(Matrix::forceSymmetric(solve(solve(B0) + t
    (X)%*%X)))
26   bn <- Bn%*(solve(B0)%*%b0 + t(X)%*%X)%*%bhat)
27   dn <- as.numeric(d0 + t(Y)%*%Y+t(b0)%*%solve(B0)%*%b0-t(bn
    )%*%solve(Bn)%*%bn)
28   an <- a0 + N
29   # Log marginal likelihood
30   logpy <- (N/2)*log(1/pi)+(a0/2)*log(d0)-(an/2)*log(dn) +
    0.5*log(det(Bn)/det(B0)) + lgamma(an/2)-lgamma(a0/2)
31   return(-logpy)
32 }
33 # Hyperparameters
34 d0 <- 0.001
35 a0 <- 0.001
36 # Empirical Bayes: Obtain c0 maximizing the log marginal
    likelihood
37 c0 <- 1000
38 EB <- optim(c0, fn = LogMarLikLM, method = "Brent", lower =
    0.0001, upper = 10^6, X = X)
39 EBnew <- optim(c0, fn = LogMarLikLM, method = "Brent", lower
    = 0.0001, upper = 10^6, X = Xnew)
40 # Change of order to take into account the -1 in the
    LogMarLikLM function
41 BFEM <- exp(EBnew$value - EB$value)
42 BFEM
43 71897025

```

The Bayes factor based on the empirical Bayes of the model with electricity price versus the model without electricity price is equal to 71897938, this gives very strong evidence to include the price in the specification.

14. Utility demand

Use the file *Utilities.csv* to estimate a multivariate linear regression model where $\mathbf{Y}_i = [\log(\text{electricity}_i) \log(\text{water}_i) \log(\text{gas}_i)]$ as function of $\log(\text{electricity price}_i)$, $\log(\text{water price}_i)$, $\log(\text{gas price}_i)$, IndSocio1_i , IndSocio2_i , Altitude_i , Nrooms_i , HouseholdMem_i , Children_i , and $\log(\text{Income}_i)$, where electricity, water and gas are monthly consumption of electricity (kWh), water (m^3) and gas (m^3), and other definitions are given in the Example of Section 4.3. Omit households that do not consume any of the utilities in this exercise.

Set a non-informative prior framework, $\mathbf{B}_0 = [0]_{11 \times 3}$, $\mathbf{V}_0 = 1000\mathbf{I}_{11}$, $\Psi_0 = 1000\mathbf{I}_3$ and $\alpha_0 = 3$, where we have $K = 11$ (regressors plus intercept) and $M = 3$ (equations) in this exercise.

- (a) Find the posterior mean estimates and the highest posterior density intervals at 95% of \mathbf{B} and Σ .
- (b) Find the Bayes factor comparing the baseline model in this exercise with the same specification but using the income in dollars. Now, calculate the Bayes factor using the income in thousand dollars. Is there any difference?
- (c) Find the predictive distribution for the monthly demand of electricity, water and gas in the baseline specification of a household located in the lowest socioeconomic condition in a municipality located below 1000 meters above the sea level, 2 rooms, 3 members with children, a monthly income equal to USD 500, an electricity price equal to USD/kWh 0.15, a water price equal to USD/ M^3 0.70, and a gas price equal to USD/ M^3 0.75.

Answer

We find that the Bayes factor of the baseline model ($\log(\text{Income})$) versus the two alternative models using income in dollars and thousand dollars are 108925764 and 0.1089261. The former gives strong evidence in favor of the baseline model, whereas the latter gives positive evidence for the model using the income in thousand dollars. This result despite that the location coefficients are the same in the two alternative specifications, except for the change in scale of the coefficients associated with income. This example shows that Bayes factors are sensitive to units of measure, and consequently, it is relevant to think carefully about the priors when performing hypothesis testing using a Bayesian framework. Observe that a nice feature in Bayesian inference is that we followed the same conceptual framework (Bayes factor) in the previous exercise and this exercise. In one

hand, the previous exercise is an example of nested models, that is, one model is a restricted version of a more general model. On the other hand, this exercise is an example of non-nested models. This is not the case in the Frequentist approach. The statistical framework is not the same when testing nested and non-nested models.

*R code. Utilities demand: Multivariate regression,
posterior inference*

```

1 rm(list = ls())
2 set.seed(010101)
3 library(dplyr)
4 # Electricity demand
5 DataUt <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/Utilities.csv
    ", sep = ",", header = TRUE, quote = "")
6 DataUtEst <- DataUt %>% filter(Electricity != 0 & Water !=0
    & Gas != 0)
7 attach(DataUtEst)
8 Y <- cbind(log(Electricity), log(Water), log(Gas))
9 X <- cbind(LnPriceElect, LnPriceWater, LnPriceGas, IndSocio1
    , IndSocio2, Altitude, Nrooms, HouseholdMem, Children,
    Lnincome, 1)
10 M <- dim(Y)[2]
11 K <- dim(X)[2]
12 N <- dim(Y)[1]
13 # Hyperparameters
14 B0 <- matrix(0, K, M)
15 c0 <- 1000
16 V0 <- c0*diag(K)
17 Psi0 <- c0*diag(M)
18 a0 <- M
19 # Posterior parameters
20 Bhat <- solve(t(X)%*%X)%*%t(X)%*%Y
21 S <- t(Y - X%*%Bhat)%*%(Y - X%*%Bhat)
22 Vn <- solve(solve(V0) + t(X)%*%X)
23 Bn <- Vn%*(solve(V0)%*%B0 + t(X)%*%X%*%Bhat)
24 Psin <- Psi0 + S + t(B0)%*%solve(V0)%*%B0 + t(Bhat)%*%t(X)%*
    %X%*%Bhat - t(Bn)%*%solve(Vn)%*%Bn
25 an <- a0 + N
26 #Posterior draws
27 s <- 10000 #Number of posterior draws
28 SIGs <- replicate(s, LaplacesDemon::rinvwishart(an, Psin))
29 Bs <- sapply(1:s, function(s) {MixMatrix::rmatrixt(n = 1,
    mean=Bn, U = Vn,V = Psin, df = an + 1 - M)})
30 summary(coda::mcmc(t(Bs)))
31 SIGMs <- t(sapply(1:s, function(l) {gdata::lowerTriangle(
    SIGs[,l], diag=TRUE, byrow=FALSE)}))
32 summary(coda::mcmc(SIGMs))
33 hdiBs <- HDInterval::hdi(t(Bs), credMass = 0.95) # Highest
    posterior density credible interval
34 hdiBs
35 hdiSIG <- HDInterval::hdi(SIGMs, credMass = 0.95) # Highest
    posterior density credible interval
36 hdiSIG
37

```

*R code. Utilities demand: Multivariate regression,
Bayes factors*

```

1 # Log marginal function (multiply by -1 due to minimization)
2 LogMarLikLM <- function(X, c0){
3   c10 <- c0[1]; c20 <- c0[2]
4   k <- dim(X)[2]
5   N <- dim(X)[1]
6   # Hyperparameters
7   V0 <- c10*diag(k)
8   Psi0 <- c20*diag(M)
9   # Posterior parameters
10  Bhat <- solve(t(X)%*%X)%*%t(X)%*%Y
11  S <- t(Y - X%*%Bhat)%*%(Y - X%*%Bhat)
12  Vn <- solve(solve(V0) + t(X)%*%X)
13  Bn <- Vn%*(solve(V0)%*%B0 + t(X)%*%X)%*%Bhat)
14  Psin <- Psi0 + S + t(B0)%*%solve(V0)%*%B0 + t(Bhat)%*%t(X)
    %*%X)%*%Bhat - t(Bn)%*%solve(Vn)%*%Bn
15  # Log marginal likelihood
16  logpy <- (N*M/2)*log(1/pi)+(a0/2)*log(det(Psi0)) - (an/2)*
    log(det(Psin)) + (M/2)*(log(det(Vn)) - log(det(V0))) +
    lgamma(an/2)-lgamma(a0/2)
17  return(-logpy)
18 }
19 c0 <- rep(1000, 2)
20 LogML <- LogMarLikLM(X=X, c0 = c0)
21 # Using income in dollars as regressor
22 Xnew <- cbind(LnPriceElect, LnPriceWater, LnPriceGas,
    IndSocio1, IndSocio2, Altitude, Nrooms, HouseholdMem,
    Children, exp(Lnincome), 1)
23 LogMLnew <- LogMarLikLM(X=Xnew, c0 = c0)
24 # Bayes factor
25 BF12 <- exp(LogMLnew - LogML)
26 BF12
27 # Using income in thousand dollars as regressor
28 XnewT <- cbind(LnPriceElect, LnPriceWater, LnPriceGas,
    IndSocio1, IndSocio2, Altitude, Nrooms, HouseholdMem,
    Children, exp(Lnincome)/1000, 1)
29 LogMLnewT <- LogMarLikLM(X=XnewT, c0 = c0)
30 # Bayes factor
31 BF13 <- exp(LogMLnewT - LogML)
32 BF13
33

```

*R code. Utilities demand: Multivariate regression,
predictive distribution*

```

1 # Predictive distribution
2 Xpred <- c(log(0.15), log(0.70), log(0.75), 1, 0, 0, 2, 3,
3           1, log(500), 1)
4 Mean <- Xpred%%Bn
5 Hn <- 1+t(Xpred)%%Vn%%Xpred
6 UtilDemand <- exp(replicate(s, MixMatrix::rmatrixt(n = 1,
7             mean=Mean, U = Hn, V = Psin, df = an + 1 - M)))
8 ElePred <- UtilDemand[1,1,]
9 WatPred <- UtilDemand[1,2,]
10 GasPred <- UtilDemand[1,3,]
11 data <- data.frame(cbind(ElePred, WatPred, GasPred)) #Data
12           frame
13 annotations1 <- data.frame(
14   x = round(quantile(data$ElePred, c(0.025, 0.5, 0.975)),1),
15   y = c(600, 1000, 600),
16   label = c("2.5%", "50%", "97.5%:")
17 )
18 annotations2 <- data.frame(
19   x = round(quantile(data$WatPred, c(0.025, 0.5, 0.975)),1),
20   y = c(600, 1000, 600),
21   label = c("2.5%", "50%", "97.5%:")
22 )
23 annotations3 <- data.frame(
24   x = round(quantile(data$GasPred, c(0.025, 0.5, 0.975)),1),
25   y = c(600, 1000, 600),
26   label = c("2.5%", "50%", "97.5%:")
27 )
28 require(ggplot2) # Cool figures
29 require(ggpubr) # Multiple figures in one page
30 require(latex2exp) # LaTeX equations in figures
31 fig1 <- ggplot(data = data, aes(ElePred)) + geom_histogram(
32   bins = 40, color = "#000000", fill = "#0099F8") + xlab(
33     "kWh") + ylab("Frequency") + ggtitle("Electricity") +
34     xlim(0, 1050) + geom_text(data = annotations1, aes(x = x,
35       y = y, label = paste(label, x)), size = 3, fontface = "
36     bold")
37 fig2 <- ggplot(data = data, aes(WatPred)) + geom_histogram(
38   bins = 40, color = "#000000", fill = "#0099F8") + xlab(
39     TeX("$M^3$")) + ylab("Frequency") + ggtitle("Water") +
40     xlim(0, 100) + geom_text(data = annotations2, aes(x = x,
41       y = y, label = paste(label, x)), size = 3, fontface = "
42     bold")
43 fig3 <- ggplot(data = data, aes(GasPred)) + geom_histogram(
44   bins = 40, color = "#000000", fill = "#0099F8") + xlab(
45     TeX("$M^3$")) + ylab("Frequency") + ggtitle("Gas") +
46     xlim(0, 80) + geom_text(data = annotations3, aes(x = x,
47       y = y, label = paste(label, x)), size = 3, fontface = "
48     bold")

```


Figures 3.3, 3.4 and 3.5 show the marginal predictive distributions of electricity, water and gas for the reference household. The median predictive values are kWh 168.8, M³ 12.3 and M³ 10.1, respectively. In addition, the 95% credible intervals are (27.7, 1028.9), (1.5, 98.7) and (1.5, 67.5) for electricity, water and gas.



FIGURE 3.3

Histogram using the posterior predictive distribution of electricity demand

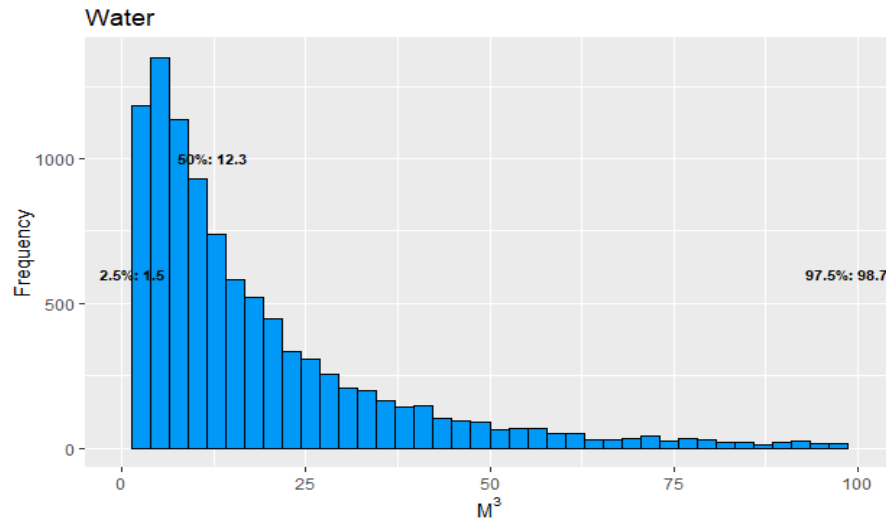
15. Ph.D. students sleeping hours [1, Chap. 2]

We are interested in learning about the proportion of Ph.D. students who sleep at least 6 hours per day. We have a sample of 52 students, where 15 report sleeping at least 6 hours, and the remaining 37 report not sleeping at least 6 hours. The prior distribution is a Beta distribution, with hyperparameters calibrated so that the prior probabilities of the proportion of students who sleep least than 6 hours being less than 0.4 and 0.75 are 0.6 and 0.95, respectively. Estimate the 95% posterior credible interval for the proportion of Ph.D. students. Then, assume there is a group of experts whose beliefs about the proportion of Ph.D. students sleeping at least 6 hours are represented in the following table:

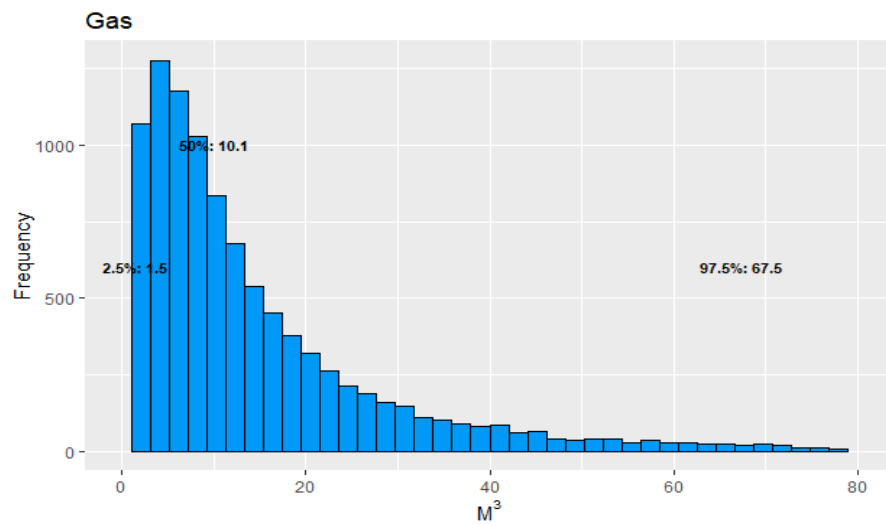
TABLE 3.1

Probability distribution: Ph.D students that sleep at least 6 hours per day.

| h | 0.05 | 0.10 | 0.15 | 0.20 | 0.25 | 0.30 | 0.35 | 0.40 | 0.45 | 0.50 | 0.55 |
|------------|------|------|------|------|------|------|------|------|------|------|------|
| $P(p = h)$ | 0.05 | 0.07 | 0.10 | 0.12 | 0.15 | 0.17 | 0.15 | 0.11 | 0.06 | 0.01 | 0.01 |

**FIGURE 3.4**

Histogram using the posterior predictive distribution of water demand

**FIGURE 3.5**

Histogram using the posterior predictive distribution of gas demand

Use Table 3.1 as prior information, and find the posterior distribution of the proportion of students that sleep at least 6 hours.

Answer

We know from the Bernoulli-beta model that the posterior distribution of the proportion of Ph.D. students that sleep at least 6 hours is beta, $\theta|\mathbf{y} \sim B(\alpha_n, \beta_n)$, $\alpha_n = \alpha_0 + 15$ and $\beta_n = \beta_0 + 37$, where $\alpha_0 = 1.44$ and $\beta_0 = 2.57$.

The following code shows how to get the posterior distribution in this exercise.

R code. Ph.D. students sleeping hours: Posterior distribution

```

1 rm(list = ls()); set.seed(010101)
2 # Function to calibrate the hyperparameters
3 elec <- function(theta, perc, q){
4   E1 <- perc[1] - pbeta(q[1], theta[1], theta[2])
5   E2 <- perc[2] - pbeta(q[2], theta[1], theta[2])
6   loss <- E1^2 + E2^2
7   return(loss)
8 }
9 q1 <- 0.4; q2 <- 0.75; q <- c(q1, q2) # Quantiles
10 p1e <- 0.6; p2e <- 0.95; perc <- c(p1e, p2e) # Cumulate
    probability from experts
11 theta0 <- c(1, 1) # Parameters
12 elec(theta0, perc, q)
13 Res <- optim(theta0, elec, perc = perc, q = q)
14 p <- seq(0, 1, length = 500)
15 a <- Res$par[1]; b <- Res$par[2]
16 pbeta(q1, a, b) # P(p <= q1) = p1e
17 pbeta(q2, a, b) # P(p <= q2) = p2e
18 s <- 15 # Success; f <- 37 # Failures
19 prior <- dbeta(p, a, b)
20 likelihood <- dbeta(p, s + 1, f + 1) # Seeing the binomial
    distribution as a likelihood is a beta distribution!!!
21 post <- dbeta(p, a+s, b+f)
22 plot(p, post, type="l", ylab="Density", main = "Proportion of
    students who sleep at least 6 hours per day", lty=2, lwd
    =3, col=gray.colors(1, start=0.1))
23 lines(p, likelihood, lty=1, lwd=3, col=gray.colors(1, start=0.4))
24 lines(p, prior, lty=3, lwd=3, col=gray.colors(1, start=0.6))
25 legend(.7, 4, c("Prior", "Likelihood", "Posterior"), lty=c
    (3, 1, 2), lwd=c(3, 3, 3), col=c(col=gray.colors(1, start=0.6),
    col=gray.colors(1, start=0.4), col=gray.colors(1, start
    =0.1)))
26 S <- 10000; postdraws1 <- rbeta(S, a+s, b+f)
27 mean(postdraws1); quantile(postdraws1, c(0.025, 0.975))
28 # Experts
29 p <- c(seq(0.05, 0.55, by = 0.05)) # Probabilities
30 prior <- c(0.05, 0.07, 0.1, 0.12, 0.15, 0.17, 0.15, 0.11,
    0.06, 0.01, 0.01) # Expert assessment
31 llikelihood <- s * log(p) + f * log(1 - p) # Log likelihood
32 likelihood2 <- exp(llikelihood - max(llikelihood)) # Scale
    the likelihood for plotting
33 product <- likelihood2 * prior # Proportional to posterior
34 posterior <- product/sum(product) # Posterior
35 # Figure
36 plot(p, prior, type = "l", ylab="Probability", lwd=2, lty=2,
    ylim=c(0, 0.99), xlim = c(0, 0.6), col=gray.colors(1,
    start=0.1), main = "Posterior distribution: Proportion
    sleep hours")
37 lines(p, posterior, type = "l", lwd=2, col=gray.colors(1, start
    =0.6))
38 lines(p, likelihood2, type = "l", lwd=4, col=gray.colors(1, start
    =0.3))
39 legend(0.45, 0.85, c('Prior', 'Likelihood', 'Posterior'), lty=c
    (2, 1, 1), col=c(gray.colors(1, start=0.1), gray.colors(1,
    start=0.3), gray.colors(1, start=0.6)), lwd=2)
40 postdraws2 <- sample(p, S, replace = TRUE, prob = posterior)
41 mean(postdraws2); quantile(postdraws2, c(0.025, 0.975))

```

Figures 3.6 and 3.7 show the prior, likelihood, and posterior distributions of the proportion of Ph.D. students who sleep at least 6 hours per day based on the binomial-beta and binomial-discrete models. The mean under both models is 29%, and the 95% credible intervals are (18%,42%) and (20%,40%), respectively.



FIGURE 3.6

Posterior distribution binomial-beta model: Proportion Ph.D. students that sleep at least 6 hours per day

**FIGURE 3.7**

Posterior distribution binomial-discrete model: Proportion Ph.D. students that sleep at least 6 hours per day

4

Simulation methods

Solutions of Exercises

1. Example: The normal model with independent priors

Let's recap the math test exercise in Chapter 3, this time assuming independent priors. Specifically, let $Y_i \sim N(\mu, \sigma^2)$, where $\mu \sim N(\mu_0, \sigma_0^2)$ and $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$. The sample size is 50, and the mean and standard deviation of the math scores are 102 and 10, respectively. We set $\mu_0 = 100$, $\sigma_0^2 = 100$, and $\alpha_0 = \delta_0 = 0.001$.

- Find the posterior distribution of μ and σ^2 .
- Program a Gibbs sampler algorithm and plot the histogram of the posterior draws of μ

Answer

The posterior distribution is

$$\begin{aligned} \pi(\mu, \sigma^2 | \mathbf{y}) &\propto (\sigma^2)^{-N/2} \exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^N (y_i - \mu)^2 \right\} \\ &\times \exp \left\{ -\frac{1}{2\sigma_0^2} (\mu - \mu_0)^2 \right\} \times \left(\frac{1}{\sigma^2} \right)^{\alpha_0/2+1} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\}. \end{aligned}$$

Thus, the conditional posterior distribution of μ is

$$\begin{aligned} \pi(\mu, \sigma^2 | \mathbf{y}) &\propto \exp \left\{ -\frac{1}{2} \left[\frac{1}{\sigma^2} \sum_{i=1}^N (y_i - \mu)^2 + \frac{1}{\sigma_0^2} (\mu - \mu_0)^2 \right] \right\} \\ &\propto \exp \left\{ -\frac{1}{2} \left[\mu^2 \left(\frac{1}{\sigma^2/N} + \frac{1}{\sigma_0^2} \right) - 2\mu \left(\frac{\bar{y}}{\sigma^2/N} + \frac{\mu_0}{\sigma_0^2} \right) \right] \right\}. \end{aligned}$$

We set $\mu_n = \sigma_n^2 \left(\frac{\bar{y}}{\sigma^2/N} + \frac{\mu_0}{\sigma_0^2} \right)$ and $\sigma_n^2 = \left(\frac{1}{\sigma^2/N} + \frac{1}{\sigma_0^2} \right)^{-1}$. Thus,

$$\begin{aligned} \pi(\mu, \sigma^2 | \mathbf{y}) &\propto \exp \left\{ -\frac{1}{2\sigma_n^2} [\mu^2 - 2\mu\mu_n + \mu_n^2 - \mu_n^2] \right\} \\ &\propto \exp \left\{ -\frac{1}{2\sigma_n^2} (\mu - \mu_n)^2 \right\}. \end{aligned}$$

This is the kernel of a normal distribution, that is, $\mu | \sigma^2, \mathbf{y} \sim N(\mu_n, \sigma_n^2)$.

The conditional posterior distribution of σ^2 is given by

$$\begin{aligned} \pi(\sigma^2 | \mu, \mathbf{y}) &\propto (\sigma^2)^{-N/2} \exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^N (y_i - \mu)^2 \right\} \\ &\quad \times \left(\frac{1}{\sigma^2} \right)^{\alpha_0/2+1} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\} \\ &\propto (\sigma^2)^{-N/2-\alpha_0/2-1} \exp \left\{ -\frac{1}{2\sigma^2} \left[\sum_{i=1}^N (y_i - \mu)^2 + \delta_0 \right] \right\}. \end{aligned}$$

Thus, $\sigma^2 | \mu, \mathbf{y} \sim IG(\alpha_n/2, \delta_n/2)$, where $\alpha_n = N + \alpha_0$ and $\delta_n = \sum_{i=1}^N (y_i - \mu)^2 + \delta_0 = N\hat{\sigma}^2 + N(\bar{y} - \mu)^2 + \delta_0$ given that $\sum_{i=1}^N (y_i - \bar{y}) = 0$, where \bar{y} and $\hat{\sigma}$ are the mean and standard deviation estimates.

As we have the conditional posterior distributions, we can use the Gibbs sampling algorithm to perform inference in this model. The following code shows how to do it.

R code. Gibbs sampler: The math example

```

1 rm(list = ls())
2 set.seed(010101)
3 N <- 50
4 # Sample size
5 muhat <- 102
6 # Sample mean
7 sig2hat <- 100
8 # Sample variance
9
10 # Hyperparameters
11 mu0 <- 100
12 sig20 <- 100
13 delta0 <- 0.001
14 alpha0 <- 0.001
15
16 MCMC <- 10000; burnin <- 1000; S <- MCMC + burnin
17 keep <- (burnin+1):S
18 # Posterior draws
19 alphan <- alpha0 + N
20 sig2Post <- rep(NA, S)
21 muPost <- rep(NA, S)
22 sig2 <- sig20
23 for(s in 1:S){
24   sig2n <- (1/(sig2/N)+1/sig20)^(-1)
25   mun <- sig2n*(muhat/(sig2/N)+mu0/sig20)
26   mu <- rnorm(1, mun, sig2n^0.5)
27   muPost[s] <- mu
28   deltan <- N*(sig2hat + (muhat - mu)^2)
29   sig2 <- invgamma::rinvgamma(1, shape = alphan, rate =
     deltan)
30   sig2Post[s] <- sig2
31 }
32 sig2s <- coda::mcmc(sig2Post[keep])
33 mus <- coda::mcmc(muPost[keep])
34 summary(sig2s)
35 summary(mus)
36 hist(mus, main = "Histogram: Posterior mean", xlab = "
   Posterior mean", col = "blue", breaks = 50)
37 muPost_tq <- quantile(mus, c(0.025, 0.5, 0.975))
38 muPost_tq
39 cutoff <- 103
40 PmuPost_tcutoff <- mean(mus > cutoff)
41 PmuPost_tcutoff

```

Figure 4.1 shows the histogram of the draws of the posterior mean of the math test results. The posterior mean and median are 101.94 and 101.95,

**FIGURE 4.1**

Histogram of posterior draws of mean: Math test

and the 95% credible interval is (99.14, 104.79).

2. Show that the Gibbs sampler is a particular case of the Metropolis-Hastings where the acceptance probability is equal to 1.

Answer

Without loss of generality let's assume that there are two blocks, $\boldsymbol{\theta} = [\boldsymbol{\theta}_1 \ \boldsymbol{\theta}_2]^\top$ such that the Metropolis-Hastings (M-H) algorithm generates a candidate sample $(\boldsymbol{\theta}_1^c)$ using a proposal distribution $q(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}^{(s-1)})$. The candidate is accepted with probability:

$$\alpha(\boldsymbol{\theta}^{(s-1)}, \boldsymbol{\theta}^c) = \min \left\{ 1, \frac{q(\boldsymbol{\theta}_1^{(s-1)} | \boldsymbol{\theta}^c) \pi(\boldsymbol{\theta}^c | \mathbf{y})}{q(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}^{(s-1)}) \pi(\boldsymbol{\theta}^{(s-1)} | \mathbf{y})} \right\}.$$

For Gibbs sampling, the candidate $\boldsymbol{\theta}_1^c$ is drawn directly from the *full conditional distribution*, so $q(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}^{(s-1)}) = \pi(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}_2^{(s-1)}, \mathbf{y})$. Since Gibbs sampling uses the full conditional distributions as the proposal, the key terms simplify. In particular, $q(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}^{(s-1)}) = \pi(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}_2^c, \mathbf{y})$, and similarly $q(\boldsymbol{\theta}_1^{(s-1)} | \boldsymbol{\theta}^c) = \pi(\boldsymbol{\theta}_1^{(s-1)} | \boldsymbol{\theta}_2^{(s-1)}, \mathbf{y})$. Thus, the acceptance probability is

given by

$$\begin{aligned}\alpha(\boldsymbol{\theta}^{(s-1)}, \boldsymbol{\theta}^c) &= \min \left\{ 1, \frac{\pi(\boldsymbol{\theta}_1^{(s-1)} | \boldsymbol{\theta}_2^{(s-1)}, \mathbf{y}) \pi(\boldsymbol{\theta}^c | \mathbf{y})}{\pi(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}_2^c, \mathbf{y}) \pi(\boldsymbol{\theta}^{(s-1)} | \mathbf{y})} \right\} \\ &= \min \left\{ 1, \frac{\pi(\boldsymbol{\theta}_1^{(s-1)} | \boldsymbol{\theta}_2^{(s-1)}, \mathbf{y}) \pi(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}_2^c, \mathbf{y}) \pi(\boldsymbol{\theta}_2^c | \mathbf{y})}{\pi(\boldsymbol{\theta}_1^c | \boldsymbol{\theta}_2^c, \mathbf{y}) \pi(\boldsymbol{\theta}_1^{(s-1)} | \boldsymbol{\theta}_2^{(s-1)}, \mathbf{y}) \pi(\boldsymbol{\theta}_2^{(s-1)} | \mathbf{y})} \right\} \\ &= 1,\end{aligned}$$

due to $\boldsymbol{\theta}_2^{(s-1)} = \boldsymbol{\theta}_2^c$. Thus, the Gibbs sampling algorithm is implicitly a M-H algorithm where the acceptance probability is 1.

3. Implement a Metropolis-Hastings (M-H) to sample from the Cauchy distribution, $C(0, 1)$, using as proposals a standard normal distribution and a Student's t distribution with 5 degrees of freedom.

Answer

The following code shows to program the M-H to get draws from the Cauchy distribution, $C(0, 1)$, using as proposal a standard normal distribution and a Student's t distribution with 5 degree of freedom.

R code. Metropolis-Hastings algorithm: Cauchy distribution

```

1 rm(list = ls()); set.seed(010101)
2 S <- 100000; df <- 5
3 theta1 <- runif(S); accept1 <- rep(0, S)
4 theta2 <- runif(S); accept2 <- rep(0, S)
5 for (s in 2:S){
6   thetac1 <- rnorm(1) # Candidate normal standard
7   thetac2 <- rt(1, df = df) # Candidate Students' t
8   #Acceptance rate
9   a1 <- (dcauchy(thetac1)*dnorm(theta1[s-1]))/(dcauchy(
10     theta1[s-1]*dnorm(thetac1))
11   a2 <- (dcauchy(thetac2)*dt(theta2[s-1], df = df))/(dcauchy(
12     theta2[s-1]*dt(thetac2, df = df))
13   U1 <- runif(1)
14   if(U1 <= a1){
15     theta1[s] <- thetac1; accept1[s] <- 1
16   }else{
17     theta1[s] <- theta1[s-1]; accept1[s] <- 0
18   }
19   if(U1 <= a2){
20     theta2[s] <- thetac2; accept2[s] <- 1
21   }else{
22     theta2[s] <- theta2[s-1]; accept2[s] <- 0
23   }
24 }
25 mean(accept1); mean(accept2)
26 plot(coda::mcmc(theta1)); plot(coda::mcmc(theta2))
27 h <- hist(theta1, breaks=50, col="blue", xlab="x", main="
28   Cauchy draws from a Metropolis-Hastings algorithm:
29   Normal standard proposal")
30 pfit <- seq(min(theta1),max(theta1),length=50)
31 yfit<-dcauchy(pfit)
32 yfit <- yfit*diff(h$mids[1:2])*length(theta1)
33 lines(pfit, yfit, col="red", lwd=2)
34 h <- hist(theta2, breaks=50, col="blue", xlab="x", main="
35   Cauchy draws from a Metropolis-Hastings algorithm:
36   Student's t proposal")
37 pfit <- seq(min(theta2),max(theta2),length=50)
38 yfit<-dcauchy(pfit)
39 yfit <- yfit*diff(h$mids[1:2])*length(theta2)
40 lines(pfit, yfit, col="red", lwd=2)

```

Figures 4.2 and 4.3 show the histograms of the posterior draws using the normal and Student's t distributions, along with the density of the Cauchy distribution. The spike in the posterior draws from the standard normal proposal is due to the algorithm being stuck for many iterations at a par-

ticular value, as the normal distribution has lighter tails compared to the Cauchy distribution. The convergence using the normal proposal is slower than when using the Student's t proposal, owing to the lighter tails of the former.

Cauchy draws from a Metropolis-Hastings algorithm: Normal standard proposal



FIGURE 4.2

Histogram of posterior draws of beta distribution and the density of the beta distribution.

4. This exercise was proposed by Professor Hedibert Freitas Lopes, who cites [31] as a useful reference for an introduction to Hamiltonian Monte Carlo in **R** and the *hmclearn* package. The task is to obtain posterior draws using the Metropolis-Hastings and Hamiltonian Monte Carlo algorithms for the posterior distribution given by

$$\pi(\theta_1, \theta_2 | \mathbf{y}) \propto \exp \left\{ -\frac{1}{2} (\theta_1^2 \theta_2^2 + \theta_1^2 + \theta_2^2 - 8\theta_1 - 8\theta_2) \right\}.$$

Answer

The following code demonstrates the implementation of the M-H and HMC algorithms for this exercise. For the M-H algorithm, the number of MCMC iterations, burn-in period, and thinning parameters are set to 20,000, 1,000, and 20, respectively. The variance of the proposal distribution is tuned to achieve an acceptance rate close to 25%.

For the HMC algorithm, the number of iterations and burn-in period are set to 5,000 and 500, respectively. The step size and number of leapfrog iterations are set to 0.001 and 100, and the mass matrix is defined as $\mathbf{M} = \mathbf{I}_2$. These parameters yield an acceptance rate near 65%.

**FIGURE 4.3**

Histogram of posterior draws of beta distribution and the density of the beta distribution.

Figures 4.4 and 4.6 present the contour plots and posterior draws from the M-H and HMC algorithms for the joint posterior distribution. It can be observed that this distribution is bimodal, and both algorithms successfully capture this feature.

*R code. Metropolis-Hastings and Hamiltonian
Monte Carlo algorithms*

```

1 rm(list = ls()); set.seed(010101)
2 # Posterior distribution
3 PostDist <- function(theta){
4   theta1 <- theta[1]; theta2 <- theta[2]
5   post <- exp(-0.5*(theta1^2*theta2^2+theta1^2+theta2^2-8*
6     theta1-8*theta2))
7   return(post)
8 }
9 # Metropolis-Hastings
10 MH <- function(theta, c2){
11   thetac <- MASS::mvrnorm(1, mu = theta, Sigma = c2*diag(2))
12   a <- PostDist(thetac)/PostDist(theta)
13   U <- runif(1)
14   if(U <= a){
15     theta <- thetac
16     accept <- 1
17   }else{
18     theta <- theta
19     accept <- 0
20   }
21   return(list(theta = theta, accept = accept))
22 }
23 # Posterior draws M-H
24 S <- 20000; burnin <- 1000; thin <- 20; tot <- S + burnin
25 K <- 2; c2 <- 1.5
26 thetaPostMH <- matrix(NA, tot, K)
27 AcceptMH <- rep(NA, tot)
28 thetaMH <- c(0, 0)
29 for(s in 1:tot){
30   ResMH <- MH(thetaMH, c2 = c2)
31   thetaMH <- ResMH$theta
32   thetaPostMH[s,] <- thetaMH
33   AcceptMH[s] <- ResMH$accept
34 }
35 keep <- seq((burnin), tot, thin)
36 mean(AcceptMH[keep])
37 thetaPostMHMCMC <- coda::mcmc(thetaPostMH[keep,])
38 plot(thetaPostMHMCMC)
39 coda::autocorr.plot(thetaPostMHMCMC)
40 # Contour plot
41 ngrid <- 400
42 theta1 <- seq(-1, 6, length = ngrid)
43 theta2 <- seq(-1, 6, length = ngrid)
44 f <- matrix(0, ngrid, ngrid)
45 for (i in 1:ngrid){
46   for (j in 1:ngrid){
47     f[i,j] = PostDist(c(theta1[i],theta2[j]))
48   }
49 }
50 plot(thetaPostMH[keep,], xlim=range(theta1), ylim=range(
51   theta2), pch=16, col=grey(0.8), xlab=expression(theta
52   [1]), ylab=expression(theta[2]))
53 contour(theta1,theta2,f, drawlabels=FALSE, add=TRUE, col = "
54   blue", lwd = 1.2)
55 title("Random walk Metropolis-Hastings")

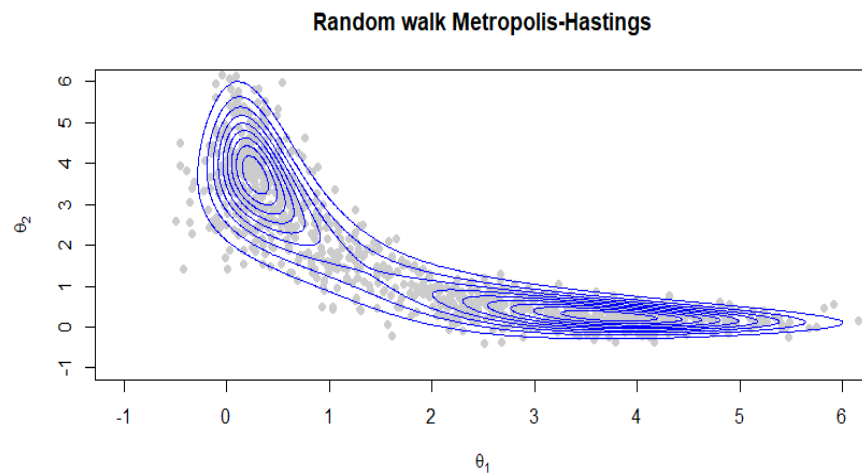
```

R code. Metropolis-Hastings and Hamiltonian Monte Carlo algorithms

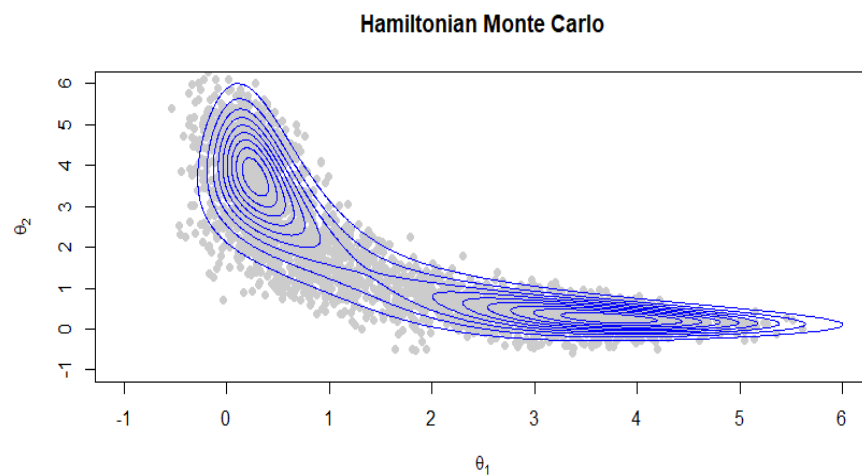
```

1 HMC <- function(theta, epsilon, L, M){
2   Minv <- solve(M); thetat <- theta
3   K <- length(thetat)
4   mom <- t(mvtnorm::rmvnorm(1, rep(0, K), M))
5   logPost_Mom_t <- log(PostDist(thetat)) + mvtnorm::dmvnorm
6     (t(mom), rep(0, K), M, log = TRUE)
7   theta1 <- theta[1]; theta2 <- theta[2]
8   for(l in 1:L){
9     if(l == 1 | l == L){
10      mom <- mom + 0.5*epsilon*(-0.5*c(2*theta1*theta2^2+2*
11        theta1-8, 2*theta2*theta1^2+2*theta2-8))
12      theta <- theta + epsilon*Minv%*%mom
13    }else{
14      mom <- mom + epsilon*(-0.5*c(2*theta1*theta2^2+2*
15        theta1-8, 2*theta2*theta1^2+2*theta2-8))
16      theta <- theta + epsilon*Minv%*%mom
17    }
18  }
19  logPost_Mom_star <- log(PostDist(theta)) + mvtnorm::
20    dmvnorm(t(mom), rep(0, K), M, log = TRUE)
21  alpha <- min(1, exp(logPost_Mom_star-logPost_Mom_t))
22  u <- runif(1)
23  if(u <= alpha){
24    thetaNew <- c(theta)
25  }else{
26    thetaNew <- thetat
27  }
28  rest <- list(theta = thetaNew, Prob = alpha)
29  return(rest)
30 }
31 # Posterior draws HMC
32 S <- 5000; burnin <- 500; tot <- S + burnin
33 epsilon <- 0.0025; L <- 100; M <- diag(2)
34 thetaPostHMC <- matrix(NA, tot, K)
35 ProbAcceptHMC <- rep(NA, tot)
36 thetaHMC <- c(0, 0)
37 for(s in 1:tot){
38   ResHMC <- HMC(theta = thetaHMC, epsilon = epsilon, L = L,
39     M = M)
40   thetaHMC <- ResHMC$theta
41   thetaPostHMC[s,] <- thetaHMC
42   ProbAcceptHMC[s] <- ResHMC$Prob
43 }
44 keep <- burnin:S
45 summary(ProbAcceptHMC[keep])
46 thetaPostHMC[keep,] <- coda::mcmc(thetaPostHMC[keep,])
47 plot(thetaPostHMC[keep,]); coda::autocorr.plot(thetaPostHMC[keep,])
48 plot(thetaPostHMC[keep,], xlim=range(theta1), ylim=range(
49   theta2), pch=16, col=grey(0.8),
50   xlab=expression(theta[1]), ylab=expression(theta[2]))
51 contour(theta1,theta2,f, drawlabels=FALSE, add=TRUE, col = "
52   blue", lwd = 1.2)
53 title("Hamiltonian Monte Carlo")

```


**FIGURE 4.4**

Contour plot: Metropolis-Hastings posterior draws.

**FIGURE 4.5**

Contour plot: Hamiltonian Monte Carlo posterior draws.

5. Ph.D. students sleeping hours continues

- (a) Use importance sampling based on a $U(0, 1)$ proposal to obtain draws

of $\theta|\mathbf{y} \sim B(16.55, 39.57)$ in the Ph.D. students' sleeping hours example in Chapter 3. Note that, based on Exercise 15 in Chapter 3, $\alpha_0 = 1.44$ and $\beta_0 = 2.57$.

- (b) Compute the marginal likelihood in this context (Bernoulli-Beta model) and compare it to the result obtained using the Gelfand-Dey method.

Answer

The posterior distribution of the Bernoulli-beta model is

$$p(\theta|\mathbf{y}) = \frac{\prod_{i=1}^N \theta^{y_i} (1-\theta)^{1-y_i} \theta^{\alpha_0-1} (1-\theta)^{\beta_0-1} \Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0) \Gamma(\beta_0) p(\mathbf{y})},$$

where

$$\begin{aligned} p(\mathbf{y}) &= \int_{\Theta} \frac{\prod_{i=1}^N \theta^{y_i} (1-\theta)^{1-y_i} \theta^{\alpha_0-1} (1-\theta)^{\beta_0-1} \Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0) \Gamma(\beta_0)} d\theta \\ &= \int_{\Theta} \frac{\theta^{\sum_{i=1}^N y_i + \alpha_0 - 1} (1-\theta)^{N - \sum_{i=1}^N y_i + \beta_0 - 1} \Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0) \Gamma(\beta_0)} d\theta \\ &= \frac{B(\alpha_n, \beta_n)}{B(\alpha_0, \beta_0)} \int_{\Theta} \frac{\theta^{\sum_{i=1}^N y_i + \alpha_0 - 1} (1-\theta)^{N - \sum_{i=1}^N y_i + \beta_0 - 1}}{B(\alpha_n, \beta_n)} d\theta \\ &= \frac{B(\alpha_n, \beta_n)}{B(\alpha_0, \beta_0)}. \end{aligned}$$

The integral is equal to 1 due to being over the support of $B(\alpha_n, \beta_n)$ distribution.

R code. Importance sampling: Bernoulli-Beta model

```

1 rm(list = ls()); set.seed(010101); S <- 50000
2 # Importance sampling from standard normal proposal
3 an <- 16.55; bn <- 39.57 # Posterior parameters
4 theta <- runif(S) # Proposal
5 ws <- dbeta(theta, an, bn) # Weights
6 wstars <- ws/sum(ws) # Standardized weights
7 L <- 20000 # Size of posterior sample
8 thetaBeta <- sample(theta, L, replace = TRUE, prob = wstars)
9 # Posterior draws
10 # Figure
11 h <- hist(thetaBeta, breaks=50, col="blue", xlab="x", main="
12   Beta draws from importance sampling: Uniform (0,1)
13   proposal")
14 pfit <- seq(min(thetaBeta), max(thetaBeta), length=50)
15 yfit <- dbeta(pfit, an, bn)
16 yfit <- yfit*diff(h$mids[1:2])*length(thetaBeta)
17 lines(pfit, yfit, col="red", lwd=2)
18 a0 <- 1.44; b0 <- 2.57 # Hyperparameters
19 s <- 15; n <- 52 # Data
20 LogMarLik <- lbeta(an, bn)-lbeta(a0, b0) # Marginal
21   likelihood
22 LogMarLik
23 # Gelfand-Day method
24 LikPrior <- function(theta){
25   Liki <- theta^s*(1-theta)^(n-s)
26   Priori <- dbeta(theta, a0, b0)
27   LikPriori <- 1 / Liki * Priori
28   return(LikPriori)
29 }
30 LogMarLikGD <- log(1/mean(sapply(thetaBeta, LikPrior)))
31 LogMarLikGD

```

Figure 4.6 shows the histogram of the posterior draws obtained using the importance sampling algorithm with a uniform proposal. The algorithm performs well. Additionally, the analytic solution for the log marginal likelihood is -32.75, while the Gelfand-Dey method yields -32.76.

6. Example 4.1 in [8] is

$$\theta_t = 0.5\theta_{t-1} + 25 \frac{\theta_{t-1}}{1 + \theta_{t-1}^2} + 8\cos(1.2t) + w_t$$

$$y_t = \frac{\theta_t^2}{20} + \mu_t,$$

where $\theta_0 \sim N(0, \sqrt{10})$, $w_t \sim N(0, \sqrt{10})$ and $\mu_t \sim N(0, \sqrt{1})$.

**FIGURE 4.6**

Importance sampling: Beta distribution.

- Perform sequential importance sampling in this example
- Perform particle (Bootstrap) filtering in this example
- Estimate the marginal likelihood in this example

Answer

The following code shows to perform sequential importance sampling and particle (Bootstrap) filtering in the Example 1 in [8]. Take into account that we use same strategy as in the dynamic linear model example in the book to calculate the mean and standard deviation of the posterior distribution.

*R code. Sequential importance sampling and
particle (Bootstrap) filtering: Gordon (1993)
Example 1.*

```

1 rm(list = ls()); set.seed(010101)
2 S <- 50000 # Number of particles
3 sigma_w <- 10^0.5 # State noise
4 sigma_mu <- 1 # Observation noise
5 T <- 200 # Sample size
6 # Simulate true states and observations
7 theta_true <- numeric(T)
8 y_obs <- numeric(T)
9 theta_true[1] <- rnorm(1, mean = 0, sd = sigma_w) # Initial
  state
10 y_obs[1] <- rnorm(1, mean = theta_true[1]^2/20, sd = sigma_
  mu)
11 for (t in 2:T) {
12   meant <- 0.5*theta_true[t-1] + 25*(theta_true[t-1]/(1+
  theta_true[t-1]^2)) + 8*cos(1.2*t)
13   theta_true[t] <- rnorm(1, mean = meant, sd = sigma_w)
14   y_obs[t] <- rnorm(1, mean = theta_true[t]^2/20, sd = sigma
  _mu)
15 }
16 plot(theta_true, type = "l"); plot(y_obs, type = "l")
17 # Sequential Importance Sampling (SIS)
18 particles <- matrix(0, nrow = S, ncol = T)
19 weights <- matrix(0, nrow = S, ncol = T)
20 weightsSt <- matrix(0, nrow = S, ncol = T)
21 # Initialization
22 particles[, 1] <- rnorm(S, mean = 0, sd = sigma_w)
23 weights[, 1] <- dnorm(y_obs[1], mean = particles[, 1]^2/20,
  sd = sigma_mu)
24 weightsSt[, 1] <- weights[, 1] / sum(weights[, 1])
25 # Sequential updating
26 for (t in 2:T) {
27   particles[, t] <- rnorm(S, mean = 0.5*particles[, t-1] +
  25*(particles[, t-1]/(1+particles[, t-1]^2)) + 8*cos(1.2
  *t), sd = sigma_w) # Compute weights
28   weights[, t] <- weightsSt[, t-1] * dnorm(y_obs[t], mean =
  particles[, t]^2/20, sd = sigma_mu)
29   weightsSt[, t] <- weights[, t] / sum(weights[, t])
30 }
31 FilterDist <- colSums(particles * weightsSt)
32 SDFilterDist <- (colSums(particles^2 * weightsSt) -
  FilterDist^2)^0.5
33 library(dplyr); library(ggplot2); library(latex2exp)
34 ggplot2::theme_set(theme_bw())
35 df <- tibble(t = 1:T, mean = FilterDist, lower = FilterDist
  - 2*SDFilterDist, upper = FilterDist + 2*SDFilterDist,
  theta_true = theta_true)
36 plot_filtering_estimates <- function(df) {
37   p <- ggplot(data = df, aes(x = t)) + geom_ribbon(aes(ymin
  = lower, ymax = upper), alpha = 1, fill = "lightblue") +
  geom_line(aes(y = theta_true), colour = "black", alpha
  = 1, linewidth = 0.5) + geom_line(aes(y = mean), colour
  = "blue", linewidth = 0.5) + ylab(TeX("$\\theta_{t}$"))
  + xlab("Time")
38   print(p)
39 }
40 plot_filtering_estimates(df)

```

***R code. Sequential importance sampling and
particle (Bootstrap) filtering: Gordon (1993)
Example 1.***

```

1 # Particle filtering
2 particles <- matrix(0, nrow = S, ncol = T)
3 particlesT <- matrix(0, nrow = S, ncol = T)
4 weights <- matrix(0, nrow = S, ncol = T)
5 weightsSt <- matrix(0, nrow = S, ncol = T)
6 weightsSTT <- matrix(1/S, nrow = S, ncol = T)
7 logalphas <- matrix(0, nrow = S, ncol = T)
8 # Initialization
9 particles[, 1] <- rnorm(S, mean = 0, sd = sigma_w) # Sample
   initial particles
10 weights[, 1] <- dnorm(y_obs[1], mean = particles[, 1]^2/20,
   sd = sigma_mu) # Importance weights
11 weightsSt[, 1] <- weights[, 1] / sum(weights[, 1]) #
   Normalize weights
12 ind <- sample(1:S, size = S, replace = TRUE, prob =
   weightsSt[, 1]) # Resample
13 particles[, 1] <- particles[ind, 1] # Resampled particles
14 particlesT[, 1] <- particles[, 1] # Resampled particles
15 # Sequential updating
16 pb <- winProgressBar(title = "progress bar", min = 0, max =
   T, width = 300)
17 for (t in 2:T) {
18   # Propagate particles
19   particles[, t] <- rnorm(S, mean = 0.5*particles[, t-1] +
   25*(particles[, t-1]/(1+particles[, t-1]^2)) + 8*cos(1.2
   *t), sd = sigma_w)
20   # Compute weights
21   logalphas[, t] <- dnorm(y_obs[t], mean = particles[, t]^2/
   20, sd = sigma_mu, log = TRUE)
22   weights[, t] <- exp(logalphas[, t])
23   weightsSt[, t] <- weights[, t] / sum(weights[, t])
24   if(t < T){
25     ind <- sample(1:S, size = S, replace = TRUE, prob =
   weightsSt[, t])
26     particles[, 1:t] <- particles[ind, 1:t]
27   }else{
28     ind <- sample(1:S, size = S, replace = TRUE, prob =
   weightsSt[, t])
29     particlesT[, 1:t] <- particles[ind, 1:t]
30   }
31   setWinProgressBar(pb, t, title=paste( round(t/T*100, 0), "
   % done"))
32 }
33 close(pb)
34 FilterDist <- colSums(particles * weightsSt)
35 SDFilterDist <- (colSums(particles^2 * weightsSt) -
   FilterDist^2)^0.5
36 FilterDistT <- colSums(particlesT * weightsSTT)
37 SDFilterDistT <- (colSums(particlesT^2 * weightsSTT) -
   FilterDistT^2)^0.5

```

***R code. Sequential importance sampling and
particle (Bootstrap) filtering: Gordon (1993)
Example 1.***

```

1 library(dplyr); library(ggplot2); library(latex2exp)
2 ggplot2::theme_set(theme_bw())
3 df <- tibble(t = 1:T, mean = FilterDist, lower = FilterDist
  - 2*SDFilterDist, upper = FilterDist+ 2*SDFilterDist,
  meanT = FilterDistT, lowerT = FilterDistT - 2*
  SDFilterDistT,
4 upperT = FilterDistT + 2*SDFilterDistT, x_true = theta_true)
5 plot_filtering_estimates <- function(df) {
6   p <- ggplot(data = df, aes(x = t)) + geom_ribbon(aes(ymin
  = lower, ymax = upper), alpha = 1, fill = "lightblue") +
  geom_line(aes(y = x_true), colour = "black", alpha = 1,
  linewidth = 0.5) + geom_line(aes(y = mean), colour = "
  blue", linewidth = 0.5) +
7   geom_line(aes(y = meanT), colour = "purple", linewidth =
  0.5) + ylab(TeX("$\\theta_{t}$")) + xlab("Time")
8   print(p)
9 }
10 plot_filtering_estimates(df)
11 MargLik <- colMeans(weights)
12 plot(MargLik, type = "l", xlab = "Time", ylab = "Marginal
  likelihood", main = "Marginal likelihood")

```

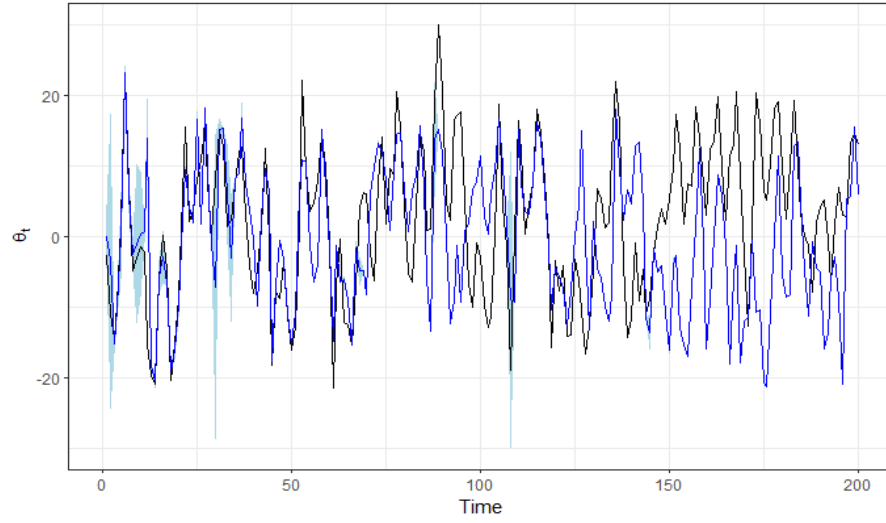
Figure 4.7 shows the true trajectory of the state vector (black line), the posterior mean (blue line), and the $\pm 2\hat{\sigma}_\theta$ posterior estimate (light blue shaded area) from the sequential importance sampling algorithm. We observe that there is no light blue shaded area after time period 40, and the algorithm exhibits poor performance after $t = 75$. This is due to weight degeneracy.

Figure 4.8 shows the performance of particle filtering (see Figure 3 in [8]). There is the true state vector (black line), the means based on $\{\theta_{1:t}^{(s)}, w_t^{*(s)}\}$ (blue line) and $\{\theta_{1:t}^{r(s)}, 1/S\}$ (purple line), and the area defined by $\pm 2\hat{\sigma}_\theta$ based on the former (light blue shaded area). Note that the particle filtering algorithm has better performance than the SIS algorithm. This is due to restarting the system every stage by resampling, which in turn mitigates the weight degeneracy issue.

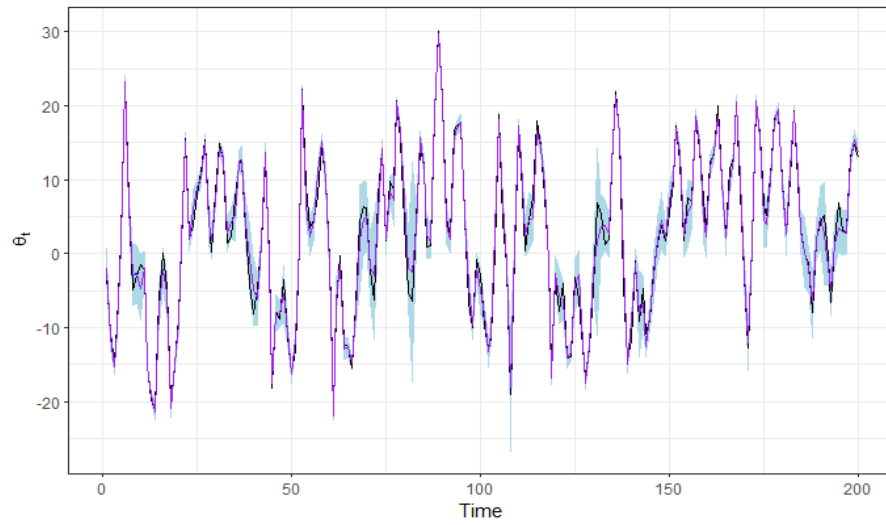
Finally, Figure 4.9 shows the posterior estimate of marginal likelihood based on the particle filtering algorithm.

7. Ph.D. students sleeping hours continues

- Perform the diagnostics of Section 4.4 in this example.

**FIGURE 4.7**

Sequential importance sampling: Example 1, [8].

**FIGURE 4.8**

Particle (Bootstrap) filtering: Example 1, [8].

- Check if there are errors in the posterior simulator of the Metropolis-Hastings algorithm in this example using the Geweke approach using as test functions the first moments of p and p^2 . Remember from Ex-

**FIGURE 4.9**

Marginal likelihood: Example 1, [8].

ercise 15 in Chapter 3 that the sample size is 52, and $\alpha_0 = 1.22$ and $\beta_0 = 2.57$.

- Run the Geweke test using $\alpha_0 = 2.57$ and $\beta_0 = 1.22$, and check the results.

Answer

We initially run the Metropolis-Hastings (M-H) algorithm for 100,000 iterations and obtain an effective sample size of 13,606. The naive and time-series standard errors are 0.00019 and 0.00052, respectively, indicating correlation—a feature also observed in the autocorrelation plot (not shown). However, the trace plot appears satisfactory. The Geweke test statistic is 1.97, marginally rejecting the null hypothesis that the means of the first 10% and the last 50% of the posterior draws are equal. Additionally, the dependence factor is 6.1, which exceeds the rule-of-thumb threshold of 5. The posterior draws pass both stages of Heidelberger and Welch's convergence diagnostic.

Given the autocorrelation issues, we set a burn-in period of 20,000 iterations and apply a thinning parameter of 10. Figures 4.10 and 4.11 display the trace and autocorrelation plots of the posterior draws. We observe that the draws appear stationary around their mean, and the autocorrelation decreases rapidly to zero.

The naive and time-series standard errors are 0.00068 and 0.00072, respectively. The similarity between these values indicates a low level of auto-

correlation, consistent with the results in Figure 4.11. The effective sample size of the posterior draws is 7,066, while the total number of posterior draws is 8,000.

The Geweke test statistic is 0.23, providing no statistical evidence to reject the null hypothesis of equal means in the two segments of the posterior draws. The Raftery and Lewis test yields a dependence factor close to 1, indicating minimal dependence. The Heidelberger and Welch test does not reject the null hypothesis of stationarity for the posterior draws and confirms that the mean is both accurate and stable.

Then, we implement the proposal by [7] to assess the reliability of the posterior simulator. We use as test functions the first moments of p and p^2 . We fail to reject the null hypothesis of equal means across the two test functions, indicating that the posterior simulator is functioning correctly. To evaluate the effectiveness of the test, we run the *marginal-conditional simulator* with prior parameters $\alpha_0 = 1.22$ and $\beta_0 = 2.57$. In contrast, for the *successive-conditional simulator*, we use prior parameters $\alpha_0 = 2.57$ and $\beta_0 = 1.22$. In this case, we reject the null hypothesis in the two test functions, suggesting that the test performs well in this example.

R code. Metropolis-Hastings algorithm: Ph.D. students sleeping hours.

