Half Title

Solution Manual
Introduction to Bayesian Econometrics: A GUIded
toolkit using R

Title Page

Solution Manual
Introduction to Bayesian Econometrics: A GUIded
toolkit using R

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To my parents, Nancy and Orlando.

Contents

III   *Advanced* methods: A brief introduction   221

Foreword

Preface

The main goal of this manual is to show the solution of the exercises of the book **Introduction to Bayesian Econometrics: A GUIded toolkit using R**. Trying to solve the exercises is important for those who want to improve their understanding about the Bayesian inferential framework more approachable.

To instructors

This book is divided into three parts: foundations (chapters 1 to 4), regression analysis (chapters 5 to 10), and *Advanced* methods (chapters 11 to 14). Our graphical user interface (GUI) is designed for the second part. The source code can be found at **https://github.com/besmarter/BSTApp**. Instructors and students can access all the code, along with simulated and real datasets. There are three ways to install our GUI:

1. Type **shiny::runGitHub("besmarter/BSTApp", launch.browser=T)** in the **R** console or any **R** code editor and execute it.

2. Visit **https://posit.cloud/content/4328505**, log in or sign up for **Posit Cloud**, navigate to the **BSTApp-master** folder in the **Files** tab of the right-bottom window, then click on the **app.R** file and select **Run App**.

3. Use a **Docker** image by typing in the **Command Prompt**

   (a) docker pull magralo95/besmartergui:latest
   (b) docker run --rm -p 3838:3838 magralo95/besmartergui

   Then users can access our GUI going to **http://localhost:3838/**. See Chapter 5 for details.

Students should have a basic understanding of probability theory and statistics, as well as some background in econometrics and time series, particularly regression analysis. Familiarity with standard univariate and multivariate probability distributions is strongly recommended. See a nice summary of useful probability distributions in [14, p. 182-191]. Additionally, students who wish to master the material in this book should have programming skills in **R** software.[1]

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[1] An excellent starting point for **R** programming is the *R Introduction Manual*: **https://cran.r-project.org/doc/manuals/r-release/R-intro.pdf**.

Instructors can send me an email to have access to this solution manual. They can use this book as a textbook for a course on introductory Bayesian Econometrics/Statistics, with a strong emphasis on implementation and applications. This book is intended to be complementary, rather than a substitute, for excellent resources on the topic, such as [9], [4], [38], [14], [12], [23], and [21].

Acknowledgments

I began developing our graphical user interface (GUI) in 2016, after being diagnosed with cervical dystonia. I worked on this side project during weekends, which I called "nerd weekends," and it served as a form of release from my health condition. Once I began to recover, I invited Mateo Graciano, my former student, business partner, and friend, to join the project. He has been instrumental in developing our GUI, and I am enormously grateful to him.

I would also like to thank the members of the BEsmarter research group at Universidad EAFIT, as well as the NUMBATs members at Monash University, for their valuable feedback and recommendations to improve our GUI.

This book is an extension of the paper *A GUIded tour of Bayesian regression* [36], which serves as a brief user guide for our GUI. I decided to write this book to explain the underlying theory and code in our GUI, and to use it as a textbook in my course on Bayesian econometrics/statistics. I am grateful to my students in this course; their insights and thoughtful questions have deepened my understanding of the material.

I would like to thank Chris Parmeter for his valuable suggestions on how to present our user guide; Professors Raúl Pericchi and Juan Carlos Correa for introducing me to Bayesian statistics; and Liana Jacobi, Tomasz Wozniak, and Chun Fung Kwok (Jackson) from the University of Melbourne, as well as David Frazier from Monash University, for their engaging discussions and fruitful collaborations in Bayesian econometrics and statistics. I am also deeply grateful to Professor Peter Diggle for his unwavering support of my career, and especially to Professor Gael Martin, who gave me the opportunity to work with her and has been a constant source of intellectual inspiration.

I also wish to acknowledge my colleagues and staff at Universidad EAFIT for their continuous support.

Finally, I acknowledge the use of ChatGPT, which assisted me in improving the grammar, clarity, and flow of the text, as well as in tidying up the code presented in this book. Nevertheless, all concepts, mathematical developments, and underlying logic are entirely my own, based on my understanding and readings of the literature. Any remaining errors are solely my responsibility, for which I apologize in advance. I sincerely thank the reader and hope that this book proves useful.

To my parents, Orlando and Nancy, who have always been there for me with their unconditional support. They have taught me that the primary aspect of human spiritual evolution is humility, a lesson I am still learning every day. To my fiancée, Estephania, for her unwavering love and support.

Symbols

Symbol Description

$\neg$	Negation symbol	$\mathbf{0}_l$	l-dimensional null vector
$\propto$	Proportional symbol	$\max_r$	Maximum over r
$\perp$	Independence symbol	$\min_r$	Minimum over r
$\mathcal{R}$	The Real set	∇	Gradiente operator
$\mathcal{R}^K$	Euclidean space of dimension K	$\overset{iid}{\sim}$	Independently and identically distributed
$\emptyset$	Empty set	$\overset{ind}{\sim}$	Independently and Not identically distributed
$\mathbb{1}$	Indicator function		
P	Probability measure	$>$	Greater than
$:=$	Is defined as	$<$	Less than
argmax	Argument of the maximum	$\approx$	Approximately equal to
argmin	Argument of the minimum	$\gtrsim$	Greater than or approximately equal to
tr	Trace operator		
vec	Vectorization operator	Δ	Difference operator
lim	Limit	$\subseteq$	Subset
$\otimes$	Kronecker product	$\subset$	Proper subset
diag$\{\cdot\}$	Diagonal matrix	$\overset{d}{\to}$	Convergence in distribution (law)
$dim\{\cdot\}$	Dimension of an object		
$\boldsymbol{I}_l$	l-dimensional identity matrix	$\overset{p}{\to}$	Convergence in probability
		$\overset{a.s.}{\to}$	Almost surely convergence

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 Blue company has 150 cabs, while the Green company has 850 cabs. A witness stated that a blue cab was involved in the accident. The court tested the reliability of the witness under similar circumstances and found that the witness correctly identified the color of the cab 80% of the time, but made an incorrect identification 25% of the time. *What is the probability that the cab involved in the accident was actually 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:

$$
\begin{aligned}
P(B|WB) &= \frac{P(B, WB)}{P(WB)} \\
&= \frac{P(WB|B) \times P(B)}{P(WB|B) \times P(B) + P(WB|\neg B) \times (1 - P(B))} \\
&= \frac{0.8 \times 0.15}{0.8 \times 0.15 + 0.25 \times 0.85} \\
&= 0.36
\end{aligned}
\tag{1.1}
$$

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,

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

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:

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

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

```r
set.seed(0101) # Set simulation seed
S <- 100000 # Simulations
Game <- function(opt = 3){
# opt: number of options. opt > 2
opts <- 1:opt
car <- sample(opts, 1) # car location
guess1 <- sample(opts, 1) # Initial guess
if(opt == 3 && car != guess1) {
 host <- opts[-c(car, guess1)]
 } else {
 host <- sample(opts[-c(car, guess1)], 1)
}
win1 <- guess1 == car # Win given no change
if(opt == 3) {
 guess2 <- opts[-c(host, guess1)]
 } else {
 guess2 <- sample(opts[-c(host, guess1)], 1)
 }
win2 <- guess2 == car # Win given change
return(c(win1, win2))
}
#Win probabilities
Prob <- rowMeans(replicate(S, Game(opt = 4)))
#Winning probabilities no changing door
Prob[1]
0.25151
#Winning probabilities changing door
Prob[2]
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,

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

$$= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \lambda^{\alpha_0 - 1} e^{-\lambda \beta_0} \right) \left(\frac{\lambda^{\sum_{i=1}^{N} y_i} e^{-N\lambda}}{\prod_{i=1}^{N} y_i!} \right)$$

$$= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \frac{1}{\prod_{i=1}^{N} y_i!} \right) \lambda^{\sum_{i=1}^{N} y_i + \alpha_0 - 1} e^{-\lambda(\beta_0 + N)}$$

$$\propto \lambda^{\sum_{i=1}^{N} y_i + \alpha_0 - 1} e^{-\lambda(\beta_0 + N)}. \tag{1.5}$$

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

$$E[\lambda|\mathbf{y}] = \frac{\alpha_n}{\beta_n} \tag{1.6}$$

$$= \frac{\sum_{i=1}^{N} y_i + \alpha_0}{\beta_0 + N}$$

$$= \left(\frac{N}{\beta_0 + N} \right) \bar{y} + \left(\frac{\beta_0}{\beta_0 + N} \right) \frac{\alpha_0}{\beta_0}$$

$$= w\bar{y} + (1 - w) E[\lambda],$$

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

$$\pi(Y_0|\mathbf{y}) = \int_0^\infty \frac{\lambda^{y_0} e^{-\lambda}}{y_0!} \pi(\lambda|\mathbf{y}) d\lambda \tag{1.7}$$

$$= \int_0^\infty \left(\frac{\lambda^{y_0} e^{-\lambda}}{y_0!} \right) \left(\frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n)} \lambda^{\alpha_n - 1} e^{-\lambda \beta_n} \right) d\lambda$$

$$= \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n) y_0!} \int_0^\infty \lambda^{y_0 + \alpha_n - 1} e^{-\lambda(1 + \beta_n)} d\lambda$$

$$= \frac{\beta_n^{\alpha_n}}{\Gamma(\alpha_n) y_0!} \frac{\Gamma(y_0 + \alpha_n)}{(1 + \beta_n)^{y_0 + \alpha_n}}$$

$$= \frac{\Gamma(y_0 + \alpha_n)}{\Gamma(\alpha_n) y_0!} \left(\frac{1}{1 + \beta_n} \right)^{y_0} \left(\frac{\beta_n}{1 + \beta_n} \right)^{\alpha_n}$$

$$= \frac{(y_0 + \alpha_n - 1)!}{(\alpha_n - 1)!y_0!} \left(\frac{1}{1 + \beta_n}\right)^{y_0} \left(\frac{\beta_n}{1 + \beta_n}\right)^{\alpha_n}$$

$$= \binom{y_0 + \alpha_n - 1}{y_0} \left(\frac{1}{1 + \beta_n}\right)^{y_0} \left(\frac{\beta_n}{1 + \beta_n}\right)^{\alpha_n}.$$

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

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

where

$$p(y) = \int_0^\infty \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0)} \lambda^{\alpha_0 - 1} e^{-\lambda \beta_0}\right) \left(\prod_{i=1}^N \frac{\lambda^{y_0} e^{-\lambda}}{y_0!}\right) d\lambda \qquad (1.8)$$

$$= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0) \prod_{i=1}^N y_i!}\right) \int_0^\infty \lambda^{\sum_{i=1}^N y_i + \alpha_0 - 1} e^{-\lambda(\beta_0 + N)} d\lambda$$

$$= \left(\frac{\beta_0^{\alpha_0}}{\Gamma(\alpha_0) \prod_{i=1}^N y_i!}\right) \left(\frac{\Gamma\left(\sum_{i=1}^N y_i + \alpha_0\right)}{(\beta_0 + N)^{\sum_{i=1}^N y_i + \alpha_0}}\right)$$

$$= \frac{\Gamma\left(\sum_{i=1}^N y_i + \alpha_0\right)}{\Gamma(\alpha_0) \prod_{i=1}^N y_i!} \left(\frac{1}{\beta_0 + N}\right)^{\sum_{i=1}^N y_i} \left(\frac{\beta_0}{\beta_0 + N}\right)^{\alpha_0}.$$

R code. Health insurance, predictive distribution using vague hyperparameters

```r
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 - pnbinom(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

```r
# Usimg Emprirical Bayes
LogMgLik <- function(theta, y){
  N <- length(y)
  #sample size
  a0 <- theta[1]
  # prior shape hyperparameter
  b0 <- theta[2]
  # prior scale hyperparameter
  aN <- sum(y) + a0
  # posterior shape parameter
  if(a0 <= 0 || b0 <= 0){
    #Avoiding negative values
    lnp <- -Inf
  }else{lnp <- lgamma(aN) - sum(y)*log(b0+N) + a0*log(b0/(b0
    +N)) - lgamma(a0)}
    # log marginal likelihood
  return(-lnp)
}
theta0 <- c(0.01, 0.01)
# Initial values
control <- list(maxit = 1000)
# Number of iterations in optimization
EmpBay <- optim(theta0, LogMgLik, method = "BFGS", control =
    control, hessian = TRUE, y = y)
# Optimization
EmpBay$convergence
# Checking convergence
EmpBay$value # Maximum
a0EB <- EmpBay$par[1]
# Prior shape using empirical Bayes
a0EB
128.383
b0EB <- EmpBay$par[2]
# Prior scale using empirical Bayes
b0EB
106.801
PriMeanEB <- a0EB / b0EB
# Prior mean
PriVarEB <- a0EB / b0EB^2
# Prior variance
PpEB <- ProbBo(y, a0 = a0EB, b0 = b0EB)
# This setting is using empirical Bayes.
PpEB
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, $Y_i \sim Ber(p)$, 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

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

$$= \frac{\Gamma(\alpha_0 + \beta_0)}{\Gamma(\alpha_0)\Gamma(\beta_0)} p^{\sum_{i=1}^{N} y_i + \alpha_0 - 1} (1-p)^{\beta_0 + N - \sum_{i=1}^{N} y_i - 1}$$

$$\propto p^{\sum_{i=1}^{N} y_i + \alpha_0 - 1} (1-p)^{\beta_0 + N - \sum_{i=1}^{N} y_i - 1}.$$

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

$$E[p|\mathbf{y}] = \frac{\alpha_n}{\alpha_n + \beta_n}$$

$$= \frac{\sum_{i=1}^{N} y_i + \alpha_0}{\alpha_0 + \beta_0 + N} \quad (1.10)$$

$$= \frac{N\bar{y}}{\alpha_0 + \beta_0 + N} + \frac{\alpha_0}{\alpha_0 + \beta_0 + N}$$

$$= \frac{N}{\alpha_0 + \beta_0 + N} (\bar{y}) + \frac{\alpha_0 + \beta_0}{\alpha_0 + \beta_0 + N} \left(\frac{\alpha_0}{\alpha_0 + \beta_0} \right)$$

$$= w(\bar{y}) + (1-w)E[p],$$

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

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

To use empirical Bayes, we have the following setting

$$\begin{bmatrix} \hat{\alpha}_0 & \hat{\beta}_0 \end{bmatrix} = \arg \max_{\alpha_0, \beta_0} \ln(p(\mathbf{y})),$$

where

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

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

```r
1  # Using Emprirical 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(
       y)) -lgamma(a0) - lgamma(b0) - lgamma(a0+b0+N)}
15   # log marginal likelihood
16   return(-lnp)
17 }
18 theta0 <- c(0.1, 0.1)
19 # Initial values
20 control <- list(maxit = 1000)
21 # Number of iterations in optimization
22 EmpBay <- optim(theta0, LogMgLik, method = "BFGS", control =
       control, hessian = TRUE, y = y)
23 # Optimization
24 EmpBay$convergence
25 # Checking convergence
26 EmpBay$value # Maximum
27 a0EB <- EmpBay$par[1]
28 # Prior shape using empirical Bayes
29 b0EB <- EmpBay$par[2]
30 # Prior scale using empirical Bayes
31 PriMeanEB <- a0EB /(a0EB + b0EB)
32 # Prior mean
33 PriVarEB <- (a0EB*b0EB)/(((a0EB+b0EB)^2)*(a0EB+b0EB+1))
34 # Prior variance
35 PpEB <- ProbBo(y, a0 = a0EB, b0 = b0EB)
36 # This setting is using empirical Bayes.
37 PpEB
38 0.47
```
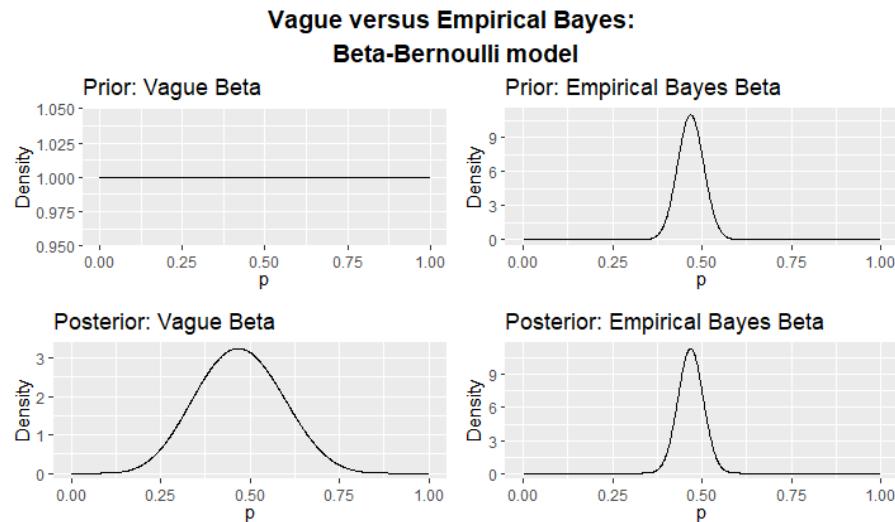
R code. Car claim, density plots

```r
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)) +
28   geom_line() +
29   xlab(TeX("$p$")) + ylab("Density") + ggtitle("Prior: Vague
       Beta")
30 fig2 <- ggplot(data = data, aes(lambda, EBPrior)) +
31   geom_line() +
32   xlab(TeX("$p$")) + ylab("Density") +
33   ggtitle("Prior: Empirical Bayes Beta")
34 fig3 <- ggplot(data = data, aes(lambda, PosteriorV)) +
35   geom_line() +
36   xlab(TeX("$p$")) + ylab("Density") +
37   ggtitle("Posterior: Vague Beta")
38 fig4 <- ggplot(data = data, aes(lambda, PosteriorEB)) +
39   geom_line() +
40   xlab(TeX("$p$")) + ylab("Density") +
41   ggtitle("Posterior: Empirical Bayes Beta")
42 FIG <- ggarrange(fig1, fig2, fig3, fig4,
43 ncol = 2, nrow = 2)
44 annotate_figure(FIG,
45 top = text_grob("Vague versus Empirical Bayes: Beta-
       Bernoulli model", color = "black", face = "bold", size =
       14))
```

Vague versus Empirical Bayes:
**Beta-Bernoulli model**
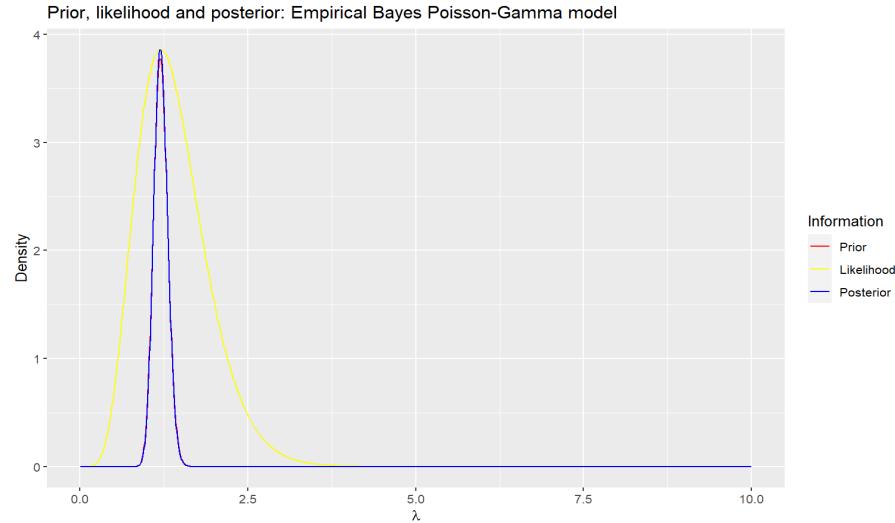
FIGURE 1.1
Vague versus Empirical Bayes: Bernoulli-Beta model.

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

```
1  # Prior , likelihood and posterior:
2  #Empirical Bayes Binonial-Beta model
3  dataNew <- data.frame(cbind(rep(lambda, 3),
4  c(EBPrior, PosteriorEB, LiksScale),
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"))
```

Prior, likelihood and posterior: Empirical Bayes Poisson-Gamma model
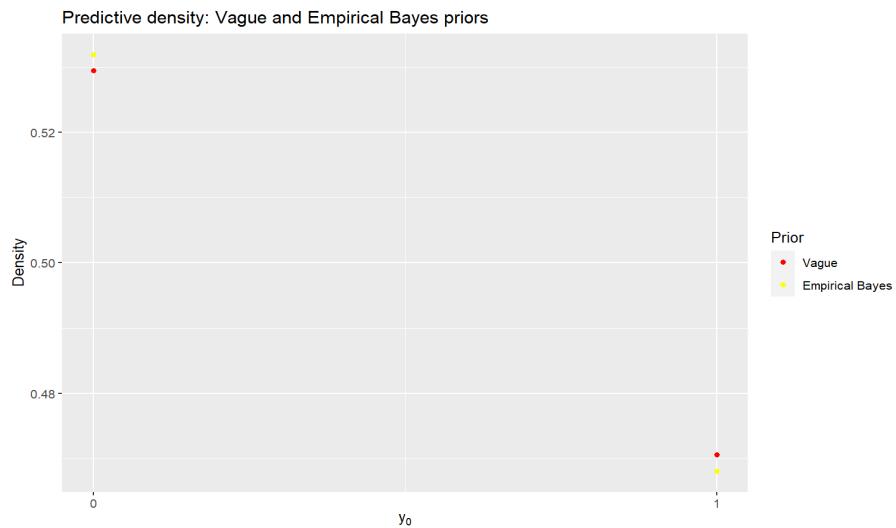
FIGURE 1.2
Prior, likelihood and posterior: Bernoulli-Beta model.

R code. Car claim, predictive probabilities plots

```r
# Predictive distributions
require(TailRank)
PredDen <- function(y, y0, a0, b0){
  N <- length(y)
  aN <- a0 + sum(y) # Posterior shape parameter
  bN <- b0 + N - sum(y) # Posterior scale parameter
  Pr <- aN/(aN+bN)
  Probs <- dbinom(y0, 1, prob = Pr)
  return(Probs)
}
y0 <- 0:1
PredVague <- PredDen(y = y, y0 = y0, a0 = a0, b0 = b0)
PredEB <- PredDen(y = y, y0 = y0, a0 = a0EB, b0 = b0EB)
dataPred <- as.data.frame(cbind(y0, PredVague, PredEB))
colnames(dataPred) <- c("y0", "PredictiveVague",
"PredictiveEB")
ggplot(data = dataPred) +
  geom_point(aes(y0, PredictiveVague, color = "red")) +
  xlab(TeX("$y_0$")) + ylab("Density") +
  ggtitle("Predictive density: Vague and Empirical Bayes
     priors") + geom_point(aes(y0, PredictiveEB, color = "
     yellow")) +
  guides(color = guide_legend(title="Prior")) +
  scale_color_manual(labels = c("Vague", "Empirical Bayes"),
     values = c("red", "yellow")) +
  scale_x_continuous(breaks=seq(0,1,by=1))
```

FIGURE 1.3
Predictive probabilities: Bernoulli-Beta model.

R code. Car claim, Bayesian model average

```r
# Posterior odds: Vague vs Empirical Bayes
PO12 <- exp(-LogMgLik(c(a0EB, b0EB), y = y))/exp(-LogMgLik(c
    (a0, b0), y = y))
PostProMEM <- PO12/(1 + PO12)
# Posterior model probability Empirical Bayes
PostProMEM
0.757
PostProbMV <- 1 - PostProMEM
# Posterior model probability vague prior
PostProbMV
0.242
# Bayesian model average (BMA)
PostMeanEB <- (a0EB + sum(y)) / (a0EB + b0EB + N)
# Posterior mean Empirical Bayes
PostMeanV <- (a0 + sum(y)) / (a0 + b0 + N)
# Posterior mean vague priors
BMAmean <- PostProMEM * PostMeanEB + PostProbMV * PostMeanV
# BMA posterior mean
PostVarEB <- (a0EB + sum(y))*(b0EB + N - sum(y)) / ((a0EB +
    b0EB + N)^2)*(a0EB + b0EB + N -1)
# Posterior variance Empirical Bayes
PostVarV <- (a0 + sum(y))*(b0 + N - sum(y)) / ((a0 + b0 + N)
    ^2)*(a0 + b0 + N -1)
# Posterior variance vague prior
BMAVar <- PostProMEM * PostVarEB + PostProbMV * PostVarV +
    PostProMEM * (PostMeanEB - BMAmean)^2 + PostProbMV * (
    PostMeanV - BMAmean)^2
# BMA posterior variance
# BMA: Predictive
BMAPred <- PostProMEM * PredEB + PostProbMV * PredVague
dataPredBMA <- as.data.frame(cbind(y0, BMAPred))
colnames(dataPredBMA) <- c("y0", "PredictiveBMA")
ggplot(data = dataPredBMA) +
  geom_point(aes(y0, PredictiveBMA, color = "red")) +
  xlab(TeX("$y_0$")) + ylab("Density") +
  ggtitle("Predictive density: BMA") +
  guides(color = guide_legend(title="BMA")) +
  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

```r
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$Post)
21 }
22 DataUp <- data.frame (cbind (rep(lambda , 15), c(PostUp), rep
       (1:15 , each = 1000)))   #Data frame
23 colnames (DataUp) <- c("Lambda", "Density", "Factor")
24 DataUp$Factor <- factor (DataUp$Factor , levels=c("1","2","3",
       "4","5","6","7","8","9","10","11","12","13","14","15"),
       labels=c("Iter_1","Iter_2","Iter_3","Iter_4","Iter_5","
       Iter_6","Iter_7","Iter_8","Iter_9","Iter_10","Iter_11","
       Iter_12","Iter_13","Iter_14","Iter_15"))
25 ggplot (data = DataUp , aes_string(x = "Lambda",
26   y = "Density", group = "Factor")) +
27   geom_line (aes(color = Factor)) +
28   xlab(TeX("$p$")) + ylab("Density") +
29   ggtitle ("Bayesian updating:
30   Beta -Binomial model with vague prior") +
31   guides (color=guide_legend(title="Update"))
```
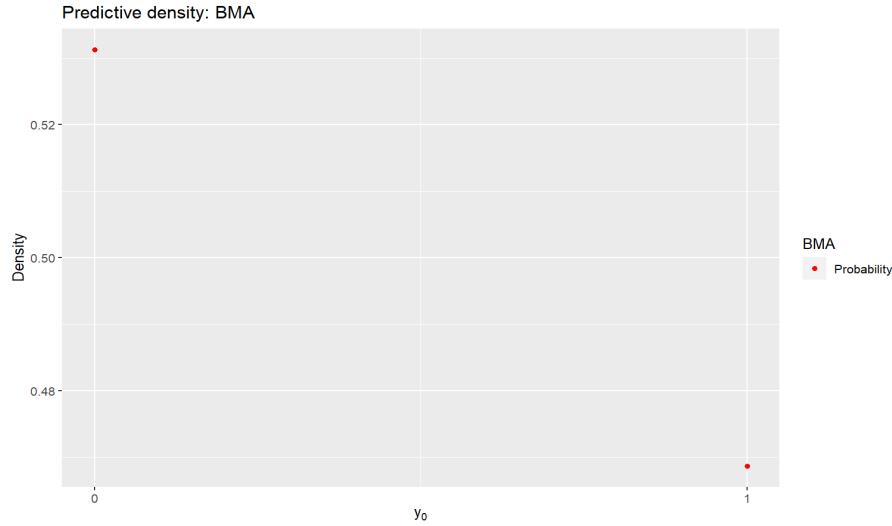
5. Show that given the loss function, $L(\theta, a) = |\theta - a|$, then the optimal decision rule minimizing the risk function, $a^*(\mathbf{y})$, is the median.
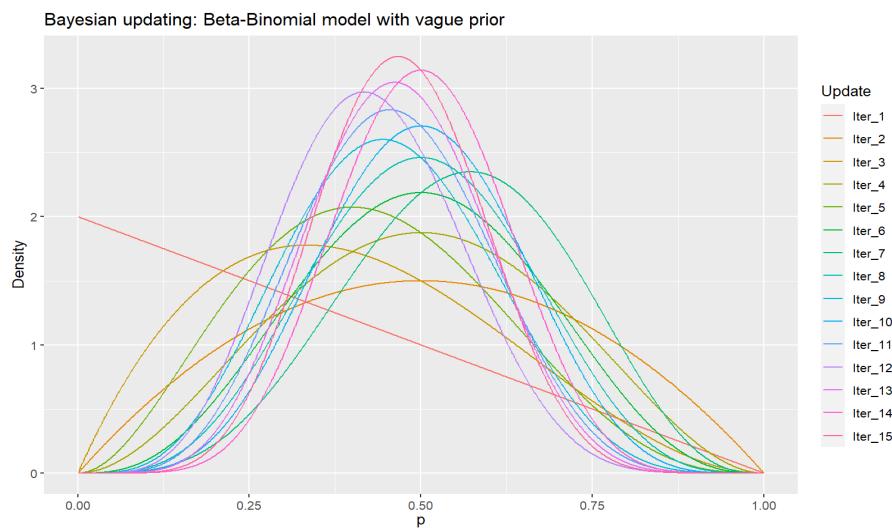
Answer

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

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

FIGURE 1.4
Predictive probabilities: Bernoulli-Beta Bayesian model average.

FIGURE 1.5
Predictive probabilities: Bernoulli-Beta Bayesian model updating.

then,

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

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** [16, 25] 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

$$p(y|H_1) = \int_0^1 \binom{N}{y} \theta^y (1-\theta)^{N-y} d\theta$$

$$= \binom{N}{y} B(y+1, N-k+1)$$

$$= \frac{\Gamma(N+1)}{\Gamma(y+1)\Gamma(n-y+1)} \frac{\Gamma(y+1)\Gamma(N-y+1)}{\Gamma(N+2)}$$

$$= \frac{N!}{(N+1)!}$$

$$= \frac{1}{N+1}$$

$$\approx 1.016 \times 10^{-5}.$$

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,

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

$$= 0.0235,$$

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]

---

[1]Observe 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 ([19] 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 $y_i \overset{iid}{\sim} N(\mu, \sigma^2)$.

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

Show that

$$p(\mathbf{y}|\mathcal{M}_1) = \frac{\pi^{-N/2}}{2}\Gamma(N/2)\left(\frac{1}{\alpha_n\hat{\sigma}^2}\right)^{N/2}\left(\frac{N}{\alpha_n\hat{\sigma}^2}\right)^{-1/2}\frac{\Gamma(1/2)\Gamma(\alpha_n/2)}{\Gamma((\alpha_N+1)/2)} \text{ and } p(\mathbf{y}|\mathcal{M}_0) =$$
$$(2\pi)^{-N/2}\left[\frac{2}{\Gamma(N/2)}\left(\frac{N}{2}\frac{\sum_{i=1}^{N}(y_i-\mu_0)^2}{N}\right)^{N/2}\right]^{-1}. \text{ Then,}$$

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

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

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

$$p(\mathbf{y}|\mathcal{M}_1) = \int_{-\infty}^{\infty}\int_{0}^{\infty}(2\pi)^{-N/2}\sigma^{-N}\exp\left\{-\frac{1}{2\sigma^2}\sum_{i=1}^{N}(y_i-\mu)^2\right\}\frac{1}{\sigma}d\sigma d\mu$$

$$= (2\pi)^{-N/2}\int_{-\infty}^{\infty}\int_{0}^{\infty}\sigma^{-(N+1)}\exp\left\{-\frac{N}{2\sigma^2}\frac{\sum_{i=1}^{N}(y_i-\mu)^2}{N}\right\}d\sigma d\mu$$

$$= (2\pi)^{-N/2}\frac{\Gamma(N/2)}{2}2^{N/2}\int_{-\infty}^{\infty}\left[\sum_{i=1}^{N}(y_i-\mu)^2\right]^{-N/2}d\mu$$

$$= (2\pi)^{-N/2}\frac{\Gamma(N/2)}{2}2^{N/2}\int_{-\infty}^{\infty}\left[\sum_{i=1}^{N}[(y_i-\bar{y})-(\mu-\bar{y})]^2\right]^{-N/2}d\mu$$

$$= (2\pi)^{-N/2}\frac{\Gamma(N/2)}{2}2^{N/2}\int_{-\infty}^{\infty}\left[\alpha_n\hat{\sigma}^2+N(\mu-\bar{y})^2\right]^{-N/2}d\mu$$

$$= (2\pi)^{-N/2}\frac{\Gamma(N/2)}{2}2^{N/2}\left(\frac{\alpha_n\hat{\sigma}^2}{\alpha_n\hat{\sigma}^2}\right)^{-N/2}\int_{-\infty}^{\infty}\left[\alpha_n\hat{\sigma}^2+N(\mu-\bar{y})^2\right]^{-N/2}d\mu$$

$$= (2\pi)^{-N/2}\frac{\Gamma(N/2)}{2}2^{N/2}(\alpha_n\hat{\sigma}^2)^{-N/2}\int_{-\infty}^{\infty}\left[1+\frac{N(\mu-\bar{y})^2}{\alpha_n\hat{\sigma}^2}\right]^{-N/2}d\mu$$

$$= \frac{\pi^{-N/2}}{2}\Gamma(N/2)\left(\frac{1}{\alpha_n\hat{\sigma}^2}\right)^{N/2}\left(\frac{N}{\alpha_n\hat{\sigma}^2}\right)^{-1/2}\frac{\Gamma(1/2)\Gamma(\alpha_n/2)}{\Gamma((\alpha_N+1)/2)}.$$

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 [48].

$$p(\mathbf{y}|\mathcal{M}_0) = \int_0^\infty (2\pi)^{-N/2} \sigma^{-N} \exp\left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^N (y_i - \mu_0)^2 \right\} \frac{1}{\sigma} d\sigma$$

$$= (2\pi)^{-N/2} \int_0^\infty \sigma^{-(N+1)} \exp\left\{ -\frac{N}{2\sigma^2} \frac{\sum_{i=1}^N (y_i - \mu_0)^2}{N} \right\} d\sigma$$

$$= (2\pi)^{-N/2} \left[\frac{2}{\Gamma(N/2)} \left(\frac{N}{2} \frac{\sum_{i=1}^N (y_i - \mu_0)^2}{N} \right)^{N/2} \right]^{-1}.$$

The third line takes into account that the integral in the second line is the kernel of an inverted-gamma distribution [48].

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

In addition,

$$PO_{01} = \frac{\Gamma((\alpha_n + 1)/2)}{\Gamma(1/2)\Gamma(\alpha_n/2)} (\alpha_n \hat\sigma^2/N)^{-1/2} \left[1 + \frac{(\mu_0 - \bar{y})^2}{\alpha_n \hat\sigma^2/N} \right]^{-\left(\frac{\alpha_n+1}{2}\right)}$$

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

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

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

```r
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 PO01 <- (gamma(N/2)*((N-1)*serror^2)^(-0.5)*(1+test^2/alpha)
      ^(-N/2))/(gamma(1/2)*gamma((N-1)/2))
13 PO01/(1+PO01)
14 0.0001705 0.0050345 0.0725330 0.3210223 0.4702050
15 # 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 $\mathbf{y} = [y_1, y_2, \ldots, y_N]^\top$ 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

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

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

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

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

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

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

Finally, the predictive distribution is

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

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 $\mathbf{y} = [y_1, y_2, \ldots, y_N]^\top$ 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

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

Finally, the predictive distribution is

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

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

$$p(\mathbf{y}|\boldsymbol{\mu},\boldsymbol{\Sigma}) = (2\pi)^{-N/2}|\boldsymbol{\Sigma}|^{-1/2}\exp\left\{-\frac{1}{2}(\mathbf{y}-\boldsymbol{\mu})^\top\boldsymbol{\Sigma}^{-1}(\mathbf{y}-\boldsymbol{\mu})\right\}$$

$$= (2\pi)^{-N/2}\exp\left\{-\frac{1}{2}\left(\mathbf{y}^\top\boldsymbol{\Sigma}^{-1}\mathbf{y}-2\mathbf{y}^\top\boldsymbol{\Sigma}^{-1}\boldsymbol{\mu}+\boldsymbol{\mu}^\top\boldsymbol{\Sigma}^{-1}\boldsymbol{\mu}+\log(|\boldsymbol{\Sigma}|)\right)\right\}$$

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

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

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

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

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

Answer

$$p(\mathbf{Y}) = \int_{\mathcal{R}^p}\int_{\mathcal{S}}(2\pi)^{-pN/2}|\boldsymbol{\Sigma}|^{-N/2}\exp\left\{-\frac{1}{2}tr[(\mathbf{S}+N(\boldsymbol{\mu}-\hat{\boldsymbol{\mu}})(\boldsymbol{\mu}-\hat{\boldsymbol{\mu}})^\top)\boldsymbol{\Sigma}^{-1}]\right\}$$

$$\times (2\pi)^{-p/2}\beta_0^{p/2}|\boldsymbol{\Sigma}|^{-1/2}\exp\left\{-\frac{\beta_0}{2}tr[(\boldsymbol{\mu}-\boldsymbol{\mu}_0)(\boldsymbol{\mu}-\boldsymbol{\mu}_0)^\top\boldsymbol{\Sigma}^{-1}]\right\}$$

$$\times |\boldsymbol{\Sigma}|^{-(\alpha_0+p+1)/2}\frac{2^{-\alpha_0 p/2}|\boldsymbol{\Psi}_0|^{\alpha_0/2}}{\Gamma_p(\alpha_0/2)}\exp\left\{-\frac{1}{2}tr(\boldsymbol{\Psi}_0\boldsymbol{\Sigma}^{-1})\right\}d\boldsymbol{\Sigma}d\boldsymbol{\mu}$$

$$= \frac{(2\pi)^{-\frac{1}{2}(pN+p)}|\boldsymbol{\Psi}_0|^{\alpha_0/2}\beta_0^{p/2}2^{-\alpha_0 p/2}}{\Gamma_p(\alpha_0/2)}\int_{\mathcal{R}^p}\int_{\mathcal{S}}|\boldsymbol{\Sigma}|^{-\frac{1}{2}(N+1+\alpha_0+p+1)}$$

$$\times \exp\left\{-\frac{1}{2}tr[(\mathbf{S}+N(\boldsymbol{\mu}-\hat{\boldsymbol{\mu}})(\boldsymbol{\mu}-\hat{\boldsymbol{\mu}})^\top+\beta_0(\boldsymbol{\mu}-\boldsymbol{\mu}_0)(\boldsymbol{\mu}-\boldsymbol{\mu}_0)^\top+\boldsymbol{\Psi}_0)\boldsymbol{\Sigma}^{-1}]\right\}d\boldsymbol{\Sigma}d\boldsymbol{\mu}.$$

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

$$p(\mathbf{Y}) = \frac{\Gamma_p\left(\frac{N+1+\alpha_0}{2}\right)|\boldsymbol{\Psi}_0|^{\alpha_0/2}\beta_0^{p/2}}{\Gamma_p(\alpha_0/2)\pi^{p(N+1)/2}}$$

$$\times \int_{\mathcal{R}^p} |\mathbf{S} + \boldsymbol{\Psi}_0 + (N+\beta_0)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top$$

$$+ N\beta_0/(N+\beta_0)(\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}_0)(\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}_0)^\top|^{-(\alpha_n+1)/2}d\boldsymbol{\mu}$$

$$= \frac{\Gamma_p\left(\frac{N+1+\alpha_0}{2}\right)|\boldsymbol{\Psi}_0|^{\alpha_0/2}\beta_0^{p/2}}{\Gamma_p(\alpha_0/2)\pi^{p(N+1)/2}}$$

$$\times \int_{\mathcal{R}^p} (|\boldsymbol{\Psi}_n||1 + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n)\boldsymbol{\Psi}_n^{-1}(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top|)^{-\frac{1}{2}(\alpha_n+1)}d\boldsymbol{\mu}$$

$$= \frac{\Gamma_p\left(\frac{\alpha_n+1}{2}\right)|\boldsymbol{\Psi}_0|^{\alpha_0/2}\beta_0^{p/2}}{\Gamma_p(\alpha_0/2)\pi^{p(N+1)/2}}|\boldsymbol{\Psi}_n|^{-\frac{1}{2}(\alpha_n+1)}$$

$$\times \int_{\mathcal{R}^p} [1 + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \boldsymbol{\Psi}_n^{-1}(\boldsymbol{\mu} - \boldsymbol{\mu}_n)]^{-\frac{1}{2}(\alpha_n+1)}d\boldsymbol{\mu}.$$

The last equality uses the definition of $\boldsymbol{\Psi}_n$, β_n and α_n, and the Sylvester's determinant theorem. Observe that we have the kernel of a multivariate t distribution. Then,

$$p(\mathbf{Y}) = \frac{\Gamma_p\left(\frac{\alpha_n+1}{2}\right)|\boldsymbol{\Psi}_0|^{\alpha_0/2}\beta_0^{p/2}}{\Gamma_p(\alpha_0/2)\pi^{p(N+1)/2}}|\boldsymbol{\Psi}_n|^{-\frac{1}{2}(\alpha_n+1)}$$

$$\times \int_{\mathcal{R}^p} \left[1 + \frac{1}{\alpha_n+1-p}(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \left(\frac{\boldsymbol{\Psi}_n}{\beta_n(\alpha_n+1-p)}\right)^{-1}(\boldsymbol{\mu} - \boldsymbol{\mu}_n)\right]^{-\frac{1}{2}(\alpha_n+1-p+p)} d\boldsymbol{\mu}$$

$$= \frac{\Gamma_p\left(\frac{\alpha_n+1}{2}\right)\Gamma_p\left(\frac{\alpha_n+1-p}{2}\right)|\boldsymbol{\Psi}_0|^{\alpha_0/2}\beta_0^{p/2}(\alpha_n+1-p)^{p/2}\pi^{p/2}|\boldsymbol{\Psi}_n|^{-\frac{1}{2}(\alpha_n+1)}}{\Gamma_p(\alpha_0/2)\pi^{p(N+1)/2}\Gamma_p\left(\frac{\alpha_n+1-p+p}{2}\right)\left|\frac{\boldsymbol{\Psi}_n}{\beta_n(\alpha_n+1-p)}\right|^{-1/2}}$$

$$= \frac{\Gamma_p\left(\frac{v_n}{2}\right)}{\Gamma_p\left(\frac{\alpha_0}{2}\right)}\frac{|\boldsymbol{\Psi}_0|^{\alpha_0/2}}{|\boldsymbol{\Psi}_n|^{\alpha_n/2}}\left(\frac{\beta_0}{\beta_n}\right)^{p/2}(\pi)^{-Np/2},$$

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

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

Answer

$$p(\mathbf{Y}_0|\mathbf{Y}) \propto \int_{\mathcal{R}^p} \int_{\mathcal{S}} |\boldsymbol{\Sigma}|^{-1/2} \exp\left\{-\frac{1}{2}tr[(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top \boldsymbol{\Sigma}^{-1}]\right\}$$

$$\times |\boldsymbol{\Sigma}|^{-1/2} \exp\left\{-\frac{\beta_n}{2}tr[(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top \boldsymbol{\Sigma}^{-1}]\right\}$$

$$\times |\boldsymbol{\Sigma}|^{-(\alpha_n+p+1)/2} \exp\left\{-\frac{1}{2}tr(\boldsymbol{\Psi}_n \boldsymbol{\Sigma}^{-1})\right\} d\boldsymbol{\Sigma} d\boldsymbol{\mu}$$

$$\propto \int_{\mathcal{R}^p} |(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top + \boldsymbol{\Psi}_n|^{-(\alpha_n+2)/2} d\boldsymbol{\mu}.$$

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

Taking into account that

$$(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top = (1 + \beta_n)\left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n\boldsymbol{\mu}_n)}{1 + \beta_n}\right)\left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n\boldsymbol{\mu}_n)}{1 + \beta_n}\right)^\top$$

$$+ \frac{\beta_n}{1 + \beta_n}(\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top.$$

Then,

$$p(\mathbf{Y}_0|\mathbf{Y}) \propto \int_{\mathcal{R}^p} |(\mathbf{y}_0 - \boldsymbol{\mu})(\mathbf{y}_0 - \boldsymbol{\mu})^\top + \beta_n(\boldsymbol{\mu} - \boldsymbol{\mu}_n)(\boldsymbol{\mu} - \boldsymbol{\mu}_n)^\top + \boldsymbol{\Psi}_n|^{-(\alpha_n+2)/2} d\boldsymbol{\mu}$$

$$= \int_{\mathcal{R}^p} \left|(1 + \beta_n)\left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n\boldsymbol{\mu}_n)}{1 + \beta_n}\right)\left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n\boldsymbol{\mu}_n)}{1 + \beta_n}\right)^\top\right.$$

$$\left. + \frac{\beta_n}{1 + \beta_n}(\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top + \boldsymbol{\Psi}_n\right|^{-(\alpha_n+2)/2} d\boldsymbol{\mu}$$

$$= \int_{\mathcal{R}^p} \left|\underbrace{\boldsymbol{\Psi}_n + \frac{\beta_n}{1 + \beta_n}(\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top}_{\boldsymbol{\Lambda}_n}\right|$$

$$\left|1 + (1 + \beta_n)\left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n\boldsymbol{\mu}_n)}{1 + \beta_n}\right)^\top \frac{1}{\alpha_n + 2 - p}\left(\frac{\boldsymbol{\Lambda}_n}{\alpha_n + 2 - p}\right)^{-1}\left(\boldsymbol{\mu} - \frac{(\mathbf{y}_0 + \beta_n\boldsymbol{\mu}_n)}{1 + \beta_n}\right)\right|^{-(\alpha_n+2-p+p)/2} d\boldsymbol{\mu}$$

$$\propto \left|\boldsymbol{\Psi}_n + \frac{\beta_n}{1 + \beta_n}(\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top\right|^{-(\alpha_n+2)/2}$$

$$\times \left|\boldsymbol{\Psi}_n + \frac{\beta_n}{1 + \beta_n}(\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top\right|^{1/2}$$

$$= \left|\boldsymbol{\Psi}_n + \frac{\beta_n}{1 + \beta_n}(\mathbf{y}_0 - \boldsymbol{\mu}_n)(\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top\right|^{-(\alpha_n+1)/2}$$

$$\propto \left[1 + (\mathbf{y}_0 - \boldsymbol{\mu}_n)^\top \frac{1}{\alpha_n + 1 - p}\left(\frac{\boldsymbol{\Psi}_n(1 + \beta_n)}{(\alpha_n + 1 - p)\beta_n}\right)^{-1}(\mathbf{y}_0 - \boldsymbol{\mu}_n)\right]^{-(\alpha_n+1-p+p)}.$$

The second equality uses the Sylvester's determinant theorem, and 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 $\mathbf{Y}_0|\mathbf{Y} \sim T_{N_0,M}(\alpha_n - M + 1, \mathbf{X}_0\mathbf{B}_n, \mathbf{I}_{N_0} + \mathbf{X}_0\mathbf{V}_n\mathbf{X}_0^\top, \boldsymbol{\Psi}_n)$.

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

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,

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

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

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

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

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

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,

$$\pi(\mathbf{Y}_0|\mathbf{Y}) \propto \left|\mathbf{\Psi}_n + (\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}_n)^\top\mathbf{C}(\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}_n)\right|^{-(N_0+\alpha_n)/2}$$

$$\propto \left|\mathbf{I}_{N_0} + \mathbf{C}(\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}_n)\mathbf{\Psi}^{-1}(\mathbf{Y}_0 - \mathbf{X}_0\mathbf{B}_n)^\top\right|^{-(\alpha_n+1-M+N_0+M-1)/2}.$$

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 $\mathbf{\Psi}_n$ 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 $\mathbf{\Psi}_n = \mathbf{\Psi}_0 + \mathbf{S} + (\hat{\mathbf{B}} - \mathbf{B}_0)^\top\mathbf{V}_n(\hat{\mathbf{B}} - \mathbf{B}_0)$ in the linear multivariate regression model.

Answer

Taking into account that

$$\delta^* = \delta_0 + \mathbf{y}^\top\mathbf{y} + \boldsymbol{\beta}_0^\top\mathbf{B}_0^{-1}\boldsymbol{\beta}_0 - \boldsymbol{\beta}_n^\top\mathbf{B}_n^{-1}\boldsymbol{\beta}_n$$

$$= \delta_0 + \mathbf{y}^\top\mathbf{y} + \boldsymbol{\beta}_0^\top\mathbf{B}_0^{-1}\boldsymbol{\beta}_0 - (\mathbf{B}_0^{-1}\boldsymbol{\beta}_0 + \mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}})^\top\mathbf{B}_n(\mathbf{B}_0^{-1}\boldsymbol{\beta}_0 + \mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}})$$

$$= \delta_0 + \mathbf{y}^\top\mathbf{y} - \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\mathbf{B}_n\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}} - 2\hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\mathbf{B}_n\mathbf{B}_0^{-1}\boldsymbol{\beta}_0 + \boldsymbol{\beta}_0^\top(\mathbf{B}_0^{-1} - \mathbf{B}_0^{-1}\mathbf{B}_n\mathbf{B}_0^{-1})\boldsymbol{\beta}_0$$

$$- \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}}$$

$$= \delta_0 + \mathbf{y}^\top\mathbf{y} - \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\beta}}^\top(\mathbf{X}^\top\mathbf{X} - \mathbf{X}^\top\mathbf{X}\mathbf{B}_n\mathbf{X}^\top\mathbf{X})\hat{\boldsymbol{\beta}}$$

$$- 2\hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\mathbf{B}_n\mathbf{B}_0^{-1}\boldsymbol{\beta}_0 + \boldsymbol{\beta}_0^\top(\mathbf{B}_0^{-1} - \mathbf{B}_0^{-1}\mathbf{B}_n\mathbf{B}_0^{-1})\boldsymbol{\beta}_0.$$

Observe that

$$(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})^\top(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}) = \mathbf{y}^\top\mathbf{y} - 2\hat{\boldsymbol{\beta}}\mathbf{X}^\top\mathbf{y} + \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}}$$

$$= \mathbf{y}^\top\mathbf{y} - 2\hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top(\mathbf{X}\hat{\boldsymbol{\beta}} + \hat{\boldsymbol{\mu}}) + \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}}$$

$$= \mathbf{y}^\top\mathbf{y} - \hat{\boldsymbol{\beta}}^\top\mathbf{X}^\top\mathbf{X}\hat{\boldsymbol{\beta}},$$

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 [42]:

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

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,

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

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 $\beta_{**} = \mathbf{X}_0\beta_n$.

Answer

Taking into account that $(\mathbf{A} + \mathbf{B})^{-1} = \mathbf{A}^{-1} - \mathbf{A}^{-1}(\mathbf{A}^{-1} + \mathbf{B}^{-1})^{-1}\mathbf{A}^{-1}$ [42], 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 $\boldsymbol{\beta}_{**} = \mathbf{X}_0\boldsymbol{\beta}_n$,

$$\boldsymbol{\beta}_{**} = \mathbf{C}^{-1}\mathbf{X}_0\mathbf{M}^{-1}\mathbf{B}_n^{-1}\boldsymbol{\beta}_n$$

$$= (\mathbf{I}_{N_0} + \mathbf{X}_0\mathbf{B}_n\mathbf{X}_0^\top)\mathbf{X}_0\mathbf{M}^{-1}\mathbf{B}_n^{-1}\boldsymbol{\beta}_n$$

$$= (\mathbf{I}_{N_0} + \mathbf{X}_0\mathbf{B}_n\mathbf{X}_0^\top)\mathbf{X}_0(\mathbf{B}_n - \mathbf{B}_n((\mathbf{X}_0^\top\mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1}\mathbf{B}_n)\mathbf{B}_n^{-1}\boldsymbol{\beta}_n$$

$$= (\mathbf{I}_{N_0} + \mathbf{X}_0\mathbf{B}_n\mathbf{X}_0^\top)(\mathbf{X}_0\boldsymbol{\beta}_n - \mathbf{X}_0\mathbf{B}_n((\mathbf{X}_0^\top\mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1}\boldsymbol{\beta}_n)$$

$$= \mathbf{X}_0\boldsymbol{\beta}_n - \mathbf{X}_0\mathbf{B}_n((\mathbf{X}_0^\top\mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1}\boldsymbol{\beta}_n + \mathbf{X}_0\mathbf{B}_n\mathbf{X}_0^\top\mathbf{X}_0\boldsymbol{\beta}_n$$

$$- \mathbf{X}_0\mathbf{B}_n\mathbf{X}_0^\top\mathbf{X}_0\mathbf{B}_n((\mathbf{X}_0^\top\mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1}\boldsymbol{\beta}_n$$

$$= \mathbf{X}_0\boldsymbol{\beta}_n - \mathbf{X}_0\mathbf{B}_n[((\mathbf{X}_0^\top\mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1} - \mathbf{X}_0^\top\mathbf{X}_0 + \mathbf{X}_0^\top\mathbf{X}_0\mathbf{B}_n((\mathbf{X}_0^\top\mathbf{X}_0)^{-1} + \mathbf{B}_n)^{-1}]\boldsymbol{\beta}_n.$$

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

Answer

$$(\mathbf{Y} - \mathbf{X}\mathbf{B})^\top(\mathbf{Y} - \mathbf{X}\mathbf{B}) = (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}} + \mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B})^\top(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}} + \mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B})$$

$$= (\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}}) + 2(\mathbf{Y} - \mathbf{X}\hat{\mathbf{B}})^\top(\mathbf{X}\hat{\mathbf{B}} - \mathbf{X}\mathbf{B})$$

$$+ (\mathbf{X}\mathbf{B} - \mathbf{X}\hat{\mathbf{B}})^\top(\mathbf{X}\mathbf{B} - \mathbf{X}\hat{\mathbf{B}})$$

$$= \mathbf{S} + (\mathbf{B} - \hat{\mathbf{B}})^\top\mathbf{X}^\top\mathbf{X}(\mathbf{B} - \hat{\mathbf{B}}),$$

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
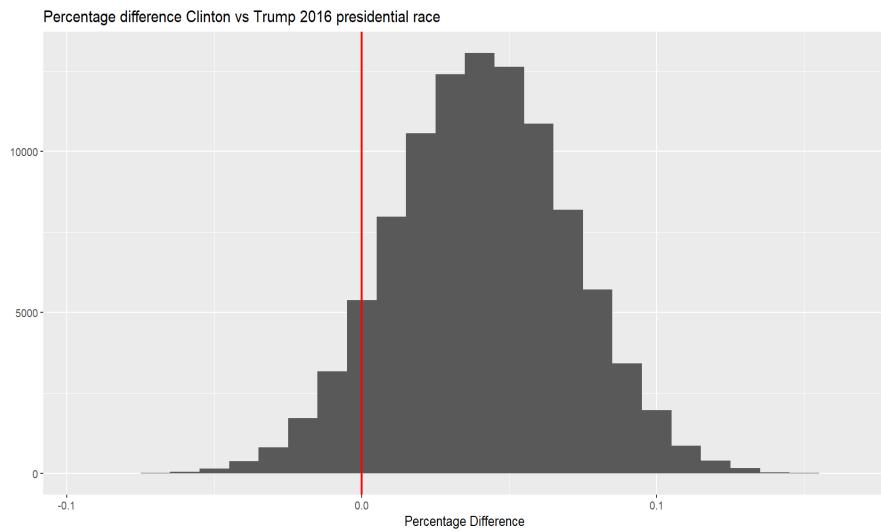
```r
set.seed(010101)
# Multinomial-Dirichlet example:
# Polling 2016 USA presidential race
y <- c(411, 373, 149)
# Clinton, Trump, Other
# Public Policy Polling September 27-28,
# 2016 five-way race
alpha0 <- rep(1, 3)
# Hyperparameters: non-informative distribution
alphan <- alpha0 + y
S <- 100000
# Sample draws of posterior
thetas <- MCMCpack::rdirichlet(S, alphan)
colnames(thetas) <- c("Clinton", "Trump", "Other")
head(thetas)
         Clinton      Trump      Other
[1,]  0.4211346  0.4188607  0.1600046
[2,]  0.4244207  0.4224523  0.1531270
[3,]  0.4349268  0.3843953  0.1806779
[4,]  0.4533499  0.4005530  0.1460972
[5,]  0.4381799  0.3968502  0.1649699
[6,]  0.4436852  0.3971321  0.1591827
dif <- thetas[,1] - thetas[,2]
# Difference of shares Hillary vs Trump
data <- data.frame(dif)
names(data) <- c("Difference")
library(ggplot2)
p <- ggplot(data) +
  geom_histogram(aes(x = Difference), binwidth = 0.01) +
  geom_vline(xintercept=0.0, lwd=1, colour="red") +
  ggtitle("Percentage difference Clinton vs Trump 2016
    presidential race") + xlab("Percentage Difference") +
    ylab("")
difmcmc <- coda::mcmc(dif)
# Declaring a MCMC object
summary(difmcmc)