```

1 rm(list = ls()); set.seed(010101); an <- 16.55; bn <- 39.57
2 S <- 100000; p <- runif(S); accept <- rep(0, S)
3 for (s in 2:S){
4   pc <- runif(1)
5   a <- dbeta(pc, an, bn)/dbeta(p[s-1], an, bn)
6   U <- runif(1)
7   if(U <= a){ p[s] <- pc; accept[s] <- 1
8   }else{p[s] <- p[s-1]; accept[s] <- 0}
9 }
10 library(coda); library(latex2exp)
11 thetaPost <- mcmc(p)
12 plot(thetaPost, density = FALSE, main = "Trace plot", ylab =
   "Proportion")
13 autocorr.plot(thetaPost, main = "Autocorrelation plot")
14 summary(thetaPost); effectiveSize(thetaPost)
15 geweke.diag(thetaPost, frac1 = 0.1, frac2 = 0.5)
16 raftery.diag(thetaPost, q = 0.025, r = 0.005, s = 0.95)
17 heidel.diag(thetaPost, eps = 0.1, pvalue = 0.05)
18 burnin <- 20000; thin <- 10; keep <- seq(burnin, S, thin)
19 thetaPostNew <- mcmc(p[keep])
20 plot(thetaPostNew, density = FALSE, main = "Trace plot",
   ylab = "Proportion")
21 autocorr.plot(thetaPostNew, main = "Autocorrelation plot")
22 summary(thetaPostNew); effectiveSize(thetaPostNew)
23 geweke.diag(thetaPostNew, frac1 = 0.1, frac2 = 0.5)
24 raftery.diag(thetaPostNew, q = 0.025, r = 0.005, s = 0.95)
25 heidel.diag(thetaPostNew, eps = 0.1, pvalue = 0.05)
26 # Marginal-conditional simulator
27 a0 <- 1.22; b0 <- 2.57; ThetaPrior <- rbeta(S,a0,b0)
28 yPrior <- rbinom(S, 1, prob = ThetaPrior)
29 parsmcmc1 <- coda::mcmc(cbind(ThetaPrior, ThetaPrior^2))
30 Summ1 <- summary(parsmcmc1)
31 # Successive-conditional simulator
32 N <- 52
33 SucConSim <- function(a0, b0, par){
34   y <- rbinom(N, 1, prob = par)
35   an <- a0 + sum(y); bn <- b0 + N - sum(y); pc <- runif(1)
36   a <- dbeta(pc, an, bn)/dbeta(par, an, bn); U <- runif(1)
37   if(U <= a){par <- pc}else{par <- par}
38   return(par)
39 }
40 a0 <- 1.22; b0 <- 2.57 # a0 <- 2.57; b0 <- 1.22
41 par2 <- rbeta(1, a0, b0); pars2 <- rep(NA, S); pars2[1] <-
   par2
42 for(s in 2:S){
43   Res <- SucConSim(a0 = a0, b0 = b0, par = pars2[s-1])
44   pars2[s] <- Res
45 }
46 parsmcmc2 <- coda::mcmc(cbind(pars2, pars2^2))
47 Summ2 <- summary(parsmcmc2)
48 TestGeweke <- function(j){
49   Test <- (Summ1[["statistics"]][j,1] - Summ2[["statistics"]
   ][j,1])/(Summ1[["statistics"]][j,4]+Summ2[["statistics"]
   ][j,4])^0.5
50   Reject <- abs(Test) > qnorm(0.975); return(list(Test =
   Test, Reject = Reject))
51 }
52 TestGeweke(1); TestGeweke(2)

```

**FIGURE 4.10**

Trace plot of posterior draws: Proportion of students that sleep at least 6 hours.

**FIGURE 4.11**

Autocorrelation plot of posterior draws: Proportion of students that sleep at least 6 hours.

Part II

Regression models: A GUIded toolkit



5

Graphical user interface

This chapter presents our graphical user interface (GUI) to carry out Bayesian regression analysis in a very friendly environment without any programming skills (drag and drop). Our GUI is based on an interactive web application using *shiny* [4], and packages like *MCMCpack* [16] and *bayesm* [26] from **R** software [20], and is designed for teaching and applied purposes at an introductory level. In the next chapters of the second part of this book we carry out some applications to highlight the potential of our GUI for applied researchers and practitioners.

5.1 Introduction

Our GUI allows performing inference using Bayesian regression analysis without requiring programming skills. The latter seems to be a significant impediment to increasing the use of the Bayesian framework [32, 13].

There are other available graphical user interfaces for carrying out Bayesian regression analysis. *ShinyStan* [30] is a very flexible open source program, but users are required to have some programming skills. *BugsXLA* [32] is open source, but less flexible. However, users do not need to have programming skills. *Bayesian regression: Nonparametric and parametric models* [13] is a very flexible and friendly GUI that is based on *MATLAB Compiler* for a 64-bit Windows computer. Its focus is on Bayesian nonparametric regressions, and it can be thought of for users who have mastered basic parametric models, such as the ones that we show in our GUI. There are also *MATLAB toolkit*, *Stata* and *BayES*, but these are not open sources.

We developed our GUI based on an interactive web application using shiny [4], and some libraries in **R** [19]. The specific libraries and commands that are used in our GUI can be seen in Table 12.1. It has ten univariate models, four multivariate, **time series models**, three hierarchical longitudinal, and seven Bayesian model averaging frameworks. In addition, it gives basic summaries and diagnostics of the posterior chains, as well as the posterior chains themselves, and different plots, such as trace, autocorrelation and densities.

In terms of its flexibility and possibilities, our GUI lies between *ShinyStan* and *BugsXLA*: users are not required to have any programming skills, but it

is not as advanced as [13]’s software. However, our GUI can be run in any operating system. Our GUI, which we call BESmarter,¹ is freely available at <https://github.com/besmarter/BSTApp>; so users have access to all our code and datasets.

Simulated and applied datasets are in the folders **DataSim** (see Table 12.2 for details), and **DataApp** (see Table 12.3 for details) of our **GitHub** repository. The former folder also includes the files that were used to simulate different processes, so, the population parameters are available, and as a consequence these files can be used as a pedagogical tool to show some statistical properties of the inferential frameworks available in our GUI. The latter folder contains the datasets used in the applications of this second part of the book. Users should use these datasets as templates to structure their own datasets.

There are three ways to install our GUI. The easiest way, but that requires installation of **R**, and potentially a **R** code editor, is to type

R code. How to display our graphical user interface

```
1 shiny::runGitHub("besmarter/BSTApp", launch.browser = T)
```

in the **R** package console or any **R** code editor. We strongly recommend to type this directly, rather than copy and paste. This is due to a potential issue with the quotation mark.

The second option is to visit <https://posit.cloud/content/4328505>, log in or sign up for **Posit Cloud**, and access the project titled **GUIDed Bayesian regression app BSTApp**. In the right-bottom window, click on the **BSTApp-master** folder under **Files**, open the **app.R** file, and finally, click the **Run App** button. However, inactivity will cause the window to close.

The third approach, and our recommendation, is using a **Docker** image by running:

1. `docker pull magralo95/besmartergui:latest`
2. `docker run -rm -p 3838:3838 magralo95/besmartergui`

in your **Command Prompt**. This creates an isolated environment for our GUI, ensuring consistent performance across systems. Note that **Docker** must be installed to deploy our GUI this way.

After implementing any of the three ways to run our GUI, users can see

¹Bayesian econometrics: Simulations, models and applications to research, teaching and encoding with responsibility.

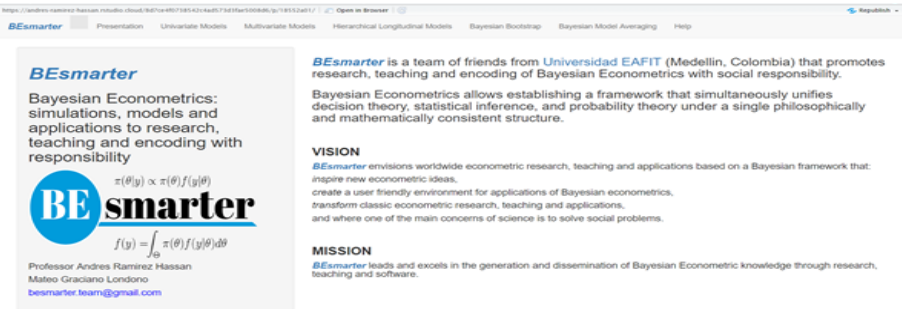


FIGURE 5.1
Display of our graphical user interface.



FIGURE 5.2
Univariate models: Specification.

a new window where a presentation of our research team is displayed (see Figure 5.1). In addition, the top panel in Figure 5.1 shows the class of models that can be estimated in our GUI.

5.2 Univariate models

After our GUI is deployed (see Figure 5.1), the user should select *Univariate Models* in the top panel. Then, the Figure 5.2 is displayed, and the user can see the radio button on the left hand side that shows the specific models inside this generic class. In particular, users can see that the normal model is selected from inside the class of univariate models.

Then, the right hand side panel displays a widget to upload the input



FIGURE 5.3
Univariate models: Results.

dataset, which should be a *csv* file with headers in the first row. Users also should select the kind of separator used in the input file: comma, semicolon, or tab (use the folders **DataSim** and **DataApp** for the input file templates). Once users upload the dataset, they can see a data preview. Range sliders help to set the number of iterations of the Markov chain Monte Carlo algorithm, the amount of burn-in, and the thinning parameter can be selected as well (see next chapters of this second part of the book for technical details). After this, users should specify the equation. This can be done with the formula builder, where users can select the dependent variable, and the independent variables, and then click on the *Build formula* tab. Users can see in the *Main Equation* space the formula expressed in the format used by **R** software (see Main equation box in Figure 5.2, $y \sim x1 + x2 + x3$). Users can modify this if necessary, for instance, including higher order or interaction terms, other transformations are also allowed. This is done directly in the *Main Equation* space taking into account that this extra terms should follow formula command structure.² Note that the class of univariate models includes the intercept by default, except ordered probit, where the specification has to do this explicitly, that is, ordered probit models do not admit an intercept, for *identification* issues (see details below).³ Hence, users should write down specifically this fact ($y \sim x1 + x2 + x3 - 1$). Finally, users should define the hyperparameters of the prior; for instance, in the normal-inverse gamma model, these are the mean vector, covariance matrix, shape, and scale parameters (see Figure 5.3). However, users should take into account that our GUI has *non-informative* hyperparameters by default in all our modelling frameworks, so the last part is not a requirement.

After this specification process, users should click the *Go!* button to initi-

²See <https://www.rdocumentation.org/packages/stats/versions/3.6.2/topics/formula>

³An *identification* issue means that multiple values for the model parameters give rise to the same value for the likelihood function.



FIGURE 5.4
Univariate models: Multinomial.

ate the estimation. Our GUI displays the summary statistics and convergence diagnostics after this process is finished (see Figure 5.3). There are also widgets to download posterior chains (*csv* file) and graphs (*pdf* and *eps* files). Note that the order of the coefficients in the results (summary, posterior chains, and graphs) is first for the location parameters, and then for the scale parameters.

Multinomial models (probit and logit) require a dataset file to have in the first column the dependent variable, then alternative specific regressors (for instance alternatives' prices), and finally, non-alternative regressors (for instance, income). The formula builder specifies the dependent variable, and independent variables that are alternative specific and non-alternative specific (see technical details in next chapter). Specification also requires defining the base category, number of alternatives (this is also required in ordered probit), number of alternative specific regressors, and number of non-alternative regressors (see Figure 5.4). Multinomial logit also allows defining a tuning parameter, the number of degrees of freedom in this case, for the Metropolis–Hastings algorithm (see technical details in next chapter). This is a feature in our GUI when the estimation of the models is based on the Metropolis–Hastings algorithm. The order of the coefficients in the results of these models is first the intercepts (cte_l appearing in the summary display, l -th alternative), and then the non-alternative specific regressors (NAS_{jl} appearing in the summary display, l -th alternative and j -th non-alternative regressor), and lastly, the coefficients for the alternative specific regressors (AS_j appearing in the summary display, j -th alternative specific regressor). Note that the non-alternative specific regressors associated with the base category are equal to zero (they do not appear in the results). In addition, some coefficients of the main diagonal of the covariance matrix are constant due to identification issues in multinomial and multivariate probit models.

In the case of the negative binomial model, users should set a dispersion parameter (see the negative binomial model in the next chapter). User should



FIGURE 5.5
Univariate models: Bootstrap.

also set the censorship points and quantiles in the Tobit and quantile models, respectively.

Bayesian bootstrap only requires uploading a dataset, specifying the number of iterations of the MCMC, the resampling size, and the equation (see Figure 5.5). The input file has the same structure as the file used in the univariate normal model.

5.3 Multivariate models

After our GUI is deployed (see Figure 5.1), the user should select *Multivariate Models* in the top panel. Then, the Figure 5.6 is displayed, and the user can see the radio button on the left hand side that shows the specific models inside this generic class.

Figure 5.6 displays the multivariate regression setting. In this case, the input file should have first the dependent variables, and then the regressors. If there are intercepts in each equation, there should be a column of 1's after the dependent variables in the input file. The user also has to set the number of dependent variables, the number of regressors, if necessary include the intercept, and the values of the hyperparameters (see Figure 5.6).

The input file in seemingly unrelated regressions should have first the dependent variables, and then the regressors by equation, including the intercept in each equation if necessary (column of 1's). Users should define the number of dependent variables (equations), the number of total regressors, that is, the sum of all regressors associated with the equation (if necessary include intercepts, each intercept is an additional regressor), and the number of regressors



FIGURE 5.6
Multivariate models: Simple multivariate.

by equation (if necessary include the intercept). Users can also set the values of the hyperparameters if there is prior information.

The results of the simple multivariate and seemingly unrelated regressions show first the posterior location parameters by equation, and then the posterior covariance matrix.

In the instrumental variable setting, users should specify the main equation and the instrumental equation. This setting includes intercepts by default. The first variable on the right hand side in the main equation has to be the variable with endogeneity issues. In the instrumental equation box, the dependent variable is the variable with endogeneity issues as a function of the instruments. Users can also specify the values of the hyperparameters if they have prior information. The input file should have the dependent variable, the endogenous regressor, the instruments, and the exogenous regressors. The results first list the posterior estimates of the endogenous regressor, then the location parameters of the auxiliary regression (instrumental equation), and the location parameters of the exogenous regressors. Last is the posterior covariance matrix.

The multivariate probit model requires an input dataset ordered by unit, for instance three choices implies repeat each unit three times. The first column has to be the identification of each unit; users should use ordered integers, then the dependent variable, just one vector, composed of 0's and 1's, then the regressors, which should include a column of 1's for the intercepts. Users should set the number of units, number of regressors, and number of choices (see Figure 5.7). The results first display the posterior location parameters by equation, and then the posterior covariance matrix.



FIGURE 5.7
Multivariate models: Multivariate probit.

5.4 Time series model

5.5 Longitudinal/panel models

After our GUI is deployed (see Figure 5.1), the user should select *Hierarchical Longitudinal Models* in the top panel. Then, the Figure 5.8 is displayed, and the user can see the radio button on the left hand side that shows the specific models inside this generic class.

The hierarchical longitudinal models tab allows for estimating models that account for within-subject correlation when the dependent variable is continuous (Normal), binary (Logit), or a count (Poisson).

The input files for hierarchical longitudinal models should have first the dependent variable, then the regressors and a cross sectional identifier ($i = 1, 2, \dots, N$). It is not a requirement to have a balanced dataset: T_i can be different for each i (see Chapter 9 for technical details). Users can see templates of datasets in the folders **DataSim** (see Table 12.2 for details), and **DataApp** (see Table 12.3 for details) of our *GitHub* repository. Users should also specify the fixed part equation and the random part equation, both in **R** format. In case of only requiring random intercepts, do not introduce anything in the latter part (see Figure 5.8). Users should also type the name of the cross sectional identifier variable. The results displayed and the posterior graphs are associated with the fixed effects and covariance matrix. However, users can download the posterior chains of all posterior estimates: fixed and random effects, and covariance matrix.



FIGURE 5.8
Hierarchical longitudinal models: Specification.

5.6 Bayesian model average

After our GUI is deployed (see Figure 5.1), the user should select *Bayesian Model Averaging* in the top panel. Then, the Figure 5.9 is displayed, and the user can see the radio button on the left hand side that shows the specific models inside this generic class.

Bayesian model averaging based on a Gaussian distribution can be carried out using the Bayesian information criterion (BIC) approximation, Markov chain Monte Carlo model composition (MC3), or instrumental variables (see Figure 5.9). The former two approaches require an input dataset where the first column is the dependent variable, and then, the potentially important regressors. Users should set the band width model selection parameter (O_R) and number of iterations for BIC and MC3, respectively (see Chapter 10 for technical details). The results include the posterior inclusion probability ($p^! = 0$), expected value (EV), and standard deviation (SD) of the coefficients associated with each regressor. The BIC framework also displays the most relevant models, including the number of regressors, the coefficient of determination (R^2), the BIC, and the posterior model probability. Users can download two *csv* files: *Best models* and *Descriptive statistics coefficients*. The former is a 0-1 matrix such that the columns are the regressors and the rows are the models; a 1 indicates the presence of a specific regressor in a specific model, 0 otherwise. Note that the last column of this file is the posterior model probability for each model (row). The latter file shows the posterior inclusion probabilities, expected values, and standard deviations associated with each regressor, taking into account the BMA procedure based on the best models.

Bayesian model averaging with endogeneity issues requires two input files. The first one has the dependent variable in the first column, the next columns are the regressors with endogeneity issues, and then the exogeneous regressors.

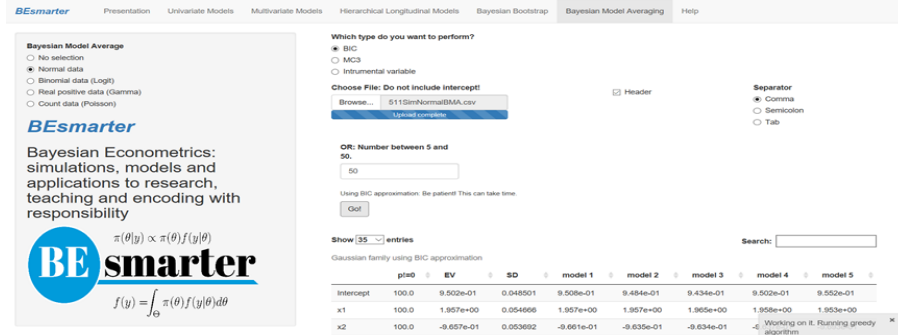


FIGURE 5.9
Bayesian model averaging: Specification and results.



FIGURE 5.10
Bayesian model averaging: Instrumental variable specification.

The user should include a column of 1's if an intercept is required. The second input file has all the instruments. Users should also introduce the number of regressors with endogeneity issues (see Figure 5.10).

The results include the posterior inclusion probabilities and expected values for each regressor. The user can find the results of the main equation, and then of the auxiliary equations. Users can download *csv* files of BMA results for both the second stage (main equation) and the first stage (auxiliary equations). In addition, users can download the posterior chains of the location parameters of the main equation, β_l , $l = 1, 2, \dots, \dim\{\beta\}$, the location parameters of the auxiliary equations, $\gamma_{j,i}$, $j = 1, 2, \dots, \dim\{\beta_s\}$ where $\dim\{\beta_s\}$ is the number of regressors with endogeneity issues, $i = 1, 2, \dots, \dim\{\gamma\}$, where $\dim\{\gamma\}$ is the number of regressors in the auxiliary regressors (exogeneous regressors + instruments), and the elements of the covariance matrix $\sigma_{j,k}$ (see Chapter 10 for technical details).

Bayesian model averaging based on BIC approximation for non-linear mod-

els, Logit, Gamma, and Poisson, requires an input dataset where the first column is the dependent variable, and the other columns are the potentially relevant regressors. Users should specify the band width model selection parameters, which are also referred to as Occam's window parameters (O_R and O_L). Our GUI displays the posterior inclusion probabilities ($p^! = 0$), the expected value of the posterior coefficients (EV), and the standard deviation (SD). In addition, users can see the results associated with the models with the highest posterior model probabilities, and download *csv* files with the results of specifications of the best models, and descriptive statistics of the posterior coefficients from the BMA procedure. These files are similar to the results of the BIC approximation of the Gaussian model.

5.7 Warning

Users should also note that sometimes our GUI shuts down. In our experience, this is due to computational issues using the implicit commands that we call when estimating some models, for instance, computationally singular systems, missing values where TRUE/FALSE needed, L-BFGS-B needs finite values of "fn", NA/NaN/Inf values, or Error in backsolve. Sometimes these issues can be solved by adjusting the dataset, for instance, avoiding high levels of multicollinearity. It should also be taken into account that when warning messages are displayed in our GUI, there is a high chance that there are convergence issues of the posterior chains. So, the results are not trustworthy. Users can identify these problems by checking the console of their *RStudio* sections, where the specific folder/file where the issue happened is specified. In any case, we would appreciate your feedback to improve and enhance our GUI.

We also should say there are many ways to improve the codes that we present in the following five chapters. For instance, the *MCMCpack* and *bayesm* packages perform most of the matrix operations in C++ using the *rcpp* package. This substantially speeds up the algorithms compared with the codes that we present in the next chapters. We could improve the computational times of our codes using parallel computing and the *rcpp* package, but this requires more advanced skills that we do not cover in this book.



6

Univariate models

Solutions of Exercises

1. Get the conditional posterior distributions of the Gaussian linear model assuming independent priors $\pi(\boldsymbol{\beta}, \sigma^2) = \pi(\boldsymbol{\beta}) \times \pi(\sigma^2)$, where $\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \mathbf{B}_0)$ and $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$.

Answer

The joint posterior distribution of the parameters is

$$\begin{aligned}
 \pi(\boldsymbol{\beta}, \sigma^2 | \mathbf{y}, \mathbf{X}) &\propto p(\mathbf{y} | \boldsymbol{\beta}, \sigma^2, \mathbf{X}) \pi(\boldsymbol{\beta}) \pi(\sigma^2) \\
 &\propto (\sigma^2)^{-\frac{N}{2}} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) \right\} \\
 &\quad \times \exp \left\{ -\frac{1}{2} (\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \mathbf{B}_0^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_0) \right\} \\
 &\quad \times \frac{(\delta_0/2)^{(\alpha_0/2)}}{\Gamma(\alpha_0/2)} \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\} \\
 &\propto \exp \left\{ -\frac{1}{2} (\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \mathbf{B}_0^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_0) \right\} \\
 &\quad \times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp \left\{ -\frac{\delta_0 + (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})}{2\sigma^2} \right\} \\
 &= \exp \left\{ -\frac{1}{2} (\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \mathbf{B}_0^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_0) \right\} \times \underbrace{\frac{1}{(\sigma^2)^{(\frac{\alpha_n}{2}+1)}} \exp \left\{ -\frac{\delta_n}{2\sigma^2} \right\}}_1.
 \end{aligned}$$

Observe that (1) is the kernel of an inverse-gamma density function. Thus, $\sigma^2 | \boldsymbol{\beta}, \mathbf{y}, \mathbf{X} \sim IG(\alpha_n/2, \delta_n/2)$, where $\alpha_n = \alpha_0 + N$ and $\delta_n = \delta_0 + (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})$.

Let's see the posterior distribution of β ,

$$\begin{aligned}
\pi(\beta, \sigma^2 | \mathbf{y}, \mathbf{X}) &\propto p(\mathbf{y} | \beta, \sigma^2, \mathbf{X}) \pi(\beta) \pi(\sigma^2) \\
&\propto (\sigma^2)^{-\frac{N}{2}} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y} - \mathbf{X}\beta)^\top (\mathbf{y} - \mathbf{X}\beta) \right\} \\
&\times \exp \left\{ -\frac{1}{2} (\beta - \beta_0)^\top \mathbf{B}_0^{-1} (\beta - \beta_0) \right\} \\
&\times \frac{(\delta_0/2)^{(\alpha_0/2)}}{\Gamma(\alpha_0/2)} \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\} \\
&= (\sigma^2)^{-\frac{N}{2}} \exp \left\{ -\frac{\sigma^{-2}}{2} [\mathbf{y}^\top \mathbf{y} - \mathbf{y}^\top \mathbf{X}\beta - \beta^\top \mathbf{X}^\top \mathbf{y} + \beta^\top \mathbf{X}^\top \mathbf{X}\beta] \right\} \\
&\times \exp \left\{ -\frac{1}{2} [\beta^\top \mathbf{B}_0^{-1} \beta - \beta^\top \mathbf{B}_0^{-1} \beta_0 - \beta_0^\top \mathbf{B}_0^{-1} \beta + \beta_0^\top \mathbf{B}_0^{-1} \beta_0] \right\} \\
&\times \frac{(\delta_0/2)^{(\alpha_0/2)}}{\Gamma(\alpha_0/2)} \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\} \\
&\propto \exp \left\{ -\frac{1}{2} [\beta^\top (\mathbf{B}_0^{-1} + \sigma^{-2} \mathbf{X}^\top \mathbf{X}) \beta - 2\beta^\top (\mathbf{B}_0^{-1} \beta_0 + \sigma^{-2} \mathbf{X}^\top \mathbf{X} \hat{\beta})] \right\} \\
&\times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp \left\{ -\frac{\delta_0 + \mathbf{y}^\top \mathbf{y}}{2\sigma^2} \right\},
\end{aligned}$$

where $\hat{\beta} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{y}$.

Adding and subtracting $\beta_n^\top \mathbf{B}_n^{-1} \beta_n$ where

$$\begin{aligned}
\mathbf{B}_n &= (\mathbf{B}_0^{-1} + \sigma^{-2} \mathbf{X}^\top \mathbf{X})^{-1} \\
\beta_n &= \mathbf{B}_n (\mathbf{B}_0^{-1} \beta_0 + \sigma^{-2} \mathbf{X}^\top \mathbf{X} \hat{\beta}) = \mathbf{B}_n (\mathbf{B}_0^{-1} \beta_0 + \sigma^{-2} \mathbf{X}^\top \mathbf{y}),
\end{aligned}$$

and completing the square

$$\begin{aligned}
\pi(\beta, \sigma^2 | \mathbf{y}, \mathbf{X}) &\propto \exp \left\{ -\frac{1}{2} [\beta^\top (\mathbf{B}_0^{-1} + \sigma^{-2} \mathbf{X}^\top \mathbf{X}) \beta - 2\beta^\top \mathbf{B}_n^{-1} \mathbf{B}_n (\mathbf{B}_0^{-1} \beta_0 + \sigma^{-2} \mathbf{X}^\top \mathbf{X} \hat{\beta}) \right. \\
&\quad \left. + \beta_n^\top \mathbf{B}_n^{-1} \beta_n - \beta_n^\top \mathbf{B}_n^{-1} \beta_n] \right\} \times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp \left\{ -\frac{\delta_0 + \mathbf{y}^\top \mathbf{y}}{2\sigma^2} \right\} \\
&= \exp \left\{ -\frac{1}{2} [\beta^\top \mathbf{B}_n^{-1} \beta - 2\beta^\top \mathbf{B}_n^{-1} \beta_n + \beta_n^\top \mathbf{B}_n^{-1} \beta_n] \right\} \\
&\times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp \left\{ -\frac{\delta_0 + \mathbf{y}^\top \mathbf{y} - \sigma^2 \beta_n^\top \mathbf{B}_n^{-1} \beta_n}{2\sigma^2} \right\} \\
&= \exp \left\{ -\frac{1}{2} (\beta - \beta_n)^\top \mathbf{B}_n^{-1} (\beta - \beta_n) \right\} \\
&\quad \underbrace{\hspace{10em}}_1 \\
&\times (\sigma^2)^{-(\frac{\alpha_n}{2}+1)} \exp \left\{ -\frac{\delta^*}{2\sigma^2} \right\},
\end{aligned}$$

where $\delta^* = \delta_0 + \mathbf{y}^\top \mathbf{y} + \sigma^2 \boldsymbol{\beta}_n^\top \mathbf{B}_n^{-1} \boldsymbol{\beta}_n$ does not depend on $\boldsymbol{\beta}$.

We can see that (1) is the kernel of a multivariate normal distribution with mean equal to $\boldsymbol{\beta}_n$ and covariance matrix \mathbf{B}_n , that is, $\boldsymbol{\beta} | \sigma^2, \mathbf{y}, \mathbf{X} \sim N(\boldsymbol{\beta}_n, \mathbf{B}_n)$.

We see that the posterior distributions are from the same family as the prior distributions.

2. Given the model $y_i \sim N(\mathbf{x}_i^\top \boldsymbol{\beta}, \sigma^2 / \tau_i)$ (Gaussian linear model with heteroskedasticity) with independent priors, $\pi(\boldsymbol{\beta}, \sigma^2, \boldsymbol{\tau}) = \pi(\boldsymbol{\beta}) \times \pi(\sigma^2) \times \prod_{i=1}^N \pi(\tau_i)$, where $\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \mathbf{B}_0)$, $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$ and $\tau_i \sim G(v/2, v/2)$. Show that $\boldsymbol{\beta} | \sigma^2, \boldsymbol{\tau}, \mathbf{y}, \mathbf{X} \sim N(\boldsymbol{\beta}_n, \mathbf{B}_n)$, $\sigma^2 | \boldsymbol{\beta}, \boldsymbol{\tau}, \mathbf{y}, \mathbf{X} \sim IG(\alpha_n/2, \delta_n/2)$ and $\tau_i | \boldsymbol{\beta}, \sigma^2, \mathbf{y}, \mathbf{X} \sim G(v_{1n}/2, v_{2in}/2)$, where $\boldsymbol{\tau} = [\tau_1, \dots, \tau_n]^\top$, $\mathbf{B}_n = (\mathbf{B}_0^{-1} + \sigma^{-2} \mathbf{X}^\top \Psi \mathbf{X})^{-1}$, $\boldsymbol{\beta}_n = \mathbf{B}_n (\mathbf{B}_0^{-1} \boldsymbol{\beta}_0 + \sigma^{-2} \mathbf{X}^\top \Psi \mathbf{y})$, $\alpha_n = \alpha_0 + N$, $\delta_n = \delta_0 + (\mathbf{y} - \mathbf{X} \boldsymbol{\beta})^\top \Psi (\mathbf{y} - \mathbf{X} \boldsymbol{\beta})$, $v_{1n} = v + 1$, $v_{2in} = v + \sigma^{-2} (y_i - \mathbf{x}_i^\top \boldsymbol{\beta})^2$, and $\Psi = \text{diagonal}\{\tau_i\}$.

Answer

The joint posterior distribution of the parameters is

$$\begin{aligned} \pi(\boldsymbol{\beta}, \sigma^2, \boldsymbol{\tau} | \mathbf{y}, \mathbf{X}) &\propto p(\mathbf{y} | \boldsymbol{\beta}, \sigma^2, \boldsymbol{\tau}, \mathbf{X}) \pi(\boldsymbol{\beta}) \pi(\sigma^2) \prod_{i=1}^N \pi(\tau_i) \\ &\propto \left(\prod_{i=1}^N \tau_i^{1/2} \right) (\sigma^2)^{-\frac{N}{2}} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y} - \mathbf{X} \boldsymbol{\beta})^\top \Psi (\mathbf{y} - \mathbf{X} \boldsymbol{\beta}) \right\} \\ &\quad \times \exp \left\{ -\frac{1}{2} (\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \mathbf{B}_0^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_0) \right\} \\ &\quad \times \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\} \prod_{i=1}^N \tau_i^{v/2-1} \exp \{-v\tau_i/2\}. \end{aligned}$$

Thus, the conditional posterior distribution of $\sigma^2 | \boldsymbol{\beta}, \boldsymbol{\tau}, \mathbf{y}, \mathbf{X}$ is given by

$$\pi(\sigma^2 | \boldsymbol{\beta}, \boldsymbol{\tau}, \mathbf{y}, \mathbf{X}) \propto (\sigma^2)^{-\frac{N+\alpha_0}{2}} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y} - \mathbf{X} \boldsymbol{\beta})^\top \Psi (\mathbf{y} - \mathbf{X} \boldsymbol{\beta}) + \delta_0 \right\}.$$

This is the kernel of an inverse-gamma distribution with shape parameter $\alpha_n/2$ and rate parameter $\delta_n/2$.

The conditional posterior distribution of $\tau_i | \boldsymbol{\beta}, \sigma^2, \mathbf{y}, \mathbf{X}$ is

$$\pi(\tau_i | \boldsymbol{\beta}, \sigma^2, \mathbf{y}, \mathbf{X}) \propto \tau_i^{(v+1)/2-1} \exp \left\{ -\frac{\tau_i}{2} [\sigma^{-2} (y_i - \mathbf{x}_i^\top \boldsymbol{\beta})^2 + v] \right\}.$$

This is the kernel of a gamma distribution with parameter $(v+1)/2$ and $(\sigma^{-2} (y_i - \mathbf{x}_i^\top \boldsymbol{\beta})^2 + v)/2$.

The conditional posterior distribution of $\beta|\sigma^2, \tau, \mathbf{y}, \mathbf{X}$ is given by

$$\pi(\beta|\sigma^2, \tau, \mathbf{y}, \mathbf{X}) \propto \exp \left\{ -\frac{1}{2} [\sigma^{-2}(\mathbf{y} - \mathbf{X}\beta)^\top \Psi(\mathbf{y} - \mathbf{X}\beta) + (\beta - \beta_0)^\top \mathbf{B}_0^{-1}(\beta - \beta_0)] \right\}.$$

Following same steps as in the previous exercise we get $\beta|\sigma^2, \tau, \mathbf{y}, \mathbf{X} \sim N(\beta_n, \mathbf{B}_n)$.

3. The market value of soccer players in Europe continues

Use the setting of the previous exercise to perform inference using a Gibbs sampling algorithm of the the market value of soccer players in Europe setting $v = 5$ and same other hyperparameters as the homoscedastic case. Is there any meaningful difference for the coefficient associated with the national team compared to the application in the homoscedastic case?

Answer

R. code. The value of soccer players, programming our Gibbs sampler (heteroskedastic case)

```

1 rm(list = ls())
2 set.seed(010101)
3 ##### Linear regression: Value of
  soccer players #####
4 Data <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/1
  ValueFootballPlayers.csv", sep = ",", header = TRUE,
  quote = "")
5 attach(Data)
6 y <- log(Value)
7 # Value: Market value in Euros (2017) of soccer players
8 # Regressors quantity including intercept
9 X <- cbind(1, Perf, Age, Age2, NatTeam, Goals, Exp, Exp2)
10 # Perf: Performance. Perf2: Performance squared. Age: Age;
  Age2: Age squared.
11 # NatTeam: Indicator of national team. Goals: Scored goals.
  Goals2: Scored goals squared
12 # Exp: Years of experience. Exp2: Years of experience
  squared. Assists: Number of assists
13 k <- dim(X)[2]
14 N <- dim(X)[1]
15 # Hyperparameters
16 d0 <- 0.001
17 a0 <- 0.001
18 b0 <- rep(0, k)
19 c0 <- 1000
20 B0 <- c0*diag(k)
21 B0i <- solve(B0)
22 v <- 5
23 # MCMC parameters
24 mcmc <- 5000
25 burnin <- 5000
26 tot <- mcmc + burnin
27 thin <- 1
28 # Posterior distributions programming the Gibbs sampling
29 # Auxiliary parameters
30 an <- a0 + N
31 v1n <- v + 1
32 # Gibbs sampling functions
33 PostSig2 <- function(Beta, tau){
34   dn <- d0 + t(y - X%%Beta)%%diag(tau)%(y - X%%Beta)
35   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
36   return(sig2)
37 }
38 PostBeta <- function(sig2, tau){
39   Bn <- solve(B0i + sig2^(-1)*t(X)%%diag(tau)%%X)
40   bn <- Bn%%(B0i%%b0 + sig2^(-1)*t(X)%%diag(tau)%%y)
41   Beta <- MASS::mvrnorm(1, bn, Bn)
42   return(Beta)
43 }
44 PostTau <- function(sig2, Beta, i){
45   v2n <- v + sig2^(-1)*(y[i]-X[i,]%%Beta)^2
46   tau1 <- rgamma(1, v1n/2, v2n/2)
47   return(tau1)
48 }

```

R. code. The value of soccer players, programming our Gibbs sampler (heteroskedastic case)

```

1 PostBetas <- matrix(0, mcmc+burnin, k)
2 PostSigma2 <- rep(0, mcmc+burnin)
3 Beta <- rep(0, k)
4 tau <- rep(1, N)
5 # create progress bar in case that you want to see
  iterations progress
6 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
7 for(s in 1:tot){
8   sig2 <- PostSig2(Beta = Beta, tau = tau)
9   PostSigma2[s] <- sig2
10  Beta <- PostBeta(sig2 = sig2, tau = tau)
11  PostBetas[s,] <- Beta
12  tau <- sapply(1:N, function(i){PostTau(sig2 = sig2, Beta =
    Beta, i)})
13  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
14 }
15 close(pb)
16 keep <- seq((burnin+1), tot, thin)
17 PosteriorBetas <- PostBetas[keep,]
18 colnames(PosteriorBetas) <- c("Intercept", "Perf", "Age", "
  Age2", "NatTeam", "Goals", "Exp", "Exp2")
19 summary(coda::mcmc(PosteriorBetas))
20 PosteriorSigma2 <- PostSigma2[keep]
21 summary(coda::mcmc(PosteriorSigma2))
22 summary(coda::mcmc(exp(PosteriorBetas[,5])-1))
23 Iterations = 1:5000
24 Thinning interval = 1
25 Number of chains = 1
26 Sample size per chain = 5000
27 1. Empirical mean and standard deviation for each variable,
28 plus standard error of the mean:
29 Mean          SD          Naive SE Time-series SE
30 1.256091      0.254974      0.003606      0.004579
31 2. Quantiles for each variable:
32 2.5%      25%      50%      75%      97.5%
33 0.8078 1.0746 1.2367 1.4189 1.7959

```

We see in this application that the value of a top soccer player in Europe increases 124% ($\exp(0.80) - 1$) on average when he has played in the national team, the credible interval at 95% is (81%, 180%). These values are not very different from the application assuming homoscedasticity in the book.

4. **Example: Determinants of hospitalization continues**

Program a Gibbs sampling algorithm in the application of determinants of hospitalization.

Answer

R. code. Determinants of hospitalization, programming our Gibbs sampler

```

1 set.seed(010101)
2 Data <- read.csv("https://raw.githubusercontent.com/
   besmarter/BSTApp/refs/heads/master/DataApp/2HealthMed.
   csv", sep = ",", header = TRUE, quote = "")
3 attach(Data)
4 str(Data)
5 y <- Hosp # Dependent variables
6 X <- cbind(1, SHI, Female, Age, Age2, Est2, Est3, Fair, Good
   , Excellent) # Regressors
7 K <- dim(X)[2]
8 N <- dim(X)[1]
9 # Hyperparameters
10 b0 <- rep(0, K) # Prio mean
11 B0 <- diag(K) # Prior covariance
12 B0i <- solve(B0)
13 mcmc <- 1000; burnin <- 500; thin <- 2; tot <- mcmc + burnin
   ; keep <- seq(burnin, tot, thin)
14 # Posterior distributions programming the Gibbs sampling
15 # Auxiliary parameters
16 XtX <- t(X)%*%X
17 # Gibbs sampling functions
18 PostBeta <- function(Yl){
19   Bn <- solve(B0i + XtX)
20   bn <- Bn%*%(B0i%*%b0 + t(X)%*%Yl)
21   Beta <- MASS::mvrnorm(1, bn, Bn)
22   return(Beta)
23 }
24 PostYl <- function(Beta, i){
25   Ylmean <- X[i,]%*%Beta
26   if(y[i] == 1){
27     Yli <- truncnorm::rtruncnorm(1, a = 0, b = Inf, mean =
       Ylmean, sd = 1)
28   }else{
29     Yli <- truncnorm::rtruncnorm(1, a = -Inf, b = 0, mean =
       Ylmean, sd = 1)
30   }
31   return(Yli)
32 }
33 PostBetas <- matrix(0, mcmc+burnin, K)
34 Beta <- rep(0, K)
35 # create progress bar in case that you want to see
   iterations progress
36 pb <- winProgressBar(title = "progress bar", min = 0, max =
   tot, width = 300)
37 for(s in 1:tot){
38   Yl <- sapply(1:N, function(i){PostYl(Beta = Beta, i)})
39   Beta <- PostBeta(Yl = Yl)
40   PostBetas[s,] <- Beta
41   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
     "% done"))
42 }
43 close(pb)
44 keep <- seq((burnin+1), tot, thin)
45 PosteriorBetas <- PostBetas[keep,]
46 colnames(PosteriorBetas) <- c("Intercept", "SHI", "Female",
   "Age", "Age2", "Est2", "Est3", "Fair", "Good", "
   Excellent")
47 summary(coda::mcmc(PosteriorBetas))

```

5. Choice of the fishing mode continues

- Run the Algorithm 3 of the book to show the results of the Geweke [6], Raftery [22] and Heidelberger [9] tests using our GUI.
- Use the command *rmnpGibbs* to do the example of the choice of the fishing mode.

Answer

R. code. Fishing choice mode, results our GUI

```

1 GewekeTestLocationCoef
2 Fraction in 1st window = 0.1
3 Fraction in 2nd window = 0.5
4 cte_1 cte_2 cte_3 NAS_1_1 NAS_1_2 NAS_1_3 AS_1 AS_2
5 -1.821 -0.714 0.792 2.275 -3.944 -2.071 1.627 -2.729
6
7 RafteryTestLocationCoef
8 Quantile (q) = 0.5
9 Accuracy (r) = +/- 0.025
10 Probability (s) = 0.95
11 Burn-in Total Lower bound Dependence
12 (M) (N) (Nmin) factor (I)
13 cte_1 780 365690 1537 238.0
14 cte_2 360 193950 1537 126.0
15 cte_3 660 340120 1537 221.0
16 NAS_1_1 120 70320 1537 45.8
17 NAS_1_2 475 243960 1537 159.0
18 NAS_1_3 440 248930 1537 162.0
19 AS_1 3010 1438135 1537 936.0
20 AS_2 550 297770 1537 194.0
21
22 HeidelTestLocationCoef
23 Stationarity start p-value
24 test iteration
25 cte_1 passed 6001 6.54e-01
26 cte_2 failed NA 3.72e-02
27 cte_3 failed NA 4.99e-02
28 NAS_1_1 failed NA 4.77e-07
29 NAS_1_2 failed NA 1.82e-05
30 NAS_1_3 failed NA 1.19e-04
31 AS_1 passed 2001 3.71e-01
32 AS_2 passed 8001 4.48e-01
33 Halfwidth Mean Halfwidth
34 test
35 cte_1 passed -0.34236 0.017025
36 cte_2 <NA> NA NA
37 cte_3 <NA> NA NA
38 NAS_1_1 <NA> NA NA
39 NAS_1_2 <NA> NA NA
40 NAS_1_3 <NA> NA NA
41 AS_1 passed -0.00708 0.000306
42 AS_2 passed 0.27982 0.009994

```

R. code. Fishing choice mode, library bayesm

```

1 remove(list = ls()); set.seed(12345)
2 Data <- read.csv("https://raw.githubusercontent.com/
   besmarter/BSTApp/refs/heads/master/DataApp/3Fishing.csv"
   , sep = ",", header = TRUE, quote = "")
3 attach(Data); str(Data)
4 p <- 4; na <- 2; nd <- 1; N <- dim(Data)[1]
5 Xa <- Data[,2:9]
6 Xd <- matrix(income, N, 1)
7 X <- bayesm::createX(p = p, na = na, nd = nd, Xa = Xa, Xd =
   Xd, INT = TRUE, base = p, DIFF = TRUE)
8 df <- list(y = mode, X = X, p = 4)
9 # Hyperparameters
10 k <- dim(X)[2]; b0 <- rep(0, k); c0 <- 1000
11 B0 <- c0*diag(k); B0i <- solve(B0)
12 a0 <- p - 1 + 3; Psi0 <- a0*diag(p-1)
13 Prior <- list(betabar = b0, A = B0i, nu = a0, V = Psi0)
14 # MCMC parameters
15 mcmc <- 100000; thin <- 5
16 Mcmc <- list(R = mcmc, keep = thin)
17 Results <- bayesm::rmnpGibbs(Data = df, Prior = Prior, Mcmc
   = Mcmc)
18 betatilde <- Results$betadraw / sqrt(Results$sigmadraw[,1])
19 attributes(betatilde)$class <- "bayesm.mat"
20 summary(coda::mcmc(betatilde))
21 Quantiles for each variable:
22      2.5%      25%      50%      75%      97.5%
23 var1 -6.371e-01 -4.670e-01 -3.834e-01 -3.028e-01 -1.422e-01
24 var2 -2.149e-01 -6.681e-02 -7.870e-03  4.414e-02  1.493e-01
25 var3 -8.873e-01 -6.071e-01 -4.982e-01 -4.040e-01 -2.446e-01
26 var4  1.859e-05  4.577e-05  5.952e-05  7.326e-05  9.861e-05
27 var5 -2.589e-05 -3.050e-06  8.212e-06  2.089e-05  5.330e-05
28 var6  4.549e-05  7.451e-05  9.144e-05  1.098e-04  1.555e-04
29 var7 -9.425e-03 -7.612e-03 -6.586e-03 -5.573e-03 -3.136e-03
30 var8  1.214e-01  2.068e-01  2.592e-01  3.154e-01  4.477e-01
31 sigmadraw <- Results$sigmadraw / Results$sigmadraw[,1]
32 attributes(sigmadraw)$class = "bayesm.var"
33 summary(coda::mcmc(sigmadraw))

```

6. Simulation exercise of the multinomial logit model continues

Perform inference in the simulation of the multinomial logit model using the command *rmnlIndepMetrop* from the *bayesm* package of **R** and using our GUI.

Answer

R. code. Simulation of the multinomial logit model