Iterations = 1:1e+05
Thinning interval = 1
Number of chains = 1
Sample size per chain = 1e+05

1. Empirical mean and standard deviation for each
variable, plus standard error of the mean:

Mean              SD         Naive SE Time-series SE
4.062e-02      2.996e-02        9.474e-05       9.474e-05
2. Quantiles for each variable:

2.5%        25%        50%       75%     97.5%
-0.01817   0.02033   0.04058   0.06089   0.09923
CW <- mean(difmcmc>0)
CW
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 =
       sum(y0), prob = p)})
4  sum(sapply(1:S, function(s) {sum(Pred[,s] == y0) == 3}))/S
5  0.00825
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[
       l]+y0[l]) - lgamma(alphan[l])-lfactorial(y0[l])}))
10   Res <- lfactorial(n)+lgamma(sum(alphan))-lgamma(sum(alphan
       )+n) + Res1
11   return(exp(Res))
12 }
13 PredY0(y0)
14 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
```
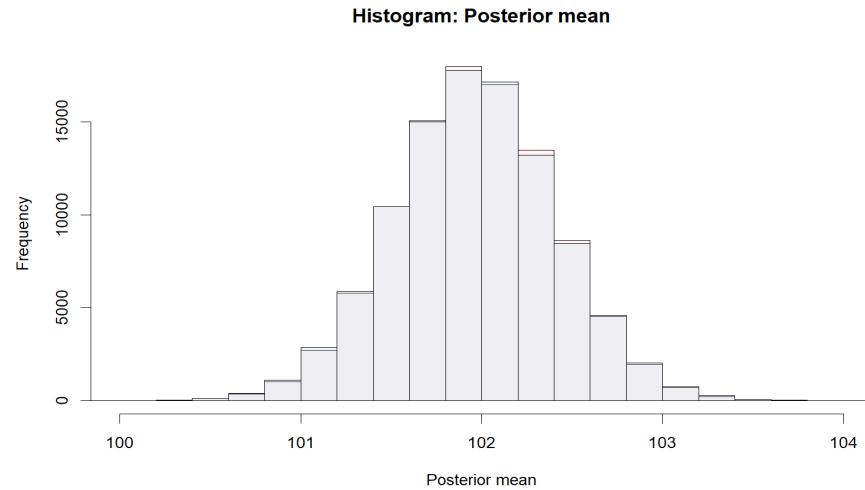
Figure 3.2 shows the posterior distribution of the mean.

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

Histogram: Posterior mean

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

```r
rm(list = ls())
set.seed(010101)
# Electricity demand
DataUt <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/Utilities.csv
    ", sep = ",", header = TRUE, quote = "")
DataUtEst <- DataUt %>%
filter(Electricity != 0)
attach(DataUtEst)
# Dependent variable: Monthly consumption (kWh) in log
Y <- log(Electricity)
N <- length(Y)
# Regressors quantity including intercept
X <- cbind(LnPriceElect, IndSocio1, IndSocio2, Altitude,
    Nrooms, HouseholdMem, Children, Lnincome, 1)
# Regressor without price
Xnew <- cbind(IndSocio1, IndSocio2, Altitude, Nrooms,
    HouseholdMem, Children, Lnincome, 1)
# Log marginal function (multiply by -1 due to minimization)
LogMarLikLM <- function(X, c0){
  k <- dim(X)[2]
  N <- dim(X)[1]
  # Hyperparameters
  B0 <- c0*diag(k)
  b0 <- rep(0, k)
  # Posterior parameters
  bhat <- solve(t(X)%*%X)%*%t(X)%*%Y
  # Force this matrix to be symmetric
  Bn <- as.matrix(Matrix::forceSymmetric(solve(solve(B0) + t
    (X)%*%X)))
  bn <- Bn%*%(solve(B0)%*%b0 + t(X)%*%X%*%bhat)
  dn <- as.numeric(d0 + t(Y)%*%Y+t(b0)%*%solve(B0)%*%b0-t(bn
    )%*%solve(Bn)%*%bn)
  an <- a0 + N
  # Log marginal likelihood
  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)
  return(-logpy)
}
# Hyperparameters
d0 <- 0.001
a0 <- 0.001
# Empirical Bayes: Obtain c0 maximizing the log marginal
    likelihood
c0 <- 1000
EB <- optim(c0, fn = LogMarLikLM, method = "Brent", lower =
    0.0001, upper = 10^6, X = X)
EBnew <- optim(c0, fn = LogMarLikLM, method = "Brent", lower
    = 0.0001, upper = 10^6, X = Xnew)
# Change of order to take into account the -1 in the
    LogMarLikLM function
BFEM <- exp(EBnew$value - EB$value)
BFEM
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, $\mathbf{B}_0 = [0]_{11 \times 3}$, $\mathbf{V}_0 = 1000\mathbf{I}_{11}$, $\mathbf{\Psi}_0 = 1000\mathbf{I}_3$ 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 $\mathbf{\Sigma}$.

(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(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

```r
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

```r
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
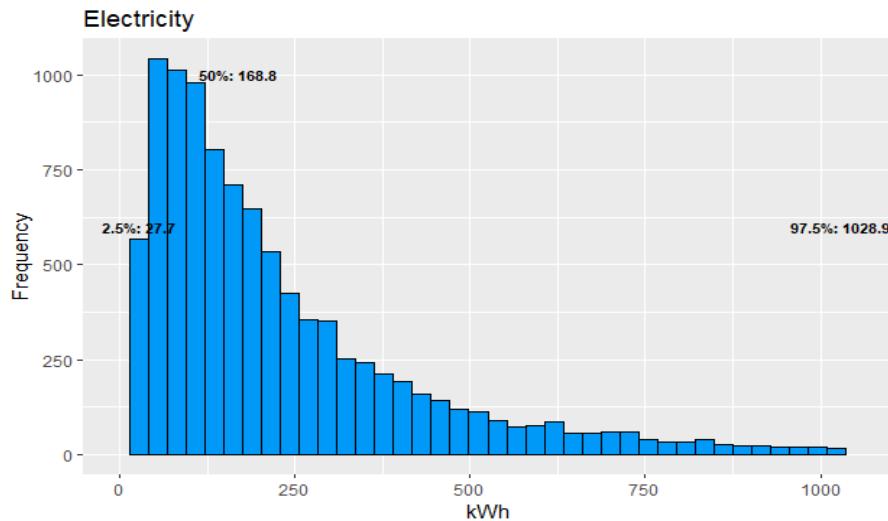
```r
# Predictive distribution
Xpred <- c(log(0.15), log(0.70), log(0.75), 1, 0, 0, 2, 3,
    1, log(500), 1)
Mean <- Xpred%*%Bn
Hn <- 1+t(Xpred)%*%Vn%*%Xpred
UtilDemand <- exp(replicate(s, MixMatrix::rmatrixt(n = 1,
    mean=Mean, U = Hn, V = Psin, df = an + 1 - M)))
ElePred <- UtilDemand[1,1,]
WatPred <- UtilDemand[1,2,]
GasPred <- UtilDemand[1,3,]
data <- data.frame(cbind(ElePred, WatPred, GasPred)) #Data
    frame
annotations1 <- data.frame(
x = round(quantile(data$ElePred, c(0.025, 0.5, 0.975)),1),
y = c(600, 1000, 600),
label = c("2.5%:", "50%:", "97.5%:")
)
annotations2 <- data.frame(
x = round(quantile(data$WatPred, c(0.025, 0.5, 0.975)),1),
y = c(600, 1000, 600),
label = c("2.5%:", "50%:", "97.5%:")
)
annotations3 <- data.frame(
x = round(quantile(data$GasPred, c(0.025, 0.5, 0.975)),1),
y = c(600, 1000, 600),
label = c("2.5%:", "50%:", "97.5%:")
)
require(ggplot2) # Cool figures
require(ggpubr) # Multiple figures in one page
require(latex2exp) # LaTeX equations in figures
fig1 <- ggplot(data = data, aes(ElePred)) + geom_histogram(
    bins = 40, color = "#000000", fill = "#0099F8") +  xlab(
    "kWh") + ylab("Frequency") + ggtitle("Electricity") +
    xlim(0, 1050) + geom_text(data = annotations1, aes(x = x
    , y = y, label = paste(label, x)), size = 3, fontface =
    "bold")
fig2 <- ggplot(data = data, aes(WatPred)) + geom_histogram(
    bins = 40, color = "#000000", fill = "#0099F8") +  xlab(
    TeX("$M^3$")) + ylab("Frequency") +  ggtitle("Water") +
    xlim(0, 100) + geom_text(data = annotations2, aes(x = x,
     y = y, label = paste(label, x)), size = 3, fontface = "
    bold")
fig3 <- ggplot(data = data, aes(GasPred)) + geom_histogram(
    bins = 40, color = "#000000", fill = "#0099F8") +  xlab(
    TeX("$M^3$")) + ylab("Frequency") +  ggtitle("Gas") +
    xlim(0, 80) + geom_text(data = annotations3, aes(x = x,
    y = y, label = paste(label, x)), size = 3, fontface = "
    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, M^3 12.3 and M^3 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.
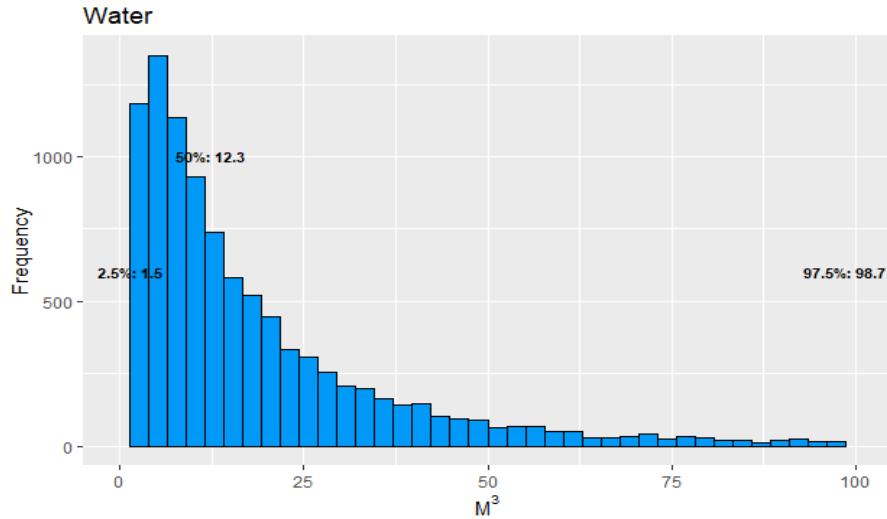
FIGURE 3.3
Histogram using the posterior predictive distribution of electricity demand

15. **Ph.D. students sleeping hours [1, Chap. 2]**
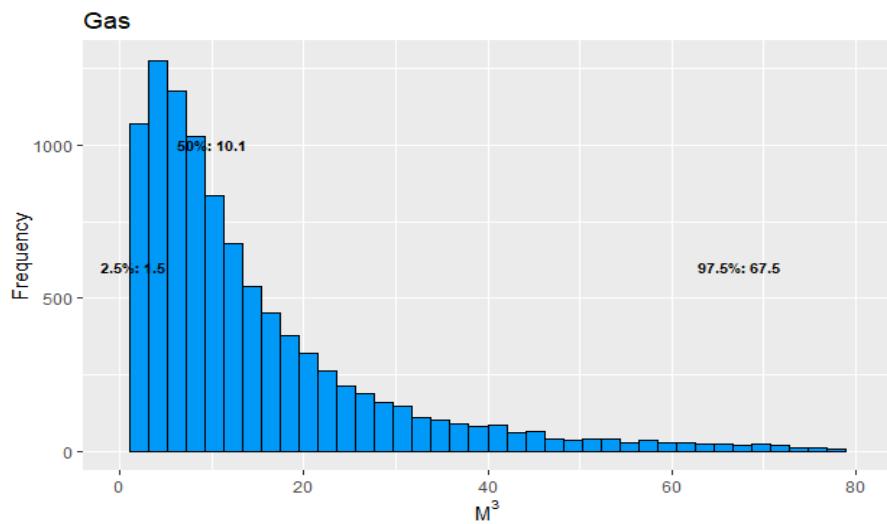
We are interested in learning about the proportion of Ph.D. students who sleep at least 6 hours per day. We have a sample of 52 students, where 15 report sleeping at least 6 hours, and the remaining 37 report not sleeping at least 6 hours. The prior distribution is a Beta distribution, with hyperparameters 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, $\theta|\boldsymbol{y} \sim B(\alpha_n, \beta_n)$, $\alpha_n = \alpha_0 + 15$ 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.
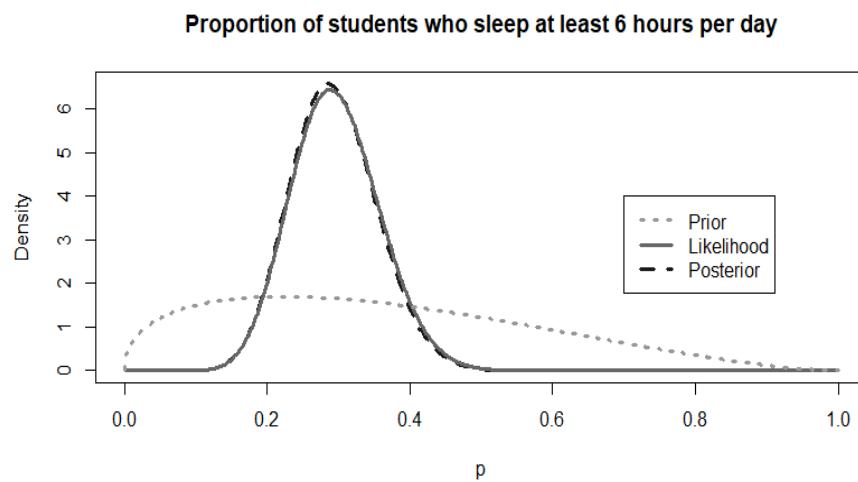
R code. Ph.D. students sleeping hours: Posterior distribution

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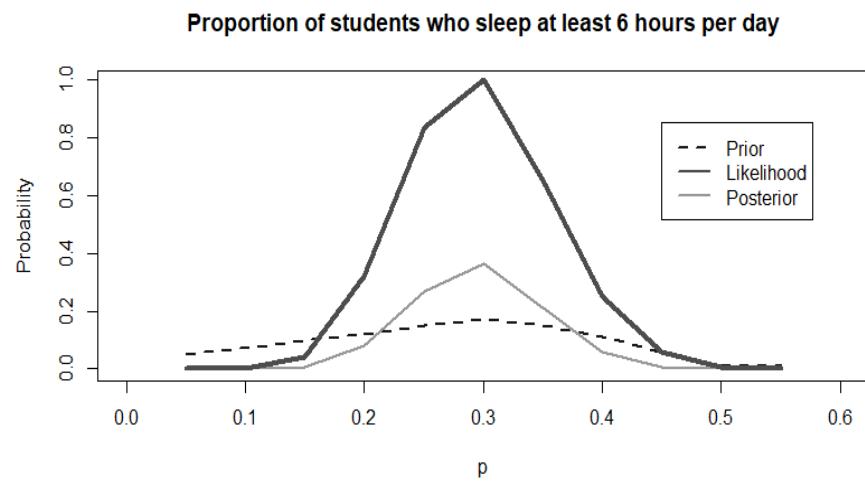
Figures 3.6 and 3.7 show the prior, likelihood, and posterior distributions of the proportion of Ph.D. students who sleep at least 6 hours per day based on the binomial-beta and binomial-discrete models. The mean under both models is 29%, and the 95% credible intervals are (18%,42%) and (20%,40%), respectively.

Proportion of students who sleep at least 6 hours per day


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

   $$\pi(\mu, \sigma^2 | \boldsymbol{y}) \propto (\sigma^2)^{-N/2} \exp\left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^{N} (y_i - \mu)^2 \right\}$$

   $$\times \exp\left\{ -\frac{1}{2\sigma_0^2} (\mu - \mu_0)^2 \right\} \times \left(\frac{1}{\sigma^2} \right)^{\alpha_0/2+1} \exp\left\{ -\frac{\delta_0}{2\sigma^2} \right\}.$$

   Thus, the conditional posterior distribution of μ is

   $$\pi(\mu, \sigma^2 | \boldsymbol{y}) \propto \exp\left\{ -\frac{1}{2} \left[\frac{1}{\sigma^2} \sum_{i=1}^{N} (y_i - \mu)^2 + \frac{1}{\sigma_0^2} (\mu - \mu_0)^2 \right] \right\}$$

   $$\propto \exp\left\{ -\frac{1}{2} \left[\mu^2 \left(\frac{1}{\sigma^2/N} + \frac{1}{\sigma_0^2} \right) - 2\mu \left(\frac{\bar{y}}{\sigma^2/N} + \frac{\mu_0}{\sigma_0^2} \right) \right] \right\}.$$

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,

$$\pi(\mu, \sigma^2 | \boldsymbol{y}) \propto \exp \left\{ -\frac{1}{2\sigma_n^2} \left[\mu^2 - 2\mu\mu_n + \mu_n^2 - \mu_n^2 \right] \right\}$$

$$\propto \exp \left\{ -\frac{1}{2\sigma_n^2} (\mu - \mu_n)^2 \right\}.$$

This is the kernel of a normal distribution, that is, $\mu | \sigma^2, \boldsymbol{y} \sim N(\mu_n, \sigma_n^2)$. The conditional posterior distribution of σ^2 is given by

$$\pi(\sigma^2 | \mu, \boldsymbol{y}) \propto (\sigma^2)^{-N/2} \exp \left\{ -\frac{1}{2\sigma^2} \sum_{i=1}^{N} (y_i - \mu)^2 \right\}$$

$$\times \left(\frac{1}{\sigma^2} \right)^{\alpha_0/2+1} \exp \left\{ -\frac{\delta_0}{2\sigma^2} \right\}$$

$$\propto (\sigma^2)^{-N/2-\alpha_0/2-1} \exp \left\{ -\frac{1}{2\sigma^2} \left[\sum_{i=1}^{N} (y_i - \mu)^2 + \delta_0 \right] \right\}.$$

Thus, $\sigma^2 | \mu, \boldsymbol{y} \sim IG(\alpha_n/2, \delta_n/2)$, 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
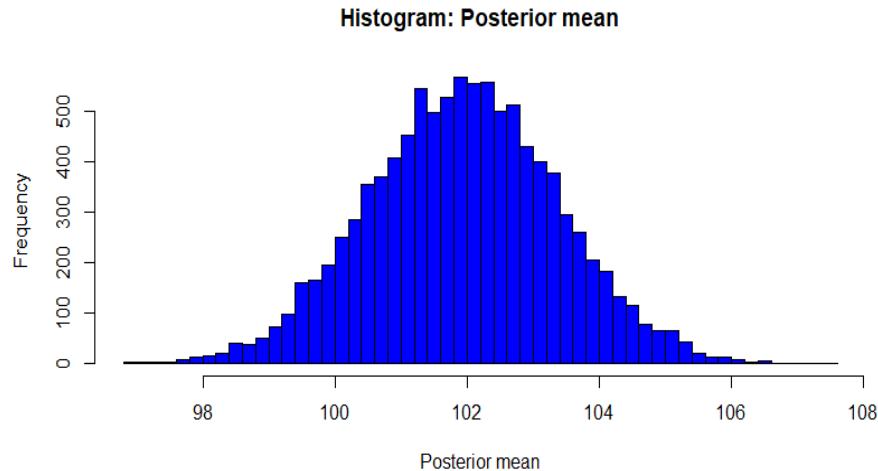
```r
1  rm(list = ls())
2  set.seed(010101)
3  N <- 50
4  # Sample size
5  muhat <- 102
6  # Sample mean
7  sig2hat <- 100
8  # Sample variance
9
10 # Hyperparameters
11 mu0 <- 100
12 sig20 <- 100
13 delta0 <- 0.001
14 alpha0 <- 0.001
15
16 MCMC <- 10000; burnin <- 1000; S <- MCMC + burnin
17 keep <- (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:

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

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

given by

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

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

$$= 1,$$

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); acept1 <- rep(0, S)
4  theta2 <- runif(S); acept2 <- 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(
       theta1[s-1])*dnorm(thetac1))
10   a2 <- (dcauchy(thetac2)*dt(theta2[s-1], df = df))/(dcauchy
       (theta2[s-1])*dt(thetac2, df = df))
11   U1 <- runif(1)
12   if(U1 <= a1){
13     theta1[s] <- thetac1; acept1[s] <- 1
14   }else{
15     theta1[s] <- theta1[s-1]; acept1[s] <- 0
16   }
17   if(U1 <= a2){
18     theta2[s] <- thetac2; acept2[s] <- 1
19   }else{
20     theta2[s] <- theta2[s-1]; acept2[s] <- 0
21   }
22 }
23 mean(acept1); mean(acept2)
24 plot(coda::mcmc(theta1)); plot(coda::mcmc(theta2))
25 h <- hist(theta1, breaks=50, col="blue", xlab="x", main="
       Cauchy draws from a Metropolis-Hastings algorithm:
       Normal standard proposal")
26 pfit <- seq(min(theta1),max(theta1),length=50)
27 yfit<-dcauchy(pfit)
28 yfit <- yfit*diff(h$mids[1:2])*length(theta1)
29 lines(pfit, yfit, col="red", lwd=2)
30 h <- hist(theta2, breaks=50, col="blue", xlab="x", main="
       Cauchy draws from a Metropolis-Hastings algorithm:
       Student's t proposal")
31 pfit <- seq(min(theta2),max(theta2),length=50)
32 yfit<-dcauchy(pfit)
33 yfit <- yfit*diff(h$mids[1:2])*length(theta2)
34 lines(pfit, yfit, col="red", lwd=2)
```
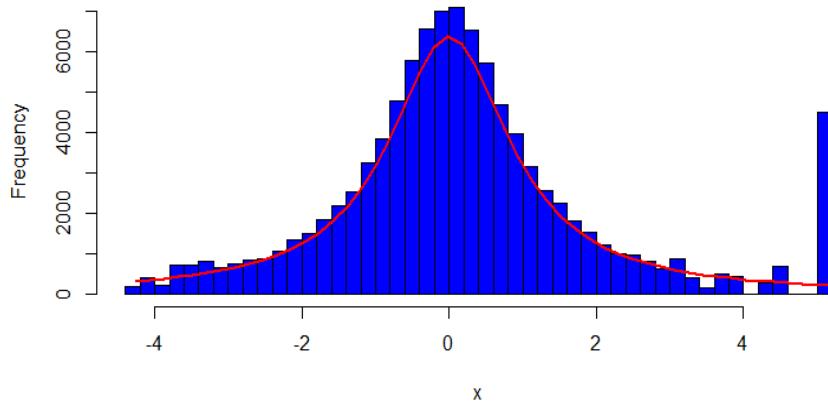
Figures 4.2 and 4.3 show the histograms of the posterior draws using the normal and Student's t distributions, along with the density of the Cauchy distribution. The spike in the posterior draws from the standard normal proposal is due to the algorithm being stuck for many iterations at a par-

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.
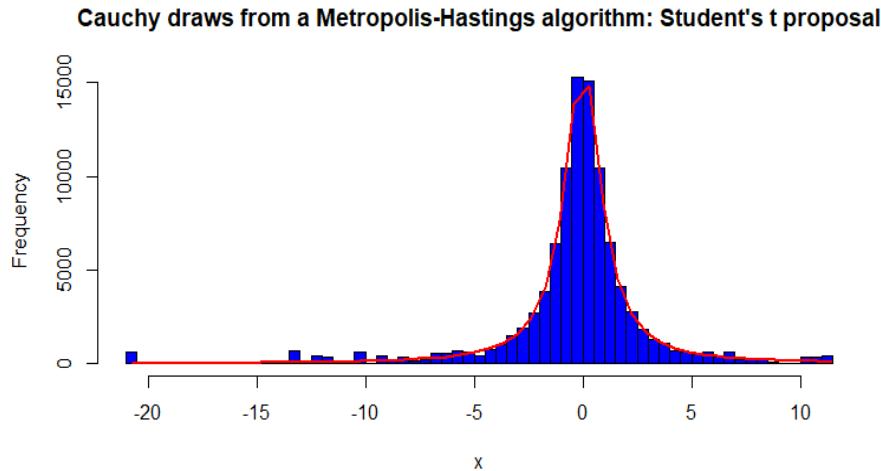
4. This exercise was proposed by Professor Hedibert Freitas Lopes, who cites [44] as a useful reference for an introduction to Hamiltonian Monte Carlo in **R** and the *hmclearn* package. The task is to obtain posterior draws using the Metropolis-Hastings and Hamiltonian Monte Carlo algorithms for the posterior distribution given by

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

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 $\boldsymbol{M} = \boldsymbol{I}_2$. These parameters yield an acceptance rate near 65%.

Cauchy draws from a Metropolis-Hastings algorithm: Student's t proposal

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

```r
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*
       theta1-8*theta2))
6    return(post)
7  }
8  # Metropolis-Hastings
9  MH <- function(theta, c2){
10   thetac <- MASS::mvrnorm(1, mu = theta, Sigma = c2*diag(2))
11   a <- PostDist(thetac)/PostDist(theta)
12   U <- runif(1)
13   if(U <= a){
14     theta <- thetac
15     accept <- 1
16   }else{
17     theta <- theta
18     accept <- 0
19   }
20   return(list(theta = theta, accept = accept))
21 }
22 # Posterior draws M-H
23 S <- 20000; burnin <- 1000; thin <- 20; tot <- S + burnin
24 K <- 2; c2 <- 1.5
25 thetaPostMH <- matrix(NA, tot, K)
26 AcceptMH <- rep(NA, tot)
27 thetaMH <- c(0, 0)
28 for(s in 1:tot){
29   ResMH <- MH(thetaMH, c2 = c2)
30   thetaMH <- ResMH$theta
31   thetaPostMH[s,] <- thetaMH
32   AcceptMH[s] <- ResMH$accept
33 }
34 keep <- seq((burnin), tot, thin)
35 mean(AcceptMH[keep])
36 thetaPostMHMCMC <- coda::mcmc(thetaPostMH[keep,])
37 plot(thetaPostMHMCMC)
38 coda::autocorr.plot(thetaPostMHMCMC)
39 # Contour plot
40 ngrid <- 400
41 theta1 <- seq(-1, 6, length = ngrid)
42 theta2 <- seq(-1, 6, length = ngrid)
43 f <- matrix(0, ngrid, ngrid)
44 for (i in 1:ngrid){
45   for (j in 1:ngrid){
46     f[i,j] = PostDist(c(theta1[i],theta2[j]))
47   }
48 }
49 plot(thetaPostMH[keep,], xlim=range(theta1), ylim=range(
       theta2), pch=16, col=grey(0.8), xlab=expression(theta
       [1]), ylab=expression(theta[2]))
50 contour(theta1,theta2,f, drawlabels=FALSE, add=TRUE, col = "
       blue", lwd = 1.2)
51 title("Random walk Metropolis-Hastings")
```
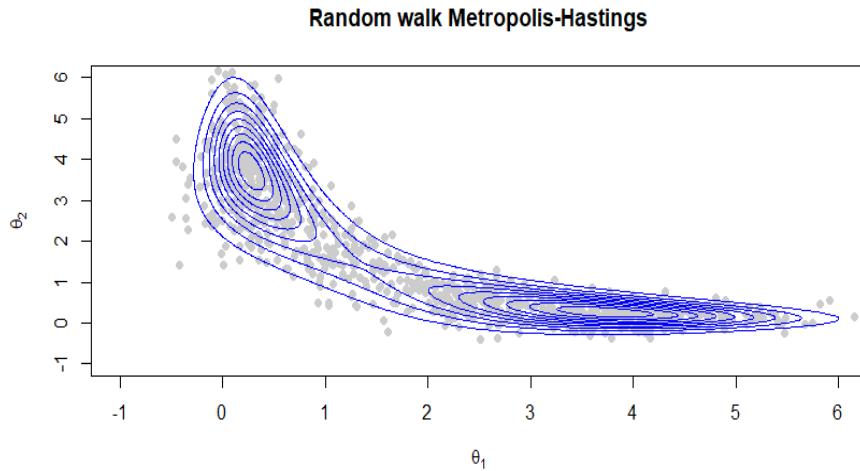
R code. Metropolis-Hastings and Hamiltonian Monte Carlo algorithms
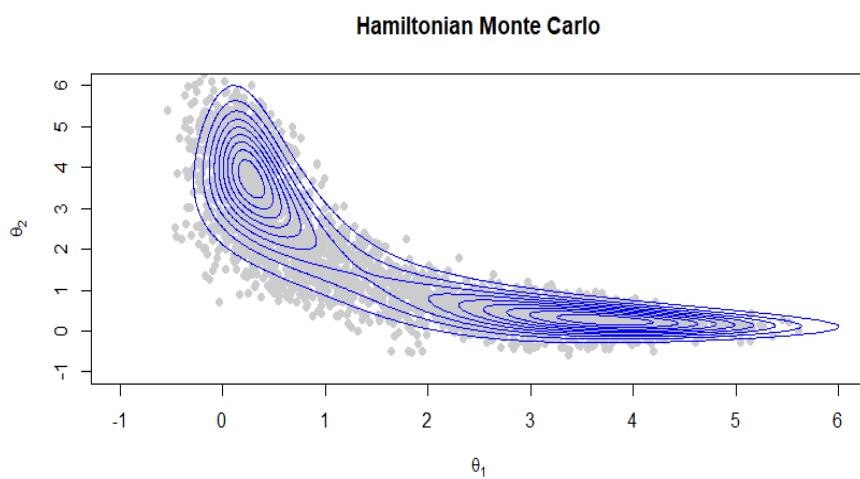
```r
1  HMC <- function(theta, epsilon, L, M){
2    Minv <- solve(M); thetat <- theta
3    K <- length(thetat)
4    mom <- t(mvtnorm::rmvnorm(1, rep(0, K), M))
5    logPost_Mom_t <- log(PostDist(thetat)) +  mvtnorm::dmvnorm
       (t(mom), rep(0, K), M, log = TRUE)
6    theta1 <- theta[1]; theta2 <- theta[2]
7    for(l in 1:L){
8      if(l == 1 | l == L){
9        mom <- mom + 0.5*epsilon*(-0.5*c(2*theta1*theta2^2+2*
       theta1-8, 2*theta2*theta1^2+2*theta2-8))
10       theta <- theta + epsilon*Minv%*%mom
11     }else{
12       mom <- mom + epsilon*(-0.5*c(2*theta1*theta2^2+2*
       theta1-8, 2*theta2*theta1^2+2*theta2-8))
13       theta <- theta + epsilon*Minv%*%mom
14     }
15   }
16   logPost_Mom_star <- log(PostDist(theta)) +  mvtnorm::
       dmvnorm(t(mom), rep(0, K), M, log = TRUE)
17   alpha <- min(1, exp(logPost_Mom_star-logPost_Mom_t))
18   u <- runif(1)
19   if(u <= alpha){
20     thetaNew <- c(theta)
21   }else{
22     thetaNew <- thetat
23   }
24   rest <- list(theta = thetaNew, Prob = alpha)
25   return(rest)
26 }
27 # Posterior draws HMC
28 S <- 5000; burnin <- 500; tot <- S + burnin
29 epsilon <- 0.0025;  L <- 100; M <- diag(2)
30 thetaPostHMC <- matrix(NA, tot, K)
31 ProbAcceptHMC  <- rep(NA, tot)
32 thetaHMC <- c(0, 0)
33 for(s in 1:tot){
34   ResHMC <- HMC(theta = thetaHMC, epsilon = epsilon, L = L,
       M = M)
35   thetaHMC <- ResHMC$theta
36   thetaPostHMC[s,] <- thetaHMC
37   ProbAcceptHMC[s] <- ResHMC$Prob
38 }
39 keep <- burnin:S
40 summary(ProbAcceptHMC[keep])
41 thetaPostHMCMCMC <- coda::mcmc(thetaPostHMC[keep,])
42 plot(thetaPostHMCMCMC); coda::autocorr.plot(thetaPostHMCMCMC
       )
43 plot(thetaPostHMC[keep,], xlim=range(theta1), ylim=range(
       theta2), pch=16, col=grey(0.8),
44 xlab=expression(theta[1]), ylab=expression(theta[2]))
45 contour(theta1,theta2,f, drawlabels=FALSE, add=TRUE, col = "
       blue", lwd = 1.2)
46 title("Hamiltonian Monte Carlo")
```

Random walk Metropolis-Hastings

FIGURE 4.4
Contour plot: Metropolis-Hastings posterior draws.

Hamiltonian Monte Carlo

FIGURE 4.5
Contour plot: Hamiltonian Monte Carlo posterior drwas.

5. **Ph.D. students sleeping hours continues**

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

of $\boldsymbol{\theta}|\boldsymbol{y} \sim B(16.55, 39.57)$ 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

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

where

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

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

<div style="border:1px solid #000; padding:1em;">

R code. Importance sampling: Bernoulli-Beta model

```r
rm(list = ls()); set.seed(010101); S <- 50000
# Importance sampling from standard normal proposal
an <- 16.55; bn <- 39.57 # Posterior parameters
theta <- runif(S) # Proposal
ws <- dbeta(theta, an, bn) # Weights
wstars <- ws/sum(ws) # Standardized weights
L <- 20000 # Size of posterior sample
thetaBeta <- sample(theta, L, replace = TRUE, prob = wstars)
    # Posterior draws
# Figure
h <- hist(thetaBeta, breaks=50, col="blue", xlab="x", main="
    Beta draws from importance sampling: Uniform (0,1)
    proposal")
pfit <- seq(min(thetaBeta),max(thetaBeta),length=50)
yfit<-dbeta(pfit, an, bn)
yfit <- yfit*diff(h$mids[1:2])*length(thetaBeta)
lines(pfit, yfit, col="red", lwd=2)
a0 <- 1.44; b0 <- 2.57 # Hyperparameters
s <- 15; n <- 52 # Data
LogMarLik <- lbeta(an, bn)-lbeta(a0, b0) # Marginal
    likelihood
LogMarLik
# Gelfand-Day method
LikPrior <- function(theta){
  Liki <- theta^s*(1-theta)^(n-s)
  Priori <- dbeta(theta, a0, b0)
  LikPriori <- 1 / Liki * Priori
  return(LikPriori)
}
LogMarLikGD <- log(1/mean(sapply(thetaBeta, LikPrior)))
LogMarLikGD
```

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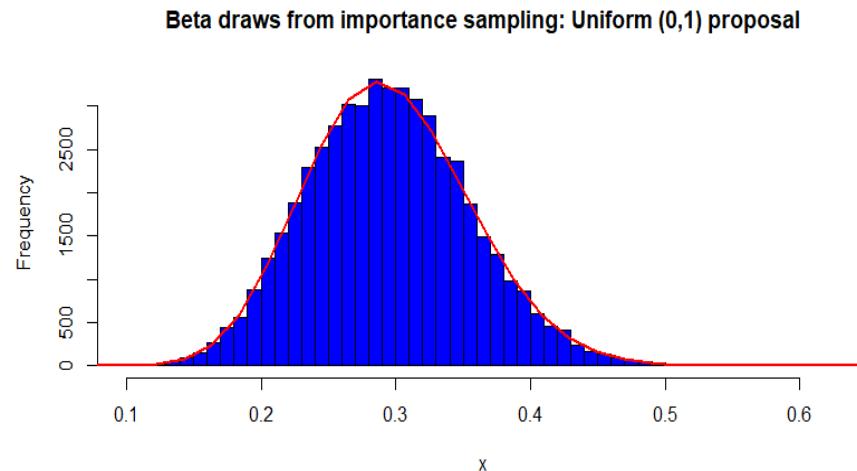
Figure 4.6 shows the histogram of the posterior draws obtained using the importance sampling algorithm with a uniform proposal. The algorithm performs well. Additionally, the analytic solution for the log marginal likelihood is -32.75, while the Gelfand-Dey method yields -32.76.

6. Example 4.1 in [13] is

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

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

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

Beta draws from importance sampling: Uniform (0,1) proposal

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 [13]. 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.

```r
rm(list = ls()); set.seed(010101)
S <- 50000 # Number of particles
sigma_w <- 10^0.5  # State noise
sigma_mu <- 1  # Observation noise
T <- 200 # Sample size
# Simulate true states and observations
theta_true <- numeric(T)
y_obs <- numeric(T)
theta_true[1] <- rnorm(1, mean = 0, sd = sigma_w)  # Initial
    state
y_obs[1] <- rnorm(1, mean = theta_true[1]^2/20, sd = sigma_
    mu)
for (t in 2:T) {
  meant <- 0.5*theta_true[t-1] + 25*(theta_true[t-1]/(1+
    theta_true[t-1]^2)) + 8*cos(1.2*t)
  theta_true[t] <-  rnorm(1, mean = meant, sd = sigma_w)
  y_obs[t] <- rnorm(1, mean = theta_true[t]^2/20, sd = sigma
    _mu)
}
plot(theta_true, type = "l"); plot(y_obs, type = "l")
# Sequential Importance Sampling (SIS)
particles <- matrix(0, nrow = S, ncol = T)
weights <- matrix(0, nrow = S, ncol = T)
weightsSt <- matrix(0, nrow = S, ncol = T)
# Initialization
particles[, 1] <- rnorm(S, mean = 0, sd = sigma_w)
weights[, 1] <- dnorm(y_obs[1], mean = particles[, 1]^2/20,
    sd = sigma_mu)
weightsSt[, 1] <- weights[, 1] / sum(weights[, 1])
# Sequential updating
for (t in 2:T) {
  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
  weights[, t] <- weightsSt[, t-1] * dnorm(y_obs[t], mean =
    particles[, t]^2/20, sd = sigma_mu)
  weightsSt[, t] <- weights[, t] / sum(weights[, t])
}
FilterDist <- colSums(particles * weightsSt)
SDFilterDist <- (colSums(particles^2 * weightsSt) -
    FilterDist^2)^0.5
library(dplyr); library(ggplot2); library(latex2exp)
ggplot2::theme_set(theme_bw())
df <- tibble(t = 1:T, mean = FilterDist, lower = FilterDist
    - 2*SDFilterDist, upper = FilterDist + 2*SDFilterDist,
    theta_true = theta_true)
plot_filtering_estimates <- function(df) {
  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")
  print(p)
}
plot_filtering_estimates(df)
```

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

```r
# Particle filtering
particles <- matrix(0, nrow = S, ncol = T)
particlesT <- matrix(0, nrow = S, ncol = T)
weights <- matrix(0, nrow = S, ncol = T)
weightsSt <- matrix(0, nrow = S, ncol = T)
weightsSTT <- matrix(1/S, nrow = S, ncol = T)
logalphas <- matrix(0, nrow = S, ncol = T)
# Initialization
particles[, 1] <- rnorm(S, mean = 0, sd = sigma_w)  # Sample
    initial particles
weights[, 1] <- dnorm(y_obs[1], mean = particles[, 1]^2/20,
    sd = sigma_mu)  # Importance weights
weightsSt[, 1] <- weights[, 1] / sum(weights[, 1])  #
    Normalize weights
ind <- sample(1:S, size = S, replace = TRUE, prob =
    weightsSt[, 1]) # Resample
particles[, 1] <- particles[ind, 1] # Resampled particles
particlesT[, 1] <- particles[, 1] # Resampled particles
# Sequential updating
pb <- txtProgressBar(min = 0, max = T, style = 3)
for (t in 2:T) {
  # Propagate particles
  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
  logalphas[, t] <- dnorm(y_obs[t], mean = particles[, t]^2/
    20, sd = sigma_mu, log = TRUE)
  weights[, t] <- exp(logalphas[, t])
  weightsSt[, t] <- weights[, t] / sum(weights[, t])
  if(t < T){
    ind <- sample(1:S, size = S, replace = TRUE, prob =
    weightsSt[, t])
    particles[, 1:t] <- particles[ind, 1:t]
  }else{
    ind <- sample(1:S, size = S, replace = TRUE, prob =
    weightsSt[, t])
    particlesT[, 1:t] <- particles[ind, 1:t]
  }
  setTxtProgressBar(pb, t)
}
close(pb)
FilterDist <- colSums(particles * weightsSt)
SDFilterDist <- (colSums(particles^2 * weightsSt) -
    FilterDist^2)^0.5
FilterDistT <- colSums(particlesT * weightsSTT)
SDFilterDistT <- (colSums(particlesT^2 * weightsSTT) -
    FilterDistT^2)^0.5
```

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