```

1  remove(list = ls())
2  set.seed(12345)
3  # Simulation of data
4  N<-1000 # Sample Size
5  B<-c(0.5,0.8,-3)
6  B1<-c(-2.5,-3.5,0)
7  B2<-c(1,1,0)
8  # Alternative specific attributes of choice 1, for instance,
   price, quality and duration of choice 1
9  X1<-matrix(cbind(rnorm(N,0,1),rnorm(N,0,1),rnorm(N,0,1)),N,
   length(B))
10 # Alternative specific attributes of choice 2, for instance,
   price, quality and duration of choice 2
11 X2<-matrix(cbind(rnorm(N,0,1),rnorm(N,0,1),rnorm(N,0,1)),N,
   length(B))
12 # Alternative specific attributes of choice 3, for instance,
   price, quality and duration of choice 3
13 X3<-matrix(cbind(rnorm(N,0,1),rnorm(N,0,1),rnorm(N,0,1)),N,
   length(B))
14 X4<-matrix(rnorm(N,1,1),N,1)
15 V1<-B2[1]+X1%*%B+B1[1]*X4
16 V2<-B2[2]+X2%*%B+B1[2]*X4
17 V3<-B2[3]+X3%*%B+B1[3]*X4
18 suma<-exp(V1)+exp(V2)+exp(V3)
19 p1<-exp(V1)/suma
20 p2<-exp(V2)/suma
21 p3<-exp(V3)/suma
22 p<-cbind(p1,p2,p3)
23 y<- apply(p,1, function(x) sample(1:3, 1, prob = x, replace =
   TRUE))
24 table(y)
25 L <- length(table(y))
26 dat <-data.frame(mode,X1[,1],X2[,1],X3[,1],X1[,2],X2[,2],X3
   [,2],X1[,3],X2[,3],X3[,3],X4)
27 colnames(dat) <- c("mode","V1.1","V1.2","V1.3","V2.1","V2.2"
   ,"V2.3","V3.1","V3.2","V3.3","V4")
28 attach(dat)
29 LongData <- mlogit::mlogit.data(dat, shape = "wide", varying
   =2:10, choice = "mode")
30 Xa <- cbind(LongData$V1, LongData$V2, LongData$V3)
31 Xa <- cbind(X1[,1],X2[,1],X3[,1],X1[,2],X2[,2],X3[,2],X1
   [,3],X2[,3],X3[,3])
32 na <- 3
33 Xd <- X4
34 X <- bayesm::createX(p = L, na = na, nd = 1, Xa = Xa, Xd =
   Xd, base = L)
35 DataMlogit <- list(y=y, X = X, p = L)
36 # MCMC parameters
37 mcmc <- 11000+1
38 thin <- 5
39 df <- 6
40 mcmcpair <- list(R = mcmc, keep = 5, nu = df)
41 PostBeta <- bayesm::rmnlIndepMetrop(Data = DataMlogit, Mcmc
   = mcmcpair)
42 summary(PostBeta[["betadraw"]])

```

7. Simulation of the ordered probit model

Simulate an ordered probit model where the first regressor distributes $N(6, 5)$ and the second distributes $G(1, 1)$, the location parameter is $\beta = [0.5 \ -0.25 \ 0.5]^\top$, and the cutoffs is the vector $\alpha = [0 \ 1 \ 2.5]^\top$. Program from scratch a Metropolis-within-Gibbs sampling algorithm to perform inference in this simulation.

Answer

R. code. Simulation of the ordered probit model

```

1 rm(list = ls()); set.seed(010101); N <- 1000
2 x1 <- rnorm(N, 6, 5); x2 <- rgamma(N, shape = 1, scale = 1)
3 X <- cbind(1, x1, x2)
4 beta <- c(0.5, -0.25, 0.5); cutoffs <- c(0, 1, 2.5)
5 e <- rnorm(N,0,1)
6 y_latent <- X%*%beta + e; y <- rep(0,N)
7 for (i in 1:N) {
8   if (y_latent[i] < cutoffs[1]){
9     y[i] <- 0}else{
10    if (y_latent[i] >= cutoffs[1] & y_latent[i] < cutoffs
11      [2]) {
12      y[i] <- 1
13    }else{
14      if (y_latent[i] >= cutoffs[2] & y_latent[i] < cutoffs
15        [3]) {
16        y[i] <- 2
17      }else{y[i] <- 3
18      }
19    }
20  }
21 }
22 # Likelihood function
23 LogLikOP <- function(param){
24   beta_g <- param[1:ncol(X)]
25   delta <- param[(ncol(X)+1):(ncol(X) + dplyr::n_distinct(y)
26     - 1)]
27   Xbeta <- X%*%beta_g
28   logLik <- 0
29   for (i in 1:length(y)){
30     if (y[i]==0){logLiki <- log(pnorm(-Xbeta[i]))
31     }else if (y[i]==1){
32       logLiki <- log(pnorm(exp(delta[1]) - Xbeta[i]) - pnorm
33         (-Xbeta[i]))
34     }else if (y[i]==2){
35       logLiki <- log(pnorm(exp(delta[2]) + exp(delta[1]) -
36         Xbeta[i]) - pnorm(exp(delta[1]) - Xbeta[i]))
37     }else {logLiki <- log(1 - pnorm(exp(delta[2]) + exp(
38       delta[1]) - Xbeta[i]))
39     }
40     logLik <- logLik + logLiki
41   }
42   return(-logLik)
43 }
44 # ML Estimation
45 param0 <- rep(0, ncol(X) + n_distinct(y)-2)
46 mle <- optim(param0, LogLikOP, hessian = T, method = "BFGS")
47 mle$par
48 exp(mle$par[length(beta)+1])
49 exp(mle$par[length(beta)+1])+exp(mle$par[length(beta)+2])
50 CovarML <- solve(mle$hessian)

```


R. code. Simulation of the ordered probit model

```

1 # M-H within Gibbs
2 mhop <- function(param0, G){
3   betasamples <- matrix(c(0), nrow = G, ncol = ncol(X))
4   betasamples[1,] <- param0[1:ncol(X)]
5   tau <- matrix(c(0), nrow = G, ncol = dplyr::n_distinct(y)
6     - 2)
7   tau[1,] <- param0[(ncol(X)+1):(ncol(X) + dplyr::n_distinct(
8     y) - 2)]
9   yl <- rep(0,length(y)); ar <- rep(0,G); B1 <- solve(t(X)%*
10     %X+solve(B0))
11   pb <- winProgressBar(title = "progress bar", min = 0, max
12     = G, width = 300)
13   for(g in 2:G){
14     bg <- betasamples[g-1,]; tg <- tau[g-1,]
15     #Random walk M-H for delta
16     delta_prime <- tg + mvtnorm::rmvnorm(1, mean = rep(0,2),
17       sigma = VarProp)
18     alpha <- min(1,(mvtnorm::dmvnorm(delta_prime, mean = d0,
19       sigma = D0)*exp(-LogLikOP(c(bg, delta_prime)) +
20       LogLikOP(c(bg, tg)))/mvtnorm::dmvnorm(tg, mean = d0,
21       sigma = D0))
22     if(is.nan(alpha) | is.na(alpha)) {
23       alpha <- 0
24     }
25     #Acceptance step
26     u <- runif(1, min = 0, max = 1)
27     if(u<=alpha){tau[g,] <- delta_prime; ar[g] <- 1
28     }else{tau[g,] <- tg
29     }
30     #Generation of latent variables
31     for (i in 1:length(y)){
32       if (y[i]==0) {
33         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
34         sd = 1, max = 0)
35       }else if(y[i]==1){
36         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
37         sd = 1, min = 0, max = exp(tau[g,1]))
38       }else if(y[i]==2){
39         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
40         sd = 1, min = exp(tau[g,1]), max = exp(tau[g,2])+exp(tau
41         [g,1]))
42       }else{
43         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
44         sd = 1, min = exp(tau[g,2])+exp(tau[g,1]))
45       }
46     }
47     #Gibbs sampling for beta
48     if(sum(is.nan(yl))>0 | sum(is.na(yl))>0 | sum(yl)==Inf){
49       betasamples[g,] <- betasamples[g-1,]
50     }else{
51       b1 <- B1%*(t(X)%*%yl + solve(B0)%*%b0)
52       betasamples[g,] <- mvrnorm(1, mu = b1, Sigma = B1)
53     }
54     setWinProgressBar(pb, g, title=paste( round(g/G*100, 0),
55       "% done"))
56   }
57   close(pb)
58   return(cbind(betasamples, tau, ar))
59 }

```

R. code. Simulation of the ordered probit model

```

1 #Hyperparameters
2 d0 <- rep(0,2)
3 D0 <- diag(2)*10000
4 b0 <- rep(0,ncol(X))
5 B0 <- diag(ncol(X))*10000
6 #Estimation
7 param0 <- rep(0, ncol(X) + dplyr::n_distinct(y)-1)
8 G <- 1000
9 tun <- 1
10 VarProp <- tun*solve(solve(CovarML[4:5, 4:5]) + solve(D0))
11 param_sample <- mhop(param0, G)
12 #Burn in
13 B <- round(0.2*G)
14 param_sample <- param_sample[(B+1):G,]
15 mcmc0 <- coda::mcmc(param_sample[, 1:(ncol(X) + dplyr::n_
    distinct(y) - 2)])
16 summary(mcmc0)
17 Iterations = 1:800
18 Thinning interval = 1
19 Number of chains = 1
20 Sample size per chain = 800
21 1. Empirical mean and standard deviation for each variable,
22 plus standard error of the mean:
23 Mean      SD Naive SE Time-series SE
24 0.49120 0.08465 0.0029929      0.007140
25 -0.24919 0.01222 0.0004319      0.001269
26 0.49440 0.03942 0.0013937      0.002739
27 0.06716 0.06419 0.0022695      0.008479
28 0.41926 0.07414 0.0026212      0.009479
29 2. Quantiles for each variable:
30 2.5%      25%      50%      75%      97.5%
31 0.31947 0.43558 0.49710 0.5479 0.6496
32 -0.27180 -0.25740 -0.24948 -0.2408 -0.2238
33 0.42229 0.46706 0.49253 0.5189 0.5762
34 -0.06338 0.02328 0.06819 0.1104 0.1932
35 0.25857 0.37195 0.41742 0.4672 0.5558
36 summary(coda::mcmc(cbind(exp(param_sample[, 4]),exp(param_
    sample[, 4])+exp(param_sample[, 5]))))
37 Iterations = 1:800
38 Thinning interval = 1
39 Number of chains = 1
40 Sample size per chain = 800
41 1. Empirical mean and standard deviation for each variable,
42 plus standard error of the mean:
43 Mean      SD Naive SE Time-series SE
44 [1,] 1.072 0.06854 0.002423      0.008999
45 [2,] 2.597 0.13593 0.004806      0.019700
46 2. Quantiles for each variable:
47 2.5%      25%      50%      75% 97.5%
48 var1 0.9386 1.024 1.071 1.117 1.213
49 var2 2.3224 2.500 2.603 2.686 2.877

```

All posterior mean estimates are close to the population parameters, and the 95% credible intervals encompass the population parameters. We use the definition of γ in the last line of the code.

8. Simulation of the negative binomial model continues

Perform inference in the simulation of the negative binomial model using the *bayesm* package in R software.

Answer

R. code. Simulation of the negative binomial model

```

1 rm(list = ls())
2 set.seed(010101)
3 N <- 2000 # Sample size
4 x1 <- runif(N); x2 <- rnorm(N)
5 X <- cbind(1, x1, x2)
6 k <- dim(X)[2]
7 B <- rep(1, k)
8 alpha <- 1.2
9 gamma <- exp(alpha)
10 lambda <- exp(X%*%B)
11 y <- rnbino(N, mu = lambda, size = gamma)
12 table(y)
13 # MCMC parameters
14 mcmc <- 10000
15 burnin <- 1000
16 thin <- 5
17 iter <- mcmc + burnin
18 keep <- seq(burnin, iter, thin)
19 sbeta <- 2.93/sqrt(k); salpha <- 2.93
20 # Hyperparameters: Priors
21 B0 <- 1000*diag(k); b0 <- rep(0, k)
22 alpha0 <- 0.5; delta0 <- 0.1
23 DataNB <- list(y = y, X = X)
24 mcmcNB <- list(R = mcmc, keep = thin, s_beta = sbeta, s_
      alpha = salpha)
25 PriorNB <- list(betabar = b0, A = solve(B0), a = alpha0, b =
      delta0)
26 ResultBayesm <- bayesm::rnegbinRw(Data = DataNB, Mcmc =
      mcmcNB, Prior = PriorNB)
27 summary(ResultBayesm$alphadraw)
28 summary(ResultBayesm$betadraw)

```

9. The market value of soccer players in Europe continues

Perform the application of the value of soccer players with left censoring

at one million Euros in our GUI using the Algorithm A7, and the hyper-parameters of the example.

Answer

These are the results of running the application in our GUI. These are very similar compared with the results in the book.

R. code. The value of soccer players with left censoring in our GUI

```

1 Summary
2 Iterations = 10001:60000
3 Thinning interval = 1
4 Number of chains = 1
5 Sample size per chain = 50000
6 1. Empirical mean and standard deviation for each variable,
7 plus standard error of the mean:
8
9      Mean      SD Naive SE Time-series SE
10 (Intercept)  1.014765 2.626395 1.175e-02      1.659e-02
11 Perf         0.033935 0.004529 2.025e-05      2.245e-05
12 Age          1.027285 0.212413 9.499e-04      1.326e-03
13 Age2         -0.021914 0.003989 1.784e-05      2.528e-05
14 NatTeam      0.847412 0.124884 5.585e-04      6.423e-04
15 Goals        0.010092 0.001644 7.351e-06      7.712e-06
16 Exp          0.175324 0.069653 3.115e-04      3.727e-04
17 Exp2         -0.005696 0.002950 1.319e-05      1.527e-05
18 sigma2       0.983337 0.096194 4.302e-04      6.724e-04
19 2. Quantiles for each variable:
20      2.5%      25%      50%      75%      97.5%
21 (Intercept) -4.212563 -0.732856 1.038281 2.796603 6.051e
22      +00
23 Perf         0.025121 0.030873 0.033896 0.036988 4.286e
24      -02
25 Age          0.618743 0.883011 1.026760 1.168860 1.450e
26      +00
27 Age2         -0.029854 -0.024580 -0.021886 -0.019203 -1.424e
28      -02
29 NatTeam      0.605030 0.763154 0.846671 0.930593 1.095e
30      +00
31 Goals        0.006893 0.008987 0.010097 0.011201 1.330e
32      -02
33 Exp          0.038522 0.128032 0.175261 0.222110 3.118e
34      -01
35 Exp2         -0.011484 -0.007671 -0.005685 -0.003706 5.502e
36      -05
37 sigma2       0.813118 0.915664 0.977298 1.043661 1.189e
38      +00

```

10. **The market value of soccer players in Europe continues**

Program from scratch the Gibbs sampling algorithm in the example of the market value of soccer players at the 0.75 quantile.

Answer

R. code. The value of soccer players, quantile regression

```

1 rm(list = ls()); set.seed(010101)
2 Data <- read.csv("https://raw.githubusercontent.com/
   besmarter/BSTApp/refs/heads/master/DataApp/1
   ValueFootballPlayers.csv", sep = ",", header = TRUE,
   quote = "")
3 attach(Data)
4 y <- log(Value); X <- cbind(1, Perf, Age, Age2, NatTeam,
   Goals, Exp, Exp2)
5 RegLS <- lm(y ~ X -1)
6 k <- dim(X)[2]; N <- dim(X)[1]
7 # Hyperparameters
8 b0 <- rep(0, k); c0 <- 1000
9 B0 <- c0*diag(k); B0i <- solve(B0)
10 # MCMC parameters
11 mcmc <- 5000; burnin <- 1000
12 tot <- mcmc + burnin; thin <- 1
13 # Quantile
14 tau <- 0.5; theta <- (1-2*tau)/(tau*(1-tau))
15 psi2 <- 2/(tau*(1-tau)); an2 <- 2+theta^2/psi2
16 # Gibbs sampler
17 PostBeta <- function(e){
18   Bn <- solve(B0i + psi2^(-1)*t(X)%*%diag(1/e)%*%X)
19   bn <- Bn%*%(B0i%*%b0 + psi2^(-1)*t(X)%*%diag(1/e)%*%(y-
   theta*e))
20   Beta <- MASS::mvrnorm(1, bn, Bn)
21   return(Beta)
22 }
23 PostE <- function(Beta, i){
24   dn2 <- (y[i]-X[i,]%*%Beta)^2/psi2
25   ei <- GIGrvg::rgig(1, chi = dn2, psi = an2, lambda = 1/2)
26   return(ei)
27 }
28 PostBetas <- matrix(0, mcmc+burnin, k)
29 Beta <- RegLS$coefficients
30 pb <- winProgressBar(title = "progress bar", min = 0, max =
   tot, width = 300)
31 for(s in 1:tot){
32   e <- sample(1:N, function(i){PostE(Beta = Beta, i)})
33   Beta <- PostBeta(e = e)
34   PostBetas[s,] <- Beta
35   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
   "% done"))
36 }
37 close(pb)
38 keep <- seq((burnin+1), tot, thin)
39 PosteriorBetas <- PostBetas[keep,]
40 colnames(PosteriorBetas) <- c("Intercept", "Perf", "Age", "
   Age2", "NatTeam", "Goals", "Exp", "Exp2")
41 summary(coda::mcmc(PosteriorBetas))

```

11. Use the *bayesboot* package to perform inference in the simulation exercise of Section 7.10, and compared the results with the ones that we get using our GUI setting $S = 10000$.

Answer

R. code. The value of soccer players, quantile regression

```

1 ##### Bayesian bootstrap: Simulation
  #####
2 rm(list = ls())
3 set.seed(010101)
4 N <- 1000 # Sample size
5 x1 <- runif(N); x2 <- rnorm(N)
6 X <- cbind(x1, x2)
7 k <- dim(X)[2]
8 B <- rep(1, k+1)
9 sig2 <- 1
10 u <- rnorm(N, 0, sig2)
11 y <- cbind(1, X)%*%B + u
12 data <- as.data.frame(cbind(y, X))
13 names(data) <- c("y", "x1", "x2")
14 Reg <- function(d){
15   Reg <- lm(y ~ x1 + x2, data = d)
16   Bhat <- Reg$coef
17   return(Bhat)
18 }
19 Reg(data)
20 S <- 10000
21 BB <- bayesboot::bayesboot(data = data, statistic = Reg, R =
  S)
22 plot(BB)

```



7

Multivariate models

Solutions of Exercises

1. Show that $\mathbb{E}[u_1 \text{PAER}] = \frac{\alpha_1}{1-\beta_1\alpha_1}\sigma_1^2$ assuming that $\mathbb{E}[u_1 u_2] = 0$ where $\text{Var}(u_1) = \sigma_1^2$ in the effect of institutions on per capita GDP.

Answer

The point of departure is the following *simultaneous structural* economic model:

$$\log(\text{pcGDP95}_i) = \beta_1 + \beta_2 \text{PAER}_i + \beta_3 \text{Africa} + \beta_4 \text{Asia} + \beta_5 \text{Other} + u_{1i}, \quad (7.1)$$

$$\text{PAER}_i = \alpha_1 + \alpha_2 \log(\text{pcGDP95}_i) + \alpha_3 \log(\text{Mort}_i) + u_{2i}, \quad (7.2)$$

where *pcGDP95*, *PAER* and *Mort* are the per capita gross domestic product (GDP) in 1995, the average index of protection against expropriation between 1985 and 1995, and the settler mortality rate during the time of colonization. *Africa*, *Asia* and *Other* are dummies for continents, with *America* as the baseline group.

Replacing Equation 7.2 into Equation 7.1, and solving for $\log(\text{pcGDP95})$,

$$\log(\text{pcGDP95}_i) = \pi_1 + \pi_2 \log(\text{Mort}_i) + \pi_3 \text{Africa} + \pi_4 \text{Asia} + \pi_5 \text{Other} + e_{1i}, \quad (7.3)$$

where $\pi_1 = \frac{\beta_1 + \beta_2 \alpha_1}{1 - \beta_2 \alpha_2}$, $\pi_2 = \frac{\beta_2 \alpha_3}{1 - \beta_2 \alpha_2}$, $\pi_3 = \frac{\beta_3}{1 - \beta_2 \alpha_2}$, $\pi_4 = \frac{\beta_4}{1 - \beta_2 \alpha_2}$, $\pi_5 = \frac{\beta_5}{1 - \beta_2 \alpha_2}$, and $e_1 = \frac{\beta_2 u_1 + u_2}{1 - \beta_2 \alpha_2}$.

Then, replacing Equation 7.3 into Equation 7.2, and solving for *PAER*,

$$\text{PAER}_i = \gamma_1 + \gamma_2 \log(\text{Mort}_i) + \gamma_3 \text{Africa} + \gamma_4 \text{Asia} + \gamma_5 \text{Other} + e_{2i}, \quad (7.4)$$

where $\gamma_1 = \frac{\alpha_1 + \alpha_2 \beta_1}{1 - \beta_2 \alpha_2}$, $\gamma_2 = \frac{\alpha_3}{1 - \beta_2 \alpha_2}$, $\gamma_3 = \frac{\alpha_2 \beta_3}{1 - \beta_2 \alpha_2}$, $\gamma_4 = \frac{\alpha_2 \beta_4}{1 - \beta_2 \alpha_2}$, $\gamma_5 = \frac{\alpha_2 \beta_5}{1 - \beta_2 \alpha_2}$, and $e_2 = \frac{\alpha_2 u_1 + u_2}{1 - \beta_2 \alpha_2}$.

Then, $\mathbb{E}[u_1 \text{PAER}] = \mathbb{E}[u_1(\gamma_1 + \gamma_2 \log(\text{Mort}_i) + \gamma_3 \text{Africa} + \gamma_4 \text{Asia} + \gamma_5 \text{Other} + e_{2i})] = \mathbb{E}\left[u_1 \left(\frac{\alpha_2 u_1 + u_2}{1 - \beta_2 \alpha_2}\right)\right] = \frac{\alpha_2}{1 - \beta_2 \alpha_2} \sigma_1^2$ given the assumptions.

2. Show that $\beta_2 = \pi_2/\gamma_2$ in the effect of institutions on per capita GDP.

Answer

Given that $\pi_2 = \frac{\beta_2 \alpha_3}{1 - \beta_2 \alpha_2}$ and $\gamma_2 = \frac{\alpha_3}{1 - \beta_2 \alpha_2}$ from the previous exercise, consequently, $\beta_2 = \pi_2/\gamma_2$.

3. **The effect of institutions on per capita gross domestic product continues**

Use the *rmultireg* command from the *bayesm* package to perform inference in the example of the effect of institutions on per capita GDP.

Answer

R code. The effect of institutions on per capita GDP

```

1 rm(list = ls())
2 set.seed(010101)
3 DataInst <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/4Institutions
  .csv", sep = ",", header = TRUE, quote = "")
4 attach(DataInst)
5 Y <- cbind(logpcGDP95, PAER)
6 X <- cbind(1, logMort, Africa, Asia, Other)
7 M <- dim(Y)[2]
8 K <- dim(X)[2]
9 # Hyperparameters
10 B0 <- matrix(0, K, M)
11 c0 <- 100
12 V0 <- c0*diag(K)
13 Psi0 <- 5*diag(M)
14 a0 <- 5
15 S <- 10000 #Number of posterior draws
16 betadraw = matrix(double(S*K*M), ncol=K*M)
17 Sigmadraw = matrix(double(S*M*M), ncol=M*M)
18 pb <- winProgressBar(title = "progress bar", min = 0, max =
  S, width = 300)
19 for (s in 1:S) {
20   Results <- bayesm::rmultireg(Y, X, Bbar = B0, A = solve(V0
    ), nu = a0, V = Psi0)
21   betadraw[s,] <- Results$B
22   Sigmadraw[s,] <- Results$Sigma
23   setWinProgressBar(pb, s, title=paste( round(s/S*100, 0), "
    % done"))
24 }
25 close(pb)
26 summary(coda::mcmc(betadraw))
27 summary(coda::mcmc(Sigmadraw))

```

4. Demand and supply simulation

Given the structural demand-supply model:

$$\begin{aligned} q_i^d &= \beta_1 + \beta_2 p_i + \beta_3 y_i + \beta_4 pc_i + \beta_5 ps_i + u_{i1} \\ q_i^s &= \alpha_1 + \alpha_2 p_i + \alpha_3 er_i + u_{i2}, \end{aligned}$$

where q^d is demand, q^s is supply, p , y , pc , ps and er are price, income, complementary price, substitute price, and exchange rate. Complementary and substitute prices are prices of a complementary and substitute goods of q . Assume that $\beta = [5 \ -0.5 \ 0.8 \ -0.4 \ 0.7]^\top$, $\alpha = [-2 \ 0.5 \ -0.4]^\top$, $u_1 \sim N(0, 0.5^2)$ and $u_2 \sim N(0, 0.5^2)$. In addition, assume that $y \sim N(10, 1)$, $pc \sim N(5, 1)$, $ps \sim N(5, 1)$ and $tc \sim N(15, 1)$.

- Find the *reduce-form* model using that in equilibrium demand and supply are equal, that is, $q^d = q^s$. This condition defines the observable quantity (q).
- Simulate p and q from the *reduce-form* equations.
- Perform inference of the *reduce-form* model using the *rmultireg* command from the *bayesm* package.
- Use the posterior draws of the *reduce-form* parameters to perform inference of the *structural* parameters. Any issue? Hint: Are all *structural* parameters exactly identified?

Answer

We should equal demand and supply, and solve for price,

$$p = \pi_1 + \pi_2 er + \pi_3 y + \pi_4 pc + \pi_5 ps + v_1,$$

where $\pi_1 = \frac{\alpha_1 - \beta_1}{\beta_2 - \alpha_2}$, $\pi_2 = \frac{\alpha_3}{\beta_2 - \alpha_2}$, $\pi_3 = \frac{-\beta_3}{\beta_2 - \alpha_2}$, $\pi_4 = \frac{-\beta_4}{\beta_2 - \alpha_2}$, $\pi_5 = \frac{-\beta_5}{\beta_2 - \alpha_2}$, and $v_1 = \frac{u_2 - u_1}{\beta_2 - \alpha_2}$ given $\beta_2 \neq \alpha_2$, that is, the equations should be independent. This condition is given by economic theory due to $\beta_2 < 0$ and $\alpha_2 > 0$, the effect of price on demand and supply should be negative and positive, respectively.

The equation of price into the demand equation gives

$$q = \tau_1 + \tau_2 er + \tau_3 y + \tau_4 pc + \tau_5 ps + v_2,$$

where $\tau_1 = \beta_1 + \beta_2 \pi_1$, $\tau_2 = \beta_2 \pi_2$, $\tau_3 = \beta_2 \pi_3 + \beta_3$, $\tau_4 = \beta_2 \pi_4 + \beta_4$, $\tau_5 = \beta_2 \pi_5 + \beta_5$, and $v_2 = \beta_2 v_1 + u_1$. We can use the equations para π_k and τ_k , $k = \{1, 2, 3, 4, 5\}$ to simulate the *reduced-form* equations.

Observe that estimating the *reduced-form* equations, we can get the *structural* parameters for the demand equation, $\beta_2 = \tau_2 / \pi_2$ ($\pi_2 \neq 0$), $\beta_3 = \tau_3 - \beta_2 \pi_3$, $\beta_4 = \tau_4 - \beta_2 \pi_4$ and $\beta_5 = \tau_5 - \beta_2 \pi_5$, whereas the *structural* parameters of the supply equation cannot be recovered just in one way,

$\alpha_2 = \beta_2 + \beta_3/\pi_3 = \beta_2 + \beta_4/\pi_4 = \beta_2 + \beta_5/\pi_5$. This in turn implies different values for $\alpha_3 = \pi_2(\beta_2 - \alpha_2)$. This is because the demand equation is *exactly identified*, whereas the supply equation is *over identified*.

In this exercise, $K = 5$, $M = 2$, $K_1 = 4$, $K_2 = 2$, $M_1 = 2$ and $M_2 = 2$. This means that $K - K_1 = 1 = M - 1$ and $K - K_2 = 3 > M - 1 = 1$, that is, the order condition says that both equations (demand and supply) satisfy the necessary condition of identification, the demand would be *exactly identified*, and the supply equation would be *over identified*.

Regarding the rank condition (necessary and sufficient), let's see the identification matrix:

TABLE 7.1

Identification matrix.

| q | p | constant | er | y | pc | ps |
|---|-------------|-------------|-------------|------------|------------|------------|
| 1 | $-\beta_2$ | $-\beta_1$ | 0 | $-\beta_3$ | $-\beta_4$ | $-\beta_5$ |
| 1 | $-\alpha_2$ | $-\alpha_1$ | $-\alpha_3$ | 0 | 0 | 0 |

The demand equation excludes the exchange rate (*exclusion restriction*), and given $\alpha_3 \neq 0$, that is, the exchange rate is relevant in the supply equation, then the rank condition is satisfied in the demand equation. The supply equation excludes the income, the complementary price and substitute price (*exclusion restrictions*), then as far as $\beta_k \neq 0$ for any $k = \{3, 4, 5\}$, the rank condition is satisfied in the supply equation.

The following code shows how to do the simulation, and perform inference in this exercise. We can see that all 95% credible intervals encompass the population parameters, and the posterior means are very close to them.

R code. Demand and supply simulation

```

1 rm(list = ls()); set.seed(12345)
2 B0 <- 5; B1 <- -0.5; B2 <- 0.8; B3 <- -0.4; B4 <- 0.7; SD <-
  0.5
3 A0 <- -2; A1 <- 0.5; A2 <- -0.4; SS <- 0.5
4 P0 <- (A0-B0)/(B1-A1); P2 <- -B2/(B1-A1); P3 <- -B3/(B1-A1);
  P1 <- A2/(B1-A1); P4 <- -B4/(B1-A1)
5 T0 <- B0+B1*P0; T2 <- B2+B1*P2; T3 <- B3+B1*P3; T1 <- B1*P1;
  T4 <- B4+B1*P4;
6 n <- 5000
7 ED <- rnorm(n, 0, SD); ES <- rnorm(n, 0, SS)
8 VP <- (ES-ED)/(B1-A1); UQ <- B1*VP+ED
9 y <- rnorm(n, 10, 1); pc <- rnorm(n, 5, 1); er <- rnorm(n,
  15, 1); ps <- rnorm(n, 5, 1);
10 p <- P0+P1*er+P2*y+P3*pc+P4*ps+VP
11 q <- T0+T1*er+T2*y+T3*pc+T4*ps+UQ
12 #Inference
13 Y <- cbind(p, q); X <- cbind(1, er, y, pc, ps)
14 M <- dim(Y)[2]; K <- dim(X)[2]
15 # Hyperparameters
16 B0 <- matrix(0, K, M); c0 <- 100; V0 <- c0*diag(K)
17 Psi0 <- 5*diag(M); a0 <- 5; S <- 10000 #Posterior draws
18 betadraw = matrix(double(S*K*M), ncol=K*M)
19 Sigmadraw = matrix(double(S*M*M), ncol=M*M)
20 pb <- winProgressBar(title = "progress bar", min = 0, max =
  S, width = 300)
21 for (s in 1:S) {
22   Results <- bayesm::rmultireg(Y, X, Bbar = B0, A = solve(V0
    ), nu = a0, V = Psi0)
23   betadraw[s,] <- Results$B
24   Sigmadraw[s,] <- Results$Sigma
25   setWinProgressBar(pb, s, title=paste( round(s/S*100, 0), "
    % done"))
26 }
27 close(pb)
28 summary(coda::mcmc(betadraw))
29 summary(coda::mcmc(Sigmadraw))
30 beta2 <- betadraw[,7]/betadraw[,2] # Effect of price on
  demand
31 summary(coda::mcmc(beta2))
32 beta3 <- betadraw[,8] - beta2*betadraw[,3] # Effect of
  income on demand
33 summary(coda::mcmc(beta3))
34 beta4 <- betadraw[,9] - beta2*betadraw[,4] # Effect of
  complementary price on demand
35 summary(coda::mcmc(beta4))
36 beta5 <- betadraw[,10] - beta2*betadraw[,5] # Effect of
  substitute price on demand
37 summary(coda::mcmc(beta5))

```

5. Utility demand continues

- Run the **Utility demand** application using our GUI and the information in the dataset *Utilities.csv*. Hint: This file should be modified to agree the structure that requires our GUI (see the dataset *5Institutions.csv* in the folder *DataApp* of our GitHub repository - <https://github.com/besmarter/BSTApp>- for a template).
- Program from scratch the Gibbs sampler algorithm in this application.

Answer

R code. Utility demand in Colombia, Gibbs sampler

```

1 rm(list = ls()); set.seed(010101); library(dplyr)
2 DataUt <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/Utilities.csv",
  sep = ",", header = TRUE, quote = "")
3 DataUtEst <- DataUt %>% filter(Electricity != 0 & Water != 0
  & Gas != 0)
4 attach(DataUtEst)
5 y1 <- log(Electricity); y2 <- log(Water); y3 <- log(Gas)
6 X1 <- cbind(1, LnPriceElect, LnPriceWater, LnPriceGas,
  IndSocio1, IndSocio2, Altitude, Nrooms, HouseholdMem,
  Lnincome)
7 X2 <- cbind(1, LnPriceElect, LnPriceWater, LnPriceGas,
  IndSocio1, IndSocio2, Nrooms, HouseholdMem)
8 X3 <- cbind(1, LnPriceElect, LnPriceWater, LnPriceGas,
  IndSocio1, IndSocio2, Altitude, Nrooms, HouseholdMem)
9 y <- c(y1, y2, y3)
10 X <- as.matrix(Matrix::bdiag(X1, X2, X3))
11 M <- 3; K1 <- dim(X1)[2]; K2 <- dim(X2)[2]; K3 <- dim(X3)[2]
12 K <- K1 + K2 + K3; N <- length(y1)
13 # Hyperparameters
14 b0 <- rep(0, K); c0 <- 100; B0 <- c0*diag(K)
15 B0i <- solve(B0); Psi0 <- 5*diag(M); Psi0i <- solve(Psi0)
16 a0 <- M; IN <- diag(N); an <- a0 + N
17 #Posterior draws
18 S <- 6000; burnin <- 1000; thin <- 1
19 tot <- S+burnin
20 # Gibbs functions
21 PostBeta <- function(Sigma){
22   Aux <- solve(Sigma)%x%IN
23   Bn <- solve(B0i + t(X)%*%Aux)%*%X
24   bn <- Bn%*%(B0i%*%b0 + t(X)%*%Aux)%*%y
25   Beta <- MASS::mvrnorm(1, bn, Bn)
26   return(Beta)
27 }
28 PostSigma <- function(Beta){
29   B1 <- Beta[1:K1]; B2 <- Beta[(K1+1):(K1+K2)]; B3 <- Beta[(
  K1+K2+1):(K1+K2+K3)]
30   U1 <- y1 - X1%*%B1; U2 <- y2 - X2%*%B2; U3 <- y3 - X3%*%B3
31   U <- cbind(U1, U2, U3)
32   Psin <- solve(Psi0i + t(U)%*%U)
33   Sigmai <- rWishart::rWishart(1, df = an, Sigma = Psin)
34   Sigma <- solve(Sigmai[, ,1])
35   return(Sigma)
36 }
37 PostBetas <- matrix(0, tot, K)
38 PostSigmas <- matrix(0, tot, M*(M+1)/2); Beta <- rep(1, K)
39 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
40 for(s in 1:tot){
41   Sigma <- PostSigma(Beta = Beta); PostSigmas[s,] <-
  matrixcalc::vech(Sigma)
42   Beta <- PostBeta(Sigma = Sigma); PostBetas[s,] <- Beta
43   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
  "% done"))
44 }
45 close(pb); keep <- seq((burnin+1), tot, thin)
46 Bs <- PostBetas[keep,]; summary(coda::mcmc(Bs))
47 Sigmas <- PostSigmas[keep,]; summary(coda::mcmc(Sigmas))

```

R code. Utility demand in Colombia, results

```

1 keep <- seq((burnin+1), tot, thin)
2 Bs <- PostBetas[keep,]; summary(coda::mcmc(Bs))
3 Sigmas <- PostSigmas[keep,]; summary(coda::mcmc(Sigmas))
4 Quantiles for each variable:
5
6      2.5%      25%      50%      75%      97.5%
7 Const      0.43304  1.04508  1.337751  1.64728  2.25228
8 LnPriceElect -2.40343 -2.05533 -1.882159 -1.70463 -1.35979
9 LnPriceWater -0.44027 -0.38524 -0.356049 -0.32676 -0.27021
10 LnPriceGas -0.21665 -0.13807 -0.098877 -0.05712  0.01673
11 IndSocio1 -0.87408 -0.78454 -0.736561 -0.68898 -0.59137
12 IndSocio2 -0.24504 -0.18344 -0.150827 -0.11845 -0.06029
13 Altitude -0.27153 -0.23866 -0.221539 -0.20468 -0.17325
14 Nrooms 0.04598 0.06191 0.069971 0.07837 0.09379
15 HouseholdMem 0.06610 0.07999 0.087320 0.09406 0.10708
16 Lnincome 0.03897 0.05516 0.063130 0.07152 0.08751
17 Const 0.88247 1.73546 2.162290 2.60793 3.48450
18 LnPriceElect -0.83128 -0.31258 -0.051838 0.20446 0.72087
19 LnPriceWater -0.49760 -0.40946 -0.363138 -0.31943 -0.23498
20 LnPriceGas 0.05880 0.16932 0.228734 0.28677 0.39226
21 IndSocio1 -0.63928 -0.50417 -0.427978 -0.35529 -0.21024
22 IndSocio2 -0.50363 -0.40976 -0.359576 -0.30929 -0.21097
23 Nrooms 0.05733 0.08126 0.093291 0.10550 0.12935
24 HouseholdMem 0.09984 0.12098 0.132126 0.14265 0.16290
25 Const -2.26403 -1.57842 -1.201124 -0.84494 -0.15985
26 LnPriceElect -2.41128 -2.00330 -1.786150 -1.57292 -1.17185
27 LnPriceWater -0.10791 -0.03978 -0.003399 0.03329 0.10082
28 LnPriceGas -0.76450 -0.67575 -0.627062 -0.57949 -0.48807
29 IndSocio1 -0.91346 -0.80094 -0.743421 -0.68334 -0.57228
30 IndSocio2 -0.31613 -0.24086 -0.202828 -0.16367 -0.08824
31 Altitude 0.24986 0.28987 0.310784 0.33183 0.37126
32 Nrooms 0.06071 0.07899 0.089606 0.09949 0.11842
33 HouseholdMem 0.14485 0.16148 0.169509 0.17797 0.19467
34 Sigmas <- PostSigmas[keep,]
35 summary(coda::mcmc(Sigmas))
36      2.5%      25%      50%      75%      97.5%
37 var1 0.19664 0.20567 0.21072 0.21593 0.22636
38 var2 0.08201 0.09289 0.09865 0.10447 0.11623
39 var3 0.05222 0.06015 0.06452 0.06903 0.07799
40 var4 0.47390 0.49575 0.50789 0.52046 0.54446
41 var5 0.07355 0.08672 0.09381 0.10061 0.11427
42 var6 0.29259 0.30618 0.31384 0.32140 0.33700

```

6. Simulation exercise of instrumental variables continues

- (a) Use the setting of the simulation exercise of instrumental variables to analyze what happens when the instrument is weak, for instance,

setting $\gamma_2 = 0.2$, and compare the performance of the posterior means of the ordinary and instrumental models.

- (b) Perform a simulation that helps to analyze how the degree of exogeneity of the instrument affects the performance of the posterior mean of the instrumental variable model.

Answer

*R code. Simulation exercise, sampling properties
of instrumental variable*

```

1 rm(list = ls())
2 set.seed(010101)
3 N <- 100
4 k <- 2
5 B <- rep(1, k)
6 G <- c(1, 0.2)
7 s12 <- 0.8
8 SIGMA <- matrix(c(1, s12, s12, 1), 2, 2)
9 z <- rnorm(N); # w <- rnorm(N)
10 Z <- cbind(1, z); w <- matrix(1,N,1)
11 S <- 100
12 U <- replicate(S, MASS::mvrnorm(n = N, mu = rep(0, 2), SIGMA
  ))
13 x <- G[1] + G[2]*z + U[,2,]
14 y <- B[1] + B[2]*x + U[,1,]
15 VarX <- G[2]^2+1 # Population variance of x
16 EU1U2 <- s12 # Covariance U1
17 BiasPopB2 <- EU1U2/VarX
18 # Hyperparameters
19 d0 <- 0.001/2
20 a0 <- 0.001/2
21 b0 <- rep(0, k)
22 c0 <- 1000
23 B0 <- c0*diag(k)
24 B0i <- solve(B0)
25 g0 <- rep(0, 2)
26 G0 <- 1000*diag(2)
27 G0i <- solve(G0)
28 nu <- 3
29 Psi0 <- nu*diag(2)
30 # MCMC parameters
31 mcmc <- 5000
32 burnin <- 1000
33 tot <- mcmc + burnin
34 thin <- 1
35 # Gibbs sampling
36 Gibbs <- function(x, y){
37   Data <- list(y = y, x = x, w = w, z = Z)
38   Mcmc <- list(R = mcmc, keep = thin, nprint = 0)
39   Prior <- list(md = g0, Ad = G0i, mbg = b0, Abg = B0i, nu =
    nu, V = Psi0)
40   RestIV <- bayesm::rivGibbs(Data = Data, Mcmc = Mcmc, Prior
    = Prior)
41   PostBIV <- mean(RestIV[["betadraw"]])
42   ResLM <- MCMCpack::MCMCregress(y ~ x + w - 1, b0 = b0, B0
    = B0i, c0 = a0, d0 = d0)
43   PostB <- mean(ResLM[,1])
44   Res <- c(PostB, PostBIV)
45   return(Res)
46 }
47 PosteriorMeans <- sapply(1:S, function(s) {Gibbs(x = x[,s],
  y = y[,s])})
48 rowMeans(PosteriorMeans)
49 1.781513 1.470648

```

**FIGURE 7.1**

Histogram of posterior means to assess the effects of *weakness* of the instrument: Ordinary and instrumental models.

Figure 7.1 shows that having a *weak instrument* generates poor performance of the posterior means of the variable instrumental model. Observe that the mean of the posterior means is less precise and biased. This is due to an identification problem in the likelihood function of y and x_s given z (see [27, Chap. 7]).

*R code. Simulation exercise, sampling properties
of instrumental variable*

```

1 # Endogenous instruments
2 rm(list = ls())
3 set.seed(010101)
4 N <- 100
5 k <- 2
6 B <- rep(1, k)
7 G <- c(1, 1)
8 delta <- 0.2 # Effect of instrument on y
9 s12 <- 0.8
10 SIGMA <- matrix(c(1, s12, s12, 1), 2, 2)
11 z <- rnorm(N); # w <- rnorm(N)
12 Z <- cbind(1, z); w <- matrix(1,N,1)
13 S <- 100
14 U <- replicate(S, MASS::mvrnorm(n = N, mu = rep(0, 2), SIGMA
  ))
15 x <- G[1] + G[2]*z + U[,2,]
16 y <- B[1] + B[2]*x + delta*z + U[,1,]
17 VarX <- G[2]^2+1 # Population variance of x
18 EU1U2 <- s12 # Covariance U1
19 BiasPopB2 <- EU1U2/VarX
20 # Hyperparameters
21 d0 <- 0.001/2
22 a0 <- 0.001/2
23 b0 <- rep(0, k)
24 c0 <- 1000
25 B0 <- c0*diag(k)
26 B0i <- solve(B0)
27 g0 <- rep(0, 2)
28 G0 <- 1000*diag(2)
29 G0i <- solve(G0)
30 nu <- 3
31 Psi0 <- nu*diag(2)
32 # MCMC parameters
33 mcmc <- 5000
34 burnin <- 1000
35 tot <- mcmc + burnin
36 thin <- 1
37 # Gibbs sampling
38 Gibbs <- function(x, y){
39   Data <- list(y = y, x = x, w = w, z = Z)
40   Mcmc <- list(R = mcmc, keep = thin, nprint = 0)
41   Prior <- list(md = g0, Ad = G0i, mbg = b0, Abg = B0i, nu =
     nu, V = Psi0)
42   RestIV <- bayesm::rivGibbs(Data = Data, Mcmc = Mcmc, Prior
     = Prior)
43   PostBIV <- mean(RestIV[["betadraw"]])
44   ResLM <- MCMCpack::MCMCregress(y ~ x + w - 1, b0 = b0, B0
     = B0i, c0 = a0, d0 = d0)
45   PostB <- mean(ResLM[,1])
46   Res <- c(PostB, PostBIV)
47   return(Res)
48 }
49 PosteriorMeans <- sapply(1:S, function(s) {Gibbs(x = x[,s],
     y = y[,s])})
50 rowMeans(PosteriorMeans)
51 1.508009 1.217419

```



FIGURE 7.2

Histogram of posterior means to assess the effects of *endogeneity* of the instrument: Ordinary and instrumental models.

A simple way to assess the effects of *endogeneity* of the instrument in the instrumental variable model is to introduce the instrument into the *structural equation*, but assume that $E[yz|x_s] = 0$. In particular, we generate $y_i = \beta_1 + \beta_2 x_{si} + \beta_3 z_i + \mu_i$, but estimate $y_i = \beta_1 + \beta_2 x_{si} + \mu_i$. Figure 7.2 shows that assuming that an instrument is exogenous, when actually it is not, generates bias in the posterior mean of the instrumental variable model. Observe that *exogeneity* of the instrument is equivalent to the dogmatic prior belief that the instrument does not affect the structural equation. Thus, [5] propose to assess the plausibility of the *exclusion restrictions* ($\beta_3 = 0$ and $\gamma_2 \neq 0$) defining *plausible exogeneity* as having prior information that the effect of the instrument in the *structural equation* is near zero, but perhaps not exactly zero.

7. Simulation exercise of instrumental variables continues II

Program from scratch the Gibbs sampling algorithm of the instrumental model for the simulation exercise of the instrumental variables.

Answer

The following code shows how to implement the Gibbs sampling algorithm from scratch. We observe that all posterior means are close to the population values, and 95% credible intervals encompass them.

*R code. Simulation exercise, Gibbs sampling
instrumental model*

```

1 rm(list = ls()); set.seed(010101)
2 N <- 100; k <- 2; kz <- 2
3 B <- rep(1, k); G <- rep(1, kz)
4 s12 <- 0.8; SIGMA <- matrix(c(1, s12, s12, 1), 2, 2)
5 z <- rnorm(N); Z <- cbind(1, z); w <- matrix(1, N, 1)
6 S <- 100; U <- MASS::mvrnorm(n = N, mu = rep(0, 2), SIGMA)
7 x <- G[1] + G[2]*z + U[,2]; y <- B[1] + B[2]*x + U[,1]
8 X <- cbind(w, x)
9 # Hyperparameters
10 b0 <- rep(0, k); c0 <- 1000; B0 <- c0*diag(k)
11 B0i <- solve(B0); g0 <- rep(0, kz)
12 G0 <- 1000*diag(kz); G0i <- solve(G0)
13 nu <- 3; Psi0 <- nu*diag(2); Psi0i <- solve(Psi0)
14 # MCMC parameters
15 mcmc <- 5000; burnin <- 1000; tot <- mcmc + burnin
16 thin <- 1
17 # Auxiliary elements
18 XtX <- t(X)%*%X; ZtZ <- t(Z)%*%Z; nun <- nu + N
19 # Gibbs sampling
20 PostBeta <- function(Sigma, Gamma){
21   w1 <- Sigma[1,1] - Sigma[1,2]^2/Sigma[2,2]
22   Bn <- solve(w1^(-1)*XtX + B0i)
23   yaux <- y - (Sigma[1,2]/Sigma[2,2])*(x - Z%*%Gamma)
24   bn <- Bn%*%(B0i%*%b0 + w1^(-1)*t(X)%*%yaux)
25   Beta <- MASS::mvrnorm(1, bn, Bn)
26   return(Beta)
27 }
28 PostGamma <- function(Sigma, Beta){
29   w2 <- Sigma[2,2] - Sigma[1,2]^2/Sigma[1,1]
30   Gn <- solve(w2^(-1)*ZtZ + G0i)
31   xaux <- x - (Sigma[1,2]/Sigma[1,1])*(y - X%*%Beta)
32   gn <- Gn%*(G0i%*%g0 + w2^(-1)*t(Z)%*%xaux)
33   Gamma <- MASS::mvrnorm(1, gn, Gn)
34   return(Gamma)
35 }
36 PostSigma <- function(Beta, Gamma){
37   Uy <- y - X%*%Beta; Ux <- x - Z%*%Gamma
38   U <- cbind(Uy, Ux)
39   Psin <- solve(Psi0i + t(U)%*%U)
40   Sigmai <- rWishart::rWishart(1, df = nun, Sigma = Psin)
41   Sigma <- solve(Sigmai[, , 1])
42   return(Sigma)
43 }

```

*R code. Simulation exercise, Gibss sampling
instrumental model*

```

1 PostBetas <- matrix(0, tot, k); PostGammas <- matrix(0, tot,
  kz)
2 PostSigmas <- matrix(0, tot, 2*(2+1)/2); Beta <- rep(0, k);
  Gamma <- rep(0, kz)
3 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
4 for(s in 1:tot){
5   Sigma <- PostSigma(Beta = Beta, Gamma = Gamma)
6   Beta <- PostBeta(Sigma = Sigma, Gamma = Gamma)
7   Gamma <- PostGamma(Sigma = Sigma, Beta = Beta)
8   PostBetas[s,] <- Beta; PostGammas[s,] <- Gamma;
    PostSigmas[s,] <- matrixcalc::vech(Sigma)
9   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
10 }
11 close(pb)
12 keep <- seq((burnin+1), tot, thin)
13 Bs <- PostBetas[keep,]
14 Gs <- PostGammas[keep,]
15 Sigmas <- PostSigmas[keep,]
16 summary(coda::mcmc(Bs))
17 1. Empirical mean and standard deviation for each variable,
18 plus standard error of the mean:
19 Mean      SD Naive SE Time-series SE
20 [1,]  1.1519 0.1683  0.00238      0.006321
21 [2,]  0.9896 0.1146  0.00162      0.005177
22 summary(coda::mcmc(Gs))
23 1. Empirical mean and standard deviation for each variable,
24 plus standard error of the mean:
25 Mean      SD Naive SE Time-series SE
26 [1,]  1.133 0.1068 0.001511      0.003096
27 [2,]  1.030 0.1066 0.001507      0.004193
28 summary(coda::mcmc(Sigmas))
29 1. Empirical mean and standard deviation for each variable,
30 plus standard error of the mean:
31 Mean      SD Naive SE Time-series SE
32 [1,]  1.3883 0.3149 0.004454      0.012707
33 [2,]  0.9992 0.2133 0.003017      0.007166
34 [3,]  1.1637 0.1685 0.002382      0.002481

```

8. The effect of institutions on per capita gross domestic product continues II

Estimate the structural Equation 7.1 using the instrumental variable model where the instrument of PAER is $\log(Mort)$. Compare the effect of prop-

erty rights on per capita GDP of this model with the effect estimated in the example of the effect of institutions on per capita gross domestic product. Use the file *6Institutions.csv* to do this exercise in our GUI, and set $\mathbf{B}_0 = 100\mathbf{I}_5$, $\boldsymbol{\beta}_0 = \mathbf{0}_5$, $\boldsymbol{\gamma}_0 = \mathbf{0}_2$, $\mathbf{G}_0 = 100\mathbf{I}_2$, $\alpha_0 = 3$ and $\boldsymbol{\Psi}_0 = 3\mathbf{I}_2$. The MCMC iterations, burn-in and thinning parameters are 50000, 1000 and 5, respectively.

Answer

The following code shows how to do this using the command *rivGibbs* from the *bayesm* package. We see that the posterior mean of the effect of property rights on per capita GDP is 0.72, and the 95% credible interval is (0.47, 1.00). The posterior mean estimate of this effect was 0.98 in the example, and the 95% credible interval was (0.56, 2.87) (see Section 8.1 in the book). We can observe that the indirect approach, where the *reduced-form* parameters are estimated, and then, plug into the equations of the *structural parameters* produce less efficient posterior estimations.

*R code. The effects of institutions on GDP,
variable instrumental model*

```

1 rm(list = ls()); set.seed(010101)
2 DataInst <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/6Institutions
  .csv", sep = ",", header = TRUE, quote = "")
3 attach(DataInst)
4 y <- logpcGDP95; x <- PAER
5 w <- cbind(1, Africa, Asia, Other); Z <- cbind(1, logMort)
6 # Hyperparameters
7 k <- 5; kz <- 2; b0 <- rep(0, k); c0 <- 100
8 B0 <- c0*diag(k); B0i <- solve(B0); g0 <- rep(0, kz)
9 G0 <- 100*diag(kz); G0i <- solve(G0); nu <- 5
10 Psi0 <- nu*diag(2)
11 # MCMC parameters
12 mcmc <- 50000; burnin <- 10000; tot <- mcmc + burnin; thin
  <- 5
13 # Gibbs sampling
14 Data <- list(y = y, x = x, w = w, z = Z)
15 Mcmc <- list(R = mcmc, keep = thin, nprint = 100)
16 Prior <- list(md = g0, Ad = G0i, mbg = b0, Abg = B0i, nu =
  nu, V = Psi0)
17 RestIV <- bayesm::rivGibbs(Data = Data, Mcmc = Mcmc, Prior =
  Prior)
18 summary(RestIV[["deltadraw"]])
19 summary(coda::mcmc(RestIV[["betadraw"]]))
20 Iterations = 1:10000
21 Thinning interval = 1
22 Number of chains = 1
23 Sample size per chain = 10000
24 1. Empirical mean and standard deviation for each variable,
25 plus standard error of the mean:
26 Mean          SD          Naive SE Time-series SE
27 0.759497      0.140874      0.001409      0.002477
28 2. Quantiles for each variable:
29 2.5%    25%    50%    75%   97.5%
30 0.5110 0.6654 0.7502 0.8424 1.0707
31 summary(RestIV[["gammadraw"]])
32 summary(RestIV[["sigmadraw"]])

```

9. Multivariate probit with different regressors

Let's do a simulation exercise where $y_{i1}^* = 0.5 - 1.2x_{i11} + 0.7x_{i12} + 0.8x_{i13} + \mu_{i1}$ and $y_{i2}^* = 1.5 - 0.8x_{i21} + 0.5x_{i22} + \mu_{i2}$, $\Sigma = \begin{Bmatrix} 1 & 0.5 \\ 0.5 & 1 \end{Bmatrix}$, where all regressors distribute standard normal, and $N = 5000$. Use $\beta_0 = \mathbf{0}$, $B_0 = 1000B$,

$\alpha_0 = 4$ and $\Psi_0 = 4\mathbf{I}_2$. Set number of iterations 2000 and a thinning parameter equal to 5.

- Perform inference using the setting of Section 7.4, that is, assuming that x_{i3} could have an effect on y_{i2} .
- Program a Gibbs sampling algorithm taking into account that there are different regressors in each binary decision, that is, x_{i3} does not have an effect on y_{i2} .

Answer

The following code shows how to perform inference assuming same number of regressors in both binary results. We can check that all 95% credible intervals encompass the population values, and the posterior mean estimates are very close to the population parameters.

R code. Multivariate probit model: Same number of regressors in each binary response