```r
library(dplyr); library(ggplot2); library(latex2exp)
ggplot2::theme_set(theme_bw())
df <- tibble(t = 1:T, mean = FilterDist, lower = FilterDist
    - 2*SDFilterDist, upper = FilterDist+ 2*SDFilterDist,
    meanT = FilterDistT, lowerT = FilterDistT - 2*
    SDFilterDistT,
upperT = FilterDistT + 2*SDFilterDistT, x_true = theta_true)
plot_filtering_estimates <- function(df) {
  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) +
  geom_line(aes(y = meanT), colour = "purple", linewidth =
    0.5) + ylab(TeX("$\\theta_{t}$")) + xlab("Time")
  print(p)
}
plot_filtering_estimates(df)
MargLik <- colMeans(weights)
plot(MargLik, type = "l", xlab = "Time", ylab = "Marginal
    likelihood", main = "Marginal likelihood")
```
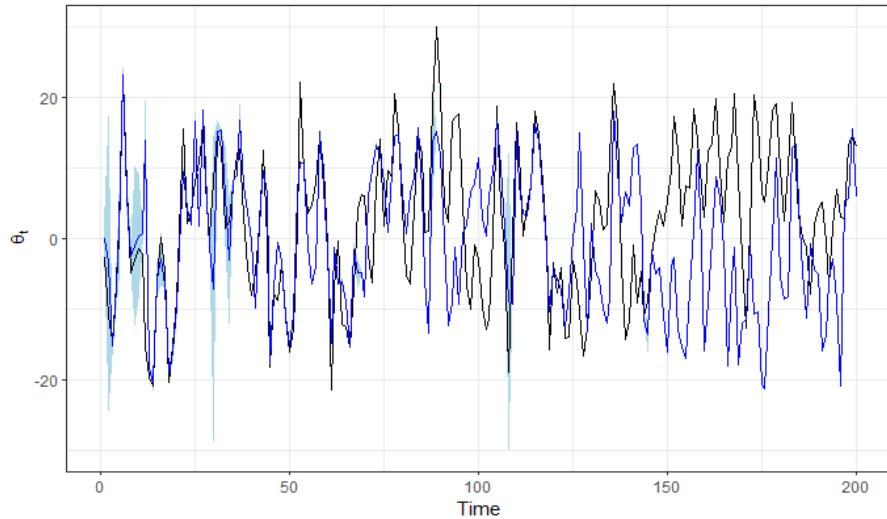
Figure 4.7 shows the true trajectory of the state vector (black line), the posterior mean (blue line), and the $\pm 2\hat{\sigma}_\theta$ posterior estimate (light blue shaded area) from the sequential importance sampling algorithm. We observe that there is no light blue shaded area after time period 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 [13]). There is the true state vector (black line), the means based on $\left\{ \boldsymbol{\theta}_{1:t}^{(s)}, w_t^{*(s)} \right\}$ (blue line) and $\left\{ \boldsymbol{\theta}_{1:t}^{r(s)}, 1/S \right\}$ (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.
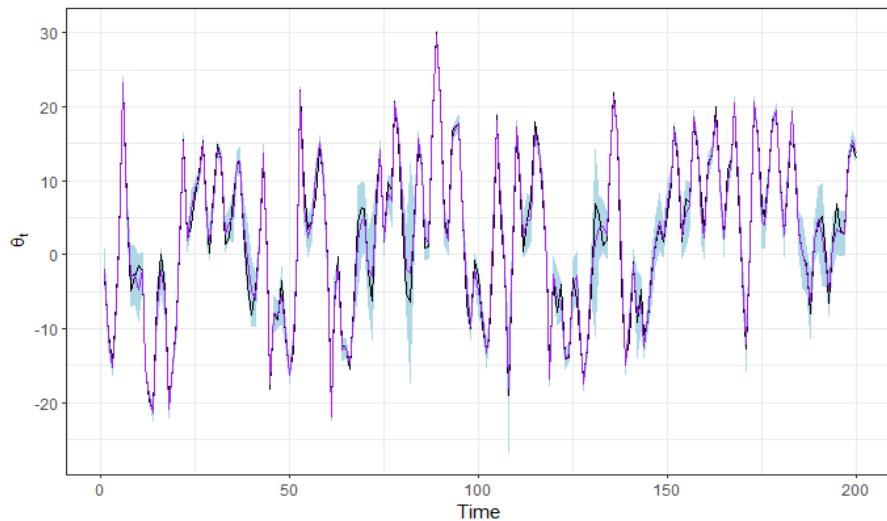
Finally, Figure 4.9 shows the posterior estimate of marginal likelihood based on the particle filtering algorithm.

7. **Ph.D. students sleeping hours continues**

   - Perform the diagnostics of Section 4.4 in this example.
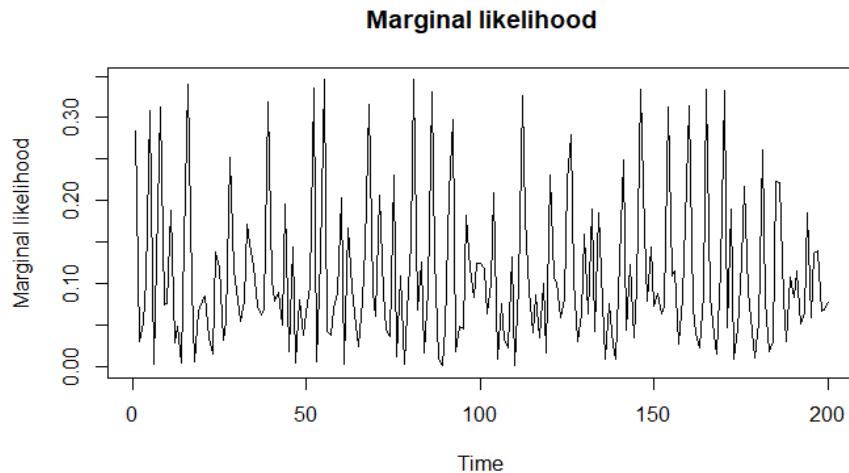
FIGURE 4.7
Sequential importance sampling: Example 1, [13].

FIGURE 4.8
Particle (Bootstrap) filtering: Example 1, [13].

- 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-

Marginal likelihood

FIGURE 4.9
Marginal likelihood: Example 1, [13].

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 [11] 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.
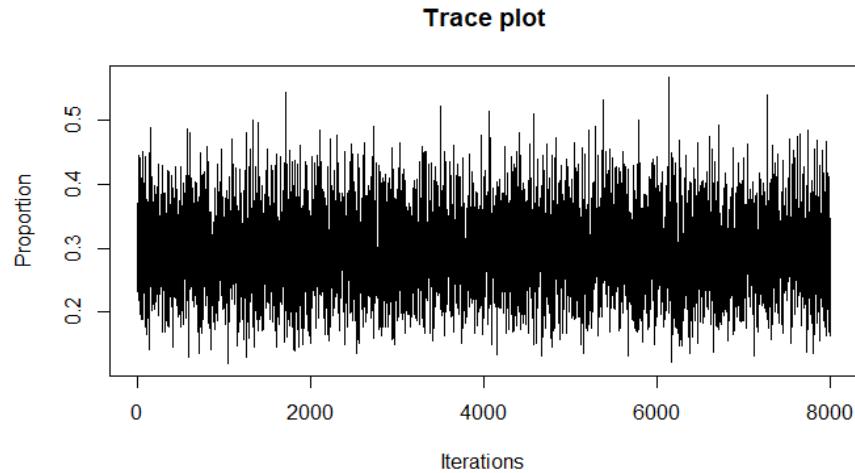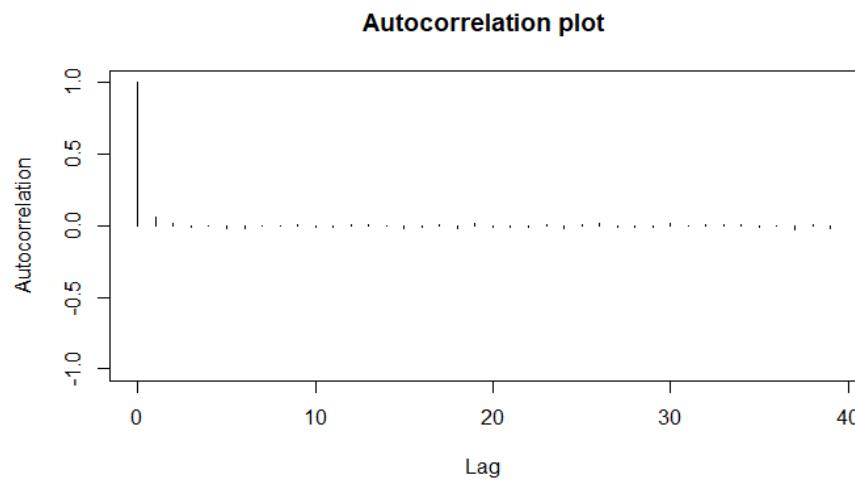
```r
1  rm(list = ls()); set.seed(010101); an <- 16.55; bn <- 39.57
2  S <- 100000; p <- runif(S); accept <- rep(0, S)
3  for (s in 2:S){
4    pc <- runif(1)
5    a <- dbeta(pc, an, bn)/dbeta(p[s-1], an, bn)
6    U <- runif(1)
7    if(U <= a){ p[s] <- pc; accept[s] <- 1
8    }else{p[s] <- p[s-1]; accept[s] <- 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)
```

Trace plot

FIGURE 4.10
Trace plot of posterior draws: Proportion of students that sleep at least 6 hours.

Autocorrelation plot

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* [5], and packages like *MCMCpack* [26] and *bayesm* [37] from **R** software [30], 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 [46, 20].

There are other available graphical user interfaces for carrying out Bayesian regression analysis. *ShinyStan* [43] is a very flexible open source program, but users are required to have some programming skills. *BugsXLA* [46] is open source, but less flexible. However, users do not need to have programming skills. *Bayesian regression: Nonparametric and parametric models* [20] 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 [5], and some libraries in **R** [29]. The specific libraries and commands that are used in our GUI can be seen in Table 14.1. 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 [20]'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 14.2 for details), and **DataApp** (see Table 14.3 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:
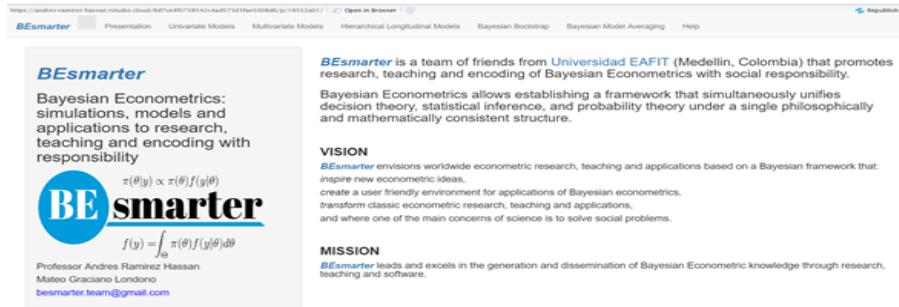
1. docker pull magralo95/besmartergui:latest

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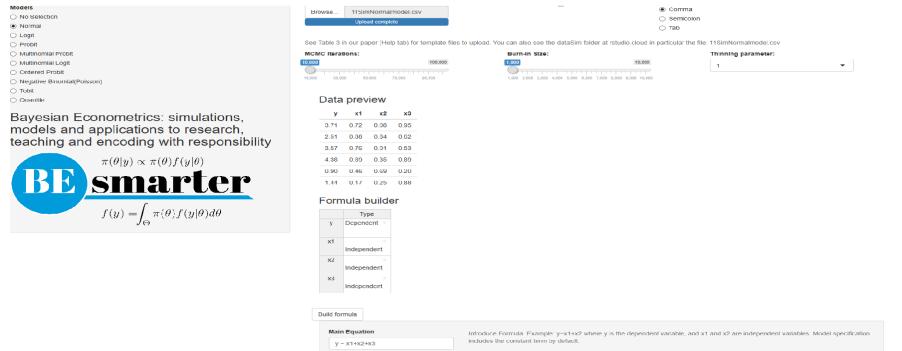
After implementing any of the three ways to run our GUI, users can see

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

FIGURE 5.1
Display of our graphical user interface.
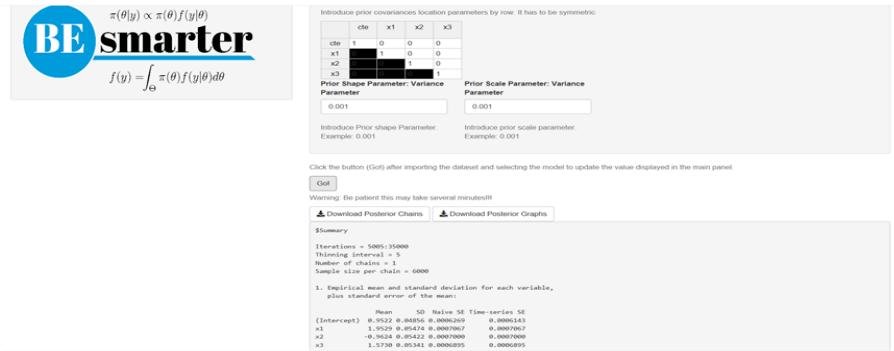
FIGURE 5.2
Univariate models: Specification.

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
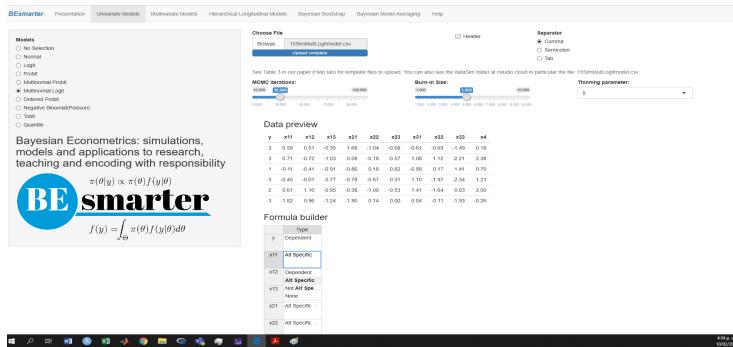
FIGURE 5.3
Univariate models: Results.

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 Equa-
tion* 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 hy-
perparameters 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-

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[2]See **https://www.rdocumentation.org/packages/stats/versions/3.6.2/topics/formula**
[3]An *identification* issue means that multiple values for the model parameters give rise
to the same value for the likelihood function.
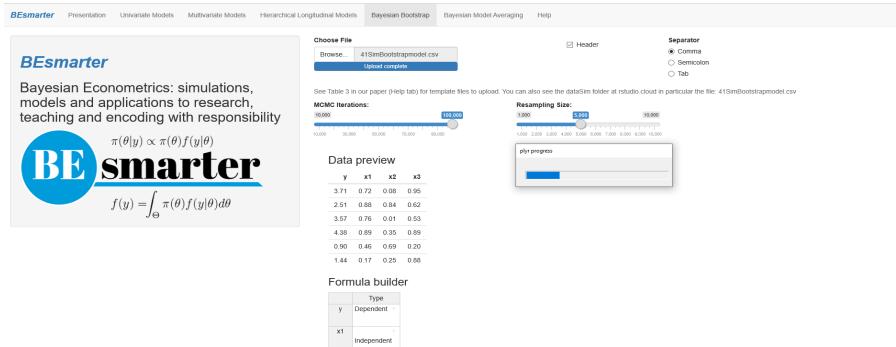
FIGURE 5.4
Univariate models: Multinomial.

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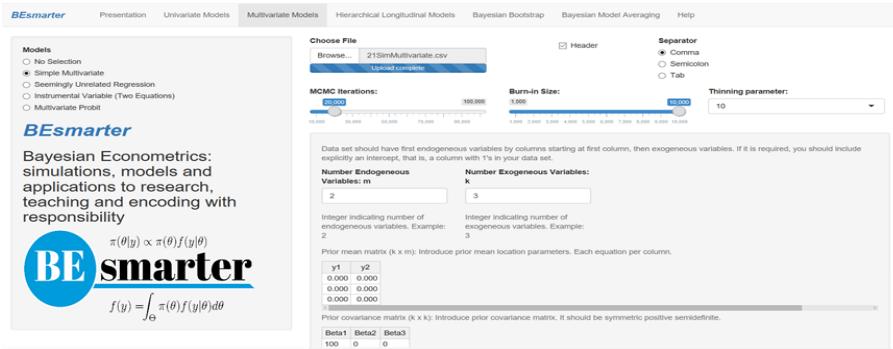
Bayesian bootstrap only requires uploading a dataset, specifying the number of iterations of the MCMC, the resampling size, and the equation (see Figure 5.5). The input file has the same structure as the file used in the univariate normal model.

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
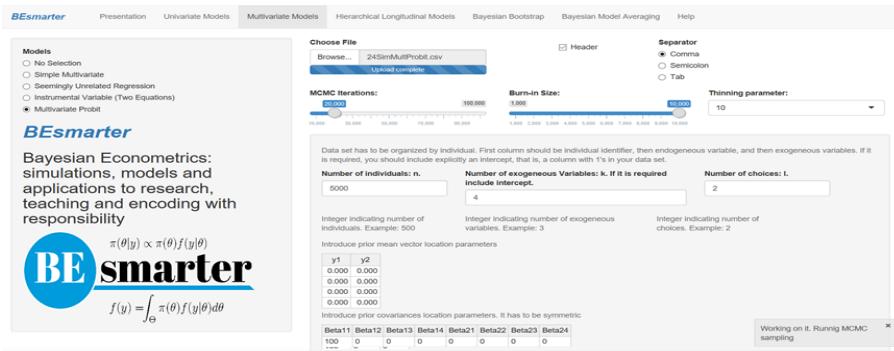
FIGURE 5.6
Multivariate models: Simple multivariate.

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
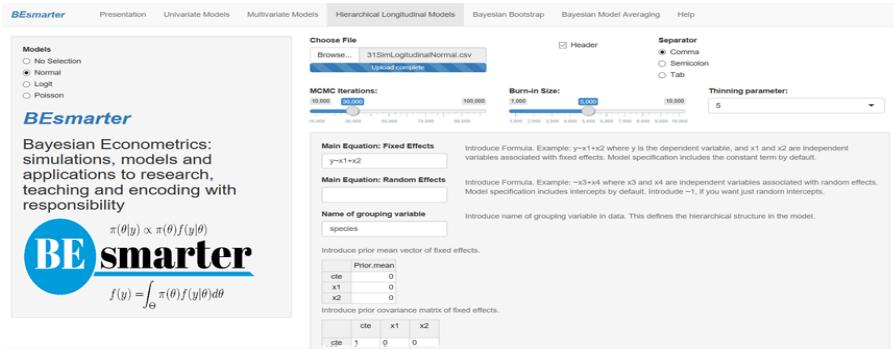
5.5   Longitudinal/panel models

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 ($i = 1, 2, \ldots, N$). 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 14.2 for details), and **DataApp** (see Table 14.3 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.
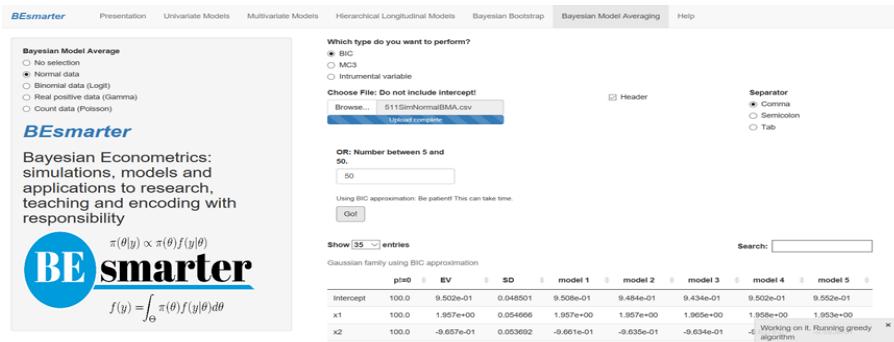
FIGURE 5.8
Hierarchical longitudinal models: Specification.

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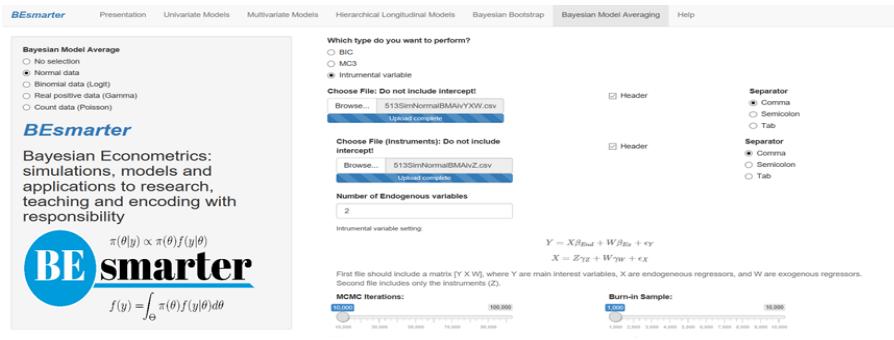
After our GUI is deployed (see Figure 5.1), the user should select *Bayesian Model Averaging* in the top panel. Then, the Figure 5.9 is displayed, and the user can see the radio button on the left hand side that shows the specific models inside this generic class.

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, $l = 1, 2, \ldots, dim\{\boldsymbol{\beta}\}$, the location parameters of the auxiliary equations, $\gamma_{j,i}$, $j = 1, 2, \ldots, dim\{\boldsymbol{\beta}_s\}$ where $dim\{\boldsymbol{\beta}_s\}$ is the number of regressors with endogeneity issues, $i = 1, 2, \ldots, dim\{\boldsymbol{\gamma}\}$, where $dim\{\boldsymbol{\gamma}\}$ 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. Derive the posterior conditional distributions of the Gaussian linear model assuming independent priors $\pi(\boldsymbol{\beta}, \sigma^2) = \pi(\boldsymbol{\beta}) \times \pi(\sigma^2)$, where $\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \boldsymbol{B}_0)$ and $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$.

Answer

The joint posterior distribution of the parameters is

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

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

Let's see the posterior distribution of $\boldsymbol{\beta}$,

$$\pi(\boldsymbol{\beta}, \sigma^2 | \boldsymbol{y}, \boldsymbol{X}) \propto p(\boldsymbol{y} | \boldsymbol{\beta}, \sigma^2, \boldsymbol{X}) \pi(\boldsymbol{\beta}) \pi(\sigma^2)$$

$$\propto (\sigma^2)^{-\frac{N}{2}} \exp\left\{ -\frac{1}{2\sigma^2} (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})^\top (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta}) \right\}$$

$$\times \exp\left\{ -\frac{1}{2} (\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \boldsymbol{B}_0^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_0) \right\}$$

$$\times \frac{(\delta_0/2)^{(\alpha_0/2)}}{\Gamma(\alpha_0/2)} \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}} \exp\left\{ -\frac{\delta_0}{2\sigma^2} \right\}$$

$$= (\sigma^2)^{-\frac{N}{2}} \exp\left\{ -\frac{\sigma^{-2}}{2} [\boldsymbol{y}^\top \boldsymbol{y} - \boldsymbol{y}^\top X\boldsymbol{\beta} - \boldsymbol{\beta}^\top \boldsymbol{X}^\top \boldsymbol{y} + \boldsymbol{\beta}^\top \boldsymbol{X}^\top \boldsymbol{X}\boldsymbol{\beta}] \right\}$$

$$\times \exp\left\{ -\frac{1}{2} [\boldsymbol{\beta}^\top \boldsymbol{B}_0^{-1} \boldsymbol{\beta} - \boldsymbol{\beta}^\top \boldsymbol{B}_0^{-1} \boldsymbol{\beta}_0 - \boldsymbol{\beta}_0^\top \boldsymbol{B}_0^{-1} \boldsymbol{\beta} + \boldsymbol{\beta}_0^\top \boldsymbol{B}_0^{-1} \boldsymbol{\beta}_0] \right\}$$

$$\times \frac{(\delta_0/2)^{(\alpha_0/2)}}{\Gamma(\alpha_0/2)} \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}} \exp\left\{ -\frac{\delta_0}{2\sigma^2} \right\}$$

$$\propto \exp\left\{ -\frac{1}{2} [\boldsymbol{\beta}^\top (\boldsymbol{B}_0^{-1} + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{X})\boldsymbol{\beta} - 2\boldsymbol{\beta}^\top (\boldsymbol{B}_0^{-1} \boldsymbol{\beta}_0 + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{X}\hat{\boldsymbol{\beta}})] \right\}$$

$$\times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp\left\{ -\frac{\delta_0 + \boldsymbol{y}^\top \boldsymbol{y}}{2\sigma^2} \right\},$$

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

Adding and subtracting $\boldsymbol{\beta}_n^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n$ where

$$\boldsymbol{B}_n = (\boldsymbol{B}_0^{-1} + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{X})^{-1}$$

$$\boldsymbol{\beta}_n = \boldsymbol{B}_n (\boldsymbol{B}_0^{-1} \boldsymbol{\beta}_0 + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{X}\hat{\boldsymbol{\beta}}) = \boldsymbol{B}_n (\boldsymbol{B}_0^{-1} \boldsymbol{\beta}_0 + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{y}),$$

and completing the square

$$\pi(\boldsymbol{\beta}, \sigma^2 | \boldsymbol{y}, \boldsymbol{X}) \propto \exp\left\{ -\frac{1}{2} [\boldsymbol{\beta}^\top (\boldsymbol{B}_0^{-1} + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{X})\boldsymbol{\beta} - 2\boldsymbol{\beta}^\top \boldsymbol{B}_n^{-1} \boldsymbol{B}_n (\boldsymbol{B}_0^{-1} \boldsymbol{\beta}_0 + \sigma^{-2} \boldsymbol{X}^\top \boldsymbol{X}\hat{\boldsymbol{\beta}}) \right.$$

$$\left. +\boldsymbol{\beta}_n^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n - \boldsymbol{\beta}_n^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n] \right\} \times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp\left\{ -\frac{\delta_0 + \boldsymbol{y}^\top \boldsymbol{y}}{2\sigma^2} \right\}$$

$$= \exp\left\{ -\frac{1}{2} [\boldsymbol{\beta}^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta} - 2\boldsymbol{\beta}^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n + \boldsymbol{\beta}_n^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n] \right\}$$

$$\times \frac{1}{(\sigma^2)^{(\alpha_0+N)/2+1}} \exp\left\{ -\frac{\delta_0 + \boldsymbol{y}^\top \boldsymbol{y} - \sigma^2 \boldsymbol{\beta}_n^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n}{2\sigma^2} \right\}$$

$$= \underbrace{\exp\left\{ -\frac{1}{2} (\boldsymbol{\beta} - \boldsymbol{\beta}_n)^\top \boldsymbol{B}_n^{-1} (\boldsymbol{\beta} - \boldsymbol{\beta}_n) \right\}}_{1}$$

$$\times (\sigma^2)^{-(\frac{\alpha_n}{2}+1)} \exp\left\{ -\frac{\delta^*}{2\sigma^2} \right\},$$

where $\delta^* = \delta_0 + \boldsymbol{y}^\top \boldsymbol{y} + \sigma^2 \boldsymbol{\beta}_n^\top \boldsymbol{B}_n^{-1} \boldsymbol{\beta}_n$ does not dependent 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 $\boldsymbol{B}_n$, that is, $\boldsymbol{\beta}|\sigma^2, \boldsymbol{y}, \boldsymbol{X} \sim N(\boldsymbol{\beta}_n, \boldsymbol{B}_n)$.

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

2. Consider the model $y_i \sim N(\boldsymbol{x}_i^\top \boldsymbol{\beta}, \sigma^2/\tau_i)$ (Gaussian linear model with heteroskedasticity) and 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 $\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \boldsymbol{B}_0)$, $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$, and $\tau_i \sim G(v/2, v/2)$.

Show that $\boldsymbol{\beta} \mid \sigma^2, \boldsymbol{\tau}, \boldsymbol{y}, \boldsymbol{X} \sim N(\boldsymbol{\beta}_n, \boldsymbol{B}_n)$, $\sigma^2 \mid \boldsymbol{\beta}, \boldsymbol{\tau}, \boldsymbol{y}, \boldsymbol{X} \sim IG(\alpha_n/2, \delta_n/2)$, and $\tau_i \mid \boldsymbol{\beta}, \sigma^2, \boldsymbol{y}, \boldsymbol{X} \sim G(v_{1n}/2, v_{2in}/2)$, where $\boldsymbol{\tau} = [\tau_1 \ \ldots \ \tau_N]^\top$, $\boldsymbol{B}_n = (\boldsymbol{B}_0^{-1} + \sigma^{-2} \boldsymbol{X}^\top \Psi \boldsymbol{X})^{-1}$, $\boldsymbol{\beta}_n = \boldsymbol{B}_n(\boldsymbol{B}_0^{-1}\boldsymbol{\beta}_0 + \sigma^{-2}\boldsymbol{X}^\top \Psi \boldsymbol{y})$, $\alpha_n = \alpha_0 + N$, $\delta_n = \delta_0 + (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})^\top \Psi (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})$, $v_{1n} = v + 1$, $v_{2in} = v + \sigma^{-2}(y_i - \boldsymbol{x}_i^\top \boldsymbol{\beta})^2$, and $\Psi = \mathrm{diag}\,(\tau_i)$.

Answer

The joint posterior distribution of the parameters is

$$\pi(\boldsymbol{\beta}, \sigma^2, \boldsymbol{\tau}|\boldsymbol{y}, \boldsymbol{X}) \propto p(\boldsymbol{y}|\boldsymbol{\beta}, \sigma^2, \boldsymbol{\tau}, \boldsymbol{X})\pi(\boldsymbol{\beta})\pi(\sigma^2)\prod_{i=1}^N \pi(\tau_i)$$

$$\propto \left(\prod_{i=1}^N \tau_i^{1/2}\right)(\sigma^2)^{-\frac{N}{2}}\exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})^\top \Psi (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})\right\}$$

$$\times \exp\left\{-\frac{1}{2}(\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \boldsymbol{B}_0^{-1}(\boldsymbol{\beta} - \boldsymbol{\beta}_0)\right\}$$

$$\times \frac{1}{(\sigma^2)^{(\alpha_0/2+1)}}\exp\left\{-\frac{\delta_0}{2\sigma^2}\right\}\prod_{i=1}^N \tau_i^{v/2-1}\exp\left\{-v\tau_i/2\right\}.$$

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

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

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 $\tau_i|\boldsymbol{\beta}, \sigma^2, \boldsymbol{y}, \boldsymbol{X}$ is

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

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

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

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

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

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 for the market value of soccer players in Europe, setting $v = 5$ and using the same hyperparameters as in the homoscedastic case. Is there any meaningful difference in the coefficient associated with the national team compared to the homoscedastic case?

   Answer

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

```r
rm(list = ls())
set.seed(010101)
######################### Linear regression: Value of
    soccer players ###########################
Data <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/1
    ValueFootballPlayers.csv", sep = ",", header = TRUE,
    quote = "")
attach(Data)
y <- log(Value)
# Value: Market value in Euros (2017) of soccer players
# Regressors quantity including intercept
X <- cbind(1, Perf, Age, Age2, NatTeam, Goals, Exp, Exp2)
# Perf: Performance. Perf2: Performance squared. Age: Age;
     Age: Age squared.
# NatTeam: Indicator of national team. Goals: Scored goals.
     Goals2: Scored goals squared
# Exp: Years of experience. Exp2: Years of experience
    squared. Assists: Number of assists
k <- dim(X)[2]
N <- dim(X)[1]
# Hyperparameters
d0 <- 0.001
a0 <- 0.001
b0 <- rep(0, k)
c0 <- 1000
B0 <- c0*diag(k)
B0i <- solve(B0)
v <- 5
# MCMC parameters
mcmc <- 5000
burnin <- 5000
tot <- mcmc + burnin
thin <- 1
# Posterior distributions programming the Gibbs sampling
# Auxiliary parameters
an <- a0 + N
v1n <- v + 1
# Gibbs sampling functions
PostSig2 <- function(Beta, tau){
  dn <- d0 + t(y - X%*%Beta)%*%diag(tau)%*%(y - X%*%Beta)
  sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
  return(sig2)
}
PostBeta <- function(sig2, tau){
  Bn <- solve(B0i + sig2^(-1)*t(X)%*%diag(tau)%*%X)
  bn <- Bn%*%(B0i%*%b0 + sig2^(-1)*t(X)%*%diag(tau)%*%y)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
PostTau <- function(sig2, Beta, i){
  v2n <- v + sig2^(-1)*(y[i]-X[i,]%*%Beta)^2
  taui <- rgamma(1, v1n/2, v2n/2)
  return(taui)
}
```

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

```r
PostBetas <- matrix(0, mcmc+burnin, k)
PostSigma2 <- rep(0, mcmc+burnin)
Beta <- rep(0, k)
tau <- rep(1, N)
# create progress bar in case that you want to see
    iterations progress
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  sig2 <- PostSig2(Beta = Beta, tau = tau)
  PostSigma2[s] <- sig2
  Beta <- PostBeta(sig2 = sig2, tau = tau)
  PostBetas[s,] <- Beta
  tau <- sapply(1:N, function(i){PostTau(sig2 = sig2, Beta =
      Beta, i)})
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
PosteriorBetas <- PostBetas[keep,]
colnames(PosteriorBetas) <- c("Intercept", "Perf", "Age", "
    Age2", "NatTeam", "Goals", "Exp", "Exp2")
summary(coda::mcmc(PosteriorBetas))
PosteriorSigma2 <- PostSigma2[keep]
summary(coda::mcmc(PosteriorSigma2))
summary(coda::mcmc(exp(PosteriorBetas[,5])-1))
Iterations = 1:5000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 5000
1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:
Mean               SD         Naive SE Time-series SE
1.256091        0.254974        0.003606        0.004579
2. Quantiles for each variable:
2.5%    25%    50%    75%  97.5%
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 for the application on the determinants of hospitalization

Answer

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

```r
set.seed(010101)
Data <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/2HealthMed.
    csv", sep = ",", header = TRUE, quote = "")
attach(Data)
str(Data)
y <- Hosp # Dependent variables
X <- cbind(1, SHI, Female, Age, Age2, Est2, Est3, Fair, Good
    , Excellent) # Regressors
K <- dim(X)[2]
N <- dim(X)[1]
# Hyperparameters
b0 <- rep(0, K) # Prio mean
B0 <- diag(K) # Prior covariance
B0i <- solve(B0)
mcmc <- 1000; burnin <- 500; thin <- 2; tot <- mcmc + burnin
    ; keep <- seq(burnin, tot, thin)
# Posterior distributions programming the Gibbs sampling
# Auxiliary parameters
XtX <- t(X)%*%X
# Gibbs sampling functions
PostBeta <- function(Yl){
  Bn <- solve(B0i + XtX)
  bn <- Bn%*%(B0i%*%b0 + t(X)%*%Yl)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
PostYl <- function(Beta, i){
  Ylmean <- X[i,]%*%Beta
  if(y[i] == 1){
    Yli <- truncnorm::rtruncnorm(1, a = 0, b = Inf, mean =
    Ylmean, sd = 1)
  }else{
    Yli <- truncnorm::rtruncnorm(1, a = -Inf, b = 0, mean =
    Ylmean, sd = 1)
  }
  return(Yli)
}
PostBetas <- matrix(0, mcmc+burnin, K)
Beta <- rep(0, K)
# create progress bar in case that you want to see
    iterations progress
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  Yl <- sapply(1:N, function(i){PostYl(Beta = Beta, i)})
  Beta <- PostBeta(Yl = Yl)
  PostBetas[s,] <- Beta
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
PosteriorBetas <- PostBetas[keep,]
colnames(PosteriorBetas) <- c("Intercept", "SHI", "Female",
    "Age", "Age2", "Est2", "Est3", "Fair", "Good", "
    Excellent")
summary(coda::mcmc(PosteriorBetas))
```

5. **Choice of fishing mode continues.**

   - Run Algorithm A9 to report the results of the Geweke [10], Raftery [32], and Heidelberger [15] tests using our GUI.

   - Use the command *rmnpGibbs* to replicate the fishing mode choice example.

   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

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

6. **Simulation exercise: Multinomial logit model continues.**

Perform inference in the simulated multinomial logit model using the command *rmnlIndepMetrop* from the *bayesm* package in **R**, and compare the results with those obtained from our GUI.

Answer

R. code. Simulation of the multinomial logit model

```r
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 mcmcpar <- list(R = mcmc, keep = 5, nu = df)
41 PostBeta <- bayesm::rmnlIndepMetrop(Data = DataMlogit, Mcmc
       = mcmcpar)
42 summary(PostBeta[["betadraw"]])
```

7. **Simulation of the ordered probit model.**

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

   Answer

R. code. Simulation of the ordered probit model

```r
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
       [2]) {
11       y[i] <- 1
12     }else{
13       if (y_latent[i] >= cutoffs[2] & y_latent[i] < cutoffs
       [3]) {
14         y[i] <- 2
15       }else{y[i] <- 3
16       }
17     }
18   }
19 }
20 # Likelihood function
21 LogLikOP <- function(param){
22   beta_g <- param[1:ncol(X)]
23   delta <- param[(ncol(X)+1):(ncol(X) + dplyr::n_distinct(y)
       - 1)]
24   Xbeta <- X%*%beta_g
25   logLik <- 0
26   for (i in 1:length(y)){
27     if (y[i]==0){logLiki <- log(pnorm(-Xbeta[i]))
28     }else if (y[i]==1){
29       logLiki <- log(pnorm(exp(delta[1]) - Xbeta[i]) - pnorm
       (-Xbeta[i]))
30     }else if (y[i]==2){
31       logLiki <- log(pnorm(exp(delta[2]) + exp(delta[1]) -
       Xbeta[i]) - pnorm(exp(delta[1]) - Xbeta[i]))
32     }else {logLiki <- log(1 - pnorm(exp(delta[2]) + exp(
       delta[1]) - Xbeta[i]))
33     }
34     logLik <- logLik + logLiki
35   }
36   return(-logLik)
37 }
38 # ML Estimation
39 param0 <- rep(0, ncol(X) + n_distinct(y)-2)
40 mle <- optim(param0, LogLikOP, hessian = T, method = "BFGS")
41 mle$par
42 exp(mle$par[length(beta)+1])
43 exp(mle$par[length(beta)+1])+exp(mle$par[length(beta)+2])
44 CovarML <- solve(mle$hessian)
```

R. code. Simulation of the ordered probit model

```r
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)
        - 2)
6    tau[1,] <- param0[(ncol(X)+1):(ncol(X) + dplyr::n_distinct
        (y) - 2)]
7    yl <- rep(0,length(y)); ar <- rep(0,G); B1 <- solve(t(X)%*
        %X+solve(B0))
8    pb <- txtProgressBar(min = 0, max = G, style = 3)
9    for(g in 2:G){
10     bg <- betasamples[g-1,]; tg <- tau[g-1,]
11     #Random walk M-H for delta
12     delta_prime <- tg + mvtnorm::rmvnorm(1, mean = rep(0,2),
         sigma = VarProp)
13     alpha <- min(1,(mvtnorm::dmvnorm(delta_prime, mean = d0,
         sigma = D0)*exp(-LogLikOP(c(bg, delta_prime)) +
        LogLikOP(c(bg, tg))))/mvtnorm::dmvnorm(tg, mean = d0,
        sigma = D0))
14     if(is.nan(alpha) | is.na(alpha)) {
15       alpha <- 0
16     }
17     #Acceptance step
18     u <- runif(1, min = 0, max = 1)
19     if(u<=alpha){tau[g,] <- delta_prime; ar[g] <- 1
20     }else{tau[g,] <- tg}
21     }
22     #Generation of latent variables
23     for (i in 1:length(y)){
24       if (y[i]==0) {
25         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
        sd = 1, max = 0)
26       }else if(y[i]==1){
27         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
        sd = 1, min = 0, max = exp(tau[g,1]))
28       }else if(y[i]==2){
29         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
        sd = 1, min = exp(tau[g,1]), max = exp(tau[g,2])+exp(tau
        [g,1]))
30       }else{
31         yl[i] <- EnvStats::rnormTrunc(1, mean = X[i,]%*%bg,
        sd = 1, min = exp(tau[g,2])+exp(tau[g,1]))
32       }
33     }
34     #Gibbs sampling for beta
35     if(sum(is.nan(yl))>0 | sum(is.na(yl))>0 | sum(yl)==Inf){
36       betasamples[g,] <- betasamples[g-1,]
37     }else{
38       b1 <- B1%*%(t(X)%*%yl + solve(B0)%*%b0)
39       betasamples[g,] <- mvrnorm(1, mu = b1, Sigma = B1)
40     }
41     setTxtProgressBar(pb, g)
42   }
43   close(pb)
44   return(cbind(betasamples, tau, ar))
45 }
```

R. code. Simulation of the ordered probit model

```r
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 simulated negative binomial model using the *bayesm* package in **R**.

Answer

R. code. Simulation of the negative binomial model

```r
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 <- rnbinom(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 on soccer players' market value with left censoring

at one million euros in our GUI using Algorithm **??** and the hyperparameters 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              Mean       SD   Naive SE Time - series SE
 9  (Intercept)  1.014765 2.626395 1.175e-02      1.659e-02
10  Perf         0.033935 0.004529 2.025e-05      2.245e-05
11  Age          1.027285 0.212413 9.499e-04      1.326e-03
12  Age2        -0.021914 0.003989 1.784e-05      2.528e-05
13  NatTeam      0.847412 0.124884 5.585e-04      6.423e-04
14  Goals        0.010092 0.001644 7.351e-06      7.712e-06
15  Exp          0.175324 0.069653 3.115e-04      3.727e-04
16  Exp2        -0.005696 0.002950 1.319e-05      1.527e-05
17  sigma2       0.983337 0.096194 4.302e-04      6.724e-04
18  2. Quantiles for each variable:
19              2.5%       25%       50%       75%       97.5%
20  (Intercept) -4.212563 -0.732856  1.038281  2.796603  6.051e
        +00
21  Perf         0.025121  0.030873  0.033896  0.036988  4.286e
        -02
22  Age          0.618743  0.883011  1.026760  1.168860  1.450e
        +00
23  Age2        -0.029854 -0.024580 -0.021886 -0.019203 -1.424e
        -02
24  NatTeam      0.605030  0.763154  0.846671  0.930593  1.095e
        +00
25  Goals        0.006893  0.008987  0.010097  0.011201  1.330e
        -02
26  Exp          0.038522  0.128032  0.175261  0.222110  3.118e
        -01
27  Exp2        -0.011484 -0.007671 -0.005685 -0.003706  5.502e
        -05
28  sigma2       0.813118  0.915664  0.977298  1.043661  1.189e
        +00
```

---

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

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

    Answer

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

```r
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 <- txtProgressBar(min = 0, max = tot, style = 3)
31 for(s in 1:tot){
32   e <- sapply(1:N, function(i){PostE(Beta = Beta, i)})
33   Beta <- PostBeta(e = e)
34   PostBetas[s,] <- Beta
35   setTxtProgressBar(pb, s)
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 **??** and compare the results with those obtained from our GUI, setting $S = 10,000$.

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 $\mathbb{E}[u_1u_2] = 0$ and $\text{Var}(u_1) = \sigma_1^2$, in the example on the effect of institutions on per capita GDP.

   Answer

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

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

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

   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 $\log(pcGDP95)$,

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

   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 $e_1 = \frac{\beta_2u_2+u_1}{1-\beta_2\alpha_2}$.

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

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

   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 $e_2 = \frac{\alpha_2u_1+u_2}{1-\beta_2\alpha_2}$.

   Then, $\mathbb{E}[u_1\text{PAER}] = \mathbb{E}\left[u_1(\gamma_1 + \gamma_2\log(\text{Mort}_i) + \gamma_3\text{Africa} + \gamma_4\text{Asia} + \gamma_5\text{Other} + e_{2i})\right] = \mathbb{E}\left[u_1\left(\frac{\alpha_2u_1+u_2}{1-\beta_2\alpha_2}\right)\right] = \frac{\alpha_2}{1-\beta_2\alpha_2}\sigma_1^2$ given the assumptions.

2. Show that $\beta_1 = \pi_1/\gamma_1$ in the example on 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 GDP continues I**

   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 <- txtProgressBar(min = 0, max = S, style = 3)
   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   setTxtProgressBar(pb, s)
   24 }
   25 close(pb)
   26 summary(coda::mcmc(betadraw))
   27 summary(coda::mcmc(Sigmadraw))
   ```

4. **Demand and supply simulation**

Consider the structural demand–supply model:

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

where q^d and q^s represent demand and supply, respectively; p, y, pc, ps, and er denote price, income, complementary price, substitute price, and exchange rate. The variables pc and ps refer to the prices of complementary and substitute goods for q. Assume that $\boldsymbol{\beta} = [5 \ -0.5 \ 0.8 \ -0.4 \ 0.7]^\top$, $\boldsymbol{\alpha} = [-2 \ 0.5 \ -0.4]^\top$, $u_1 \sim N(0, 0.5^2)$, and $u_2 \sim N(0, 0.5^2)$. Additionally, assume that $y \sim N(10, 1)$, $pc \sim N(5, 1)$, $ps \sim N(5, 1)$, and $er \sim N(15, 1)$.

- Derive the *reduced-form* model under the equilibrium condition $q^d = q^s$, which defines the observable quantity q.

- Simulate p and q from the *reduced-form* equations.

- Perform inference for the *reduced-form* model using the *rmultireg* command from the *bayesm* package.

- Use the posterior draws of the *reduced-form* parameters to perform inference for the *structural* parameters. Discuss any potential issues. *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

```r
rm(list = ls()); set.seed(12345)
B0 <- 5; B1 <- -0.5; B2 <- 0.8; B3 <- -0.4; B4 <- 0.7; SD <-
    0.5
A0 <- -2; A1 <- 0.5; A2 <- -0.4; SS <- 0.5
P0 <- (A0-B0)/(B1-A1); P2 <- -B2/(B1-A1); P3 <- -B3/(B1-A1);
    P1 <- A2/(B1-A1); P4 <- -B4/(B1-A1)
T0 <- B0+B1*P0; T2 <- B2+B1*P2; T3 <- B3+B1*P3; T1 <- B1*P1;
    T4 <- B4+B1*P4;
n <- 5000
ED <- rnorm(n, 0, SD); ES <- rnorm(n, 0, SS)
VP <- (ES-ED)/(B1-A1); UQ <- B1*VP+ED
y <- rnorm(n, 10, 1); pc <- rnorm(n, 5, 1); er <- rnorm(n,
    15, 1); ps <- rnorm(n, 5, 1);
p <- P0+P1*er+P2*y+P3*pc+P4*ps+VP
q <- T0+T1*er+T2*y+T3*pc+T4*ps+UQ
#Inference
Y <- cbind(p, q); X <- cbind(1, er, y, pc, ps)
M <- dim(Y)[2]; K <- dim(X)[2]
# Hyperparameters
B0 <- matrix(0, K, M); c0 <- 100; V0 <- c0*diag(K)
Psi0 <- 5*diag(M); a0 <- 5; S <- 10000 #Posterior draws
betadraw = matrix(double(S*K*M), ncol=K*M)
Sigmadraw = matrix(double(S*M*M), ncol=M*M)
pb <- txtProgressBar(min = 0, max = S, style = 3)
for (s in 1:S) {
  Results <- bayesm::rmultireg(Y, X, Bbar = B0, A = solve(V0
    ), nu = a0, V = Psi0)
  betadraw[s,] <- Results$B
  Sigmadraw[s,] <- Results$Sigma
  setTxtProgressBar(pb, s)
}
close(pb)
summary(coda::mcmc(betadraw))
summary(coda::mcmc(Sigmadraw))
beta2 <- betadraw[,7]/betadraw[,2] # Effect of price on
    demand
summary(coda::mcmc(beta2))
beta3 <- betadraw[,8] - beta2*betadraw[,3] # Effect of
    income on demand
summary(coda::mcmc(beta3))
beta4 <- betadraw[,9] - beta2*betadraw[,4] # Effect of
    complementary price on demand
summary(coda::mcmc(beta4))
beta5 <- betadraw[,10] - beta2*betadraw[,5] # Effect of
    substitute price  on demand
summary(coda::mcmc(beta5))
```

5. **Utility demand continues**

- Run the **Utility demand** application using our GUI and the dataset *Utilities.csv*. *Hint:* This file must be modified to match the structure required by our GUI (see the dataset *5Institutions.csv* in the *DataApp* folder of our GitHub repository—**https://github.com/besmarter/BSTApp**—as a template).

- Program the Gibbs sampling algorithm for this application from scratch.

Answer

R code. Utility demand in Colombia, Gibss sampler

```r
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 <- txtProgressBar(min = 0, max = tot, style = 3)
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   setTxtProgressBar(pb, s)
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                  2.5%      25%       50%        75%      97.5%
6  Const          0.43304   1.04508   1.337751   1.64728   2.25228
7  LnPriceElect  -2.40343  -2.05533  -1.882159  -1.70463  -1.35979
8  LnPriceWater  -0.44027  -0.38524  -0.356049  -0.32676  -0.27021
9  LnPriceGas    -0.21665  -0.13807  -0.098877  -0.05712   0.01673
10 IndSocio1     -0.87408  -0.78454  -0.736561  -0.68898  -0.59137
11 IndSocio2     -0.24504  -0.18344  -0.150827  -0.11845  -0.06029
12 Altitude      -0.27153  -0.23866  -0.221539  -0.20468  -0.17325
13 Nrooms         0.04598   0.06191   0.069971   0.07837   0.09379
14 HouseholdMem   0.06610   0.07999   0.087320   0.09406   0.10708
15 Lnincome       0.03897   0.05516   0.063130   0.07152   0.08751
16 Const          0.88247   1.73546   2.162290   2.60793   3.48450
17 LnPriceElect  -0.83128  -0.31258  -0.051838   0.20446   0.72087
18 LnPriceWater  -0.49760  -0.40946  -0.363138  -0.31943  -0.23498
19 LnPriceGas     0.05880   0.16932   0.228734   0.28677   0.39226
20 IndSocio1     -0.63928  -0.50417  -0.427978  -0.35529  -0.21024
21 IndSocio2     -0.50363  -0.40976  -0.359576  -0.30929  -0.21097
22 Nrooms         0.05733   0.08126   0.093291   0.10550   0.12935
23 HouseholdMem   0.09984   0.12098   0.132126   0.14265   0.16290
24 Const         -2.26403  -1.57842  -1.201124  -0.84494  -0.15985
25 LnPriceElect  -2.41128  -2.00330  -1.786150  -1.57292  -1.17185
26 LnPriceWater  -0.10791  -0.03978  -0.003399   0.03329   0.10082
27 LnPriceGas    -0.76450  -0.67575  -0.627062  -0.57949  -0.48807
28 IndSocio1     -0.91346  -0.80094  -0.743421  -0.68334  -0.57228
29 IndSocio2     -0.31613  -0.24086  -0.202828  -0.16367  -0.08824
30 Altitude       0.24986   0.28987   0.310784   0.33183   0.37126
31 Nrooms         0.06071   0.07899   0.089606   0.09949   0.11842
32 HouseholdMem   0.14485   0.16148   0.169509   0.17797   0.19467
33 Sigmas <- PostSigmas[keep,]
34 summary(coda::mcmc(Sigmas))
35         2.5%      25%      50%      75%     97.5%
36 var1 0.19664  0.20567  0.21072  0.21593  0.22636
37 var2 0.08201  0.09289  0.09865  0.10447  0.11623
38 var3 0.05222  0.06015  0.06452  0.06903  0.07799
39 var4 0.47390  0.49575  0.50789  0.52046  0.54446
40 var5 0.07355  0.08672  0.09381  0.10061  0.11427
41 var6 0.29259  0.30618  0.31384  0.32140  0.33700
```

6. **Simulation exercise of instrumental variables continues I**

   - Use the setting of the simulation exercise with instrumental variables to analyze the impact of a weak instrument. For example, set $\gamma_2 =$

0.2 and compare the posterior mean estimates of the ordinary and instrumental variable models.

- Perform a simulation to analyze how the degree of exogeneity of the instrument affects the performance of the posterior mean in the instrumental variable model.

Answer

R code. Simulation exercise, sampling properties of instrumental variable
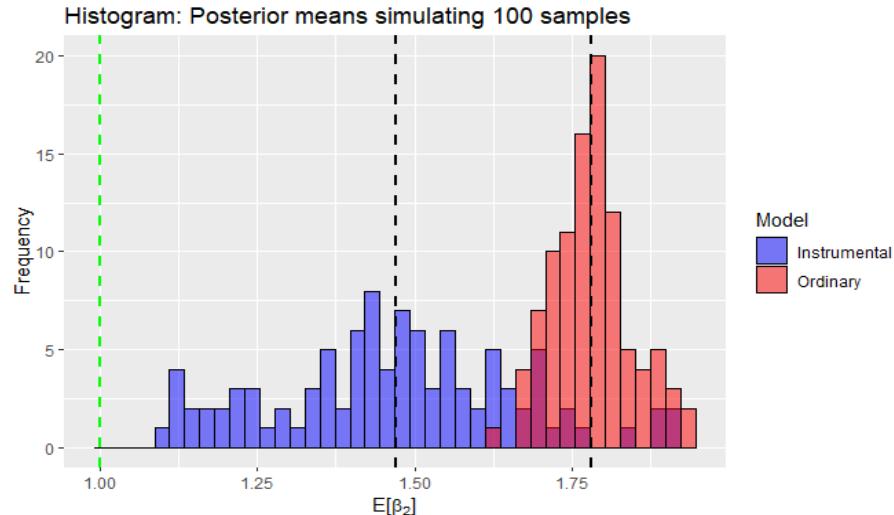
```r
1  rm(list = ls())
2  set.seed(010101)
3  N <- 100
4  k <- 2
5  B <- rep(1, k)
6  G <- c(1, 0.2)
7  s12 <- 0.8
8  SIGMA <- matrix(c(1, s12, s12, 1), 2, 2)
9  z <- rnorm(N); # w <- rnorm(N)
10 Z <- cbind(1, z); w <- matrix(1,N,1)
11 S <- 100
12 U <- replicate(S, MASS::mvrnorm(n = N, mu = rep(0, 2), 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 [39, Chap. 7]).

R code. Simulation exercise, sampling properties of instrumental variable
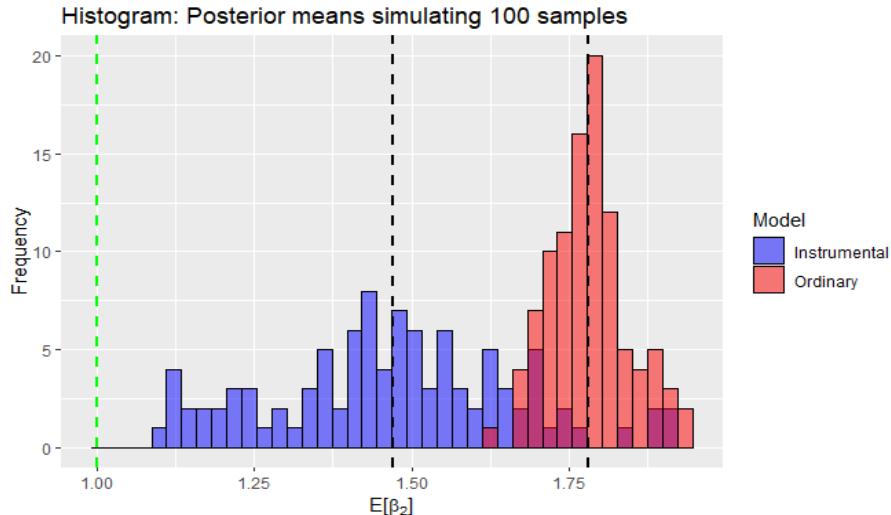
```r
1  # Endogenous instruments
2  rm(list = ls())
3  set.seed(010101)
4  N <- 100
5  k <- 2
6  B <- rep(1, k)
7  G <- c(1, 1)
8  delta <- 0.2 # Effect of instrument on y
9  s12 <- 0.8
10 SIGMA <- matrix(c(1, s12, s12, 1), 2, 2)
11 z <- rnorm(N); # w <- rnorm(N)
12 Z <- cbind(1, z); w <- matrix(1,N,1)
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 $\mathbb{E}[yz|x_s] = 0$. 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, [6] 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 the Gibbs sampling algorithm for the instrumental variable model from scratch.

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, Gibss sampling instrumental model

```r
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

```r
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 <- txtProgressBar(min = 0, max = tot, style = 3)
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   setTxtProgressBar(pb, s)
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 GDP continues II**

Estimate the structural Equation 7.1 using the instrumental variable model, where log(*Mort*) serves as the instrument for PAER. Compare the estimated effect of property rights on per capita GDP with that obtained in the example on the effect of institutions on per capita GDP. Use the file *6Institutions.csv* to conduct this exercise in our GUI, setting $B_0 = 100I_5$,

$\boldsymbol{\beta}_0 = \mathbf{0}_5$, $\boldsymbol{\gamma}_0 = \mathbf{0}_2$, $\boldsymbol{G}_0 = 100\boldsymbol{I}_2$, $\alpha_0 = 3$, and $\boldsymbol{\Psi}_0 = 3\boldsymbol{I}_2$. Set the MCMC parameters as follows: 50,000 iterations, 1,000 burn-in, and a thinning interval of 5.

Answer

The following code shows how to do this using the command *rivGibss* 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

```r
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**

   Simulate the model

   $$y_{i1}^* = 0.5 - 1.2x_{i11} + 0.7x_{i12} + 0.8x_{i3} + \mu_{i1}, \quad y_{i2}^* = 1.5 - 0.8x_{i21} + 0.5x_{i22} + \mu_{i2},$$

   with

   $$\boldsymbol{\Sigma} = \begin{bmatrix} 1 & 0.5 \\ 0.5 & 1 \end{bmatrix},$$

where all regressors follow a standard normal distribution and $N = 5000$. Use $\boldsymbol{\beta}_0 = \mathbf{0}$, $\boldsymbol{B}_0 = 1000\boldsymbol{I}$, $\alpha_0 = 4$, and $\boldsymbol{\Psi}_0 = 4\boldsymbol{I}_2$. Set the number of iterations to 2,000 and the thinning parameter to 5.

- Perform inference under the setting of Section 7.4, assuming that x_{i3} may affect y_{i2}.

- Program a Gibbs sampling algorithm that accounts for different regressors in each binary decision, that is, where x_{i3} does not affect 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

```r
remove(list = ls())
n <-5000   #Individuals
p <-2  #Number dependent variables (For instance to buy or
    not to buy different products)
xo <- 2  #Number of choice dependent variables (For instance
     price of products)
xi <- 1  #Number of regressors that dependt on individuals (
    For instance income)
B1 <- c(0.5,-1.2,0.7,0.8)
B2 <- c(1.5,-0.8,0.5,0) # The last regressor is not relevant
     for the second product
Cor <- matrix(c(1,0.5,0.5,1),p,p)
yX <- NULL; yl <- NULL
for (i in 1:n){
  ei <- MASS::mvrnorm(1, c(0,0), Cor);  xs <- rnorm(xi)
  x1i <- c(1, rnorm(xo), xs);   yl1i <- sum(x1i*B1)
  y1i <- yl1i + ei[1] > 0;  x2i <- c(1, rnorm(xo), xs)
  yl2i <- sum(x2i*B2);  y2i <- yl2i + ei[2] > 0
  yXi <- rbind(c(y1i, x1i), c(y2i, x2i))
  yXi <- cbind(i, yXi)
  colnames(yXi) <- c("id", "y", "cte", "x1o", "x2o", "xi")
  yX <- rbind(yX, yXi)
  yl <- c(yl, c(yl1i + ei[1], yl2i + ei[2]))
}

nd <- 4 # Number of regressors
Xd <- as.matrix(yX[,3:6])
XcreateMP<-function(p,nxs,nind,Data){
  pandterm = function(message) {
    stop(message, call. = FALSE)
  }
  if (missing(nxs))
  pandterm("requires number of regressors: include intercept
      if required")
  if (missing(nind))
  pandterm("requires number of units (individuals)")
  if (missing(Data))
  pandterm("requires dataset")
  if (nrow(Data)!=nind*2)
  pandterm("check dataset! number of units times number
      alternatives should be equal to dataset rows")
  XXDat<-array(0,c(p,1+nxs,nind))
  XX<-array(0,c(p,nxs*p,nind))
  YY<-array(0,c(p,1,nind))
  is<- seq(p,nind*p,p)
  cis<- seq(nxs,nxs*p+1,nxs)
  for(i in is){
    j<-which(i==is)
    XXDat[,,j]<-as.matrix(Data[c((i-(p-1)):i),-1])
    YY[,,j]<-XXDat[,1,j]
    for(l in 1:p){
      XX[l,((cis[l]-(nxs-1)):cis[l]),j]<-XXDat[l,-1,j]
    }
  }
  return(list(y=YY,X=XX))
}
Dat <- XcreateMP(p = p, nxs = nd, nind = n, Data = yX)
```

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

```r
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 algo-rithm using the *bayesm* package, particularly, the *rmvpGibbs* command.

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

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

```r
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,
       mean = Ylmean1, sd = t11^0.5)
37     }else{
38       Ylnew[i] <- truncnorm::rtruncnorm(1, a = -Inf, b = 0,
       mean = Ylmean1, sd = t11^0.5)
39     }
40     Ylmean2 <- Xnew[i+1,]%*%Beta + f2*(Ylnew[i] - Xnew[i,]%*
       %Beta)
41     if(y[i+1] == 1){
42       Ylnew[i+1] <- truncnorm::rtruncnorm(1, a = 0, b = Inf,
        mean = Ylmean2, sd = t22^0.5)
43     }else{
44       Ylnew[i+1] <- truncnorm::rtruncnorm(1, a = -Inf, b =
       0, mean = Ylmean2, sd = t22^0.5)
45     }
46   }
47   return(Ylnew)
48 }
```

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

```r
an <- a0 + n
Psi0i <- solve(Psi0)
K1 <- 4; K2 <- 3; K <- K1 + K2
tot <- mcmc + burnin
PostBetas <- matrix(0, tot, K)
PostSigmas <- matrix(0, tot, p*(p+1)/2)
Beta <- rep(1, K)
Sigma <- diag(p)
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  Yl <- PostYlNew(Beta = Beta, Sigma = Sigma, Yl = yl)
  Sigma <- PostSigmaNew(Beta = Beta, Yl = Yl)
  Beta <- PostBetaNew(Sigma = Sigma, Yl = Yl)
  PostBetas[s,] <- Beta
  PostSigmas[s,] <- matrixcalc::vech(Sigma)
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
Bs <- PostBetas[keep,]
betatilde1 <- Bs[,1:K1] / sqrt(PostSigmas[keep,1])
summary(coda::mcmc(betatilde1))
betatilde2 <- Bs[,(K1+1):(K1+K2)] / sqrt(PostSigmas[keep,3])
summary(coda::mcmc(betatilde2))
sigmadraw12 <-  PostSigmas[keep,2] / (PostSigmas[keep,1]*
    PostSigmas[keep,3])^0.5
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 $G_t = 1$, $t = 1, \ldots, 100$. 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 *dlm* package in **R**.

R code. Simulation: Scenarios signal-to-noise ratio
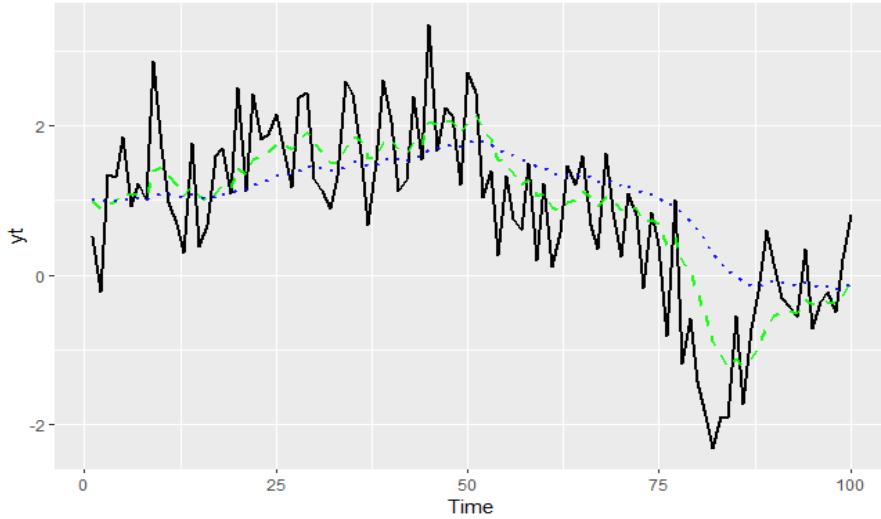
```
1  rm(list = ls()); set.seed(010101)
2  T <- 100; sig2 <- 0.5^2; r <- 0.5; sigW2 <- sig2*r
3  x <- rnorm(T, mean = 1, sd = 0.1*sig2^0.5)
4  e <- rnorm(T, mean = 0, sd = sig2^0.5)
5  w <- rnorm(T, mean = 0, sd = sigW2^0.5)
6  K <- 1
7  Bt <- matrix(NA, T, K); Bt[1] <- 1
8  yt <- rep(NA, T)
9  yt[1] <- 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
         [2]), m0 = rep(1, K),
21    C0 = sigW2*diag(K), addInt = FALSE)
22    return(Mod)
23 }
24 sig2New <- sig2*25
25 RegFilter1 <- dlm::dlmFilter(yt, ModelReg(c(sig2New, sig2New
         *0.5)))
26 ytfil1 <- RegFilter1[["m"]][-1]
27 RegFilter2 <- dlm::dlmFilter(yt, ModelReg(c(sig2New, sig2New
         *0.1)))
28 ytfil2 <- RegFilter2[["m"]][-1]
29 Time <- 1:T
30 df1 <- as.data.frame(cbind(Time,yt, ytfil1, ytfil2))
31 library(ggplot2)
32 ggplot(df1, aes(x=Time)) +
33 geom_line(aes(y=yt), colour="black", linewidth=1, linetype
         =1) +
34 geom_line(aes(y=ytfil1), colour="green", linewidth=1, alpha
         =0.9, linetype=2) +
35 geom_line(aes(y=ytfil2), color="blue", linewidth=1, alpha
         =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 $\sigma^2 = 1$, $t = 1, \ldots, 100$. 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

```r
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,
       Omega = sigW2, sig2 = sig2)
31   b0 <- KFrest[["bt"]]; B0 <- KFrest[["Bt"]]
32   KFresb[[t]] <- b0; KFresB[[t]] <- B0
33 }
34 ModelReg <- function(par){
35   Mod <- dlm::dlmModReg(xt, dV = exp(par[1]), dW = exp(par
       [2]), m0 = rep(0, K),
36   C0 = sigW2*diag(K), addInt = FALSE)
37   return(Mod)
38 }
39 RegFilter1 <- dlm::dlmFilter(yt, ModelReg(c(sig2, sigW2)))
40 plot(Bt, type = "l")
41 lines(unlist(KFresb), type = "l", col = "red")
42 lines(RegFilter1[["m"]][-1], type = "l", col = "blue")
```

> ### *R code. Simulation: Filtering and smoothing recursions from scratch*
>
> ```r
> # Smoothing
> BSR <- function(b, B, slead, Slead, Omega){
>   b = bfilter[t]; B = Bfilter[t]; slead = slead; Slead =
>     slead; Omega = sigW2
>   R1 <- B + Omega
>   s <- b + B%*%solve(R1)%*%(slead - b)
>   S <- B - B%*%solve(R1)%*%(R1 - Slead)%*%solve(R1)%*%B
>   Result <- list(st = s, St = S)
>   return(Result)
> }
> bfilter <- unlist(KFresb); Bfilter <- unlist(KFresB)
> slead <- bfilter[T]; Slead <- Bfilter[T]
> smooth <- rep(slead, T); Smooth <- rep(Slead, T);
> for(t in (T-1):1){
>   BSRrest <- BSR(b = bfilter[t], B = Bfilter[t], slead =
>     slead, Slead = Slead, Omega = sigW2)
>   slead <- BSRrest[["st"]]; Slead <- BSRrest[["st"]]
>   smooth[t] <- slead
> }
> RegSmoth <- dlm::dlmSmooth(yt, ModelReg(c(sig2, sigW2)))
> VarSmooth <- dlm::dlmSvd2var(u = RegSmoth[["U.S"]], RegSmoth
>     [["D.S"]])
> SDVarSmoothB2 <- sapply(2:(T+1), function(t){VarSmooth[[t]][
>     K,K]^0.5})
> plot(Bt, type = "l")
> lines(smooth, type = "l", col = "orange")
> lines(RegSmoth[["s"]][-1], type = "l", col = "green")
> ```

3. Simulate the process $y_t = \alpha z_t + \beta_t x_t + \boldsymbol{h}^\top \boldsymbol{\epsilon}_t$, $\beta_t = \beta_{t-1} + \boldsymbol{H}^\top \boldsymbol{\epsilon}_t$, where $\boldsymbol{h}^\top = [1\ 0]$, $\boldsymbol{H}^\top = [0\ 1/\tau]$, $\boldsymbol{v}_t \sim N(\boldsymbol{0}_2, \sigma^2 \boldsymbol{I}_2)$, $x_t \sim N(1, 2\sigma^2)$, $z_t \sim N(0, 2\sigma^2)$, $\alpha = 2$, $\tau^2 = 5$ and $\sigma^2 = 0.1$, $t = 1, \ldots, 200$. 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

```r
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

```r
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 <- txtProgressBar(min = 0, max = tot, style = 3)
```

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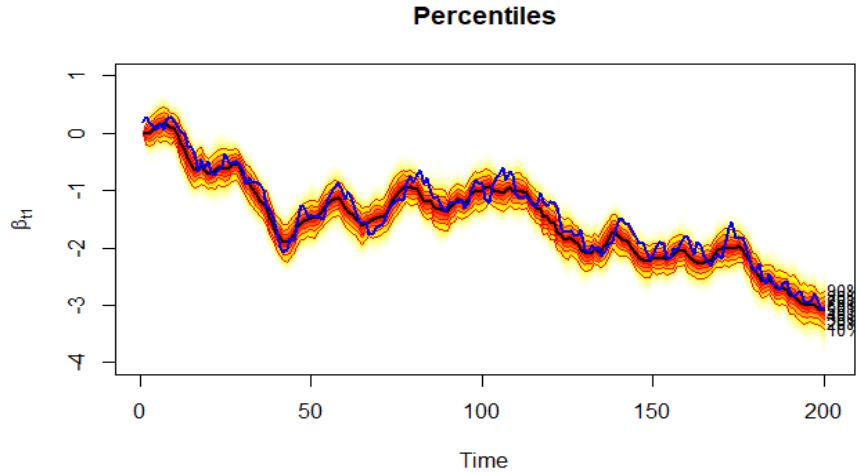
```r
1  for (s in 1:tot){
2    b0 <- 0; B0 <- sigW2
3    KFDSresb <- list(); KFDSresB <- list()
4    KFDSresE <- list(); KFDSresK <- list(); KFDSresQ <- list()
5    for(t in 1:T){
6      KFDSrest <- KFRDSnew(y = yt[t], z = zt[t], x = xt[t], b
       = b0, B = B0, alpha = alphapost, tau2 = tau2post)
7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

Percentiles

FIGURE 8.2
State vector: Dynamic linear model.

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

Answer

The conditional posterior distribution can be got as follows:

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

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

last expression is the kernel of a multivariate normal distribution with mean $\boldsymbol{\phi}_n$ and variance matrix $\boldsymbol{\Phi}_n$.

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 $Var[Y_t] = \frac{\sigma^2(1-\phi_2)}{1-\phi_2-\phi_1^2-\phi_1^2\phi_2-\phi_2^2+\phi_2^3}$.

Answer

A necessary condition to achieve second-order stationarity in the $AR(2)$ process is that roots of 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 $\gamma_0 = \frac{\sigma^2(1-\phi_2)}{1-\phi_2-\phi_1^2-\phi_1^2\phi_2-\phi_2^2+\phi_2^3}$.

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

```r
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[
       t-2], sd = sig2^0.5, log = TRUE)
18     logLik <- c(logLik, logLikt)
19   }
20   logLik <- sum(logLik)
21   logPrior <- dnorm(mu, mean = mu0, sd = MU0^0.5, log = TRUE
       ) + dnorm(phi1, mean = phi0[1], sd = Phi0[1,1]^0.5, log
       = TRUE) + dnorm(phi2, mean = phi0[2], sd = Phi0
       [2,2]^0.5, log = TRUE) + invgamma::dinvgamma(sig2, shape
       = a0/2, rate = d0/2, log = TRUE)
22   logPosterior <- logLik + logPrior + tau
23   return(-logPosterior) # Multiply by -1 to minimize using
       optim
24 }
25 theta0 <- c(mean(y), 0, 0, var(y))
26 Opt <- optim(theta0, LogPost, y = y, hessian = TRUE)
27 theta0 <- Opt$par; VarPost <- solve(Opt$hessian)
28 # Gradient log posterior
29 GradientTheta <- function(theta, y){
30   mu <- theta[1]; phi1 <- theta[2]; phi2 <- theta[3]
31   tau <- theta[4]; sig2 <- exp(tau); SumLik <- matrix(0, 3,
       1)
32   SumLik2 <- NULL
33   for(t in 3:T){
34     xt <- matrix(c(1, y[t-1], y[t-2]), 3, 1)
35     SumLikt <- (y[t] - (mu + phi1*y[t-1] + phi2*y[t-2]))*xt
36     SumLik2t <- (y[t] - (mu + phi1*y[t-1] + phi2*y[t-2]))^2
37     SumLik <- rowSums(cbind(SumLik, SumLikt))
38     SumLik2 <- sum(SumLik2, SumLik2t)
39   }
40   Grad_mu <- SumLik[1]/sig2 - (1/MU0)*(mu - mu0)
41   Grad_phi1 <- SumLik[2]/exp(tau) - 1/Phi0[1,1]*(phi1 - phi0
       [1])
42   Grad_phi2 <- SumLik[3]/exp(tau) - 1/Phi0[2,2]*(phi2 - phi0
       [2])
43   Grad_tau <- -(T-2)/2 + SumLik2/(2*exp(tau)) - (a0/2 + 1) +
       d0/(2*exp(tau)) + 1
44   Grad <- c(Grad_mu, Grad_phi1, Grad_phi2, Grad_tau)
45   return(Grad)
46 }
```

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

```r
StatRest <- function(phi1, phi2){
  if(abs(phi2) < 1 & phi1 + phi2 < 1 & phi2 - phi1 < 1){
    check <- 1
  }else{
    check <- 0
  }
  return(check)
}
HMC <- function(theta, y, epsilon, M){
  L <- ceiling(1/epsilon)
  Minv <- solve(M)
  thetat <- theta
  K <- length(thetat)
  mom <- t(mvtnorm::rmvnorm(1, rep(0, K), M))
  logPost_Mom_t <- -LogPost(thetat, y) +  mvtnorm::dmvnorm(t
    (mom), rep(0, K), M, log = TRUE)
  for(l in 1:L){
    if(l == L){
      mom <- mom + 0.5*epsilon*GradientTheta(theta, y)
      theta <- theta + epsilon*Minv%*%mom
    }else{
      mom <- mom + epsilon*GradientTheta(theta, y)
      theta <- theta + epsilon*Minv%*%mom
    }
  }
  logPost_Mom_star <- -LogPost(theta, y) +  mvtnorm::dmvnorm
    (t(mom), rep(0, K), M, log = TRUE)
  alpha <- min(1, exp(logPost_Mom_star-logPost_Mom_t))
  u <- runif(1)
  if(u <= alpha & StatRest(phi1 = theta[2], phi2 = theta[3])
     == 1){
    thetaNew <- c(theta)
  }else{
    thetaNew <- thetat
  }
  rest <- list(theta = thetaNew, Prob = alpha)
  return(rest)
}
```

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

```r
1  # Posterior draws
2  S <- 1000; burnin <- 1000; thin <- 2; tot <- S + burnin
3  thetaPost <- matrix(NA, tot, K)
4  ProbAcept <- 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 <- txtProgressBar(min = 0, max = tot, style = 3)
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    ProbAcept[s] <- HMCs$Prob
16    setTxtProgressBar(pb, s)
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  ProbAceptF <- coda::mcmc(ProbAcept[keep])
26  summary(ProbAceptF)
```

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
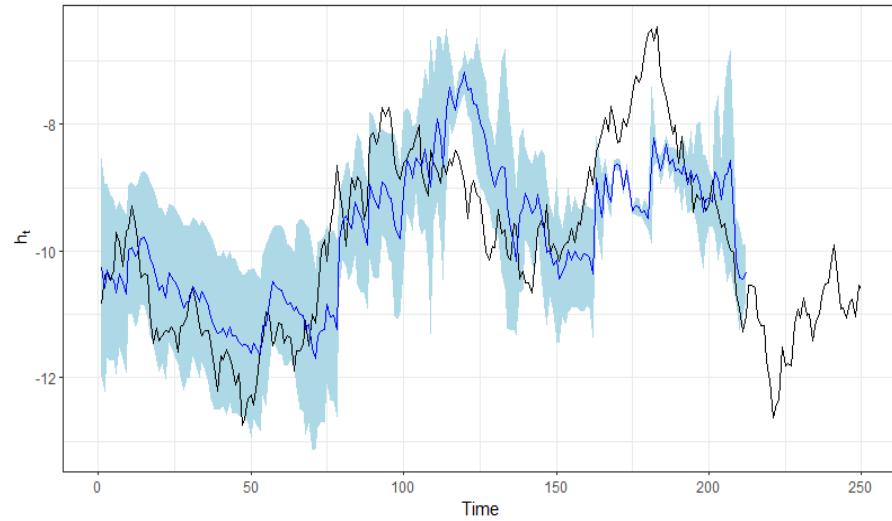
We observe that, initially, sequential importance sampling performs relatively well. However, particle degeneracy occurs around ($t = 50$), causing the algorithm's performance to deteriorate rapidly (see Figure 8.3). We can see in Figure 8.4 how the effective sample size (ESS) of the particles decreases rapidly.

### R code. Stochastic volatility model: Sequential importance sampling
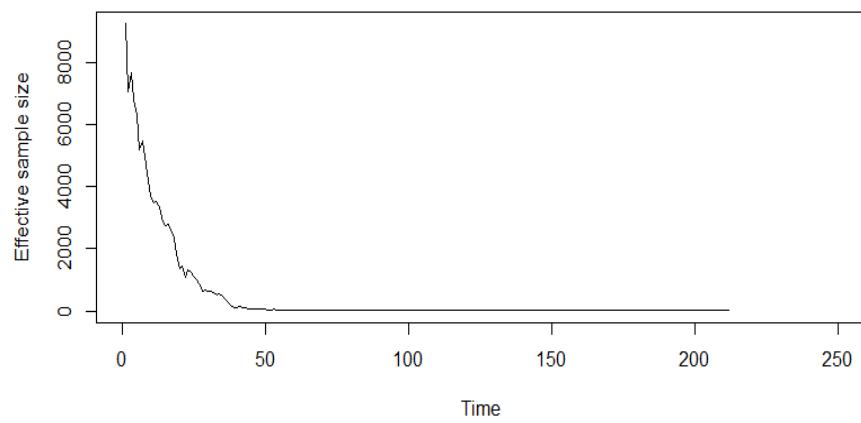
```r
1  rm(list = ls()); set.seed(010101)
2  T <- 250; K <- 2; mu <- -10; phi <- 0.95; sigma <- 0.3
3  h <- numeric(T); y <- numeric(T)
4  h[1] <- rnorm(1, mu, sigma / sqrt(1 - phi^2))
5  y[1] <- rnorm(1, 0, exp(h[1] / 2))
6  for (t in 2:T) {
7    h[t] <- mu + phi*(h[t-1]-mu) + rnorm(1, 0, sigma)
8    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 es 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

```r
rm(list = ls()); set.seed(010101)
T <- 1250; mu <- -10; phi <- 0.95; sigma <- 0.3
h <- numeric(T); y <- numeric(T)
h[1] <- rnorm(1, mu, sigma / sqrt(1 - phi^2))
y[1] <- rnorm(1, 0, exp(h[1] / 2))
for (t in 2:T) {
  h[t] <- mu + phi*(h[t-1]-mu) + rnorm(1, 0, sigma)
  y[t] <- rnorm(1, 0, sd = exp(0.5*h[t]))
}
N <- 10000
log_Weights <- matrix(NA, N, T)  # Log weights
Weights <- matrix(NA, N, T)  # Weights
WeightsST <- matrix(NA, N, T)  # Normalized weights
WeightsSTT <- matrix(1/N, N, T)  # Normalized weights bar
particles <- matrix(NA, N, T)   # Particles
particlesT <- matrix(NA, N, T)   # Particles bar
logalphas <- matrix(NA, N, T)   # Incremental import. weig.
ESS <- rep(NA, T) # Efective sample size
cutoff <- 0.5
particles[, 1] <- rnorm(N, mu, sigma / sqrt(1 - phi^2))
log_Weights[, 1] <- dnorm(y[1], 0, sd = exp(0.5*particles
    [,1]), log = TRUE)
Weights[, 1] <- exp(log_Weights[, 1])
WeightsST[, 1] <- Weights[, 1] / sum(Weights[, 1])
ESS[1] <- (sum(WeightsST[, 1]^2))^(-1)
ind <- sample(1:N, size = N, replace = TRUE, prob =
    WeightsST[, 1]) # Resample
particles[, 1] <- particles[, 1] # Resampled particles
particlesT[, 1] <- particles[ind, 1] # Resampled particles
WeightsST[, 1] <- rep(1/N, N) # Resampled weights
pb <- txtProgressBar(min = 0, max = T, style = 3)
for (t in 2:T) {
  particles[, t] <- rnorm(N, mu + phi*(particles[, t - 1] -
    mu), sigma)  # Sample from proposal
  logalphas[, t] <- dnorm(y[t], 0, sd = exp(0.5*particles[,t
    ]), log = TRUE)
  Weights[, t] <- exp(logalphas[, t])
  WeightsST[, t] <- Weights[, t] / sum(Weights[, t])
  ESS[t] <- (sum(WeightsST[, t]^2))^(-1)
  particlesT[, t] <- particles[, t]
  if(ESS[t] < N*cutoff){
    ind <- sample(1:N, size = N, replace = TRUE, prob =
    WeightsST[, t])
    particles[, 1:t] <- particles[ind, 1:t]
    WeightsST[, t] <- 1/N
  }else{if(t == T & ESS[t] < N*cutoff)
    ind <- sample(1:N, size = N, replace = TRUE, prob =
    WeightsST[, t])
    particlesT[, 1:t] <- particles[ind, 1:t]
  }
  setTxtProgressBar(pb, t)
}
close(pb)
```

R code. Stochastic volatility model: Sequential Monte Carlo
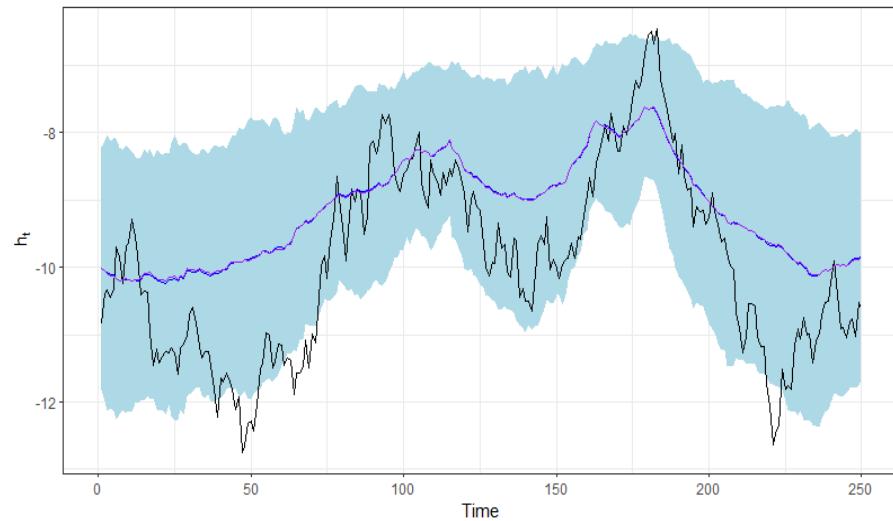
```
1  FilterDist <- colSums(particles * WeightsST)
2  SDFilterDist <- (colSums(particles^2 * WeightsST) -
       FilterDist^2)^0.5
3  FilterDistT <- colSums(particlesT * WeightsSTT)
4  SDFilterDistT <- (colSums(particlesT^2 * WeightsSTT) -
       FilterDistT^2)^0.5
5  MargLik <- colMeans(Weights)
6  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   geom_line(aes(y = meanT), colour = "purple", linewidth =
       0.5) +
30   ylab(TeX("$h_{t}$")) + xlab("Time")
31   print(p)
32 }
33 plot_filtering_estimates(df)
```

8. Estimate the vanilla stochastic volatility model using the dataset *17Ex-cRate.csv* provided by [35] 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
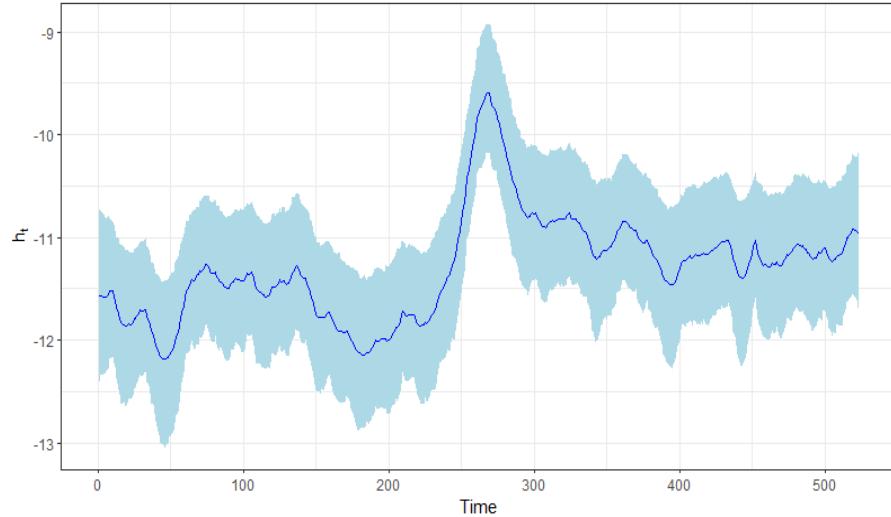
```
1  rm(list = ls()); set.seed(010101)
2  DataExcRate <- read.csv("https://raw.githubusercontent.com/
       besmarter/BSTApp/refs/heads/master/DataApp/17ExcRate.csv
       ", sep = ",", header = TRUE, quote = "")
3  attach(DataExcRate)
4  MCMC <- 10000; burnin <- 10000; thin <- 5
5  y <- USDEUR - 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   ylab(TeX("$h_{t}$")) + xlab("Time")
42   print(p)
43 }
44 plot_filtering_estimates(df)
```

FIGURE 8.6
Stochastic volatility model: Exchange rate log daily returns from USD/EUR.

9. Simulate the VAR(1) process

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

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

- Use vague independent priors setting $\boldsymbol{\beta}_0 = \mathbf{0}$, $\boldsymbol{B}_0 = 100\boldsymbol{I}$, $\boldsymbol{V}_0 = 5\boldsymbol{I}$ 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 $\boldsymbol{\Phi}_s = \sum_{l=1}^{s} \boldsymbol{\Phi}_{s-l} \boldsymbol{A}_l$, $\boldsymbol{A}_l = \mathbf{0}$, $l > p$ and $s = 1, 2, ..$, we get $\boldsymbol{\Phi}_s = \boldsymbol{A}_1^s$. In addition, we know that $\boldsymbol{\Theta}_s = \boldsymbol{\Phi}_S \boldsymbol{P}$. 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 $\boldsymbol{\Sigma}$, 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  U <- MASS::mvrnorm(T, rep(0, M), SIGMA)
5  A <- matrix(c(0.5, 0.1, 0, 0, 0.1, 0.2, 0, 0.3, 0.3), M, M )
6  v <- c(1.4, 1.9, 1.1); Y <- matrix(NA, T, M)
7  Y[1, ] <- solve(diag(M)-A)%*%v + U[1,]
8  for(t in 2:T){
9    Y[t, ] <- v + A%*%Y[t-1,] + U[t,]
10 }
11 plot(Y[,1], type = "l"); plot(Y[,2], type = "l"); plot(Y
       [,3], type = "l")
12 y1 <- Y[-1,1]; y2 <- Y[-1,2]; y3 <- Y[-1,3]
13 X1 <- cbind(1, lag(Y)); X1 <- X1[-1,]
14 X2 <- cbind(1, lag(Y)); X2 <- X2[-1,]
15 X3 <- cbind(1, lag(Y)); X3 <- X3[-1,]
16 regdata <- NULL
17 regdata[[1]] <- list(y = y1, X = X1); regdata[[2]] <- list(y
       = y2, X = X2); regdata[[3]] <- list(y = y3, X = X3)
18 M <- length(regdata); K1 <- dim(X1)[2]; K2 <- dim(X2)[2]; K3
       <- dim(X3)[2]
19 K <- K1 + K2 + K3
20 # Hyperparameters
21 b0 <- rep(0, K); c0 <- 100
22 B0 <- c0*diag(K); V <- 5*diag(M); a0 <- M
23 Prior <- list(betabar = b0, A = solve(B0), nu = a0, V = V)
24 #Posterior draws
25 MCMC <- 10000; thin <- 5; burnin <- 1000; tot <- MCMC +
       burnin
26 Mcmc <- list(R = tot, keep = thin)
27 PosteriorDraws <- bayesm::rsurGibbs(Data = list(regdata =
       regdata), Mcmc = Mcmc, Prior = Prior)
28 keep <- seq(round(burnin/thin)+1, round(tot/thin))
29 Bs <- PosteriorDraws[["betadraw"]][keep,]
30 SIGMAs <- PosteriorDraws[["Sigmadraw"]][keep,]
31 S <- dim(Bs)[1]
32 As <- array(NA, c(M, M, S))
33 for(s in 1:S){
34   As[,,s] <- matrix(Bs[s, -c(1, 5, 9)], M, M, byrow = TRUE)
35 }
36 # Impulse response functions
37 H <- 10; Ptrue <- t(chol(SIGMA))
38 Phistrue <-  array(NA, c(M, M, H))
39 Phistrue[,,1] <- diag(M); PhistrueAccum <-  Phistrue
40 PhistrueAccum[,,1] <- diag(M)
41 Thetastrue <- Phistrue; Thetastrue[,,1] <- Ptrue
42 ThetastrueAccum <-  Thetastrue; ThetastrueAccum[,,1] <-
       Ptrue
43 for(h in 2:H){
44   Phistrue[,,h] <- Phistrue[,,h-1]%*%A
45   PhistrueAccum[,,h] <- PhistrueAccum[,,h-1] + Phistrue[,,h]
46   Thetastrue[,,h] <- Phistrue[,,h]%*%Ptrue
47   PhistrueAccum[,,h] <- ThetastrueAccum[,,h-1] + Thetastrue
       [,,h]
48 }
49 P <- array(NA, c(M, M, S))
```

R code. Vector autoregressive model: Simulation

```r
for(s in 1:S){
  P[,,s] <- t(chol(matrix(SIGMAs[s,], M, M)))
}
Phis <- list(); PhisAcum <- list()
Thetas <- list(); ThetasAcum <- list()
for(h in 0:H){
  if(h == 0){
    Phis[[h+1]] <- array(diag(M), c(M,M,S))
    Thetas <- Phis
    for(s in 1:S){
      Thetas[[h+1]][,,s] <- Phis[[h+1]][,,s]%*%P[,,s]
    }
    PhisAcum[[h+1]] <- Phis[[h+1]]
    ThetasAcum[[h+1]] <- Thetas[[h+1]]
  }else{
    Phis[[h+1]] <- array(diag(M), c(M,M,S))
    Thetas[[h+1]] <- Phis[[h+1]]
    for(s in 1:S){
      Phis[[h+1]][,,s] <- Phis[[h]][,,s]%*%As[,,s]
      Thetas[[h+1]][,,s] <- Phis[[h+1]][,,s]%*%P[,,s]
    }
    PhisAcum[[h+1]] <- PhisAcum[[h]] + Phis[[h+1]]
    ThetasAcum[[h+1]] <- ThetasAcum[[h]] + Thetas[[h+1]]
  }
}
library(dplyr); library(ggplot2); require(latex2exp)
ggplot2::theme_set(theme_bw())
plot_filtering_estimates <- function(df) {
  p <- ggplot(data = df, aes(x = t)) +
  geom_ribbon(aes(ymin = lower1, ymax = upper1), alpha = 1,
  fill = "blue") +
  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)
    +
  ylab("Impulse response") + xlab("Time") + xlim(0,H-1)
  print(p)
}
```
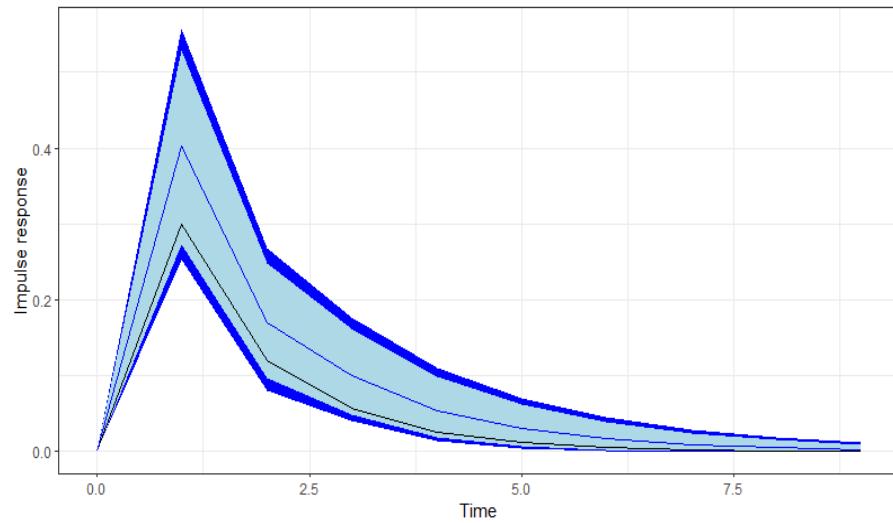
R code. Vector autoregressive model: Simulation

```r
IR <- function(m, j, Accumulated = "FALSE", Type = "Ordinary
    "){
  if(Type == "Cholesky"){
    IRtrue <- Thetastrue[m,j,]
    if(Accumulated == FALSE){
      RES <- Thetas; IRtrue <- IRtrue
    }else{
      RES <- ThetasAcum; IRtrue <- cumsum(IRtrue)
    }
    Mean <- sapply(1:H, function(h){mean(RES[[h]][m,j,])})
    LimInf1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.025)})
    LimSup1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.975)})
    LimInf <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.05)})
    LimSup <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.95)})
  }else{
    IRtrue <- Phistrue[m,j,]
    if(Accumulated == FALSE){
      RES <- Phis; IRtrue <- IRtrue
    }else{
      RES <- PhisAcum; IRtrue <- cumsum(IRtrue)
    }
    Mean <- sapply(1:H, function(h){mean(RES[[h]][m,j,])})
    LimInf1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.025)})
    LimSup1 <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.975)})
    LimInf <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.05)})
    LimSup <- sapply(1:H, function(h){quantile(RES[[h]][m,j
      ,], 0.95)})
  }
  df <- tibble(t = 0:(H-1), mean = Mean, lower1 = LimInf1,
    upper1 = LimSup1, lower = LimInf, upper = LimSup, x_true
     = IRtrue)
  Fig <- plot_filtering_estimates(df)
  return(Fig)
}
m <- 2; j <- 3
IR(m,j, Accumulated = "FALSE", Type = "Cholesky")
Ynew <- ts(Y)
model <- bvartools::gen_var(Ynew, p = 1, deterministic = "
    const", iterations = MCMC, burnin = burnin) # Model
model <- bvartools::add_priors(model, coef = list(v_i = b0
    [1], v_i_det = b0[1]), sigma = list(df = a0, scale = V
    [1,1]/a0)) # Prior
object <- bvartools::draw_posterior(model) # Pposterior
ir <- bvartools::irf.bvar(object, impulse = "Series 2",
    response = "Series 3") # Calculate IR
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 $\boldsymbol{\beta}|\sigma^2, \boldsymbol{D}$ is $N(\boldsymbol{\beta}_n, \boldsymbol{B}_n)$, where $\boldsymbol{B}_n = (\boldsymbol{B}_0^{-1} + \sum_{i=1}^N \boldsymbol{X}_i^\top \boldsymbol{V}_i^{-1} \boldsymbol{X}_i)^{-1}$ and $\boldsymbol{\beta}_n = \boldsymbol{B}_n(\boldsymbol{B}_0^{-1}\boldsymbol{\beta}_0 + \sum_{i=1}^N \boldsymbol{X}_i^\top \boldsymbol{V}_i^{-1}\boldsymbol{y}_i)$.

Answer

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

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

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

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

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 $\boldsymbol{\beta}_0 = \mathbf{0}_5$, $\boldsymbol{B}_0 = \boldsymbol{I}_5$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 5$ and $\boldsymbol{D}_0 = \boldsymbol{I}_1$.

- 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

```r
rm(list = ls())
set.seed(12345)
DataGSP <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/8PublicCap.
    csv", sep = ",", header = TRUE, quote = "")
attach(DataGSP)
N <- length(unique(id))
y <- log(gsp)
NT <- length(y)
X <- cbind(1, log(pcap), log(pc), log(emp), unemp)
K1 <- dim(X)[2]
W <- matrix(rep(1, NT), NT, 1)
K2 <- dim(W)[2]
mcmc <- 10000; burnin <- 5000; thin <- 1; tot <- mcmc +
    burnin
b0 <- rep(0, K1); B0 <- diag(K1); B0i <- solve(B0)
r0 <- 5; R0 <- diag(K2); a0 <- 0.001; d0 <- 0.001
PostBeta <- function(sig2, D){
  XVX <- matrix(0, K1, K1)
  XVy <- matrix(0, K1, 1)
  for(i in 1:N){
    ids <- which(id == i)
    Ti <- length(ids)
    Wi <- W[ids, ]
    Vi <- sig2*diag(Ti) + Wi%*%D%*%t(Wi)
    ViInv <- solve(Vi)
    Xi <- X[ids, ]
    XVXi <- t(Xi)%*%ViInv%*%Xi
    XVX <- XVX + XVXi
    yi <- y[ids]
    XVyi <- t(Xi)%*%ViInv%*%yi
    XVy <- XVy + XVyi
  }
  Bn <- solve(B0i + XVX)
  bn <- Bn%*%(B0i%*%b0 + XVy)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
```

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

```r
Postb <- function(Beta, sig2, D){
  Di <- solve(D)
  bis <- matrix(0, N, K2)
  for(i in 1:N){
    ids <- which(id == i)
    Wi <- W[ids, ]
    Xi <- X[ids, ]
    yi <- y[ids]
    Wtei <- sig2^(-1)*t(Wi)%*%(yi - Xi%*%Beta)
    Bni <- solve(sig2^(-1)*t(Wi)%*%Wi + Di)
    bni <- Bni%*%Wtei
    bi <- MASS::mvrnorm(1, bni, Bni)
    bis[i, ] <- bi
  }
  return(as.matrix(bis))
}
PostSig2 <- function(Beta, bs){
  an <- a0 + 0.5*NT
  ete <- 0
  for(i in 1:N){
    ids <- which(id == i)
    Xi <- X[ids, ]
    yi <- y[ids]
    Wi <- W[ids, ]
    ei <- yi - Xi%*%Beta - Wi*bs[i, ]
    etei <- t(ei)%*%ei
    ete <- ete + etei
  }
  dn <- d0 + 0.5*ete
  sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
  return(sig2)
}
PostD <- function(bs){
  rn <- r0 + N
  btb <- matrix(0, K2, K2)
  for(i in 1:N){
    bsi <- bs[i, ]
    btbi <- bsi%*%t(bsi)
    btb <- btb + btbi
  }
  Rn <- d0*R0 + btb
  Sigma <- MCMCpack::riwish(v = rn, S = Rn)
  return(Sigma)
}
```

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

```r
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 <- txtProgressBar(min = 0, max = tot, style = 3)
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   setTxtProgressBar(pb, s)
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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```r
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     taui <- tau[ids]
24     Vi <- sig2*solve(diag(1/taui)) + 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

```r
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]; taui <- tau[ids]
7      Taui <- solve(diag(1/taui))
8      Wtei <- sig2^(-1)*t(Wi)%*%Taui%*%(yi - Xi%*%Beta)
9      Bni <- solve(sig2^(-1)*t(Wi)%*%Taui%*%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, ]; taui <- tau[ids]
22     Taui <- solve(diag(1/taui))
23     ei <- yi - Xi%*%Beta - Wi*bs[i]
24     etei <- t(ei)%*%Taui%*%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

```r
PostBetas <- matrix(0, tot, K1); PostDs <- matrix(0, tot, K2
    *(K2+1)/2)
PostSig2s <- rep(0, tot); Postbs <- array(0, c(N, K2, tot))
PostTaus <- matrix(0, tot, NT); RegLS <- lm(y ~ X - 1)
SumLS <- summary(RegLS); Beta <- SumLS[["coefficients"]][,1]
sig2 <- SumLS[["sigma"]]^2; D <- diag(K2)
tau <- rgamma(NT, shape = v/2, rate = v/2)
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  bs <- Postb(Beta = Beta, sig2 = sig2, D = D, tau = tau)
  D <- PostD(bs = bs)
  Beta <- PostBeta(sig2 = sig2, D = D, tau = tau)
  sig2 <- PostSig2(Beta = Beta, bs = bs, tau = tau)
  tau <- PostTau(sig2 = sig2, Beta = Beta, bs = bs)
  PostBetas[s,] <- Beta
  PostDs[s,] <- matrixcalc::vech(D)
  PostSig2s[s] <- sig2
  Postbs[, , s] <- bs
  PostTaus[s,] <- tau
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
Bs <- PostBetas[keep,]
Ds <- PostDs[keep,]
bs <- Postbs[, , keep]
sig2s <- PostSig2s[keep]
taus <- PostTaus[keep,]
summary(coda::mcmc(Bs))
Quantiles for each variable:
          2.5%        25%        50%        75%       97.5%
var1   1.61764   1.891242   2.029985   2.165677   2.427349
var2  -0.07088  -0.016921   0.013080   0.044681   0.107360
var3   0.27259   0.312197   0.333106   0.353678   0.395123
var4   0.59507   0.664490   0.699526   0.734612   0.796977
var5  -0.01046  -0.008533  -0.007586  -0.006666  -0.004918
summary(coda::mcmc(Ds))
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 $x_{itk} \sim N(0,1)$, $k = 1,2,3$, $z_{i1} \sim B(0.5)$, $w_{it1} \sim N(0,1)$, $b_i \sim N(0, 0.7^{1/2})$, $b_{i1} \sim N(0, 0.6^{1/2})$, $\mu_{it} \sim N(0, 0.1^{1/2})$ $\boldsymbol{\beta} = [0.4\ 0.6\ -0.6\ 0.7]^\top$,

$i = 1, 2, \ldots, 50$, and the sample size is 2000 in an *unbalanced panel structure*. In addition, we assume that $\boldsymbol{b}_i$ dependents on $\boldsymbol{z}_i = \begin{bmatrix} 1 & z_{i1} \end{bmatrix}^\top$ such that $\boldsymbol{b}_i \sim N(\boldsymbol{Z}_i\boldsymbol{\gamma}, \boldsymbol{D})$ where $\boldsymbol{Z}_i = \boldsymbol{I}_{K_2} \otimes \boldsymbol{z}_i^\top$, and $\boldsymbol{\gamma} = \begin{bmatrix} 1 & 1 & 1 & 1 \end{bmatrix}$. The prior for $\boldsymbol{\gamma}$ is $N(\boldsymbol{\gamma}_0, \boldsymbol{\Gamma}_0)$ where we set $\boldsymbol{\gamma}_0 = \boldsymbol{0}_4$ and $\boldsymbol{\Gamma}_0 = \boldsymbol{I}_4$. In addition, Set $\boldsymbol{\beta}_0 = \boldsymbol{0}_4$, $\boldsymbol{B}_0 = \boldsymbol{I}_4$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 2$ and $\boldsymbol{D}_0 = \boldsymbol{I}_2$.

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

- Perform inference in this model taking into account the dependence between $\boldsymbol{b}_i$ 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

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

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

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

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

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

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

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

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

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

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

The following code shwos 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, $\boldsymbol{\beta}_0 = \boldsymbol{0}_5$, $\boldsymbol{B}_0 = \boldsymbol{I}_5$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 2$, $\boldsymbol{D}_0 = \boldsymbol{I}_2$, $\boldsymbol{\gamma}_0 = \boldsymbol{0}_4$ and $\boldsymbol{\Gamma}_0 = \boldsymbol{I}_4$.

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

```r
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

```r
PostBeta <- function(sig2, Gamma, D){
  XVX <- matrix(0, K1, K1)
  XVy <- matrix(0, K1, 1)
  for(i in 1:N){
    ids <- which(id == i)
    Ti <- length(ids)
    Wi <- W[ids, ]
    Vi <- sig2*diag(Ti) + Wi%*%D%*%t(Wi)
    ViInv <- solve(Vi)
    Xi <- X[ids, ]
    XVXi <- t(Xi)%*%ViInv%*%Xi
    XVX <- XVX + XVXi
    Zi <- Z[i, ]
    yi <- y[ids]
    ZGi <- t(kronecker(diag(K2), Zi))%*%Gamma
    XVyi <- t(Xi)%*%ViInv%*%(yi - Wi%*%ZGi)
    XVy <- XVy + XVyi
  }
  Bn <- solve(B0i + XVX)
  bn <- Bn%*%(B0i%*%b0 + XVy)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
Postb <- function(Beta, sig2, Gamma, D){
  Di <- solve(D)
  bis <- matrix(0, N, K2)
  for(i in 1:N){
    ids <- which(id == i)
    Wi <- W[ids, ]
    Xi <- X[ids, ]
    yi <- y[ids]
    Wtei <- sig2^(-1)*t(Wi)%*%(yi - Xi%*%Beta)
    Bni <- solve(sig2^(-1)*t(Wi)%*%Wi + Di)
    Zi <- Z[i, ]
    ZGi <- t(kronecker(diag(K2), Zi))%*%Gamma
    bni <- Bni%*%(Wtei + Di%*%ZGi)
    bi <- MASS::mvrnorm(1, bni, Bni)
    bis[i, ] <- bi
  }
  return(bis)
}
PostSig2 <- function(Beta, bs){
an <- a0 + 0.5*NT
ete <- 0
for(i in 1:N){
  ids <- which(id == i)
  Xi <- X[ids, ]
  yi <- y[ids]
  Wi <- W[ids, ]
  ei <- yi - Xi%*%Beta - Wi%*%bs[i, ]
  etei <- t(ei)%*%ei
  ete <- ete + etei
}
dn <- d0 + 0.5*ete
sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
return(sig2)
}
```

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

```r
PostGamma <- function(bs, D){
  Di <- solve(D)
  ZDZ <- matrix(0, K2*K3, K2*K3)
  ZDb <- matrix(0, K2*K3, 1)
  for(i in 1:N){
    Zi <- Z[i, ]
    ZZi <- t(kronecker(diag(K2), Zi))
    ZDZi <- t(ZZi)%*%Di%*%ZZi
    ZDZ <- ZDZ + ZDZi
    bi <- bs[i,]
    ZDbi <- t(ZZi)%*%Di%*%bi
    ZDb <- ZDb + ZDbi
  }
  Gn <- solve(G0i + ZDZ); gn <- Gn%*%(G0i%*%g0 + ZDb)
  Gamma <- MASS::mvrnorm(1, gn, Gn)
  return(Gamma)
}
PostD <- function(bs, Gamma){
  rn <- r0 + N
  btb <- matrix(0, K2, K2)
  for(i in 1:N){
    bsi <- bs[i, ]
    Zi <- Z[i, ]
    ZGi <- t(kronecker(diag(K2), Zi))%*%Gamma
    btbi <- (bsi-ZGi)%*%t(bsi-ZGi)
    btb <- btb + btbi
  }
  Rn <- d0*R0 + btb
  Sigma <- MCMCpack::riwish(v = rn, S = Rn)
  return(Sigma)
}
PostBetas <- matrix(0, tot, K1); PostGammas <- matrix(0, tot
    , K2*K3)
PostDs <- matrix(0, tot, K2*(K2+1)/2); PostSig2s <- rep(0,
    tot)
Postbs <- array(0, c(N, K2, tot)); RegLS <- lm(y ~ X - 1)
SumLS <- summary(RegLS); Beta <- SumLS[["coefficients"]][,1]
sig2 <- SumLS[["sigma"]]^2; Gamma <- rep(0, K2*K3)
D <- diag(K2); b0 <- rep(0, K1); B0 <- diag(K1); B0i <-
    solve(B0)
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  bs <- Postb(Beta = Beta, sig2 = sig2, Gamma = Gamma, D = D
    )
  D <- PostD(bs = bs, Gamma = Gamma)
  Beta <- PostBeta(sig2 = sig2, Gamma = Gamma, D = D)
  sig2 <- PostSig2(Beta = Beta, bs = bs)
  Gamma <- PostGamma(bs = bs, D = D)
  PostBetas[s,] <- Beta; PostDs[s,] <- matrixcalc::vech(D)
  PostSig2s[s] <- sig2; Postbs[, , s] <- bs
  PostGammas[s,] <- Gamma
  setTxtProgressBar(pb, s)
}
```

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 $x_{itk} \sim N(0,1)$, $k = 1, 2, 3$, $w_{it1} \sim N(0,1)$, $b_i \sim N(0, 0.7^{1/2})$, $b_{i1} \sim N(0, 0.6^{1/2})$, $\boldsymbol{\beta} = [0.5\ 0.4\ 0.6\ -0.6]^\top$, $i = 1, 2, \ldots, 50$, 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 $\boldsymbol{\beta}_0 = \mathbf{0}_4$, $\boldsymbol{B}_0 = \boldsymbol{I}_4$, $\alpha_0 = \delta_0 = 0.001$, $d_0 = 2$ and $\boldsymbol{D}_0 = \boldsymbol{I}_2$.

- 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

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

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

```r
1  PostD <- function(bs){
2    rn <- r0 + N
3    btb <- matrix(0, K2, K2)
4    for(i in 1:N){
5      bsi <- bs[i, ]; btbi <- bsi%*%t(bsi)
6      btb <- btb + btbi
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 SumLogit <- summary(RegLogit)
37 Beta <- SumLogit[["coefficients"]][,1]
38 sig2 <- sum(SumLogit[["deviance.resid"]]^2)/SumLogit[["df.
       residual"]]
39 ss0 <- sig2; D <- diag(K2)
40 bs1 <- rnorm(N, 0, sd = D[1]^0.5)
41 bs2 <- rnorm(N, 0, sd = D[2]^0.5)
42 bs <- cbind(bs1, bs2)
43 tuning <- 0.1; ropt <- 0.44
44 tunepariter <- seq(round(tot/10, 0), tot, round(tot/10, 0));
        l <- 1
45 pb <- txtProgressBar(min = 0, max = tot, style = 3)
```

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

```r
for(s in 1:tot){
  LatY <- LatentMHV1(tuning = tuning, Beta = Beta, bs = bs,
     sig2 = sig2)
  ylhat <- LatY[["ylhat"]]
  bs <- Postb(Beta = Beta, D = D, ylhat = ylhat, sig2 = sig2
     )
  D <- PostD(bs = bs)
  Beta <- PostBeta(D = D, ylhat = ylhat, sig2 = sig2)
  sig2 <- PostSig2(Beta = Beta, bs = bs, ylhat = ylhat, ss =
     ss0)
  PostBetas[s,] <- Beta
  PostDs[s,] <- matrixcalc::vech(D)
  Postbs[, , s] <- bs
  PostSig2s[s] <- sig2
  AcceptRate <- LatY[["accept"]]
  Accepts[s] <- AcceptRate
  if(AcceptRate > ropt){
    tuning = tuning*(2-(1-AcceptRate)/(1-ropt))
  }else{
    tuning = tuning/(2-AcceptRate/ropt)
  }
  if(s == tunepariter[l]){
    print(AcceptRate)
    l <- l + 1
  }
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
Bs <- PostBetas[keep,]
Ds <- PostDs[keep,]
bs <- Postbs[, , keep]
sig2s <- PostSig2s[keep]
summary(coda::mcmc(Bs))
Quantiles for each variable:
      2.5%      25%      50%      75%    97.5%
var1  0.3195   0.5266   0.6325   0.7452   0.9427
var2  0.1780   0.3563   0.4521   0.5436   0.7352
var3  0.3596   0.5197   0.6140   0.7165   0.9149
var4 -0.8994  -0.7153  -0.6125  -0.5135  -0.3240
summary(coda::mcmc(Ds))
Quantiles for each variable:
      2.5%         25%          50%        75%    97.5%
var1  0.0002003   0.0007473   0.0022547 0.0124378 0.09575
var2 -0.0534437  -0.0029207  -0.0001433 0.0009905 0.02296
var3  0.0002150   0.0009101   0.0026712 0.0119391 0.14863
summary(coda::mcmc(sig2s))
Quantiles for each variable:
2.5%     25%      50%      75% 97.5%
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 datatset *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

```r
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[i]
28     ylhatmeani <- X[i,]%*%Beta + W[i,]%*%bs[id[i],]
29     ylhati <- rnorm(1, ylhatmeani, 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) +
      dnorm(ylhati, ylhatmeani, sig2^0.5, log = TRUE))
35     logPostpropi <- sum(dpois(yi, lambdapropi, log = TRUE) +
       dnorm(ylpropi, ylhatmeani, sig2^0.5, log = TRUE))
36     alphai <- min(1, exp(logPostpropi - logPosthati))
37     ui <- runif(1)
38     if(ui <= alphai){
39       ylhati <- ylpropi; accepti <- 1
40     }else{
41       ylhati <- ylhati; accepti <- 0
42     }
43     ylhat[i] <- ylhati
44     accept <- c(accept, accepti)
45   }
46   res <- list(ylhat = ylhat, accept = mean(accept))
47   return(res)
48 }
```

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

```r
PostBeta <- function(D, ylhat, sig2){
  XVX <- matrix(0, K1, K1); XVy <- matrix(0, K1, 1)
  for(i in 1:N){
    ids <- which(id == i); Ti <- length(ids)
    Wi <- matrix(W[ids, ], Ti, K2)
    Vi <- diag(Ti)*sig2 + Wi%*%D%*%t(Wi)
    ViInv <- solve(Vi); Xi <- matrix(X[ids, ], Ti, K1)
    XVXi <- t(Xi)%*%ViInv%*%Xi
    XVX <- XVX + XVXi; yi <- ylhat[ids]
    XVyi <- t(Xi)%*%ViInv%*%yi; XVy <- XVy + XVyi
  }
  Bn <- solve(B0i + XVX); bn <- Bn%*%(B0i%*%b0 + XVy)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
Postb <- function(Beta, D, ylhat, sig2){
  Di <- solve(D); bis <- matrix(0, N, K2)
  for(i in 1:N){
    ids <- which(id == i); Ti <- length(ids)
    Wi <- matrix(W[ids, ], Ti, K2)
    Xi <- matrix(X[ids, ], Ti, K1)
    yi <- ylhat[ids]
    Wtei <- sig2^(-1)*t(Wi)%*%(yi - Xi%*%Beta)
    Bni <- solve(sig2^(-1)*t(Wi)%*%Wi + Di)
    bni <- Bni%*%Wtei
    bi <- MASS::mvrnorm(1, bni, Bni)
    bis[i, ] <- bi
  }
  return(bis)
}
PostD <- function(bs){
  rn <- r0 + N; btb <- matrix(0, K2, K2)
  for(i in 1:N){
    bsi <- bs[i, ]; btbi <- bsi%*%t(bsi)
    btb <- btb + btbi
  }
  Rn <- d0*R0 + btb; Sigma <- MCMCpack::riwish(v = rn, S =
    Rn)
  return(Sigma)
}
PostSig2 <- function(Beta, bs, ylhat){
  an <- a0 + 0.5*NT; ete <- 0
  for(i in 1:N){
    ids <- which(id == i)
    Ti <- length(ids)
    Xi <- matrix(X[ids, ], Ti, K1); yi <- ylhat[ids]
    Wi <- matrix(W[ids, ], Ti, K2)
    ei <- yi - Xi%*%Beta - Wi%*%bs[i, ]
    etei <- t(ei)%*%ei; ete <- ete + etei
  }
  dn <- d0 + 0.5*ete
  sig2 <- MCMCpack::rinvgamma(1, shape = an, scale = dn)
  return(sig2)
}
```

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

```r
PostBetas <- matrix(0, tot, K1)
PostDs <- matrix(0, tot, K2*(K2+1)/2)
Postbs <- array(0, c(N, K2, tot))
PostSig2s <- rep(0, tot); ccepts <- rep(NULL, tot)
RegPois <- glm(DocNum ~ Age + Male + Sport + LogInc +
    GoodHealth + BadHealth, family = poisson(link = "log"))
SumPois <- summary(RegPois)
Beta <- SumPois[["coefficients"]][,1]
sig2 <- sum(SumPois[["deviance.resid"]]^2)/SumPois[["df.
    residual"]]
D <- diag(K2)
bs1 <- rnorm(N, 0, sd = D[1,1]^0.5)
bs2 <- rnorm(N, 0, sd = D[2,2]^0.5)
bs <- cbind(bs1, bs2); tuning <- 0.1; ropt <- 0.44
tunepariter <- seq(round(tot/10, 0), tot, round(tot/10, 0));
        l <- 1
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  LatY <- LatentMHV1(tuning = tuning, Beta = Beta, bs = bs,
    sig2 = sig2)
  ylhat <- LatY[["ylhat"]]
  bs <- Postb(Beta = Beta, D = D, ylhat = ylhat, sig2 = sig2
    )
  D <- PostD(bs = bs)
  Beta <- PostBeta(D = D, ylhat = ylhat, sig2 = sig2)
  sig2 <- PostSig2(Beta = Beta, bs = bs, ylhat = ylhat)
  PostBetas[s,] <- Beta; PostDs[s,] <- matrixcalc::vech(D)
  Postbs[, , s] <- bs; PostSig2s[s] <- sig2
  AcceptRate <- LatY[["accept"]]; Accepts[s] <- AcceptRate
  if(AcceptRate > ropt){
    tuning = tuning*(2-(1-AcceptRate)/(1-ropt))
  }else{
    tuning = tuning/(2-AcceptRate/ropt)
  }
  if(s == tunepariter[l]){
    print(AcceptRate)
    l <- l + 1
  }
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
Bs <- PostBetas[keep,]; Ds <- PostDs[keep,]
bs <- Postbs[, , keep]; sig2s <- PostSig2s[keep]
summary(coda::mcmc(Bs))
Quantiles for each variable:
2.5%        25%          50%        75%      97.5%
var1 -1.250036 -0.269211   0.1995811   0.69139   1.59234
var2 -0.001542   0.004852   0.0083935   0.01147   0.01815
var3 -0.484097 -0.331748  -0.2586891  -0.19011  -0.04787
var4 -0.023677   0.123336   0.1973927   0.26883   0.41314
var5 -0.196732 -0.071421  -0.0001036   0.06601   0.19356
var6 -0.815499 -0.657182  -0.5784964  -0.49969  -0.36882
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 $\boldsymbol{\mu}_m \sim N(\mathbf{0}, \sigma^2 \boldsymbol{I}_n)$, and $\boldsymbol{X}_m$ does not have the column of ones. Assuming that $\pi(\sigma^2) \propto 1/\sigma^2$, $\pi(\alpha) \propto 1$, and $\boldsymbol{\beta}_m|\sigma^2 \sim N(\mathbf{0}_{k_m}, \sigma^2(g_m\boldsymbol{X}_m^\top\boldsymbol{X}_m)^{-1})$.