```

1 remove(list = ls())
2 n <- 5000 #Individuals
3 p <- 2 #Number dependent variables (For instance to buy or
4       #not to buy different products)
5 xo <- 2 #Number of choice dependent variables (For instance
6       #price of products)
7 xi <- 1 #Number of regressors that dependt on individuals (
8       #For instance income)
9 B1 <- c(0.5, -1.2, 0.7, 0.8)
10 B2 <- c(1.5, -0.8, 0.5, 0) # The last regressor is not relevant
11      #for the second product
12 Cor <- matrix(c(1, 0.5, 0.5, 1), p, p)
13 yX <- NULL; y1 <- NULL
14 for (i in 1:n){
15   ei <- MASS::mvrnorm(1, c(0,0), Cor); xs <- rnorm(xi)
16   x1i <- c(1, rnorm(xo), xs); y11i <- sum(x1i*B1)
17   y1i <- y11i + ei[1] > 0; x2i <- c(1, rnorm(xo), xs)
18   y12i <- sum(x2i*B2); y2i <- y12i + ei[2] > 0
19   yXi <- rbind(c(y1i, x1i), c(y2i, x2i))
20   yXi <- cbind(i, yXi)
21   colnames(yXi) <- c("id", "y", "cte", "x1o", "x2o", "xi")
22   yX <- rbind(yX, yXi)
23   y1 <- c(y1, c(y11i + ei[1], y12i + ei[2]))
24 }
25 nd <- 4 # Number of regressors
26 Xd <- as.matrix(yX[,3:6])
27 XcreateMP <- function(p, nxs, nind, Data){
28   pandterm = function(message) {
29     stop(message, call. = FALSE)
30   }
31   if (missing(nxs))
32     pandterm("requires number of regressors: include intercept
33             #if required")
34   if (missing(nind))
35     pandterm("requires number of units (individuals)")
36   if (missing(Data))
37     pandterm("requires dataset")
38   if (nrow(Data) != nind*2)
39     pandterm("check dataset! number of units times number
40             #alternatives should be equal to dataset rows")
41   XXDat <- array(0, c(p, 1+nxs, nind))
42   XX <- array(0, c(p, nxs*p, nind))
43   YY <- array(0, c(p, 1, nind))
44   is <- seq(p, nind*p, p)
45   cis <- seq(nxs, nxs*p+1, nxs)
46   for(i in is){
47     j <- which(i==is)
48     XXDat[,j] <- as.matrix(Data[c((i-(p-1)):i), -1])
49     YY[,j] <- XXDat[,1,j]
50     for(l in 1:p){
51       XX[l, (cis[l]-(nxs-1)):cis[l], j] <- XXDat[l, -1, j]
52     }
53   }
54   return(list(y=YY, X=XX))
55 }
56 Dat <- XcreateMP(p = p, nxs = nd, nind = n, Data = yX)

```

R code. Multivariate probit model: Same number of regressors in each binary response

```

1 y<-NULL
2 X<-NULL
3 for(i in 1:dim(Dat$y)[3]){
4   y<-c(y,Dat$y[,i])
5   X<-rbind(X,Dat$X[,i])
6 }
7 DataMP = list(p=p, y=y, X=X)
8 # Hyperparameters
9 k <- dim(X)[2]
10 b0 <- rep(0, k)
11 c0 <- 1000
12 B0 <- c0*diag(k)
13 B0i <- solve(B0)
14 a0 <- p - 1 + 3
15 Psi0 <- a0*diag(p)
16 Prior <- list(betabar = b0, A = B0i, nu = a0, V = Psi0)
17 # MCMC parameters
18 mcmc <- 2000
19 burnin <- 1000
20 thin <- 5
21 Mcmc <- list(R = mcmc, keep = thin)
22 Results <- bayesm::rmvpGibbs(Data = DataMP, Mcmc = Mcmc,
   Prior = Prior)
23 betatildeEq1 <- Results$betadraw[,1:4] / sqrt(Results$
   sigmadraw[,1])
24 summary(coda::mcmc(betatildeEq1))
25 betatildeEq2 <- Results$betadraw[,5:8] / sqrt(Results$
   sigmadraw[,4])
26 summary(coda::mcmc(betatildeEq2))
27 sigmadraw12 <- Results$sigmadraw[,2] / (Results$sigmadraw
   [,1]*Results$sigmadraw[,4])^0.5
28 summary(coda::mcmc(sigmadraw12))

```

The following code shows the implementation of a Gibbs sampling algorithm using the *bayesm* package, particularly, the *rmvpGibbs* command.

R code. Multivariate probit model: Different number of regressors in each binary response, the rmvpGibbs command

```

1 # Omitting last regressor for y2
2 Xnew <- X[,-8]
3 DataMP = list(p=p, y=y, X=Xnew)
4 # Hyperparameters
5 k <- dim(Xnew)[2]
6 b0 <- rep(0, k)
7 c0 <- 1000
8 B0 <- c0*diag(k)
9 B0i <- solve(B0)
10 Prior <- list(betabar = b0, A = B0i, nu = a0, V = Psi0)
11 Results <- bayesm::rmvpGibbs(Data = DataMP, Mcmc = Mcmc,
    Prior = Prior)
12 betatildeEq1 <- Results$betadraw[,1:4] / sqrt(Results$
    sigmadraw[,1])
13 summary(coda::mcmc(betatildeEq1))
14 betatildeEq2 <- Results$betadraw[,5:7] / sqrt(Results$
    sigmadraw[,4])
15 summary(coda::mcmc(betatildeEq2))
16 sigmadraw12 <- Results$sigmadraw[,2] / (Results$sigmadraw
    [,1]*Results$sigmadraw[,4])^0.5
17 summary(coda::mcmc(sigmadraw12))

```

The following code shows how to implement a Gibbs sampling algorithm from scratch.

R code. Multivariate probit model: Different number of regressors in each binary response, Gibbs from scratch

```

1 PostBetaNew <- function(Sigma, Yl){
2   Sigmai <- solve(Sigma); C <- chol(Sigmai)
3   Xstar <- matrix(0, n*p, k); Ystar <- matrix(0, n*p, 1)
4   for(i in seq(1, n*p, 2)){
5     Xstari <- C%%Xnew[i:(i+1),]
6     Xstar[i:(i+1),] <- Xstari
7     Ystari <- C%%Yl[i:(i+1)]
8     Ystar[i:(i+1)] <- Ystari
9   }
10  Bn <- solve(B0i + t(Xstar)%%Xstar)
11  bn <- Bn%*(B0i%%b0 + t(Xstar)%%Ystar)
12  Beta <- MASS::mvrnorm(1, bn, Bn)
13  return(Beta)
14 }
15 PostSigmaNew <- function(Beta, Yl){
16  U <- matrix(0, p, p)
17  for(i in seq(1, n*p, 2)){
18    Ui <- (Yl[i:(i+1)] - Xnew[i:(i+1),]%%Beta)%%t(Yl[i:(i+1)] - Xnew[i:(i+1),]%%Beta)
19    U <- U + Ui
20  }
21  Psin <- solve(Psi0i + U)
22  Sigmai <- rWishart::rWishart(1, df = an, Sigma = Psin)
23  Sigma <- solve(Sigmai[, ,1])
24 }
25 PostYlNew <- function(Beta, Sigma, Yl){
26  w1 <- Sigma[1, ]
27  w2 <- Sigma[2, ]
28  f1 <- w1[-1]*Sigma[2, 2]^(-1)
29  f2 <- w2[-2]*Sigma[1, 1]^(-1)
30  t11 <- Sigma[1, 1] - w1[-1]*Sigma[2, 2]^(-1)*w1[-1]
31  t22 <- Sigma[2, 2] - w2[-2]*Sigma[1, 1]^(-1)*w2[-2]
32  Ylnew <- Yl
33  for(i in seq(1, n*p, 2)){
34    Ylmean1 <- Xnew[i,]%%Beta + f1*(Yl[i+1] - Xnew[i+1,]%%Beta)
35    if(y[i] == 1){
36      Ylnew[i] <- truncnorm::rtruncnorm(1, a = 0, b = Inf,
37        mean = Ylmean1, sd = t11^0.5)
38    }else{
39      Ylnew[i] <- truncnorm::rtruncnorm(1, a = -Inf, b = 0,
40        mean = Ylmean1, sd = t11^0.5)
41    }
42    Ylmean2 <- Xnew[i+1,]%%Beta + f2*(Ylnew[i] - Xnew[i,]%%Beta)
43    if(y[i+1] == 1){
44      Ylnew[i+1] <- truncnorm::rtruncnorm(1, a = 0, b = Inf,
45        mean = Ylmean2, sd = t22^0.5)
46    }else{
47      Ylnew[i+1] <- truncnorm::rtruncnorm(1, a = -Inf, b = 0,
48        mean = Ylmean2, sd = t22^0.5)
49    }
50  }
51  return(Ylnew)
52 }

```

R code. Multivariate probit model: Different number of regressors in each binary response, Gibbs from scratch

```

1 an <- a0 + n
2 Psi0i <- solve(Psi0)
3 K1 <- 4; K2 <- 3; K <- K1 + K2
4 tot <- mcmc + burnin
5 PostBetas <- matrix(0, tot, K)
6 PostSigmas <- matrix(0, tot, p*(p+1)/2)
7 Beta <- rep(1, K)
8 Sigma <- diag(p)
9 pb <- winProgressBar(title = "progress bar", min = 0, max =
    tot, width = 300)
10 for(s in 1:tot){
11   Yl <- PostYlNew(Beta = Beta, Sigma = Sigma, Yl = yl)
12   Sigma <- PostSigmaNew(Beta = Beta, Yl = Yl)
13   Beta <- PostBetaNew(Sigma = Sigma, Yl = Yl)
14   PostBetas[s,] <- Beta
15   PostSigmas[s,] <- matrixcalc::vech(Sigma)
16   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
17 }
18 close(pb)
19 keep <- seq((burnin+1), tot, thin)
20 Bs <- PostBetas[keep,]
21 betatilde1 <- Bs[,1:K1] / sqrt(PostSigmas[keep,1])
22 summary(coda::mcmc(betatilde1))
23 betatilde2 <- Bs[, (K1+1):(K1+K2)] / sqrt(PostSigmas[keep,3])
24 summary(coda::mcmc(betatilde2))
25 sigmadraw12 <- PostSigmas[keep,2] / (PostSigmas[keep,1] *
    PostSigmas[keep,3])^0.5
26 summary(coda::mcmc(sigmadraw12))

```



8

Time series models

Solutions of Exercises

1. Simulate the *dynamic linear model* assuming $X_t \sim N(1, 0.1\sigma^2)$, $w_t \sim N(0, 0.5\sigma^2)$, $\mu_t \sim N(0, \sigma^2)$, $\beta_0 = 1$, $B_0 = 0.5\sigma^2$, $\sigma^2 = 0.25$, and $G_t = 1$, $t = 1, \dots, 100$. Then, perform the filtering recursion fixing $\Sigma = 25 \times 0.25$, $\Omega_1 = 0.5\Sigma$ (high signal-to-noise ratio) and $\Omega_2 = 0.1\Sigma$ (low signal-to-noise ratio). Plot and compare the results.

Answer

The following code shows how to perform this simulation and perform the filtering recursion using the *dln* package in **R**.

R code. Simulation: Scenarios signal-to-noise ratio

```

1 rm(list = ls()); set.seed(010101)
2 T <- 100; sig2 <- 0.5^2; r <- 0.5; sigW2 <- sig2*r
3 x <- rnorm(T, mean = 1, sd = 0.1*sig2^0.5)
4 e <- rnorm(T, mean = 0, sd = sig2^0.5)
5 w <- rnorm(T, mean = 0, sd = sigW2^0.5)
6 K <- 1
7 Bt <- matrix(NA, T, K); Bt[1] <- 1
8 yt <- rep(NA, T)
9 yt[1] <- x[1]*Bt[1] + e[1]
10 for(t in 1:T){
11   if(t == 1){
12     Bt[t,] <- w[t]
13   }else{
14     Bt[t,] <- Bt[t-1,] + w[t]
15   }
16   yt[t] <- x[t]*Bt[t,] + e[t]
17 }
18 # State space model
19 ModelReg <- function(par){
20   Mod <- dlm::dlmModReg(x, dV = exp(par[1]), dW = exp(par
21     [2]), m0 = rep(1, K),
22   CO = sigW2*diag(K), addInt = FALSE)
23   return(Mod)
24 }
25 sig2New <- sig2*25
26 RegFilter1 <- dlm::dlmFilter(yt, ModelReg(c(sig2New, sig2New
27   *0.5)))
28 ytfil1 <- RegFilter1[["m"]][-1]
29 RegFilter2 <- dlm::dlmFilter(yt, ModelReg(c(sig2New, sig2New
30   *0.1)))
31 ytfil2 <- RegFilter2[["m"]][-1]
32 Time <- 1:T
33 df1 <- as.data.frame(cbind(Time,yt, ytfil1, ytfil2))
34 library(ggplot2)
35 ggplot(df1, aes(x=Time)) +
36   geom_line(aes(y=yt), colour="black", linewidth=1, linetype
37     =1) +
38   geom_line(aes(y=ytfil1), colour="green", linewidth=1, alpha
39     =0.9, linetype=2) +
40   geom_line(aes(y=ytfil2), color="blue", linewidth=1, alpha
41     =0.9, linetype=3)

```

Figure 8.1 shows the results of the filtering recursion. We see in this figure that the filtered recursion associated with the high signal-to-noise ratio (green dashed line) follows closer the data than the low signal-to-noise

**FIGURE 8.1**

Signal-to-noise ratio: Dynamic linear model.

ratio scenario (blue dotted line). We see that the latter is smoother as it gives more weight to the prior mean, which takes into account historical information.

2. Simulate the *dynamic linear model* $y_t = \beta_t x_t + \mu_t$, $\beta_t = \beta_{t-1} + w_t$, where $x_t \sim N(1, 0.1\sigma^2)$, $w_t \sim N(0, 0.5\sigma^2)$, $\mu_t \sim N(0, \sigma^2)$, $\beta_0 = 0$, $B_0 = 0.5\sigma^2$, and $\sigma^2 = 1$, $t = 1, \dots, 100$. Perform the filtering and smoothing recursions from scratch.

Answer

The following code shows how to perform this simulation and perform the filtering recursion from scratch in **R**.

*R code. Simulation: Filtering and smoothing
recursions from scratch*

```

1 rm(list = ls()); set.seed(010101)
2 T <- 100; sig2 <- 1; r <- 0.5; sigW2 <- sig2*r
3 xt <- rnorm(T, mean = 1, sd = 0.1*sig2^0.5)
4 e <- rnorm(T, mean = 0, sd = sig2^0.5)
5 w <- rnorm(T, mean = 0, sd = sigW2^0.5)
6 K <- 1; Bt <- matrix(NA, T, K); Bt[1] <- 0
7 yt <- rep(NA, T)
8 for(t in 1:T){
9   if(t == 1){
10     Bt[t,] <- w[t]
11   }else{
12     Bt[t,] <- Bt[t-1,] + w[t]
13   }
14   yt[t] <- xt[t]%*%Bt[t,] + e[t]
15 }
16 # Filtering
17 KFR <- function(y, x, b1, B1, Omega, sig2){
18   e <- as.numeric(y - t(x)%*%b1) # Error
19   R <- B1 + Omega
20   q <- as.numeric(t(x)%*%R%*%x + sig2)
21   K <- (R%*%x)/q
22   bt <- b1 + K*e
23   Bt <- R - R%*%x%*%t(x)%*%R/q
24   Result <- list(bt = bt, Bt = Bt)
25   return(Result)
26 }
27 KFresb <- list(); KFresB <- list()
28 b0 <- 0; B0 <- sigW2
29 for(t in 1:T){
30   KFrest <- KFR(y = yt[t], x = xt[t], b1 = b0, B1 = B0,
31     Omega = sigW2, sig2 = sig2)
32   b0 <- KFrest[["bt"]]; B0 <- KFrest[["Bt"]]
33   KFresb[[t]] <- b0; KFresB[[t]] <- B0
34 }
35 ModelReg <- function(par){
36   Mod <- dlm::dlmModReg(xt, dV = exp(par[1]), dW = exp(par
37     [2]), m0 = rep(0, K),
38   C0 = sigW2*diag(K), addInt = FALSE)
39   return(Mod)
40 }
41 RegFilter1 <- dlm::dlmFilter(yt, ModelReg(c(sig2, sigW2)))
42 plot(Bt, type = "l")
43 lines(unlist(KFresb), type = "l", col = "red")
44 lines(RegFilter1[["m"]][-1], type = "l", col = "blue")

```

R code. Simulation: Filtering and smoothing recursions from scratch

```

1 # Smoothing
2 BSR <- function(b, B, slead, Slead, Omega){
3   b = bfilter[t]; B = Bfilter[t]; slead = slead; Slead =
4     slead; Omega = sigW2
5   R1 <- B + Omega
6   s <- b + B%*%solve(R1)%*(slead - b)
7   S <- B - B%*%solve(R1)%*(R1 - Slead)%*%solve(R1)%*B
8   Result <- list(st = s, St = S)
9   return(Result)
10 }
11 bfilter <- unlist(KFresb); Bfilter <- unlist(KFresB)
12 slead <- bfilter[T]; Slead <- Bfilter[T]
13 smooth <- rep(slead, T); Smooth <- rep(Slead, T);
14 for(t in (T-1):1){
15   BSRrest <- BSR(b = bfilter[t], B = Bfilter[t], slead =
16     slead, Slead = Slead, Omega = sigW2)
17   slead <- BSRrest[["st"]]; Slead <- BSRrest[["St"]]
18   smooth[t] <- slead
19 }
20 RegSmoth <- dlm::dlmSmooth(yt, ModelReg(c(sig2, sigW2)))
21 VarSmooth <- dlm::dlmSvd2var(u = RegSmoth[["U.S"]], RegSmoth
22   [["D.S"]])
23 SDVarSmoothB2 <- sapply(2:(T+1), function(t){VarSmooth[[t]][
24   K,K]^0.5})
25 plot(Bt, type = "l")
26 lines(smooth, type = "l", col = "orange")
27 lines(RegSmoth[["s"]][-1], type = "l", col = "green")

```

3. Simulate the process $y_t = \alpha z_t + \beta_t x_t + \mathbf{h}^\top \boldsymbol{\epsilon}_t$, $\beta_t = \beta_{t-1} + \mathbf{H}^\top \boldsymbol{\epsilon}_t$, where $\mathbf{h}^\top = [1 \ 0]$, $\mathbf{H}^\top = [0 \ 1/\tau]$, $\mathbf{v}_t \sim N(\mathbf{0}_2, \sigma^2 \mathbf{I}_2)$, $x_t \sim N(1, 2\sigma^2)$, $z_t \sim N(0, 2\sigma^2)$, $\alpha = 2$, $\tau^2 = 5$ and $\sigma^2 = 0.1$, $t = 1, \dots, 200$. Assume $\pi(\beta_0, \alpha, \sigma^2, \tau) = \pi(\beta_0)\pi(\alpha)\pi(\sigma^2)\pi(\tau^2)$ where $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$, $\tau^2 \sim G(v_0/2, v_0/2)$, $\alpha \sim N(a_0, A_0)$ and $\beta_0 \sim N(b_0, B_0)$ such that $\alpha_0 = \delta_0 = 1$, $v_0 = 5$, $a_0 = 0$, $A_0 = 1$, $\beta_0 = 0$, $B_0 = \sigma^2/\tau^2$. Program the MCMC algorithm including the *simulation smoother*.

Answer

*R code. Simulation: MCMC algorithm with
simulation smoother*

```

1 rm(list = ls()); set.seed(010101)
2 T <- 200; sig2 <- 0.1; tau2 <- 5; tau <- tau2^0.5; sigW2 <-
  sig2/tau2
3 xt <- rnorm(T, mean = 1, sd = 2*sig2^0.5)
4 zt <- rnorm(T, mean = 1, sd = 2*sig2^0.5)
5 alpha <- 2
6 e <- MASS::mvrnorm(T, mu = c(0, 0), Sigma = sig2*diag(2))
7 K <- 1
8 h1 <- matrix(c(1, 0), K + 1, 1); h2 <- matrix(c(0, 1/tau), K
  + 1, 1); t(h1)%*%h2
9 e1 <- e%*%h1; e2 <- e%*%h2; var(e1); var(e2)
10 Bt <- matrix(NA, T, K); Bt[1] <- 0
11 yt <- rep(NA, T)
12 for(t in 1:T){
13   if(t == 1){
14     Bt[t,] <- e2[t]
15   }else{
16     Bt[t,] <- Bt[t-1,] + e2[t]
17   }
18   yt[t] <- zt[t]*alpha + xt[t]*Bt[t] + e1[t]
19 }
20 # Recursion functions
21 # Filter
22 KFRDSnew <- function(y, z, x, b, B, alpha, tau2){
23   e <- as.numeric(y - z*alpha - t(x)%*%b)
24   q <- as.numeric(t(x)%*%B%*%x + t(h1)%*%h1)
25   K <- (B%*%x)/q
26   bt <- b + K*e
27   h2 <- matrix(c(0, 1/tau2^0.5))
28   Bt <- B - B%*%x%*%t(K) + t(h2)%*%h2
29   Result <- list(bt = bt, Bt = Bt, et = e, Kt = K, qt = q)
30   return(Result)
31 }
32 # Smooth
33 BSRDSnew <- function(r, M, Q, e, K, x, sig2, tau2){
34   h2 <- matrix(c(0, 1/tau2^0.5))
35   Lambda <- t(h2)%*%h2
36   C <- Lambda - Lambda%*%M%*%t(Lambda)
37   xi <- rnorm(1, 0, sd = (sig2*C)^0.5)
38   L <- 1 - K*x
39   V <- Lambda%*%M%*%L
40   rtl <- x*e/Q + t(L)*r - t(V)%*%solve(C)%*%xi
41   Mtl <- x%*%t(x)/Q + t(L)%*%M%*%L + t(V)%*%solve(C)%*%V
42   eta <- Lambda%*%r + xi
43   Result <- list(rtl = rtl, Mtl = Mtl, etat = eta)
44   return(Result)
45 }
46 # Gibbs functions
47 PostSig2 <- function(bbt, alpha, tau2){
48   an <- T*(K + 1) + alpha0
49   term1 <- diff(c(0, bbt))
50   term2 <- c(yt - alpha*zt - xt*bbt)
51   dn <- delta0 + sum(term1^2)*tau2 + sum(term2^2)
52   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
53   return(sig2)
54 }

```

*R code. Simulation: MCMC algorithm with
simulation smoother*

```

1 PosAlpha <- function(bbt, sig2){
2   An <- solve(A0i + sig2^(-1)*t(zt)%*%zt)
3   term <- yt-xt*bbt
4   an <- An%*%(A0i%*%a0 + sig2^(-1)*t(zt)%*%term)
5   Alpha <- MASS::mvrnorm(1, an, An)
6   return(Alpha)
7 }
8 PostTau2 <- function(bbt, sig2){
9   v1n <- v0 + T
10  term1 <- diff(c(0,bbt))
11  v2n <- v0 + sig2^(-1)*sum(term1^2)
12  tau2 <- rgamma(1, v1n/2, v2n/2)
13  return(tau2)
14 }
15 # Hyperparameter
16 alpha0 <- 1; delta0 <- 1; v0 <- 5
17 a0 <- 0; A0 <- 1; A0i <- 1/A0
18 tau2post <- 2; sig2post <- 0.2; alphapost <- 0
19 # Inference
20 S <- 2000; burnin <- 500; tot <- S + burnin; thin <- 5
21 # Posterior draws
22 sig2s <- rep(NA, tot); tau2s <- rep(NA, tot)
23 alphas <- rep(NA, tot); betas <- matrix(NA, tot, T)
24 pb <- winProgressBar(title = "progress bar", min = 0, max =
   tot, width = 300)

```

*R code. Simulation: MCMC algorithm with
simulation smoother*

```

1  for (s in 1:tot){
2    b0 <- 0; B0 <- sigW2
3    KFDSresb <- list(); KFDSresB <- list()
4    KFDSresE <- list(); KFDSresK <- list(); KFDSresQ <- list()
5    for(t in 1:T){
6      KFDSrest <- KFRDSnew(y = yt[t], z = zt[t], x = xt[t], b
7      = b0, B = B0, alpha = alphapost, tau2 = tau2post)
8      b0 <- KFDSrest[["bt"]]; B0 <- KFDSrest[["Bt"]]
9      KFDSresb[[t]] <- b0; KFDSresB[[t]] <- B0
10     KFDSresE[[t]] <- KFDSrest[["et"]]; KFDSresK[[t]] <-
11     KFDSrest[["Kt"]]; KFDSresQ[[t]] <- KFDSrest[["qt"]]
12   }
13   et <- unlist(KFDSresE); Qt <- unlist(KFDSresQ); Kt <-
14   unlist(KFDSresK)
15   rT <- 0; MT <- 0
16   BSRDSreseta <- rep(0, T); BSRDSresetaMean <- rep(0, T)
17   for(t in (T-1):1){
18     BSRDSrest <- BSRDSnew(r = rT, M = MT, Q = Qt[t+1], e =
19     et[t+1], K = Kt[t+1], x = xt[t+1], sig2 = sig2post, tau2
20     = tau2post)
21     rT <- BSRDSrest[["rt1"]]; MT <- BSRDSrest[["Mt1"]]
22     BSRDSreseta[t+1] <- BSRDSrest[["etat"]]
23   }
24   Bt1DSpost <- rep(0,T)
25   for(t in 1:T){
26     if(t == 1){
27       Bt1DSpost[t] <- BSRDSreseta[t]
28     }else{
29       Bt1DSpost[t] <- Bt1DSpost[t-1] + BSRDSreseta[t]
30     }
31   }
32   sig2post <- PostSig2(bbt = Bt1DSpost, alpha = alphapost,
33   tau2 = tau2post)
34   alphapost <- PosAlpha(bbt = Bt1DSpost, sig2 = sig2post)
35   tau2post <- PostTau2(bbt = Bt1DSpost, sig2 = sig2post)
36   sig2s[s] <- sig2post
37   tau2s[s] <- tau2post
38   alphas[s] <- alphapost
39   betas[s,] <- Bt1DSpost
40   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
41   "% done"))
42 }
43 close(pb); keep <- seq((burnin+1), tot, thin)
44 betasF <- betas[keep,]; sig2sF <- coda::mcmc(sig2s[keep])
45 tau2sF <- coda::mcmc(tau2s[keep]); alphasF <- coda::mcmc(
46   alphas[keep])
47 summary(sig2sF); plot(sig2sF)
48 summary(tau2sF); plot(tau2sF)
49 summary(alphasF); plot(alphasF)
50 library(fanplot); df <- as.data.frame(betasF)
51 plot(NULL, main="Percentiles", xlim = c(1, T+1), ylim = c
52   (-4, 1), xlab = "Time", ylab = TeX("$\\beta_{t1}$"))
53 fan(data = df); lines(colMeans(betasF), col = "black", lw =
54   2)
55 lines(Bt, col = "blue")

```


Figure 8.2 shows the path of the state vector (blue line), and the results from the *simulation smoother* using posterior draws, the black line is the mean, and the red-yellow shadows are different deciles.



FIGURE 8.2

State vector: Dynamic linear model.

4. Show that the posterior distribution of $\phi|\beta, \sigma^2, \mathbf{y}, \mathbf{X}$ in the model $Y_t = \mathbf{x}_t^\top \beta + \mu_t$ where $\phi(L)\mu_t = \epsilon_t$ and $\epsilon_t \stackrel{iid}{\sim} N(0, \sigma^2)$ is $N(\phi_n, \Phi_n) \mathbb{1}[\phi \in S_\phi]$, where $\Phi_n = (\Phi_0^{-1} + \sigma^{-2} \mathbf{U}^\top \mathbf{U})$, $\phi_n = \Phi_n(\Phi_0^{-1} \phi_0 + \sigma^{-2} \mathbf{U}^\top \boldsymbol{\mu})$, and S_ϕ is the stationary region of ϕ .

Answer

The conditional posterior distribution can be got as follows:

$$\begin{aligned} \pi(\phi|\beta, \sigma^2, \mathbf{y}) &\propto \exp \left\{ -\frac{1}{2\sigma^2} (\boldsymbol{\mu} - \mathbf{U}\phi)^\top (\boldsymbol{\mu} - \mathbf{U}\phi) \right\} \\ &\quad \times \exp \left\{ -\frac{1}{2} (\phi - \phi_0)^\top \Phi_0^{-1} (\phi - \phi_0) \right\} \\ &\propto \exp \left\{ -\frac{1}{2} [\phi^\top (\sigma^{-2} \mathbf{U}^\top \mathbf{U} + \Phi_0^{-1}) \phi - 2\phi^\top (\sigma^{-2} \mathbf{U}^\top \boldsymbol{\mu} + \Phi_0^{-1} \phi_0) \right. \\ &\quad \left. + \phi_n^\top \Phi_n^{-1} \phi_n - \phi_n^\top \Phi_n^{-1} \phi_n] \right\} \\ &\propto \exp \left\{ -\frac{1}{2} [(\phi - \phi_n)^\top \Phi_n^{-1} (\phi - \phi_n)] \right\}, \end{aligned}$$

where $\Phi_n = (\sigma^{-2} \mathbf{U}^\top \mathbf{U} + \Phi_0^{-1})^{-1}$ and $\phi_n = \Phi_n(\sigma^{-2} \mathbf{U}^\top \boldsymbol{\mu} + \Phi_0^{-1} \phi_0)$. The

last expression is the kernel of a multivariate normal distribution with mean ϕ_n and variance matrix Φ_n .

5. Show that in the $AR(2)$ stationary process, $Y_t = \mu + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \epsilon_t$, where $\epsilon_t \sim N(0, \sigma^2)$, $\mathbb{E}[Y_t] = \frac{\mu}{1-\phi_1-\phi_2}$, and $Var[Y_t] = \frac{\sigma^2(1-\phi_2)}{1-\phi_2-\phi_1^2\phi_2-\phi_2^2+\phi_2^3}$.

Answer

A necessary condition to achieve second-order stationarity in the $AR(2)$ process is that roots of the polynomial $1 - \phi_1 L - \phi_2 L^2 = 0$ lie outside the unit circle. This is achieved if $|\phi_2| < 1$, $\phi_1 + \phi_2 < 1$ and $\phi_2 - \phi_1 < 1$.

Let's calculate the expected value:

$$\begin{aligned}\mathbb{E}[Y_t] &= \bar{\mu} \\ &= \mathbb{E}[\mu + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \epsilon_t] \\ &= \mu + \phi_1 \mathbb{E}[Y_{t-1}] + \phi_2 \mathbb{E}[Y_{t-2}] + \mathbb{E}[\epsilon_t] \\ &= \mu + \phi_1 \bar{\mu} + \phi_2 \bar{\mu},\end{aligned}$$

then, $\bar{\mu}(1 - \phi_1 - \phi_2) = \mu$, then, $\mathbb{E}[Y_t] = \bar{\mu} = \frac{\mu}{1-\phi_1-\phi_2}$.

See that $Y_t = \mu + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \epsilon_t$ implies that $Y_t = \bar{\mu}(1 - \phi_1 - \phi_2) + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \epsilon_t$, which means that $Y_t - \bar{\mu} = \phi_1(Y_{t-1} - \bar{\mu}) + \phi_2(Y_{t-2} - \bar{\mu}) + \epsilon_t$, and setting $z_t = Y_t - \bar{\mu}$, we have $z_t = \phi_1 z_{t-1} + \phi_2 z_{t-2} + \epsilon_t$ where $\mathbb{E}[z_t] = 0$. Then, we can calculate the variance of Y_t using z_t , given that both have same variance.

Let's define $\gamma_s = Cov(z_t, z_{t-s}) = \mathbb{E}[z_t z_{t-s}]$, then the Yule-Walker equations are:

$$\begin{aligned}\gamma_0 &= \phi_1 \gamma_1 + \phi_2 \gamma_2 + \sigma^2 \\ \gamma_1 &= \phi_1 \gamma_0 + \phi_2 \gamma_1 \\ \gamma_2 &= \phi_1 \gamma_1 + \phi_2 \gamma_0.\end{aligned}$$

Solving this system of equations for γ_0 , γ_1 and γ_2 , we find that $\gamma_0 = \frac{\sigma^2(1-\phi_2)}{1-\phi_2-\phi_1^2\phi_2-\phi_2^2+\phi_2^3}$.

6. Program a Hamiltonian Monte Carlo (HMC) taking into account the stationary restrictions on ϕ_1 and ϕ_2 , and ϵ_0 such that the acceptance rate is near 65%.

Answer

We know from the previous exercise that $|\phi_2| < 1$, $\phi_1 + \phi_2 < 1$ and $\phi_2 - \phi_1 < 1$ satisfied the stationary condition of the process. Thus, we should impose this restrictions in the HMC. The following code does this.

*R code. AR(2) model: Hamiltonian Monte Carlo
with stationary restrictions*

```

1 # Simulation AR(2)
2 rm(list = ls()); set.seed(010101); T <- 1000; K <- 4
3 mu <- 0.5; phi1 <- 0.5; phi2 <- 0.3; sig <- 0.5
4 Ey <- mu/(1-phi1-phi2); Sigy <- sig*((1-phi2)/(1-phi2-phi1
   ^2-phi2*phi1^2-phi2^2+phi2^3))^0.5
5 y <- rnorm(T, mean = Ey, sd = Sigy); e <- rnorm(T, mean = 0,
   sd = sig)
6 for(t in 3:T){
7   y[t] <- mu + phi1*y[t-1] + phi2*y[t-2] + e[t]
8 }
9 # Hyperparameters
10 d0 <- 0.01; a0 <- 0.01; mu0 <- 0; MU0 <- 1
11 phi0 <- c(0, 0); Phi0 <- diag(2)
12 # Log posterior multiply by -1 to use optim
13 LogPost <- function(theta, y){
14   mu <- theta[1]; phi1 <- theta[2]; phi2 <- theta[3]
15   tau <- theta[4]; sig2 <- exp(tau); logLik <- NULL
16   for(t in 3:T){
17     logLikt <- dnorm(y[t], mean = mu + phi1*y[t-1] + phi2*y[
18       t-2], sd = sig2^0.5, log = TRUE)
19     logLik <- c(logLik, logLikt)
20   }
21   logLik <- sum(logLik)
22   logPrior <- dnorm(mu, mean = mu0, sd = MU0^0.5, log = TRUE
23     ) + dnorm(phi1, mean = phi0[1], sd = Phi0[1,1]^0.5, log
24     = TRUE) + dnorm(phi2, mean = phi0[2], sd = Phi0
25     [2,2]^0.5, log = TRUE) + invgamma::dinvgamma(sig2, shape
26     = a0/2, rate = d0/2, log = TRUE)
27   logPosterior <- logLik + logPrior + tau
28   return(-logPosterior) # Multiply by -1 to minimize using
29     optim
30 }
31 theta0 <- c(mean(y), 0, 0, var(y))
32 Opt <- optim(theta0, LogPost, y = y, hessian = TRUE)
33 theta0 <- Opt$par; VarPost <- solve(Opt$hessian)
34 # Gradient log posterior
35 GradientTheta <- function(theta, y){
36   mu <- theta[1]; phi1 <- theta[2]; phi2 <- theta[3]
37   tau <- theta[4]; sig2 <- exp(tau); SumLik <- matrix(0, 3,
38     1)
39   SumLik2 <- NULL
40   for(t in 3:T){
41     xt <- matrix(c(1, y[t-1], y[t-2]), 3, 1)
42     SumLikt <- (y[t] - (mu + phi1*y[t-1] + phi2*y[t-2]))*xt
43     SumLik2t <- (y[t] - (mu + phi1*y[t-1] + phi2*y[t-2]))^2
44     SumLik <- rowSums(cbind(SumLik, SumLikt))
45     SumLik2 <- sum(SumLik2, SumLik2t)
46   }
47   Grad_mu <- SumLik[1]/sig2 - (1/MU0)*(mu - mu0)
48   Grad_phi1 <- SumLik[2]/exp(tau) - 1/Phi0[1,1]*(phi1 - phi0
49     [1])
50   Grad_phi2 <- SumLik[3]/exp(tau) - 1/Phi0[2,2]*(phi2 - phi0
51     [2])
52   Grad_tau <- -(T-2)/2 + SumLik2/(2*exp(tau)) - (a0/2 + 1) +
53     d0/(2*exp(tau)) + 1
54   Grad <- c(Grad_mu, Grad_phi1, Grad_phi2, Grad_tau)
55   return(Grad)
56 }

```

***R code. AR(2) model: Hamiltonian Monte Carlo
with stationary restrictions***

```

1 StatRest <- function(phi1, phi2){
2   if(abs(phi2) < 1 & phi1 + phi2 < 1 & phi2 - phi1 < 1){
3     check <- 1
4   }else{
5     check <- 0
6   }
7   return(check)
8 }
9 HMC <- function(theta, y, epsilon, M){
10  L <- ceiling(1/epsilon)
11  Minv <- solve(M)
12  thetat <- theta
13  K <- length(thetat)
14  mom <- t(mvtnorm::rmvnorm(1, rep(0, K), M))
15  logPost_Mom_t <- -LogPost(thetat, y) + mvtnorm::dmvnorm(t
    (mom), rep(0, K), M, log = TRUE)
16  for(l in 1:L){
17    if(l == L){
18      mom <- mom + 0.5*epsilon*GradientTheta(theta, y)
19      theta <- theta + epsilon*Minv%%mom
20    }else{
21      mom <- mom + epsilon*GradientTheta(theta, y)
22      theta <- theta + epsilon*Minv%%mom
23    }
24  }
25  logPost_Mom_star <- -LogPost(theta, y) + mvtnorm::dmvnorm
    (t(mom), rep(0, K), M, log = TRUE)
26  alpha <- min(1, exp(logPost_Mom_star-logPost_Mom_t))
27  u <- runif(1)
28  if(u <= alpha & StatRest(phi1 = theta[2], phi2 = theta[3])
    == 1){
29    thetaNew <- c(theta)
30  }else{
31    thetaNew <- thetat
32  }
33  rest <- list(theta = thetaNew, Prob = alpha)
34  return(rest)
35 }

```

*R code. AR(2) model: Hamiltonian Monte Carlo
with stationary restrictions*

```

1 # Posterior draws
2 S <- 1000; burnin <- 1000; thin <- 2; tot <- S + burnin
3 thetaPost <- matrix(NA, tot, K)
4 ProbAccept <- rep(NA, tot)
5 # theta0 <- theta0
6 theta0 <- c(mean(y), 0, 0, exp(var(y)))
7 M <- solve(VarPost); epsilon0 <- 0.4
8 pb <- winProgressBar(title = "progress bar", min = 0, max =
9   tot, width = 300)
9 for(s in 1:tot){
10   epsilon <- runif(1, 0, 2*epsilon0)
11   L <- ceiling(1/epsilon)
12   HMCs <- HMC(theta = theta0, y, epsilon, M)
13   theta0 <- HMCs$theta
14   thetaPost[s,] <- HMCs$theta
15   ProbAccept[s] <- HMCs$Prob
16   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
17     "% done"))
17 }
18 close(pb)
19 keep <- seq((burnin+1), tot, thin)
20 thetaF <- coda::mcmc(thetaPost[keep,])
21 summary(thetaF)
22 plot(thetaF)
23 summary(exp(thetaF[,K]))
24 plot(exp(thetaF[,K]))
25 ProbAcceptF <- coda::mcmc(ProbAccept[keep])
26 summary(ProbAcceptF)

```

7. Stochastic volatility model

- Program a sequential importance sampling (SIS) from scratch in the vanilla stochastic volatility model setting $\mu = -10$, $\phi = 0.95$, $\sigma = 0.3$ and $T = 250$. Check what happen with its performance.
- Modify the sequential Monte Carlo (SMC) to perform multinomial resampling when the effective sample size is lower than 50% the number of particles.

Answer

We observe that, initially, sequential importance sampling performs relatively well. However, particle degeneracy occurs around ($t = 50$), causing the algorithm's performance to deteriorate rapidly (see Figure 8.3). We

can see in Figure 8.4 how the effective sample size (ESS) of the particles decreases rapidly.

R code. Stochastic volatility model: Sequential importance sampling

```

1 rm(list = ls()); set.seed(010101)
2 T <- 250; K <- 2; mu <- -10; phi <- 0.95; sigma <- 0.3
3 h <- numeric(T); y <- numeric(T)
4 h[1] <- rnorm(1, mu, sigma / sqrt(1 - phi^2))
5 y[1] <- rnorm(1, 0, exp(h[1] / 2))
6 for (t in 2:T) {
7   h[t] <- mu + phi*(h[t-1]-mu) + rnorm(1, 0, sigma)
8   y[t] <- rnorm(1, 0, sd = exp(0.5*h[t]))
9 }
10 N <- 10000
11 log_Weights <- matrix(NA, N, T) # Log weights
12 Weights <- matrix(NA, N, T) # Weights
13 WeightsST <- matrix(NA, N, T) # Normalized weights
14 particles <- matrix(NA, N, T) # Particles
15 logalphas <- matrix(NA, N, T) # Incremental importance
    weights
16 ESS <- rep(NA, T) # Effective sample size
17 particles[, 1] <- rnorm(N, mu, sigma / sqrt(1 - phi^2))
18 log_Weights[, 1] <- dnorm(y[1], 0, sd = exp(0.5*particles
    [,1]), log = TRUE)
19 Weights[, 1] <- exp(log_Weights[, 1])
20 WeightsST[, 1] <- Weights[, 1] / sum(Weights[, 1])
21 ESS[1] <- (sum(WeightsST[, 1]^2))^-1
22 for (t in 2:T) {
23   particles[, t] <- rnorm(N, mu + phi*(particles[, t - 1] -
    mu), sigma) # Sample from proposal
24   logalphas[, t] <- dnorm(y[t], 0, sd = exp(0.5*particles[, t]
    ), log = TRUE)
25   log_Weights[, t] <- log_Weights[, t - 1] + logalphas[, t]
26   Weights[, t] <- exp(log_Weights[, t])
27   WeightsST[, t] <- Weights[, t] / sum(Weights[, t])
28   ESS[t] <- (sum(WeightsST[, t]^2))^-1
29 }
30 FilterDist <- colSums(particles * WeightsST)
31 SDFilterDist <- (colSums(particles^2 * WeightsST) -
    FilterDist^2)^0.5
32 MargLik <- colMeans(Weights)
33 library(dplyr); library(ggplot2); require(latex2exp)
34 ggplot2::theme_set(theme_bw())
35 df <- tibble(t = seq(1, T), mean = FilterDist, lower =
    FilterDist - 1.96*SDFilterDist, upper = FilterDist +
    1.96*SDFilterDist, x_true = h)
36 plot_filtering_estimates <- function(df) {
37   p <- ggplot(data = df, aes(x = t)) + geom_ribbon(aes(ymin
    = lower, ymax = upper), alpha = 1, fill = "lightblue") +
    geom_line(aes(y = x_true), colour = "black", alpha = 1,
    linewidth = 0.5) + geom_line(aes(y = mean), colour = "
    blue", linewidth = 0.5) +
38   ylab(TeX("$h_{t}$")) + xlab("Time")
39   print(p)
40 }
41 plot_filtering_estimates(df)
42 plot(ESS, type = "l", ylab = "Effective sample size", xlab =
    "Time")

```

**FIGURE 8.3**

Stochastic volatility model: Sequential importance sampling (SIS).

**FIGURE 8.4**

Stochastic volatility model: Effective sample size (ESS) of the particles.

This code shows how to program the SMC algorithm performing multinomial resampling when the effective sample size is lower than 50% the initial number of particles. It seems that in this example is better to perform re-

sampling every time period as the mean recursion (blue and purple lines) are not good following in state (black line). However, the bands corresponding to plus/minus two standard deviations (light blue shading) encompass the state vector; although, it is too wide.

R code. Stochastic volatility model: Sequential Monte Carlo

```

1 rm(list = ls()); set.seed(010101)
2 T <- 1250; mu <- -10; phi <- 0.95; sigma <- 0.3
3 h <- numeric(T); y <- numeric(T)
4 h[1] <- rnorm(1, mu, sigma / sqrt(1 - phi^2))
5 y[1] <- rnorm(1, 0, exp(h[1] / 2))
6 for (t in 2:T) {
7   h[t] <- mu + phi*(h[t-1]-mu) + rnorm(1, 0, sigma)
8   y[t] <- rnorm(1, 0, sd = exp(0.5*h[t]))
9 }
10 N <- 10000
11 log_Weights <- matrix(NA, N, T) # Log weights
12 Weights <- matrix(NA, N, T) # Weights
13 WeightsST <- matrix(NA, N, T) # Normalized weights
14 WeightsSTT <- matrix(1/N, N, T) # Normalized weights bar
15 particles <- matrix(NA, N, T) # Particles
16 particlesT <- matrix(NA, N, T) # Particles bar
17 logalphas <- matrix(NA, N, T) # Incremental import. weig.
18 ESS <- rep(NA, T) # Effective sample size
19 cutoff <- 0.5
20 particles[, 1] <- rnorm(N, mu, sigma / sqrt(1 - phi^2))
21 log_Weights[, 1] <- dnorm(y[1], 0, sd = exp(0.5*particles
  [,1]), log = TRUE)
22 Weights[, 1] <- exp(log_Weights[, 1])
23 WeightsST[, 1] <- Weights[, 1] / sum(Weights[, 1])
24 ESS[1] <- (sum(WeightsST[, 1]^2))^(-1)
25 ind <- sample(1:N, size = N, replace = TRUE, prob =
  WeightsST[, 1]) # Resample
26 particles[, 1] <- particles[, 1] # Resampled particles
27 particlesT[, 1] <- particles[ind, 1] # Resampled particles
28 WeightsST[, 1] <- rep(1/N, N) # Resampled weights
29 pb <- winProgressBar(title = "progress bar", min = 0, max =
  T, width = 300)
30 for (t in 2:T) {
31   particles[, t] <- rnorm(N, mu + phi*(particles[, t - 1] -
    mu), sigma) # Sample from proposal
32   logalphas[, t] <- dnorm(y[t], 0, sd = exp(0.5*particles[, t
    ]), log = TRUE)
33   Weights[, t] <- exp(logalphas[, t])
34   WeightsST[, t] <- Weights[, t] / sum(Weights[, t])
35   ESS[t] <- (sum(WeightsST[, t]^2))^(-1)
36   particlesT[, t] <- particles[, t]
37   if(ESS[t] < N*cutoff){
38     ind <- sample(1:N, size = N, replace = TRUE, prob =
      WeightsST[, t])
39     particles[, 1:t] <- particles[ind, 1:t]
40     WeightsST[, t] <- 1/N
41   }else{if(t == T & ESS[t] < N*cutoff)
42     ind <- sample(1:N, size = N, replace = TRUE, prob =
      WeightsST[, t])
43     particlesT[, 1:t] <- particles[ind, 1:t]
44   }
45   setWinProgressBar(pb, t, title=paste( round(t/T*100, 0), "
    % done"))
46 }
47 close(pb)

```

R code. Stochastic volatility model: Sequential Monte Carlo

```

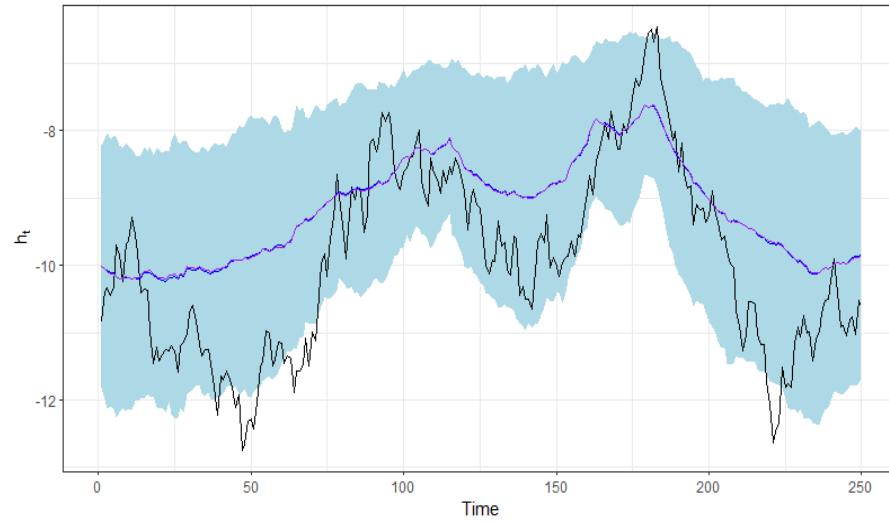
1 FilterDist <- colSums(particles * WeightsST)
2 SDFilterDist <- (colSums(particles^2 * WeightsST) -
  FilterDist^2)^0.5
3 FilterDistT <- colSums(particlesT * WeightsSTT)
4 SDFilterDistT <- (colSums(particlesT^2 * WeightsSTT) -
  FilterDistT^2)^0.5
5 MargLik <- colMeans(Weights)
6 plot(MargLik, type = "l")
7 plot(ESS, type = "l")
8 library(dplyr)
9 library(ggplot2)
10 require(latex2exp)
11 ggplot2::theme_set(theme_bw())
12 Tfig <- 250
13 keepFig <- 1:Tfig
14 df <- tibble(t = keepFig,
15 mean = FilterDist[keepFig],
16 lower = FilterDist[keepFig] - 2*SDFilterDist[keepFig],
17 upper = FilterDist[keepFig] + 2*SDFilterDist[keepFig],
18 meanT = FilterDistT[keepFig],
19 lowerT = FilterDistT[keepFig] - 2*SDFilterDistT[keepFig],
20 upperT = FilterDistT[keepFig] + 2*SDFilterDistT[keepFig],
21 x_true = h[keepFig])
22 plot_filtering_estimates <- function(df) {
23   p <- ggplot(data = df, aes(x = t)) +
24     geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 1,
25     fill = "lightblue") +
26     geom_line(aes(y = x_true), colour = "black", alpha = 1,
27     linewidth = 0.5) +
28     geom_line(aes(y = mean), colour = "blue", linewidth = 0.5)
29     +
30     geom_line(aes(y = meanT), colour = "purple", linewidth =
31     0.5) +
32     ylab(TeX("$h_{t}$")) + xlab("Time")
33   print(p)
34 }
35 plot_filtering_estimates(df)

```

8. Estimate the vanilla stochastic volatility model using the dataset *17ExchangeRate.csv* provided by [25] of the exchange rate log daily returns from USD/EUR, USD/GBP and GBP/EUR one year before and after the WHO declared the COVID-19 pandemic on 11 March 2020.

Answer

The following code shows the results of modeling the exchange rate log

**FIGURE 8.5**

Stochastic volatility model: Sequential Monte Carlo (SMC).

daily returns from USD/EUR using a stochastic volatility model. Similar code can be used to estimate the other two models.

R code. Stochastic volatility model: Exchange rate log daily returns from USD/EUR