   - Show that the conditional posterior distribution of $\boldsymbol{\beta}_m$ is $N(\boldsymbol{\beta}_{mn}, \sigma^2\boldsymbol{B}_{mn})$, where $\boldsymbol{\beta}_{mn} = \boldsymbol{B}_{mn}\boldsymbol{X}_m^\top\boldsymbol{y}$ and $\boldsymbol{B}_{mn} = ((1+g_m)\boldsymbol{X}_m^\top\boldsymbol{X}_m)^{-1}$.

   - Show that the marginal the marginal likelihood associated with model $\mathcal{M}_m$ is proportional to

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

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

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

Answer

The marginal likelihood of this model is

$$p(\mathbf{y}) = \int_0^\infty \int_{R^K} \int_R \pi(\boldsymbol{\beta}|\sigma^2)\pi(\sigma^2)\pi(\alpha)p(\mathbf{y}|\boldsymbol{\beta}, \sigma^2, \alpha)d\alpha d\boldsymbol{\beta}d\sigma^2$$

$$\propto \int_0^\infty \int_{R^K} \int_R (\sigma^2)^{-k_m/2}|g_m\boldsymbol{X}_m^\top\boldsymbol{X}_m|^{1/2}\exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{\beta}^\top(g_m\boldsymbol{X}_m^\top\boldsymbol{X}_m)\boldsymbol{\beta})\right\}(\sigma^2)^{-1}$$

$$\times (\sigma^2)^{-N/2}\exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{y} - \alpha\boldsymbol{i}_N - \boldsymbol{X}_m\boldsymbol{\beta})^\top(\boldsymbol{y} - \alpha\boldsymbol{i}_N - \boldsymbol{X}_m\boldsymbol{\beta})\right\}d\alpha d\boldsymbol{\beta}d\sigma^2.$$

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

$$p(\mathbf{y}) \propto \int_0^\infty \int_{R^K} (\sigma^2)^{-k_m/2} |g_m \boldsymbol{X}_m^\top \boldsymbol{X}_m|^{1/2} \exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{\beta}^\top(g_m \boldsymbol{X}_m^\top \boldsymbol{X}_m)\boldsymbol{\beta})\right\} (\sigma^2)^{-1}$$

$$\times (\sigma^2)^{-N/2} \exp\left\{-\frac{1}{2\sigma^2}[(\boldsymbol{y}-\boldsymbol{X}_m\boldsymbol{\beta})^\top(\boldsymbol{y}-\boldsymbol{X}_m\boldsymbol{\beta})-N\bar{y}^2]\right\}$$

$$\times \int_R \exp\left\{-\frac{1}{2\sigma^2}(N(\alpha-\bar{y})^2)\right\} d\alpha d\boldsymbol{\beta} d\sigma^2.$$

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

$$p(\mathbf{y}) \propto \int_0^\infty \int_{R^K} (\sigma^2)^{-k_m/2} |g_m \boldsymbol{X}_m^\top \boldsymbol{X}_m|^{1/2} \exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{\beta}^\top(g_m \boldsymbol{X}_m^\top \boldsymbol{X}_m)\boldsymbol{\beta})\right\} (\sigma^2)^{-1}$$

$$\times (\sigma^2)^{-N/2}(\sigma^2)^{1/2} \exp\left\{-\frac{1}{2\sigma^2}[(\boldsymbol{y}-\boldsymbol{X}_m\boldsymbol{\beta})^\top(\boldsymbol{y}-\boldsymbol{X}_m\boldsymbol{\beta})-N\bar{y}^2]\right\} d\boldsymbol{\beta} d\sigma^2.$$

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

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

$$\times (\sigma^2)^{-N/2}(\sigma^2)^{1/2} \int_{R^K} \exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{\beta}-\boldsymbol{\beta}_{mn})^\top\boldsymbol{B}_{mn}^{-1}(\boldsymbol{\beta}-\boldsymbol{\beta}_{mn})\right\} d\boldsymbol{\beta} d\sigma^2.$$

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

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

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

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

2. **Determinants of export diversification I**

[17] 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 [17] 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

```r
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 BMAsdmc3 <- (colSums(PMPmc3*Varsmc3)  + colSums(PMPmc3*(
      Meansmc3-matrix(rep(BMAmeansmc3, each = nModels),
      nModels, K))^2))^0.5
47 plot(BMAmeansmc3)
48 plot(BMAsdmc3)
49 Ratio <- BMAmeansmc3/BMAsdmc3
50 RessulMC3 <- as.data.frame(cbind(PIPmc3, Models[1,],
      BMAmeansmc3, BMAsdmc3, 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 1.1e+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 ($<< 2^{40}$) 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

```r
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))
       %*%(y - mean(y)))/(1 + gr))
18     PX <- Xr%*%solve(t(Xr)%*%Xr)%*%t(Xr)
19     s2pos <- c((t(y - mean(y))%*%(y - mean(y))) - t(y)%*%PX%
       *%y/(1 + gr))
20     mllMod <- (kr/2)*log(gr/(1+gr))-(N-1)/2*log(s2pos)
21   }else{
22     gr <- ifelse(N > kr^2, 1/N, kr^(-2))
23     # PX <- diag(N)
24     # s2pos <- c(t(y)%*%PX%*%y/(1 + gr) + gr*(t(y - mean(y))
       %*%(y - mean(y)))/(1 + gr))
25     s2pos <- c((t(y - mean(y))%*%(y - mean(y))))
26     mllMod <- (kr/2)*log(gr/(1+gr))-(N-1)/2*log(s2pos)
27   }
28   return(mllMod)
29 }
30 Xnew <- apply(X, 2, scale); M <- 100
31 Models <- matrix(rbinom(K*M, 1, p = 0.5), ncol = K, nrow = M
       + 800)
32 Models <- unique(Models)[1:M,]
33 mllnew <- sapply(1:M, function(s){LogMLfunt(matrix(Models[s
       ,], 1, K))})
34 oind <- order(mllnew, decreasing = TRUE)
35 mllnew <- mllnew[oind]
36 Models <- Models[oind, ]
37 iter <- 50000; s <- 1
38 pb <- txtProgressBar(min = 0, max = iter, style = 3)
```

R code. Markov chain Monte Carlo model composition

```r
while(s <= iter){
  ActModel <- Models[M,]
  idK <- which(ActModel == 1)
  Kact <- length(idK)
  Continue <- 0
  while(Continue == 0){
    if(Kact < K & Kact > 1){
      CardMol <- K
      opt <- sample(1:3, 1)
      if(opt == 1){ # Same
        CandModel <- ActModel
      }else{
        if(opt == 2){ # Add
          All <- 1:K
          NewX <- sample(All[-idK], 1)
          CandModel <- ActModel
          CandModel[NewX] <- 1
        }else{ # Subtract
          LessX <- sample(idK, 1)
          CandModel <- ActModel
          CandModel[LessX] <- 0
        }
      }
    }else{
      CardMol <- K + 1
      if(Kact == K){
        opt <- sample(1:2, 1)
        if(opt == 1){ # Same
          CandModel <- ActModel
        }else{ # Subtract
          LessX <- sample(1:K, 1)
          CandModel <- ActModel
          CandModel[LessX] <- 0
        }
      }else{
        if(K == 1){
          opt <- sample(1:3, 1)
          if(opt == 1){ # Same
            CandModel <- ActModel
          }else{
            if(opt == 2){ # Add
              All <- 1:K
              NewX <- sample(All[-idK], 1)
              CandModel <- ActModel
              CandModel[NewX] <- 1
            }else{ # Subtract
              LessX <- sample(idK, 1)
              CandModel <- ActModel
              CandModel[LessX] <- 0
            }
          }
        }else{ # Add
          NewX <- sample(1:K, 1)
          CandModel <- ActModel
          CandModel[NewX] <- 1
        }
      }
    }
```

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 setTxtProgressBar(pb, s)
33 }
34 close(pb)
35 ModelsUni <- unique(Models)
36 mllnewUni <- sapply(1:dim(ModelsUni)[1], function(s){
        LogMLfunt(matrix(ModelsUni[s,], 1, K))})
37 StMarLik <- exp(mllnewUni-mllnewUni[1])
38 PMP <- StMarLik/sum(StMarLik)
39 PIP <- NULL
40 for(k in 1:K){
41 PIPk <- sum(PMP[which(ModelsUni[,k] == 1)])
42 PIP <- c(PIP, PIPk)
43 }
44 PIP
```

R code. Markov chain Monte Carlo model composition

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

R code. BIC and MC3 in model with endogeneity

```r
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
       (BMAmeans, each = nModels), nModels, K))^2))^0.5
17 plot(BMAmeans)
18 plot(BMAsd)
19 plot(BMAmeans/BMAsd)
```

The previous results are intuitive, as the PMP are calculated based on fit (and penalty for complexity), for instance, $BIC = k_m \log(N) - 2\log(p(\hat{\boldsymbol{\theta}}_m|\boldsymbol{y}))$, where $\hat{\boldsymbol{\theta}}_m$ 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

```r
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-
        matrix(rep(BMAmeans, each = nModels), nModels, K))^2))
        ^0.5
23  BMAmeans
24  5.589366e-01 -9.431664e-01  1.035593e+00 -1.967444e-05
        -1.429801e-04 -3.310215e-04  4.036846e-04 4.651796e-03
        -2.673730e-03  6.462503e-05  4.286529e-04 -1.829889e-04
         5.073229e-03 -1.007356e-04 -5.377972e-04  1.644475e-03
        -4.029205e-04 -1.457381e-04  6.421582e-04  2.211994e-04
         2.216503e-04
25  plot(BMAsd)
26  plot(BMAmeans/BMAsd)
27  17.764095075 -23.233601133   34.734610916   -0.005600369
        -0.039168667   -0.071895067    0.080909448 0.274994618
        -0.210854131    0.018790592    0.061271650   -0.047117887
         0.305639285   -0.028830411  -0.092463544    0.169455952
        -0.058299940   -0.038099792    0.102373567    0.056074670
         0.055500343
28
```

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 [17] 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

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

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

7. [33, 34] 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. [41] 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 [41] 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 [47, 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 Bostwana

```
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

```r
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 <- txtProgressBar(min = 0, max = iter, style = 3)
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     }
```

R code. BMA Logit model

```r
  }else{
CardMol <- K + 1
if(Kact == K){
  opt <- sample(1:2, 1)
  if(opt == 1){ # Same
    CandModel <- ActModel
  }else{ # Subtract
    LessX <- sample(1:K, 1)
    CandModel <- ActModel
    CandModel[LessX] <- 0
  }
}else{
  if(K == 1){
    opt <- sample(1:3, 1)
    if(opt == 1){ # Same
      CandModel <- ActModel
    }else{
      if(opt == 2){ # Add
        All <- 1:K
        NewX <- sample(All[-idK], 1)
        CandModel <- ActModel
        CandModel[NewX] <- 1
      }else{ # Subtract
        LessX <- sample(idK, 1)
        CandModel <- ActModel
        CandModel[LessX] <- 0
      }
    }
  }else{ # Add
    NewX <- sample(1:K, 1)
    CandModel <- ActModel
    CandModel[NewX] <- 1
  }
}
}
LogMLact <- BICfunt(matrix(ActModel, 1, K))
LogMLcand <- BICfunt(matrix(CandModel, 1, K))
alpha <- min(1, exp(LogMLcand-LogMLact)) # Let's reasonably
    assume same prior model probability for candidate and
    actual, and same carnality of neighbor models
u <- runif(1)
if(u <= alpha){
mllnew[M] <- LogMLcand
Models[M, ] <- CandModel
oind <- order(mllnew, decreasing = TRUE)
mllnew <- mllnew[oind]
Models <- Models[oind, ]
}else{
mllnew <- mllnew
Models <- Models
}
s <- s + 1
setTxtProgressBar(pb, s)
}
close(pb)

```

R code. BMA Logit model

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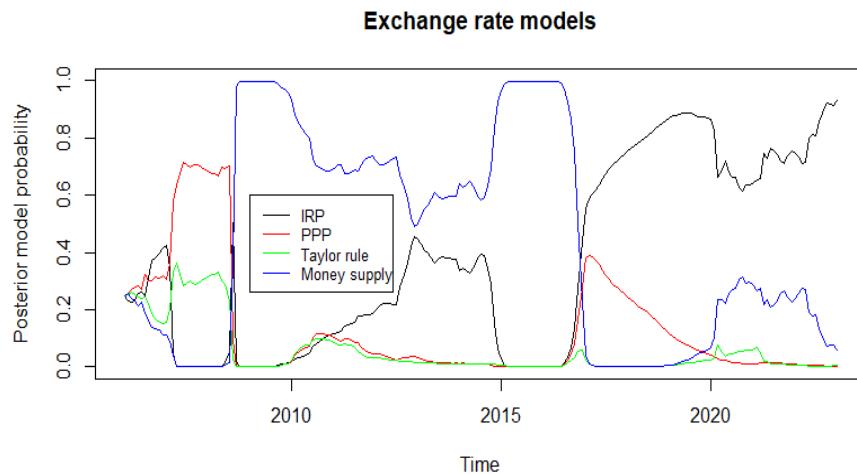
R code. Dynamic Bayesian model average: Theories to explain (forecast) exchange rate

```r
rm(list = ls()); set.seed(010101)
DataMain <- read.csv("https://raw.githubusercontent.com/
    besmarter/BSTApp/refs/heads/master/DataApp/19
    ExchangeRateCOPUSD.csv", sep = ",", header = TRUE, quote
    = "")
X <- DataMain[-c(1:12,227),c(4, 5, 7, 9, 11, 13, 14, 15)]
DifIntRat <- X[,8] - X[,7]; DifInf <- X[,1] - X[,2]
DifGrowth <- X[,3] - X[,4]; DifM3 <- X[,6] - X[,5]
XDif <- cbind(DifIntRat, DifInf, DifGrowth, DifM3)
matplot(XDif, type = "l")
y <- DataMain[-c(1:13),17] # Var exchange rate depends on
    lag of other variables
plot(y, type = "l")
IRP <- c(1, 0, 0, 0); PPP <- c(0, 1, 0, 0)
Taylor <- c(0, 1, 1, 0); Money <- c(0, 0, 1, 1)
Models <- rbind(IRP, PPP, Taylor, Money)
T0 <- 50
dma.test <- dma::dma(XDif, y, Models, lambda=.99, gamma=.99,
    initialperiod = T0)
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)
require(latex2exp)
plot_filtering_estimates <- function(df) {
  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")
  print(p)
}
menathetaIRP <- dma.test[["thetahat"]][4,,4]
SDthetaIRP <- (dma.test[["Vtheta"]][4,,4])^0.5
LimInf <- menathetaIRP - 2*SDthetaIRP
LimSup <- menathetaIRP + 2*SDthetaIRP
library(ggplot2,tibble,dplyr)
df <- tibble(t = 1:214, mean = menathetaIRP, lower = LimInf,
    upper = LimSup)
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.

Exchange rate models
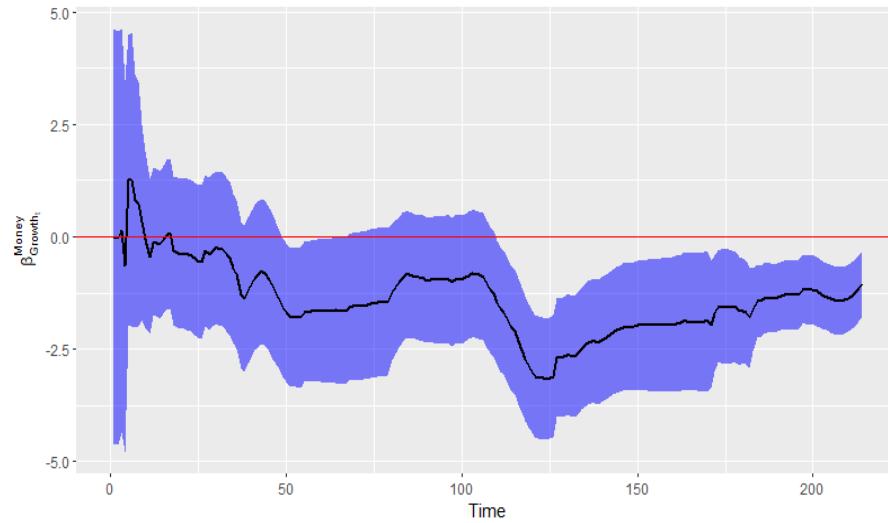
FIGURE 10.1

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 $1/T$, $\beta_{3t} = \begin{Bmatrix} -1, & 1 < t \le 0.5T \\ 0, & 0.5T < t \le T \end{Bmatrix}$, and $\beta_4 = 1.2$. Then, $\boldsymbol{x}_t^\top \boldsymbol{\beta}_t = \beta_1 + \beta_{2t} x_{2t} + \beta_{3t} x_{3t} + \beta_4 x_{4t}$, where $P[Y_t = 1 | \boldsymbol{x}_t, \boldsymbol{\beta}_t] = \exp(\boldsymbol{x}_t^\top \boldsymbol{\beta}_t)/(1 + \exp(\boldsymbol{x}_t^\top \boldsymbol{\beta}_t))$, $t = 1, 2, \ldots, 1100$. 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
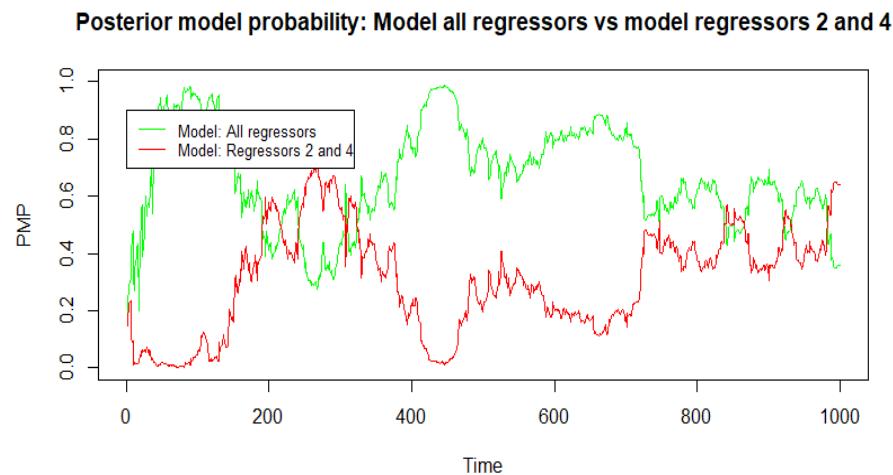
```r
rm(list = ls()); set.seed(010101)
T <- 1100; K <- 3
X <- matrix(rnorm(T*K, mean = 0.5, sd = 0.8), T, K)
combs <- expand.grid(c(0,1), c(0,1), c(0,1))
B1 <- 0.5; B2t <- seq(1, 2, length.out=T )
a <- 0.5
B3t <- c(rep(-1,round(a*T)), rep(0,round((1-a)*T)))
B4 <- 1.2
yl <- B1 + X[,1]*B2t + X[,2]*B3t + X[,3]*B4
py <- exp(yl)/(1 + exp(yl))
y <- rbinom(T, 1, prob = py)
table(y)
T0 <- 100
dma.test <- dma::logistic.dma(X, y, combs[-1,], lambda =
    0.99, alpha = 0.99, initialsamp = T0)
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))
lines(dma.test[["pmp"]][5,-c(1:T0)], col = "red")
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)
dma.test1 <- dma::logistic.dma(X, y, combs[-1,], lambda =
    0.99, alpha = 0.95, initialsamp = T0)
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))
lines(dma.test1[["pmp"]][5,-c(1:T0)], col = "red")
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.

Posterior model probability: Model all regressors vs model regressors 2 and 4

FIGURE 10.3
Posterior model probability: Dynamic Bayesian model average, forgetting parameter equal to 0.99.
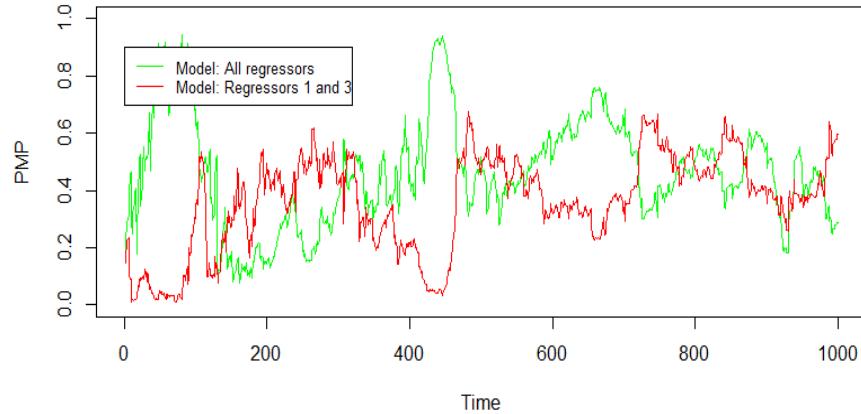
13. Show that

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

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

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

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 $\alpha_{h0} = \delta_{h0} = 0.01$, $\boldsymbol{\beta}_0 = \mathbf{0}_2$, $\boldsymbol{B}_0 = \boldsymbol{I}_2$, $\mu_{h0} = 0$, $\sigma_{\mu0}^2 = 10$, and $\boldsymbol{\alpha}_0 = [1/H \ \ldots \ 1/H]^\top$. 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

```r
rm(list = ls()); set.seed(010101)
# Simulate data from a 2-component mixture model
n <- 1000
x1 <- rnorm(n); x2 <- rnorm(n)
B <- c(0.5, -1.2); X <- cbind(x1, x2)
z <- rbinom(n, 1, 0.3)  # Latent class indicator
mu <- ifelse(z == 0, rnorm(n, -0.5, 0.5), rnorm(n, 1, 0.8))
plot(density(mu))
y <- X%*%B + mu
# Hyperparameters
d0 <- 0.001; a0 <- 0.001
b0 <- rep(0, 2); B0 <- diag(2); B0i <- solve(B0)
mu0 <- 0; sig2mu0 <- 10
H <- 5; a0h <- rep(1/H, H)
# MCMC parameters
mcmc <- 2000
burnin <- 4000
tot <- mcmc + burnin
thin <- 2
# Gibbs sampling functions
PostSig2 <- function(Beta, muh, Xh, yh){
  Nh <- length(yh)
  an <- a0 + Nh
  dn <- d0 + t(yh - muh - Xh%*%Beta)%*%(yh - muh - Xh%*%Beta
    )
  sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
  return(sig2)
}
PostBeta <- function(sig2, mu, X, y, Psi){
  XtX <- matrix(0, 2, 2)
  Xty <- matrix(0, 2, 1)
  Hs <- length(mu)
  for(h in 1:Hs){
    idh <- which(Psi == h)
    if(length(idh) == 1){
      Xh <- matrix(X[idh,], 1, 2)
      XtXh <- sig2[h]^(-1)*t(Xh)%*%Xh
      yh <- y[idh]
      Xtyh <- sig2[h]^(-1)*t(Xh)%*%(yh - mu[h])
    }else{
      Xh <- X[idh,]
      XtXh <- sig2[h]^(-1)*t(Xh)%*%Xh
      yh <- y[idh]
      Xtyh <- sig2[h]^(-1)*t(Xh)%*%(yh - mu[h])
    }
    XtX <- XtX + XtXh
    Xty <- Xty + Xtyh
  }
  Bn <- solve(B0i + XtX)
  bn <- Bn%*%(B0i%*%b0 + Xty)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
```

R code. Simulation: Semi-parametric Gaussian mixture

```r
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 <- txtProgressBar(min = 0, max = tot, style = 3)
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
      ], Sig2[h]^0.5)
30       lambdai <- c(lambdai, lambdaih)
31     }
32     Psi[i] <- sample(1:Hs, 1, prob = lambdai)
33   }
34   PostPsi[s, ] <- Psi
35   Hs <- length(table(Psi))
36   for(h in 1:Hs){
37     idh <- which(Psi == h)
38     Sig2[h] <- PostSig2(Beta = Beta, muh = MU[h], Xh = X[idh
      ,], yh = y[idh])
39     MU[h] <- Postmu(sig2h = Sig2[h], Beta = Beta, Xh = X[idh
      ,], yh = y[idh])
40   }
41   PostSigma2[[s]] <- Sig2
42   PostMu[[s]] <- MU
43   Beta <- PostBeta(sig2 = Sig2, mu = MU, X = X, y = y, Psi =
       Psi)
44   PostBetas[s,] <- Beta
45   Lambda <- sort(MCMCpack::rdirichlet(1, a0h[1:Hs] + table(
      Psi)), decreasing = TRUE)
46   PostLambda[[s]] <- Lambda
47   setTxtProgressBar(pb, s)
48 }
49 close(pb)
```

R code. Simulation: Semi-parametric Gaussian mixture

```r
keep <- seq(burnin, tot, thin)
PosteriorBetas <- coda::mcmc(PostBetas[keep,])
summary(PosteriorBetas); plot(PosteriorBetas)
PosteriorPsi <- PostPsi[keep,]
Clusters <- sapply(1:length(keep), function(i){length(table(
    PosteriorPsi[i,]))})
PosteriorSIGMA <- matrix(NA, length(keep), 2)
PosteriorMU <- matrix(NA, length(keep), 2)
PosteriorLAMBDA <- matrix(NA, length(keep), 2)
l <- 1
for (s in keep){
  PosteriorSIGMA[l,] <- PostSigma2[[s]][1:2]
  PosteriorMU[l,] <- PostMu[[s]][1:2]
  PosteriorLAMBDA[l,] <- PostLambda[[s]][1:2]
  l <- l + 1
}
summary(coda::mcmc(PosteriorSIGMA))
summary(coda::mcmc(PosteriorMU))
summary(coda::mcmc(PosteriorLAMBDA))
mus <- seq(-3, 4, 0.01)
DensityEst <- function(par, eval){
  lambda1 <- par[1]; lambda2 <- par[2]
  mu1 <- par[3]; mu2 <- par[4]
  sd1 <- par[5]; sd2 <- par[6]
  Dens <- lambda1 * dnorm(eval, mu1, sd1) + lambda2 * dnorm(
    eval, mu2, sd2)
  return(Dens)
}
par <- cbind(PosteriorLAMBDA, PosteriorMU, PosteriorSIGMA
    ^0.5)
DensEval <- matrix(NA, length(keep), length(mus))
DensPop <- rep(NA, length(mus))
for(r in 1:length(mus)){
  for(l in 1:length(keep)){
    DensEval[l, r] <- DensityEst(par = par[l,], eval = mus[r
    ])
  }
  DensPop[r] <- DensityEst(par = c(0.7, 0.3, -0.5, 1, 0.5,
    0.8), eval = mus[r])
}
library(dplyr); library(ggplot2); require(latex2exp)
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))
plot_filtering_estimates <- function(df) {
  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("$\\mu$")) + ylab("
    Density") +   labs(title = "Density: Stochastic Errors",
     color = "") + theme_minimal()
  print(p)
}
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 *LogPrice-Crack*). The sample size is 1,156.

Estimate a finite Gaussian mixture regression using non-informative priors, that is, $\alpha_0 = \delta_0 = 0.01$, $\boldsymbol{\beta}_0 = \mathbf{0}_K$, $\boldsymbol{B}_0 = \boldsymbol{I}_K$, and and $\boldsymbol{\alpha}_0 = [1/H \ \ldots \ 1/H]^\top$, 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

```r
rm(list = ls()); set.seed(010101)
Data <- read.csv("https://raw.githubusercontent.com/
    BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
    MarijuanaColombia.csv")
attach(Data)
y <- LogMarijuana; X <- as.matrix(cbind(1, Data[,-1]))
Reg <- lm(y ~ X - 1); summary(Reg)
k <- dim(X)[2]; N <- dim(X)[1]
# Plot
library(ggplot2)
ggplot(Data, aes(x = LogMarijuana)) + geom_density(fill = "
    blue", alpha = 0.3) + labs(title = "Density Plot", x = "
    y", y = "Density") + theme_minimal()
# Hyperparameters
d0 <- 0.001; a0 <- 0.001
b0 <- rep(0, k); B0 <- diag(k); B0i <- solve(B0)
H <- 5; a0h <- rep(1/H, H)
# MCMC parameters
mcmc <- 2000; burnin <- 500
tot <- mcmc + burnin; thin <- 2
# Gibbs sampling functions
PostSig2 <- function(Betah, Xh, yh){
  Nh <- length(yh); an <- a0 + Nh
  dn <- d0 + t(yh - Xh%*%Betah)%*%(yh - Xh%*%Betah)
  sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
  return(sig2)
}
PostBeta <- function(sig2h, Xh, yh){
  if(length(yh) == 1){
    Xh <- matrix(Xh, k, 1)
    Bn <- solve(B0i + sig2h^(-1)*Xh%*%t(Xh))
    bn <- Bn%*%(B0i%*%b0 + sig2h^(-1)*Xh%*%yh)
  }else{
    Bn <- solve(B0i + sig2h^(-1)*t(Xh)%*%Xh)
    bn <- Bn%*%(B0i%*%b0 + sig2h^(-1)*t(Xh)%*%yh)
  }
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
PostBetas <- list(); PostSigma2 <- list(); PostLambda <-
    list()
PostPsi <- matrix(0, tot, N); Psi <- sample(1:H, N, replace
    = TRUE, prob = a0h)
Beta <- matrix(rep(Reg$coefficients, H), k, H); Hs <- H
```

R code. Marijuana in Colombia: Gaussian mixture

```r
 1 pb <- txtProgressBar(min = 0, max = tot, style = 3)
 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   setTxtProgressBar(pb, s)
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:

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

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

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

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

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

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

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

where $e_i = y_i - \boldsymbol{x}_i^\top \boldsymbol{\beta}$ 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

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

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

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,

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

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

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,

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

where $H^{(i)}$ is the number of clusters excluding i, which may have its own cluster (singleton cluster), $q_c^* = \frac{q_c}{q_0 + \sum_h q_h}$, $q_c = \{q_0, q_h\}$, $q_h = \frac{N_h^{(i)}}{\alpha + N - 1} f_N(e_i \mid \mu_h, \sigma_h^2)$ 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 $IG\left(\alpha_n/2, \delta_n/2\right)$, a new μ_h is sample from $N(\mu_i, \sigma_h^2/\beta_n)$, where $\mu_i = \frac{e_i + \beta_0 \mu_0}{1 + \beta_0}$.

Discarding $\boldsymbol{\theta}_h$'s from last step, we use $\boldsymbol{s}$ 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 $\mu_h \mid \sigma_h^2, \boldsymbol{e} \sim N\left(\mu_{hn}, \frac{\sigma_h^2}{\beta_0 + N_h} \right)$, where $\mu_{hn} = \frac{\beta_0 \mu_0 + N_h \bar{e}}{\beta_0 + N_h}$, $h = 1, 2, \ldots, H$. Note that μ_{hn} is equal to μ_i when $N_h = 1$.

The posterior distribution of $\boldsymbol{\beta}$ is given by

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

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

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 $\alpha_0 = \delta_0 = 0.01$, $\boldsymbol{\beta}_0 = \boldsymbol{0}_2$, $\boldsymbol{B}_0 = \boldsymbol{I}_2$, 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 bi-modality, 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

```r
PostBeta <- function(sig2, mu, X, y, Clust){
  XtX <- matrix(0, k, k); Xty <- matrix(0, k, 1)
  Hs <- length(mu)
  for(h in 1:Hs){
    idh <- which(Clust == h)
    if(length(idh) == 1){
      Xh <- matrix(X[idh,], k, 1); XtXh <- sig2[h]^(-1)*Xh%*%t(Xh)
      yh <- y[idh]; Xtyh <- sig2[h]^(-1)*Xh%*%(yh - mu[h])
    }else{
      Xh <- X[idh,]; XtXh <- sig2[h]^(-1)*t(Xh)%*%Xh
      yh <- y[idh]; Xtyh <- sig2[h]^(-1)*t(Xh)%*%(yh - mu[h])
    }
    XtX <- XtX + XtXh; Xty <- Xty + Xtyh
  }
  Bn <- solve(B0i + XtX); bn <- Bn%*%(B0i%*%b0 + Xty)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
PostAlpha <- function(Clust, alpha){
  H <- length(unique(Clust))
  psi <- rbeta(1, alpha + 1, N)
  pi.ratio <- (a + H - 1) / (N * (b - log(psi)))
  pi <- pi.ratio / (1 + pi.ratio)
  components <- sample(1:2, prob = c(pi, (1 - pi)), size = 1)
  cs <- c(a + H, a + H - 1); ds <- b - log(psi)
  alpha <- rgamma(1, cs[components], ds)
  return(alpha)
}
LogMarLikLM <- function(xh, yh, Beta){
  xh <- matrix(xh, k, 1); ei <- c(yh - t(xh)%*%Beta)
  betan <- beta0 + 1; an <- a0 + 1
  dn <- d0 +beta0/(beta0 + 1)*(ei - mu0)^2
  logpy <- (1/2)*log(1/pi)+(a0/2)*log(d0)-(an/2)*log(dn) +
    0.5*log(beta0/betan) + lgamma(an/2)-lgamma(a0/2)
  return(logpy)
}
PostS <- function(Beta, SIGMA, MU, Alpha, Clust, i){
  Nl <- table(Clust[-i]); H <- length(Nl)
  ei <- c(y[i] - t(X[i,])%*%Beta)
  qh <- sapply(1:H, function(h){(Nl[h]/(N+Alpha-1))*dnorm(ei
    , mean = MU[h], sd = SIGMA[h])})
  q0 <- (Alpha/(N+Alpha-1))*exp(LogMarLikLM(xh = X[i,], yh =
    y[i], Beta = Beta))
  qh <- c(q0, qh)
  Clust <- as.numeric(names(Nl))
  si <- sample(c(0, Clust), 1, prob = qh)
  if(si == 0){si <- Clust[H] + 1
    Sig2New <- PostSig2(Xh = X[i,], yh = y[i], Beta = Beta)
    SIGMA <- c(SIGMA, Sig2New^0.5)
    MuNew <- Postmu(sig2h = Sig2New, Beta = Beta, Xh = X[i
    ,], yh = y[i])
    MU <- cbind(MU, MuNew)
  }else{si == si}
  return(list(si = si, MU = MU, SIGMA = SIGMA))
}
```

R code. Simulation: Semi-parametric Dirichlet process mixture

```r
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$coefficients[1], 3)
10 Alpha <- rgamma(1, a, b)
11 pb <- txtProgressBar(min = 0, max = tot, style = 3)
12 for(s in 1:tot){
13   for(i in 1:N){
14     Rests <- PostS(Beta = BETA, SIGMA = SIGMA, MU = MU,
       Alpha = Alpha, Clust = Clust, i = i)
15     Clust[i] <- Rests$si
16     MU <- Rests$MU; SIGMA <- Rests$SIGMA
17   }
18   sFreq <- table(Clust)
19   lt <- 1
20   for(li in as.numeric(names(sFreq))){
21     Index <- which(Clust == li)
22     if(li == lt){Clust[Index] <- li
23     } else {Clust[Index] <- lt
24     }
25     lt <- lt + 1
26   }
27   Alpha <- PostAlpha(Clust = Clust, alpha = Alpha)
28   Nl <- table(Clust); H <- length(Nl)
29   SIGMA <- rep(NA, H)
30   MU <- rep(NA, H)
31   l <- 1
32   for(h in unique(Clust)){
33     Idh <- which(Clust == h)
34     SIGMA[l] <- (PostSig2(Beta = BETA, Xh = X[Idh, ], yh = y
       [Idh]))^0.5
35     MU[l] <- Postmu(Beta = BETA, sig2h = SIGMA[l]^2, Xh = X[
       Idh, ], yh = y[Idh])
36     l <- l + 1
37   }
38   BETA <- PostBeta(sig2 = SIGMA, mu = MU, X = X, y = y,
       Clust = Clust)
39   PostBetas[s,] <- BETA
40   PostSigma[[s]] <- SIGMA
41   PostMu[[s]] <- MU
42   Posts[s, ] <- Clust
43   PostAlphas[s] <- Alpha
44   setTxtProgressBar(pb, s)
45 }
46 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:
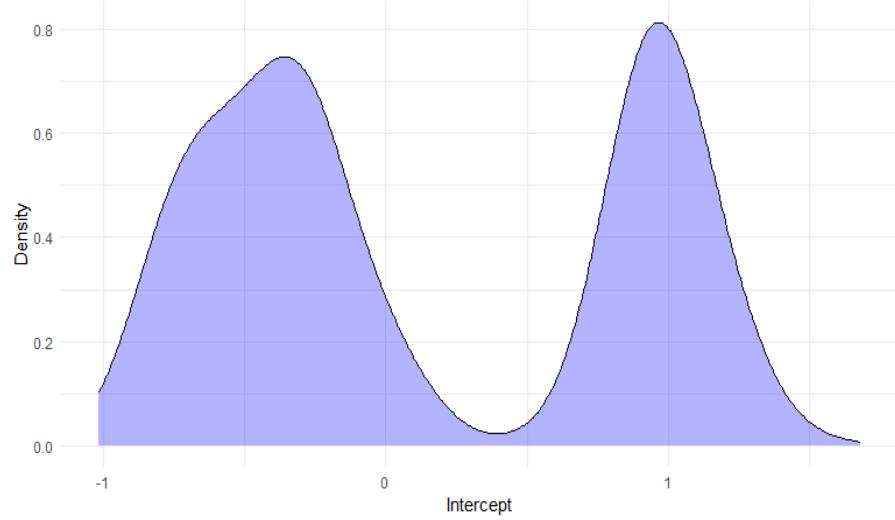
A simple strategy to address label switching in this simulation exercise is to fix the number of clusters to three, given that this is the typical number of clusters obtained after performing the DPM. Recall that, according to the simulation setup, there are only two clusters:

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

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

---

[1] Another approach is to use finite Dirichlet processes [27, 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

```r
rm(list = ls()); set.seed(010101)
# Simulate data from a 2-component mixture model
n <- 1000; x <- rnorm(n)
z <- rbinom(n, 1, 0.5)
y <- ifelse(z == 0, rnorm(n, 2 + 1.5*x, 1), rnorm(n, -1 +
    0.5*x, 0.8))
data <- data.frame(y, x)
# Hyperparameters
d0 <- 0.001; a0 <- 0.001
b0 <- rep(0, 2); B0 <- diag(2); B0i <- solve(B0)
H <- 3; a0h <- rep(1/H, H)
# MCMC parameters
mcmc <- 10000; burnin <- 2000
tot <- mcmc + burnin; thin <- 2
# Gibbs sampling functions
PostSig2 <- function(Betah, Xh, yh){
  Nh <- length(yh); an <- a0 + Nh
  dn <- d0 + t(yh - Xh%*%Betah)%*%(yh - Xh%*%Betah)
  sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
  return(sig2)
}
PostBeta <- function(sig2h, Xh, yh){
  Bn <- solve(B0i + sig2h^(-1)*t(Xh)%*%Xh)
  bn <- Bn%*%(B0i%*%b0 + sig2h^(-1)*t(Xh)%*%yh)
  Beta <- MASS::mvrnorm(1, bn, Bn)
  return(Beta)
}
PostBetas1 <- matrix(0, tot, 2)
PostBetas2 <- matrix(0, tot, 2)
PostBetas3 <- matrix(0, tot, 2)
PostSigma2 <- matrix(0, tot, H)
PostPsi <- matrix(0, tot, n)
PostLambda <- matrix(0, tot, H)
Reg <- lm(y ~ x)
SumReg <- summary(Reg)
BETA <- cbind(Reg$coefficients, Reg$coefficients, Reg$
    coefficients)
SIG2 <- rep(SumReg$sigma, H)
X <- cbind(1, x); Psi <- rep(NA, n)
Lambda1 <- 1/H; Lambda2 <- 1/H; Lambda3 <- 1/H
perutatms <- gtools::permutations(3, 3, 1:H)
```

R code. Simulation: Random permutation of latent classes

```r
 1 pb <- txtProgressBar(min = 0, max = tot, style = 3)
 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   setTxtProgressBar(pb, s)
42 }
43 close(pb)
```

<div style="border:1px solid">

R code. Simulation: Random permutation of latent classes

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

</div>
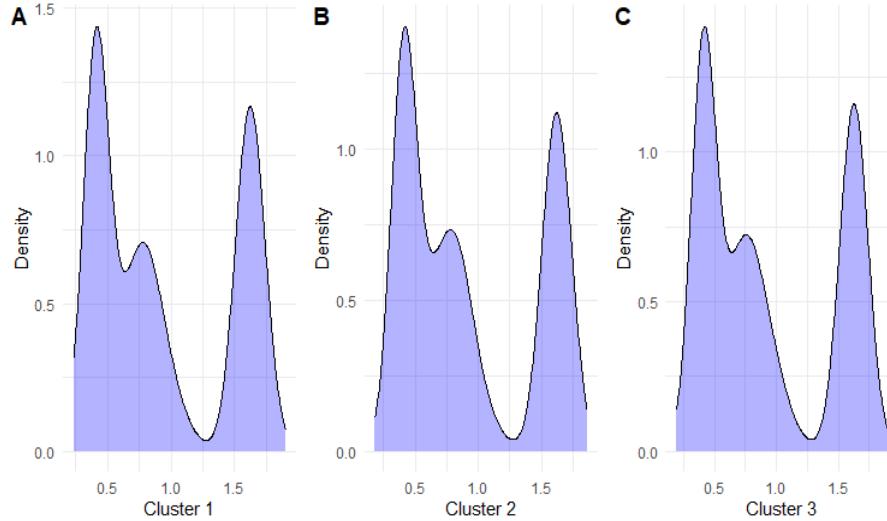
Figure 11.3 shows the posterior density estimates of the three clusters. We observe that they have similar shapes, as they are targeting the same posterior distributions. There are two modes with large values around the population parameters, and an additional mode around 0. This occurs because we are 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.

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

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

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

R code. Simulation: Density from Dirichlet process mixture

```r
PostAlpha <- function(s, alpha){
  H <- length(unique(s))
  psi <- rbeta(1, alpha + 1, N)
  pi.ratio <- (a + H - 1) / (N * (b - log(psi)))
  pi <- pi.ratio / (1 + pi.ratio)
  components <- sample(1:2, prob = c(pi, (1 - pi)), size =
    1)
  cs <- c(a + H, a + H - 1)
  ds <- b - log(psi)
  alpha <- rgamma(1, cs[components], ds)
  return(alpha)
}
LogMarLikLM <- function(xh, yh){
  xh <- matrix(xh, k, 1)
  Bn <- solve(xh%*%t(xh) + B0i)
  Bni <- solve(Bn)
  bn <- Bn%*%(B0i%*%b0 + xh%*%yh)
  an <- a0 + 1
  dn <- d0 + yh^2 + t(b0)%*%B0i%*%b0 - t(bn)%*%Bni%*%bn
  # Log marginal likelihood
  logpy <- (1/2)*log(1/pi)+(a0/2)*log(d0)-(an/2)*log(dn) +
    0.5*log(det(Bn)/det(B0)) + lgamma(an/2)-lgamma(a0/2)
  return(logpy)
}
PostS <- function(BETA, SIGMA, Alpha, s, i){
  Nl <- table(s[-i]); H <- length(Nl)
  qh <- sapply(1:H, function(h){(Nl[h]/(N+Alpha-1))*dnorm(y[
    i], mean = t(X[i,])%*%BETA[,h], sd = SIGMA[h])})
  q0 <- (Alpha/(N+Alpha-1))*exp(LogMarLikLM(xh = X[i,], yh =
    y[i]))
  qh <- c(q0, qh)
  Clust <- as.numeric(names(Nl))
  si <- sample(c(0, Clust), 1, prob = qh)
  if(si == 0){
    si <- Clust[H] + 1
    Sig2New <- PostSig2(Xh = X[i,], yh = y[i])
    SIGMA <- c(SIGMA, Sig2New^0.5)
    BetaNew <- PostBeta(sig2h = Sig2New, Xh = X[i,], yh = y[
    i])
    BETA <- cbind(BETA, BetaNew)
  }else{si == si
  }
  return(list(si = si, BETA = BETA, SIGMA = SIGMA))
}
PostBetas <- list(); PostSigma <- list()
Posts <- matrix(0, tot, N); PostAlphas <- rep(0, tot)
S <- sample(1:3, N, replace = T, prob = c(0.5, 0.3, 0.2))
BETA <- cbind(Reg$coefficients, Reg$coefficients, Reg$
    coefficients)
SIGMA <- rep(SumReg$sigma, 3)
Alpha <- rgamma(1, a, b)
```

R code. Simulation: Density from Dirichlet process mixture

```r
pb <- txtProgressBar(min = 0, max = tot, style = 3)
for(s in 1:tot){
  for(i in 1:N){
    Rests <- PostS(BETA = BETA, SIGMA = SIGMA, Alpha = Alpha
    , s = S, i = i)
    S[i] <- Rests$si
    BETA <- Rests$BETA; SIGMA <- Rests$SIGMA
  }
  sFreq <- table(S)
  lt <- 1
  for(li in as.numeric(names(sFreq))){
    Index <- which(S == li)
    if(li == lt){S[Index] <- li
    } else {S[Index] <- lt
    }
    lt <- lt + 1
  }
  Alpha <- PostAlpha(s = S, alpha = Alpha)
  Nl <- table(S); H <- length(Nl)
  SIGMA <- rep(NA, H)
  BETA <- matrix(NA, k, H)
  l <- 1
  for(h in unique(S)){
    Idh <- which(S == h)
    SIGMA[l] <- (PostSig2(Xh = X[Idh, ], yh = y[Idh]))^0.5
    BETA[,l] <- PostBeta(sig2h = SIGMA[l]^2, Xh = X[Idh, ],
    yh = y[Idh])
    l <- l + 1
  }
  PostBetas[[s]] <- BETA
  PostSigma[[s]] <- SIGMA
  Posts[s, ] <- S
  PostAlphas[s] <- Alpha
  setTxtProgressBar(pb, s)
}
close(pb)
keep <- seq((burnin+1), tot, thin)
PosteriorS<- Posts[keep,]
Clusters <- sapply(1:length(keep), function(i){length(table(
    PosteriorS[i,]))})
table(Clusters)
Clusters <- sapply(1:length(keep), function(i){table(
    PosteriorS[i,])})
PosteriorBeta <- PostBetas[keep]
PosteriorSigma <- PostSigma[keep]
PosteriorAlpha <- PostAlphas[keep]
```

R code. Simulation: Density from Dirichlet process mixture
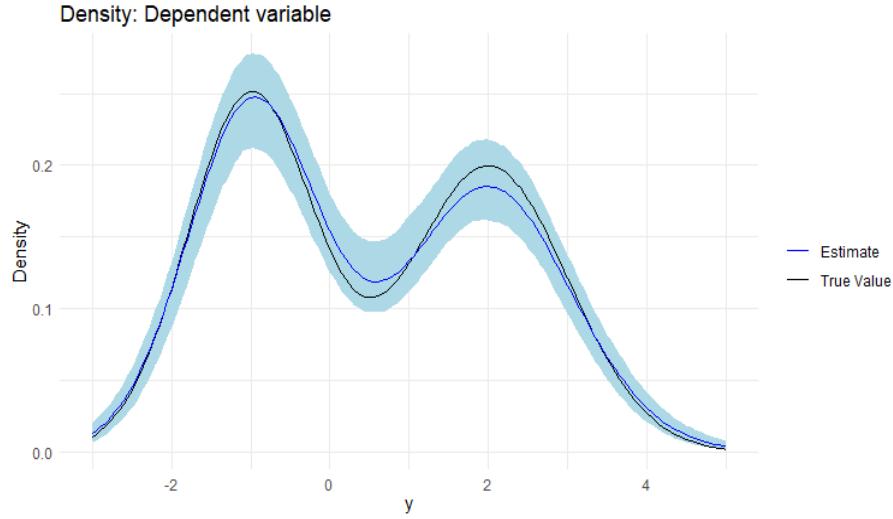
```r
DensityFunc <- function(yobs = 0, xobs = c(1, 0), s){
  dens <- NULL
  for(j in 1:length(Clusters[[s]])){
    densj <- Clusters[[s]][j]/(PosteriorAlpha[s] + N + 1) *
    dnorm(yobs, t(PosteriorBeta[[s]][,j])%*%xobs,
    PosteriorSigma[[s]][j])
    dens <- c(dens, densj)
  }
  dens <- c(dens, PosteriorAlpha[s]/(PosteriorAlpha[s] + N +
      1)*exp(LogMarLikLM(yh = yobs, xh = xobs)))
  return(sum(dens))
}
xobs <- c(1, 0)
ys <- seq(-3, 5, 0.05)
pdfy <- 0.5*dnorm(ys, 2 + 1.5*xobs[2], 1) + 0.5*dnorm(ys, -1
    + 0.5*xobs[2], 0.8)
DensEval <- matrix(NA, length(keep), length(ys))
for(r in 1:length(ys)){
  for(l in 1:length(keep)){
    DensEval[l, r] <- DensityFunc(yobs = ys[r], xobs = xobs,
    s = l)
  }
}
library(dplyr)
library(ggplot2)
require(latex2exp)
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))
plot_filtering_estimates <- function(df) {
  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()
  print(p)
}
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:

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

where y_i is the (log) marijuana monthly consumption, $\boldsymbol{z}_i$ 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 $\{0, 0.05, \ldots, 0.95, 1\}$ 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.
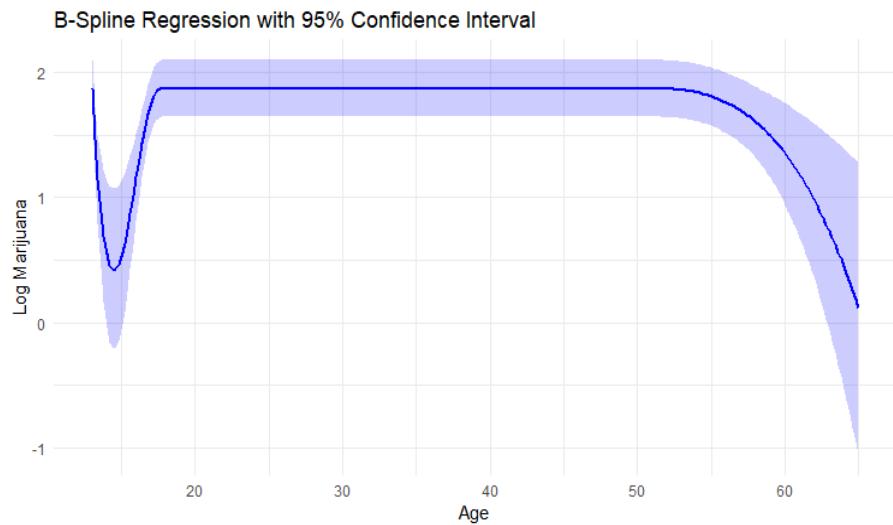
After this, we proceed with inference using a linear regression with conjugate prior distributions. Figure 11.5 shows the fit, with the mean (blue line) and 95% credible intervals (shaded blue). This curve is simpler than the one using all the B-splines: there appears to be a hook-shaped pattern at the 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

```r
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()
```

B-Spline Regression with 95% Confidence Interval

FIGURE 11.5
Spline: Marijuana monthly consumption vs age.

12

Bayesian machine learning

Solutions of Exercises

1. **Simulation exercise: the Bayesian LASSO continues**

   Program the Gibbs sampler for the Bayesian LASSO from scratch, assuming a hierarchical structure for the global shrinkage parameter, where both the shape and rate parameters are set to 1. Perform inference using this sampler in the Bayesian LASSO simulation exercise and compare the results with those obtained using the *monomvn* package.

   Answer

   The following code illustrates how to implement the Gibbs sampler for the Bayesian LASSO. Overall, the results are very similar to those obtained using the *monomvn* package (see Figure 12.1).

R code. Simulation: The Bayesian LASSO

```r
1  rm(list = ls()); set.seed(10101)
2  library(monomvn)
3  # Parameters
4  n <- 500   # sample size
5  k <- 100   # number of predictors
6  s <- 10    # number of non-zero coefficients
7  # Generate design matrix
8  X <- matrix(rnorm(n * k), nrow = n, ncol = k)
9  # True beta: first s coefficients are non-zero, rest are
       zero
10 beta_true <- c(runif(s, -3, 3), rep(0, k - s))
11 # Generate response with some noise
12 sigma <- 1
13 y <- X %*% beta_true + rnorm(n, sd = sigma)
14 df <- data.frame(X,y)
15 ### Using monomvn ###
16 library(monomvn)
17 library(statmod)
18 # Fit model using Bayesian LASSO
19 fit <- monomvn::blasso(X, y, T = 5000, verb = 0)
20 # burn-in removal
21 burnin <- 1000
22 beta_samples <- fit$beta[(burnin + 1):5000, ]  # exclude
       burn-in
23 intercept_samples <- fit$mu[(burnin + 1):5000] # intercept
       posterior draws
24 # Posterior mean of coefficients
25 beta_post_mean <- colMeans(beta_samples)
26 # Intercept summary
27 mean(intercept_samples)
28 quantile(intercept_samples, c(0.025, 0.975))
29 # Local shrinkage parameters
30 colMeans(is.na(fit$tau2i))  # proportion of NA values per
       coefficient
31
32 #### Gibss sampler ####
33 # Hyperparameters
34 r0 <- 1; d0 <- 1
35 # MCMC parameters
36 mcmc <- 5000; burnin <- 5000
37 tot <- mcmc + burnin; thin <- 1
38 # Posterior distributions programming the Gibbs sampling
39 # Standardized variables
40 W <- scale(X)
41 yh <- y - mean(y)
42 # Gibbs sampling functions
43 PostBeta <- function(sig2, tau2){
44   Bn <- solve(diag(1/tau2) + t(W)%*%W)
45   bn <- Bn%*%t(W)%*%yh
46   Beta <- MASS::mvrnorm(1, bn, sig2*Bn)
47   return(Beta)
48 }
```

R code. Simulation: The Bayesian LASSO

```r
1  PostSig2 <- function(Beta, tau2){
2    an <- n - 1 + k
3    dn <- t(yh - W%*%Beta)%*%(yh - W%*%Beta) + t(Beta)%*%diag
       (1/tau2)%*%Beta
4    sig2 <- invgamma::rinvgamma(1, shape = an/2, rate = dn/2)
5    return(sig2)
6  }
7  PostTau2 <- function(sig2, Beta, lambda, p){
8    mukn <- (lambda^2*sig2/Beta[p]^2)^0.5
9    lambdan <- lambda^2
10   tauk2k <- rinvgauss(1, mean = mukn, shape = lambdan)
11   return(tauk2k)
12 }
13 PostLambda2 <- function(tau2){
14   sh <- k + r0
15   rat <- 0.5 * sum(tau2) + d0
16   lambda2 <- rgamma(1, shape = sh, rate = rat)
17   return(lambda2^0.5)
18 }
19 PostBeta0 <- function(sig2){
20   beta0 <- rnorm(1, mean = mean(y), sd = (sig2/n)^0.5)
21   return(beta0)
22 }
23 PostBetas <- matrix(0, mcmc+burnin, k)
24 PostSigma2 <- rep(0, mcmc+burnin)
25 PostTaus2 <- matrix(0, mcmc+burnin, k)
26 PostLambda <- rep(0, mcmc+burnin)
27 PostBetas0 <- rep(0, mcmc+burnin)
28 Beta <- rep(0, k); tau2 <- rep(1, k); lambda <- 1
29 # create progress bar in case that you want to see
       iterations progress
30 pb <- txtProgressBar(min = 0, max = tot, style = 3)
31 for(s in 1:tot){
32   sig2 <- PostSig2(Beta = Beta, tau2 = tau2)
33   PostSigma2[s] <- sig2
34   Beta <- PostBeta(sig2 = sig2, tau2 = tau2)
35   PostBetas[s,] <- Beta
36   tau2 <- sapply(1:k, function(i){PostTau2(sig2 = sig2, Beta
       = Beta, lambda = lambda, p = i)})
37   PostTaus2[s,] <- tau2
38   lambda <- PostLambda2(tau2 = tau2)
39   PostLambda[s] <- lambda
40   beta0 <- PostBeta0(sig2 = sig2)
41   PostBetas0[s] <- beta0
42   setTxtProgressBar(pb, s)
43 }
44 close(pb)
45 keep <- seq((burnin+1), tot, thin)
46 PosteriorBetas <- PostBetas[keep,]
47 summary(coda::mcmc(PosteriorBetas))
48 PosteriorBeta0 <- PostBetas0[keep]
49 summary(coda::mcmc(PosteriorBeta0))
50 PosteriorSigma2 <- PostSigma2[keep]
51 summary(coda::mcmc(PosteriorSigma2))
52 PosteriorTau2s <- PostTaus2[keep,]
53 summary(coda::mcmc(PosteriorTau2s))
54 PosteriorLambda <- PostLambda[keep]
55 summary(coda::mcmc(PosteriorLambda))
```
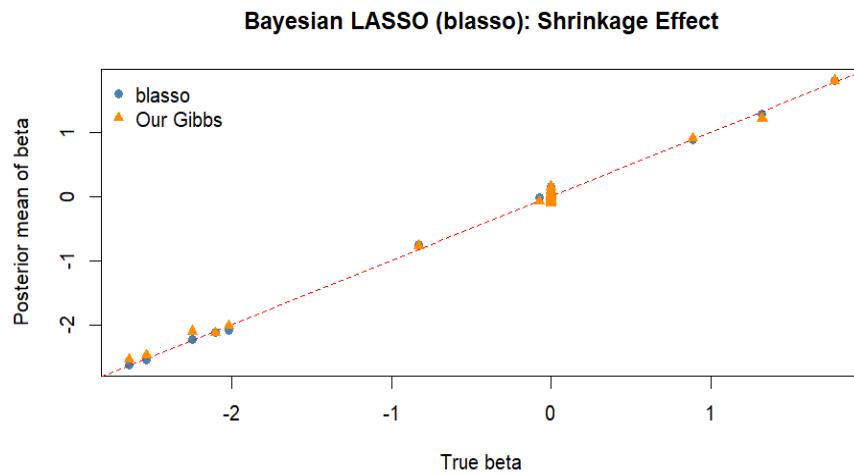
R code. Simulation: The Bayesian LASSO

```r
# Posterior mean of coefficients
beta_post_meanNew <- colMeans(PosteriorBetas)
# Plot true vs estimated betas
plot(beta_true, beta_post_mean, pch = 19, col = "steelblue",
xlab = "True beta", ylab = "Posterior mean of beta",
main = "Bayesian LASSO (blasso): Shrinkage Effect")
abline(0, 1, col = "red", lty = 2)
# Add another set of posterior means
points(beta_true, beta_post_meanNew, pch = 17, col = "
    darkorange")
# Add legend
legend("topleft", legend = c("blasso", "Our Gibbs"),
col = c("steelblue", "darkorange"),
pch = c(19, 17), bty = "n")

```


FIGURE 12.1
Comparison of LASSO performance: Package vs Gibbs from scratch.

2. [18] employ stochastic search variable selection (SSVS) to identify the main drivers of civil conflict in the post-Cold War era, considering a set of 35 potential determinants across 175 countries worldwide. We use a subset of their dataset provided in *Conflict.xlsx*, where the dependent variable

is *conflictcw*, a binary indicator of civil conflict. Perform SSVS using the *BoomSpikeSlab* package, specifically the *lm.spike* function, to identify the best subset of models.

Answer

The following code illustrates how to implement SSVS in this application, based on [18], using 15,000 iterations and the default settings for the hyperparameters. We find that infant mortality rate, population, peace, and political rights are the most relevant drivers of the incidence of civil conflict. *Peace* exhibits a negative 95% credible interval, while the other variables have positive credible intervals. The model with the highest posterior probability (30%) includes the first three regressors.

R code. Application: Drivers of civil conflict in the post-Cold War era using a linear model

```r
1  rm(list = ls())
2  set.seed(010101)
3  Data <- read.csv("https://raw.githubusercontent.com/
       BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
       Conflict.csv", sep = ",", header = TRUE, quote = "")
4
5  # Scale regressors
6  W <- as.matrix(scale(Data[, -c(1, 2)]))
7  niter <- 15000
8  y <- unlist(Data[, 2])
9
10 # Linear model
11 SSBoomLinear <- lm.spike(y ~ W, niter = niter)
12 Models <- SSBoomLinear$beta != 0
13 PIP <- colMeans(SSBoomLinear$beta != 0)
14 # Convert the logical matrix to a data frame and then to a
       tibble
15 df <- as.data.frame(Models); df_tbl <- as_tibble(df)
16 # Count identical rows
17 row_counts <- df_tbl %>% count(across(everything()), name =
       "frequency") %>% arrange(desc(frequency))
18 colnames(W)
19 # Get indices of best model
20 for(l in 1:5) {
21    print(which(row_counts[l,] == 1))
22    print(row_counts[l, dim(row_counts)[2]]/niter)
23 }
24 # Coefficients
25 SummarySS <- summary(coda::mcmc(SSBoomLinear$beta))
26 SummarySS
```

3. [45] proposes an SSVS approach for binary response models. Use the dataset *Conflict.xlsx*, where the dependent variable is *conflictcw*, to perform SSVS using the *BoomSpikeSlab* package, specifically the `logit.spike` function, in order to identify the best subset of models. Compare the results with those obtained in Exercise 2.

Answer

The following code illustrates how to implement SSVS in this application, based on [18], using 15,000 iterations and the default settings for the hyperparameters with a logit model.

We find that the results using a logit model are very similar to those ob-

tained with a linear model. Once again, infant mortality rate, population, peace, and political rights emerge as the most relevant drivers of the incidence of civil conflict. *Peace* exhibits a negative 95% credible interval, while the other variables have positive credible intervals. In this case, the model with the highest posterior probability (35%) includes infant mortality rate and peace. However, the model with the second-highest posterior probability (17%) includes the first three drivers.

R code. Application: Drivers of civil conflict in the post-Cold War era using a logit model

```r
1  rm(list = ls())
2  set.seed(010101)
3  Data <- read.csv("https://raw.githubusercontent.com/
      BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
      Conflict.csv", sep = ",", header = TRUE, quote = "")
4
5  # Scale regressors
6  W <- as.matrix(scale(Data[, -c(1, 2)]))
7  niter <- 15000
8  y <- unlist(Data[, 2])
9
10 # Logit model
11 SSBoomLogit <- logit.spike(y ~ W, niter = niter)
12 ModelsLogit <- SSBoomLogit$beta != 0
13 PIPLogit <- colMeans(SSBoomLogit$beta != 0)
14 # Convert the logical matrix to a data frame and then to a
      tibble
15 df <- as.data.frame(ModelsLogit); df_tbl <- as_tibble(df)
16 # Count identical rows
17 row_counts <- df_tbl %>% count(across(everything()), name =
      "frequency") %>% arrange(desc(frequency))
18 colnames(W)
19 # Get indices of best model
20 for(l in 1:5) {
21    print(which(row_counts[l,] == 1))
22    print(row_counts[l, dim(row_counts)[2]]/niter)
23 }
24 # Coefficients
25 SummarySSlogit <- summary(coda::mcmc(SSBoomLogit$beta))
26 SummarySSlogit
27
```

---

4. **Example: Simulation exercise $K > N$**

Use the simulation setting from the Bayesian LASSO and SSVS examples, but now assume there are 600 features. This setup implies that the number

of features exceeds the sample size. In such a scenario, there is no unique solution to the least squares estimator because the determinant of $\mathbf{W}^\top \mathbf{W}$ is zero. This means the matrix is not invertible, and consequently, standard inference procedures based on the least squares estimator cannot be applied. On the other hand, Bayesian inference in this setup is well-defined because the prior helps regularize the problem, which is a key motivation for these methods.

Answer

The following code shows how to perform this exercise using the *bayesreg* and *BoomSpikeSlab* packages. We observe that both the Bayesian LASSO and SSVS perform well (see Figure 12.2) and allow for valid inference.

R code. Simulation: Performance of the Bayesian LASSO and SSVS when $K > N$
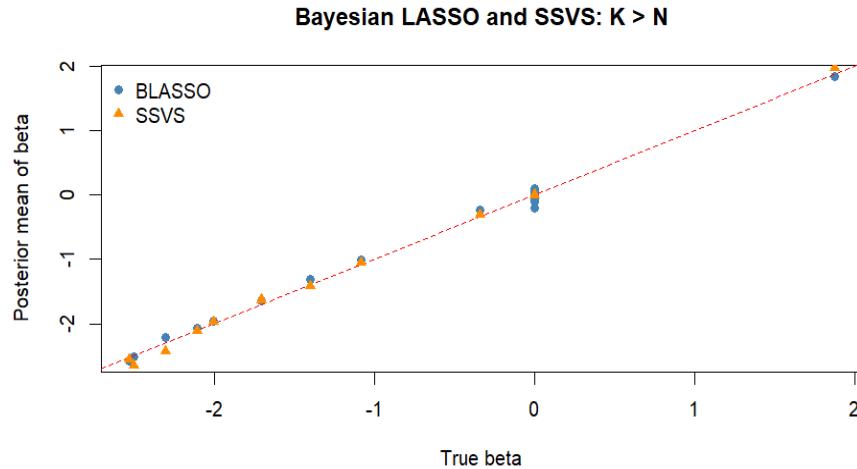
```r
1  rm(list = ls()); set.seed(10101)
2  library(BoomSpikeSlab)
3  library(dplyr)
4  library(tibble)
5  library(bayesreg)
6  # Parameters
7  n <- 500   # sample size
8  k <- 600   # number of predictors
9  s <- 10    # number of non-zero coefficients
10 # Generate design matrix
11 X <- matrix(rnorm(n * k), nrow = n, ncol = k)
12 # True beta: first s coefficients are non-zero, rest are
       zero
13 beta_true <- c(runif(s, -3, 3), rep(0, k - s))
14 # Generate response with some noise
15 sigma <- 1
16 y <- X %*% beta_true + rnorm(n, sd = sigma)
17 df <- data.frame(X,y)
18 ### Using BoomSpikeSlab ###
19 #Scale regressors
20 W <- scale(X); yh <- y - mean(y)
21 niter <- 5000
22 ######Estimate model########
23 # Least squared
24 Reg <- lm(y ~ X)
25 summary(Reg)
26 ## BLASSO ##
27 # Fit the model
28 fit <- bayesreg::bayesreg(y ~ X, data = df, model = "
       gaussian", prior = "lasso",
29 n.samples = niter, burnin = 1000)
30 # Check summary
31 summary(fit)
32 # Extract posterior means of beta
33 beta_post_meanLASSO <- rowMeans(fit$beta)
34
35 ## SSVS ##
36 SSBoomNew <- lm.spike(yh ~ W - 1, niter = niter)
37 # Coefficients
38 SummarySS <- summary(coda::mcmc(SSBoomNew$beta))
39 # Extract posterior means of beta
40 beta_post_meanSSVS <- SummarySS$statistics[, 1]
41
42 # Compare true vs estimated
43 plot(beta_true, beta_post_meanLASSO, pch = 19, col = "
       steelblue",
44 xlab = "True beta", ylab = "Posterior mean of beta",
45 main = "Bayesian LASSO and SSVS")
46 abline(0, 1, col = "red", lty = 2)
47 # Add another set of posterior means
48 points(beta_true, beta_post_meanSSVS, pch = 17, col = "
       darkorange")
49 # Add legend
50 legend("topleft", legend = c("BLASSO", "SSVS"),
51 col = c("steelblue", "darkorange"),
52 pch = c(19, 17), bty = "n")
```

FIGURE 12.2
Performance of the Bayesian LASSO and SSVS: $K > N$.

5. **Simulation exercise: the BART model continues**

Compute Friedman's partial dependence functions [8] for all variables in the BART model simulation example, and plot the posterior mean along with the 95% credible intervals.

Answer

The following code illustrates how to compute the posterior distribution of Friedman's partial dependence functions. Figures 12.3 and 12.4 display the results for variables 1 and 10. From the simulation setup, we know that variable 1 is relevant, whereas variable 10 is irrelevant. This is reflected in the partial dependence functions: the function for variable 10 is flat, indicating no effect, while the function for variable 1 shows a positive relationship with the outcome variable.

R code. Simulation: Partial dependence functions from BART models
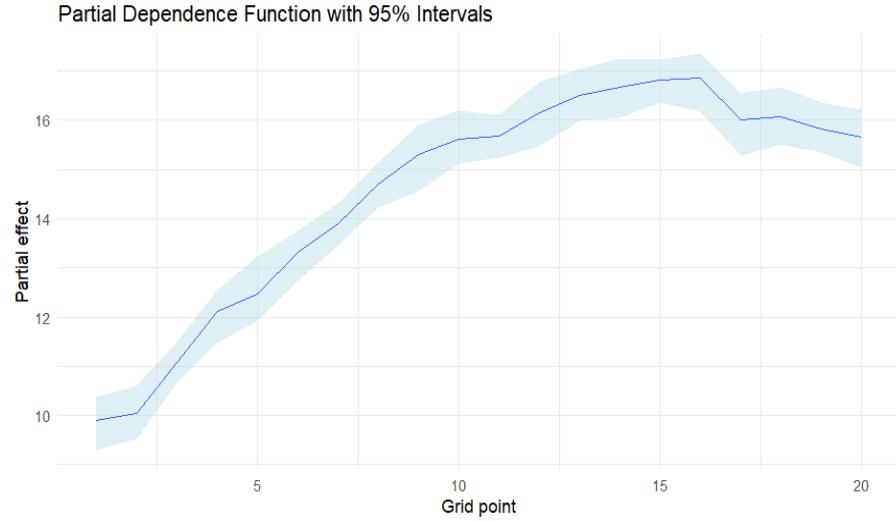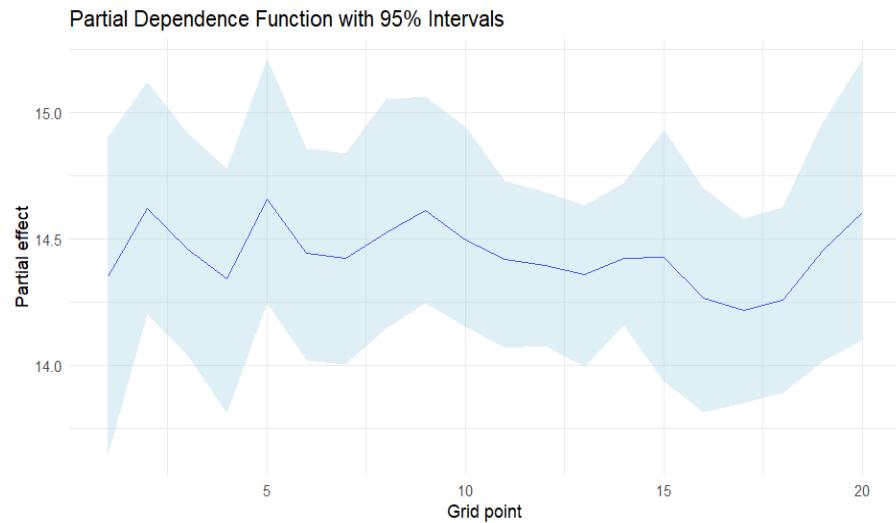
```r
1  rm(list = ls()); set.seed(10101)
2  library(BART); library(ggplot2); library(dplyr); library(
       tidyr)
3  N <- 500; K <- 10
4  # Simulate the dataset
5  MeanFunct <- function(x){
6    f <- 10*sin(pi*x[,1]*x[,2]) + 20*(x[,3]-.5)^2+10*x[,4]+5*x
       [,5]
7    return(f)
8  }
9  sig2 <- 1
10 e <- rnorm(N, 0, sig2^0.5)
11 X <- matrix(runif(N*K),N,K)
12 y <- MeanFunct(X[,1:5]) + e
13 # Hyperparameters
14 alpha <- 0.95; beta <- 2; k <- 2
15 v <- 3; q <- 0.9; J <- 200
16 # MCMC parameters
17 MCMCiter <- 1000; burnin <- 100; thinning <- 1
18 # Partial dependence function
19 BARTfit <- wbart(x.train = X, y.train = y, base = alpha,
20 power = beta, k = k, sigdf = v, sigquant = q, ntree = J,
21 ndpost = MCMCiter, nskip = burnin, keepevery = thinning)
22 k <- 1; L <- 20
23 x <- seq(min(X[, k]), max(X[, k]), length.out = L)
24 X.test <- X
25 X.test[,k] <- x[1]
26 for(j in 2:L){
27   X.k <- X
28   X.k[,k] <- x[j]
29   X.test <- rbind(X.test, X.k)
30 }
31 pred <- predict(BARTfit, X.test)
32 partial <- matrix(nrow = MCMCiter, ncol = L)
33 for(j in 1:L) {
34   h <- (j - 1) * N + 1:N
35   partial[, j] <- apply(pred[, h], 1, mean)
36 }
37 partial_df <- as.data.frame(partial)
38 partial_df$draw <- 1:nrow(partial_df)
39 long_df <- pivot_longer(partial_df, cols = -draw, names_to =
       "x", values_to = "value")
40 long_df$x <- as.numeric(gsub("V", "", long_df$x))
41 summary_df <- long_df %>% group_by(x) %>%
42 summarise(mean = mean(value), lower = quantile(value, 0.025)
       , upper = quantile(value, 0.975)
43 )
44 ggplot(summary_df, aes(x = x, y = mean)) + geom_line(color =
       "blue") + geom_ribbon(aes(ymin = lower, ymax = upper),
       fill = "lightblue", alpha = 0.4) + labs(x = "Grid point"
       , y = "Partial effect", title = "Partial Dependence
       Function with 95% Intervals") + theme_minimal()
```

FIGURE 12.3
Partial dependence function: Variable 1.

FIGURE 12.4
Partial dependence function: Variable 10.

6. [45] proposes an SSVS approach for binary response models. Use the dataset *Conflict.csv*, where the dependent variable is *conflictcw*, to perform SSVS using the *BoomSpikeSlab* package, specifically the `logit.spike`

function, in order to identify the best subset of models. Compare the results with those obtained in Exercise 2.

Answer

The following code demonstrates how to perform probit BART for binary classification. According to the results obtained using 10 trees, the most relevant regressors are *infant mortality rate*, *peace*, *political rights*, and *population*. Note that this agrees with previous exercises using this dataset.

R code. Application: Probit BART for binary classification

```r
1  rm(list = ls()); set.seed(10101)
2  library(BART); library(tidyr)
3  library(pROC); library(caret)
4  # Load and prepare data
5  Data <- read.csv("https://raw.githubusercontent.com/
       BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
       Conflict.csv", sep = ",", header = TRUE, quote = "")
6  X <- as.matrix(Data[, -c(1, 2)])
7  y <- unlist(Data[, 2])
8  # MCMC parameters
9  niter <- 1000; burnin <- 200; J <- 200
10 # Create 5-fold cross-validation indices
11 folds <- createFolds(y, k = 5, list = TRUE, returnTrain =
       FALSE)
12 thresholds <- seq(0.01, 0.99, by = 0.01)
13 scores <- matrix(0, nrow = 5, ncol = length(thresholds))
14 for (i in 1:5) {
15   test_idx <- folds[[i]]; train_idx <- setdiff(1:length(y),
       test_idx)
16   X.train <- X[train_idx, ];  y.train <- y[train_idx]
17   X.test <- X[test_idx, ]; y.test <- y[test_idx]
18   pf <- pbart(x.train = X.train, y = y.train, x.test = X.
       train, ntree = J, ndpost = niter, nskip = burnin)
19   prob_train <- pf$prob.test.mean
20   for (j in 1:length(thresholds)) {
21     thresh <- thresholds[j]
22     preds <- ifelse(prob_train > thresh, 1, 0)
23     TP <- sum(preds == 1 & y.train == 1)
24     TN <- sum(preds == 0 & y.train == 0)
25     FP <- sum(preds == 1 & y.train == 0)
26     FN <- sum(preds == 0 & y.train == 1)
27     TPR <- TP / (TP + FN + 1e-8)
28     TNR <- TN / (TN + FP + 1e-8)
29     scores[i, j] <- TPR + TNR
30   }
31 }
32 mean_scores <- colMeans(scores)
33 best_thresh <- thresholds[which.max(mean_scores)]
34 cat("Optimal threshold by CV:", best_thresh, "\n")
35 # Train/test split to evaluate final performance
36 N <- nrow(X); K <- ncol(X)
37 N.train <- floor(0.8 * N); X.train <- X[1:N.train, ]; y.
       train <- y[1:N.train]
38 X.test <- X[(N.train + 1):N, ]; y.test <- y[(N.train + 1):N]
39 pf_final <- pbart(x.train = X.train, y = y.train, x.test = X
       .test, ntree = 200, ndpost = 1000, nskip = 200)
40 prob_test <- pf_final$prob.test.mean
41 y_pred_test <- ifelse(prob_test > best_thresh, 1, 0)
42 conf_mat <- table(Predicted = y_pred_test, Actual = y.test)
43 accuracy <- mean(y_pred_test == y.test)
44 print(conf_mat)
45 cat("Test set accuracy:", round(accuracy, 3), "\n")
```

R code. Application: Probit BART for binary classification

```r
# Relevant regressors
Js <- c(10, 20, 50, 100, 200)
VarImportance <- matrix(0, length(Js), K)
l <- 1
for (j in Js){
  BARTfit <- BART::pbart(x.train = X.train, y = y.train, x.
      test = X.test, ntree = j, ndpost = niter, nskip = burnin
      )
  VarImportance[l, ] <- BARTfit[["varcount.mean"]]/j
  l <- l + 1
}
# Assign row and column names for clarity
rownames(VarImportance) <- as.character(Js)
colnames(VarImportance) <- as.character(1:K)
# Convert to long format
importance_df <- as.data.frame(VarImportance) %>%
mutate(trees = rownames(.)) %>%
pivot_longer(
cols = -trees,
names_to = "variable",
values_to = "percent_used"
)
# Make variable numeric for plotting
importance_df$variable <- as.numeric(importance_df$variable)
importance_df$trees <- factor(importance_df$trees, levels =
    c("10", "20", "50", "100", "200"))

ggplot(importance_df, aes(x = variable, y = percent_used,
    color = trees, linetype = trees)) +
geom_line() + geom_point() + scale_color_manual(values = c("
    10" = "red", "20" = "green", "50" = "blue", "100" = "
    cyan", "200" = "magenta")) + scale_x_continuous(breaks =
    1:K) + labs(x = "variable", y = "percent used", color =
    "#trees", linetype = "#trees") + theme_minimal()

data.frame(Nanes = colnames(X), Frequency = VarImportance
    [1,])
```

7. **Simulation exercise: The Gaussian Process simulation continues**

   Simulate the process

   $$f_i = \sin(2\pi x_{i1}) + \cos(2\pi x_{i2}) + \sin(x_{i1}x_{i2}) + \mu_i,$$

   where $\mu_i \overset{\text{i.i.d.}}{\sim} N(0, 0.1^2)$, $x_{ik} \sim U(0,1)$ for $k = 1, 2$, and the sample size is 500.

Define a grid of 20 evenly spaced values between 0 and 1 for each covariate x_{ik}, and use this grid to perform prediction.

Estimate the hyperparameters of the Gaussian Process by maximizing the log marginal likelihood. Then, use the *km* function from the *DiceKriging* package to fit the Gaussian Process, fixing the noise variance at the value that maximizes the log marginal likelihood.

Finally, use the fitted model to predict the outputs on the grid points, and produce a 3D plot showing the predicted surface along with the training data points.

Answer

We use the Cholesky decomposition to optimize time calculating the inverse of the covariance matrix. In particular, let $\mathbf{K} \in \mathbb{R}^{N \times N}$ be a symmetric positive definite matrix. Then, it admits a Cholesky decomposition:

$$\mathbf{K} = \mathbf{L}\mathbf{L}^\top,$$

where $\mathbf{L}$ is a lower triangular matrix with positive diagonal entries.

The determinant of $\mathbf{K}$ can be computed using the Cholesky factor:

$$\det(\mathbf{K}) = \det(\mathbf{L}\mathbf{L}^\top) = \det(\mathbf{L})^2.$$

Since $\mathbf{L}$ is lower triangular, its determinant is the product of its diagonal elements:

$$\det(\mathbf{K}) = \left(\prod_{i=1}^{N} L_{ii} \right)^2.$$

Equivalently, the log-determinant is:

$$\log |\mathbf{K}| = 2 \sum_{i=1}^{N} \log L_{ii}.$$

The inverse of $\mathbf{K}$ can also be computed using the Cholesky factor:

$$\mathbf{K}^{-1} = (\mathbf{L}\mathbf{L}^\top)^{-1} = (\mathbf{L}^\top)^{-1}\mathbf{L}^{-1}.$$

This is useful computationally because triangular systems can be solved efficiently via forward and backward substitution:

(a) Solve $\mathbf{L}\mathbf{z} = \mathbf{b}$ for $\mathbf{z}$ (forward solve),

(b) Solve $\mathbf{L}^\top \mathbf{x} = \mathbf{z}$ for $\mathbf{x}$ (backward solve),

then, $\mathbf{x} = (\mathbf{L}^\top)^{-1}\mathbf{z} = (\mathbf{L}^\top)^{-1}\mathbf{L}^{-1}\mathbf{b} = (\mathbf{LL}^\top)^{-1}\mathbf{b} = \mathbf{K}^{-1}\mathbf{b}$. Thus, we avoid computing the matrix inverse, which requires $O(N^3)$ operations. Instead, it is more efficient and numerically stable to solve triangular systems of equations, which arise naturally from the Cholesky decomposition.

The following code shows how to perform this exercise, and Figure 12.5 displays the 3D plot.

R code. Simulation:
$$f_i = \sin(2\pi x_{i1}) + \cos(2\pi x_{i2}) + \sin(x_{i1}x_{i2}) + \mu_i \textbf{ and}$$
Gaussian process
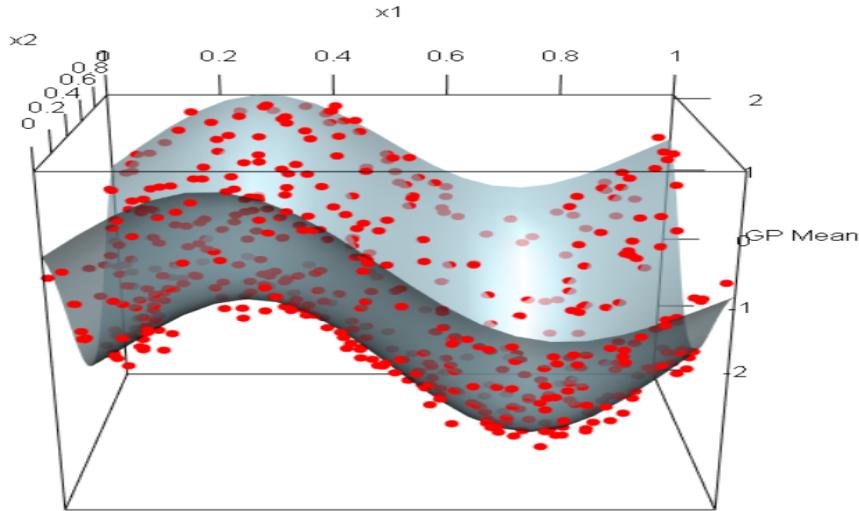
```r
rm(list = ls()); set.seed(10101)
library(fields); library(DiceKriging); library(ggplot2)
# Simulate training data
n_train <- 500
x1 <- runif(n_train); x2 <- runif(n_train)
X_train <- data.frame(x1 = x1, x2 = x2)
sig <- 0.1; u <- rnorm(n_train, mean = 0, sd = sig)
# True function without noise
f_train <- sin(2 * pi * X_train$x1) + cos(2 * pi * X_train$
    x2) + sin(X_train$x1 * X_train$x2)
y_train <- scale(f_train + u)
# Empirical Bayes: Optimize the log marginal likelihood
log_marginal_likelihood <- function(par, X, y) {
  sigma2_f <- par[1]; l2 <- par[2]; sigma2_n <- par[3]; n <-
      nrow(X)
  # Ensure parameters are positive
  if (sigma2_f <= 0 | l2 <= 0 | sigma2_n <= 0) return(Inf)
  # Squared exponential kernel
  dists <- rdist(X)
  K <- sigma2_f * exp(-0.5 * (dists^2) / l2)
  # Add noise variance + jitter for numerical stability
  K <- K + (sigma2_n + 1e-8) * diag(n)
  # Cholesky decomposition
  L <- tryCatch(chol(K), error = function(e) return(NULL))
  if (is.null(L)) return(Inf)
  alpha <- backsolve(t(L), forwardsolve(L, y)) #--> K^{-1}y
  log_det_K <- 2 * sum(log(diag(L)))
  lml <- -0.5 * t(y) %*% alpha - 0.5 * log_det_K - 0.5 * n *
      log(2 * pi)
  return(-as.numeric(lml))  # Negative log-marginal
      likelihood
}
par0 <- rep(1, 3)
ResOpt <- optim(par = par0, fn = log_marginal_likelihood,
    method = "L-BFGS-B", lower = c(1e-5, 1e-5), X = X_train,
    y = y_train)
theta_hat <- ResOpt$par
sigma2_f_hat <- theta_hat[1]; l2_hat <- theta_hat[2]; sigma2
    _n_hat <- theta_hat[3]
# Grid for prediction
grid_points <- 20
x1_seq <- seq(0, 1, length.out = grid_points)
x2_seq <- seq(0, 1, length.out = grid_points)
X_new <- expand.grid(x1 = x1_seq, x2 = x2_seq)
# Fit Gaussian Process
fit_km <- km(design = X_train, response = y_train, covtype =
    "gauss", noise.var = rep(sigma2_n_hat, n_train))
# Predict GP surface
pred <- predict(fit_km, newdata = X_new, type = "UK")
z_pred <- matrix(pred$mean, nrow = grid_points, ncol = grid_
    points)
# Plot
persp3d(x = x1_seq, y = x2_seq, z = z_pred, col = "lightblue
    ", alpha = 0.7, xlab = "x1", ylab = "x2", zlab = "GP
    Mean")
points3d(x = X_train$x1, y = X_train$x2, z = y_train, col =
    "red", size = 8)
```

FIGURE 12.5
Simulation: $f_i = \sin(2\pi x_{i1}) + \cos(2\pi x_{i2}) + \sin(x_{i1} x_{i2}) + \mu_i$ and Gaussian process

8. **Simulation exercise: Stochastic gradient MCMC continues**

   Program from scratch the stochastic gradient Langevin dynamic algorithm for the logit simulation exercise implementing the control variate version performing 1,500 stochastic gradient descent iterations to locate the posterior mode, which should be then used as the initial value for 1,000 subsequent MCMC iterations using a step size set to 1×10^{-4}.

   Answer

   The following code illustrates how to implement the Stochastic Gradient Langevin Dynamics (SGLD) algorithm with a control variate. Figure 12.6 shows the posterior distributions obtained from the SGLD algorithm with a control variate and the Metropolis-Hastings algorithm. We observe that the former is well centered, but exhibits overdispersion; however, the control variate helps reduce the variability compared to the naive SGLD algorithm (see Figure 12.10 in the book).

R code. Stochastic Gradient Langevin Dynamic control variate (SGLDcv): Logit regression

```r
1  rm(list = ls()); set.seed(10101)
2  library(mvtnorm); library(MCMCpack)
3  library(ggplot2); library(dplyr)
4  #--- Generate correlated covariates
5  genCovMat <- function(K, rho = 0.4) {
6    Sigma0 <- matrix(1, K, K)
7    for (i in 2:K) {
8      for (j in 1:(i - 1)) {
9        Sigma0[i, j] <- runif(1, -rho, rho)^(i - j)
10     }
11   }
12   Sigma0 <- Sigma0 * t(Sigma0)
13   diag(Sigma0) <- 1
14   return(Sigma0)
15 }
16 #--- Simulate logistic regression data
17 simulate_logit_data <- function(K, N, beta_true) {
18   Sigma0 <- genCovMat(K)
19   X <- rmvnorm(N, mean = rep(0, K), sigma = Sigma0)
20   linpred <- X %*% beta_true
21   p <- 1 / (1 + exp(-linpred))
22   y <- rbinom(N, 1, p)
23   list(y = y, X = X)
24 }
25 #--- One SGD step
26 SGD_step <- function(beta, y, X, lr, batch_size, prior_var =
        10) {
27   N <- nrow(X)
28   K <- length(beta)
29   ids <- sample(1:N, size = batch_size, replace = FALSE)
30
31   grad <- rep(0, K)
32   for (i in ids) {
33     xi <- X[i, ]
34     eta <- sum(xi * beta)
35     pi <- 1 / (1 + exp(-eta))
36     grad_i <- -(y[i] - pi) * xi
37     grad <- grad + grad_i
38   }
39
40   grad <- grad / batch_size + beta / prior_var * 1 / N
41
42   beta_new <- beta - lr * grad
43   return(beta_new)
44 }
45 #--- Parameters
46 K <- 10; N <- 100000
47 beta_true <- rep(0.5, K); batch_prop <- 0.01
48 batch_size <- round(N*batch_prop); n_iter <- 1000
49 n_iterSGD <- 1500; kappa <- 0.55
50 stepsize <- 1e-4; prior_var <- 10
51 k_target <- 5  # beta5
52
53 sim_data <- simulate_logit_data(K, N, beta_true)
54 y <- sim_data$y
55 X <- scale(sim_data$X)
```

R code. Stochastic Gradient Langevin Dynamic control variate (SGLDcv): Logit regression

```r
1  beta_mat <- matrix(0, n_iterSGD, K)
2  beta_mat[1, ] <- rep(0, K)
3  for (s in 2:n_iterSGD) {
4    beta_mat[s, ] <- SGD_step(beta_mat[s - 1, ], y = y, X = X,
        lr = s^(-kappa), batch_size = batch_size, prior_var =
        prior_var)
5  }
6  matplot(beta_mat, type = "l"); betahat <- beta_mat[s, ]
7  gradhat <- rep(0, K)
8  for (i in 1:N) {
9    xi <- X[i, ]
10   etahat <- sum(xi * betahat)
11   pihat <- 1 / (1 + exp(-etahat))
12   grad_ihat <- -(y[i] - pihat) * xi
13   gradhat <- gradhat + grad_ihat
14 }
15 #--- One SGLD control variate step
16 SGLDcv_step <- function(beta, betahat, gradhat, y, X,
        stepsize, batch_size, prior_var = 10) {
17   N <- nrow(X)
18   K <- length(beta)
19   ids <- sample(1:N, size = batch_size, replace = FALSE)
20   grad_dif <- rep(0, K)
21   for (i in ids) {
22     xi <- X[i, ]
23     eta <- sum(xi * beta)
24     pi <- 1 / (1 + exp(-eta))
25     etahat <- sum(xi * betahat)
26     pihat <- 1 / (1 + exp(-etahat))
27     grad_dif_i <- (pi - pihat) * xi
28     grad_dif <- grad_dif + grad_dif_i
29   }
30   grad <- gradhat + grad_dif / batch_size * N
31   grad <- grad + beta / prior_var  # gradient of log-prior
32   noise <- rnorm(K, 0, sqrt(stepsize))
33   beta_new <- beta - 0.5 * stepsize * grad + noise
34   return(beta_new)
35 }
36
37 #--- SGLD algorithm
38 run_SGLDcv <- function(y, X, stepsize, batch_prop, n_iter,
        beta_init = NULL, prior_var = prior_var) {
39   N <- nrow(X)
40   K <- ncol(X)
41   batch_size <- round(batch_prop * N)
42   beta_mat <- matrix(0, n_iter, K)
43   beta_mat[1, ] <- if (is.null(beta_init)) rep(0, K) else
        beta_init
44   for (s in 2:n_iter) {
45     beta_mat[s, ] <- SGLDcv_step(beta_mat[s - 1, ], betahat
        = betahat, gradhat = gradhat, y, X, stepsize, batch_size
        )
46   }
47   return(beta_mat)
48 }
49 #--- Run SGLD cv
50 posterior_sgldcv <- run_SGLDcv(y, X, stepsize, batch_prop, n
        _iter)
```

R code. Stochastic Gradient Langevin Dynamic control variate (SGLDcv): Logit regression

```r
1 #--- Run MCMCpack logit
2 df <- as.data.frame(X)
3 colnames(df) <- paste0("X", 1:K)
4 df$y <- y
5 formula <- as.formula(paste("y ~", paste(colnames(df)[1:K],
      collapse = " + "), "-1"))
6 posterior_mh <- MCMClogit(formula, data = df, b0 = 0, B0 =
      0.1,
7 burnin = n_iterSGD, mcmc = n_iter)
8 #--- Compare densities for beta5
9 df_plot <- data.frame(
10 value = c(posterior_sgldcv[, k_target], posterior_mh[, k_
      target]),
11 method = rep(c("SGLDcv", "MCMC"), each = n_iter)
12 )
13 ggplot(df_plot, aes(x = value, fill = method, color = method
      )) + geom_density(alpha = 0.4) + geom_vline(xintercept =
       beta_true[k_target], linetype = "dashed", color = "
      black") + labs(title = expression(paste("Posterior
      density of ", beta[k_target])), x = expression(beta[k_
      target]), y = "Density") + theme_minimal() + xlim(0.45,
      0.55)
```

9. Perform the simulation according to the model $y_i = 1 - 2x_{i1} + 0.5x_{i2} + \mu_i$, where $\mu_i \sim N(0,1)$, the sample size is 100,000, and the covariates $\mathbf{x}_i \sim N(\mathbf{0}, \mathbf{I}_2)$. Use 5,000 MCMC iterations and a batch size of 1,000 to implement the SGLD algorithm. Set a learning rate schedule that yields sensible results.

   Assume independent priors $\pi(\boldsymbol{\beta}, \sigma^2) = \pi(\boldsymbol{\beta}) \times \pi(\sigma^2)$, with $\boldsymbol{\beta} \sim N(\mathbf{0}, \mathbf{I}_3)$ and $\sigma^2 \sim IG(\alpha_0/2, \delta_0/2)$, where $\alpha_0 = \delta_0 = 0.01$.
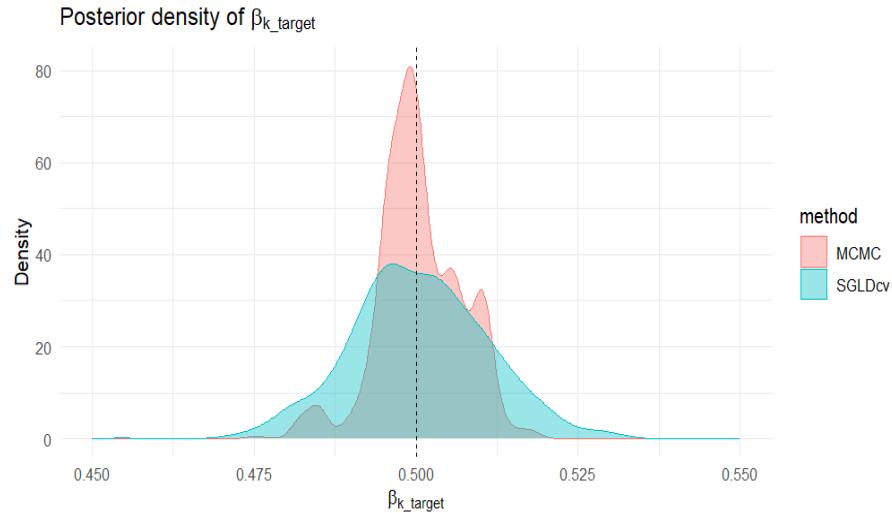
   Answer

   Take into account that SGLD was originally developed for parameter spaces in $\mathbb{R}^K$. In this exercise, we use SGLD to perform inference on $\boldsymbol{\beta}$, while obtaining draws from the conditional posterior distribution of $\sigma^2 \sim IG(\alpha_n/2, \delta_n/2)$, where $\alpha_n = N + \alpha_0$ and $\delta_n = (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\top(\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \delta_0$.

   Additionally, recall the gradients involved in the SGLD updates:

   $$\nabla_{\boldsymbol{\beta}} \log p(\mathbf{y} \mid \boldsymbol{\beta}, \sigma^2) = \frac{1}{\sigma^2} \mathbf{X}^\top(\mathbf{y} - \mathbf{X}\boldsymbol{\beta}),$$
   $$\nabla_{\boldsymbol{\beta}} \log \pi(\boldsymbol{\beta}) = -\boldsymbol{\beta}.$$

Posterior density of β_{k_target}

FIGURE 12.6
Simulation: Posterior distributions from logit simulation exercise

The following code illustrates how to implement this procedure. We note that the results for the location parameters $\boldsymbol{\beta}$ are satisfactory; however, the algorithm appears to exhibit a positive bias in the estimation of σ^2.

R code. Stochastic Gradient MCMC (SG-MCMC): Linear regression

```r
1  rm(list = ls()); set.seed(10101)
2  # Simulated data
3  N <- 100000; K <- 3
4  X <- cbind(1, matrix(rnorm(N * (K - 1)), N, K - 1))  #
       design matrix
5  beta_true <- c(1, -2, 0.5); sigma2_true <- 1
6  y <- X %*% beta_true + rnorm(N, 0, sqrt(sigma2_true))
7  X[, 2:3] <- scale(X[, 2:3])
8  # SGLD settings
9  iterations <- 5000
10 batch_size <- 1000
11 initial_stepsize <- 1e-4
12 decay_rate <- 0.55
13 schedule <- 1000
14 # Priors
15 a0 <- 0.01; b0 <- 0.01
16 # Storage
17 trace_beta <- matrix(NA, nrow = iterations, ncol = K)
18 trace_sigma2 <- rep(NA, iterations)
19 # Initialization
20 beta <- rep(0, K)
21 sigma2 <- 0.5
22 # Gradient of log-posterior w.r.t. beta (scaled)
23 grad_log_post <- function(beta, X_batch, y_batch, N, sigma2)
       {
24   grad_loglik <- t(X_batch) %*% (y_batch - X_batch %*% beta)
       / sigma2
25   grad_logprior <- -beta  # derivative of log N(0, I)
26   return((N / nrow(X_batch)) * grad_loglik + grad_logprior)
27 }
```

R code. Stochastic Gradient MCMC (SG-MCMC): Linear regression

```r
# SGLD algorithm
for (t in 1:iterations) {
  # Step size
  stepsize_t <- initial_stepsize / (1 + t / schedule)^decay_
      rate
  # Sample mini-batch
  idx <- sample(1:N, batch_size)
  X_batch <- X[idx, ]
  y_batch <- y[idx]
  # Beta update via SGLD
  grad <- grad_log_post(beta, X_batch, y_batch, N, sigma2)
  noise <- rnorm(K, 0, sqrt(stepsize_t))
  beta <- beta + 0.5 * stepsize_t * grad + noise
  # Sigma2 update via inverse-gamma (full conditional)
  resid <- y - X %*% beta
  shape <- (a0 + N) / 2
  rate <- (b0 + sum(resid^2)) / 2
  sigma2 <- 1 / rgamma(1, shape = shape, rate = rate)
  # Store draws
  trace_beta[t, ] <- beta
  trace_sigma2[t] <- sigma2
}
# Plot trace of beta[2]
plot(trace_beta[4001:5000, 2], type = "l", col = "blue", lwd
     = 2,
main = expression("SGLD: Evolution of " * beta[2]),
xlab = "Iteration", ylab = expression(beta[2]))
abline(h = beta_true[2], col = "red", lty = 2)
# Plot trace of sigma2
plot(trace_sigma2[4001:5000], type = "l", col = "darkgreen",
      lwd = 2,
main = expression("Trace plot of " * sigma^2),
xlab = "Iteration", ylab = expression(sigma^2))
abline(h = sigma2_true, col = "red", lty = 2)
```

13

Causal inference

Solutions of Exercises

1. Show that the Average Treatment Effect (ATE) in the simple linear regression framework

$$Y_i = \beta_0 + \tau D_i + \mu_i,$$

assuming non-informative prior distributions, so that the posterior mean of the location parameter coincides with the maximum likelihood estimator, is equal to

$$\bar{y}_1 - \bar{y}_0.$$

Answer

Consider the simple linear regression model

$$Y_i = \beta_0 + \tau D_i + \mu_i, \qquad i = 1, \dots, N,$$

where $D_i \in \{0, 1\}$ is a treatment indicator. In matrix notation:

$$\mathbf{y} = X\boldsymbol{\beta} + \boldsymbol{\mu}, \qquad X = \begin{pmatrix} 1 & D_1 \\ \vdots & \vdots \\ 1 & D_n \end{pmatrix}, \qquad \boldsymbol{\beta} = \begin{pmatrix} \beta_0 \\ \tau \end{pmatrix}.$$

Under the usual Gaussian likelihood and a non-informative prior $\pi(\boldsymbol{\beta}, \sigma^2) \propto \sigma^{-2}$, the posterior mean of $\boldsymbol{\beta}$ coincides with the maximum likelihood estimator (MLE), which is the ordinary least squares (OLS) estimator:

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

Compute $\mathbf{X}^\top \mathbf{X}$ and $\mathbf{X}^\top \mathbf{y}$:

$$\mathbf{X}^\top \mathbf{X} = \begin{pmatrix} N & N_1 \\ N_1 & N_1 \end{pmatrix}, \qquad \mathbf{X}^\top \mathbf{y} = \begin{pmatrix} \sum_{i=1}^{N} y_i \\ \sum_{i:D_i=1} y_i \end{pmatrix},$$

where $N_1 = \sum_i D_i$ and $N_0 = N - N_1$. Let $\bar{y}_1 = \frac{1}{N_1} \sum_{i:D_i=1} y_i$ and $\bar{y}_0 = \frac{1}{N_0} \sum_{i:D_i=0} y_i$.

Compute the inverse:

$$(\mathbf{X}^\top \mathbf{X})^{-1} = \frac{1}{N_0 N_1} \begin{pmatrix} N_1 & -N_1 \\ -N_1 & N \end{pmatrix}.$$

Thus:

$$\widehat{\boldsymbol{\beta}} = \frac{1}{N_0 N_1} \begin{pmatrix} N_1 & -N_1 \\ -N_1 & N \end{pmatrix} \begin{pmatrix} \sum_{i=1}^{N} y_i \\ \sum_{i:D_i=1} y_i \end{pmatrix} = \begin{pmatrix} \bar{y}_0 \\ \bar{y}_1 - \bar{y}_0 \end{pmatrix}.$$

Therefore, the intercept equals the mean outcome for the control group ($\bar{y}_0$), and the slope equals the difference in means between treated and control groups:

$$\widehat{\tau} = \bar{y}_1 - \bar{y}_0.$$

Since under a non-informative prior the posterior mean equals the ML estimator, the posterior mean of τ coincides with the sample difference in means:

$$\text{ATE} = \mathbb{E}[\tau \mid \mathbf{y}] = \bar{y}_1 - \bar{y}_0.$$

2. Some readers may question the assumption that potential outcomes are normally distributed. However, it is important to note that the normal distribution is the *maximum entropy* continuous distribution given a specified mean μ and finite variance σ^2. In other words, among all distributions with the same mean and variance, the normal distribution represents the one with the greatest level of uncertainty or unpredictability [7].

Show that the normal distribution is the *maximum entropy* continuous distribution given a specified mean μ and finite variance σ^2 by considering the formal definition of entropy:

$$H(f) = -\int_{-\infty}^{\infty} f(y) \log f(y) \, dy,$$

where $f(y)$ is a probability density function.

Answer

We want to maximize $H(f)$ subject to the constraints:

$$\int_{-\infty}^{\infty} f(y) \, dy = 1, \qquad \int_{-\infty}^{\infty} y f(y) \, dy = \mu, \qquad \int_{-\infty}^{\infty} (y - \mu)^2 f(y) \, dy = \sigma^2.$$

Form the Lagrangian:

$$\mathcal{L}(f) = -\int f(y) \log f(y) \, dy + \lambda_0 \left(\int f(y) \, dy - 1 \right) + \lambda_1 \left(\int y f(y) \, dy - \mu \right) + \lambda_2 \left(\int (y - \mu)^2 f(y) \, dy - \sigma^2 \right).$$

Taking the functional derivative with respect to $f(y)$:

$$\frac{\delta \mathcal{L}}{\delta f} = -(\log f(y) + 1) + \lambda_0 + \lambda_1 y + \lambda_2 (y - \mu)^2 = 0.$$

Thus:

$$\log f(y) = \lambda_0' + \lambda_1 y + \lambda_2 (y - \mu)^2,$$

where λ_0' absorbs constants. Exponentiating:

$$f(y) \propto \exp\left(\lambda_1 y + \lambda_2 (y - \mu)^2\right).$$

For integrability, $\lambda_2 < 0$. Completing the square:

$$f(y) \propto \exp\left(-\frac{(y - \mu)^2}{2\sigma^2}\right),$$

which is the kernel of a normal density. Normalizing:

$$f(y) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(y - \mu)^2}{2\sigma^2}\right).$$

Therefore, the maximum entropy distribution for a given mean μ and variance σ^2 is

$$Y \sim N(\mu, \sigma^2).$$

3. Use the package *dagity* to construct the DAG in Figure 13.5, verify that it is acyclic, and check whether the causal effect of D on Y is identifiable by controlling for $\mathbf{X}$.

   Answer

R code. Simple exercise in dagity package: Conditional independence assumption