```

1 rm(list = ls()); set.seed(010101)
2 DataExcRate <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/17ExcRate.csv",
  sep = ",", header = TRUE, quote = "")
3 attach(DataExcRate)
4 MCMC <- 10000; burnin <- 10000; thin <- 5
5 y <- USDEUR - mean(USDEUR)
6 plot(y, type = "l")
7 res <- stochvol::svsample(y, draws = MCMC, burnin = burnin,
  thin = thin, priormu = c(0, 100), priorsigma = c(1),
  priorphi = c(5, 1.5), priorbeta = c(0, 10000))
8 summary(res[["para"]][[1]][, -c(4,5)])
9 Iterations = 10005:20000
10 Thinning interval = 5
11 Number of chains = 1
12 Sample size per chain = 2000
13 1. Empirical mean and standard deviation for each variable,
14 plus standard error of the mean:
15 Mean      SD Naive SE Time-series SE
16 mu      -11.2886 0.28916 0.0064657      0.006466
17 phi       0.9618 0.02202 0.0004923      0.001421
18 sigma    0.1664 0.04501 0.0010064      0.003722
19 2. Quantiles for each variable:
20      2.5%      25%      50%      75%      97.5%
21 mu      -11.81067 -11.4287 -11.2902 -11.1448 -10.7699
22 phi       0.90719  0.9512  0.9657  0.9774  0.9913
23 sigma    0.09615  0.1327  0.1607  0.1926  0.2666
24 plot(res)
25 ht <- res[["latent"]][[1]]
26 library(dplyr)
27 library(ggplot2)
28 require(latex2exp)
29 ggplot2::theme_set(theme_bw())
30 x_means <- colMeans(ht)
31 x_quantiles <- apply(ht, 2, function(x) quantile(x, probs =
  c(0.025, 0.975)))
32 df <- tibble(t = 1:length(y),
33 mean = x_means,
34 lower = x_quantiles[1, ],
35 upper = x_quantiles[2, ])
36 plot_filtering_estimates <- function(df) {
37   p <- ggplot(data = df, aes(x = t)) +
38     geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 1,
39     fill = "lightblue") +
40     geom_line(aes(y = mean), colour = "blue", linewidth = 0.5)
41   +
42   ylab(TeX("$h_{t}$")) + xlab("Time")
43   print(p)
44 }
45 plot_filtering_estimates(df)

```

**FIGURE 8.6**

Stochastic volatility model: Exchange rate log daily returns from USD/EUR.

9. Simulate the VAR(1) process

$$\begin{bmatrix} y_{1t} \\ y_{2t} \\ y_{3t} \end{bmatrix} = \begin{bmatrix} 2.8 \\ 2.2 \\ 1.3 \end{bmatrix} + \begin{bmatrix} 0.5 & 0 & 0 \\ 0.1 & 0.1 & 0.3 \\ 0 & 0.2 & 0.3 \end{bmatrix} \begin{bmatrix} y_{1t-1} \\ y_{2t-1} \\ y_{3t-1} \end{bmatrix} + \begin{bmatrix} \mu_{1t} \\ \mu_{2t} \\ \mu_{3t} \end{bmatrix},$$

$$\text{where } \Sigma = \begin{bmatrix} 2.25 & 0 & 0 \\ 0 & 1 & 0.5 \\ 0 & 0.5 & 0.74 \end{bmatrix}.$$

- Use vague independent priors setting $\beta_0 = \mathbf{0}$, $B_0 = 100I$, $V_0 = 5I$ and $\alpha_0 = 3$, and estimate a VAR(1) model using the *rsurGibbs* function from the package *bayesm*. Then, program from scratch algorithms to perform inference of the *forecast error* and *ortogonalized* impulse response functions, and compare with the population impulse response functions, that is, using the population parameters.
- Using the previous setting perform inference of the *forecast error* and the *ortogonalized* impulse responses using the package *bvartools*.

Answer

Using the recursion $\Phi_s = \sum_{l=1}^s \Phi_{s-l} A_l$, $A_l = \mathbf{0}$, $l > p$ and $s = 1, 2, \dots$, we get $\Phi_s = A_1^s$. In addition, we know that $\Theta_s = \Phi_s P$. Then, we can get these impulse response functions.

The following code shows how to perform from scratch the impulse response

functions. Figure 8.7 shows the *forecast error impulse response* of y_{2t} to shocks in μ_{3t} . We see that the 95% (blue shadow) and 90% (light blue shadow) credible intervals of the impulse response functions embrace the true impulse response (black line); although the mean impulse response (blue line) overestimates the true impulse. In addition, we can see that the results from the *bvartools* package have the same patterns compared to the ones that we get programming the algorithm from scratch. Remember that the *bvartools* package uses the inverse Wishart distribution as prior for Σ , where the hyperparameters are the degrees of freedom of the error term, and the prior error variance of endogenous variables.

R code. Vector autoregressive model: Simulation

```

1 rm(list = ls()); set.seed(010101)
2 T <- 300; M <- 3
3 SIGMA <- matrix(c(2.25, 0, 0, 0, 1, 0.5, 0, 0.5, 0.74), M, M
4 )
5 U <- MASS::mvrnorm(T, rep(0, M), SIGMA)
6 A <- matrix(c(0.5, 0.1, 0, 0, 0.1, 0.2, 0, 0.3, 0.3), M, M )
7 v <- c(1.4, 1.9, 1.1); Y <- matrix(NA, T, M)
8 Y[1, ] <- solve(diag(M)-A)%%v + U[1,]
9 for(t in 2:T){
10   Y[t, ] <- v + A%%Y[t-1,] + U[t,]
11 }
12 plot(Y[,1], type = "l"); plot(Y[,2], type = "l"); plot(Y
13   [,3], type = "l")
14 y1 <- Y[-1,1]; y2 <- Y[-1,2]; y3 <- Y[-1,3]
15 X1 <- cbind(1, lag(Y)); X1 <- X1[-1,]
16 X2 <- cbind(1, lag(Y)); X2 <- X2[-1,]
17 X3 <- cbind(1, lag(Y)); X3 <- X3[-1,]
18 regdata <- NULL
19 regdata[[1]] <- list(y = y1, X = X1); regdata[[2]] <- list(y
20   = y2, X = X2); regdata[[3]] <- list(y = y3, X = X3)
21 M <- length(regdata); K1 <- dim(X1)[2]; K2 <- dim(X2)[2]; K3
22   <- dim(X3)[2]
23 K <- K1 + K2 + K3
24 # Hyperparameters
25 b0 <- rep(0, K); c0 <- 100
26 B0 <- c0*diag(K); V <- 5*diag(M); a0 <- M
27 Prior <- list(betabar = b0, A = solve(B0), nu = a0, V = V)
28 #Posterior draws
29 MCMC <- 10000; thin <- 5; burnin <- 1000; tot <- MCMC +
30   burnin
31 Mcmc <- list(R = tot, keep = thin)
32 PosteriorDraws <- bayesm::rsurGibbs(Data = list(regdata =
33   regdata), Mcmc = Mcmc, Prior = Prior)
34 keep <- seq(round(burnin/thin)+1, round(tot/thin))
35 Bs <- PosteriorDraws[["betadraw"]][keep,]
36 SIGMAs <- PosteriorDraws[["Sigmadraw"]][keep,]
37 S <- dim(Bs)[1]
38 As <- array(NA, c(M, M, S))
39 for(s in 1:S){
40   As[,s] <- matrix(Bs[s, -c(1, 5, 9)], M, M, byrow = TRUE)
41 }
42 # Impulse response functions
43 H <- 10; Ptrue <- t(chol(SIGMA))
44 Phistrue <- array(NA, c(M, M, H))
45 Phistrue[,1] <- diag(M); PhistrueAccum <- Phistrue
46 PhistrueAccum[,1] <- diag(M)
47 Thetatrue <- Phistrue; Thetatrue[,1] <- Ptrue
48 ThetatrueAccum <- Thetatrue; ThetatrueAccum[,1] <-
49   Ptrue
50 for(h in 2:H){
51   Phistrue[,h] <- Phistrue[,h-1]%%A
52   PhistrueAccum[,h] <- PhistrueAccum[,h-1] + Phistrue[,h]
53   Thetatrue[,h] <- Phistrue[,h]%%Ptrue
54   PhistrueAccum[,h] <- ThetatrueAccum[,h-1] + Thetatrue
55     [,h]
56 }
57 P <- array(NA, c(M, M, S))

```


R code. Vector autoregressive model: Simulation

```

1 for(s in 1:S){
2   P[,s] <- t(chol(matrix(SIGMAs[s,], M, M)))
3 }
4 Phis <- list(); PhisAcum <- list()
5 Thetas <- list(); ThetasAcum <- list()
6 for(h in 0:H){
7   if(h == 0){
8     Phis[[h+1]] <- array(diag(M), c(M,M,S))
9     Thetas <- Phis
10    for(s in 1:S){
11      Thetas[[h+1]][,s] <- Phis[[h+1]][,s]*%P[,s]
12    }
13    PhisAcum[[h+1]] <- Phis[[h+1]]
14    ThetasAcum[[h+1]] <- Thetas[[h+1]]
15  }else{
16    Phis[[h+1]] <- array(diag(M), c(M,M,S))
17    Thetas[[h+1]] <- Phis[[h+1]]
18    for(s in 1:S){
19      Phis[[h+1]][,s] <- Phis[[h]][,s]*%As[,s]
20      Thetas[[h+1]][,s] <- Phis[[h+1]][,s]*%P[,s]
21    }
22    PhisAcum[[h+1]] <- PhisAcum[[h]] + Phis[[h+1]]
23    ThetasAcum[[h+1]] <- ThetasAcum[[h]] + Thetas[[h+1]]
24  }
25 }
26 library(dplyr); library(ggplot2); require(latex2exp)
27 ggplot2::theme_set(theme_bw())
28 plot_filtering_estimates <- function(df) {
29   p <- ggplot(data = df, aes(x = t)) +
30     geom_ribbon(aes(ymin = lower1, ymax = upper1), alpha = 1,
31               fill = "blue") +
32     geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 1,
33               fill = "lightblue") +
34     geom_line(aes(y = x_true), colour = "black", alpha = 1,
35              linewidth = 0.5) +
36     geom_line(aes(y = mean), colour = "blue", linewidth = 0.5)
37   +
38   ylab("Impulse response") + xlab("Time") + xlim(0,H-1)
39   print(p)
40 }

```

R code. Vector autoregressive model: Simulation

```

1 IR <- function(m, j, Accumulated = "FALSE", Type = "Ordinary
  ") {
2   if (Type == "Cholesky") {
3     IRtrue <- Thetastrue[m,j,]
4     if (Accumulated == FALSE) {
5       RES <- Thetas; IRtrue <- IRtrue
6     } else {
7       RES <- ThetasAcum; IRtrue <- cumsum(IRtrue)
8     }
9     Mean <- sapply(1:H, function(h){mean(RES[[h]][m,j,])})
10    LimInf1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
11    ,], 0.025)})
12    LimSup1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
13    ,], 0.975)})
14    LimInf <- sapply(1:H, function(h){quantile(RES[[h]][m,j
15    ,], 0.05)})
16    LimSup <- sapply(1:H, function(h){quantile(RES[[h]][m,j
17    ,], 0.95)})
18  } else {
19    IRtrue <- Phistrue[m,j,]
20    if (Accumulated == FALSE) {
21      RES <- Phis; IRtrue <- IRtrue
22    } else {
23      RES <- PhisAcum; IRtrue <- cumsum(IRtrue)
24    }
25    Mean <- sapply(1:H, function(h){mean(RES[[h]][m,j,])})
26    LimInf1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
27    ,], 0.025)})
28    LimSup1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
29    ,], 0.975)})
30    LimInf <- sapply(1:H, function(h){quantile(RES[[h]][m,j
31    ,], 0.05)})
32    LimSup <- sapply(1:H, function(h){quantile(RES[[h]][m,j
33    ,], 0.95)})
34  }
35  df <- tibble(t = 0:(H-1), mean = Mean, lower1 = LimInf1,
36    upper1 = LimSup1, lower = LimInf, upper = LimSup, x_true
37    = IRtrue)
38  Fig <- plot_filtering_estimates(df)
39  return(Fig)
40 }
41 m <- 2; j <- 3
42 IR(m,j, Accumulated = "FALSE", Type = "Cholesky")
43 Ynew <- ts(Y)
44 model <- bvartools::gen_var(Ynew, p = 1, deterministic = "
45   const", iterations = MCMC, burnin = burnin) # Model
46 model <- bvartools::add_priors(model, coef = list(v_i = b0
47   [1], v_i_det = b0[1]), sigma = list(df = a0, scale = V
48   [1,1]/a0)) # Prior
49 object <- bvartools::draw_posterior(model) # Pposterior
50 ir <- bvartools::irf.bvar(object, impulse = "Series 2",
51   response = "Series 3") # Calculate IR
52 plot(ir) # Plot IR

```

**FIGURE 8.7**

Forecast error impulse response: Response in y_{2t} to shock in μ_{3t} .



9

Longitudinal/Panel data models

Solutions of Exercises

1. Show that the posterior distribution of $\beta|\sigma^2, \mathbf{D}$ is $N(\beta_n, \mathbf{B}_n)$, where $\mathbf{B}_n = (\mathbf{B}_0^{-1} + \sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{X}_i)^{-1}$ and $\beta_n = \mathbf{B}_n(\mathbf{B}_0^{-1}\beta_0 + \sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{y}_i)$.

Answer

$$\begin{aligned}
 \pi(\beta|\sigma^2, \mathbf{D}, \mathbf{y}, \mathbf{X}, \mathbf{W}) &\propto \exp \left\{ -\frac{1}{2} \sum_{i=1}^N (\mathbf{y}_i - \mathbf{X}_i \beta)^\top \mathbf{V}_i^{-1} (\mathbf{y}_i - \mathbf{X}_i \beta) \right\} \\
 &\quad \times \exp \left\{ -\frac{1}{2} (\beta - \beta_0)^\top \mathbf{B}_0^{-1} (\beta - \beta_0) \right\} \\
 &\propto \exp \left\{ -\frac{1}{2} \left(-2\beta^\top \left(\sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{y}_i + \mathbf{B}_0^{-1} \beta_0 \right) + \beta^\top \left(\sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{X}_i + \mathbf{B}_0^{-1} \right) \beta \right) \right\} \\
 &= \exp \left\{ -\frac{1}{2} (-2\beta^\top \mathbf{B}_n^{-1} \mathbf{B}_n \left(\sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{y}_i + \mathbf{B}_0^{-1} \beta_0 \right) + \beta^\top \mathbf{B}_n^{-1} \beta) \right\} \\
 &= \exp \left\{ -\frac{1}{2} (-2\beta^\top \mathbf{B}_n^{-1} \beta_n + \beta^\top \mathbf{B}_n^{-1} \beta) \right\}.
 \end{aligned}$$

We can complete the square in this expression by adding and subtracting $\beta_n^\top \mathbf{B}_n^{-1} \beta_n$. Thus,

$$\begin{aligned}
 \pi(\beta|\sigma^2, \mathbf{D}, \mathbf{y}, \mathbf{X}, \mathbf{W}) &\propto \exp \left\{ -\frac{1}{2} (-2\beta^\top \mathbf{B}_n^{-1} \beta_n + \beta^\top \mathbf{B}_n^{-1} \beta + \beta_n^\top \mathbf{B}_n^{-1} \beta_n - \beta_n^\top \mathbf{B}_n^{-1} \beta_n) \right\} \\
 &\propto \exp \left\{ -\frac{1}{2} (\beta - \beta_n)^\top \mathbf{B}_n^{-1} (\beta - \beta_n) \right\}.
 \end{aligned}$$

This is the kernel of a multivariate random variable with mean β_n and variance matrix \mathbf{B}_n .

2. **The relation between productivity and public investment example continues**

- Perform inference of this example using our GUI.

- Program from scratch a Gibbs sampling algorithm to perform this application. Set $\beta_0 = \mathbf{0}_5$, $B_0 = I_5$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 5$ and $D_0 = I_1$.
- Perform inference in this example assuming that $\mu_{it}|\tau_{it} \sim N(0, \sigma^2/\tau_{it})$ and $\tau_{it} \sim G(v/2, v/2)$ setting $v = 5$.

Answer

R code. The relationship between productivity and public investment, programming from scratch the Gibbs sampler

```

1 rm(list = ls())
2 set.seed(12345)
3 DataGSP <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/8PublicCap.
  csv", sep = ",", header = TRUE, quote = "")
4 attach(DataGSP)
5 N <- length(unique(id))
6 y <- log(gsp)
7 NT <- length(y)
8 X <- cbind(1, log(pcap), log(pc), log(emp), unemp)
9 K1 <- dim(X)[2]
10 W <- matrix(rep(1, NT), NT, 1)
11 K2 <- dim(W)[2]
12 mcmc <- 10000; burnin <- 5000; thin <- 1; tot <- mcmc +
  burnin
13 b0 <- rep(0, K1); B0 <- diag(K1); B0i <- solve(B0)
14 r0 <- 5; R0 <- diag(K2); a0 <- 0.001; d0 <- 0.001
15 PostBeta <- function(sig2, D){
16   XVX <- matrix(0, K1, K1)
17   XVy <- matrix(0, K1, 1)
18   for(i in 1:N){
19     ids <- which(id == i)
20     Ti <- length(ids)
21     Wi <- W[ids, ]
22     Vi <- sig2*diag(Ti) + Wi*%D*%t(Wi)
23     ViInv <- solve(Vi)
24     Xi <- X[ids, ]
25     XVXi <- t(Xi)*%ViInv*%Xi
26     XVX <- XVX + XVXi
27     yi <- y[ids]
28     XVyi <- t(Xi)*%ViInv*%yi
29     XVy <- XVy + XVyi
30   }
31   Bn <- solve(B0i + XVX)
32   bn <- Bn*%(B0i*%b0 + XVy)
33   Beta <- MASS::mvrnorm(1, bn, Bn)
34   return(Beta)
35 }

```

R code. The relationship between productivity and public investment, programming from scratch the Gibbs sampler

```

1 Postb <- function(Beta, sig2, D){
2   Di <- solve(D)
3   bis <- matrix(0, N, K2)
4   for(i in 1:N){
5     ids <- which(id == i)
6     Wi <- W[ids, ]
7     Xi <- X[ids, ]
8     yi <- y[ids]
9     Wtei <- sig2^(-1)*t(Wi)%*(yi - Xi%*Beta)
10    Bni <- solve(sig2^(-1)*t(Wi)%*Wi + Di)
11    bni <- Bni%*Wtei
12    bi <- MASS::mvrnorm(1, bni, Bni)
13    bis[i, ] <- bi
14  }
15  return(as.matrix(bis))
16 }
17 PostSig2 <- function(Beta, bs){
18   an <- a0 + 0.5*NT
19   ete <- 0
20   for(i in 1:N){
21     ids <- which(id == i)
22     Xi <- X[ids, ]
23     yi <- y[ids]
24     Wi <- W[ids, ]
25     ei <- yi - Xi%*Beta - Wi*bs[i, ]
26     etei <- t(ei)%*ei
27     ete <- ete + etei
28   }
29   dn <- d0 + 0.5*ete
30   sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
31   return(sig2)
32 }
33 PostD <- function(bs){
34   rn <- r0 + N
35   btb <- matrix(0, K2, K2)
36   for(i in 1:N){
37     bsi <- bs[i, ]
38     btbi <- bsi%*t(bsi)
39     btb <- btb + btbi
40   }
41   Rn <- d0*R0 + btb
42   Sigma <- MCMCpack::riwish(v = rn, S = Rn)
43   return(Sigma)
44 }

```


R code. The relationship between productivity and public investment, programming from scratch the Gibbs sampler

```

1 PostBetas <- matrix(0, tot, K1); PostDs <- matrix(0, tot, K2
  *(K2+1)/2)
2 PostSig2s <- rep(0, tot); Postbs <- array(0, c(N, K2, tot))
3 RegLS <- lm(y ~ X - 1); SumLS <- summary(RegLS)
4 Beta <- SumLS[["coefficients"]][,1]
5 sig2 <- SumLS[["sigma"]]^2; D <- diag(K2)
6 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
7 for(s in 1:tot){
8   bs <- Postb(Beta = Beta, sig2 = sig2, D = D)
9   D <- PostD(bs = bs)
10  Beta <- PostBeta(sig2 = sig2, D = D)
11  # Beta <- PostBetaNew(sig2 = sig2, D = D)
12  sig2 <- PostSig2(Beta = Beta, bs = bs)
13  PostBetas[s,] <- Beta
14  PostDs[s,] <- matrixcalc::vech(D)
15  PostSig2s[s] <- sig2
16  Postbs[, , s] <- bs
17  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
18 }
19 close(pb)
20 keep <- seq((burnin+1), tot, thin)
21 Bs <- PostBetas[keep,]; Ds <- PostDs[keep,]
22 bs <- Postbs[, , keep]; sig2s <- PostSig2s[keep]
23 summary(coda::mcmc(Bs))
24 Quantiles for each variable:
25      2.5%      25%      50%      75%      97.5%
26 var1  1.727227  1.934457  2.037411  2.138829  2.325961
27 var2 -0.033664  0.001015  0.018974  0.037977  0.076626
28 var3  0.274521  0.303619  0.318302  0.332881  0.363323
29 var4  0.652937  0.692479  0.712605  0.730885  0.768415
30 var5 -0.008724 -0.007265 -0.006548 -0.005844 -0.004508
31 summary(coda::mcmc(Ds))
32 summary(coda::mcmc(sig2s))
33 # Convergence diagnostics
34 coda::geweke.diag(Bs)
35 coda::raftery.diag(Bs,q=0.5,r=0.05,s = 0.95)
36 coda::heidel.diag(Bs)

```

The likelihood function in the case with heteroskedasticity is proportional

to

$$p(\boldsymbol{\beta}, \mathbf{b}, \sigma^2, \boldsymbol{\tau} | \mathbf{y}, \mathbf{X}, \mathbf{W}) \propto \prod_{i=1}^N |\sigma^2 \boldsymbol{\Psi}_i|^{-1/2} \\ \times \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y}_i - \mathbf{X}_i \boldsymbol{\beta} - \mathbf{W}_i \mathbf{b}_i)^\top \boldsymbol{\Psi}_i^{-1} (\mathbf{y}_i - \mathbf{X}_i \boldsymbol{\beta} - \mathbf{W}_i \mathbf{b}_i) \right\},$$

where $\mathbf{b} = [\mathbf{b}_1^\top, \mathbf{b}_2^\top, \dots, \mathbf{b}_N^\top]^\top$, $\boldsymbol{\tau} = [\tau_{it}]^\top$ and $\boldsymbol{\Psi}_i = \text{diag} \{ \tau_{it}^{-1} \}$.

Following the same procedure as in Section 9.1 of the book, and Exercise 1 of this chapter, we have that

$$\boldsymbol{\beta} | \sigma^2, \boldsymbol{\tau}, \mathbf{D}, \mathbf{y}, \mathbf{X}, \mathbf{W} \sim N(\boldsymbol{\beta}_n, \mathbf{B}_n),$$

where $\mathbf{B}_n = (\mathbf{B}_0^{-1} + \sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{X}_i)^{-1}$, $\boldsymbol{\beta}_n = \mathbf{B}_n (\mathbf{B}_0^{-1} \boldsymbol{\beta}_0 + \sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{y}_i)$ and $\mathbf{V}_i = \sigma^2 \boldsymbol{\Psi}_i + \sigma_b^2 \mathbf{i}_{T_i} \mathbf{i}_{T_i}^\top$.

$$\mathbf{b}_i | \boldsymbol{\beta}, \sigma^2, \boldsymbol{\tau}, \mathbf{D}, \mathbf{y}, \mathbf{X}, \mathbf{W} \sim N(\mathbf{b}_{ni}, \mathbf{B}_{ni}),$$

where $\mathbf{B}_{ni} = (\sigma^{-2} \mathbf{W}_i^\top \boldsymbol{\Psi}_i^{-1} \mathbf{W}_i + \mathbf{D}^{-1})^{-1}$ and $\mathbf{b}_{ni} = \mathbf{B}_{ni} (\sigma^{-2} \mathbf{W}_i^\top \boldsymbol{\Psi}_i^{-1} (\mathbf{y}_i - \mathbf{X}_i \boldsymbol{\beta}))$.

$$\sigma^2 | \boldsymbol{\beta}, \mathbf{b}, \boldsymbol{\tau}, \mathbf{y}, \mathbf{X}, \mathbf{W} \sim IG(\alpha_n, \delta_n),$$

where $\alpha_n = \alpha_0 + \frac{1}{2} \sum_{i=1}^N T_i$ and $\delta_n = \delta_0 + \frac{1}{2} \sum_{i=1}^N (\mathbf{y}_i - \mathbf{X}_i \boldsymbol{\beta} - \mathbf{W}_i \mathbf{b}_i)^\top \boldsymbol{\Psi}_i^{-1} (\mathbf{y}_i - \mathbf{X}_i \boldsymbol{\beta} - \mathbf{W}_i \mathbf{b}_i)$.

$$\mathbf{D} | \mathbf{b} \sim IW(d_n, \mathbf{D}_n),$$

where $d_n = d_0 + N$ and $\mathbf{D}_n = d_0 \mathbf{D}_0 + \sum_{i=1}^N \mathbf{b}_i \mathbf{b}_i^\top$. And

$$\tau_{it} | \sigma^2, \boldsymbol{\beta}, \mathbf{b}, \mathbf{y}, \mathbf{X}, \mathbf{W} \sim G(v_{1n}/2, v_{2ni}/2),$$

where $v_{1n} = v + 1$ and $v_{2ni} = v + \sigma^{-2} (\mathbf{y}_{it} - \mathbf{x}_{it}^\top \boldsymbol{\beta} - \mathbf{w}_{it}^\top \mathbf{b}_i)^2$.

The following code shows to implement this for the productivity application. The results of the *fixed effects* are very similar compared to the results without taken into account heteroskedasticity.

R code. The relationship between productivity and public investment, programming from scratch the Gibbs sampler with heteroskedasticity

```

1 rm(list = ls())
2 set.seed(12345)
3 DataGSP <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/8PublicCap.
  csv", sep = ",", header = TRUE, quote = "")
4 attach(DataGSP)
5 N <- length(unique(id))
6 y <- log(gsp)
7 NT <- length(y)
8 X <- cbind(1, log(pcap), log(pc), log(emp), unemp)
9 K1 <- dim(X)[2]
10 W <- matrix(rep(1, NT), NT, 1)
11 K2 <- dim(W)[2]
12 mcmc <- 10000; burnin <- 5000; thin <- 1; tot <- mcmc +
  burnin
13 b0 <- rep(0, K1); B0 <- diag(K1); B0i <- solve(B0)
14 r0 <- 5; R0 <- diag(K2); a0 <- 0.001; d0 <- 0.001; v <- 5
15 # Gibbs by hand
16 PostBeta <- function(sig2, D, tau){
17   XVX <- matrix(0, K1, K1)
18   XVy <- matrix(0, K1, 1)
19   for(i in 1:N){
20     ids <- which(id == i)
21     Ti <- length(ids)
22     Wi <- W[ids, ]
23     tau_i <- tau[ids]
24     Vi <- sig2*solve(diag(1/tau_i)) + Wi%*%D%*%t(Wi)
25     ViInv <- solve(Vi)
26     Xi <- X[ids, ]
27     XVXi <- t(Xi)%*%ViInv%*%Xi
28     XVX <- XVX + XVXi
29     yi <- y[ids]
30     XVyi <- t(Xi)%*%ViInv%*%yi
31     XVy <- XVy + XVyi
32   }
33   Bn <- solve(B0i + XVX)
34   bn <- Bn%*%(B0i%*%b0 + XVy)
35   Beta <- MASS::mvrnorm(1, bn, Bn)
36   return(Beta)
37 }

```

R code. The relationship between productivity and public investment, programming from scratch the Gibbs sampler with heteroskedasticity

```

1 Postb <- function(Beta, sig2, D, tau){
2   Di <- solve(D);   bis <- matrix(0, N, K2)
3   for(i in 1:N){
4     ids <- which(id == i)
5     Wi <- W[ids, ]; Xi <- X[ids, ]
6     yi <- y[ids]; tau_i <- tau[ids]
7     Tau_i <- solve(diag(1/tau_i))
8     Wtei <- sig2^(-1)*t(Wi)%*%Tau_i%*(yi - Xi%*Beta)
9     Bni <- solve(sig2^(-1)*t(Wi)%*%Tau_i%*Wi + Di)
10    bni <- Bni%*%Wtei
11    bi <- MASS::mvrnorm(1, bni, Bni)
12    bis[i, ] <- bi
13  }
14  return(bis)
15 }
16 PostSig2 <- function(Beta, bs, tau){
17   an <- a0 + 0.5*NT; ete <- 0
18   for(i in 1:N){
19     ids <- which(id == i)
20     Xi <- X[ids, ]; yi <- y[ids]
21     Wi <- W[ids, ]; tau_i <- tau[ids]
22     Tau_i <- solve(diag(1/tau_i))
23     ei <- yi - Xi%*Beta - Wi*bs[i]
24     etei <- t(ei)%*%Tau_i%*ei
25     ete <- ete + etei
26   }
27   dn <- d0 + 0.5*ete
28   sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
29   return(sig2)
30 }
31 PostD <- function(bs){
32   rn <- r0 + N
33   btb <- matrix(0, K2, K2)
34   for(i in 1:N){
35     bsi <- bs[i, ]
36     btbi <- bsi%*%t(bsi)
37     btb <- btb + btbi
38   }
39   Rn <- d0*R0 + btb
40   Sigma <- MCMCpack::riwish(v = rn, S = Rn)
41   return(Sigma)
42 }
43 PostTau <- function(sig2, Beta, bs){
44   v1n <- v + 1
45   v2n <- NULL
46   for(i in 1:NT){
47     Xi <- X[i, ]; yi <- y[i]
48     Wi <- W[i, ]; bi <- bs[id[i],]
49     v2ni <- v + sig2^(-1)*(yi - Xi%*Beta - Wi%*bi)^2
50     v2n <- c(v2n, v2ni)
51   }
52   tau <- rgamma(NT, shape = rep(v1n/2, NT), rate = v2n/2)
53   return(tau)
54 }

```

R code. The relationship between productivity and public investment, programming from scratch the Gibbs sampler with heteroskedasticity

```

1 PostBetas <- matrix(0, tot, K1); PostDs <- matrix(0, tot, K2
  *(K2+1)/2)
2 PostSig2s <- rep(0, tot); Postbs <- array(0, c(N, K2, tot))
3 PostTaus <- matrix(0, tot, NT); RegLS <- lm(y ~ X - 1)
4 SumLS <- summary(RegLS); Beta <- SumLS[["coefficients"]][,1]
5 sig2 <- SumLS[["sigma"]]^2; D <- diag(K2)
6 tau <- rgamma(NT, shape = v/2, rate = v/2)
7 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
8 for(s in 1:tot){
9   bs <- Postb(Beta = Beta, sig2 = sig2, D = D, tau = tau)
10  D <- PostD(bs = bs)
11  Beta <- PostBeta(sig2 = sig2, D = D, tau = tau)
12  sig2 <- PostSig2(Beta = Beta, bs = bs, tau = tau)
13  tau <- PostTau(sig2 = sig2, Beta = Beta, bs = bs)
14  PostBetas[s,] <- Beta
15  PostDs[s,] <- matrix(calc::vech(D)
16  PostSig2s[s] <- sig2
17  Postbs[, , s] <- bs
18  PostTaus[s,] <- tau
19  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
20 }
21 close(pb)
22 keep <- seq((burnin+1), tot, thin)
23 Bs <- PostBetas[keep,]
24 Ds <- PostDs[keep,]
25 bs <- Postbs[, , keep]
26 sig2s <- PostSig2s[keep]
27 taus <- PostTaus[keep,]
28 summary(coda::mcmc(Bs))
29 Quantiles for each variable:
30      2.5%      25%      50%      75%      97.5%
31 var1  1.61764  1.891242  2.029985  2.165677  2.427349
32 var2 -0.07088 -0.016921  0.013080  0.044681  0.107360
33 var3  0.27259  0.312197  0.333106  0.353678  0.395123
34 var4  0.59507  0.664490  0.699526  0.734612  0.796977
35 var5 -0.01046 -0.008533 -0.007586 -0.006666 -0.004918
36 summary(coda::mcmc(Ds))
37 summary(coda::mcmc(sig2s))

```

3. Simulation exercise of the longitudinal normal model continues

Assume that $y_{it} = \beta_1 x_{it1} + \beta_2 x_{it2} + \beta_3 x_{it3} + \beta_4 z_{i1} + b_i + w_{it1} b_{i1} + \mu_{it}$ where $x_{itk} \sim N(0, 1)$, $k = 1, 2, 3$, $z_{i1} \sim B(0.5)$, $w_{it1} \sim N(0, 1)$, $b_i \sim$

$N(0, 0.7^{1/2})$, $b_{i1} \sim N(0, 0.6^{1/2})$, $\mu_{it} \sim N(0, 0.1^{1/2})$ $\beta = [0.4 \ 0.6 \ -0.6 \ 0.7]^\top$, $i = 1, 2, \dots, 50$, and the sample size is 2000 in an *unbalanced panel structure*. In addition, we assume that \mathbf{b}_i depends on $\mathbf{z}_i = [1 \ z_{i1}]^\top$ such that $\mathbf{b}_i \sim N(\mathbf{Z}_i \boldsymbol{\gamma}, \mathbf{D})$ where $\mathbf{Z}_i = \mathbf{I}_{K_2} \otimes \mathbf{z}_i^\top$, and $\boldsymbol{\gamma} = [1 \ 1 \ 1 \ 1]$. The prior for $\boldsymbol{\gamma}$ is $N(\boldsymbol{\gamma}_0, \boldsymbol{\Gamma}_0)$ where we set $\boldsymbol{\gamma}_0 = \mathbf{0}_4$ and $\boldsymbol{\Gamma}_0 = \mathbf{I}_4$. In addition, Set $\beta_0 = \mathbf{0}_4$, $\mathbf{B}_0 = \mathbf{I}_4$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 2$ and $\mathbf{D}_0 = \mathbf{I}_2$.

- Perform inference in this model without taking into account the dependence between \mathbf{b}_i and z_{i1} , and compare the posterior estimates with the population parameters.
- Perform inference in this model taking into account the dependence between \mathbf{b}_i and z_{i1} , and compare the posterior estimates with the population parameters.

Answer

Following the same procedure as in Section 9.1 of the book, and Exercise 1 of this chapter, we have that

$$\beta | \sigma^2, \gamma, \mathbf{D}, \mathbf{y}, \mathbf{X}, \mathbf{W}, \mathbf{Z} \sim N(\beta_n, \mathbf{B}_n),$$

where $\mathbf{B}_n = (\mathbf{B}_0^{-1} + \sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} \mathbf{X}_i)^{-1}$, $\beta_n = \mathbf{B}_n(\mathbf{B}_0^{-1} \beta_0 + \sum_{i=1}^N \mathbf{X}_i^\top \mathbf{V}_i^{-1} (\mathbf{y}_i - \mathbf{W}_i \mathbf{Z}_i \boldsymbol{\gamma}))$ and $\mathbf{V}_i = \sigma^2 \mathbf{I}_{T_i} + \sigma_b^2 \mathbf{i}_{T_i} \mathbf{i}_{T_i}^\top$.

$$\mathbf{b}_i | \beta, \sigma^2, \gamma, \mathbf{D}, \mathbf{y}, \mathbf{X}, \mathbf{W}, \mathbf{Z} \sim N(\mathbf{b}_{ni}, \mathbf{B}_{ni}),$$

where $\mathbf{B}_{ni} = (\sigma^{-2} \mathbf{W}_i^\top \mathbf{W}_i + \mathbf{D}^{-1})^{-1}$ and $\mathbf{b}_{ni} = \mathbf{B}_{ni}(\sigma^{-2} \mathbf{W}_i^\top (\mathbf{y}_i - \mathbf{X}_i \beta) + \mathbf{D}^{-1} \mathbf{Z}_i \boldsymbol{\gamma})$.

$$\sigma^2 | \beta, \mathbf{b}, \tau, \mathbf{y}, \mathbf{X}, \mathbf{W} \sim IG(\alpha_n, \delta_n),$$

where $\alpha_n = \alpha_0 + \frac{1}{2} \sum_{i=1}^N T_i$ and $\delta_n = \delta_0 + \frac{1}{2} \sum_{i=1}^N (\mathbf{y}_i - \mathbf{X}_i \beta - \mathbf{W}_i \mathbf{b}_i)^\top (\mathbf{y}_i - \mathbf{X}_i \beta - \mathbf{W}_i \mathbf{b}_i)$.

$$\mathbf{D} | \mathbf{b}, \gamma, \mathbf{Z} \sim IW(d_n, \mathbf{D}_n),$$

where $d_n = d_0 + N$ and $\mathbf{D}_n = d_0 \mathbf{D}_0 + \sum_{i=1}^N (\mathbf{b}_i - \mathbf{Z}_i \boldsymbol{\gamma})(\mathbf{b}_i - \mathbf{Z}_i \boldsymbol{\gamma})^\top$. And

$$\boldsymbol{\gamma} | \mathbf{b}, \mathbf{D}, \mathbf{Z} \sim N(\boldsymbol{\gamma}_n, \boldsymbol{\Gamma}_n),$$

where $\boldsymbol{\Gamma}_n = (\sum_{i=1}^N \mathbf{Z}_i^\top \mathbf{D}^{-1} \mathbf{Z}_i + \boldsymbol{\Gamma}_0^{-1})^{-1}$ and $\boldsymbol{\gamma}_n = \boldsymbol{\Gamma}_n(\sum_{i=1}^N \mathbf{Z}_i^\top \mathbf{D}^{-1} \mathbf{b}_i + \boldsymbol{\Gamma}_0^{-1} \boldsymbol{\gamma}_0)$.

The following code shows how to implement this longitudinal normal model where *random effects* are correlated with regressors. We set MCMC iterations, burn-in and thinning parameters equal to 15000, 5000 and 5, respectively. In addition, $\beta_0 = \mathbf{0}_5$, $\mathbf{B}_0 = \mathbf{I}_5$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 2$, $\mathbf{D}_0 = \mathbf{I}_2$, $\boldsymbol{\gamma}_0 = \mathbf{0}_4$ and $\boldsymbol{\Gamma}_0 = \mathbf{I}_4$.

R code. Simulation exercise: Longitudinal normal model with fixed effects correlated to regressors

```

1 rm(list = ls())
2 set.seed(010101)
3 NT <- 2000
4 N <- 50
5 id <- c(1:N, sample(1:N, NT - N, replace=TRUE))
6 table(id)
7 x1 <- rnorm(NT); x2 <- rnorm(NT)
8 x3 <- rnorm(NT); z1 <- rbinom(N, 1, 0.5)
9 zdata <- NULL
10 for(i in 1:NT){
11   zdatai <- z1[id[i]]
12   zdata <- c(zdata, zdatai)
13 }
14 X <- cbind(x1, x2, x3, zdata)
15 K1 <- dim(X)[2]
16 w1 <- rnorm(NT)
17 W <- cbind(1, w1)
18 K2 <- dim(W)[2]
19 B <- c(0.5, 0.4, 0.6, -0.6, 0.7)
20 D <- c(0.7, 0.6)
21 sig2 <- 0.1
22 u <- rnorm(NT, 0, sd = sig2^0.5)
23 Z <- cbind(1, z1)
24 K3 <- dim(Z)[2]
25 G <- rep(1, K3*K2)
26 b <- matrix(0, N, K2)
27 for(i in 1:N){
28   ZGi <- t(kronecker(diag(K2), Z[i, ]))%*%G
29   b[i, ] <- MASS::mvrnorm(1, ZGi, diag(D))
30 }
31 y <- NULL
32 for(i in 1:NT){
33   yi <- X[i,]%*%B + W[i,]%*%b[id[i],] + u[i]
34   y <- c(y, yi)
35 }
36 Data <- as.data.frame(cbind(y, x1, x2, x3, zdata, w1, id))
37 mcmc <- 15000; burnin <- 5000; thin <- 10; tot <- mcmc +
   burnin
38 b0 <- rep(0, K1+1); B0 <- diag(K1+1); B0i <- solve(B0)
39 r0 <- K2; R0 <- diag(K2); a0 <- 0.001; d0 <- 0.001
40 g0 <- rep(0, K2*K3); G0 <- diag(K2*K3); G0i <- solve(G0)
41 Resultshreg <- MCMCpack::MCMChregress(fixed = y~x1 + x2 + x3
   + zdata, random = ~w1, group="id", data = Data, burnin
   = burnin, mcmc = mcmc, thin = thin,
42 mubeta = b0, Vbeta = B0, r = r0, R = R0, nu = a0, delta = d0
   )
43 Betas <- Resultshreg[["mcmc"]][,1:(K1+1)]
44 Sigma2RanEff <- Resultshreg[["mcmc"]][,c(K2*N+K1+2, 2*N+K1
   +1+K2^2)]
45 Sigma2 <- Resultshreg[["mcmc"]][,K2*N+K1+K2^2+2]
46 summary(Betas)
47 summary(Sigma2RanEff)
48 summary(Sigma2)

```

R code. Simulation exercise: Longitudinal normal model with fixed effects correlated to regressors

```

1 PostBeta <- function(sig2, Gamma, D){
2   XVX <- matrix(0, K1, K1)
3   XVy <- matrix(0, K1, 1)
4   for(i in 1:N){
5     ids <- which(id == i)
6     Ti <- length(ids)
7     Wi <- W[ids, ]
8     Vi <- sig2*diag(Ti) + Wi%*%D%*%t(Wi)
9     ViInv <- solve(Vi)
10    Xi <- X[ids, ]
11    XVXi <- t(Xi)%*%ViInv%*%Xi
12    XVX <- XVX + XVXi
13    Zi <- Z[i, ]
14    yi <- y[ids]
15    ZGi <- t(kronecker(diag(K2), Zi))%*%Gamma
16    XVyi <- t(Xi)%*%ViInv%*%(yi - Wi%*%ZGi)
17    XVy <- XVy + XVyi
18  }
19  Bn <- solve(B0i + XVX)
20  bn <- Bn%*%(B0i%*%b0 + XVy)
21  Beta <- MASS::mvrnorm(1, bn, Bn)
22  return(Beta)
23 }
24 Postb <- function(Beta, sig2, Gamma, D){
25   Di <- solve(D)
26   bis <- matrix(0, N, K2)
27   for(i in 1:N){
28     ids <- which(id == i)
29     Wi <- W[ids, ]
30     Xi <- X[ids, ]
31     yi <- y[ids]
32     Wtei <- sig2^(-1)*t(Wi)%*%(yi - Xi%*%Beta)
33     Bni <- solve(sig2^(-1)*t(Wi)%*%Wi + Di)
34     Zi <- Z[i, ]
35     ZGi <- t(kronecker(diag(K2), Zi))%*%Gamma
36     bni <- Bni%*%(Wtei + Di%*%ZGi)
37     bi <- MASS::mvrnorm(1, bni, Bni)
38     bis[i, ] <- bi
39   }
40   return(bis)
41 }
42 PostSig2 <- function(Beta, bs){
43   an <- a0 + 0.5*NT
44   ete <- 0
45   for(i in 1:N){
46     ids <- which(id == i)
47     Xi <- X[ids, ]
48     yi <- y[ids]
49     Wi <- W[ids, ]
50     ei <- yi - Xi%*%Beta - Wi%*%bs[i, ]
51     etei <- t(ei)%*%ei
52     ete <- ete + etei
53   }
54   dn <- d0 + 0.5*ete
55   sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
56   return(sig2)
57 }

```


R code. Simulation exercise: Longitudinal normal model with fixed effects correlated to regressors

```

1 PostGamma <- function(bs, D){
2   Di <- solve(D)
3   ZDZ <- matrix(0, K2*K3, K2*K3)
4   ZDb <- matrix(0, K2*K3, 1)
5   for(i in 1:N){
6     Zi <- Z[i, ]
7     ZZi <- t(kronecker(diag(K2), Zi))
8     ZDZi <- t(ZZi)%*%Di%*%ZZi
9     ZDZ <- ZDZ + ZDZi
10    bi <- bs[i,]
11    ZDbi <- t(ZZi)%*%Di%*%bi
12    ZDb <- ZDb + ZDbi
13  }
14  Gn <- solve(G0i + ZDZ); gn <- Gn%*%(G0i%*%g0 + ZDb)
15  Gamma <- MASS::mvrnorm(1, gn, Gn)
16  return(Gamma)
17 }
18 PostD <- function(bs, Gamma){
19   rn <- r0 + N
20   btb <- matrix(0, K2, K2)
21   for(i in 1:N){
22     bsi <- bs[i, ]
23     Zi <- Z[i, ]
24     ZGi <- t(kronecker(diag(K2), Zi))%*%Gamma
25     btbi <- (bsi-ZGi)%*%t(bsi-ZGi)
26     btb <- btb + btbi
27   }
28   Rn <- d0*R0 + btb
29   Sigma <- MCMCpack::riwish(v = rn, S = Rn)
30   return(Sigma)
31 }
32 PostBetas <- matrix(0, tot, K1); PostGammas <- matrix(0, tot,
33   , K2*K3)
34 PostDs <- matrix(0, tot, K2*(K2+1)/2); PostSig2s <- rep(0,
35   tot)
36 Postbs <- array(0, c(N, K2, tot)); RegLS <- lm(y ~ X - 1)
37 SumLS <- summary(RegLS); Beta <- SumLS[["coefficients"]][,1]
38 sig2 <- SumLS[["sigma"]]2; Gamma <- rep(0, K2*K3)
39 D <- diag(K2); b0 <- rep(0, K1); B0 <- diag(K1); B0i <-
40   solve(B0)
41 pb <- winProgressBar(title = "progress bar", min = 0, max =
42   tot, width = 300)
43 for(s in 1:tot){
44   bs <- Postb(Beta = Beta, sig2 = sig2, Gamma = Gamma, D = D)
45   D <- PostD(bs = bs, Gamma = Gamma)
46   Beta <- PostBeta(sig2 = sig2, Gamma = Gamma, D = D)
47   sig2 <- PostSig2(Beta = Beta, bs = bs)
48   Gamma <- PostGamma(bs = bs, D = D)
49   PostBetas[s,] <- Beta; PostDs[s,] <- matrixcalc::vech(D)
50   PostSig2s[s] <- sig2; Postbs[, , s] <- bs
51   PostGammas[s,] <- Gamma
52   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
53     "% done"))
54 }

```

R code. Simulation exercise: Longitudinal normal model with fixed effects correlated to regressors

```

1 close(pb)
2 keep <- seq((burnin+1), tot, thin)
3 Bs <- PostBetas[keep,]
4 Ds <- PostDs[keep,]
5 bs <- Postbs[, , keep]
6 sig2s <- PostSig2s[keep]
7 Gs <- PostGammas[keep, ]
8 summary(coda::mcmc(Bs))
9 Quantiles for each variable:
10      2.5%      25%      50%      75%      97.5%
11 var1  0.3629  0.3812  0.3880  0.3945  0.4120
12 var2  0.5844  0.6032  0.6098  0.6176  0.6381
13 var3 -0.6114 -0.5950 -0.5880 -0.5809 -0.5605
14 var4 -0.4455  0.4155  0.8598  1.3047  2.0654
15 summary(coda::mcmc(Ds))
16 Quantiles for each variable:
17      2.5%      25%      50%      75%      97.5%
18 var1  0.5858  0.7798  0.9173  1.13381  2.0153
19 var2 -0.3914 -0.1901 -0.1104 -0.03585  0.1250
20 var3  0.4285  0.5495  0.6314  0.72342  0.9662
21 summary(coda::mcmc(sig2s))
22 Quantiles for each variable:
23 Quantiles for each variable:
24      2.5%      25%      50%      75%      97.5%
25 0.09609 0.11486 0.17790 0.35215 1.12537
26 summary(coda::mcmc(Gs))
27 Quantiles for each variable:
28      2.5%      25%      50%      75%      97.5%
29 var1  0.6552  0.8998  1.0288  1.162  1.402
30 var2 -0.4463  0.4056  0.7882  1.242  2.144
31 var3  0.8583  1.0599  1.1623  1.271  1.482
32 var4  0.5525  0.8430  1.0038  1.147  1.416

```

In one hand, the 95% credible intervals of the model without taking into account the dependence between the *random effects* and z_{i1} overestimates the posterior mean of β_4 and the variance of b_{i1} . In addition, the credible intervals are very narrow. However, the variance of μ_i is well estimated. On the other hand, all the 95% credible intervals of the model taking into account the dependence between the *random effects* and z_{i1} encompass the population parameters. However, there is a lot of variability in β_4 posterior estimates. The posterior mean estimate of the variance of b_{i1} is close to the population value, and the location parameters associated with z_{i1} in the mean of the *random effects* are also well estimated by the posterior mean. However, the variance of the model is overestimated.

4. Doctor visits in Germany continues I

Replicate this example using our GUI, which by default does not fix the over-dispersion parameter (σ^2), and compare the results with the results of this example in Section 9.2.

Answer

This code replicates what we get using our GUI.

R code. Doctor visits in Germany, results

```

1 rm(list = ls())
2 set.seed(12345)
3 Data <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/9VisitDoc.csv",
  sep = ",", header = TRUE, quote = "\"")
4 attach(Data)
5 K1 <- 7; K2 <- 2; N <- 9197
6 b0 <- rep(0, K1); B0 <- diag(K1)
7 r0 <- 5; R0 <- diag(K2)
8 a0 <- 0.001; d0 <- 0.001
9 RegLogit <- glm(DocVis ~ Age + Male + Sport + LogInc +
  GoodHealth + BadHealth, family = binomial(link = "logit"
  ))
10 SumLogit <- summary(RegLogit)
11 Beta0 <- SumLogit[["coefficients"]][,1]
12 mcmc <- 10000; burnin <- 1000; thin <- 10
13 # MCMChlogit
14 Resultshlogit <- MCMCpack::MCMChlogit(fixed = DocVis ~ Age +
  Male + Sport + LogInc + GoodHealth + BadHealth, random
  = ~Sozh, group="id", data = Data, burnin = burnin, mcmc
  = mcmc, thin = thin, mubeta = b0, Vbeta = B0, r = r0, R
  = R0, nu = a0, delta = d0, beta.start = Beta0, FixOD =
  0)
15 Betas <- Resultshlogit[["mcmc"]][,1:K1]
16 Sigma2RanEff <- Resultshlogit[["mcmc"]][,c(K2*N+K1+1, 2*N+K1
  +K2^2)]
17 summary(Betas)
18 summary(Sigma2RanEff)
19 summary(Sigma2)
20 Quantiles for each variable:
21      2.5%      25%      50%      75%      97.5%
22 Intercept -9.48e-01 -5.27e-01 -2.86e-01 -6.28e-02 2.99e-01
23 Age        4.88e-03 7.27e-03 8.35e-03 9.31e-03 1.09e-02
24 Male      -9.90e-01 -9.52e-01 -9.31e-01 -9.10e-01 -8.75e-01
25 Sport      1.80e-01 2.25e-01 2.55e-01 2.85e-01 3.47e-01
26 LogInc     1.38e-01 1.85e-01 2.15e-01 2.49e-01 3.01e-01
27 GoodHealth -9.56e-01 -9.18e-01 -8.97e-01 -8.75e-01 -8.36e-01
28 BadHealth  1.08e+00 1.14e+00 1.19e+00 1.23e+00 1.28e+00
29 D11        1.43e+00 1.53e+00 1.58e+00 1.62e+00 1.70e+00
30 D21       -2.67e-01 1.94e-02 1.85e-01 4.08e-01 5.81e-01
31 D12       -2.67e-01 1.94e-02 1.85e-01 4.08e-01 5.81e-01
32 D22        6.05e-01 7.99e-01 9.75e-01 1.21e+00 1.62e+00
33 sigma2     6.37e-02 7.76e-02 1.01e-01 1.15e-01 1.58e-01

```

We see in this example running our GUI that we get qualitatively same results as the results fixing the over-dispersion parameter in Section 9.2 in the book. However, there small numerical differences in the *fixed effects*,

and the differences are greater in the posterior results of the covariance matrix of the *random effects*.

5. Simulation exercise of the longitudinal logit model

Perform a simulation exercise to assess the performance of the hierarchical longitudinal logit model. The point of departure is to assume that $y_{it}^* = \beta_0 + \beta_1 x_{it1} + \beta_2 x_{it2} + \beta_3 x_{it3} + b_i + w_{it1} b_{i1}$ where $x_{itk} \sim N(0, 1)$, $k = 1, 2, 3$, $w_{it1} \sim N(0, 1)$, $b_i \sim N(0, 0.7^{1/2})$, $b_{i1} \sim N(0, 0.6^{1/2})$, $\beta = [0.5 \ 0.4 \ 0.6 \ -0.6]^\top$, $i = 1, 2, \dots, 50$, and $y_{it} \sim B(\pi_{it})$, where $\pi_{it} = 1/(1 + \exp(-y_{it}^*))$. The sample size is 1000 in an *unbalanced panel structure*.

- Perform inference using the command *MCMChlogit* fixing the over-dispersion parameter, and using $\beta_0 = \mathbf{0}_4$, $\mathbf{B}_0 = \mathbf{I}_4$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 2$ and $\mathbf{D}_0 = \mathbf{I}_2$.
- Program from scratch a Metropolis-within-Gibbs algorithm to perform inference in this simulation.

Answer

The following code shows the simulation setting, and the results using the *MCMChlogit* command. We see that all posterior estimates encompass the population values.

R code. Simulation exercise: Hierarchical longitudinal logit model using MCMChlogit