```
1  library(dagitty)
2  library(ggdag)
3
4  Gd = dagitty('dag{
5    X [pos="-1,1"]
6    D [exposure, pos="0,0"]
7    Y [outcome, pos="1,1"]
8    X -> D
9    X -> Y
10   D -> Y
11 }')
12
13 ggdag(Gd) +  theme_dag()
14
15 isAcyclic(Gd)
16
17 for( n in names(Gd) ){
18   for( m in children(Gd,n) ){
19     a <- adjustmentSets(Gd, n, m, effect = c("direct"), type
       = c("minimal"))
20     if( length(a) > 0 ){
21       cat("The effect ",n,"->",m,
22       " is identifiable by controlling for:\n",sep="")
23       print( a, prefix=" * " )
24     }
25   }
26 }
```

4. Use the package *dagitty* to construct the DAG in Figure 13.8, verify that it is acyclic, and check that the causal effect of D on Y is identifiable by controlling for **X** but not for C.

   Answer

R code. Simple exercise in dagity package: Collider bias

```r
#### DAG: Collider bias    ####
library(dagitty)
library(ggdag)

Gd = dagitty('dag{
  X [pos="-1,1"]
  D [exposure, pos="0,0"]
  Y [outcome, pos="1,1"]
  C [pos="0,0.5"]
  X -> D
  X -> Y
  X -> C
  D -> Y
  D -> C
}')

ggdag(Gd) +  theme_dag()

isAcyclic(Gd)

adjustmentSets(Gd, exposure = "D", outcome = "Y")

for( n in names(Gd) ){
  for( m in children(Gd,n) ){
    a <- adjustmentSets(Gd, n, m, effect = c("direct"), type
      = c("minimal"))
    if( length(a) > 0 ){
      cat("The effect ",n,"->",m,
      " is identifiable by controlling for:\n",sep="")
      print( a, prefix=" * " )
    }
  }
}
```

5. Use the package *dagitty* to construct the DAG in Figure 13.11, taking into account that **U** is unobserved (latent). Verify that it is acyclic, check that Z is a valid instrument, and determine whether the causal effect of D on Y is identifiable.

Answer

<div style="border:1px solid #000">

R code. Simple exercise in dagity package: Instrumental variable

```
1  #### DAG: Instruments   ####
2  library(dagitty)
3  library(ggdag)
4
5  Gd = dagitty('dag{
6     U [latent, pos="-1,1"]
7     D [exposure, pos="0,0"]
8     Y [outcome, pos="1,1"]
9     Z [pos="0,0.5"]
10    U -> D
11    U -> Y
12    D -> Y
13    Z -> D
14 }')
15
16 ggdag(Gd) +  theme_dag()
17
18 isAcyclic(Gd)
19
20 instrumentalVariables(Gd)
21
22 adjustmentSets(Gd, exposure = "D", outcome = "Y")
```

</div>

6. **401(k) participation on net financial assets continues I**

Apply the framework from this example to compute the intention-to-treat effect, the local average treatment effect, and the effect of eligibility on participation.

Answer

Taking into account that

$$\tau_{LATE} = \mathbb{E}[Y_i(1) - Y_i(0) \mid D(1) = 1, D(0) = 0]$$
$$= \frac{\mathbb{E}[Y_i \mid Z_i = 1] - \mathbb{E}[Y_i \mid Z_i = 0]}{\mathbb{E}[D_i \mid Z_i = 1] - \mathbb{E}[D_i \mid Z_i = 0]},$$

we can recover the ITT effect by multiplying the LATE by the effect of eligibility on participation. The following code illustrates this procedure and plots the ITT. The posterior distribution of the ITT is shown in Figure 13.1, which closely resembles the posterior distribution of the effect of eligibility reported in the main text.

R code. Treatment effect: 401(k) participation on net financial assets

```r
1  rm(list = ls()); set.seed(10101)
2  library(coda); library(ggplot2)
3  mydata <- read.csv("https://raw.githubusercontent.com/
        BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
        401k.csv", sep = ",", header = TRUE, quote = "")
4  # Attach variables
5  attach(mydata)
6  y <- net_tfa/1000  # Outcome: net financial assets
7  x <- as.vector(p401) # Endogenous regressor: participation
8  w <- as.matrix(cbind(1, age, inc, fsize, educ, marr, twoearn
        , db, pira, hown))  # Exogenous regressors with
        intercept
9  z <- as.matrix(e401)  # Instrument: eligibility (NO
        intercept here)
10 X <- cbind(x, w); Z <- cbind(z, w)
11 # Dimensions
12 k <- ncol(X); kz <- ncol(Z)
13 # Priors
14 b0 <- rep(0, k); B0i <- diag(1e-5, k)
15 g0 <- rep(0, kz); G0i <- diag(1e-5, kz)
16 nu <- 3; Psi0 <- nu * 1000 * diag(2); Psi0i <- solve(Psi0)
17 # MCMC parameters
18 mcmc <- 5000; burnin <- 1000
19 tot <- mcmc + burnin; thin <- 1
20 # Auxiliary elements
21 XtX <- t(X)%*%X; ZtZ <- t(Z)%*%Z; nun <- nu + length(y)
22 # Gibbs sampling
23 PostBeta <- function(Sigma, Gamma){
24   w1 <- Sigma[1,1] - Sigma[1,2]^2/Sigma[2,2]
25   Bn <- solve(w1^(-1)*XtX + B0i)
26   yaux <- y - (Sigma[1,2]/Sigma[2,2])*(x - Z%*%Gamma)
27   bn <- Bn%*%(B0i%*%b0 + w1^(-1)*t(X)%*%yaux)
28   Beta <- MASS::mvrnorm(1, bn, Bn)
29   return(Beta)
30 }
31 PostGamma <- function(Sigma, Beta){
32   w2 <- Sigma[2,2] - Sigma[1,2]^2/Sigma[1,1]
33   Gn <- solve(w2^(-1)*ZtZ + G0i)
34   xaux <- x - (Sigma[1,2]/Sigma[1,1])*(y - X%*%Beta)
35   gn <- Gn%*%(G0i%*%g0 + w2^(-1)*t(Z)%*%xaux)
36   Gamma <- MASS::mvrnorm(1, gn, Gn)
37   return(Gamma)
38 }
39 PostSigma <- function(Beta, Gamma){
40   Uy <- y - X%*%Beta; Ux <- x - Z%*%Gamma
41   U <- cbind(Uy, Ux)
42   Psin <- solve(Psi0i + t(U)%*%U)
43   Sigmai <- rWishart::rWishart(1, df = nun, Sigma = Psin)
44   Sigma <- solve(Sigmai[,,1])
45   return(Sigma)
46 }
```
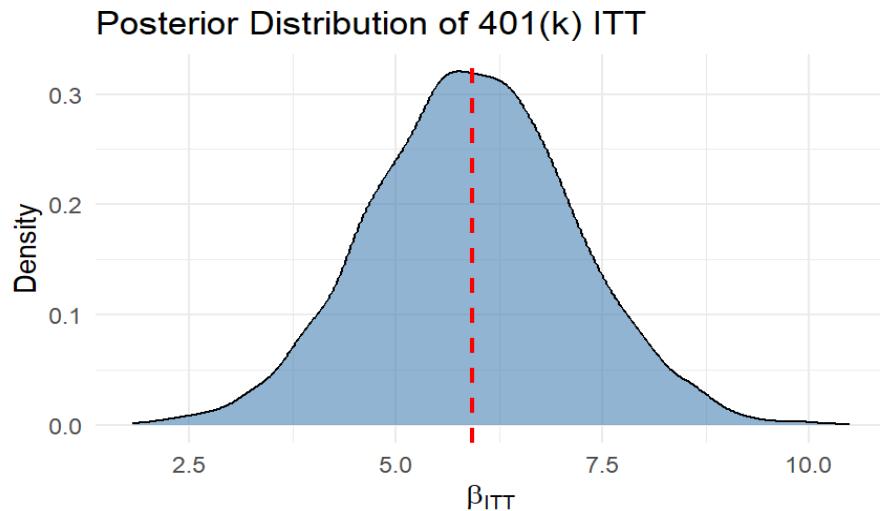
R code. Treatment effect: 401(k) participation on net financial assets

```
1 ITT <- Bs[,1]*Gs[,1]
2 summary(coda::mcmc(ITT))
3 # Convert to data frame for ggplot
4 df_ITT <- data.frame(ITT = as.vector(ITT))
5
6 # Plot posterior distribution of treatment effect
7 ggplot(df_ITT, aes(x = ITT)) + geom_density(fill = "
      steelblue", alpha = 0.6) +
8 geom_vline(xintercept = mean(ITT), color = "red", linetype =
      "dashed", linewidth = 1) + labs(title = "Posterior
      Distribution of 401(k) ITT", x = expression(beta["ITT"])
      , y = "Density") + theme_minimal(base_size = 14)
```


FIGURE 13.1
Posterior distribution: Intention-to-treat effect 401k participation on net financial assets.

7. **401(k) participation on net financial assets continues II**

Perform inference in this example assuming that the stochastic errors follow a Dirichlet process, using the function *rivDP* from the *bayesm* package to

analyze 401(k) participation and its effect on net financial assets under the same specification as in the main text, and plot the LATE.

Answer

The following code implements the exercise, and Figure 13.2 display the posterior distribution of the LATE. The results are very similar to the ones in the main text assuming a normal distribution; however, the degree of dispersion of higher using a Dirichlet process for the stochastic errors.

R code. Treatment effect: 401(k) participation on net financial assets using Dirichlet process
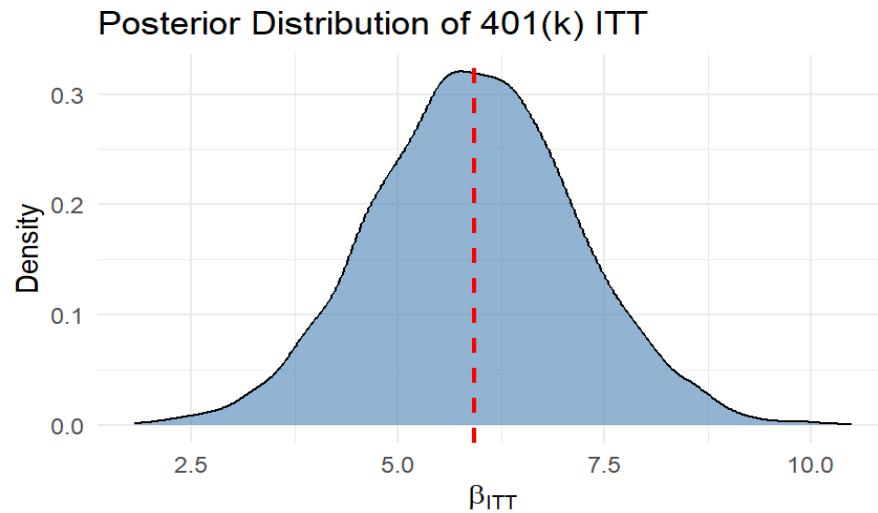
```r
1  rm(list = ls()); set.seed(10101)
2  library(ggplot2); library(bayesm)
3  # Load data
4  mydata <- read.csv("https://raw.githubusercontent.com/
      BEsmarter-consultancy/BSTApp/refs/heads/master/DataApp/
      401k.csv",
5  sep = ",", header = TRUE, quote = "")
6  # Attach variables
7  attach(mydata)
8  y <- net_tfa/1000      # Outcome: net financial assets
9  x <- as.vector(p401)   # Endogenous regressor: participation
10 w <- as.matrix(cbind(age, inc, fsize, educ, marr, twoearn,
      db, pira, hown))   # Exogenous regressors with intercept
11 z <- as.matrix(e401)   # Instrument: eligibility (NO
      intercept here)
12
13 # specify data input and mcmc parameters
14 Data = list();
15 Data$z <- z
16 Data$x <- x
17 Data$y <- y
18 Data$w <- w
19
20 Mcmc = list()
21 Mcmc$maxuniq <- 100
22 Mcmc$R <- 5000
23 keep <- seq((1000+1), Mcmc$R)
24
25 out <- rivDP(Data=Data, Mcmc=Mcmc)
26
27 # Plot posterior distribution of treatment effect
28 df_ITT <- data.frame(ITT = out[["betadraw"]][kepp])
29 ggplot(df_ITT, aes(x = ITT)) + geom_density(fill = "
      steelblue", alpha = 0.6) + geom_vline(xintercept = mean(
      ITT), color = "red", linetype = "dashed", linewidth = 1)
       + labs(title = "Posterior Distribution of 401(k) ITT:
      Dirichlet process", x = expression(beta["ITT"]), y = "
      Density") + theme_minimal(base_size = 14)
```

8. **Difference-in-Differences simulation continues**

   Perform the simulation of the DiD example, and perform inference using the specification:

$$Y_{it} = \alpha + \alpha_i + \phi_t + \tau_2 \left[D_i \cdot \mathbb{1}(t = 2) \right] + \epsilon_{it}.$$

Posterior Distribution of 401(k) ITT

FIGURE 13.2
Posterior distribution: Local average treatment effect 401k participation on net financial assets using a Dirichlet process.

Answer

You can check that we get same results as in example in the main book.

R code. Difference-in-Differences: Simulation exercise

```r
1  rm(list = ls()); set.seed(10101)
2  library(ggplot2); library(dplyr); library(fastDummies)
3  # Parameters
4  N_per_group <- 200          # units per group
5  T_periods    <- 2           # keep 2x2 for clarity
6  tau_true     <- 1           # ATT
7  sigma_eps    <- 0.5         # noise SD
8  # Panel index
9  id  <- rep(1:(2*N_per_group), each = T_periods)
10 t   <- rep(1:T_periods, times = 2*N_per_group)
11 # Group: treated (D=1) vs control (D=0)
12 D   <- rep(c(rep(0, N_per_group), rep(1, N_per_group)), each
       = T_periods)
13 # Post indicator (t=2 is post)
14 post <- as.integer(t == 2)
15 # Unit fixed effects (random heterogeneity)
16 alpha_i <- rnorm(2*N_per_group, 0, 0.8)
17 alpha   <- alpha_i[id]
18 # Time effects
19 phi_t <- c(0, -1.8)  # common decline from t=1 to t=2
20 phi   <- phi_t[t]
21 treat_effect <- tau_true * (D * post)
22 # Outcome
23 eps <- rnorm(length(id), 0, sigma_eps)
24 Y   <- alpha + phi + treat_effect + eps
25 did <- data.frame(id, t, D, post, Y)
26 plot_data <- did %>%
27 group_by(D, t) %>%
28 summarise(meanY = mean(Y), .groups = "drop") %>%
29 mutate(Group = ifelse(D == 1, "Treated", "Control"))
30 ggp <- ggplot(plot_data, aes(x = t, y = meanY, group = Group
       , linetype = Group)) +
31 geom_line(linewidth = 1) + geom_point() + scale_x_continuous
       (breaks = c(1, 2), labels = c("t = 1 (pre)", "t = 2 (
       post)")) + labs(x = "Time", y = "Mean outcome", title =
       "Synthetic DiD: Parallel Trends & No Anticipation") +
       theme_minimal(base_size = 12)
32 print(ggp)
33 # Bayesian inference: Model with interaction treatment x
       post period
34 post_fit1 <- MCMCpack::MCMCregress(Y ~ 1 + factor(id) +
       factor(t) + I(D * post), data = did, burnin = 100, mcmc
       = 1000)
35 tau_draws1 <- post_fit1[, "I(D * post)"]
36 quantile(tau_draws1, c(.025,.5,.975))
```

9. **Difference-in-Differences simulation continues II**

Note that another strategy to perform inference on the ATT is to estimate the saturated model

$$Y_{it} = \sum_{t,d} \mu_{tl} \big[D_{il} \cdot \mathbb{1}(t = t) \big] + \epsilon_{it}, \quad t = 1, 2, \ d = 1, 0,$$

and then use the posterior draws to compute

$$\tau_2 = (\mu_{21} - \mu_{11}) - (\mu_{20} - \mu_{10}).$$

Explain why inference on τ_2 using this approach in the simulation setting shows that the posterior mean is similar to that from the previous approaches, but the level of uncertainty is higher.

Answer

There is more uncertainty because performing inference on τ_2 uses four parameters in this setting, whereas in the previous we use only one parameter.

R code. Difference-in-Differences: Simulation exercise

```r
1  rm(list = ls()); set.seed(10101)
2  library(ggplot2); library(dplyr); library(fastDummies)
3  # Parameters
4  N_per_group <- 200          # units per group
5  T_periods    <- 2          # keep 2x2 for clarity
6  tau_true     <- 1          # ATT
7  sigma_eps    <- 0.5        # noise SD
8  # Panel index
9  id  <- rep(1:(2*N_per_group), each = T_periods)
10 t    <- rep(1:T_periods, times = 2*N_per_group)
11 # Group: treated (D=1) vs control (D=0)
12 D    <- rep(c(rep(0, N_per_group), rep(1, N_per_group)), each
        = T_periods)
13 # Post indicator (t=2 is post)
14 post <- as.integer(t == 2)
15 # Unit fixed effects (random heterogeneity)
16 alpha_i <- rnorm(2*N_per_group, 0, 0.8)
17 alpha    <- alpha_i[id]
18 # Time effects
19 phi_t <- c(0, -1.8)  # common decline from t=1 to t=2
20 phi    <- phi_t[t]
21 # No anticipation: effect is zero in pre, equals tau in post
        *only for treated*
22 treat_effect <- tau_true * (D * post)
23 # Outcome: Y_it(0) = alpha_i + phi_t + linear trend if you
        want; here just FE + shock
24 eps <- rnorm(length(id), 0, sigma_eps)
25 Y    <- alpha + phi + treat_effect + eps
26 did <- data.frame(id, t, D, post, Y)
27 # Calculating the means at each level, and then ATT
28 # ---- Build 2x2 cell indicators (no intercept model) ----
29 did$c_pre  <- as.integer(did$D == 0 & did$t == 1)
30 did$c_post <- as.integer(did$D == 0 & did$t == 2)
31 did$t_pre  <- as.integer(did$D == 1 & did$t == 1)
32 did$t_post <- as.integer(did$D == 1 & did$t == 2)
33 # Sanity check: each row must belong to exactly one cell
34 stopifnot(all(did$c_pre + did$c_post + did$t_pre + did$t_
        post == 1))
35 # ---- Bayesian saturated cell-mean model (compatible priors
        ) ----
36 # No intercept: each coefficient IS a cell mean.
37 fit_cells <- MCMCpack::MCMCregress(
38 Y ~ 0 + c_pre + c_post + t_pre + t_post, data  = did, burnin
        = 1000, mcmc = 10000, thin = 5)
39 draws_cells <- as.matrix(fit_cells)
40 colnames(draws_cells)  # should be c("c_pre","c_post","t_pre
        ","t_post", "sigma2")
41 # Posterior of the four cell means
42 mu_c_pre_draw  <- draws_cells[, "c_pre"]; mu_c_post_draw <-
        draws_cells[, "c_post"]
43 mu_t_pre_draw  <- draws_cells[, "t_pre"]; mu_t_post_draw <-
        draws_cells[, "t_post"]
44 # ATT = (mu_t,post - mu_t,pre) - (mu_c,post - mu_c,pre)
45 ATT_cells_draw <- (mu_t_post_draw - mu_t_pre_draw) - (mu_c_
        post_draw - mu_c_pre_draw)
46 quantile(ATT_cells_draw, c(.025, .5, .975))
```

10. Perform a simulation exercise to assess the ability of BETEL to identify the causal effect when an instrument is used to address the omission of relevant regressors. Illustrate the consequences of varying the dependence between the omitted regressor and the observed regressor.

Answer

We simulate the observed process $X_i = 0.5Z_i + e_i$, with the unobserved regressor defined as $W_i = H_i + \nu_i$, where

$$\begin{bmatrix} e_i \\ \nu_i \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} 1 & \rho \\ \rho & 1 \end{bmatrix} \right).$$

Thus, ρ defines the degree of correlation between X_i and W_i, and we perform two exercises with $\rho \in \{0.0, 0.7\}$. The variables Z_i and H_i are standard normal. The dependent variable is specified as

$$Y_i = 1 + 1.2X_i - 0.7W_i + \mu_i,$$

where μ_i follows a mixture of two normal distributions with means 0.5 and -0.5, and standard deviations 0.5 and 1.2. The sample size is 2,000, the burn-in is 1,000, and the number of MCMC draws retained after burn-in is 10,000. We adopt the default hyperparameter values provided in the *betel* package. For comparison, we also perform the analysis under the assumption of no endogeneity using the package *MCMCpack* using default values for the hyperparameters.

The following code shows the implementation, and Figure 13.3 displays the posterior distributions. When $\rho = 0$, implying no association between the regressors, there are no endogeneity issues, and assuming exogeneity yields more efficient posterior estimates. In contrast, when $\rho = 0.7$, endogeneity arises, and assuming exogeneity produces a biased posterior distribution. BETEL performs relatively well in both settings, although it is less efficient.

R code. BETEL: Omission of a relevant regressor
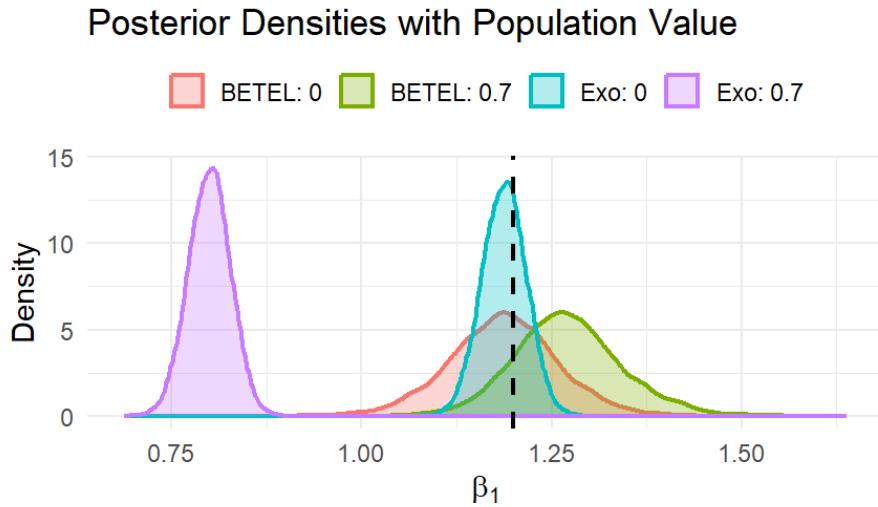
```r
1  rm(list = ls()); set.seed(10101)
2  library(betel); library(ucminf)
3  # Simulate data
4  N <- 2000; d <- 2; k <- 2
5  gamma <- 0.5; beta <- c(1, 1.2, -0.7); rho <- 0.7
6  # Mixture
7  mum1 <- 1/2; mum2 <- -1/2
8  mu1 <- rnorm(N, mum1, 0.5); mu2 <- rnorm(N, mum2, 1.2)
9  mu <- sapply(1:N, function(i){sample(c(mu1[i], mu2[i]), 1,
       prob = c(0.5, 0.5))})
10 z <- rnorm(N) # Instrument
11 E <- MASS::mvrnorm(n = N, mu = c(0, 0), Sigma = matrix(c(1,
       rho,rho,1),2,2))
12 x <- gamma*z + E[,1] # Observed regressor
13 w <- rnorm(N) + E[,2] # Unobserved correlated regressor
14 X <- cbind(1, x, w)
15 y <- X%*%beta + mu
16 dat <- cbind(1, x, z) # Data
17 # Function g_i by row in BETEL
18 gfunc <- function(psi = psi, y = y, dat = dat) {
19    X <- dat[,1:2]
20    e <- y - X %*% psi
21    E <- e %*% rep(1,d)
22    Z <- dat[,c(1,3)]
23    G <- E * Z;
24    return(G)
25 }
26 nt <- round(N * 0.1, 0); # training sample size for prior
27 psi0 <- lm(y[1:nt]~x[1:nt])$coefficients # Starting value of
       psi = (theta, v), v is the slack parameter in CSS
       (2018)
28 names(psi0) <- c("alpha","beta")
29 psi0_ <- as.matrix(psi0) # Prior mean of psi
30 Psi0_ <- 5*rep(1,k) # Prior dispersions of psi
31 lam0 <- .5*rnorm(d) # Starting value of lambda
32 nu <- 2.5 # df of the prior student-t
33 nuprop <- 15 # df of the student-t proposal
34 n0 <- 1000 # burn-in
35 m <- 10000 # iterations beyond burn-in
36 # MCMC ESTIMATION BY THE CSS (2018) method
37 psim2 <- betel::bayesetel(gfunc = gfunc, y = y[-(1:nt)], dat
       = dat[-(1:nt),], psi0 = psi0, lam0 = lam0, psi0_ = psi0
       _, Psi0_ = Psi0_, nu = nu, nuprop = nuprop,
38 controlpsi = list(maxiterpsi = 50, mingrpsi = 1.0e-8), #
       list of parameters in maximizing likelihood over psi
39 controllam = list(maxiterlam = 50, # list of parameters in
       minimizing dual over lambda
40 mingrlam = 1.0e-7),
41 n0 = n0, m = m)
42 MCMCreg2 <- MCMCpack::MCMCregress(y~x)
```

Posterior Densities with Population Value

FIGURE 13.3
Posterior distribution slope parameter given omission of relevant regressor: betel and MCMCregress

11. **Simultaneous causality continues**

Use the demand–supply simulation and the moment conditions to infer the causal effect of a 10% tax, implementing a BETEL algorithm from scratch.

Answer

The following code shows how to program a BETEL from scratch for the demand-supply simulation exercise. Figure 13.4 displays the posterior distribution of the causal effect. The 95% credible interval contains the population value, and the posterior mean lies close to it.

R code. BETEL: Simultaneous causality

```r
1  # Simulation
2  rm(list = ls()); set.seed(12345)
3  # Population parameters demand
4  B1 <- 5; B2 <- -0.5; B3 <- 0.8; B4 <- -0.4; B5 <- 0.7; SD <-
       0.5
5  # Population parameters supply
6  A1 <- -2; A2 <- 0.5; A3 <- -0.4; SS <- 0.5
7  # Reduced form parameters
8  P0 <- (A1-B1)/(B2-A2); P2 <- -B3/(B2-A2); P3 <- -B4/(B2-A2);
       P1 <- A3/(B2-A2); P4 <- -B5/(B2-A2)
9  T0 <- B1+B2*P0; T2 <- B3+B2*P2; T3 <- B4+B2*P3; T1 <- B2*P1;
       T4 <- B5+B2*P4;
10 n <- 5000
11 ED <- rnorm(n, 0, SD); ES <- rnorm(n, 0, SS)
12 VP <- (ES-ED)/(B2-A2); UQ <- B2*VP+ED
13 y <- rnorm(n, 10, 1); pc <- rnorm(n, 5, 1); er <- rnorm(n,
       15, 1); ps <- rnorm(n, 5, 1);
14 p <- P0+P1*er+P2*y+P3*pc+P4*ps+VP
15 q <- T0+T1*er+T2*y+T3*pc+T4*ps+UQ
16
17 ### Supply ###
18 p_s  <- as.numeric(scale(p,  TRUE, TRUE))
19 er_s <- as.numeric(scale(er, TRUE, TRUE))
20
21 X <- cbind(1, p_s, er_s)  # k = 3  (STRUCTURAL: intercept, p
       , er)
22 Z <- cbind(1,
23 as.numeric(scale(y,  TRUE, TRUE)),
24 as.numeric(scale(pc, TRUE, TRUE)),
25 as.numeric(scale(ps, TRUE, TRUE)),
26 er_s)           # EXCLUDED instruments y,pc,ps, plus er
27
28 k <- ncol(X); d <- ncol(Z)
29
30 # Objective function
31 lambdafunc <- function(lambda, theta, q, X, Z){
32   e <- as.numeric(q - X %*% theta); if (!all(is.finite(e)))
       return(1e300)
33   G <- Z * e
34   eta <- as.numeric(G %*% lambda); if (!all(is.finite(eta)))
        return(1e300)
35   m <- max(eta); m + log(mean(exp(eta - m)))
36 }
37
38 # ----- Profile ETEL log-likelihood (use this in MH) -----
39 loglik_etel <- function(theta, q, X, Z){
40   e <- as.numeric(q - X %*% theta); if (!all(is.finite(e)))
       return(-Inf)
41   G <- Z * e
42   op <- optim(par = rep(0, ncol(G)), fn = function(l){
43     eta <- as.numeric(G %*% l); m <- max(eta)
44     m + log(mean(exp(eta - m)))
45   }, method="BFGS", control=list(maxit=2000))
46   if (!is.finite(op$value)) return(-Inf)
47   lam <- op$par
48   eta <- as.numeric(G %*% lam)
49   sum(eta) - length(e) * log(sum(exp(eta)))
50 }
```

R code. BETEL: Simultaneous causality

```r
theta0 <- coef(lm(q ~ p_s + er_s))
# ----- MH using profile ETEL -----
b0 <- rep(0, k); B0 <- 1000*diag(k)
S <- 10000; burnin <- 2000; thin <- 5; tot <- S + burnin
BETA <- matrix(NA, tot, k); accept <- logical(tot)
step <- c(0.05, 0.02, 0.02)                        #
    preconditioned steps
BETA[1,] <- theta0
LL <- loglik_etel(BETA[1,], q, X, Z)
pb <- txtProgressBar(min=0, max=tot, style=3)
for(s in 2:tot){
  cand <- BETA[s-1,] + rnorm(k, 0, step)
  LLc  <- loglik_etel(cand, q, X, Z)
  priorRat <- mvtnorm::dmvnorm(cand, b0, B0, log=TRUE) -
  mvtnorm::dmvnorm(BETA[s-1,], b0, B0, log=TRUE)
  loga <- (LLc - LL) + priorRat
  if (is.finite(loga) && log(runif(1)) <= loga) {
    BETA[s,] <- cand; LL <- LLc; accept[s] <- TRUE
  } else {
    BETA[s,] <- BETA[s-1,]; accept[s] <- FALSE
  }
  if (s %% 200 == 0) {            # gentle adaptation
    acc <- mean(accept[(s-199):s])
    if (acc > 0.4) step <- step * 1.25
    if (acc < 0.15) step <- step / 1.25
  }
  setTxtProgressBar(pb, s)
}
close(pb)
cat("\nAcceptance rate:", mean(accept), "\n")
keep <- seq(burnin, tot, by = thin)
post_s <- BETA[keep, , drop=FALSE]   # posterior draws in
    scaled space
## ---------- Back-transform each draw to original scale
    ----------
p_mu <- mean(p);   p_sd <- sd(p); er_mu <- mean(er); er_sd
    <- sd(er)
alpha_draws <- cbind(
alpha0  = post_s[,1] - post_s[,2] * (p_mu/p_sd) - post_s[,3]
    * (er_mu/er_sd),
alphap  = post_s[,2] / p_sd,
alphaer = post_s[,3] / er_sd
)
## ---------- Summaries ----------
summ <- function(x) c(mean=mean(x), sd=sd(x), quantile(x, c
    (.025,.25,.5,.75,.975)))
cat("\nPosterior (original scale):\n")
print(rbind(
alpha0  = summ(alpha_draws[,"alpha0"]), alphap  = summ(alpha
    _draws[,"alphap"]), alphaer = summ(alpha_draws[,"alphaer
    "])))
cat("\nTrue (original scale):\n")
print(c(alpha0=A1, alphap=A2, alphaer=A3))
ElastSupPrice <- alpha_draws[,2]
#### Demand ####
y_s <- as.numeric(scale(y)); pc_s <- as.numeric(scale(pc))
ps_s <- as.numeric(scale(ps)); Xdem <- cbind(1, p_s, y_s, pc
    _s, ps_s)
k <- ncol(Xdem); d <- ncol(Z); theta0 <- coef(lm(q ~ p_s + y
    _s + pc_s + ps_s))
```
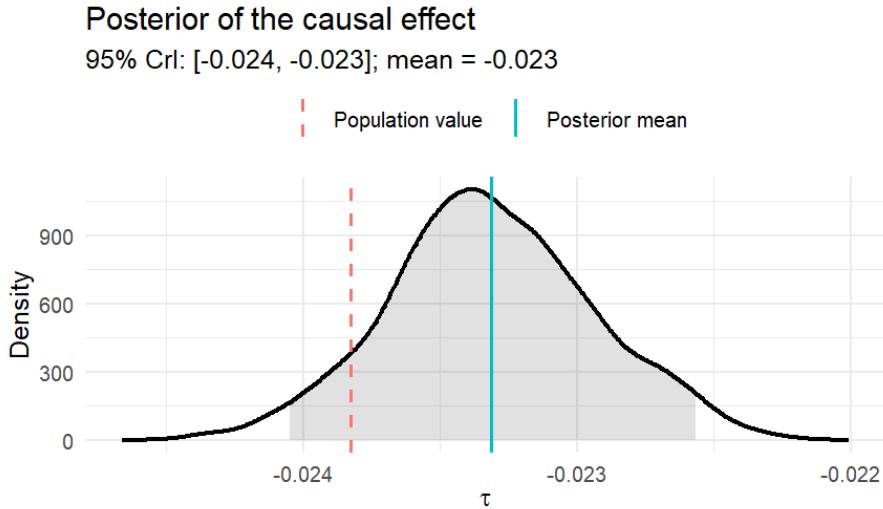
R code. BETEL: Simultaneous causality

```r
1  # ----- MH using profile ETEL -----
2  b0 <- rep(0, k); B0 <- 1000*diag(k)
3  S <- 10000; burnin <- 2000; thin <- 5; tot <- S + burnin
4  BETAdem <- matrix(NA, tot, k); accept <- logical(tot)
5  step <- c(0.05, 0.02, 0.02); BETAdem[1,] <- theta0
6  LL <- loglik_etel(BETAdem[1,], q, X = Xdem, Z)
7  pb <- txtProgressBar(min=0, max=tot, style=3)
8  for(s in 2:tot){
9    cand <- BETAdem[s-1,] + rnorm(k, 0, step)
10   LLc  <- loglik_etel(cand, q, X = Xdem, Z)
11   priorRat <- mvtnorm::dmvnorm(cand, b0, B0, log=TRUE) -
12   mvtnorm::dmvnorm(BETAdem[s-1,], b0, B0, log=TRUE)
13   loga <- (LLc - LL) + priorRat
14   if (is.finite(loga) && log(runif(1)) <= loga) {
15     BETAdem[s,] <- cand; LL <- LLc; accept[s] <- TRUE
16   } else {
17     BETAdem[s,] <- BETAdem[s-1,]; accept[s] <- FALSE
18   }
19   if (s %% 200 == 0) {    # gentle adaptation
20     acc <- mean(accept[(s-199):s])
21     if (acc > 0.4) step <- step * 1.25
22     if (acc < 0.15) step <- step / 1.25
23   }
24   setTxtProgressBar(pb, s)
25 }
26 close(pb)
27 cat("\nAcceptance rate:", mean(accept), "\n")
28 keep <- seq(burnin, tot, by = thin)
29 postDem_s <- BETAdem[keep, , drop=FALSE]
30 p_mu <- mean(p);   p_sd <- sd(p); y_mu <- mean(y); y_sd <-
       sd(y)
31 pc_mu <- mean(pc); pc_sd <- sd(pc); ps_mu <- mean(ps); ps_sd
        <- sd(ps)
32 alphaDem_draws <- cbind(
33 alpha0  = postDem_s[,1] - postDem_s[,2] * (p_mu/p_sd) -
       postDem_s[,3] * (y_mu/y_sd)
34 - postDem_s[,4] * (pc_mu/pc_sd) - postDem_s[,5] * (pc_mu/pc_
       sd),
35 alphap  = postDem_s[,2] / p_sd, alphay = postDem_s[,3] / y_
       sd, alphapc = postDem_s[,4] / pc_sd, alphaps = postDem_s
       [,5] / ps_sd)
36 summ <- function(x) c(mean=mean(x), sd=sd(x), quantile(x, c
       (.025,.25,.5,.75,.975)))
37 cat("\nPosterior (original scale):\n")
38 print(rbind(
39 alpha0  = summ(alphaDem_draws[,"alpha0"]), alphap  = summ(
       alphaDem_draws[,"alphap"]), alphay = summ(alphaDem_draws
       [,"alphay"]),
40 alphapc = summ(alphaDem_draws[,"alphapc"]), alphaps = summ(
       alphaDem_draws[,"alphaps"])))
41 cat("\nTrue (original scale):\n")
42 print(c(alpha0=B1, alphap=B2, alphay=B3, alphpc=B4, alphaps=
       B5))
43 ElastDemPrice <- alphaDem_draws[,2]; tax <- 0.1
44 CausalEffect <- (ElastSupPrice*ElastDemPrice)*log(1+tax)/(
       ElastSupPrice-ElastDemPrice)
45 popCauEff <- (A2 * B2)/(A2 - B2) * log(1 + tax)
```

Posterior of the causal effect

95% CrI: [-0.024, -0.023]; mean = -0.023

FIGURE 13.4
Posterior distribution causal effect: BETEL

12. Perform a simulation of the instrumental variable quantile regression, and then perform inference using the general Bayes posterior framework. Use the Laplace asymmetric distribution to simulate the stochastic error, such that

$$\int_{-\infty}^{0} f_\tau(\mu_i) \, d\mu_i = \tau,$$

which implies that the τ-th quantile of μ_i is 0. In addition, let

$$q_\tau(Y_i \mid X_i, D_i) = \beta_0 + \beta_1 X_i + \beta_2 D_i$$

denote the τ-th quantile regression function of Y_i given X_i and D_i, with $0 < \tau < 1$. Specifically, consider the model

$$Y_i = \beta_{0\tau} + \beta_{1\tau} X_i + \beta_{2\tau} D_i + \mu_i,$$

together with

$$D_i = \gamma Z_i + \delta \mu_i, \quad Z_i \sim N(0, 1).$$

Answer:

The following code shows how to perform inference in this simulation. The 95% credible intervals encompass the population values, and the posterior means are also close to these values.

R code. Instrumental Variable Quantile Regression: General Bayes posteriors

```r
1  rm(list = ls()); set.seed(10101); library(quantreg)
2  ### Simulation ####
3  # Asymmetric Laplace
4  rALD <- function(n, tau) {
5    stopifnot(tau > 0, tau < 1)
6    theta <- (1 - 2*tau) / (tau * (1 - tau))
7    psi   <- 2 / (tau * (1 - tau))
8    v  <- rexp(n, rate = 1)
9    z  <- rnorm(n)
10   mu <- theta * v + sqrt(psi * v) * z
11   return(mu)
12 }
13 ## --- Simulator for a given tau ---
14 simulate_qr <- function(n = 5000, tau = 0.5,
15 beta0 = 0.7,
16 beta1_tau = 1.5,
17 beta2_tau = 1,
18 gamma = 1,
19 delta = 0.5) {
20   # Nonnegative regressor stabilizes intercept & preserves
         tau-ordering of slopes
21   x <- runif(n, 0, 1)
22   # optional: anchor a portion at 0 to pin intercept
23   x[sample.int(n, size = round(0.1*n))] <- 0
24   mu <- rALD(n, tau = tau) # ALD error
25   z <- rnorm(n) # Instrument
26   d <- gamma * z + delta * mu
27   y <- beta0 + beta1_tau * x + beta2_tau * d + mu
28   df <- data.frame(y, x, d, z)
29 }
30 tau <- 0.75
31 df <- simulate_qr(tau = tau, beta0 = 1, beta1_tau = 1,
32 beta2_tau = 1, gamma = 1, delta = 1, n = 5000)
33 Reg <- MCMCpack::MCMCquantreg(y~x+d, data = df, tau = tau)
34 summary(Reg)
35 summary(rq(y ~ x + d, tau = tau, data = df))
36 LossFunct <- function(par, tau, y, z, x, d){
37   n <- length(y)
38   X <- cbind(1, x, d)
39   Z <- cbind(1, x, z)
40   Ind <- as.numeric(y <= X%*%par)
41   gn <- colMeans((tau - Ind) * Z)
42   Wni <- lapply(1:n, function(i) {Z[i,] %*% t(Z[i,])})
43   Wn <- 1 / (tau * (1 - tau)) * solve(Reduce("+", Wni)/n)
44   Ln <- - 0.5 * n * t(gn) %*% Wn %*% gn
45   return(Ln)
46 }
47 par0 <- rnorm(3)
48 LossFunct(par = par0, tau = tau, y = df$y, z = df$z, x = df$
       x, d = df$d)
```

R code. Instrumental Variable Quantile Regression: General Bayes posteriors

```r
# ----- MH using Ln -----
k <- 3
b0 <- rep(0, k); B0 <- 1000*diag(k)
S <- 5000; burnin <- 6000; thin <- 5; tot <- S + burnin
BETA <- matrix(NA, tot, k); accept <- logical(tot)
step <- 0.05
BETA[1,] <- par0
LL <- LossFunct(par = BETA[1,], tau = tau, y = df$y, z = df$
    z, x = df$x, d = df$d)
pb <- txtProgressBar(min=0, max=tot, style=3)
for(s in 2:tot){
  cand <- BETA[s-1,] + rnorm(k, 0, step)
  LLc  <- LossFunct(par = cand, tau = tau, y = df$y, z = df$
    z, x = df$x, d = df$d)
  priorRat <- mvtnorm::dmvnorm(cand, b0, B0, log=TRUE) -
  mvtnorm::dmvnorm(BETA[s-1,], b0, B0, log=TRUE)
  loga <- (LLc - LL) + priorRat
  if (is.finite(loga) && log(runif(1)) <= loga) {
    BETA[s,] <- cand; LL <- LLc; accept[s] <- TRUE
  } else {
    BETA[s,] <- BETA[s-1,]; accept[s] <- FALSE
  }
  if (s <= burnin && s %% 200 == 0) {
    acc <- mean(accept[(s-199):s])
    if (acc > 0.4) step <- step * 1.25
    if (acc < 0.15) step <- step / 1.25
  }
  setTxtProgressBar(pb, s)
}
close(pb)
cat("\nAcceptance rate:", mean(accept), "\n")
keep <- seq(burnin, tot, by = thin)
post <- BETA[keep, , drop=FALSE]   # posterior draws in
    scaled space
colnames(post) <- c("beta0","beta_x","beta_d")
# Posterior summaries
post_mean <- colMeans(post)
post_ci   <- apply(post, 2, quantile, c(0.025, 0.975))
round(post_mean, 3); round(post_ci, 3)
```

13. **Example: Doubly robust Bayesian inference continues**

   Perform a simulation exercise to assess the consequences of misspecifying
   the propensity score function and the outcome regression in doubly robust
   Bayesian inference.

Answer:

Let us simulate the process

$$\eta_i^\pi = -0.3 + 0.8X_{i1} - 0.5X_{i2} + 0.7X_{i3} + 0.7X_{i1}X_{i3} + 0.5sin(X_{i1}),$$

$$\eta_i^m = -0.2 + 0.6D_i + 0.5X_{i1} - 0.4X_{i2} + 0.3X_{i3} + 0.6X_{i1}^2 - 0.5X_{i1}X_{i2},$$

where $X_1 \sim N(0,1)$, $X_2 \sim$ Bernoulli(0.5), and $X_3 \sim U(-1,1)$, and the sample size is 2,000.

The following code implements the algorithm.

R code. Doubly robust Bayesian inference: Misspecified simulation

```r
rm(list = ls()); set.seed(123); library(glmnet)

## simulate covariates
n   <- 2000
X1 <- rnorm(n)                   # continuous
X2 <- rbinom(n, 1, 0.5)          # binary
X3 <- runif(n, -1, 1)            # continuous
Z <- cbind(X1, X2, X3)
# True propensity and outcome
logit <- function(t) 1/(1+exp(-t))
true_pi  <- function(X){ logit(-0.3 + 0.8*X[,1] -0.5*X[,2] +
        0.7*X[,3] + 0.7*X[,1]*X[,3] + 0.5*sin(X[,1])) }
true_eta <- function(d,X){ -0.2 + 0.6*d + 0.5*X[,1] -0.4*X
        [,2] + 0.3*X[,3] + 0.6*(X[,1]^2) - 0.5*X[,1]*X[,2] }
true_p    <- function(d,X){ logit(true_eta(d,X)) }
ATE   <- mean(true_p(1,Z) - true_p(0,Z))
pi <- true_pi(Z)
D   <- rbinom(n,1,pi)
P   <- true_p(D,Z)
Y   <- rbinom(n,1,P)
dat <- data.frame(Y, D, X1, X2 = factor(X2), X3)
######### Doubly Robust Bayesian: Implementation #########
# OK specification propensity score
Z <- cbind(X1, X2, X3, X1*X3, sin(X1)); p <- dim(Z)[2]
covars <- c("X1","X2","X3", "X1X3", "sinX1")
# # OK specification outcome regression
# Z <- cbind(X1, X2, X3, X1*X2, X1^2); p <- dim(Z)[2]
# covars <- c("X1","X2","X3", "X1X2", "X12")
cvfit <- cv.glmnet(Z, D, family = "binomial", alpha=1,
        nfolds = 10) # lasso,min
ps.coef <- coef(cvfit, s = "lambda.min")[0:p+1]
ps_hat <- predict(cvfit, newx = Z, s = "lambda.min",type = "
        response")
ps_hat <- pmin(pmax(ps_hat, 1e-6), 1 - 1e-6)
# Riesz representer
riesz_fun <- function(d, ps) d/ps - (1 - d)/(1 - ps)
# GP model
make_gp <- function(X_train, y_bin, use_correction = FALSE,
        gamma_scaled = NULL,
approx_method = gplite::approx_laplace(),
init_lscale = 0.3) {
  stopifnot(length(y_bin) == nrow(X_train))
  cf_se <- gplite::cf_sexp(vars = colnames(X_train), lscale
        = init_lscale, magn = 1, normalize = TRUE)
  cfs <- list(cf_se)
  if (use_correction) {
    stopifnot(!is.null(gamma_scaled))
    cf_lin <- gplite::cf_lin(vars = "gamma", magn = 1,
        normalize = FALSE)
    cfs <- list(cf_se, cf_lin)
  }
  gp <- gplite::gp_init(cfs = cfs, lik = gplite::lik_
        bernoulli(), approx = approx_method)
  gp <- gplite::gp_optim(gp, x = X_train, y = y_bin, maxiter
        = 1000, restarts = 3, tol = 1e-05)
  return(gp)
}
```

R code. Doubly robust Bayesian inference: Simulation exercise

```r
1  posterior_draws_prob <- function(gp, X_test, ndraws = 5000)
       {
2    out <- gplite::gp_draw(gp, xnew = X_test, draws = ndraws,
       transform = TRUE, target = FALSE, jitter = 1e-6)
3    return(t(out))
4  }
5  # Main function
6  run_trim <- function(t_trim = 0.10, N_post = 5000, h_r = 1/
       2, cor_size = 1) {
7    # Trim by estimated PS
8    keep <- which(ps_hat >= t_trim & ps_hat <= (1 - t_trim))
9    n_eff <- length(keep)
10   if (n_eff < 50) stop("Too few observations after trimming.
       ")
11   Yk  <- Y[keep]
12   Dk  <- D[keep]
13   Zk  <- Z[keep, , drop = FALSE]
14   psk <- ps_hat[keep]
15   # Riesz representer and sigma_n choice
16   gamma_k <- riesz_fun(Dk, psk)
17   sigma_n <- cor_size * (log(n_eff) / ( (n_eff)^(h_r) * mean
       (abs(gamma_k)) ))
18   gamma_scaled <- sigma_n * gamma_k
19   # Training inputs for GP: [Z, D] and, if corrected, an
       extra column 'gamma'
20   X_train_nc <- data.frame(Zk)
21   X_train_nc$D <- Dk
22   colnames(X_train_nc) <- c(covars, "D")
23   X_train_c <- X_train_nc
24   X_train_c$gamma <- gamma_scaled
25   # Test inputs: for each i, (Z_i, d=0) and (Z_i, d=1)
26   X_t0 <- X_train_nc; X_t0$D <- 0
27   X_t1 <- X_train_nc; X_t1$D <- 1
28   X_t0c <- X_t0; X_t1c <- X_t1
29   X_t0c$gamma <- sigma_n * riesz_fun(0, psk)
30   X_t1c$gamma <- sigma_n * riesz_fun(1, psk)
31   # GP WITHOUT prior correction #
32   gp_nc <- make_gp(X_train = X_train_nc, y_bin = Yk, use_
       correction = FALSE)
33   # joint draws for [m(Z,0); m(Z,1)]
34   M_nc_0 <- posterior_draws_prob(gp_nc, X_t0, ndraws = N_
       post)  # N_post x n_eff
35   M_nc_1 <- posterior_draws_prob(gp_nc, X_t1, ndraws = N_
       post)
36   # observed arm probabilities
37   M_nc_obs <- ifelse(matrix(Dk, nrow = N_post, ncol = n_eff,
       byrow = TRUE) == 1, M_nc_1, M_nc_0)
38   # GP WITH prior correction #
39   gp_c <- make_gp(X_train = X_train_c, y_bin = Yk, use_
       correction = TRUE, gamma_scaled = gamma_scaled)
40   M_c_0 <- posterior_draws_prob(gp_c, X_t0c, ndraws = N_post
       )
41   M_c_1 <- posterior_draws_prob(gp_c, X_t1c, ndraws = N_post
       )
42   M_c_obs <- ifelse(matrix(Dk, nrow = N_post, ncol = n_eff,
       byrow = TRUE) == 1, M_c_1, M_c_0)
```

R code. Doubly robust Bayesian inference: Simulation exercise