```

1 rm(list = ls()); set.seed(010101)
2 NT <- 1000; N <- 50
3 id <- c(1:N, sample(1:N, NT - N, replace=TRUE))
4 x1 <- rnorm(NT); x2 <- rnorm(NT); x3 <- rnorm(NT)
5 X <- cbind(1, x1, x2, x3); K1 <- dim(X)[2]
6 w1 <- rnorm(NT); W <- cbind(1, w1); K2 <- dim(W)[2]
7 B <- c(0.5, 0.4, 0.6, -0.6); D <- c(0.7, 0.6)
8 sig2 <- 0.1
9 b1 <- rnorm(N, 0, sd = D[1]^0.5)
10 b2 <- rnorm(N, 0, sd = D[2]^0.5)
11 b <- cbind(b1, b2)
12 yl <- NULL
13 for(i in 1:NT){
14   ylmeani <- X[i,]%*%B + W[i,]%*%b[id[i],]
15   yli <- rnorm(1, ylmeani, sig2^0.5)
16   yl <- c(yl, yli)
17 }
18 pit <- 1/(1+exp(-yl))
19 y <- rbinom(NT, 1, prob = pit)
20 Data <- as.data.frame(cbind(y, x1, x2, x3, w1, id))
21 mcmc <- 15000; burnin <- 5000; thin <- 10; tot <- mcmc +
   burnin
22 b0 <- rep(0, K1); B0 <- diag(K1); B0i <- solve(B0)
23 r0 <- K2; R0 <- diag(K2); a0 <- 0.001; d0 <- 0.001
24 RegLogit <- glm(y ~ X - 1, family = binomial(link = "logit")
   )
25 SumLogit <- summary(RegLogit)
26
27 Beta0 <- SumLogit[["coefficients"]][,1]
28 sig20 <- sum(SumLogit[["deviance.resid"]]^2)/SumLogit[["df.
   residual"]]
29 Resultshlogit <- MCMCpack::MCMChlogit(fixed = y~x1 + x2 + x3
   , random = ~w1, group="id", data = Data, burnin = burnin
   , mcmc = mcmc, thin = thin,
30 mubeta = b0, Vbeta = B0, r = r0, R = R0, nu = a0, delta = d0
   ,
31 beta.start = Beta0, FixOD = 1, sigma2.start = sig20)
32 Betas <- Resultshlogit[["mcmc"]][,1:K1]
33 Sigma2RanEff <- Resultshlogit[["mcmc"]][,c(K2*N+K1+1, 2*N+K1
   +K2^2)]
34 Sigma2 <- Resultshlogit[["mcmc"]][,K2*N+K1+K2^2+1]
35 summary(Betas)
36 Quantiles for each variable:
37      2.5%      25%      50%      75%      97.5%
38 beta.(Intercept)  0.4258  0.6165  0.7140  0.8155  1.0041
39 beta.x1           0.3294  0.4372  0.4999  0.5617  0.6684
40 beta.x2           0.5555  0.6763  0.7388  0.8062  0.9377
41 beta.x3          -0.9327 -0.7957 -0.7276 -0.6591 -0.5383
42 summary(Sigma2RanEff)
43 Quantiles for each variable:
44      2.5%      25%      50%      75% 97.5%
45 D11 0.3394 0.5366 0.6962 0.8652 1.338
46 D22 0.4101 0.6478 0.8091 1.0039 1.611

```

The following code shows the algorithm step by step.

R code. Simulation exercise: Hierarchical longitudinal logit model from scratch

```

1 LatentMHV1 <- function(tuning, Beta, bs, sig2){
2   ylhat <- rep(0, NT)
3   accept <- NULL
4   for(i in 1:NT){
5     ids <- which(id == i)
6     yi <- y[i]
7     ylhatmean1 <- X[i,]%*Beta + W[i,]%*bs[id[i],]
8     ylhati <- rnorm(1, ylhatmean1, sd = sig2^0.5)
9     pihati <- 1/(1+exp(-ylhati))
10    ei <- rnorm(1, 0, sd = tuning)
11    ylpropi <- ylhati + ei; pipropi <- 1/(1+exp(-ylpropi))
12    logPosthati <- sum(dbinom(yi, 1, prob = pihati, log =
13    TRUE) + dnorm(ylhati, ylhatmean1, sig2^0.5, log = TRUE))
14    logPostpropi <- sum(dbinom(yi, 1, prob = pipropi, log =
15    TRUE) + dnorm(ylpropi, ylhatmean1, sig2^0.5, log = TRUE)
16    )
17    alphai <- min(1, exp(logPostpropi - logPosthati))
18    ui <- runif(1)
19    if(ui <= alphai){
20      ylhati <- ylpropi; accepti <- 1
21    }else{
22      ylhati <- ylhati; accepti <- 0
23    }
24    ylhat[i] <- ylhati; accept <- c(accept, accepti)
25  }
26  res <- list(ylhat = ylhat, accept = mean(accept))
27  return(res)
28 }
29
30 PostBeta <- function(D, ylhat, sig2){
31   XVX <- matrix(0, K1, K1); XVy <- matrix(0, K1, 1)
32   for(i in 1:N){
33     ids <- which(id == i); Ti <- length(ids)
34     Wi <- W[ids, ]; Vi <- diag(Ti)*sig2 + Wi%*D%*t(Wi)
35     ViInv <- solve(Vi); Xi <- X[ids, ]
36     XVXi <- t(Xi)%*ViInv%*Xi; XVX <- XVX + XVXi
37     yi <- ylhat[ids]; XVyi <- t(Xi)%*ViInv%*yi
38     XVy <- XVy + XVyi
39   }
40   Bn <- solve(B0i + XVX)
41   bn <- Bn%*(B0i%*b0 + XVy)
42   Beta <- MASS::mvrnorm(1, bn, Bn)
43   return(Beta)
44 }
45
46 Postb <- function(Beta, D, ylhat, sig2){
47   Di <- solve(D); bis <- matrix(0, N, K2)
48   for(i in 1:N){
49     ids <- which(id == i)
50     Wi <- W[ids, ]; Xi <- X[ids, ]
51     yi <- ylhat[ids]
52     Wtei <- sig2^(-1)*t(Wi)%*(yi - Xi%*Beta)
53     Bni <- solve(sig2^(-1)*t(Wi)%*Wi + Di)
54     bni <- Bni%*Wtei; bi <- MASS::mvrnorm(1, bni, Bni)
55     bis[i, ] <- bi
56   }
57   return(bis)
58 }

```


R code. Simulation exercise: Hierarchical longitudinal logit model from scratch

```

1 PostD <- function(bs){
2   rn <- r0 + N
3   btb <- matrix(0, K2, K2)
4   for(i in 1:N){
5     bsi <- bs[i, ]; btb_i <- bsi%*%t(bsi)
6     btb <- btb + btb_i
7   }
8   Rn <- d0*R0 + btb
9   Sigma <- MCMCpack::riwish(v = rn, S = Rn)
10  return(Sigma)
11 }
12 PostSig2 <- function(Beta, bs, ylhat, ss){
13   an <- a0 + 0.5*NT; ete <- 0
14   for(i in 1:N){
15     ids <- which(id == i)
16     Xi <- X[ids, ]; yi <- ylhat[ids]
17     Wi <- W[ids, ]
18     ei <- yi - Xi%*%Beta - Wi%*%bs[i, ]
19     etei <- t(ei)%*%ei; ete <- ete + etei
20   }
21   dn <- d0 + 0.5*ete
22   sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
23   if(sig2 > ss){
24     sig2 <- ss
25   }else{
26     sig2 <- sig2
27   }
28   return(sig2)
29 }
30 PostBetas <- matrix(0, tot, K1)
31 PostDs <- matrix(0, tot, K2*(K2+1)/2)
32 Postbs <- array(0, c(N, K2, tot))
33 PostSig2s <- rep(0, tot)
34 Accepts <- rep(NULL, tot)
35 RegLogit <- glm(y ~ X - 1, family = binomial(link = "logit")
36 )
37 SumLogit <- summary(RegLogit)
38 Beta <- SumLogit[["coefficients"]][,1]
39 sig2 <- sum(SumLogit[["deviance.resid"]]^2)/SumLogit[["df.
40 residual"]]
41 ss0 <- sig2; D <- diag(K2)
42 bs1 <- rnorm(N, 0, sd = D[1]^0.5)
43 bs2 <- rnorm(N, 0, sd = D[2]^0.5)
44 bs <- cbind(bs1, bs2)
45 tuning <- 0.1; ropt <- 0.44
46 tuneapariter <- seq(round(tot/10, 0), tot, round(tot/10, 0));
47   l <- 1
48 pb <- winProgressBar(title = "progress bar", min = 0, max =
49   tot, width = 300)

```

R code. Simulation exercise: Hierarchical longitudinal logit model from scratch

```

1 for(s in 1:tot){
2   LatY <- LatentMHV1(tuning = tuning, Beta = Beta, bs = bs,
3     sig2 = sig2)
4   ylhat <- LatY[["ylhat"]]
5   bs <- Postb(Beta = Beta, D = D, ylhat = ylhat, sig2 = sig2)
6   D <- PostD(bs = bs)
7   Beta <- PostBeta(D = D, ylhat = ylhat, sig2 = sig2)
8   sig2 <- PostSig2(Beta = Beta, bs = bs, ylhat = ylhat, ss =
9     ss0)
10  PostBetas[s,] <- Beta
11  PostDs[s,] <- matrixcalc::vech(D)
12  Postbs[, , s] <- bs
13  PostSig2s[s] <- sig2
14  AcceptRate <- LatY[["accept"]]
15  Accepts[s] <- AcceptRate
16  if(AcceptRate > ropt){
17    tuning = tuning*(2-(1-AcceptRate)/(1-ropt))
18  }else{
19    tuning = tuning/(2-AcceptRate/ropt)
20  }
21  if(s == tunepariter[1]){
22    print(AcceptRate)
23    l <- l + 1
24  }
25  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
26    "% done"))
27 }
28 close(pb)
29 keep <- seq((burnin+1), tot, thin)
30 Bs <- PostBetas[keep,]
31 Ds <- PostDs[keep,]
32 bs <- Postbs[, , keep]
33 sig2s <- PostSig2s[keep]
34 summary(coda::mcmc(Bs))
35 Quantiles for each variable:
36      2.5%      25%      50%      75%      97.5%
37 var1  0.3195  0.5266  0.6325  0.7452  0.9427
38 var2  0.1780  0.3563  0.4521  0.5436  0.7352
39 var3  0.3596  0.5197  0.6140  0.7165  0.9149
40 var4 -0.8994 -0.7153 -0.6125 -0.5135 -0.3240
41 summary(coda::mcmc(Ds))
42 Quantiles for each variable:
43      2.5%      25%      50%      75%      97.5%
44 var1  0.0002003  0.0007473  0.0022547  0.0124378  0.09575
45 var2 -0.0534437 -0.0029207 -0.0001433  0.0009905  0.02296
46 var3  0.0002150  0.0009101  0.0026712  0.0119391  0.14863
47 summary(coda::mcmc(sig2s))
48 Quantiles for each variable:
49      2.5%      25%      50%      75%      97.5%
50 0.1321  0.5174  0.8674  1.0788  1.1909

```

The 95% credible intervals of the *fixed effects* encompass all the population values. However, we do not get good posterior estimates of the covariance matrix and over-dispersion parameters.

6. Doctor visits in Germany continues II

Take a sub-sample of the first 500 individuals of the dataset *9VisitDoc.csv* to perform inference in the number of visits to doctors (*DocNum*) with the same specification of the example of **Doctor visits in Germany** of Section 9.2.

Answer

This algorithm shows how to perform inference in this application programming from scratch the algorithm.

R code. Doctor visits in Germany: Hierarchical longitudinal Poisson model from scratch

```

1 rm(list = ls())
2 set.seed(12345)
3 Data <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/9VisitDoc.csv",
  sep = ",", header = TRUE, quote = "")
4 library(dplyr)
5 Data <- Data %>%
6 filter(id <= 500)
7 attach(Data)
8 K1 <- 7; K2 <- 2; N <- 9197
9 b0 <- rep(0, K1); B0 <- diag(K1)
10 r0 <- 5; R0 <- diag(K2)
11 a0 <- 0.001; d0 <- 0.001
12 NT <- dim(Data)[1]
13 N <- length(unique(id))
14 X <- cbind(1, Age, Male, Sport, LogInc, GoodHealth,
  BadHealth)
15 K1 <- dim(X)[2]
16 W <- cbind(1, Sozh)
17 K2 <- dim(W)[2]
18 y <- DocNum
19 mcmc <- 15000; burnin <- 5000; thin <- 10; tot <- mcmc +
  burnin
20 b0 <- rep(0, K1); B0 <- diag(K1); B0i <- solve(B0)
21 r0 <- K2; R0 <- diag(K2); a0 <- 0.001; d0 <- 0.001
22 LatentMHV1 <- function(tuning, Beta, bs, sig2){
23   ylhat <- rep(0, NT)
24   accept <- NULL
25   for(i in 1:NT){
26     ids <- which(id == i)
27     yi <- y[ids]
28     ylhatmean1 <- X[ids,]%*%Beta + W[ids,]%*%bs[id[ids],]
29     ylhati <- rnorm(1, ylhatmean1, sd = sig2^0.5)
30     lambdahati <- exp(ylhati)
31     ei <- rnorm(1, 0, sd = tuning)
32     ylpropi <- ylhati + ei
33     lambdapropi <- exp(ylpropi)
34     logPosthati <- sum(dpois(yi, lambdahati, log = TRUE) +
35       dnorm(ylhati, ylhatmean1, sig2^0.5, log = TRUE))
36     logPostpropi <- sum(dpois(yi, lambdapropi, log = TRUE) +
37       dnorm(ylpropi, ylhatmean1, sig2^0.5, log = TRUE))
38     alphai <- min(1, exp(logPostpropi - logPosthati))
39     ui <- runif(1)
40     if(ui <= alphai){
41       ylhati <- ylpropi; accepti <- 1
42     }else{
43       ylhati <- ylhati; accepti <- 0
44     }
45     ylhat[i] <- ylhati
46     accept <- c(accept, accepti)
47   }
48   res <- list(ylhat = ylhat, accept = mean(accept))
49   return(res)
50 }

```

R code. Doctor visits in Germany: Hierarchical longitudinal Poisson model from scratch

```

1 PostBeta <- function(D, ylhat, sig2){
2   XVX <- matrix(0, K1, K1); XVy <- matrix(0, K1, 1)
3   for(i in 1:N){
4     ids <- which(id == i); Ti <- length(ids)
5     Wi <- matrix(W[ids, ], Ti, K2)
6     Vi <- diag(Ti)*sig2 + Wi%*%D%*%t(Wi)
7     ViInv <- solve(Vi); Xi <- matrix(X[ids, ], Ti, K1)
8     XVXi <- t(Xi)%*%ViInv%*%Xi
9     XVX <- XVX + XVXi; yi <- ylhat[ids]
10    XVyi <- t(Xi)%*%ViInv%*%yi; XVy <- XVy + XVyi
11  }
12  Bn <- solve(B0i + XVX); bn <- Bn%*%(B0i%*%b0 + XVy)
13  Beta <- MASS::mvrnorm(1, bn, Bn)
14  return(Beta)
15 }
16 Postb <- function(Beta, D, ylhat, sig2){
17   Di <- solve(D); bis <- matrix(0, N, K2)
18   for(i in 1:N){
19     ids <- which(id == i); Ti <- length(ids)
20     Wi <- matrix(W[ids, ], Ti, K2)
21     Xi <- matrix(X[ids, ], Ti, K1)
22     yi <- ylhat[ids]
23     Wtei <- sig2^(-1)*t(Wi)%*%(yi - Xi%*%Beta)
24     Bni <- solve(sig2^(-1)*t(Wi)%*%Wi + Di)
25     bni <- Bni%*%Wtei
26     bi <- MASS::mvrnorm(1, bni, Bni)
27     bis[i, ] <- bi
28   }
29   return(bis)
30 }
31 PostD <- function(bs){
32   rn <- r0 + N; btb <- matrix(0, K2, K2)
33   for(i in 1:N){
34     bsi <- bs[i, ]; btbi <- bsi%*%t(bsi)
35     btb <- btb + btbi
36   }
37   Rn <- d0*R0 + btb; Sigma <- MCMCpack::riwish(v = rn, S =
38     Rn)
39   return(Sigma)
40 }
41 PostSig2 <- function(Beta, bs, ylhat){
42   an <- a0 + 0.5*NT; ete <- 0
43   for(i in 1:N){
44     ids <- which(id == i)
45     Ti <- length(ids)
46     Xi <- matrix(X[ids, ], Ti, K1); yi <- ylhat[ids]
47     Wi <- matrix(W[ids, ], Ti, K2)
48     ei <- yi - Xi%*%Beta - Wi%*%bs[i, ]
49     etei <- t(ei)%*%ei; ete <- ete + etei
50   }
51   dn <- d0 + 0.5*ete
52   sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
53   return(sig2)
54 }

```

R code. Doctor visits in Germany: Hierarchical longitudinal Poisson model from scratch

```

1 PostBetas <- matrix(0, tot, K1)
2 PostDs <- matrix(0, tot, K2*(K2+1)/2)
3 Postbs <- array(0, c(N, K2, tot))
4 PostSig2s <- rep(0, tot); ccepts <- rep(NULL, tot)
5 RegPois <- glm(DocNum ~ Age + Male + Sport + LogInc +
  GoodHealth + BadHealth, family = poisson(link = "log"))
6 SumPois <- summary(RegPois)
7 Beta <- SumPois[["coefficients"]][,1]
8 sig2 <- sum(SumPois[["deviance.resid"]]2)/SumPois[["df.
  residual"]]
9 D <- diag(K2)
10 bs1 <- rnorm(N, 0, sd = D[1,1]0.5)
11 bs2 <- rnorm(N, 0, sd = D[2,2]0.5)
12 bs <- cbind(bs1, bs2); tuning <- 0.1; ropt <- 0.44
13 tuneapariter <- seq(round(tot/10, 0), tot, round(tot/10, 0));
  l <- 1
14 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
15 for(s in 1:tot){
16   LatY <- LatentMHV1(tuning = tuning, Beta = Beta, bs = bs,
    sig2 = sig2)
17   ylhat <- LatY[["ylhat"]]
18   bs <- Postb(Beta = Beta, D = D, ylhat = ylhat, sig2 = sig2
    )
19   D <- PostD(bs = bs)
20   Beta <- PostBeta(D = D, ylhat = ylhat, sig2 = sig2)
21   sig2 <- PostSig2(Beta = Beta, bs = bs, ylhat = ylhat)
22   PostBetas[s,] <- Beta; PostDs[s,] <- matrixcalc::vech(D)
23   Postbs[, , s] <- bs; PostSig2s[s] <- sig2
24   AcceptRate <- LatY[["accept"]]; Accepts[s] <- AcceptRate
25   if(AcceptRate > ropt){
26     tuning = tuning*(2-(1-AcceptRate)/(1-ropt))
27   }else{
28     tuning = tuning/(2-AcceptRate/ropt)
29   }
30   if(s == tuneapariter[l]){
31     print(AcceptRate)
32     l <- l + 1
33   }
34   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
35 }
36 close(pb)
37 keep <- seq((burnin+1), tot, thin)
38 Bs <- PostBetas[keep,]; Ds <- PostDs[keep,]
39 bs <- Postbs[, , keep]; sig2s <- PostSig2s[keep]
40 summary(coda::mcmc(Bs))
41 Quantiles for each variable:
42 2.5%      25%      50%      75%      97.5%
43 var1 -1.250036 -0.269211  0.1995811  0.69139  1.59234
44 var2 -0.001542  0.004852  0.0083935  0.01147  0.01815
45 var3 -0.484097 -0.331748 -0.2586891 -0.19011 -0.04787
46 var4 -0.023677  0.123336  0.1973927  0.26883  0.41314
47 var5 -0.196732 -0.071421 -0.0001036  0.06601  0.19356
48 var6 -0.815499 -0.657182 -0.5784964 -0.49969 -0.36882
49 var7  0.613990  0.799534  0.8982645  1.00161  1.18880

```

We see that males with good perception of health status visit less frequently the physicians, and women with bad perception of health status visit more frequently the physicians.



10

Bayesian model average

Solutions of Exercises

1. The Gaussian linear model specifies $\mathbf{y} = \alpha \mathbf{i}_N + \mathbf{X}_m \boldsymbol{\beta}_m + \boldsymbol{\mu}_m$ such that $\boldsymbol{\mu}_m \sim N(\mathbf{0}, \sigma^2 \mathbf{I}_n)$, and \mathbf{X}_m does not have the column of ones. Assuming that $\pi(\sigma^2) \propto 1/\sigma^2$, $\pi(\alpha) \propto 1$, and $\boldsymbol{\beta}_m | \sigma^2 \sim N(\mathbf{0}_{k_m}, \sigma^2 (g_m \mathbf{X}_m^\top \mathbf{X}_m)^{-1})$.
 - Show that the conditional posterior distribution of $\boldsymbol{\beta}_m$ is $N(\boldsymbol{\beta}_{mn}, \sigma^2 \mathbf{B}_{mn})$, where $\boldsymbol{\beta}_{mn} = \mathbf{B}_{mn} \mathbf{X}_m^\top \mathbf{y}$ and $\mathbf{B}_{mn} = ((1 + g_m) \mathbf{X}_m^\top \mathbf{X}_m)^{-1}$.
 - Show that the marginal the marginal likelihood associated with model \mathcal{M}_m is proportional to

$$p(\mathbf{y} | \mathcal{M}_m) \propto \left(\frac{g_m}{1 + g_m} \right)^{k_m/2} \left[(\mathbf{y} - \bar{y} \mathbf{i}_N)^\top (\mathbf{y} - \bar{y} \mathbf{i}_N) - \frac{1}{1 + g_m} (\mathbf{y}^\top \mathbf{P}_{X_m} \mathbf{y}) \right]^{-(N-1)/2},$$

where all parameter are indexed to model \mathcal{M}_m , $\mathbf{P}_{X_m} = \mathbf{X}_m (\mathbf{X}_m^\top \mathbf{X}_m)^{-1} \mathbf{X}_m$ is the projection matrix on the space generated by the columns of \mathbf{X}_m , and \bar{y} is the sample mean of \mathbf{y} .

Hint: Take into account that $\mathbf{i}_N^\top \mathbf{X}_m = \mathbf{0}_{k_m}$ due to all columns being centered with respect to their means.

Answer

The marginal likelihood of this model is

$$\begin{aligned} p(\mathbf{y}) &= \int_0^\infty \int_{R^K} \int_R \pi(\boldsymbol{\beta} | \sigma^2) \pi(\sigma^2) \pi(\alpha) p(\mathbf{y} | \boldsymbol{\beta}, \sigma^2, \alpha) d\alpha d\boldsymbol{\beta} d\sigma^2 \\ &\propto \int_0^\infty \int_{R^K} \int_R (\sigma^2)^{-k_m/2} |g_m \mathbf{X}_m^\top \mathbf{X}_m|^{1/2} \exp \left\{ -\frac{1}{2\sigma^2} (\boldsymbol{\beta}^\top (g_m \mathbf{X}_m^\top \mathbf{X}_m) \boldsymbol{\beta}) \right\} (\sigma^2)^{-1} \\ &\quad \times (\sigma^2)^{-N/2} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y} - \alpha \mathbf{i}_N - \mathbf{X}_m \boldsymbol{\beta})^\top (\mathbf{y} - \alpha \mathbf{i}_N - \mathbf{X}_m \boldsymbol{\beta}) \right\} d\alpha d\boldsymbol{\beta} d\sigma^2. \end{aligned}$$

Taking into account that $(\mathbf{y} - \alpha \mathbf{i}_N - \mathbf{X}_m \boldsymbol{\beta})^\top (\mathbf{y} - \alpha \mathbf{i}_N - \mathbf{X}_m \boldsymbol{\beta}) = (\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta}) + N(\alpha - \bar{y})^2 - N\bar{y}^2$,

$$\begin{aligned}
p(\mathbf{y}) &\propto \int_0^\infty \int_{R^K} (\sigma^2)^{-k_m/2} |g_m \mathbf{X}_m^\top \mathbf{X}_m|^{1/2} \exp \left\{ -\frac{1}{2\sigma^2} (\boldsymbol{\beta}^\top (g_m \mathbf{X}_m^\top \mathbf{X}_m) \boldsymbol{\beta}) \right\} (\sigma^2)^{-1} \\
&\quad \times (\sigma^2)^{-N/2} \exp \left\{ -\frac{1}{2\sigma^2} [(\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta}) - N\bar{y}^2] \right\} \\
&\quad \times \int_R \exp \left\{ -\frac{1}{2\sigma^2} (N(\alpha - \bar{y})^2) \right\} d\alpha d\boldsymbol{\beta} d\sigma^2.
\end{aligned}$$

The last term is the kernel of a normal density function with mean \bar{y} and variance σ^2/N , then

$$\begin{aligned}
p(\mathbf{y}) &\propto \int_0^\infty \int_{R^K} (\sigma^2)^{-k_m/2} |g_m \mathbf{X}_m^\top \mathbf{X}_m|^{1/2} \exp \left\{ -\frac{1}{2\sigma^2} (\boldsymbol{\beta}^\top (g_m \mathbf{X}_m^\top \mathbf{X}_m) \boldsymbol{\beta}) \right\} (\sigma^2)^{-1} \\
&\quad \times (\sigma^2)^{-N/2} (\sigma^2)^{1/2} \exp \left\{ -\frac{1}{2\sigma^2} [(\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta}) - N\bar{y}^2] \right\} d\boldsymbol{\beta} d\sigma^2.
\end{aligned}$$

Collecting terms for $\boldsymbol{\beta}$, we have $(\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta})^\top (\mathbf{y} - \mathbf{X}_m \boldsymbol{\beta}) - N\bar{y}^2 + \boldsymbol{\beta}^\top (g_m \mathbf{X}_m^\top \mathbf{X}_m) \boldsymbol{\beta} = (\boldsymbol{\beta} - \boldsymbol{\beta}_{mn})^\top \mathbf{B}_{mn}^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_{mn}) + \mathbf{y}^\top \mathbf{y} - N\bar{y}^2 - \boldsymbol{\beta}_{mn}^\top \mathbf{B}_{mn} \boldsymbol{\beta}_{mn}$ where $\boldsymbol{\beta}_{mn} = \mathbf{B}_{mn} \mathbf{X}_m^\top \mathbf{y}$ and $\mathbf{B}_{mn} = ((1 + g_m) \mathbf{X}_m^\top \mathbf{X}_m)^{-1}$. Then,

$$\begin{aligned}
p(\mathbf{y}) &\propto \int_0^\infty (\sigma^2)^{-k_m/2} |g_m \mathbf{X}_m^\top \mathbf{X}_m|^{1/2} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y}^\top \mathbf{y} - N\bar{y}^2 - \boldsymbol{\beta}_{mn}^\top \mathbf{B}_{mn} \boldsymbol{\beta}_{mn}) \right\} (\sigma^2)^{-1} \\
&\quad \times (\sigma^2)^{-N/2} (\sigma^2)^{1/2} \int_{R^K} \exp \left\{ -\frac{1}{2\sigma^2} (\boldsymbol{\beta} - \boldsymbol{\beta}_{mn})^\top \mathbf{B}_{mn}^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_{mn}) \right\} d\boldsymbol{\beta} d\sigma^2.
\end{aligned}$$

The last term is the kernel of a multivariate normal density with mean $\boldsymbol{\beta}_{mn}$ and variance \mathbf{B}_{mn} (proof of the first bullet). Then,

$$p(\mathbf{y}) \propto \int_0^\infty \left(\frac{g_m}{1 + g_m} \right)^{k_m/2} (\sigma^2)^{-(N-1)/2-1} \exp \left\{ -\frac{1}{2\sigma^2} (\mathbf{y}^\top \mathbf{y} - N\bar{y}^2 - \boldsymbol{\beta}_{mn}^\top \mathbf{B}_{mn} \boldsymbol{\beta}_{mn}) \right\} d\sigma^2.$$

This is the kernel of an inverse-gamma density with parameters $\alpha_n = (N-1)/2$ and $\delta_n = \mathbf{y}^\top \mathbf{y} - N\bar{y}^2 - \boldsymbol{\beta}_{mn}^\top \mathbf{B}_{mn} \boldsymbol{\beta}_{mn}$, where $\mathbf{y}^\top \mathbf{y} - N\bar{y}^2 - \boldsymbol{\beta}_{mn}^\top \mathbf{B}_{mn} \boldsymbol{\beta}_{mn} = (\mathbf{y} - \mathbf{i}_N \bar{y})^\top (\mathbf{y} - \mathbf{i}_N \bar{y}) - (1 + g_m)^{-1} \mathbf{y}^\top (\mathbf{X} (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top) \mathbf{y}$. Then,

$$p(\mathbf{y} | \mathcal{M}_m) \propto \left(\frac{g_m}{1 + g_m} \right)^{k_m/2} \left[(\mathbf{y} - \bar{y} \mathbf{i}_N)^\top (\mathbf{y} - \bar{y} \mathbf{i}_N) - \frac{1}{1 + g_m} (\mathbf{y}^\top \mathbf{P}_{X_m} \mathbf{y}) \right]^{-(N-1)/2},$$

2. Determinants of export diversification I

[11] use BMA to study the determinants of export diversification. Use the dataset *10ExportDiversificationHHI.csv* to perform BMA using the BIC approximation and MC3 with 10000 iterations to check if these two approaches agree.

Answer

The first aspect to note is that the BIC approximation is faster by far than the MC3 algorithm. We see from the results that the two approaches show that the most relevant variables to determine export diversification are *avgedu5* (primary education) and *avgnatres* (natural resources). See [11] for details of all variables. The model with the highest PMP using MC3 includes these two variables (PMP = 0.16), while the model with the highest PMP using the BIC approximation in addition to these two variables also includes Portugal former colony and population (PMP = 0.03). Both methods agree that export diversification increases with primary education, and decreases with natural resources.

R code. Determinants of export diversification

```

1 rm(list = ls()); set.seed(010101)
2 Data <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/10
  ExportDiversificationHHI.csv", sep = ",", header = TRUE,
  quote = "\"")
3 attach(Data)
4 y <- Data[,1]; X <- as.matrix(Data[, -1]); K <- dim(X)[2]
5 BMAglm <- BMA::bicreg(X, y, strict = FALSE, OR = 50)
6 summary(BMAglm)
7 BMAreg <- BMA::MC3.REG(y, X, num.its=10000)
8 Models <- unique(BMAreg[["variables"]])
9 nModels <- dim(Models)[1]
10 nVistModels <- dim(BMAreg[["variables"]])[1]
11 PMPmc3 <- NULL
12 for(m in 1:nModels){
13   idModm <- NULL
14   for(j in 1:nVistModels){
15     if(sum(Models[m,] == BMAreg[["variables"]][j,]) == K){
16       idModm <- c(idModm, j)
17     }else{
18       idModm <- idModm
19     }
20   }
21   PMPm <- sum(BMAreg[["post.prob"]][idModm])
22   PMPmc3 <- c(PMPmc3, PMPm)
23 }
24 PMPmc3
25 PIPmc3 <- NULL
26 for(k in 1:K){
27   PIPk <- sum(PMPmc3[which(Models[,k] == 1)])
28   PIPmc3 <- c(PIPmc3, PIPk)
29 }
30 plot(PIPmc3)
31 Meansmc3 <- matrix(0, nModels, K)
32 Varsmc3 <- matrix(0, nModels, K)
33 for(m in 1:nModels){
34   idXs <- which(Models[m,] == 1)
35   if(length(idXs) == 0){
36     Regm <- lm(y ~ 1)
37   }else{
38     Xm <- X[, idXs]
39     Regm <- lm(y ~ Xm)
40     SumRegm <- summary(Regm)
41     Meansmc3[m, idXs] <- SumRegm[["coefficients"]][-1,1]
42     Varsmc3[m, idXs] <- SumRegm[["coefficients"]][-1,2]^2
43   }
44 }
45 BMAmeansmc3 <- colSums(Meansmc3*PMPmc3)
46 BMAstdmc3 <- (colSums(PMPmc3*Varsmc3) + colSums(PMPmc3*(
  Meansmc3-matrix(rep(BMAmeansmc3, each = nModels),
  nModels, K))^2))^0.5
47 plot(BMAmeansmc3)
48 plot(BMAstdmc3)
49 Ratio <- BMAmeansmc3/BMAstdmc3
50 ResselMC3 <- as.data.frame(cbind(PIPmc3, Models[1,],
  BMAmeansmc3, BMAstdmc3, Ratio))
51 PMPmc3

```

3. Simulation exercise of the Markov chain Monte Carlo model composition continues

Program an algorithm to perform MC3 where the final S models are unique. Use the simulation setting of Section 10.2 of the book increasing the number of regressors to 40, this implies approximately 1.1×10^{12} models.

Answer

The following code shows how to perform BMA using MC3 with the consideration that all final S models should be different.

After running the algorithm 50000 ($\ll 2^{40}$) times, we can see that the PIP is 1 for variables x_1 , x_5 and x_{10} , which are the variables in the data generating process (population statistical model). However, we can see that variable x_{23} has a high PIP (0.49), this makes that the PMP of the model including x_1 , x_5 , x_{10} and x_{23} is the highest, followed by the model including x_1 , x_5 and x_{10} , which is the population statistical model. This highlights the relevance of performing BMA; selecting just one model based on the highest PMP would induce a mistake. Although selecting the median probability model would uncover the population statistical model.

Estimating the BMA mean shows that we get values very close to the population values, a remarkable results is all other BMA posterior means are close to 0, including the mean coefficient of x_{23} despite that its PIP is almost 0.5. We calculate the posterior ratio between the mean and standard deviation, and get values higher than 2 just for x_1 , x_5 and x_{10} , again given evidence for the data generating process.

R code. Markov chain Monte Carlo model composition

```

1 rm(list = ls()); set.seed(010101)
2 N <- 1000
3 K1 <- 6; K2 <- 4; K3 <- 30; K <- K1 + K2 + K3
4 X1 <- matrix(rnorm(N*K1,1,1), N, K1)
5 X2 <- matrix(rbinom(N*K2, 1, 0.5), N, K2)
6 X3 <- matrix(rnorm(N*K3,1,1), N, K3)
7 X <- cbind(X1, X2, X3); e <- rnorm(N, 0, 0.5)
8 B <- c(1,0,0,0,0.5,0,0,0,0,-0.7, rep(0, 30))
9 y <- 1 + X%B + e
10 LogMLfunt <- function(Model){
11   indr <- Model == 1
12   kr <- sum(indr)
13   if(kr > 0){
14     gr <- ifelse(N > kr^2, 1/N, kr^(-2))
15     Xr <- matrix(Xnew[, indr], ncol = kr)
16     # PX <- diag(N) - Xr%*%solve(t(Xr)%*%Xr)%*%t(Xr)
17     # s2pos <- c(t(y)%*%PX%*%y/(1 + gr) + gr*(t(y - mean(y))
18     # %*%(y - mean(y)))/(1 + gr))
19     PX <- Xr%*%solve(t(Xr)%*%Xr)%*%t(Xr)
20     s2pos <- c((t(y - mean(y))%*%(y - mean(y))) - t(y)%*%PX%
21     # %*%y/(1 + gr))
22     mllMod <- (kr/2)*log(gr/(1+gr))-(N-1)/2*log(s2pos)
23   }else{
24     gr <- ifelse(N > kr^2, 1/N, kr^(-2))
25     # PX <- diag(N)
26     # s2pos <- c(t(y)%*%PX%*%y/(1 + gr) + gr*(t(y - mean(y))
27     # %*%(y - mean(y)))/(1 + gr))
28     s2pos <- c((t(y - mean(y))%*%(y - mean(y))))
29     mllMod <- (kr/2)*log(gr/(1+gr))-(N-1)/2*log(s2pos)
30   }
31   return(mllMod)
32 }
33 Xnew <- apply(X, 2, scale); M <- 100
34 Models <- matrix(rbinom(K*M, 1, p = 0.5), ncol = K, nrow = M
35 + 800)
36 Models <- unique(Models)[1:M,]
37 mllnew <- sapply(1:M, function(s){LogMLfunt(matrix(Models[s
38 ], 1, K))})
39 oind <- order(mllnew, decreasing = TRUE)
40 mllnew <- mllnew[oind, ]
41 Models <- Models[oind, ]
42 iter <- 50000; s <- 1
43 pb <- winProgressBar(title = "progress bar", min = 0, max =
44   iter, width = 300)

```

*R code. Markov chain Monte Carlo model
composition*

```

1 while(s <= iter){
2   ActModel <- Models[M,]
3   idK <- which(ActModel == 1)
4   Kact <- length(idK)
5   Continue <- 0
6   while(Continue == 0){
7     if(Kact < K & Kact > 1){
8       CardMol <- K
9       opt <- sample(1:3, 1)
10      if(opt == 1){ # Same
11        CandModel <- ActModel
12      }else{
13        if(opt == 2){ # Add
14          All <- 1:K
15          NewX <- sample(All[-idK], 1)
16          CandModel <- ActModel
17          CandModel[NewX] <- 1
18        }else{ # Subtract
19          LessX <- sample(idK, 1)
20          CandModel <- ActModel
21          CandModel[LessX] <- 0
22        }
23      }
24    }else{
25      CardMol <- K + 1
26      if(Kact == K){
27        opt <- sample(1:2, 1)
28        if(opt == 1){ # Same
29          CandModel <- ActModel
30        }else{ # Subtract
31          LessX <- sample(1:K, 1)
32          CandModel <- ActModel
33          CandModel[LessX] <- 0
34        }
35      }else{
36        if(K == 1){
37          opt <- sample(1:3, 1)
38          if(opt == 1){ # Same
39            CandModel <- ActModel
40          }else{
41            if(opt == 2){ # Add
42              All <- 1:K
43              NewX <- sample(All[-idK], 1)
44              CandModel <- ActModel
45              CandModel[NewX] <- 1
46            }else{ # Subtract
47              LessX <- sample(idK, 1)
48              CandModel <- ActModel
49              CandModel[LessX] <- 0
50            }
51          }
52        }else{ # Add
53          NewX <- sample(1:K, 1)
54          CandModel <- ActModel
55          CandModel[NewX] <- 1
56        }
57      }
58    }

```

R code. Markov chain Monte Carlo model composition

```

1      check <- NULL
2      for(j in 1:M){
3          if(sum(Models[j,] == CandModel) == K){
4              checkj <- 0
5              check <- c(check, checkj)
6          }else{
7              checkj <- 1
8              check <- c(check, checkj)
9          }
10     }
11     dimUniModels <- sum(check)
12     if(dimUniModels == M){
13         Continue <- 1
14     }else{
15         Continue <- 0
16     }
17 }
18 LogMLact <- LogMLfunt(matrix(ActModel, 1, K))
19 LogMLcand <- LogMLfunt(matrix(CandModel, 1, K))
20 alpha <- min(1, exp(LogMLcand-LogMLact)); u <- runif(1)
21 if(u <= alpha){
22     mllnew[M] <- LogMLcand
23     Models[M, ] <- CandModel
24     oind <- order(mllnew, decreasing = TRUE)
25     mllnew <- mllnew[oind]
26     Models <- Models[oind, ]
27 }else{
28     mllnew <- mllnew
29     Models <- Models
30 }
31 s <- s + 1
32 setWinProgressBar(pb, s, title=paste( round(s/iter*100, 0), "%
    done"))
33 }
34 close(pb)
35 ModelsUni <- unique(Models)
36 mllnewUni <- sapply(1:dim(ModelsUni)[1], function(s){
37     LogMLfunt(matrix(ModelsUni[s,], 1, K))})
38 StMarLik <- exp(mllnewUni-mllnewUni[1])
39 PMP <- StMarLik/sum(StMarLik)
40 PIP <- NULL
41 for(k in 1:K){
42     PIPk <- sum(PMP[which(ModelsUni[,k] == 1)])
43     PIP <- c(PIP, PIPk)
44 }
45 PIP

```


R code. Markov chain Monte Carlo model composition

```

1 Means <- matrix(0, M, K)
2 Vars <- matrix(0, M, K)
3 for(m in 1:M){
4   idXs <- which(ModelsUni[m,] == 1)
5   if(length(idXs) == 0){
6     Regm <- lm(y ~ 1)
7   }else{
8     Xm <- X[, idXs]
9     Regm <- lm(y ~ Xm)
10    SumRegm <- summary(Regm)
11    Means[m, idXs] <- SumRegm[["coefficients"]][-1,1]
12    Vars[m, idXs] <- SumRegm[["coefficients"]][-1,2]^2
13  }
14 }
15 BMMeans <- colSums(Means*PMP)
16 BMAsd <- (colSums(PMP*Vars) + colSums(PMP*(Means-matrix(rep
17   (BMMeans, each = M), M, K))^2))^0.5
18 plot(BMMeans)
19 plot(BMAsd)
20 plot(BMMeans/BMAsd)

```

4. Simulation exercise of IV BMA continues

Use the simulation setting with endogeneity in Section 10.2 to perform BMA based on the BIC approximation and MC3.

Answer

The following code shows how to perform BMA using the BIC approximation and MC3 in this simulation setting with endogeneity. We see from the results that the BIC approximation and MC3 do a good job with the PMP and the PIP, as the data generating process gets the highest PMP using both approaches, and the PIPs of the variables in the data generating process are equal 1. The critical point is the BMA posterior means of the endogenous regressors, as these are far from the population values. The population values of x_{i1} and x_{i2} are 0.5 and -1, whereas the posterior means are 0.97 and -0.52.

R code. BIC and MC3 in model with endogeneity

```

1 rm(list = ls())
2 set.seed(010101)
3 simIV <- function(delta1,delta2,beta0,betas1,betas2,beta2,
4   Sigma,n,z) {
5   eps <- matrix(rnorm(3*n),ncol=3) %%% chol(Sigma)
6   xs1 <- z%*%delta1 + eps[,1]
7   xs2 <- z%*%delta2 + eps[,2]
8   x2 <- rnorm(dim(z)[1])
9   y <- beta0+betas1*xs1+betas2*xs2+beta2*x2 + eps[,3]
10  X <- as.matrix(cbind(xs1,xs2,1,x2))
11  colnames(X) <- c("x1en","x2en","cte","xex")
12  y <- matrix(y,dim(z)[1],1)
13  colnames(y) <- c("y")
14  list(X=X,y=y)
15 }
16 n <- 1000 ; p <- 3
17 z <- matrix(runif(n*p),ncol=p)
18 rho31 <- 0.8; rho32 <- 0.5;
19 Sigma <- matrix(c(1,0,rho31,0,1,rho32,rho31,rho32,1),ncol=3)
20 delta1 <- c(4,-1,2); delta2 <- c(-2,3,-1); betas1 <- .5;
21 betas2 <- -1; beta2 <- 1; beta0 <- 2
22 simiv <- simIV(delta1,delta2,beta0,betas1,betas2,beta2,Sigma,
23   n,z)
24 nW <- 18
25 W <- matrix(rnorm(nW*dim(z)[1]),dim(z)[1],nW)
26 YXW<-cbind(simiv$y, simiv$X, W)
27 y <- YXW[,1]; X <- YXW[,2:3]; W <- YXW[,-c(1:4)]
28 Xnew <- cbind(X, W)
29 BMAglm <- BMA::bicreg(Xnew, y, strict = FALSE, OR = 50)
30 summary(BMAglm)
31 BMAREg <- BMA::MC3.REG(y, Xnew, num.its=10000)
32 Models <- unique(BMAREg[["variables"]])
33 nModels <- dim(Models)[1]
34 nVistModels <- dim(BMAREg[["variables"]])[1]
35 K <- dim(Xnew)[2]
36 PMP <- NULL
37 for(m in 1:nModels){
38   idModm <- NULL
39   for(j in 1:nVistModels){
40     if(sum(Models[m,] == BMAREg[["variables"]][j,]) == K){
41       idModm <- c(idModm, j)
42     }else{
43       idModm <- idModm
44     }
45   }
46   PMPm <- sum(BMAREg[["post.prob"]][idModm])
47   PMP <- c(PMP, PMPm)
48 }
49 PMP
50 PIP <- NULL
51 for(k in 1:K){
52   PIPk <- sum(PMP[which(Models[,k] == 1)])
53   PIP <- c(PIP, PIPk)
54 }
55 plot(PIP)

```

R code. BIC and MC3 in model with endogeneity

```

1 Means <- matrix(0, nModels, K)
2 Vars <- matrix(0, nModels, K)
3 for(m in 1:nModels){
4   idXs <- which(Models[m,] == 1)
5   if(length(idXs) == 0){
6     Regm <- lm(y ~ 1)
7   }else{
8     Xm <- Xnew[, idXs]
9     Regm <- lm(y ~ Xm)
10    SumRegm <- summary(Regm)
11    Means[m, idXs] <- SumRegm[["coefficients"]][-1,1]
12    Vars[m, idXs] <- SumRegm[["coefficients"]][-1,2]^2
13  }
14 }
15 BMAMEANS <- colSums(Means*PMP)
16 BMASD <- (colSums(PMP*Vars) + colSums(PMP*(Means-matrix(rep
17   (BMAMEANS, each = nModels), nModels, K))^2))^0.5
18 plot(BMAMEANS)
19 plot(BMASD)
20 plot(BMAMEANS/BMASD)

```

The previous results are intuitive, as the PMP are calculated based on fit (and penalty for complexity), for instance, $BIC = k_m \log(N) - 2\log(p(\hat{\theta}_m|\mathbf{y}))$, where $\hat{\theta}_m$ is the maximum likelihood estimator. Observe that the fit is not affected by endogeneity. Thus, the PMP are well calculated. However, the coefficients are not well identified.

This suggests a simple strategy to perform BMA taking into account endogeneity, calculate the PMPs using standard BMA approaches, for instance, BIC approximation, and then estimate the BMA means using these PMPs, but estimating the different models using instrumental variables. This approach is easily implemented using packages from **R**. The following code does this:

R code. Easy IV BMA

```

1 BMAglm <- BMA::bicreg(Xnew, y, strict = FALSE, OR = 50)
2 summary(BMAglm)
3 PMPBIC <- BMAglm[["postprob"]]
4 ModelsBIC <- BMAglm[["which"]]
5 nModels <- dim(ModelsBIC)[1]
6 K <- dim(Xnew)[2]
7 Means <- matrix(0, nModels, K)
8 Vars <- matrix(0, nModels, K)
9 for(m in 1:nModels){
10   idXs <- which(ModelsBIC[m,] == 1)
11   if(length(idXs) == 0){
12     Regm <- lm(y ~ 1)
13   }else{
14     Xm <- Xnew[, idXs]
15     Regm <- ivreg::ivreg(y ~ Xm | z + W)
16     SumRegm <- summary(Regm)
17     Means[m, idXs] <- SumRegm[["coefficients"]][-1,1]
18     Vars[m, idXs] <- SumRegm[["coefficients"]][-1,2]^2
19   }
20 }
21 BMAMEANS <- colSums(Means*PMPBIC)
22 BMASd <- (colSums(PMPBIC*Vars) + colSums(PMPBIC*(Means -
23   matrix(rep(BMAMEANS, each = nModels), nModels, K))^2))
24   ^0.5
25 BMAMEANS
26 5.589366e-01 -9.431664e-01 1.035593e+00 -1.967444e-05
27 -1.429801e-04 -3.310215e-04 4.036846e-04 4.651796e-03
28 -2.673730e-03 6.462503e-05 4.286529e-04 -1.829889e-04
29 5.073229e-03 -1.007356e-04 -5.377972e-04 1.644475e-03
30 -4.029205e-04 -1.457381e-04 6.421582e-04 2.211994e-04
31 2.216503e-04
32
33 plot(BMASd)
34 plot(BMAMEANS/BMASd)
35 17.764095075 -23.233601133 34.734610916 -0.005600369
36 -0.039168667 -0.071895067 0.080909448 0.274994618
37 -0.210854131 0.018790592 0.061271650 -0.047117887
38 0.305639285 -0.028830411 -0.092463544 0.169455952
39 -0.058299940 -0.038099792 0.102373567 0.056074670
40 0.055500343

```

We observe that the Easy IV BMA means of the endogenous regressors are 0.59 and -0.94, which are closer to the population values (0.5 and -1) than the exogenous BMA means (0.97 and -0.52) and align closely with the IV BMA means calculated using conditional Bayes factors (0.51 and -0.98; see Section 10.2 in the book). Additionally, the ratios between the Easy IV

BMA means and their standard deviations exceed 2 in absolute value for these variables, and the t-intervals encompass the population values

5. Determinants of export diversification II

Use the datasets *11ExportDiversificationHHI.csv* and *12ExportDiversificationHHIInstr.csv* to perform IV BMA assuming that the log of per capita gross domestic product is endogenous (*avglgdpcap*). See [11] for details.

Answer

The results show that primary education (*avgedu5*) and natural resources (*avgnatres*) have again the highest PIP, 0.77 and 0.92, respectively. The former variable increases export diversification, and the latter decreases export diversification. However, it seems that endogeneity is not a concern in this application, as the 95% credible interval of σ_{12} is (-0.014, 0.024).

R code. IV BMA in export diversification

```

1 rm(list = ls())
2 set.seed(010101)
3 DataMain <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/11
  ExportDiversificationHHI.csv", sep = ",", header = TRUE,
  quote = "")
4 DataInst <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/12
  ExportDiversificationHHIInstr.csv", sep = ",", header =
  TRUE, quote = "")
5 attach(DataMain)
6 attach(DataInst)
7 y <- DataMain[,1]
8 X <- as.matrix(DataMain[,2])
9 W <- as.matrix(DataMain[,c(1:2)])
10 Z <- as.matrix(DataInst)
11 S <- 10000; burnin <- 1000
12 regivBMA <- ivbma::ivbma(Y = y, X = X, Z = Z, W = W, s = S+
  burnin, b = burnin, odens = S, print.every = round(S/10)
  , run.diagnostics = FALSE)
13 PIPmain <- regivBMA[["L.bar"]] # PIP outcome
14 PIPmain
15 EVmain <- regivBMA[["rho.bar"]] # Posterior mean outcome
16 EVmain
17 PIPaux <- regivBMA[["M.bar"]] # PIP auxiliary
18 PIPaux
19 EVaux <- regivBMA[["lambda.bar"]] # Posterior mean auxiliary
20 plot(EVaux[,1])
21 EVsigma <- regivBMA[["Sigma.bar"]] # Posterior mean variance
  matrix
22 EVsigma
23 summary(coda::mcmc(regivBMA[["Sigma"]][1,2,]))
24 Iterations = 1:10000
25 Thinning interval = 1
26 Number of chains = 1
27 Sample size per chain = 10000
28 1. Empirical mean and standard deviation for each variable,
29 plus standard error of the mean:
30 Mean          SD          Naive SE Time-series SE
31 3.944e-03      9.592e-03      9.592e-05      4.043e-04
32 2. Quantiles for each variable:
33 2.5%          25%          50%          75%          97.5%
34 -0.014155     -0.002415     0.003592     0.009988     0.024047

```

6. Show that the link function in the case of the Bernoulli distribution is $\log\left(\frac{\theta}{1-\theta}\right)$.

Answer

$$\begin{aligned}
 p(\mathbf{y}|\theta) &= \theta^y(1-\theta)^{1-y} \\
 &= (1-\theta) \exp \left\{ y \log \left(\frac{\theta}{1-\theta} \right) \right\} \\
 &= \exp \left\{ y \log \left(\frac{\theta}{1-\theta} \right) + \log(1-\theta) \right\},
 \end{aligned}$$

then $\eta(\theta) = \log \left(\frac{\theta}{1-\theta} \right)$, and this density in the canonical form is $p(y|\eta) = \exp \{ y\eta - \log(1 + \exp(\eta)) \}$ consequently, $\mathbb{E}[Y|\mathbf{x}] = \nabla (\log(1 + \exp(\eta))) = \frac{\exp(\eta)}{1 + \exp(\eta)} = \theta = \frac{\exp(\mathbf{x}^\top \boldsymbol{\beta})}{1 + \exp(\mathbf{x}^\top \boldsymbol{\beta})}$. Then, the link function in the Bernoulli case is the *logit* function.

7. [23, 24] perform variable selection using the file *13InternetMed.csv*. In this data set, the dependent variable is an indicator of Internet adoption (internet) for 5000 households in Medellín (Colombia) during the period 2006–2014. This dataset contains information about 18 potential determinants, which means 262144 (2^{18}) potential models just taking into account variable uncertainty (see these papers for details about the data set). Perform BMA using the logit link function using this data set.

Answer

R code. BMA logit in internet adoption

```

1 rm(list = ls())
2 set.seed(010101)
3 DataMain <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/13InternetMed
  .csv", sep = ",", header = TRUE, quote = "")
4 attach(DataMain)
5 ### BIC approximation
6 y <- DataMain[,1]
7 X <- as.matrix(DataMain[, -1])
8 BMAGlm <- BMA::bic.glm(X, y, strict = FALSE, OR = 50, glm.
  family = binomial(link="logit"))
9 summary(BMAGlm)
10

```

The results show that the best model has a posterior model probability equal to 31%, and the second best model has a PMP equal to 30%. It seems that age, squared age, years of education of the head of the household, total expenses, having pay TV, any household member studying, and number of children in the household are relevant determinants of Internet adoption.

8. [28] use the file *14ValueFootballPlayers.csv* to analyze the market value of soccer players in the most important leagues in Europe. In particular, there are 26 potential determinants of the market value (dependent variable) of a stratified sample of 335 soccer players in the five most important leagues in Europe (see [28] for details). Use this data set to perform BMA using the gamma distribution with the log link function, and setting default values for Occam's window.

Answer

R code. BMA gamma in market value of soccer players in Europe

```

1 rm(list = ls())
2 set.seed(010101)
3 DataMain <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/14
  ValueFootballPlayers.csv", sep = ",", header = TRUE,
  quote = "")
4 attach(DataMain)
5 ### BIC approximation
6 y <- DataMain[,1]
7 X <- as.matrix(DataMain[,-1])
8 BMAGlm <- BMA::bic.glm(X, y, strict = FALSE, OR = 50, glm.
  family = Gamma(link="log"))
9 summary(BMAGlm)

```

The results show that performance, age, squared age, participation in national team, scored goals, and appearance in the UEFA champions league have PIPs equal 1. All these variables increase the market value of soccer players, except squared age.

9. Use the dataset *15Fertile2.csv* from [33, p. 547] to perform BMA using the Poisson model with the log link. This data set has information about 1,781 women from Botswana in 1988 (for details, see <https://rdrr.io/cran/wooldridge/man/fertil2.html>, and take into account that we deleted some variables and omitted observations with NA values). The dependent variable is the number of children ever born (ceb), which is a count variable, as a function of 19 potential determinants.

Answer

***R code. BMA Poisson in determinants of fertility
in Botswana***

```

1 rm(list = ls())
2 set.seed(010101)
3 DataMain <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/15Fertil2.csv",
  sep = ",", header = TRUE, quote = "")
4 attach(DataMain)
5 ### BIC approximation
6 y <- DataMain[,1]
7 X <- as.matrix(DataMain[,-1])
8 BMAglm <- BMA::bic.glm(X, y, strict = FALSE, OR = 50, glm.
  family = poisson(link="log"))
9 summary(BMAglm)

```

We found that the best model, for which the PMP is equal to 27%, has as regressors age, squared age, age at first birth, use birth control, husband's years of education, woman's years of education, and living in an urban area. The first five variables have PIPs equal to 100. For instance, we found that women using birth control have approximately 15% fewer children on average than women who are not using birth control.

10. Perform BMA in the logit model using MC3 and the BIC approximation using the simulation setting of Section 10.3.

Answer

R code. BMA Logit model

```

1 rm(list = ls()); set.seed(010101)
2 n<-1000; B<-c(0.5,0.8,-1.2)
3 X<-matrix(cbind(rep(1,n),rnorm(n,0,1),rnorm(n,0,1)),n,length
  (B))
4 p <- exp(X%*%B)/(1+exp(X%*%B))
5 y <- rbinom(n, 1, p); table(y)
6 nXgar<-25; Xgar<-matrix(rnorm(nXgar*n),n,nXgar)
7 df<-as.data.frame(cbind(y,X[, -1],Xgar))
8 colnames(df) <- c("y", "x1", "x2", "x3", "x4", "x5", "x6", "
  x7", "x8", "x9", "x10", "x11", "x12", "x13", "x14", "x15
  ", "x16", "x17", "x18", "x19", "x20", "x21", "x22", "x23
  ", "x24", "x25", "x26", "x27")
9 Xnew <- apply(df[, -1], 2, scale)
10 BICfunt <- function(Model){
11   indr <- Model == 1
12   kr <- sum(indr)
13   if(kr > 0){
14     Xr <- as.matrix(Xnew[, indr])
15     model <- glm(y ~ Xr, family = binomial(link = "logit"))
16     model_bic <- BIC(model)
17     mllMod <- -model_bic/2
18   }else{
19     model <- glm(y ~ 1, family = binomial(link = "logit"))
20     model_bic <- BIC(model)
21     mllMod <- -model_bic/2
22   }
23   return(mllMod)
24 }
25 M <- 500; K <- dim(df)[2] - 1
26 Models <- matrix(rbinom(K*M, 1, p = 0.5), ncol = K, nrow = M
  )
27 mllnew <- sapply(1:M, function(s){BICfunt(matrix(Models[s,],
  1, K))})
28 oind <- order(mllnew, decreasing = TRUE)
29 mllnew <- mllnew[oind]; Models <- Models[oind, ]
30 iter <- 25000; s <- 1
31 pb <- winProgressBar(title = "progress bar", min = 0, max =
  iter, width = 300)
32 while(s <= iter){
33   ActModel <- Models[M,]
34   idK <- which(ActModel == 1)
35   Kact <- length(idK)
36   if(Kact < K & Kact > 1){
37     CardMol <- K; opt <- sample(1:3, 1)
38     if(opt == 1){ # Same
39       CandModel <- ActModel
40     }else{
41       if(opt == 2){ # Add
42         All <- 1:K; NewX <- sample(All[-idK], 1)
43         CandModel <- ActModel; CandModel[NewX] <- 1
44       }else{ # Subtract
45         LessX <- sample(idK, 1)
46         CandModel <- ActModel; CandModel[LessX] <- 0
47       }
48     }
49   }
50 }

```

R code. BMA Logit model

```

1   }else{
2   CardMol <- K + 1
3   if(Kact == K){
4     opt <- sample(1:2, 1)
5     if(opt == 1){ # Same
6       CandModel <- ActModel
7     }else{ # Subtract
8       LessX <- sample(1:K, 1)
9       CandModel <- ActModel
10      CandModel[LessX] <- 0
11    }
12  }else{
13    if(K == 1){
14      opt <- sample(1:3, 1)
15      if(opt == 1){ # Same
16        CandModel <- ActModel
17      }else{
18        if(opt == 2){ # Add
19          All <- 1:K
20          NewX <- sample(All[-idK], 1)
21          CandModel <- ActModel
22          CandModel[NewX] <- 1
23        }else{ # Subtract
24          LessX <- sample(idK, 1)
25          CandModel <- ActModel
26          CandModel[LessX] <- 0
27        }
28      }
29    }else{ # Add
30      NewX <- sample(1:K, 1)
31      CandModel <- ActModel
32      CandModel[NewX] <- 1
33    }
34  }
35  }
36  LogMLact <- BICfunt(matrix(ActModel, 1, K))
37  LogMLcand <- BICfunt(matrix(CandModel, 1, K))
38  alpha <- min(1, exp(LogMLcand-LogMLact)) # Let's reasonably
39  assume same prior model probability for candidate and
40  actual, and same carnality of neighbor models
41  u <- runif(1)
42  if(u <= alpha){
43    mllnew[M] <- LogMLcand
44    Models[M, ] <- CandModel
45    oind <- order(mllnew, decreasing = TRUE)
46    mllnew <- mllnew[oind]
47    Models <- Models[oind, ]
48  }else{
49    mllnew <- mllnew
50    Models <- Models
51  }
52  s <- s + 1
53  setWinProgressBar(pb, s, title=paste( round(s/iter*100, 0),"
54    % done"))
55  }
56  close(pb)

```

R code. BMA Logit model

```

1 ModelsUni <- unique(Models)
2 mllnewUni <- sapply(1:dim(ModelsUni)[1], function(s){BICfunt
  (matrix(ModelsUni[s,], 1, K))})
3 StMarLik <- exp(mllnewUni-mllnewUni[1])
4 PMP <- StMarLik/sum(StMarLik) # PMP based on unique selected
  models
5 plot(PMP)
6 ModelsUni[1,]
7 PIP <- NULL
8 for(k in 1:K){
9   PIPk <- sum(PMP[which(ModelsUni[,k] == 1)])
10  PIP <- c(PIP, PIPk)
11 }
12 plot(PIP)
13 Xnew <- df[,-1]
14 nModels <- dim(ModelsUni)[1]
15 Means <- matrix(0, nModels, K)
16 Vars <- matrix(0, nModels, K)
17 for(m in 1:nModels){
18   idXs <- which(ModelsUni[m,] == 1)
19   if(length(idXs) == 0){
20     Regm <- glm(y ~ 1, family = binomial(link = "logit"))
21   }else{
22     Xm <- as.matrix(Xnew[, idXs])
23     Regm <- glm(y ~ Xm, family = binomial(link = "logit"))
24     SumRegm <- summary(Regm)
25     Means[m, idXs] <- SumRegm[["coefficients"]][-1,1]
26     Vars[m, idXs] <- SumRegm[["coefficients"]][-1,2]^2
27   }
28 }
29 BMAMEANS <- colSums(Means*PMP)
30 BMASD <- (colSums(PMP*Vars) + colSums(PMP*(Means-matrix(rep
  (BMAMEANS, each = nModels), nModels, K))^2))^0.5
31 plot(BMAMEANS)
32 plot(BMASD)
33 plot(BMAMEANS/BMASD)

```

The simulation setting implies 2^{27} models, which implies approximately 135 million models in the model space. We run our MC3 algorithm using the BIC approximation with 25000 iterations. This takes by far more time than the BIC approximation from the *BMA* package, but it seems to do a good job finding the data generating process as the highest PMP is associated with it, the PIPs of x_{i1} and x_{i2} are 1, the posterior means are 0.85 and -1.1, which are very close to the population values (0.8 and -1.2), and the

t-ratios are by far higher than 2. The PIPs of the other regressors are lower than 20%, and the BMA means are close to 0.

11. Use the dataset *19ExchangeRateCOPUSD.csv* to estimate four different *state-space models* to explain the annual variation of the COP to USD exchange rate:

- Interest rate parity

$$\Delta e_t = \beta_{1t}^{IRP} + \beta_{2t}^{IRP}(i_{t-1}^{Col} - i_{t-1}^{USA}) + \mu_t^{IRP}$$

- Purchasing power parity

$$\Delta e_t = \beta_{1t}^{PPP} + \beta_{2t}^{PPP}(\pi_{t-1}^{Col} - \pi_{t-1}^{USA}) + \mu_t^{PPP}$$

- Taylor rule

$$\Delta e_t = \beta_{1t}^{Taylor} + \beta_{2t}^{Taylor}(\pi_{t-1}^{Col} - \pi_{t-1}^{USA}) + \beta_{2t}^{Taylor}(g_{t-1}^{Col} - g_{t-1}^{USA}) + \mu_t^{IRP}$$

- Money supply

$$\Delta e_t = \beta_{1t}^{Money} + \beta_{2t}^{Money}(g_{t-1}^{Col} - g_{t-1}^{USA}) + \beta_{2t}^{Money}(m_{t-1}^{Col} - m_{t-1}^{USA}) + \mu_t^{Money}$$

where $varTRM$ (Δe_t) is the annual variation rate of the exchange rate COP to USD, TES_COL10 (i_t^{Col}) and TES_USA10 (i_t^{USA}) are the annual return rates of Colombian and USA public debts in 10 years, $inflation_COL$ (π_t^{Col}) and $inflation_USA$ (π_t^{USA}) are the annual inflation rates, $varISE_COL$ (g_t^{Col}) and $varISE_USA$ (g_t^{USA}) are annual variation of economic activity indices, and $varCOL_M3$ (m_t^{Col}) and $varUSA_M3$ (m_t^{USA}) are annual variations of money supply. We have monthly variations between January 2006 and November 2023.

Perform Bayesian model averaging using these four models to explain the annual variation of the exchange rate, get the posterior model probabilities, and plot the posterior mean and credible interval of β_{2t}^{Money} .

Answer

*R code. Dynamic Bayesian model average:
Theories to explain (forecast) exchange rate*

```

1 rm(list = ls()); set.seed(010101)
2 DataMain <- read.csv("https://raw.githubusercontent.com/
  besmarter/BSTApp/refs/heads/master/DataApp/19
  ExchangeRateCOPUSD.csv", sep = ",", header = TRUE, quote
    = "")
3 X <- DataMain[-c(1:12,227),c(4, 5, 7, 9, 11, 13, 14, 15)]
4 DifIntRat <- X[,8] - X[,7]; DifInf <- X[,1] - X[,2]
5 DifGrowth <- X[,3] - X[,4]; DifM3 <- X[,6] - X[,5]
6 XDif <- cbind(DifIntRat, DifInf, DifGrowth, DifM3)
7 matplot(XDif, type = "l")
8 y <- DataMain[-c(1:13),17] # Var exchange rate depends on
  lag of other variables
9 plot(y, type = "l")
10 IRP <- c(1, 0, 0, 0); PPP <- c(0, 1, 0, 0)
11 Taylor <- c(0, 1, 1, 0); Money <- c(0, 0, 1, 1)
12 Models <- rbind(IRP, PPP, Taylor, Money)
13 T0 <- 50
14 dma.test <- dma::dma(XDif, y, Models, lambda=.99, gamma=.99,
  initialperiod = T0)
15 plot(ts(dma.test[["pmp"]][,1], start = 2006, end = 2023,
  frequency = 12), type = "l", main = "Exchange rate
  models", ylab = "Posterior model probability", ylim = c
    (0,1)) lines(ts(dma.test[["pmp"]][,2], start = 2006, end
    = 2023, frequency = 12), col = "red") lines(ts(dma.test
    [["pmp"]][,3], start = 2006, end = 2023, frequency = 12)
    , col = "green") lines(ts(dma.test[["pmp"]][,4], start =
    2006, end = 2023, frequency = 12), col = "blue") legend
    (x = 2009, y = 0.6, legend = c("IRP", "PPP", "Taylor
    rule", "Money supply"), col = c("black", "red", "green",
    "blue"), lty=1:1, cex=0.8)
16 require(latex2exp)
17 plot_filtering_estimates <- function(df) {
18   p <- ggplot(data = df, aes(x = t)) + geom_ribbon(aes(ymin
    = lower, ymax = upper), alpha = 0.5, fill = "blue") +
    geom_line(aes(y = mean), colour = "black", linewidth =
    0.8) + geom_hline(yintercept=0, colour = "red") + ylab(
    TeX("$\\beta_{Growth_t}^{\\{Money\\}}$")) + xlab("Time")
19   print(p)
20 }
21 menathetaIRP <- dma.test[["thetahat"]][4,,4]
22 SDthetaIRP <- (dma.test[["Vtheta"]][4,,4])^0.5
23 LimInf <- menathetaIRP - 2*SDthetaIRP
24 LimSup <- menathetaIRP + 2*SDthetaIRP
25 library(ggplot2,tibble,dplyr)
26 df <- tibble(t = 1:214, mean = menathetaIRP, lower = LimInf,
  upper = LimSup)
27 Fig <- plot_filtering_estimates(df)

```

Figure 10.1 shows the posterior model probabilities. We see that at the beginning, between 2006 and 2007, the purchasing power parity theory (PPP) had the highest PMP (70% on average) to explain the annual variations of the COP/USD exchange rate. Then, the money supply theory (Money) got the highest PMP (80% on average) between 2008 and 2017. Finally, the interest rate parity got the highest PMP (80% on average) between 2018 and 2023.

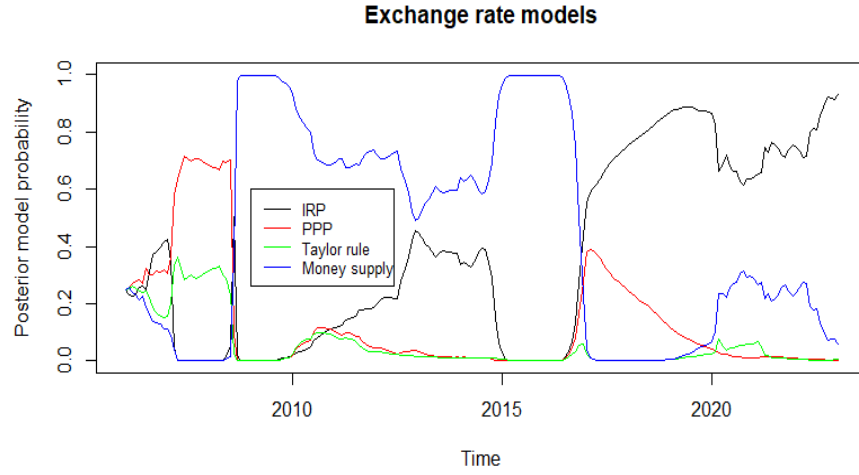


FIGURE 10.1

Dynamic posterior model probability: Models to explain variations of the COP to USD exchange rate.

Figure 10.2 shows the dynamic posterior mean (black line) and credible interval (blue shadow) of the coefficient related to the differential of economic growths (Colombia vs the USA) in the money supply equation to explain the annual variations of the exchange rate. We observe that increasing this economic growth differential implies appreciation of the COP relatively to USD.

12. Perform a simulation of the dynamic logistic model, where there are 7 ($2^3 - 1$, the model without regressors is excluded) competing models originated from 3 regressors, $x_{tk} \sim N(0.5, 0.8^2)$, $k = 2, 3, 4$, and $\beta_1 = 0.5$, β_{2t} is a sequence from 1 to 2 in steps given by $1/T$, $\beta_{3t} = \begin{cases} -1, & 1 < t \leq 0.5T \\ 0, & 0.5T < t \leq T \end{cases}$, and $\beta_4 = 1.2$. Then, $\mathbf{x}_t^\top \boldsymbol{\beta}_t = \beta_1 + \beta_{2t}x_{2t} + \beta_{3t}x_{3t} + \beta_4x_{4t}$, where $P[Y_t = 1 | \mathbf{x}_t, \boldsymbol{\beta}_t] = \exp(\mathbf{x}_t^\top \boldsymbol{\beta}_t) / (1 + \exp(\mathbf{x}_t^\top \boldsymbol{\beta}_t))$, $t = 1, 2, \dots, 1100$. Use the function *logistic.dma* from the *dma* package to get the posterior model probabilities

**FIGURE 10.2**

State coefficient money supply theory: Differential of economic growths (Colombia vs the USA).

setting the forgetting parameter of the models equal to 0.99, and then to 0.95. Compare the results.

Answer

The following code shows the simulation exercise, and the results of the dynamic Bayesian model average of logistic models.

R code. Dynamic Bayesian model average: Logit model

```

1 rm(list = ls()); set.seed(010101)
2 T <- 1100; K <- 3
3 X <- matrix(rnorm(T*K, mean = 0.5, sd = 0.8), T, K)
4 combs <- expand.grid(c(0,1), c(0,1), c(0,1))
5 B1 <- 0.5; B2t <- seq(1, 2, length.out=T)
6 a <- 0.5
7 B3t <- c(rep(-1, round(a*T)), rep(0, round((1-a)*T)))
8 B4 <- 1.2
9 yl <- B1 + X[,1]*B2t + X[,2]*B3t + X[,3]*B4
10 py <- exp(yl)/(1 + exp(yl))
11 y <- rbinom(T, 1, prob = py)
12 table(y)
13 T0 <- 100
14 dma.test <- dma::logistic.dma(X, y, combs[-1,], lambda =
    0.99, alpha = 0.99, initialsamp = T0)
15 plot(dma.test[["pmp"]][7, -c(1:T0)], type = "l", col = "
    green", main = "Posterior model probability: Model all
    regressors vs model regressors 1 and 3", xlab = "Time",
    ylab = "PMP", ylim = c(0, 1))
16 lines(dma.test[["pmp"]][5, -c(1:T0)], col = "red")
17 legend(x = 0, y = 0.9, legend = c("Model: All regressors", "
    Model: Regressors 1 and 3"), col = c("green", "red"),
    lty=1:1, cex=0.8)
18 dma.test1 <- dma::logistic.dma(X, y, combs[-1,], lambda =
    0.99, alpha = 0.95, initialsamp = T0)
19 plot(dma.test1[["pmp"]][7, -c(1:T0)], type = "l", col = "
    green", main = "Posterior model probability: Model all
    regressors vs model regressors 1 and 3", xlab = "Time",
    ylab = "PMP", ylim = c(0, 1))
20 lines(dma.test1[["pmp"]][5, -c(1:T0)], col = "red")
21 legend(x = 0, y = 0.9, legend = c("Model: All regressors", "
    Model: Regressors 1 and 3"), col = c("green", "red"),
    lty=1:1, cex=0.8)

```

Figure 10.3 shows the posterior model probabilities of the model with all the regressors (green line), and the model with regressors 2 and 4 (red line), setting the forgetting parameter of the models equal to 0.99. In one hand, we see that the model with all regressors, which is the data generating process in the first period ($t \leq 0.5T$), gets high posterior model probabilities. We see that the PMPs decrease around $T = 700$, whereas the change in the data generating process is at $T = 550$. This means that there is a lack to identify the data generating process, which is a consequence of the high forgetting parameter of the models. Consequently, the PMPs of the model with regressors 2 and 4 increases around $T = 700$, but it is lower than the

PMPs of the model with all regressors, despite that in this time period the data generating process is given by the model with regressors 2 and 4.

Figure 10.4 shows the posterior model probabilities using a forgetting parameter equal to 0.95. We can see that as the forgetting parameter decreases, the process of identifying the data generating process is faster, and consequently, the PMP of the model with regressors 2 and 4 increases around $T = 550$, which is the turning point in the data generating process. This does not mean that we should set small forgetting parameters. These parameters should be set based on model performance, for instance, small mean squared error in a cross validation period.



FIGURE 10.3

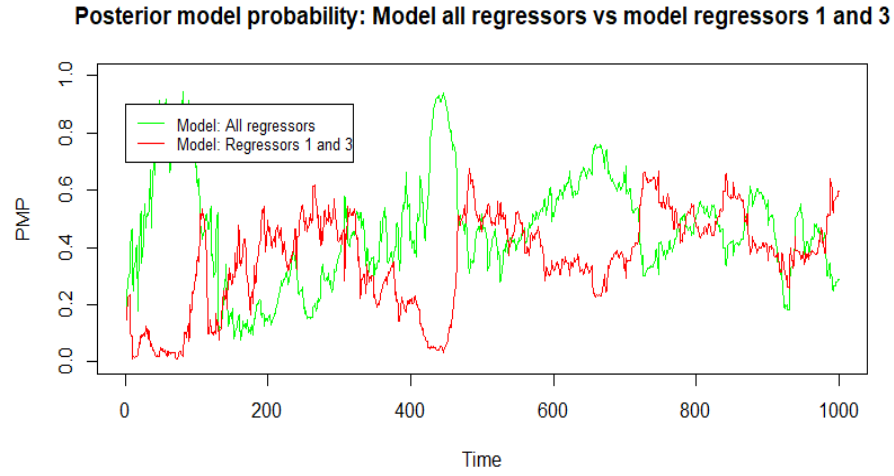
Posterior model probability: Dynamic Bayesian model average, forgetting parameter equal to 0.99.

13. Show that

$$\mathbb{E} \left[\frac{q(\boldsymbol{\theta})}{\pi(\boldsymbol{\theta}|\mathcal{M}_m)p(\mathbf{y}|\boldsymbol{\theta}_m, \mathcal{M}_m)} \middle| \mathbf{y}, \mathcal{M}_m \right] = \frac{1}{p(\mathbf{y}|\mathcal{M}_m)},$$

where the expected value is with respect to the posterior distribution given the model \mathcal{M}_m , and $q(\boldsymbol{\theta})$ is the proposal distribution whose support is $\boldsymbol{\Theta}$.

Answer

**FIGURE 10.4**

Posterior model probability: Dynamic Bayesian model average, forgetting parameter equal to 0.95.

Given a probability density function $q(\boldsymbol{\theta})$, whose support is in $\boldsymbol{\Theta}$, then

$$\begin{aligned}
 \mathbb{E} \left[\frac{q(\boldsymbol{\theta})}{\pi(\boldsymbol{\theta}|\mathcal{M}_m)p(\mathbf{y}|\boldsymbol{\theta}_m, \mathcal{M}_m)} \middle| \mathbf{y}, \mathcal{M}_m \right] &= \int_{\boldsymbol{\Theta}} \left[\frac{q(\boldsymbol{\theta})}{\pi(\boldsymbol{\theta}|\mathcal{M}_m)p(\mathbf{y}|\boldsymbol{\theta}_m, \mathcal{M}_m)} \right] \pi(\boldsymbol{\theta}|\mathbf{y}, \mathcal{M}_m) d\boldsymbol{\theta} \\
 &= \int_{\boldsymbol{\Theta}} \left[\frac{q(\boldsymbol{\theta})}{\pi(\boldsymbol{\theta}|\mathcal{M}_m)p(\mathbf{y}|\boldsymbol{\theta}_m, \mathcal{M}_m)} \right] \frac{\pi(\boldsymbol{\theta}|\mathcal{M}_m)p(\mathbf{y}|\boldsymbol{\theta}_m, \mathcal{M}_m)}{p(\mathbf{y}|\mathcal{M}_m)} d\boldsymbol{\theta} \\
 &= \frac{1}{p(\mathbf{y}|\mathcal{M}_m)} \int_{\boldsymbol{\Theta}} q(\boldsymbol{\theta}) d\boldsymbol{\theta} \\
 &= \frac{1}{p(\mathbf{y}|\mathcal{M}_m)}.
 \end{aligned}$$



Part III

Advanced methods: A brief introduction



11

Semi-parametric and non-parametric models

Solutions of Exercises

1. Simulate a semi-parametric regression where

$$y_i = 0.5x_{i1} - 1.2x_{i2} + \mu_i,$$
$$p(\mu_i) = 0.3\phi(\mu_i \mid -0.5, 0.5^2) + 0.7\phi(\mu_i \mid 1, 0.8^2).$$

Assume that x_{i1} and x_{i2} follow a standard normal distribution and that the sample size is 1,000. Perform inference in this model assuming that the number of components is unknown. Start with $H = 5$ and use non-informative priors, setting $\alpha_{h0} = \delta_{h0} = 0.01$, $\beta_0 = \mathbf{0}_2$, $\mathbf{B}_0 = \mathbf{I}_2$, $\mu_{h0} = 0$, $\sigma_{\mu 0}^2 = 10$, and $\boldsymbol{\alpha}_0 = [1/H \ \dots \ 1/H]^\top$. Use 6,000 MCMC iterations, a burn-in period of 4,000, and a thinning parameter of 2. Compare the population parameters with the posterior estimates and plot the population density along with the posterior density estimate of $\boldsymbol{\mu}$ (the mean, and the 95% credible interval).

Answer

We can see from the posterior estimates that three components disappear after the burn-in iterations. The 95% credible intervals encompass the population values of all parameters, and the posterior density estimate closely matches the population density. See Figure 11.1, where the black line represents the population density, the blue line denotes the posterior mean density estimate, and the shaded light blue area corresponds to the 95% credible interval.

R code. Simulation: Semi-parametric Gaussian mixture

```

1 rm(list = ls()); set.seed(010101)
2 # Simulate data from a 2-component mixture model
3 n <- 1000
4 x1 <- rnorm(n); x2 <- rnorm(n)
5 B <- c(0.5, -1.2); X <- cbind(x1, x2)
6 z <- rbinom(n, 1, 0.3) # Latent class indicator
7 mu <- ifelse(z == 0, rnorm(n, -0.5, 0.5), rnorm(n, 1, 0.8))
8 plot(density(mu))
9 y <- X%*%B + mu
10 # Hyperparameters
11 d0 <- 0.001; a0 <- 0.001
12 b0 <- rep(0, 2); B0 <- diag(2); B0i <- solve(B0)
13 mu0 <- 0; sig2mu0 <- 10
14 H <- 5; a0h <- rep(1/H, H)
15 # MCMC parameters
16 mcmc <- 2000
17 burnin <- 4000
18 tot <- mcmc + burnin
19 thin <- 2
20 # Gibbs sampling functions
21 PostSig2 <- function(Beta, muh, Xh, yh){
22   Nh <- length(yh)
23   an <- a0 + Nh
24   dn <- d0 + t(yh - muh - Xh%*%Beta)%*(yh - muh - Xh%*%Beta)
25   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
26   return(sig2)
27 }
28 PostBeta <- function(sig2, mu, X, y, Psi){
29   XtX <- matrix(0, 2, 2)
30   Xty <- matrix(0, 2, 1)
31   Hs <- length(mu)
32   for(h in 1:Hs){
33     idh <- which(Psi == h)
34     if(length(idh) == 1){
35       Xh <- matrix(X[idh,], 1, 2)
36       XtXh <- sig2[h]^(-1)*t(Xh)%*%Xh
37       yh <- y[idh]
38       Xtyh <- sig2[h]^(-1)*t(Xh)%*(yh - mu[h])
39     }else{
40       Xh <- X[idh,]
41       XtXh <- sig2[h]^(-1)*t(Xh)%*%Xh
42       yh <- y[idh]
43       Xtyh <- sig2[h]^(-1)*t(Xh)%*(yh - mu[h])
44     }
45     XtX <- XtX + XtXh
46     Xty <- Xty + Xtyh
47   }
48   Bn <- solve(B0i + XtX)
49   bn <- Bn%*(B0i%*%b0 + Xty)
50   Beta <- MASS::mvrnorm(1, bn, Bn)
51   return(Beta)
52 }

```


R code. Simulation: Semi-parametric Gaussian mixture

```

1 Postmu <- function(sig2h, Beta, Xh, yh){
2   Nh <- length(yh)
3   sig2mu <- (1/sig2mu0 + Nh/sig2h)^(-1)
4   mun <- sig2mu*(mu0/sig2mu0 + sum((yh - Xh*%Beta))/sig2h)
5   mu <- rnorm(1, mun, sig2mu^0.5)
6   return(mu)
7 }
8 PostBetas <- matrix(0, mcmc+burnin, 2)
9 PostPsi <- matrix(0, mcmc+burnin, n)
10 PostSigma2 <- list(); PostMu <- list()
11 PostLambda <- list(); Reg <- lm(y ~ X)
12 Beta <- Reg$coefficients[2:3]; Res <- Reg$residuals
13 plot(density(Res))
14 Resq <- quantile(Res, c(0.2, 0.4, 0.6, 0.8))
15 Id1 <- which(Res <= Resq[1])
16 Id2 <- which(Res > Resq[1] & Res <= Resq[2])
17 Id3 <- which(Res > Resq[2] & Res <= Resq[3])
18 Id4 <- which(Res > Resq[3] & Res <= Resq[4])
19 Id5 <- which(Res > Resq[4])
20 Nh <- rep(n/H, H); Lambda <- rep(1/H, H)
21 MU <- c(mean(Res[Id1]), mean(Res[Id2]), mean(Res[Id3]), mean(
  Res[Id4]), mean(Res[Id5]))
22 Sig2 <- c(var(Res[Id1]), var(Res[Id2]), var(Res[Id3]), var(
  Res[Id4]), var(Res[Id5]))
23 Psi <- rep(NA, n); Hs <- length(MU)
24 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
25 for(s in 1:tot){
26   for(i in 1:n){
27     lambdai <- NULL
28     for(h in 1:Hs){
29       lambdaih <- Lambda[h]*dnorm(y[i] - X[i,]*Beta, MU[h],
30       Sig2[h]^0.5)
31       lambdai <- c(lambdai, lambdaih)
32     }
33     Psi[i] <- sample(1:Hs, 1, prob = lambdai)
34   }
35   PostPsi[s, ] <- Psi
36   Hs <- length(table(Psi))
37   for(h in 1:Hs){
38     idh <- which(Psi == h)
39     Sig2[h] <- PostSig2(Beta = Beta, muh = MU[h], Xh = X[idh,],
40     yh = y[idh])
41     MU[h] <- Postmu(sig2h = Sig2[h], Beta = Beta, Xh = X[idh,],
42     yh = y[idh])
43   }
44   PostSigma2[[s]] <- Sig2
45   PostMu[[s]] <- MU
46   Beta <- PostBeta(sig2 = Sig2, mu = MU, X = X, y = y, Psi =
47   Psi)
48   PostBetas[s,] <- Beta
49   Lambda <- sort(MCMCpack::rdirichlet(1, a0h[1:Hs] + table(
50   Psi)), decreasing = TRUE)
51   PostLambda[[s]] <- Lambda
52   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
53   "% done"))
54 }
55 close(pb)

```

R code. Simulation: Semi-parametric Gaussian mixture

```

1 keep <- seq(burnin, tot, thin)
2 PosteriorBetas <- coda::mcmc(PostBetas[keep,])
3 summary(PosteriorBetas); plot(PosteriorBetas)
4 PosteriorPsi <- PostPsi[keep,]
5 Clusters <- sapply(1:length(keep), function(i){length(table(
  PosteriorPsi[i,]))})
6 PosteriorSIGMA <- matrix(NA, length(keep), 2)
7 PosteriorMU <- matrix(NA, length(keep), 2)
8 PosteriorLAMBDA <- matrix(NA, length(keep), 2)
9 l <- 1
10 for (s in keep){
11   PosteriorSIGMA[l,] <- PostSigma2[[s]][1:2]
12   PosteriorMU[l,] <- PostMu[[s]][1:2]
13   PosteriorLAMBDA[l,] <- PostLambda[[s]][1:2]
14   l <- l + 1
15 }
16 summary(coda::mcmc(PosteriorSIGMA))
17 summary(coda::mcmc(PosteriorMU))
18 summary(coda::mcmc(PosteriorLAMBDA))
19 mus <- seq(-3, 4, 0.01)
20 DensityEst <- function(par, eval){
21   lambda1 <- par[1]; lambda2 <- par[2]
22   mu1 <- par[3]; mu2 <- par[4]
23   sd1 <- par[5]; sd2 <- par[6]
24   Dens <- lambda1 * dnorm(eval, mu1, sd1) + lambda2 * dnorm(
    eval, mu2, sd2)
25   return(Dens)
26 }
27 par <- cbind(PosteriorLAMBDA, PosteriorMU, PosteriorSIGMA
  ^0.5)
28 DensEval <- matrix(NA, length(keep), length(mus))
29 DensPop <- rep(NA, length(mus))
30 for(r in 1:length(mus)){
31   for(l in 1:length(keep)){
32     DensEval[l, r] <- DensityEst(par = par[l,], eval = mus[r]
  )}
33 }
34 DensPop[r] <- DensityEst(par = c(0.7, 0.3, -0.5, 1, 0.5,
  0.8), eval = mus[r])
35 }
36 library(dplyr); library(ggplot2); require(latex2exp)
37 DataDens <- tibble(t = mus, Pop = DensPop, lower = apply(
  DensEval, 2, quantile, probs = 0.025), upper = apply(
  DensEval, 2, quantile, probs = 0.975), meanT = colMeans(
  DensEval))
38 plot_filtering_estimates <- function(df) {
39   p <- ggplot(data = df, aes(x = t)) + geom_ribbon(aes(ymin
    = lower, ymax = upper), alpha = 1, fill = "lightblue")
    + geom_line(aes(y = Pop, color = "True Value"),
    linewidth = 0.5) + geom_line(aes(y = meanT, color = "
    Estimate"), linewidth = 0.5) +
40   scale_color_manual(values = c("True Value" = "black", "
    Estimate" = "blue")) + xlab(TeX("$\\mu$")) + ylab("
    Density") + labs(title = "Density: Stochastic Errors",
    color = "") + theme_minimal()
41   print(p)
42 }
43 plot_filtering_estimates(DataDens)

```



FIGURE 11.1
Posterior density estimate: Stochastic errors.

2. Use the dataset *MarijuanaColombia.csv* from our GitHub repository to perform inference on the demand for marijuana in Colombia. This dataset contains information on the (log) monthly demand in 2019 from the National Survey of the Consumption of Psychoactive Substances. It includes variables such as the presence of a drug dealer in the neighborhood (*Dealer*), gender (*Female*), indicators of good physical and mental health (*PhysicalHealthGood* and *MentalHealthGood*), age (*Age* and *Age2*), years of schooling (*YearsEducation*), and (log) prices of marijuana, cocaine, and crack by individual (*LogPriceMarijuana*, *LogPriceCocaine*, and *LogPriceCrack*). The sample size is 1,156.

Estimate a finite Gaussian mixture regression using non-informative priors, that is, $\alpha_0 = \delta_0 = 0.01$, $\beta_0 = \mathbf{0}_K$, $\mathbf{B}_0 = \mathbf{I}_K$, and $\alpha_0 = [1/H \dots 1/H]^\top$, K is the number of regressors, 11 including the intercept. The number of MCMC iterations is 5,000, the burn-in is 1,000, and the thinning parameter is 2. Start with five potential clusters. Obtain the posterior distribution of the own-price elasticity of marijuana and the cross-price elasticities of marijuana demand with respect to the prices of cocaine and crack.

Answer:

The following code demonstrates how to perform inference in this model. The results indicate the presence of four clusters, with mean probabilities of 0.64, 0.14, 0.12 and 0.10, and 95% credible intervals of (0.60, 0.67), (0.12, 0.16), (0.10, 0.14) and (0.08, 0.12), respectively.

The 95% posterior credible interval for the own-price elasticities of the most representative group, which comprises two-thirds of the sample, is $(-0.55, -0.26)$. Additionally, the 95% credible interval for the cross-price elasticities with respect to cocaine is $(0.01, 0.35)$, while that with respect to crack is $(0.07, 0.43)$.

These results suggest that marijuana is an inelastic good for these individuals and that there is substitution between marijuana and both cocaine and crack: an increase in the prices of the latter leads to higher marijuana demand in the most representative cluster of individuals. However, these findings should be interpreted with caution due to potential endogeneity issues that must be addressed for a rigorous scientific analysis. The primary goal of this exercise is pedagogical.

R code. Marijuana in Colombia: Gaussian mixture

```

1 rm(list = ls()); set.seed(010101)
2 Data <- read.csv("https://raw.githubusercontent.com/
   BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
   MarijuanaColombia.csv")
3 attach(Data)
4 y <- LogMarijuana; X <- as.matrix(cbind(1, Data[, -1]))
5 Reg <- lm(y ~ X - 1); summary(Reg)
6 k <- dim(X)[2]; N <- dim(X)[1]
7 # Plot
8 library(ggplot2)
9 ggplot(Data, aes(x = LogMarijuana)) + geom_density(fill = "
   blue", alpha = 0.3) + labs(title = "Density Plot", x = "
   y", y = "Density") + theme_minimal()
10 # Hyperparameters
11 d0 <- 0.001; a0 <- 0.001
12 b0 <- rep(0, k); B0 <- diag(k); B0i <- solve(B0)
13 H <- 5; a0h <- rep(1/H, H)
14 # MCMC parameters
15 mcmc <- 2000; burnin <- 500
16 tot <- mcmc + burnin; thin <- 2
17 # Gibbs sampling functions
18 PostSig2 <- function(Betah, Xh, yh){
19   Nh <- length(yh); an <- a0 + Nh
20   dn <- d0 + t(yh - Xh%*%Betah)%*(yh - Xh%*%Betah)
21   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
22   return(sig2)
23 }
24 PostBeta <- function(sig2h, Xh, yh){
25   if(length(yh) == 1){
26     Xh <- matrix(Xh, k, 1)
27     Bn <- solve(B0i + sig2h^(-1)*Xh%*%t(Xh))
28     bn <- Bn%*(B0i%*%b0 + sig2h^(-1)*Xh%*%yh)
29   }else{
30     Bn <- solve(B0i + sig2h^(-1)*t(Xh)%*%Xh)
31     bn <- Bn%*(B0i%*%b0 + sig2h^(-1)*t(Xh)%*%yh)
32   }
33   Beta <- MASS::mvrnorm(1, bn, Bn)
34   return(Beta)
35 }
36 PostBetas <- list(); PostSigma2 <- list(); PostLambda <-
   list()
37 PostPsi <- matrix(0, tot, N); Psi <- sample(1:H, N, replace
   = TRUE, prob = a0h)
38 Beta <- matrix(rep(Reg$coefficients, H), k, H); Hs <- H

```

R code. Marijuana in Colombia: Gaussian mixture

```

1 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
2 for(s in 1:tot){
3   Sig2 <- rep(NA, Hs)
4   for(h in 1:Hs){
5     idh <- which(Psi == h)
6     Sig2[h] <- PostSig2(Betah = Beta[, h], Xh = X[idh,], yh
  = y[idh])
7   }
8   Hs <- length(Sig2)
9   Beta <- matrix(NA, k, Hs)
10  for(h in 1:Hs){
11    idh <- which(Psi == h)
12    Beta[, h] <- PostBeta(sig2h = Sig2[h], Xh = X[idh,], yh
  = y[idh])
13  }
14  Lambda <- sort(MCMCpack::rdirichlet(1, a0h[1:Hs] + table(
  Psi)), decreasing = TRUE)
15  for(i in 1:N){
16    lambdai <- NULL
17    for(h in 1:Hs){
18      idh <- which(Psi == h)
19      lambdaih <- Lambda[h]*dnorm(y[i], X[i,]%*%Beta[h],
  Sig2[h]^0.5)
20      lambdai <- c(lambdai, lambdaih)
21    }
22    Psi[i] <- sample(1:Hs, 1, prob = lambdai)
23  }
24  Hs <- length(table(Psi))
25  PostBetas[[s]] <- Beta; PostSigma2[[s]] <- Sig2
26  PostLambda[[s]] <- Lambda; PostPsi[s, ] <- Psi
27  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
  "% done"))
28 }
29 close(pb)
30 keep <- seq((burnin+1), tot, thin)
31 PosteriorPsi <- PostPsi[keep,]
32 Clusters <- sapply(1:length(keep), function(i){length(table(
  PosteriorPsi[i,]))})
33 NClus <- 4
34 PosteriorSIGMA <- matrix(NA, length(keep), NClus)
35 PosteriorBETA <- array(NA, c(k,NClus,length(keep)))
36 PosteriorLAMBDA <- matrix(NA, length(keep), NClus)
37 l <- 1
38 for (s in keep){
39   PosteriorSIGMA[l,] <- PostSigma2[[s]][1:NClus]
40   PosteriorLAMBDA[l,] <- PostLambda[[s]][1:NClus]
41   PosteriorBETA[,l] <- PostBetas[[s]]
42   l <- l + 1
43 }
44 summary(coda::mcmc(PosteriorSIGMA)); summary(coda::mcmc(
  PosteriorLAMBDA))
45 for(l in 1:NClus){
46   PosteriorBeta <- t(PosteriorBETA[,l,])
47   colnames(PosteriorBeta) <- c("Ct", names(Data[, -1]))
48   print(summary(coda::mcmc(PosteriorBeta)))
49 }

```

3. Get the posterior sampler in the semi-parametric setting using a Dirichlet process mixture:

$$y_i = \mathbf{x}_i^\top \boldsymbol{\beta} + e_i$$

$$e_i \mid \mu_i, \sigma_i^2 \stackrel{iid}{\sim} N(\mu_i, \sigma_i^2),$$

Do not include the intercept in $\boldsymbol{\beta}$ to get flexibility in the distribution of the stochastic errors.

Let's assume $\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \mathbf{B}_0)$, $\sigma_i^2 \sim IG(\alpha_0/2, \delta_0/2)$, $\mu_i \sim N(\mu_0, \sigma_i^2/\beta_0)$, $\alpha \sim G(a, b)$ such that introducing the latent variable $\xi \mid \alpha, N \sim Be(\alpha+1, N)$, allows to easily sample the posterior draws of $\alpha \mid \xi, H, \pi_\xi \sim \pi_\xi G(a+H, b - \log(\xi)) + (1 - \pi_\xi)G(a+H-1, b - \log(\xi))$, where $\frac{\pi_\xi}{1-\pi_\xi} = \frac{a+H-1}{N(b-\log(\xi))}$, H is the number of atoms (mixture components).

Answer:

This mixture model can be expressed in a hierarchical structure:

$$e_i \mid \boldsymbol{\theta}_i \stackrel{ind}{\sim} f_{\boldsymbol{\theta}_i}$$

$$\boldsymbol{\theta}_i \mid G \stackrel{iid}{\sim} G$$

$$G \mid \alpha, G_0 \sim DP(\alpha G_0),$$

where $e_i = y_i - \mathbf{x}_i^\top \boldsymbol{\beta}$ and $\boldsymbol{\theta}_i = [\mu_i \ \sigma_i^2]^\top$.

Thus,

$$s_i \sim \sum_{h=0}^{\infty} \lambda_h \delta_h,$$

$$e_i \mid s_i, \boldsymbol{\theta}_{s_i} \sim N(\mu_{s_i}, \sigma_{s_i}^2),$$

where $\lambda_h = P(\boldsymbol{\theta}_i = \boldsymbol{\theta}_h^*)$.

The conditional posterior distribution of $\boldsymbol{\theta}_i$ is

$$\boldsymbol{\theta}_i \mid \{\boldsymbol{\theta}_{i'}, \mathbf{s}_{i'} : i' \neq i\}, e_i, \alpha \sim \sum_{i' \neq i} \frac{N_h^{(i)}}{\alpha + N - 1} f_N(e_i \mid \mu_h, \sigma_h^2)$$

$$+ \frac{\alpha}{\alpha + N - 1} \int_{\mathcal{R}} \int_0^\infty f_N(e_i \mid \mu, \sigma^2) f_N\left(\mu \mid \mu_0, \frac{\sigma^2}{\beta_0}\right) f_{IG}(\sigma^2 \mid \alpha_0, \delta_0) d\sigma^2 d\mu,$$

where $N_h^{(i)}$ is the number of observations such that $s_{i'} = h$, $i' \neq i$.

Observe that the integral in the previous equation has exactly the same form as in the marginal likelihood presented in Section 3.2 in the book in the normal-normal/inverse gamma model. Thus,

$$p(e_i) = \int_{\mathcal{R}} \int_0^\infty f_N(e_i \mid \mu, \sigma^2) f_N\left(\mu \mid \mu_0, \frac{\sigma^2}{\beta_0}\right) f_{IG}(\sigma^2 \mid \alpha_0, \delta_0) d\sigma^2 d\mu$$

$$= \frac{\Gamma\left(\frac{\alpha_n}{2}\right) (\delta_0/2)^{\alpha_0/2}}{\Gamma\left(\frac{\alpha_0}{2}\right) (\delta_n/2)^{\alpha_n/2}} \left(\frac{\beta_0}{\beta_n}\right)^{1/2} (\pi)^{-1/2},$$

where $\alpha_n = 1 + \alpha_0$, $\delta_n = \delta_0 + \frac{\beta_0}{1+\beta_0}(e_i - \mu_0)^2$ and $\beta_n = 1 + \beta_0$. Therefore, we sample s_i as follows,

$$s_i | \{\mu_{i'}, \sigma_{i'}^2, \mathbf{s}_{i'} : i' \neq i\}, e_i, \alpha \sim \left\{ \begin{array}{l} P(s_i = 0 | \cdot) = q_0^* \\ P(s_i = h | \cdot) = q_h^*, h = 1, 2, \dots, H^{(i)} \end{array} \right\},$$

where $H^{(i)}$ is the number of clusters excluding i , which may have its own cluster (singleton cluster), $q_c^* = \frac{q_c}{q_0 + \sum_h q_h}$, $q_c = \{q_0, q_h\}$, $q_h = \frac{N_h^{(i)}}{\alpha + N - 1} f_N(e_i | \mu_h, \sigma_h^2)$ and $q_0 = \frac{\alpha}{\alpha + N - 1} p(e_i)$.

If $s_i = 0$ is sampled, then $s_i = H + 1$, and a new σ_h^2 is sampled from $IG(\alpha_n/2, \delta_n/2)$, a new μ_h is sampled from $N(\mu_i, \sigma_h^2/\beta_n)$, where $\mu_i = \frac{e_i + \beta_0 \mu_0}{1 + \beta_0}$.

Discarding θ_h 's from last step, we use \mathbf{s} and total number of components to sample σ_h^2 from

$$IG\left(\frac{\alpha_0 + N_h}{2}, \frac{\delta_0 + \sum_{i \in \mathcal{C}_h} (e_i - \bar{e})^2 + \frac{\beta_0 N_h}{\beta_0 + N_h} (\bar{e} - \mu_0)^2}{2}\right),$$

where $\bar{e} = \frac{\sum_{i \in \mathcal{C}_h} e_i}{N_h}$, that is, the mean uses individuals in cluster \mathcal{C}_h . Note that when $N_h = 1$, $\delta_0 + \sum_{i \in \mathcal{C}_h} (e_i - \bar{e})^2 + \frac{\beta_0 N_h}{\beta_0 + N_h} (\bar{e} - \mu_0)^2$ is equal to δ_n .

We sample $\mu_h | \sigma_h^2, \mathbf{e} \sim N\left(\mu_{hn}, \frac{\sigma_h^2}{\beta_0 + N_h}\right)$, where $\mu_{hn} = \frac{\beta_0 \mu_0 + N_h \bar{e}}{\beta_0 + N_h}$, $h = 1, 2, \dots, H$. Note that μ_{hn} is equal to μ_i when $N_h = 1$.

The posterior distribution of β is given by

$$\beta \sim N(\beta_n, \mathbf{B}_n),$$

where $\mathbf{B}_n = (\mathbf{B}_0^{-1} + \sum_{h=1}^H \sum_{i \in \mathcal{C}_h} \sigma_h^{-2} \mathbf{x}_i \mathbf{x}_i^\top)^{-1}$ and $\beta_n = \mathbf{B}_n (\mathbf{B}_0^{-1} \beta_0 + \sum_{h=1}^H \sum_{i \in \mathcal{C}_h} \sigma_h^{-2} \mathbf{x}_i (y_i - \mu_h))$.

4. Example: Exercise 1 and 3 continue

Perform inference in the simulation of the semi-parametric model of Exercise 1 using the sampler of Exercise 3. Use non-informative priors, setting $\alpha_0 = \delta_0 = 0.01$, $\beta_0 = \mathbf{0}_2$, $\mathbf{B}_0 = \mathbf{I}_2$, and $a = b = 0.1$. The number of MCMC iterations is 5,000, the burn-in is 1,000, and the thinning parameter is 2.

Answer:

The following code implements the Gibbs sampling algorithm to perform inference using the DPM in the semi-parametric simulation. From the summary statistics of the posterior chains, we can see that the 95% credible intervals encompass the population values. Figure 11.2 shows the posterior

density of the intercept associated with the second cluster. We observe bimodality, with the two modes located around the population means of the clusters.

R code. Simulation: Semi-parametric Dirichlet process mixture

```

1 rm(list = ls())
2 set.seed(010101)
3 # Simulate data from a 2-component mixture model
4 n <- 1000
5 x1 <- rnorm(n); x2 <- rnorm(n)
6 B <- c(0.5, -1.2)
7 X <- cbind(x1, x2)
8 z <- rbinom(n, 1, 0.3) # Latent class indicator
9 mu <- ifelse(z == 0, rnorm(n, -0.5, 0.5), rnorm(n, 1, 0.8))
10 y <- X%*%B + mu
11 k <- dim(X)[2]
12 N <- dim(X)[1]
13 # Hyperparameters
14 a0 <- 0.001; d0 <- 0.001
15 b0 <- rep(0, k); B0 <- diag(k)
16 B0i <- solve(B0)
17 a <- 0.1; b <- 0.1
18 mu0 <- 0
19 sig2mu0 <- 10
20 beta0 <- 0.1
21 # MCMC parameters
22 mcmc <- 5000; burnin <- 1000
23 tot <- mcmc + burnin; thin <- 2
24 # Gibbs sampling functions
25 PostSig2 <- function(Xh, yh, Beta){
26   Nh <- length(yh)
27   if(Nh == 1){
28     Xh <- matrix(Xh, k, 1)
29     XhB <- t(Xh)%*%Beta
30   }else{
31     Xh <- matrix(Xh, Nh, k)
32     XhB <- Xh%*%Beta
33   }
34   eh <- matrix(yh, Nh, 1) - XhB
35   an <- a0 + Nh
36   dn <- d0 + sum((eh - mean(eh))^2) + beta0*Nh/(beta0 + Nh)*
     (mean(eh) - mu0)^2
37   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
38   return(sig2)
39 }
40 Postmu <- function(sig2h, Beta, Xh, yh){
41   Nh <- length(yh)
42   if(Nh == 1){
43     Xh <- matrix(Xh, k, 1)
44     XhB <- t(Xh)%*%Beta
45   }else{
46     Xh <- matrix(Xh, Nh, k)
47     XhB <- Xh%*%Beta
48   }
49   eh <- matrix(yh, Nh, 1) - XhB
50   sig2mu <- sig2h/(beta0 + Nh)
51   mun <- (beta0*mu0 + Nh*mean(eh))/(beta0 + Nh)
52   mu <- rnorm(1, mun, sig2mu^0.5)
53   return(mu)
54 }

```

*R code. Simulation: Semi-parametric Dirichlet
process mixture*

```

1 PostBeta <- function(sig2, mu, X, y, Clust){
2   XtX <- matrix(0, k, k); Xty <- matrix(0, k, 1)
3   Hs <- length(mu)
4   for(h in 1:Hs){
5     idh <- which(Clust == h)
6     if(length(idh) == 1){
7       Xh <- matrix(X[idh,], k, 1); XtXh <- sig2[h]^(-1)*Xh%*
8       %t(Xh)
9       yh <- y[idh]; Xtyh <- sig2[h]^(-1)*Xh%*(yh - mu[h])
10      }else{
11        Xh <- X[idh,]; XtXh <- sig2[h]^(-1)*t(Xh)%*Xh
12        yh <- y[idh]; Xtyh <- sig2[h]^(-1)*t(Xh)%*(yh - mu[h
13        ])
14      }
15      XtX <- XtX + XtXh; Xty <- Xty + Xtyh
16    }
17    Bn <- solve(B0i + XtX); bn <- Bn%*(B0i%*b0 + Xty)
18    Beta <- MASS::mvrnorm(1, bn, Bn)
19    return(Beta)
20  }
21 PostAlpha <- function(Clust, alpha){
22   H <- length(unique(Clust))
23   psi <- rbeta(1, alpha + 1, N)
24   pi.ratio <- (a + H - 1) / (N * (b - log(psi)))
25   pi <- pi.ratio / (1 + pi.ratio)
26   components <- sample(1:2, prob = c(pi, (1 - pi)), size =
27   1)
28   cs <- c(a + H, a + H - 1); ds <- b - log(psi)
29   alpha <- rgamma(1, cs[components], ds)
30   return(alpha)
31 }
32 LogMarLikLM <- function(xh, yh, Beta){
33   xh <- matrix(xh, k, 1); ei <- c(yh - t(xh)%*Beta)
34   betan <- beta0 + 1; an <- a0 + 1
35   dn <- d0 + beta0/(beta0 + 1)*(ei - mu0)^2
36   logpy <- (1/2)*log(1/pi)+(a0/2)*log(d0)-(an/2)*log(dn) +
37   0.5*log(beta0/betan) + lgamma(an/2)-lgamma(a0/2)
38   return(logpy)
39 }
40 PostS <- function(Beta, SIGMA, MU, Alpha, Clust, i){
41   N1 <- table(Clust[-i]); H <- length(N1)
42   ei <- c(y[i] - t(X[i,])%*Beta)
43   qh <- sapply(1:H, function(h){(N1[h]/(N+Alpha-1))*dnorm(ei
44   , mean = MU[h], sd = SIGMA[h])})
45   q0 <- (Alpha/(N+Alpha-1))*exp(LogMarLikLM(xh = X[i,], yh =
46   y[i], Beta = Beta))
47   qh <- c(q0, qh)
48   Clust <- as.numeric(names(N1))
49   si <- sample(c(0, Clust), 1, prob = qh)
50   if(si == 0){si <- Clust[H] + 1
51     Sig2New <- PostSig2(Xh = X[i,], yh = y[i], Beta = Beta)
52     SIGMA <- c(SIGMA, Sig2New^0.5)
53     MuNew <- Postmu(sig2h = Sig2New, Beta = Beta, Xh = X[i
54     ], yh = y[i])
55     MU <- cbind(MU, MuNew)
56   }else{si == si}
57   return(list(si = si, MU = MU, SIGMA = SIGMA))
58 }

```

*R code. Simulation: Semi-parametric Dirichlet
process mixture*

```

1 PostBetas <- matrix(NA, tot, k)
2 PostSigma <- list(); PostMu <- list()
3 Posts <- matrix(0, tot, N); PostAlphas <- rep(0, tot)
4 Clust <- sample(1:3, N, replace=T, prob = c(0.5, 0.3, 0.2))
5 Reg <- lm(y ~ X)
6 SumReg <- summary(Reg)
7 BETA <- Reg$coefficients[-1]
8 SIGMA <- rep(SumReg$sigma, 3)
9 MU <- rep(Reg$coefficients[1], 3)
10 Alpha <- rgamma(1, a, b)
11 pb <- winProgressBar(title = "progress bar", min = 0, max =
    tot, width = 300)
12 for(s in 1:tot){
13   for(i in 1:N){
14     Rests <- PostS(Beta = BETA, SIGMA = SIGMA, MU = MU,
15       Alpha = Alpha, Clust = Clust, i = i)
16     Clust[i] <- Rests$si
17     MU <- Rests$MU; SIGMA <- Rests$SIGMA
18   }
19   sFreq <- table(Clust)
20   lt <- 1
21   for(li in as.numeric(names(sFreq))){
22     Index <- which(Clust == li)
23     if(li == lt){Clust[Index] <- li
24     } else {Clust[Index] <- lt
25     }
26     lt <- lt + 1
27   }
28   Alpha <- PostAlpha(Clust = Clust, alpha = Alpha)
29   N1 <- table(Clust); H <- length(N1)
30   SIGMA <- rep(NA, H)
31   MU <- rep(NA, H)
32   l <- 1
33   for(h in unique(Clust)){
34     Idh <- which(Clust == h)
35     SIGMA[l] <- (PostSig2(Beta = BETA, Xh = X[Idh, ], yh = y
36       [Idh]))^0.5
37     MU[l] <- Postmu(Beta = BETA, sig2h = SIGMA[l]^2, Xh = X[
38       Idh, ], yh = y[Idh])
39     l <- l + 1
40   }
41   BETA <- PostBeta(sig2 = SIGMA, mu = MU, X = X, y = y,
42     Clust = Clust)
43   PostBetas[s,] <- BETA
44   PostSigma[[s]] <- SIGMA
45   PostMu[[s]] <- MU
46   Posts[s, ] <- Clust
47   PostAlphas[s] <- Alpha
48   setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
49     "% done"))
50 }
51 close(pb)

```

R code. Simulation: Semi-parametric Dirichlet process mixture

```

1 keep <- seq(burnin, tot, thin)
2 PosteriorBetas <- coda::mcmc(PostBetas[keep,])
3 summary(PosteriorBetas)
4 plot(PosteriorBetas)
5 PosteriorPsi <- Posts[keep,]
6 Clusters <- sapply(1:length(keep), function(i){length(table(
  PosteriorPsi[i,]))})
7 table(Clusters)
8 PosteriorSIGMA <- matrix(NA, length(keep), 2)
9 PosteriorMU <- matrix(NA, length(keep), 2)
10 l <- 1
11 for (s in keep){
12   PosteriorSIGMA[l,] <- PostSigma[[s]][1:2]
13   PosteriorMU[l,] <- PostMu[[s]][1:2]
14   l <- l + 1
15 }
16 summary(coda::mcmc(PosteriorSIGMA))
17 summary(coda::mcmc(PosteriorMU))
18 plot(coda::mcmc(PosteriorMU))
19 DataMU2 <- data.frame(Posterior = PosteriorMU[,2])
20 library(ggplot2)
21 densMU <- ggplot(DataMU2, aes(x = Posterior)) + geom_density
  (fill = "blue", alpha = 0.3) + labs(x = "Intercept", y =
    "Density") + theme_minimal()
22 densMU

```

5. Example: Simulation exercise continues

Fix the label-switching problem of the simulation exercise of the DPM using *random permutation of latent classes*.

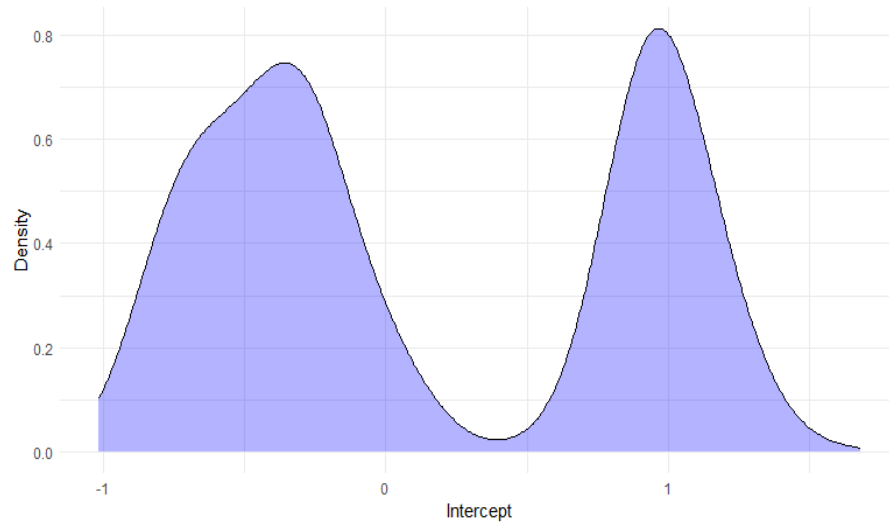
Answer:

A simple strategy to address label switching in this simulation exercise is to fix the number of clusters to three, given that this is the typical number of clusters obtained after performing the DPM. Recall that, according to the simulation setup, there are only two clusters:

$$p(y_i | \mathbf{x}_i) = 0.5\phi(y_i | 2 + 1.5x_i, 1^2) + 0.5\phi(y_i | -1 + 0.5x_i, 0.8^2).$$

Thus, we can use a finite Gaussian mixture model with $H = 3$.¹

¹Another approach is to use finite Dirichlet processes [17, Chap. 2] and set a random permutation of latent classes.

**FIGURE 11.2**

Posterior density estimate: Mean of the stochastic errors.

The following code illustrates the algorithm.

*R code. Simulation: Random permutation of
latent classes*

```

1 rm(list = ls()); set.seed(010101)
2 # Simulate data from a 2-component mixture model
3 n <- 1000; x <- rnorm(n)
4 z <- rbinom(n, 1, 0.5)
5 y <- ifelse(z == 0, rnorm(n, 2 + 1.5*x, 1), rnorm(n, -1 +
6   0.5*x, 0.8))
7 data <- data.frame(y, x)
8 # Hyperparameters
9 d0 <- 0.001; a0 <- 0.001
10 b0 <- rep(0, 2); B0 <- diag(2); B0i <- solve(B0)
11 H <- 3; a0h <- rep(1/H, H)
12 # MCMC parameters
13 mcmc <- 10000; burnin <- 2000
14 tot <- mcmc + burnin; thin <- 2
15 # Gibbs sampling functions
16 PostSig2 <- function(Betah, Xh, yh){
17   Nh <- length(yh); an <- a0 + Nh
18   dn <- d0 + t(yh - Xh%*%Betah)%*(yh - Xh%*%Betah)
19   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
20   return(sig2)
21 }
22 PostBeta <- function(sig2h, Xh, yh){
23   Bn <- solve(B0i + sig2h^(-1)*t(Xh)%*%Xh)
24   bn <- Bn%*(B0i%*%b0 + sig2h^(-1)*t(Xh)%*%yh)
25   Beta <- MASS::mvrnorm(1, bn, Bn)
26   return(Beta)
27 }
28 PostBetas1 <- matrix(0, tot, 2)
29 PostBetas2 <- matrix(0, tot, 2)
30 PostBetas3 <- matrix(0, tot, 2)
31 PostSigma2 <- matrix(0, tot, H)
32 PostPsi <- matrix(0, tot, n)
33 PostLambda <- matrix(0, tot, H)
34 Reg <- lm(y ~ x)
35 SumReg <- summary(Reg)
36 BETA <- cbind(Reg$coefficients, Reg$coefficients, Reg$
37   coefficients)
38 SIG2 <- rep(SumReg$sigma, H)
39 X <- cbind(1, x); Psi <- rep(NA, n)
40 Lambda1 <- 1/H; Lambda2 <- 1/H; Lambda3 <- 1/H
41 perutatms <- gtools::permutations(3, 3, 1:H)

```

R code. Simulation: Random permutation of latent classes

```

1 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
2 for(s in 1:tot){
3   for(i in 1:n){
4     lambdai1 <- Lambda1*dnorm(y[i], X[i,]*BETA[,1], SIG2
      [1]^0.5)
5     lambdai2 <- Lambda2*dnorm(y[i], X[i,]*BETA[,2], SIG2
      [2]^0.5)
6     lambdai3 <- Lambda3*dnorm(y[i], X[i,]*BETA[,3], SIG2
      [3]^0.5)
7     Psi[i] <- sample(1:H, 1, prob = c(lambdai1, lambdai2,
      lambdai3))
8   }
9   NH <- NULL
10  for(h in 1:H){
11    Idh <- which(Psi == h)
12    Nh <- length(Idh)
13    NH <- c(NH, Nh)
14    SIG2[h] <- PostSig2(Betah = BETA[,h], Xh = X[Idh, ], yh
      = y[Idh])
15    BETA[,h] <- PostBeta(sig2h = SIG2[h], Xh = X[Idh, ], yh
      = y[Idh])
16  }
17  Lambda <- sort(MCMCpack::rdirichlet(1, a0h + NH),
    decreasing = TRUE)
18  IndPer <- sample(1:dim(perutatms)[1], 1)
19  Clust <- perutatms[IndPer, ]
20  SIG2 <- SIG2[Clust]
21  BETA <- BETA[,Clust]
22  Lambda <- Lambda[Clust]
23  for(i in 1:n){
24    if(Psi[i] == 1){
25      Psi[i] <- Clust[1]
26    }else{
27      if(Psi[i] == 2){
28        Psi[i] <- Clust[2]
29      }else{
30        Psi[i] <- Clust[3]
31      }
32    }
33  }
34  Lambda1 <- Lambda[1]; Lambda2 <- Lambda[2]; Lambda3 <-
    Lambda[3]
35  PostPsi[s, ] <- Psi
36  PostSigma2[s, ] <- SIG2
37  PostBetas1[s, ] <- BETA[,1]
38  PostBetas2[s, ] <- BETA[,2]
39  PostBetas3[s, ] <- BETA[,3]
40  PostLambda[s, ] <- Lambda
41  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
42 }
43 close(pb)

```


R code. Simulation: Random permutation of latent classes

```

1 keep <- seq((burnin+1), tot, thin)
2 PosteriorBetas1 <- coda::mcmc(PostBetas1[keep,])
3 PosteriorBetas2 <- coda::mcmc(PostBetas2[keep,])
4 PosteriorBetas3 <- coda::mcmc(PostBetas3[keep,])
5 PosteriorSigma2 <- coda::mcmc(PostSigma2[keep,])
6 summary(PosteriorSigma2)
7 PosteriorLambda <- coda::mcmc(PostLambda[keep,])
8 summary(PosteriorLambda)
9 DataBetas <- data.frame(Cluster1 = as.numeric(
    PosteriorBetas1[,2]), Cluster2 = as.numeric(
    PosteriorBetas2[,2]), Cluster3 = as.numeric(
    PosteriorBetas3[,2]))
10 library(ggplot2)
11 dens1 <- ggplot(DataBetas, aes(x = Cluster1)) + geom_density
    (fill = "blue", alpha = 0.3) + labs(x = "Cluster 1", y =
    "Density") + theme_minimal()
12 dens2 <- ggplot(DataBetas, aes(x = Cluster2)) + geom_density
    (fill = "blue", alpha = 0.3) + labs(x = "Cluster 2", y =
    "Density") + theme_minimal()
13 dens3 <- ggplot(DataBetas, aes(x = Cluster3)) + geom_density
    (fill = "blue", alpha = 0.3) + labs(x = "Cluster 3", y =
    "Density") + theme_minimal()
14 library(ggpubr)
15 ggarrange(dens1, dens2, dens3, labels = c("A", "B", "C"),
    ncol = 3, nrow = 1, legend = "bottom", common.legend =
    TRUE)
16

```

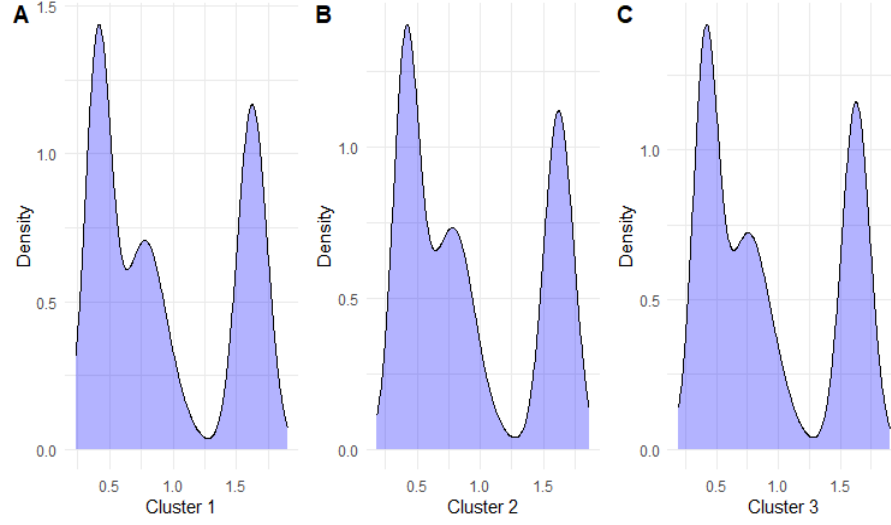
Figure 11.3 shows the posterior density estimates of the three clusters. We observe that they have similar shapes, as they are targeting the same posterior distributions. There are two modes with large values around the population parameters, and an additional mode around 0. This occurs because we are forcing three clusters, even though the data-generating process contains only two.

6. Example: Simulation exercise continues II

Obtain the density estimate of y in the simulation exercise of the DPM, evaluated at $x = 0$.

Answer:

The following code shows how to perform inference, and get the density estimate using the DPM. Note that the density estimate is given by

**FIGURE 11.3**

Posterior density estimates slope parameter: Population values are 1.5 and 0.5.

$$y \mid \boldsymbol{\theta}_h, \mathbf{s}, \alpha \sim \sum_{h=1}^H \frac{N_h}{\alpha + N + 1} f_N(y \mid \mathbf{x}_h^\top \boldsymbol{\beta}_h, \sigma_h^2) + \frac{\alpha}{\alpha + N + 1} p(y),$$

where N_h is the number of individuals in cluster h , H is the total observed clusters after estimation, and $p(y)$ is the marginal likelihood given in Section 11.1.2 in the book.

Figure 11.4 shows the density plots, population (black line), mean (blue line), and 95% credible interval (shaded blue). We observe that the DPM performs very well despite having more clusters than the actual data generating process.

*R code. Simulation: Density from Dirichlet
process mixture*

```

1 rm(list = ls()); set.seed(010101)
2 # Simulate data from a 2-component mixture model
3 N <- 1000; x <- rnorm(N); z <- rbinom(N, 1, 0.5)
4 y <- ifelse(z == 0, rnorm(N, 2 + 1.5*x, 1), rnorm(N, -1 +
5   0.5*x, 0.8))
6 X <- cbind(1, x); k <- 2
7 data <- data.frame(y, x); Reg <- lm(y ~ x)
8 SumReg <- summary(Reg)
9 # Hyperparameters
10 a0 <- 0.001; d0 <- 0.001
11 b0 <- rep(0, k); B0 <- diag(k)
12 B0i <- solve(B0)
13 a <- 0.1; b <- 0.1
14 # MCMC parameters
15 mcmc <- 5000; burnin <- 1000
16 tot <- mcmc + burnin; thin <- 2
17 # Gibbs sampling functions
18 PostSig2 <- function(Xh, yh){
19   Nh <- length(yh)
20   yh <- matrix(yh, Nh, 1)
21   if(Nh == 1){
22     Xh <- matrix(Xh, k, 1)
23     Bn <- solve(Xh%*%t(Xh) + B0i)
24     bn <- Bn%*(B0i%*%b0 + Xh%*%yh)
25   }else{
26     Xh <- matrix(Xh, Nh, k)
27     Bn <- solve(t(Xh)%*%Xh + B0i)
28     bn <- Bn%*(B0i%*%b0 + t(Xh)%*%yh)
29   }
30   Bni <- solve(Bn)
31   an <- a0 + Nh
32   dn <- d0 + t(yh)%*%yh + t(b0)%*%B0i%*%b0 - t(bn)%*%Bni%*%
33     bn
34   sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
35   return(sig2)
36 }
37 PostBeta <- function(sig2h, Xh, yh){
38   Nh <- length(yh)
39   yh <- matrix(yh, Nh, 1)
40   if(Nh == 1){
41     Xh <- matrix(Xh, k, 1)
42     Bn <- solve(Xh%*%t(Xh) + B0i)
43     bn <- Bn%*(B0i%*%b0 + Xh%*%yh)
44   }else{
45     Xh <- matrix(Xh, Nh, k)
46     Bn <- solve(t(Xh)%*%Xh + B0i)
47     bn <- Bn%*(B0i%*%b0 + t(Xh)%*%yh)
48   }
49   Beta <- MASS::mvrnorm(1, bn, sig2h*Bn)
50   return(Beta)
51 }

```

*R code. Simulation: Density from Dirichlet
process mixture*

```

1 PostAlpha <- function(s, alpha){
2   H <- length(unique(s))
3   psi <- rbeta(1, alpha + 1, N)
4   pi.ratio <- (a + H - 1) / (N * (b - log(psi)))
5   pi <- pi.ratio / (1 + pi.ratio)
6   components <- sample(1:2, prob = c(pi, (1 - pi)), size =
7     1)
8   cs <- c(a + H, a + H - 1)
9   ds <- b - log(psi)
10  alpha <- rgamma(1, cs[components], ds)
11  return(alpha)
12 }
13 LogMarLikLM <- function(xh, yh){
14   xh <- matrix(xh, k, 1)
15   Bn <- solve(xh%*%t(xh) + B0i)
16   Bni <- solve(Bn)
17   bn <- Bn%*%(B0i%*%b0 + xh%*%yh)
18   an <- a0 + 1
19   dn <- d0 + yh^2 + t(b0)%*%B0i%*%b0 - t(bn)%*%Bni%*%bn
20   # Log marginal likelihood
21   logpy <- (1/2)*log(1/pi)+(a0/2)*log(d0)-(an/2)*log(dn) +
22     0.5*log(det(Bn)/det(B0)) + lgamma(an/2)-lgamma(a0/2)
23   return(logpy)
24 }
25 PostS <- function(BETA, SIGMA, Alpha, s, i){
26   N1 <- table(s[-i]); H <- length(N1)
27   qh <- sapply(1:H, function(h){(N1[h]/(N+Alpha-1))*dnorm(y[
28     i], mean = t(X[i,])%*%BETA[,h], sd = SIGMA[h])})
29   q0 <- (Alpha/(N+Alpha-1))*exp(LogMarLikLM(xh = X[i,], yh =
30     y[i]))
31   qh <- c(q0, qh)
32   Clust <- as.numeric(names(N1))
33   si <- sample(c(0, Clust), 1, prob = qh)
34   if(si == 0){
35     si <- Clust[H] + 1
36     Sig2New <- PostSig2(Xh = X[i,], yh = y[i])
37     SIGMA <- c(SIGMA, Sig2New^0.5)
38     BetaNew <- PostBeta(sig2h = Sig2New, Xh = X[i,], yh = y[
39       i])
40     BETA <- cbind(BETA, BetaNew)
41   }else{si == si}
42   }
43   return(list(si = si, BETA = BETA, SIGMA = SIGMA))
44 }
45 PostBetas <- list(); PostSigma <- list()
46 Posts <- matrix(0, tot, N); PostAlphas <- rep(0, tot)
47 S <- sample(1:3, N, replace = T, prob = c(0.5, 0.3, 0.2))
48 BETA <- cbind(Reg$coefficients, Reg$coefficients, Reg$
49   coefficients)
50 SIGMA <- rep(SumReg$sigma, 3)
51 Alpha <- rgamma(1, a, b)

```

*R code. Simulation: Density from Dirichlet
process mixture*

```

1 pb <- winProgressBar(title = "progress bar", min = 0, max =
  tot, width = 300)
2 for(s in 1:tot){
3   for(i in 1:N){
4     Rests <- PostS(BETA = BETA, SIGMA = SIGMA, Alpha = Alpha
      , s = S, i = i)
5     S[i] <- Rests$si
6     BETA <- Rests$BETA; SIGMA <- Rests$SIGMA
7   }
8   sFreq <- table(S)
9   lt <- 1
10  for(li in as.numeric(names(sFreq))){
11    Index <- which(S == li)
12    if(li == lt){S[Index] <- li
13    } else {S[Index] <- lt
14    }
15    lt <- lt + 1
16  }
17  Alpha <- PostAlpha(s = S, alpha = Alpha)
18  N1 <- table(S); H <- length(N1)
19  SIGMA <- rep(NA, H)
20  BETA <- matrix(NA, k, H)
21  l <- 1
22  for(h in unique(S)){
23    Idh <- which(S == h)
24    SIGMA[l] <- (PostSig2(Xh = X[Idh, ], yh = y[Idh]))^0.5
25    BETA[,l] <- PostBeta(sig2h = SIGMA[l]^2, Xh = X[Idh, ],
      yh = y[Idh])
26    l <- l + 1
27  }
28  PostBetas[[s]] <- BETA
29  PostSigma[[s]] <- SIGMA
30  Posts[s, ] <- S
31  PostAlphas[s] <- Alpha
32  setWinProgressBar(pb, s, title=paste( round(s/tot*100, 0),
    "% done"))
33 }
34 close(pb)
35 keep <- seq((burnin+1), tot, thin)
36 PosteriorS<- Posts[keep,]
37 Clusters <- sapply(1:length(keep), function(i){length(table(
  PosteriorS[i,]))})
38 table(Clusters)
39 Clusters <- sapply(1:length(keep), function(i){table(
  PosteriorS[i,]))})
40 PosteriorBeta <- PostBetas[keep]
41 PosteriorSigma <- PostSigma[keep]
42 PosteriorAlpha <- PostAlphas[keep]

```

R code. Simulation: Density from Dirichlet process mixture

```

1 DensityFunc <- function(yobs = 0, xobs = c(1, 0), s){
2   dens <- NULL
3   for(j in 1:length(Clusters[[s]])){
4     densj <- Clusters[[s]][j]/(PosteriorAlpha[s] + N + 1) *
       dnorm(yobs, t(PosteriorBeta[[s]][,j])%*%xobs,
       PosteriorSigma[[s]][j])
5     dens <- c(dens, densj)
6   }
7   dens <- c(dens, PosteriorAlpha[s]/(PosteriorAlpha[s] + N +
       1)*exp(LogMarLikLM(yh = yobs, xh = xobs)))
8   return(sum(dens))
9 }
10 xobs <- c(1, 0)
11 ys <- seq(-3, 5, 0.05)
12 pdfy <- 0.5*dnorm(ys, 2 + 1.5*xobs[2], 1) + 0.5*dnorm(ys, -1
       + 0.5*xobs[2], 0.8)
13 DensEval <- matrix(NA, length(keep), length(ys))
14 for(r in 1:length(ys)){
15   for(l in 1:length(keep)){
16     DensEval[l, r] <- DensityFunc(yobs = ys[r], xobs = xobs,
       s = 1)
17   }
18 }
19 library(dplyr)
20 library(ggplot2)
21 require(latex2exp)
22 DataDens <- tibble(t = ys, Pop = pdfy, lower = apply(
       DensEval, 2, quantile, probs = 0.025), upper = apply(
       DensEval, 2, quantile, probs = 0.975), meanT = colMeans(
       DensEval))
23 plot_filtering_estimates <- function(df) {
24   p <- ggplot(data = df, aes(x = t)) + geom_ribbon(aes(ymin
       = lower, ymax = upper), alpha = 1, fill = "lightblue") +
       geom_line(aes(y = Pop, color = "True Value"), linewidth
       = 0.5) + geom_line(aes(y = meanT, color = "Estimate"),
       linewidth = 0.5) + scale_color_manual(values = c("True
       Value" = "black", "Estimate" = "blue")) + xlab(TeX("y"))
       + ylab("Density") + labs(title = "Density: Dependent
       variable", color = "") + theme_minimal()
25   print(p)
26 }
27 plot_filtering_estimates(DataDens)

```

7. Example: Consumption of marijuana in Colombia continues II

Perform the application of marijuana consumption with the following spec-



FIGURE 11.4
Density from Dirichlet process mixture.

ification:

$$y_i = \mathbf{z}_i^\top \boldsymbol{\gamma} + f(\text{Age}_i) + \mu_i,$$

where y_i is the (log) marijuana monthly consumption, \mathbf{z}_i represents the presence of a drug dealer in the neighborhood (*Dealer*), gender (*Female*), indicators of good physical and mental health (*PhysicalHealthGood* and *MentalHealthGood*), years of education (*YearsEducation*), and the (log) prices of marijuana, cocaine, and crack by individual.

Initially, set the knots as the percentiles $\{0, 0.05, \dots, 0.95, 1\}$ of age and use cubic B-splines. Then, apply the BIC approximation to perform variable selection in this model with non-informative conjugate priors, 5,000 MCMC iterations, and 5,000 burn-in iterations.

Do you think that using a linear regression with a second-degree polynomial in age provides a good approximation to the relationship found using splines in this application?

Answer:

The following code illustrates this exercise. We use the function *bicreg* from the package *BMA* to perform variable selection. Initially, we construct the design matrix, excluding the B-splines that cause perfect multicollinearity, and then select the variables with a posterior inclusion probability greater than 50%. This also corresponds to the model with the highest posterior probability.

After this, we proceed with inference using a linear regression with conjugate prior distributions. Figure 11.5 shows the fit, with the mean (blue line) and 95% credible intervals (shaded blue). This curve is simpler than the one using all the B-splines: there appears to be a hook-shaped pattern at the beginning, where teenagers consume less marijuana than individuals in their 20s to 50s. After age 55, consumption decreases significantly. Given this pattern, assuming a second-degree polynomial appears to be a reasonable choice.

*R code. Simulation: Semi-parametric Dirichlet
process mixture*

```

1 rm(list = ls()); set.seed(010101)
2 library(splines); library(ggplot2)
3 Data <- read.csv("https://raw.githubusercontent.com/
   BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
   MarijuanaColombia.csv")
4 attach(Data)
5 IdOrd <- order(Age); y <- LogMarijuana[IdOrd]
6 Z <- as.matrix(cbind(Data[IdOrd,-c(1, 6, 7)]))
7 x <- Age[IdOrd]
8 knots <- quantile(x, seq(0, 1, 0.05))
9 BS <- bs(x, knots = knots, degree = 3, Boundary.knots =
   range(x), intercept = FALSE)
10 matplot(x, BS, type = "l", lty = 1, col = rainbow(ncol(BS)))
11 # Function to check if a column is constant
12 is_constant <- function(col) {
13   return(length(unique(col)) == 1)
14 }
15 constant_columns <- apply(BS, 2, is_constant)
16 X <- cbind(BS[, -c(which(constant_columns == TRUE))], Z)
17 BMAGlm <- BMA::bicreg(X, y, strict = FALSE, OR = 50)
18 summary(BMAGlm)
19 idReg <- c(2, 23, 24, 27:29) # Relevant regressors, PIP >
   0.5
20 Xnew <- cbind(1, X[, idReg])
21 N <- dim(Xnew)[1]; k <- dim(Xnew)[2]
22 # Hyperparameters
23 d0 <- 0.001; a0 <- 0.001
24 b0 <- rep(0, k); c0 <- 1000
25 B0 <- c0*diag(k); B0i <- solve(B0)
26 # MCMC parameters
27 mcmc <- 5000; burnin <- 5000
28 tot <- mcmc + burnin; thin <- 1
29 posterior <- MCMCpack::MCMCregress(y~Xnew-1, b0=b0, B0 =
   B0i, c0 = a0, d0 = d0, burnin = burnin, mcmc = mcmc,
   thin = thin)
30 summary(coda::mcmc(posterior))
31 # Predict values with 95% credible intervals
32 xfit <- seq(min(x), max(x), 0.2); H <- length(xfit)
33 i <- 675 # Pick a particular individual
34 idfit <- sample(1:N, H)
35 BSfit <- bs(xfit, knots = knots, degree = 3, Boundary.knots
   = range(x), intercept = FALSE)
36 Xfit <- cbind(1, BSfit[, c(2,23)], Z[rep(i, H), c(1,4:6)]) #
   Relevant regressors, PIP > 0.5
37 Fit <- matrix(NA, mcmc, H)
38 for(s in 1:mcmc){
39   Fit[s,] <- Xfit%*%posterior[s,1:7]
40 }
41 plot_data <- data.frame(x = xfit, fit = colMeans(Fit),
   liminf = apply(Fit, 2, quantile, 0.025), limsup = apply(
   Fit, 2, quantile, 0.975))
42
43 ggplot() + geom_line(data = plot_data, aes(x, fit), color =
   "blue", linewidth = 1) + geom_ribbon(data = plot_data,
   aes(x, ymin = liminf, ymax = limsup), fill = "blue",
   alpha = 0.2) + labs(title = "B-Spline Regression with
   95% Confidence Interval", x = "Age",
44 y = "Log Marijuana") + theme_minimal()

```

**FIGURE 11.5**

Spline: Marijuana monthly consumption vs age.

12

Approximate Bayesian methods

Solutions of Exercises

1. g-and-k distribution for financial returns continues I

Simulate a dataset following the specification given in the g-and-k distribution for financial returns example. Set $\theta_1 = 0.8$, $a = 1$, $b = 0.5$, $g = -1$, and $k = 1$, with a sample size of 500, and use the same priors as in that example. Implement the ABC accept/reject algorithm from scratch using one million prior draws, selecting the 1,000 draws with the smallest distance.¹

- Perform a linear regression adjustment using the posterior draws of our ABC-AR algorithm (ABC-AR-Adj).
- Compare the results with those obtained using the ABC-AR implementation in the *EasyABC* package, ensuring that the computational time is relatively similar between both implementations.
- Compare the posterior results of ABC-AR, ABC-AR-Adj and EasyABC with the population values.

Answer:

The following code implements our ABC-AR algorithm, following the steps outlined in the ABC-AR Algorithm of the book. Users can observe that a linear regression adjustment is applied; however, due to multicollinearity issues, one summary statistic is omitted in the prediction step (see the *abc* package for alternative regression adjustments).

Figure 12.1 presents the posterior distributions of θ_1 , g , and k using both our ABC implementations and the *EasyABC* package. We observe that our algorithms provide less information about θ_1 compared to the *EasyABC* implementation. Conversely, our algorithms offer more information about g and k than the *EasyABC* function. Additionally, regression adjustment helps center the posterior distributions of g and k around the population parameters. But, this is not the case regarding θ_1 . Moreover, applying regression adjustment introduces a degree of smoothness to the distributions.

¹Note that this setting does not satisfy the asymptotic requirements for Bayesian consistency. However, it serves as a pedagogical exercise.

Overall, in all implementations, the 95% credible intervals encompass the population values.

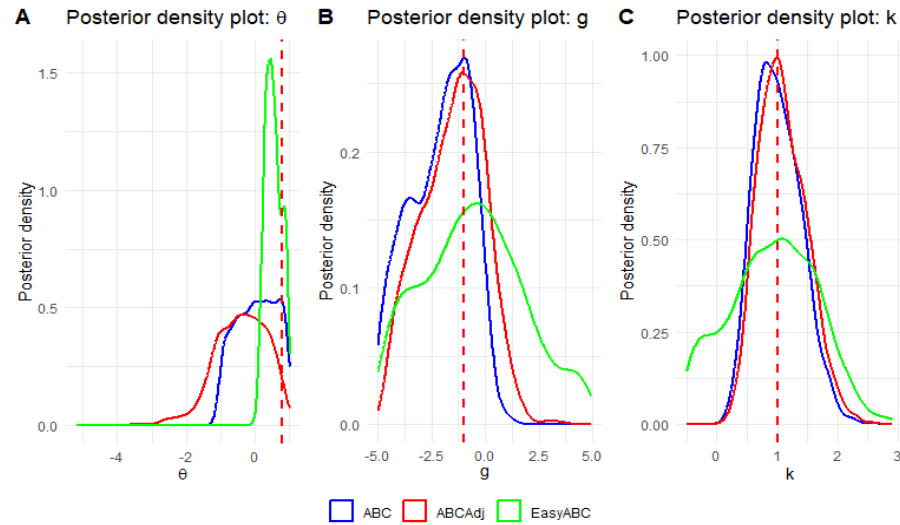


FIGURE 12.1

Posterior distributions using approximate Bayesian computation accept/reject: g-and-k distribution.

*R code. Approximate Bayesian computation
accept/reject algorithm: g-and-k distribution
simulation*

```

1 rm(list = ls()); set.seed(010101)
2 # Simulate g-and-k data
3 RGKnew <- function(par) {
4   z <- NULL
5   theta <- par[1]; a <- par[2]; b <- par[3]; g <- par[4]; k
     <- par[5]
6   e <- rnorm(n + 1)
7   for(t in 2:(n + 1)){
8     zt <- e[t] + theta * e[t-1]
9     z <- c(z, zt)
10  }
11  zs <- z / (1 + theta^2)^0.5
12  x <- a + b * (1 + 0.8 * (1 - exp(-g * zs)) / (1 + exp(-g *
     zs))) * (1 + zs^2)^k * zs
13  return(x)
14 }
15 # Summary statistics
16 SumSt <- function(y) {
17   Oct <- quantile(y, c(0.125, 0.25, 0.375, 0.5, 0.625, 0.75,
     0.875))
18   eta1 <- Oct[6] - Oct[2]
19   eta2 <- (Oct[6] + Oct[2] - 2 * Oct[4]) / eta1
20   eta3 <- (Oct[7] - Oct[5] + Oct[3] - Oct[1]) / eta1
21   autocor <- acf(y, lag = 2, plot = FALSE)
22   autocor[["acf"]][2:3]
23   Etag <- c(Oct, eta1, eta2, eta3, autocor[["acf"]][2:3])
24   return(Etag)
25 }
26 # Population parameters
27 theta1 <- 0.8; a <- 1; b <- 0.5; g <- -1; k <- 1
28 parpop <- c(theta1, a, b, g, k)
29 n <- 500
30 y <- RGKnew(par = parpop)
31 ##### ABC Function#####
32 ABC <- function(S, a, y) {
33   prior <- cbind(runif(S,-1,1), runif(S,0,5), runif(S,0,5),
     runif(S,-5,5), runif(S,-0.5,5))
34   Z <- apply(prior, 1, RGKnew)
35   EtasZ <- apply(Z, 2, SumSt)
36   Etag <- SumSt(y)
37   Dist <- sapply(1:S, function(l) {
38     dist(rbind(Etag, EtasZ[, l]))
39   })
40   OrdPrior <- prior[order(Dist), ]
41   SelPrior <- OrdPrior[1:round(S * a), ]
42   SelSumSt <- t(EtasZ)[1:round(S * a), ]
43   return(list(SelPrior = SelPrior, SelSumSt = SelSumSt))
44 }
45 S <- 1000000
46 a <- 0.001
47 tick <- Sys.time()
48 ResABC <- ABC(S = S, a = 0.001, y = y)
49 tock <- Sys.time()
50 tock - tick
51 PostABC_Arown <- ResABC[["SelPrior"]]

```

*R code. Approximate Bayesian computation
accept/reject algorithm: g-and-k distribution
simulation*

```

1 # Regression adjusted ABC
2 X <- ResABC[["SelSumSt"]]-matrix(SumSt(y), S*a, 12, byrow =
  TRUE)
3 PostABC_ARownRegAd <- PostABC_ARown
4 for(j in 1:5){
5   Reg <- lm(PostABC_ARown[,j] ~ X)
6   # Coefficient of regressor 9 is na.
7   PostABC_ARownRegAd[,j] <- PostABC_ARown[,j] - X[,-9]%*%Reg
  $coefficients[-c(1,9)]
8 }
9 RGKnewSum <- function(par) {
10   z <- NULL
11   theta <- par[1]; a <- par[2]; b <- par[3]; g <- par[4]; k
    <- par[5]
12   e <- rnorm(n + 1)
13   for(t in 2:(n + 1)){
14     zt <- e[t] + theta * e[t-1]
15     z <- c(z, zt)
16   }
17   zs <- z / (1 + theta^2)^0.5
18   x <- a + b * (1 + 0.8 * (1 - exp(-g * zs)) / (1 + exp(-g *
    zs))) * (1 + zs^2)^k * zs
19   Etaz <- SumSt(x)
20   return(Etaz)
21 }
22 sum_stat_obs <- SumSt(y)
23 toy_prior <- list(c("unif",-1,1), c("unif",0,5), c("unif",
  0,5), c("unif", -5,5), c("unif", -0.5,5))
24 library(EasyABC)
25 tick <- Sys.time()
26 ABC_AR <- ABC_rejection(model=RGKnewSum, prior=toy_prior,
27 summary_stat_target = sum_stat_obs, nb_simul=260000, tol =
  0.00385,
28 progress_bar = TRUE)
29 tock <- Sys.time()
30 tock - tick
31 PostABC_AR <- coda::mcmc(ABC_AR$param)
32 # Summary
33 summary(coda::mcmc(PostABC_ARown))
34 summary(coda::mcmc(PostABC_ARownRegAd))
35 summary(coda::mcmc(PostABC_AR))

```

*R code. Approximate Bayesian computation
accept/reject algorithm: g-and-k distribution
simulation*

```

1 library(ggplot2); library(latex2exp)
2 Sp <- 1000
3
4 df1 <- data.frame(Value = c(PostABC_AR[1:Sp,1], PostABC_
  ARown[1:Sp,1], PostABC_ARownRegAd[1:Sp,1]), Distribution
  = factor(c(rep("EasyABC", Sp), rep("ABC", Sp), rep("
    ABCAdj", Sp))))
5 dentheta <- ggplot(df1, aes(x = Value, color = Distribution)
  ) + geom_density(linewidth = 1) + geom_vline(xintercept
  = theta1, linetype = "dashed", color = "red", linewidth
  = 1) +
6 labs(title = TeX("Posterior density plot:  $\theta$ "), x = TeX
  (" $\theta$ "), y = "Posterior density") + scale_color_
  manual(values = c("blue", "red", "green")) + theme_
  minimal() +
7 theme(legend.title = element_blank())
8
9 df2 <- data.frame(Value = c(PostABC_AR[1:Sp,4], PostABC_
  ARown[1:Sp,4], PostABC_ARownRegAd[1:Sp,4]), Distribution
  = factor(c(rep("EasyABC", Sp), rep("ABC", Sp), rep("
    ABCAdj", Sp))))
10 deng <- ggplot(df2, aes(x = Value, color = Distribution)) +
  geom_density(linewidth = 1) + geom_vline(xintercept =
  g, linetype = "dashed", color = "red", linewidth = 1) +
  labs(title = TeX("Posterior density plot: g"), x = TeX("
    g"), y = "Posterior density") +
11 scale_color_manual(values = c("blue", "red", "green")) +
  theme_minimal() + theme(legend.title = element_blank())
12
13 df3 <- data.frame(Value = c(PostABC_AR[1:Sp,5], PostABC_
  ARown[1:Sp,5], PostABC_ARownRegAd[1:Sp,5]), Distribution
  = factor(c(rep("EasyABC", Sp), rep("ABC", Sp), rep("
    ABCAdj", Sp))))
14 denk <- ggplot(df3, aes(x = Value, color = Distribution)) +
  geom_density(linewidth = 1) + geom_vline(xintercept =
  k, linetype = "dashed", color = "red", linewidth = 1) +
15 labs(title = TeX("Posterior density plot: k"), x = TeX(" $k$ "),
  y = "Posterior density") +
16 scale_color_manual(values = c("blue", "red", "green")) +
  theme_minimal() + theme(legend.title = element_blank())
17
18 library(ggpubr)
19 ggarrange(dentheta, deng, denk, labels = c("A", "B", "C"),
  ncol = 3, nrow = 1,
20 legend = "bottom", common.legend = TRUE)

```

2. g-and-k distribution for financial returns continues II

Perform inference in the financial returns example using Bayesian synthetic likelihood, setting $M = 500$, $S = 11,000$, a burn-in of 1,000, and a thinning parameter of 10. This setting results in a similar computational time to the ABC algorithm. Use a random walk proposal distribution in the *BSL* package in **R**, and compare the results with those from ABC.

Answer:

The following code shows how to perform inference in this exercise, and Figure 12.2 shows the posterior plots. We find that there is marginal positive evidence that the moving average coefficient is positive. Since the posterior distribution of g is centered around zero, the distribution appears to be symmetric around its median. Meanwhile, a positive k indicates that the distribution has heavier tails than a normal distribution, implying a higher likelihood of extreme values (outliers) in the exchange rate USD/EURO.

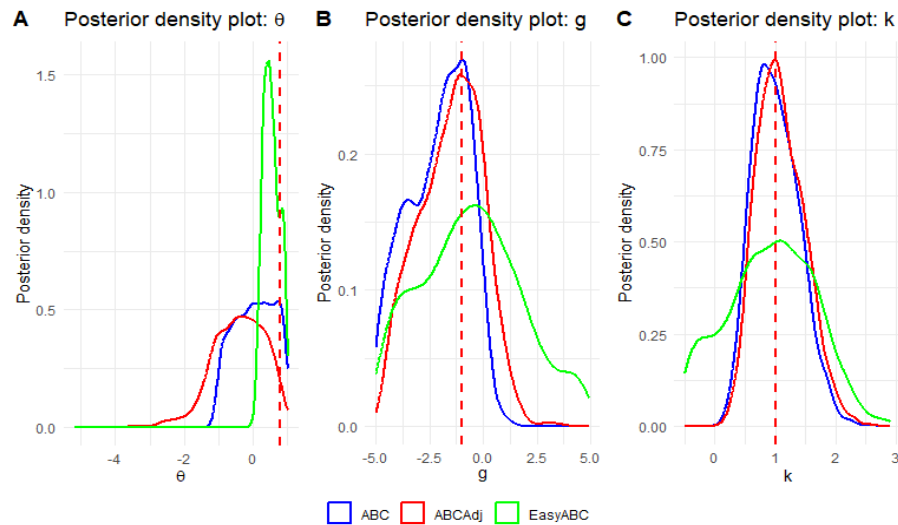


FIGURE 12.2

Posterior distributions using Bayesian synthetic likelihood: Financial returns USD/EURO example.

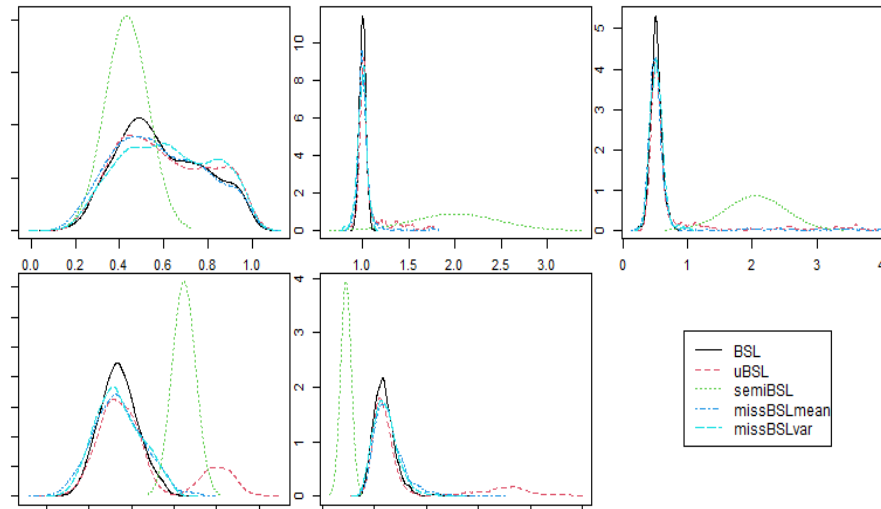


FIGURE 12.3

Posterior distributions using Bayesian synthetic likelihood: Simulation exercise g-and-k distribution.

R code. Bayesian synthetic likelihood: Financial log returns USD/EURO

```

1  library(ggplot2); library(latex2exp)
2  Sp <- 1000
3
4  df1 <- data.frame(Value = c(PostABC_AR[1:Sp,1],
5  PostABC_ARown[1:Sp,1], PostABC_ARownRegAd[1:Sp,1]),
6  Distribution = factor(c(rep("EasyABC", Sp), rep("ABC",
7  Sp), rep("ABCAdj", Sp))))
8  dentheta <- ggplot(df1, aes(x = Value, color =
9  Distribution)) + geom_density(linewidth = 1) + geom_
10 vline(xintercept = theta1, linetype = "dashed", color =
11 "red", linewidth = 1) +
12 labs(title = TeX("Posterior density plot:  $\theta$ "), x
13 = TeX(" $\theta$ "), y = "Posterior density") + scale_
14 color_manual(values = c("blue", "red", "green")) +
15 theme_minimal() +
16 theme(legend.title = element_blank())
17
18 df2 <- data.frame(Value = c(PostABC_AR[1:Sp,4],
19 PostABC_ARown[1:Sp,4], PostABC_ARownRegAd[1:Sp,4]),
20 Distribution = factor(c(rep("EasyABC", Sp), rep("ABC",
21 Sp), rep("ABCAdj", Sp))))
22 deng <- ggplot(df2, aes(x = Value, color =
23 Distribution)) + geom_density(linewidth = 1) + geom_
24 vline(xintercept = g, linetype = "dashed", color = "red",
25 linewidth = 1) + labs(title = TeX("Posterior density
26 plot: g"), x = TeX("g"), y = "Posterior density") +
27 scale_color_manual(values = c("blue", "red", "green"))
28 + theme_minimal() + theme(legend.title = element_blank
29 ())
30
31 df3 <- data.frame(Value = c(PostABC_AR[1:Sp,5],
32 PostABC_ARown[1:Sp,5], PostABC_ARownRegAd[1:Sp,5]),
33 Distribution = factor(c(rep("EasyABC", Sp), rep("ABC",
34 Sp), rep("ABCAdj", Sp))))

```



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Appendix

TABLE 12.1

Libraries and commands in BEsmarter GUI.

| Univariate models | | | |
|----------------------------------|-----------|-----------------|-----------|
| Model | Library | Command | Reference |
| Normal | MCMCpack | MCMCregress | [16] |
| Logit | MCMCpack | MCMClogit | [16] |
| Probit | bayesm | rbprobitGibbs | [26] |
| Multinomial(Mixed) Probit | bayesm | rmnpGibbs | [26] |
| Multinomial(Mixed) Logit | bayesm | rmnlIndepMetrop | [26] |
| Ordered Probit | bayesm | rordprobitGibbs | [26] |
| Negative Binomial(Poisson) | bayesm | rnegbinRw | [26] |
| Tobit | MCMCpack | MCMCtobit | [16] |
| Quantile | MCMCpack | MCMCquantreg | [16] |
| Bayesian bootstrap | bayesboot | bayesboot | [2] |
| Multivariate models | | | |
| Model | Library | Command | Reference |
| Multivariate | bayesm | rmultireg | [26] |
| Seemingly Unrelated Regression | bayesm | rsurGibbs | [26] |
| Instrumental Variable | bayesm | rivGibbs | [26] |
| Bivariate Probit | bayesm | rmvpGibbs | [26] |
| Hierarchical longitudinal models | | | |
| Model | Library | Command | Reference |
| Normal | MCMCpack | MCMChregress | [16] |
| Logit | MCMCpack | MCMChlogit | [16] |
| Poisson | MCMCpack | MCMChpoisson | [16] |
| Bayesian model averaging | | | |
| Model | Library | Command | Reference |
| Normal (BIC) | BMA | bic.glm | [21] |
| Normal (MC ³) | BMA | MC3.REG | [21] |
| Normal (instrumental variables) | ivbma | ivbma | [14] |
| Logit (BIC) | BMA | bic.glm | [21] |
| Gamma (BIC) | BMA | bic.glm | [21] |
| Poisson (BIC) | BMA | bic.glm | [21] |
| Diagnostics | | | |
| Diagnostic | Library | Command | Reference |
| Trace plot | coda | traceplot | [18] |
| Autocorrelation plot | coda | autocorr.plot | [18] |
| Geweke test | coda | geweke.diag | [18] |
| Raftery & Lewis test | coda | raftery.diag | [18] |
| Heidelberger & Welch test | coda | heidel.diag | [18] |

TABLE 12.2Datasets templates in folder *DataSim*.

| Univariate models | | |
|----------------------------------|-----------------------------|---------------------------|
| Model | Data set file | Data set simulation |
| Normal | 11SimNormalmodel.csv | 11SimNormal.R |
| Logit | 12SimLogitmodel.csv | 12SimLogit |
| Probit | 13SimProbitmodel.csv | 13SimProbit.R |
| Multinomial(Mixed) Probit | 14SimMultProbmodel.csv | 14SimMultinomialProbit.R |
| Multinomial(Mixed) Logit | 15SimMultLogitmodel.csv | 15SimMultinomialLogit.R |
| Ordered Probit | 16SimOrderedProbitmodel.csv | 16SimOrderedProbit.R |
| Negative Binomial(Poisson) | 17SimNegBinmodel.csv | 17SimNegBin.R |
| Tobit | 18SimTobitmodel.csv | 18SimTobit.R |
| Quantile | 19SimQuantilemodel.csv | 19SimQuantile.R |
| Bayesian bootstrap | 41SimBootstrapmodel.csv | 41SimBootstrapmodel.R |
| Multivariate models | | |
| Model | Data set file | Data set simulation |
| Multivariate | 21SimMultivariate.csv | 21SimMultReg.R |
| Seemingly Unrelated Regression | 22SimSUR.csv | 22SimSUR.R |
| Instrumental Variable | 23SimIV.csv | 23SimIV.R |
| Bivariate Probit | 24SimMultProbit.csv | 24SimMultProbit.R |
| Hierarchical longitudinal models | | |
| Model | Data set file | Data set simulation |
| Normal | 31SimLogitudinalNormal.csv | 31SimLogitudinalNormal.R |
| Logit | 32SimLogitudinalLogit.csv | 32SimLogitudinalLogit.R |
| Poisson | 33SimLogitudinalPoisson.csv | 33SimLogitudinalPoisson.R |
| Bayesian model averaging | | |
| Model | Data set file | Data set simulation |
| Normal (BIC) | 511SimNormalBMA.csv | 511SimNormalBMA.R |
| Normal (MC ³) | 512SimNormalBMA.csv | 512SimNormalBMA.R |
| Normal (instrumental variables) | 513SimNormalBMAivYXW.csv | 513SimNormalBMAiv.R |
| | 513SimNormalBMAivZ.csv | |
| Logit (BIC) | 52SimLogitBMA.csv | 52SimLogitBMA.R |
| Gamma (BIC) | 53SimGammaBMA.csv | 53SimGammaBMA.R |
| Poisson (BIC) | 53SimPoissonBMA.csv | 53SimPoissonBMA.R |

TABLE 12.3Real datasets in folder *DataApp*.

| Univariate models | | |
|----------------------------------|-------------------------------------|--------------------------|
| Model | Data set file | Dependent variable |
| Normal | 1ValueFootballPlayers.csv | log(Value) |
| Logit | 2HealthMed.csv | Hosp |
| Probit | 2HealthMed.csv | Hosp |
| Multinomial(Mixed) Probit | Fishing.csv | mode |
| Multinomial(Mixed) Logit | Fishing.csv | mode |
| Ordered Probit | 2HealthMed.csv | MedVisPrevOr |
| Negative Binomial(Poisson) | 2HealthMed.csv | MedVisPrev |
| Tobit | 1ValueFootballPlayers.csv | log(ValueCens) |
| Quantile | 1ValueFootballPlayers.csv | log(Value) |
| Bayesian bootstrap | 1ValueFootballPlayers.csv | log(Value) |
| Multivariate models | | |
| Model | Data set file | Dependent variable |
| Multivariate | 4Institutions.csv | logpcGDP95 and PAER |
| Seemingly Unrelated Regression | 5Institutions.csv | logpcGDP95 and PAER |
| Instrumental Variable | 6Institutions.csv | logpcGDP95 and PAER |
| Bivariate Probit | 7HealthMed.csv | $y = [\text{Hosp SHI}]'$ |
| Hierarchical longitudinal models | | |
| Model | Data set file | Dependent variable |
| Normal | 8PublicCap.csv | log(gsp) |
| Logit | 9VisitDoc.csv | DocVis |
| Poisson | 9VisitDoc.csv | DocNum |
| Bayesian model averaging | | |
| Model | Data set file | Dependent variable |
| Normal (BIC) | 10ExportDiversificationHHI.csv | avghhi |
| Normal (MC ³) | 10ExportDiversificationHHI.csv | avghhi |
| Normal (instrumental variables) | 11ExportDiversificationHHI.csv | avghhi and avglgdp |
| Logit (BIC) | 12ExportDiversificationHHIInstr.csv | cap |
| Gamma (BIC) | 13InternetMed.csv | internet |
| Poisson (BIC) | 14ValueFootballPlayers.csv | log market value |
| | 15Fertile2.csv | ceb |