```r
1   # Bayesian bootstrap weights #
2   W <- matrix(rexp(N_post * n_eff, rate = 1), nrow = N_post)
3   W <- W / rowSums(W)
4   # ATEs
5   # (1) Unadjusted Bayes
6   Ate_nc_draws <- rowSums((M_nc_1 - M_nc_0) * W)
7   # (2) Prior-adjusted Bayes
8   Ate_c_draws  <- rowSums((M_c_1 - M_c_0) * W)
9   # (3) DR Bayes (posterior recentering)
10  # Pre-centering using UNcorrected GP posterior means
11  mu_nc_diff <- colMeans(M_nc_1 - M_nc_0)
12  mu_nc_obs  <- colMeans(M_nc_obs)
13  ATE_dr_pre <- mean(mu_nc_diff + gamma_k * (Yk - mu_nc_obs)
     )
14  # Recenter draws using corrected GP draws
15  DR_rec_1 <- (matrix(gamma_k, nrow = N_post, ncol = n_eff,
     byrow = TRUE)) * (matrix(Yk, nrow = N_post, ncol = n_eff
     , byrow = TRUE) - M_c_obs)
16  # The first component is \tau_{\eta}^s in Algorithm 1
17  # The second component is \hat{m} a scalar. This has
     positive sign because
18  # minus x minus, the bias is with minus, and then, this
     component enters with minus in the bias term
19  # The third component is \gamma_k x (y-m(d,x)), m(d,x) is
     with prior correction
20  # The fourth component is m(1,x)-m(0,x) also with
     correction in the prior
21  Ate_drb_draws <- rowSums((M_c_1 - M_c_0) * W) + ATE_dr_pre
     - rowSums(DR_rec_1) / n_eff - rowSums(M_c_1 - M_c_0) /
     n_eff
22
23  qfun <- function(x) {
24    qs <- quantile(x, c(0.025, 0.975))
25    c(mean   = mean(x),   median = median(x), lo = qs[1], hi
     = qs[2], len = diff(qs)
     )
26    )
27  }
28  vals <- list(
29  Bayes       = qfun(Ate_nc_draws),
30  'PA Bayes' = qfun(Ate_c_draws),
31  'DR Bayes' = qfun(Ate_drb_draws)
32  )
33  out_df <- as.data.frame(do.call(rbind, vals), check.names
     = FALSE)
34  list(t_trim = t_trim, results = out_df)
35 }
36 N_post <- 5000
37 h_r    <- 1/2
38 cor_size <- 1
39 trim <- 0.05
40 res_list <- run_trim(t_trim = trim, N_post = N_post, h_r = h
     _r, cor_size = cor_size)
41 print(res_list$results)
```

14

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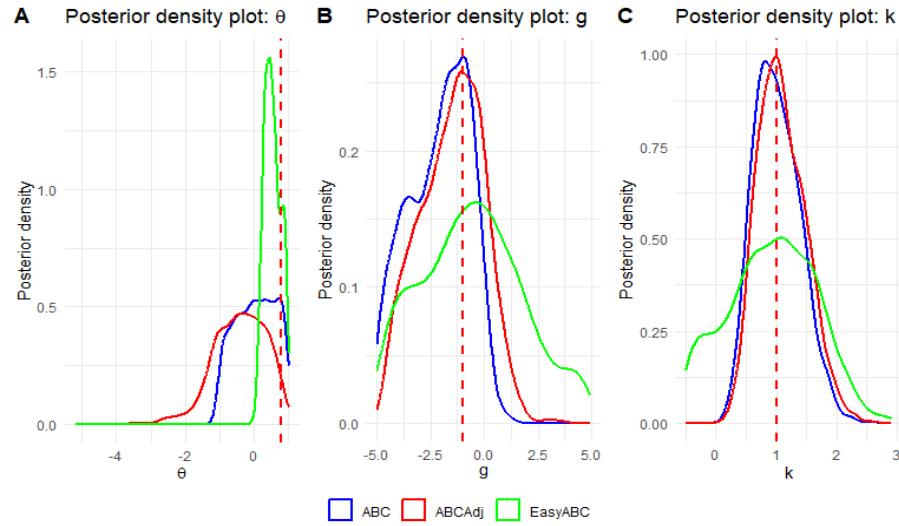
   The following code implements our ABC-AR algorithm, following the steps outlined in the ABC-AR Algorithm of the book. Users can observe that a linear regression adjustment is applied; however, due to multicollinearity issues, one summary statistic is omitted in the prediction step (see the *abc* package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

   Figure 14.1 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 no the case regarding θ_1. Moreover, applying regression adjustment introduces a degree of smoothness to the distributions.

   ---

   [1]Note 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 14.1
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

```r
rm(list = ls()); set.seed(010101)
# Simulate g-and-k data
RGKnew <- function(par) {
  z <- NULL
  theta <- par[1]; a <- par[2]; b <- par[3]; g <- par[4]; k
    <- par[5]
  e <- rnorm(n + 1)
  for(t in 2:(n + 1)){
    zt <- e[t] + theta * e[t-1]
    z <- c(z, zt)
  }
  zs <- z / (1 + theta^2)^0.5
  x <- a + b * (1 + 0.8 * (1 - exp(-g * zs)) / (1 + exp(-g *
    zs))) * (1 + zs^2)^k * zs
  return(x)
}
# Summary statistics
SumSt <- function(y) {
  Oct <- quantile(y, c(0.125, 0.25, 0.375, 0.5, 0.625, 0.75,
    0.875))
  eta1 <- Oct[6] - Oct[2]
  eta2 <- (Oct[6] + Oct[2] - 2 * Oct[4]) / eta1
  eta3 <- (Oct[7] - Oct[5] + Oct[3] - Oct[1]) / eta1
  autocor <- acf(y, lag = 2, plot = FALSE)
  autocor[["acf"]][2:3]
  Etay <- c(Oct, eta1, eta2, eta3, autocor[["acf"]][2:3])
  return(Etay)
}
# Population parameters
theta1 <- 0.8; a <- 1; b <- 0.5; g <- -1; k <- 1
parpop <- c(theta1, a, b, g, k)
n <- 500
y <- RGKnew(par = parpop)
##### ABC Function#####
ABC <- function(S, a, y) {
  prior <- cbind(runif(S,-1,1), runif(S,0,5), runif(S,0,5),
    runif(S,-5,5), runif(S,-0.5,5))
  Z <- apply(prior, 1, RGKnew)
  EtasZ <- apply(Z, 2, SumSt)
  Etay <- SumSt(y)
  Dist <- sapply(1:S, function(l) {
    dist(rbind(Etay, EtasZ[, l]))
  })
  OrdPrior <- prior[order(Dist), ]
  SelPrior <- OrdPrior[1:round(S * a), ]
  SelSumSt <- t(EtasZ)[1:round(S * a), ]
  return(list(SelPrior = SelPrior, SelSumSt = SelSumSt))
}
S <- 1000000
a <- 0.001
tick <- Sys.time()
ResABC <- ABC(S = S, a = 0.001, y = y)
tock <- Sys.time()
tock - tick
PostABC_ARown <- ResABC[["SelPrior"]]
```

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

```r
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

```r
library(ggplot2); library(latex2exp)
Sp <- 1000

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))))
dentheta <- ggplot(df1, aes(x = Value, color = Distribution)
    ) + geom_density(linewidth = 1) + geom_vline(xintercept
    = theta1, linetype = "dashed", color = "red", linewidth
    = 1) +
labs(title = TeX("Posterior density plot: $theta$"), x = TeX
    ("$theta$"), y = "Posterior density") + scale_color_
    manual(values = c("blue", "red", "green")) +  theme_
    minimal() +
theme(legend.title = element_blank())

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))))
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") +
scale_color_manual(values = c("blue", "red", "green")) +
    theme_minimal() + theme(legend.title = element_blank())

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))))
denk <- ggplot(df3, aes(x = Value, color = Distribution)) +
     geom_density(linewidth = 1) + geom_vline(xintercept =
    k, linetype = "dashed", color = "red", linewidth = 1) +
labs(title = TeX("Posterior density plot: k"), x = TeX("$k$"
    ), y = "Posterior density") +
scale_color_manual(values = c("blue", "red", "green")) +
    theme_minimal() + theme(legend.title = element_blank())

library(ggpubr)
ggarrange(dentheta, deng, denk, labels = c("A", "B", "C"),
    ncol = 3, nrow = 1,
legend = "bottom", common.legend = TRUE)
```
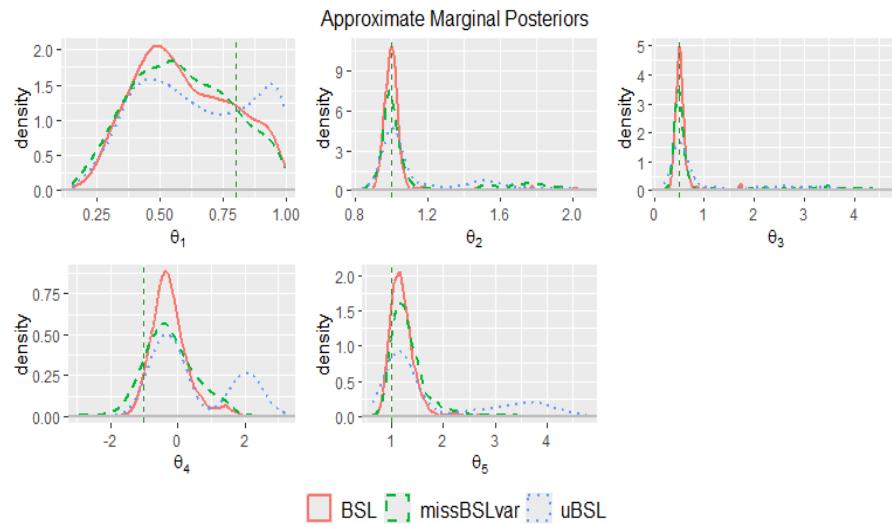
2. **Simulation: g-and-k distribution continues**

Perform the simulation example of the Bayesian synthetic likelihood presented in the book, using the same population parameters and setting $M = 500$, $S = 6,000$, with burn-in and thinning parameters set to 1,000 and 5, respectively. Use the *BSL* package in **R** to perform inference using the vanilla, unbiased, semi-parametric, and misspecified (mean and variance) versions of BSL. Compare the posterior distributions of the methods with the true population parameters.

Answer:

The following code shows how to perform inference in this exercise. The results using the semi-parametric and misspecified settings in mean are very different compared to the other methods. In general, the performance of these methods are not good in this particular exercise and setting.

Figure 14.2 shows the posterior plots of the vanilla, unbiased and misspecified in variance settings. All the 95% credible intervals encompass the population variables; the posterior distributions of a, b and k are really good.


FIGURE 14.2
Posterior distributions using Bayesian synthetic likelihood: Simulation exercise g-and-k distribution.

R code. Bayesian synthetic likelihood: Simulation exercise g-and-k distribution.

```r
1  rm(list = ls()); set.seed(010101)
2  library(BSL)
3  # Simulate g-and-k data
4  RGKnew <- function(par) {
5    z <- NULL
6    theta <- par[1]; a <- par[2]; b <- par[3]; g <- par[4]; k
        <- par[5]
7    e <- rnorm(n + 1)
8    for(t in 2:(n + 1)){
9      zt <- e[t] + theta * e[t-1]
10     z <- c(z, zt)
11   }
12   zs <- z / (1 + theta^2)^0.5
13   x <- a + b * (1 + 0.8 * (1 - exp(-g * zs)) / (1 + exp(-g *
        zs))) * (1 + zs^2)^k * zs
14   return(x)
15 }
16 # Summary statistics
17 SumSt <- function(y) {
18   Oct <- quantile(y, c(0.125, 0.25, 0.375, 0.5, 0.625, 0.75,
        0.875))
19   eta1 <- Oct[6] - Oct[2]
20   eta2 <- (Oct[6] + Oct[2] - 2 * Oct[4]) / eta1
21   eta3 <- (Oct[7] - Oct[5] + Oct[3] - Oct[1]) / eta1
22   autocor <- acf(y, lag = 2, plot = FALSE)
23   autocor[["acf"]][2:3]
24   Etay <- c(Oct[4], eta1, eta2, eta3, autocor[["acf"]][2:3])
25   return(Etay)
26 }
27 # Prior function
28 LogPrior <- function(par){
29   LogPi <- log(par[1] > -1 & par[1] < 1 & par[2] > 0 & par
        [2] < 5 & par[3] > 0 & par[3] < 5 & par[4] > -5 & par[4]
         < 5 & par[5] > -0.5 & par[5] < 5)
30   return(LogPi)
31 }
32 # Population parameters
33 theta1 <- 0.8; a <- 1; b <- 0.5; g <- -1; k <- 1
34 parpop <- c(theta1, a, b, g, k)
35 K <- 5
36 n <- 500
37 y <- RGKnew(par = parpop)
38 # Algorithm parameters
39 M <- 200 # Number of iterations to calculate mu and sigma
40 S <- 1100 # Number of MCMC iterations
41 burnin <- 100 # Burn in iterations
42 thin <- 2 # Thining parameter
43 keep <- seq(burnin + 1, S, thin)
44 par0 <- c(0.5, 2, 1, 0, 1)
45 Modelgk <- newModel(fnSim = RGKnew, fnSum = SumSt, theta0 =
        par0, fnLogPrior = LogPrior, verbose = FALSE)
46 validObject(Modelgk)
47 keep <- seq(burnin + 1, S, thin)
48 tune <- 0.1 # Tuning parameter RW MH
49 simgk <- simulation(Modelgk, n = M, theta = par0, seed = 10)
50 par(mfrow = c(2, 3))
```

R code. Bayesian synthetic likelihood: Simulation exercise g-and-k distribution.

```r
# Check if the summary statistics are roughly normal
for (i in 1:6){
  eval <- seq(min(simgk$ssx[, i]), max(simgk$ssx[, i]),
    0.001)
  densnorm <- dnorm(eval, mean = mean(simgk$ssx[, i]), sd(
    simgk$ssx[, i]))
  plot(density(simgk$ssx[, i]), main = "", xlab = "")
  lines(eval, densnorm, col = "red")
}
Lims <- matrix(c(-1, 0, 0, -5, -0.5, 1, rep(5, 4)), 5, 2)
tick <- Sys.time()
Resultsgk <- bsl(y = y, n = M, M = S, model = Modelgk,
    covRandWalk = tune*diag(5),
method = "BSL", thetaNames = expression(theta, a, b, g, k),
logitTransformBound = Lims, plotOnTheFly = TRUE)
tock <- Sys.time()
tock - tick
PostChain <- coda::mcmc(Resultsgk@theta[keep,])
CovarRWnew <- var(PostChain)
M <- 500 # Number of iterations to calculate mu and sigma
S <- 6000 # Number of MCMC iterations
burnin <- 1000 # Burn in iterations
thin <- 5 # Thining parameter
keep <- seq(burnin + 1, S, thin)
tune <- 1 # Tuning parameter RW MH
ModelgkNew <- newModel(fnSim = RGKnew, fnSum = SumSt, theta0
    = par0, fnLogPrior = LogPrior, verbose = FALSE)
logitTransform <- function(par, a, b){
  logtrans <- log((par - a)/(b - par))
  return(logtrans)
}
ParTrans <- matrix(NA, dim(PostChain)[1], 5)
for(j in 1:5){
  ParTrans[,j] <- logitTransform(par = PostChain[,j], a =
    Lims[j,1], b = Lims[j,2])
}
CovarRW <- var(ParTrans)
# Vanilla BLS
tick <- Sys.time()
ResultsgkVanila <- bsl(y = y, n = M, M = S, model =
    ModelgkNew, covRandWalk = tune*CovarRW, method = "BSL",
    thetaNames = expression(theta, a, b, g, k),
    logitTransformBound = Lims, plotOnTheFly = TRUE)
tock <- Sys.time()
tock - tick
# Unbiased BLS
tick <- Sys.time()
ResultsgkuBLS <- bsl(y = y, n = M, M = S, model = ModelgkNew
    , covRandWalk = tune*CovarRW,
method = "uBSL", thetaNames = expression(theta, a, b, g, k),
logitTransformBound = Lims, plotOnTheFly = TRUE)
tock <- Sys.time()
tock - tick
```

R code. Bayesian synthetic likelihood: Simulation exercise g-and-k distribution.

```r
1  # Semi-parametric BLS
2  tick <- Sys.time()
3  ResultsgksemiBLS <- bsl(y = y, n = M, M = S, model =
       ModelgkNew, covRandWalk = tune*CovarRW, method = "
       semiBSL", thetaNames = expression(theta, a, b, g, k),
4  logitTransformBound = Lims, plotOnTheFly = TRUE)
5  tock <- Sys.time()
6  tock - tick
7  # Misspecified BLS in mean
8  tick <- Sys.time()
9  ResultsgkmisspecBLSmean <- bsl(y = y, n = M, M = S, model =
       ModelgkNew, covRandWalk = tune*CovarRW, method = "
       BSLmisspec", thetaNames = expression(theta, a, b, g, k),
10 logitTransformBound = Lims, misspecType = "mean", tau = 0.5,
        plotOnTheFly = TRUE)
11 tock <- Sys.time()
12 tock - tick
13 # Misspecified BLS in variance
14 tick <- Sys.time()
15 ResultsgkmisspecBLSvar <- bsl(y = y, n = M, M = S, model =
       ModelgkNew, covRandWalk = tune*CovarRW, method = "
       BSLmisspec", thetaNames = expression(theta, a, b, g, k),
16 logitTransformBound = Lims, misspecType = "variance", tau =
       0.5, plotOnTheFly = TRUE)
17 tock <- Sys.time()
18 tock - tick
19 # Summary all models
20 gkResults <- list(ResultsgkVanila, ResultsgkuBLS,
       ResultsgksemiBLS, ResultsgkmisspecBLSmean,
       ResultsgkmisspecBLSvar)
21 names(gkResults) <- c("BSL", "uBSL", "semiBLS", "missBSLmean
       ", "missBSLvar")
22 t(sapply(gkResults, summary))
23 combinePlotsBSL(gkResults, which = 2, thetaTrue = parpop,
       thin = thin, options.linetype = list(values = 1:8),
       options.size = list(values = rep(1, 8)), options.theme =
        list(plot.margin = grid::unit(rep(0.03, 4), "npc"),
       axis.title = ggplot2::element_text(size = 12), axis.text
        = ggplot2::element_text(size = 8),
24 legend.text = ggplot2::element_text(size = 12)))
25 # semi BSL and miss BSL mean are totally diferent to other
       methods
26 gkResultsNew <- list(gkResults[["BSL"]], gkResults[["uBSL"
       ]], gkResults[["missBSLvar"]])
27 names(gkResultsNew) <- c("BSL", "uBSL", "missBSLvar")
28 combinePlotsBSL(gkResultsNew, which = 2, thetaTrue = parpop,
        thin = thin, options.linetype = list(values = 1:8),
       options.size = list(values = rep(1, 8)), options.theme =
        list(plot.margin = grid::unit(rep(0.03, 4), "npc"),
       legend.text = ggplot2::element_text(size = 12)))
```

3. Simulate a multinomial logit model (see Section 6.5 in the book) with 3 alternatives, 2 alternative-specific regressors, and 1 individual-specific regressor. The population parameters for the alternative-specific regressors are -0.3 and 1.2, while the population values for the individual-specific regressor are 0.3, 0, and 0.5. All regressors are assumed to follow a standard normal distribution, and the sample size is 1,000.

   Perform inference using the *INLA* package, and note that the Poisson trick should be used for multinomial models in this exercise (see [40] for details).

   Answer:

R code. Multinomial model in INLA: Simulation exercise.

```r
1  rm(list = ls()); set.seed(010101)
2  library(INLA)
3  beta1 <- -0.3; beta2 <- 1.2; gamma <- c(0.3, 0, 0.5)
4  param <- c(beta1, beta2, gamma); n <- 1000
5  # Alternative specific regressors
6  x11 <- rnorm(n); x12 <- rnorm(n); x13 <- rnorm(n)
7  x21 <- rnorm(n); x22 <- rnorm(n); x23 <- rnorm(n)
8  # Individual specific regressor
9  Z <- rnorm(n)
10 Multinom.sample = function(N){
11   Y <- matrix(NA, ncol = 3, nrow = n)
12   for(i in 1:n){
13     V1 <- beta1*x11[i] + beta2*x21[i] + gamma[1]*Z[i]
14     V2<- beta1*x12[i] + beta2*x22[i] + gamma[2]*Z[i]
15     V3 <- beta1*x13[i] + beta2*x23[i] + gamma[3]*Z[i]
16     probs <- c(V1, V2, V3)
17     probs <- exp(probs)/sum(exp(probs))
18     samp <- rmultinom(1, N, prob = probs)
19     Y[i,] = as.vector(samp)
20   }
21   colnames(Y ) = c("Y1", "Y2", "Y3")
22   return(Y)
23 }
24 Y <- Multinom.sample(1)
25 df <- data.frame(cbind(Y, x11, x12, x13, x21, x22, x23, Z))
26 Data.structure = function(df){
27   Data = matrix(NA, ncol = 6, nrow = n*3)
28   for(i in 1:n){
29     # simulated variable
30     Data[((i-1)*3+1):(i*3), 1] = c(df$Y1[i], df$Y2[i], df$Y3
       [i])
31     # alternative specific with generic coeff
32     Data[((i-1)*3+1):(i*3), 2] = c(df$x11[i], df$x12[i], df$
       x13[i])
33     # alternative specific with generic coeff
34     Data[((i-1)*3+1):(i*3), 3] = c(df$x21[i], df$x22[i], df$
       x23[i])
35     # individual specific with alternative coeff
36     Data[((i-1)*3+1):(i*3), 4] = rep(df$Z[i],3)
37     # choice situation index
38     Data[((i-1)*3+1):(i*3), 5] = rep(i,3)
39     # choice alternative index
40     Data[((i-1)*3+1):(i*3), 6] = c(1, 2, 3)
41   }
42   Data = data.frame(Data)
43   names(Data) = c('Y', "X1", "X2", "Z",'phi','alt.idx')
44   return(Data)
45 }
46 formula = Y ~ -1 + X1 + X2 + f(phi, initial = -10, fixed = T
       ) + f(alt.idx, Z, fixed = T, constr = T)
47 Data = Data.structure(df)
48 model = inla(formula, data = Data, family = 'Poisson')
49 result = rbind(model$summary.fixed[1:5], model$summary.
       random$alt.idx[2:6])
50 result = cbind(result, true = param)
```

R code. Multinomial model in INLA: Simulation exercise.

```
1 row.names(result) = c("beta1", "beta2", "gamma.A","gamma.B",
      "gamma.C" )
2 round(result,3)
3 diff.result = cbind("0.025quant"= diff(model$summary.random$
      alt.idx$'0.025quant'), "0.5quant" = diff(model$summary.
      random$alt.idx$'0.5quant'), "0.975quant" = diff(model$
      summary.random$alt.idx$'0.975quant'), "true" = diff(
      gamma))
4 row.names(diff.result) = c("gamma.B - gamma.A", "gamma.C -
      gamma.B")
5 round(diff.result,3)
```

4. Get the expression for the ELBO in the linear regression model with conjugate family.

   Answer:

$$
\begin{aligned}
\text{ELBO}(q(\boldsymbol{\beta}, \sigma^2)) &= \mathbb{E}_{\boldsymbol{\beta},\sigma^2}[\log p(\boldsymbol{y}, \boldsymbol{\beta}, \sigma^2 \mid \boldsymbol{X})] - \mathbb{E}_{\boldsymbol{\beta},\sigma^2}[\log q(\boldsymbol{\beta}, \sigma^2)] \\
&= \mathbb{E}_{\boldsymbol{\beta},\sigma^2}[\log p(\boldsymbol{y} \mid \boldsymbol{\beta}, \sigma^2, \boldsymbol{X}) + \log \pi(\boldsymbol{\beta} \mid \sigma^2) + \log(\sigma^2)] \\
&\quad - \mathbb{E}_{\boldsymbol{\beta},\sigma^2}[\log q(\boldsymbol{\beta}) + \log q(\sigma^2)] \\
&= \mathbb{E}_{\boldsymbol{\beta},\sigma^2}\left[-\frac{N}{2}\log(2\pi) - \frac{N}{2}\log\sigma^2 - \frac{1}{2\sigma^2}(\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})^\top(\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta}) \right. \\
&\quad -\frac{K}{2}\log(2\pi) - \frac{K}{2}\log(\sigma^2) - \frac{1}{2}\log|\boldsymbol{B}_0| - \frac{1}{2\sigma^2}(\boldsymbol{\beta} - \boldsymbol{\beta}_0)^\top \boldsymbol{B}_0^{-1}(\boldsymbol{\beta} - \boldsymbol{\beta}_0) \\
&\quad \left. - (\alpha_0/2 + 1)\log\sigma^2 - \frac{\delta_0}{2\sigma^2} + \alpha_0/2\log(\delta_0/2) - \log\Gamma(\alpha_0/2)\right] \\
&\quad - \left\{\mathbb{E}_{\boldsymbol{\beta},\sigma^2}\left[\frac{K}{2}\log\mathbb{E}_{\sigma^2}(1/\sigma^2) - \frac{1}{2}\log|\boldsymbol{B}_n| - \frac{1}{2}\mathbb{E}_{\sigma^2}(1/\sigma^2)(\boldsymbol{\beta} - \boldsymbol{\beta}_n)^\top \boldsymbol{B}_n^{-1}(\boldsymbol{\beta} - \boldsymbol{\beta}_n)\right.\right. \\
&\quad \left.\left. - \frac{K}{2}\log(2\pi) - (\alpha_n/2 + 1)\log\sigma^2 - \frac{\delta_n}{2\sigma^2} + \alpha_n/2\log(\delta_n/2) - \log\Gamma(\alpha_n/2)\right]\right\} \\
&= -\frac{N}{2}\log(2\pi) - \frac{1}{2}\log|\boldsymbol{B}_0| + \frac{1}{2}\log|\boldsymbol{B}_n| + \alpha_0/2\log(\delta_0/2) \\
&\quad - \alpha_n/2\log(\delta_n/2) - \log\Gamma(\alpha_0/2) + \log\Gamma(\alpha_n/2) - \frac{K}{2}\log\mathbb{E}_{\sigma^2}(1/\sigma^2) \\
&\quad + \frac{1}{2}\mathbb{E}_{\sigma^2}(1/\sigma^2)\mathbb{E}_{\boldsymbol{\beta}}\left[(\boldsymbol{\beta} - \boldsymbol{\beta}_n)^\top \boldsymbol{B}_n^{-1}(\boldsymbol{\beta} - \boldsymbol{\beta}_n)\right] \\
&= -\frac{N}{2}\log(2\pi) - \frac{1}{2}\log|\boldsymbol{B}_0| + \frac{1}{2}\log|\boldsymbol{B}_n| + \alpha_0/2\log(\delta_0/2) \\
&\quad - \alpha_n/2\log(\delta_n/2) - \log\Gamma(\alpha_0/2) + \log\Gamma(\alpha_n/2) - \frac{K}{2}\log(\alpha_n/\delta_n) \\
&\quad + 0.5 tr\left\{Var(\boldsymbol{\beta})\boldsymbol{B}_n^{-1}\right\}
\end{aligned}
$$

We take into account in the fourth equality that the terms collecting $\log\sigma^2$ and $\frac{1}{2\sigma^2}$ cancel out by the definitions of α_n and δ_n, respectively.

5. **Linear regression continues**

Perform inference in the linear regression example using stochastic variational inference via the automatic differentiation variational inference (ADVI) approach [22], implemented in `rstan` package. In particular, consider the model $y_i = \boldsymbol{x}_i^\top \boldsymbol{\beta} + \mu_i$, assuming non-informative independent priors: $\boldsymbol{\beta} \sim N(\boldsymbol{\beta}_0, \boldsymbol{B}_0)$ and $\sigma^2 \sim \text{IG}(\alpha_0/2, \delta_0/2)$, where $\boldsymbol{\beta}_0 = \boldsymbol{0}_3$, $\boldsymbol{B}_0 = 1000\boldsymbol{I}_3$, and $\alpha_0 = \delta_0 = 0.01$. The sample size is one hundred thousand.

Answer:

The posterior mean values are very close to the population parameters, but the 95% credible intervals are too narrow and do not contain the true values.

R code. Stochastic variational inference: Simulation exercise linear regression.

```r
1  library(rstan)
2  # --- Simulated data ---
3  N <- 100000; K <- 2; B <- rep(1, K + 1); sig2 <- 1
4  X <- cbind(1, matrix(rnorm(N * K), N, K))
5  y <- X %*% B + rnorm(N, 0, sig2^0.5)
6  # --- Priors ---
7  b0 <- 0; B0 <- 1000; a0 <- 0.01; d0 <- 0.01
8  # --- Prepare data for Stan ---
9  data_list <- list(
10 N = N,
11 K = K + 1,   # K+1 because of the intercept
12 X = X,
13 y = as.vector(y),
14 b0 = b0,
15 B0 = B0,
16 a0 = a0,
17 d0 = d0
18 )
19 # --- Stan model compilation ---
20 stan_model_code <- "
21 data {
22   int<lower=0> N;          // number of data points
23   int<lower=0> K;          // number of predictors
24   matrix[N, K] X;          // predictor matrix
25   vector[N] y;             // response vector
26   real b0;                 // location parameter prior on beta
27   real<lower=0> B0;        // variance parameter prior on beta
28   real<lower=0> a0;        // shape parameter prior on sigma^2
29   real<lower=0> d0;        // rate parameter prior on sigma^2
30 }
31 parameters {
32   vector[K] beta;          // coefficients of the linear model
33   real<lower=0> sigma2;    // variance parameter (sigma^2)
34 }
35 model {
36   // Priors
37   beta ~ normal(b0, B0);        // Normal prior on beta
38   sigma2 ~ inv_gamma(a0/2, d0/2); // Inverse Gamma prior
39
40   // Likelihood
41   y ~ normal(X * beta, sqrt(sigma2)); // Normal likelihood
     with linear predictor
42 }
43 generated quantities {
44   vector[N] y_pred;
45   for (n in 1:N) {
46     y_pred[n] = normal_rng(dot_product(X[n], beta), sqrt(
     sigma2));
47   }
48 }
49 "
```

```
1  # Compile Stan model
2  stan_model <- stan_model(model_code = stan_model_code)
3  # --- Perform Stochastic Variational Inference (SVI) ---
4  fit <- vb(stan_model, data = data_list, algorithm = "
       meanfield", iter = 10000)
5  # --- Extract the results ---
6  mu_estimate <- extract(fit)$beta
7  summary(coda::mcmc(mu_estimate))
8  sigma2_estimate <- extract(fit)$sigma2
9  summary(coda::mcmc(as.vector(sigma2_estimate)))
10
```

6. Let's retake the mixture regression model of Chapter 11, that is, the simple regression mixture with two components such that $z_{i1} \sim \text{Ber}(0.5)$, consequently, $z_{i2} = 1 - z_{i1}$, and assume one regressor, $x_i \sim N(0, 1)$, $i = 1, 2, \ldots, 1,000$. Then,

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

Let's set $\alpha_{h0} = \delta_{h0} = 0.01$, $\boldsymbol{\beta}_{h0} = \boldsymbol{0}_2$, $\boldsymbol{B}_{h0} = \boldsymbol{I}_2$, and $\boldsymbol{a}_0 = [1/2 \ 1/2]^\top$.

Perform VB inference in this model using the CAVI algorithm.

Answer:

The likelihood function in this model is $p(\boldsymbol{y} \mid \boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2) = \prod_{i=1}^{N} \prod_{h=1}^{H} \phi(y_i \mid \boldsymbol{x}_i^\top \boldsymbol{\beta}_h, \sigma_h^2)^{z_{ih}}$, and $\pi(\boldsymbol{z} \mid \boldsymbol{\lambda}) = \prod_{i=1}^{N} \prod_{h=1}^{H} \lambda_h^{z_{ih}}$, $\boldsymbol{\lambda} \sim Dir(\boldsymbol{a}_0)$, $\boldsymbol{\beta}_h \sim N(\boldsymbol{\beta}_{h0}, \boldsymbol{B}_{h0})$ and $\sigma_h^2 \sim IG(\alpha_{h0}/2, \delta_{h0}/2)$. In this notation, $\boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2$ and $\boldsymbol{\lambda}$ stacks all the latent indicators, all locations and scale parameters of each cluster, and all the probabilities, respectively.

Let's work with the mean-field variational family $q(\boldsymbol{z}, \boldsymbol{\lambda}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2) = q(\boldsymbol{z})q(\boldsymbol{\lambda})\prod_{h=1}^{H} q(\boldsymbol{\beta}_h)\prod_{h=1}^{H} q(\sigma_h^2)$.

Then,

$$
\begin{aligned}
\log q(\boldsymbol{z}) =& \mathbb{E}_{\boldsymbol{\lambda},\boldsymbol{\beta},\boldsymbol{\sigma}^2}\left[\log p(\boldsymbol{y},\boldsymbol{z},\boldsymbol{\beta},\boldsymbol{\sigma}^2)\right] + c_1 \\
=& \mathbb{E}_{\boldsymbol{\lambda},\boldsymbol{\beta},\boldsymbol{\sigma}^2}\left[\log p(\boldsymbol{y}\mid\boldsymbol{z},\boldsymbol{\beta},\boldsymbol{\sigma}^2) + \log\pi(\boldsymbol{z}\mid\boldsymbol{\lambda})\right] + c_2 \\
=& \mathbb{E}_{\boldsymbol{\lambda},\boldsymbol{\beta},\boldsymbol{\sigma}^2}\left[\sum_{i=1}^{N}\sum_{h=1}^{H} z_{ih}\left\{-0.5\log 2\pi - 0.5\log\sigma_h^2 - \right.\right. \\
& \left.\left. -\frac{1}{2\sigma_h^2}(y_i - \boldsymbol{x}_i\boldsymbol{\beta}_h)^2 + \log\lambda_h\right\}\right] + c_2 \\
=& \sum_{i=1}^{N}\sum_{h=1}^{H}\psi_{ih}\log\rho_{ih} + c_2.
\end{aligned}
$$

Thus, $q(\boldsymbol{z}) = \prod_{i=1}^{N}\prod_{h=1}^{H} r_{ih}^{z_{ih}}$, such that $\mathbb{E}_{z_{ih}}[z_{ih}] = r_{ih}$, where $r_{ih} = \frac{\rho_{ih}}{\sum_{j=1}^{H}\rho_{ij}}$, and

$$
\log\rho_{ih} = -0.5\log 2\pi - 0.5\mathbb{E}_{\sigma_h^2}\log\sigma_h^2 - 0.5\mathbb{E}_{\sigma_h^2}\left(\frac{1}{\sigma_h^2}\right)\mathbb{E}_{\boldsymbol{\beta}_h}(y_i - \boldsymbol{x}_i^{\top}\boldsymbol{\beta}_h)^2 + \mathbb{E}_{\lambda_h}\log\lambda_h.
$$

$$
\begin{aligned}
\log q(\boldsymbol{\lambda}) &= \mathbb{E}_{\boldsymbol{z},\boldsymbol{\beta},\boldsymbol{\sigma}^2}\left[\log p(\boldsymbol{y},\boldsymbol{z},\boldsymbol{\beta},\boldsymbol{\sigma}^2)\right] + c_1 \\
&= \mathbb{E}_{\boldsymbol{z}}\left[\log\pi(\boldsymbol{z}\mid\boldsymbol{\lambda}) + \log\pi(\boldsymbol{\lambda})\right] + c_2 \\
&= \mathbb{E}_{\boldsymbol{z}}\left[\sum_{i=1}^{N}\sum_{h=1}^{H} z_{ih}\log\lambda_h + \sum_{h=1}^{H}(a_{h0}-1)\log\lambda_h\right] + c_3 \\
&= \sum_{i=1}^{N}\sum_{h=1}^{H}\mathbb{E}_{z_{ih}}[z_{ih}]\log\lambda_h + \sum_{h=1}^{H}(a_{h0}-1)\log\lambda_h + c_3 \\
&= \sum_{i=1}^{N}\sum_{h=1}^{H} r_{ih}\log\lambda_h + \sum_{h=1}^{H}(a_{h0}-1)\log\lambda_h + c_3 \\
&= \sum_{h=1}^{H}\left(\sum_{i=1}^{N} r_{ih} + a_{h0} - 1\right)\log\lambda_h + c_3.
\end{aligned}
$$

This implies that $q(\boldsymbol{\lambda})$ is Dirichlet with parameters $a_{hn} = a_{h0} + \sum_{i=1}^{N} r_{ih}$.

$$
\begin{aligned}
\log q(\boldsymbol{\beta}_h) &= \mathbb{E}_{\boldsymbol{\lambda},\boldsymbol{z},\boldsymbol{\sigma}^2}\left[\log p(\boldsymbol{y},\boldsymbol{z},\boldsymbol{\beta},\boldsymbol{\sigma}^2)\right] + c_1 \\
&= \mathbb{E}_{\boldsymbol{z},\boldsymbol{\sigma}^2}\left[\log p(\boldsymbol{y}\mid\boldsymbol{z},\boldsymbol{\beta},\boldsymbol{\sigma}^2) + \log\pi(\boldsymbol{\beta}_h)\right] + c_2 \\
&= \mathbb{E}_{\boldsymbol{z},\boldsymbol{\sigma}^2}\left[\sum_{i=1}^{N}\sum_{h=1}^{H} z_{ih}\left\{-\frac{1}{2\sigma_h^2}(y_i - \boldsymbol{x}_i^{\top}\boldsymbol{\beta}_h)^2\right\}\right. \\
& \left. -0.5(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{h0})^{\top}\boldsymbol{B}_{h0}^{-1}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{h0})\right] + c_3.
\end{aligned}
$$

Following same steps as those to obtain the posterior distribution,

and taking into account the expected values, we have that $q(\boldsymbol{\beta}_h)$ is $N(\boldsymbol{\beta}_{hn}, \boldsymbol{B}_{hn})$, where $\boldsymbol{B}_{hn} = \left(\boldsymbol{B}_{h0}^{-1} + \mathbb{E}_{\sigma_h^2}\left(\frac{1}{\sigma_h^2}\right)\sum_{i=1}^N r_{ih}\boldsymbol{x}_i\boldsymbol{x}_i^\top\right)^{-1}$ and $\boldsymbol{\beta}_{hn} = \boldsymbol{B}_{hn}\left(\boldsymbol{B}_{h0}^{-1}\boldsymbol{\beta}_{h0} + \mathbb{E}_{\sigma_h^2}\left(\frac{1}{\sigma_h^2}\right)\sum_{i=1}^N r_{ih}\boldsymbol{x}_i y_i\right)$.

$$\log q(\sigma_h^2) = \mathbb{E}_{\boldsymbol{\lambda},\boldsymbol{z},\boldsymbol{\beta}}\left[\log p(\boldsymbol{y}, \boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2)\right] + c_1$$
$$= \mathbb{E}_{\boldsymbol{z},\boldsymbol{\beta}}\left[\log p(\boldsymbol{y} \mid \boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2) + \log \pi(\sigma_h^2)\right] + c_2$$
$$= \mathbb{E}_{\boldsymbol{z},\boldsymbol{\beta}}\left[\sum_{i=1}^N\sum_{h=1}^H z_{ih}\left\{-0.5\log\sigma_h^2 - \frac{1}{2\sigma_h^2}(y_i - \boldsymbol{x}_i^\top\boldsymbol{\beta}_h)^2\right\}\right.$$
$$\left. -(\alpha_{h0}/2 + 1)\log\sigma_h^2 - \frac{\delta_{h0}}{2\sigma_h^2}\right] + c_1.$$

Collecting terms we see that $q(\sigma_h^2)$ is $IG(\alpha_{hn}/2, \delta_{hn}/2)$, where $\alpha_{hn} = \sum_{i=1}^N r_{ih} + \alpha_{h0}$ and $\delta_{hn} = \sum_{i=1}^N r_{ih}\mathbb{E}_{\boldsymbol{\beta}_h}(y_i - \boldsymbol{x}_i^\top\boldsymbol{\beta}_h)^2 + \delta_{h0}$.

Note that the previous results imply that $\mathbb{E}_{\sigma_h^2}\left(\frac{1}{\sigma_h^2}\right) = \alpha_{hn}/\delta_{hn}$, $\mathbb{E}_{\boldsymbol{\beta}_h}(y_i - \boldsymbol{x}_i^\top\boldsymbol{\beta}_h)^2 = (y_i - \boldsymbol{x}_i^\top\boldsymbol{\beta}_{hn})^2 + \boldsymbol{x}_i^\top\boldsymbol{B}_{hn}\boldsymbol{x}_i$, and

$$\log\rho_{ih} = -0.5\log 2\pi - 0.5\mathbb{E}_{\sigma_h^2}\log\sigma_h^2 - 0.5\mathbb{E}_{\sigma_h^2}\left(\frac{1}{\sigma_h^2}\right)\mathbb{E}_{\boldsymbol{\beta}_h}(y_i - \boldsymbol{x}_i^\top\boldsymbol{\beta}_h)^2 + \mathbb{E}_{\lambda_h}\log\lambda_h$$
$$= -0.5\log 2\pi - 0.5(\log(\delta_{hn}/2) - \psi(\alpha_{hn}/2)) - 0.5(\alpha_{hn}/\delta_{hn})(y_i - \boldsymbol{x}_i^\top\boldsymbol{\beta}_{hn})^2$$
$$+ \boldsymbol{x}_i^\top\boldsymbol{B}_{hn}\boldsymbol{x}_i^\top + \psi(a_{hn}) - \psi\left(\sum_{h=1}^H a_{hn}\right),$$

where ψ is the digamma function.

In addition, the evidence lower bound (ELBO) is given by

$$\text{ELBO}(q(\boldsymbol{\theta})) = \mathbb{E}_q\left[\log p(\boldsymbol{y}, \boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2)\right] - \mathbb{E}_q[\log q(\boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2)]$$

$$= \mathbb{E}_q\left[\log p(\boldsymbol{y} \mid \boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2) + \log \pi(\boldsymbol{z} \mid \boldsymbol{\lambda}) + \log \pi(\boldsymbol{\lambda}) + \sum_{h=1}^{H}(\log \pi(\boldsymbol{\beta}_h) + \log \pi(\sigma_h^2))\right]$$

$$- \mathbb{E}_q\left[\log q(\boldsymbol{z}) + \log \pi(\boldsymbol{\lambda}) + \sum_{h=1}^{H}(\log q(\boldsymbol{\beta}_h) + \log \pi(\sigma_h^2))\right]$$

$$= \mathbb{E}_q\left[\sum_{i=1}^{N}\sum_{h=1}^{H} z_{ih}\left\{-0.5\log(2\pi) - 0.5\log \sigma_h^2 - 0.5\frac{1}{\sigma_h^2}(y_i - \boldsymbol{x}_i^\top \boldsymbol{\beta}_h)^2\right\}\right.$$

$$+ \sum_{i=1}^{N}\sum_{h=1}^{H} z_{ih}\log \lambda_h + \sum_{h=1}^{H}\left\{-\frac{K}{2}\log(2\pi) - 0.5\log|\boldsymbol{B}_{h0}| - 0.5(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{h0})^\top \boldsymbol{B}_{h0}^{-1}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{h0})\right\}$$

$$\left.+ \sum_{h=1}^{H}\left\{-(\alpha_{h0}/2 + 1)\log \sigma_h^2 - \frac{\delta_{h0}}{2\sigma_h^2} + (\alpha_{h0}/2)\log(\delta_{h0}/2) - \log \Gamma(\alpha_0/2)\right\}\right]$$

$$- \mathbb{E}_q\left[\sum_{i=1}^{N}\sum_{h=1}^{H} z_{ih}\log r_{ih} - \log B(\boldsymbol{a}_n) + \sum_{h=1}^{H}(a_{hn} - 1)\log \lambda_h\right.$$

$$+ \sum_{h=1}^{H}\left\{-\frac{K}{2}\log(2\pi) - 0.5\log|\boldsymbol{B}_{hn}| - 0.5(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})^\top \boldsymbol{B}_{hn}^{-1}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})\right\}$$

$$\left.+ \sum_{h=1}^{H}\left\{-(\alpha_{hn}/2 + 1)\log \sigma_h^2 - \frac{\delta_{hn}}{2\sigma_h^2} + (\alpha_{hn}/2)\log(\delta_{hn}/2) - \log \Gamma(\alpha_{hn}/2)\right\}\right].$$

The first part of this expression, that is, $\mathbb{E}_q\left[\log p(\boldsymbol{y}, \boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2)\right]$, is given by
$\sum_{i=1}^{N}\sum_{h=1}^{H} r_{ih}\left\{-0.5\log(2\pi) - 0.5(\log(\delta_{hn}/2) - \psi(\alpha_{hn}/2)) - \frac{\alpha_{hn}}{2\delta_{hn}}[(y_i - \boldsymbol{x}_i^\top \boldsymbol{\beta}_{hn})^2 + \boldsymbol{x}_i^\top \boldsymbol{B}_{hn}\boldsymbol{x}_i]\right\} +$
$\sum_{i=1}^{N}\sum_{h=1}^{H} r_{ih}\log r_{it} + \sum_{h=1}^{H}\left\{-\frac{K}{2}\log(2\pi) - 0.5\log|\boldsymbol{B}_{h0}| - tr(\boldsymbol{B}_{hn}\boldsymbol{B}_{h0}^{-1}) - (\boldsymbol{\beta}_{hn} - \boldsymbol{\beta}_{h0})^\top(\boldsymbol{\beta}_{hn} - \boldsymbol{\beta}_{h0})\right\} +$
$\sum_{h=1}^{H}\left\{-(\alpha_{h0}/2 + 1)(\log(\delta_{hn}/2) - \psi(\alpha_{hn}/2)) - \frac{\delta_{h0}}{2}\frac{\alpha_{hn}}{\delta_{hn}} + (\alpha_{h0}/2)\log(\delta_{h0}/2) - \log \Gamma(\alpha_0/2)\right\}.$

The second part of the ELBO, that is, $\mathbb{E}_q[\log q(\boldsymbol{z}, \boldsymbol{\beta}, \boldsymbol{\sigma}^2)]$ is given by
$\sum_{i=1}^{N}\sum_{h=1}^{H} r_{ih}\log r_{ih} - \log B(\boldsymbol{a}_n) + \sum_{h=1}^{H}(a_{hn} - 1)\left(\psi(a_{hn}) - \psi\left(\sum_{h=1}^{H} a_{hn}\right)\right) +$
$\sum_{h=1}^{H} -\frac{K}{2}(\log(2\pi) + 1) - 0.5\log|\boldsymbol{B}_{hn}| + (\alpha_{hn}/2 + 1)\psi(\alpha_{hn}/2) - 0.5\alpha_{hn} -$
$\log(\delta_{hn}/2) - \log \Gamma(\alpha_{hn}/2)$. We use

$$\mathbb{E}_{\boldsymbol{\beta}_h}[(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})^\top \boldsymbol{B}_{hn}^{-1}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})] = tr\left\{\mathbb{E}_{\boldsymbol{\beta}_h}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})^\top \boldsymbol{B}_{hn}^{-1}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})\right\}$$

$$= \mathbb{E}_{\boldsymbol{\beta}_h}[tr\left\{(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})^\top \boldsymbol{B}_{hn}^{-1}(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})\right\}]$$

$$= tr\left\{\mathbb{E}_{\boldsymbol{\beta}_h}[(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})(\boldsymbol{\beta}_h - \boldsymbol{\beta}_{hn})^\top \boldsymbol{B}_{hn}^{-1}]\right\}$$

$$= tr\left\{Var(\boldsymbol{\beta}_h)\boldsymbol{B}_{hn}^{-1}\right\}$$

$$= tr\left\{\boldsymbol{I}_K\right\}$$

$$= K$$

R code. Variational Bayes: Mixture Gaussian regression.

```r
1  rm(list = ls())
2  set.seed(010101)
3  # Simulate data from a 2-component mixture model
4  n <- 1000
5  K <- 2; H <- 2
6  x <- rnorm(n)
7  z <- rbinom(n, 1, 0.5)  # Latent class indicator
8  y <- ifelse(z == 0, rnorm(n, 2 + 1.5*x, 1), rnorm(n, -1 +
        0.5*x, 0.8))
9  X <- cbind(1,x)
10 # Iterations
11 S <- 10000
12 ##### From scratch ######
13 # Hyperparameters
14 b0h <- rep(0, K); B0h <- diag(1000,K); B0hi <- solve(B0h)
15 a0h <- 0.01; d0h <- 0.01; a0 <- rep(1/H, H)
16 # Innitial values
17 dhn <- c(50, 50); ahn <- c(500, 500)
18 bhn <- matrix(c(2, 1.5, -1, 0.5), K, H)
19 Bhn <- array(c(1,0,0,1,1,0,0,1), c(K, K, H))
20 an <- c(500, 500)
21 VarParPsi <- function(dhn, ahn, bhn, Bhn, an){
22   logrhoih <- matrix(NA, n, H)
23   for(i in 1:n){
24     for(h in 1:H){
25       logrhoih[i,h] <- -0.5*log(2*pi) - 0.5*(log(dhn[h]/2) -
        digamma(ahn[h]/2)) -
26       0.5*(ahn[h]/dhn[h])*((y[i] - t(X[i,])%*%bhn[,h])^2 + t
        (X[i,])%*%Bhn[,,h]%*%X[i,]) +
27       digamma(an[h]) - digamma(sum(an))
28     }
29   }
30   rhoih <- exp(logrhoih - apply(logrhoih, 1, max))
31   rih <- rhoih / rowSums(rhoih)
32   return(rih)
33 }
34 Rih <- VarParPsi(dhn = dhn, ahn = ahn, bhn = bhn, Bhn = Bhn,
        an = an)
35 VarParLambda <- function(rih){
36   an <- a0 + colSums(rih)
37   return(an)
38 }
39 VarParLambda(rih = Rih)
40 VarParBetah <- function(ahn, dhn, rh){
41   rXX <- matrix(0, K, K)
42   rXy <- matrix(0, K, 1)
43   for(i in 1:n){
44     rXXi <- rh[i]*X[i,]%*%t(X[i,])
45     rXX <- rXX + rXXi
46     rXyi <- rh[i]*X[i,]*y[i]
47     rXy <- rXy + rXyi
48   }
49   Bhn <- solve(B0hi + ahn/dhn * rXX)
50   bhn <- Bhn%*%(B0hi%*%b0h + ahn/dhn * rXy)
51   return(list(bhn = bhn, Bhn = Bhn))
52 }
```

R code. Variational Bayes: Mixture Gaussian regression.

```r
VarParSigma2h <- function(bhn, Bhn, rh){
  ahn <- a0h + sum(rh); dhnterm <- 0
  for(i in 1:n){
    dhntermi <- rh[i]*((y[i] - t(X[i,])%*%bhn)^2 + t(X[i,])%
    *%Bhn%*%X[i,])
    dhnterm <- dhnterm + dhntermi
  }
  dhn <- dhnterm + d0h; return(list(ahn = ahn, dhn = dhn))
}
multivariate_beta <- function(alpha) {
  prod_gammas <- sum(sapply(alpha, lgamma))
  sum_alpha <- sum(alpha)
  gamma_sum_alpha <- lgamma(sum_alpha)
  return(prod_gammas - gamma_sum_alpha)
}
ELBO <- function(rih, dhn, ahn, bhn, Bhn, an){
  LogLikh <- 0; LogPrioPsih <- 0
  LogPriorBeta <- 0; LogPriorSig2 <- 0
  for(h in 1:H){
    for(i in 1:n){
      LogLikih <- rih[i, h]*(-0.5*log(2*pi) - 0.5*(log(dhn[h
      ]/2) - digamma(ahn[h]/2)) - 0.5*(ahn[h]/dhn[h])*((y[i] -
      t(X[i,])%*%bhn[,h])^2 + t(X[i,])%*%Bhn[,,h]%*%X[i,]))
      LogLikh <- LogLikh + LogLikih
      LogPrioPsiih <- rih[i, h]*(digamma(an[h]) - digamma(
      sum(an)))
      LogPrioPsih <- LogPrioPsih + LogPrioPsiih
    }
    LogPriorBetah <- -0.5*K*log(2*pi) - 0.5*log(det(B0h)) -
    sum(diag(Bhn[,,h]%*%B0hi)) - t(bhn[,h] - b0h)%*%B0hi%*%(
    bhn[,h] - b0h)
    LogPriorBeta <- LogPriorBeta + LogPriorBetah
    LogPriorSig2h <- -(a0h/2+1)*(log(dhn[h]/2) - digamma(ahn
    [h]/2)) - 0.5*d0h*(ahn[h]/dhn[h]) + (a0h/2)*log(d0h/2) -
     lgamma(a0h/2)
    LogPriorSig2 <- LogPriorSig2 + LogPriorSig2h
  }
  LogJoint <- LogLikh + LogPrioPsih + LogPriorBeta +
    LogPriorSig2
  logqPsi <- 0; logqLambda <- 0; logqBeta <- 0;logqSig2 <- 0
  for(h in 1:H){
    for(i in 1:n){
      logqPsiih <- rih[i, h] * log(rih[i, h])
      logqPsi <- logqPsi + logqPsiih
    }
    logqLambdah <- (an[h] - 1)*(digamma(an[h]) - digamma(sum
    (an)))
    logqLambda <- logqLambda + logqLambdah
    logqBetah <- -0.5*K*log(2*pi + 1) - 0.5*log(det(Bhn[,,h
    ]))
    logqBeta <- logqBeta + logqBetah
    logqSig2h <- -log(dhn[h]/2) + (ahn[h]/2+1)*digamma(ahn[h
    ]/2) - ahn[h]/2 - lgamma(ahn[h]/2)
    logqSig2 <- logqSig2 + logqSig2h
  }
  logqLambda <- logqLambda - multivariate_beta(alpha = an)
  logq <- logqPsi + logqLambda + logqBeta + logqSig2
  ELBO <- LogJoint - logq
  return(ELBO)
}
```

R code. Variational Bayes: Mixture Gaussian regression.

```r
# Initial values
fit_lm1 <- lm(y ~ x)
bhn[,1] <- coef(fit_lm1)
bhn[,2] <- coef(fit_lm1) + rnorm(K, 0, 0.5)
Bhn[,,1] <- diag(0.1, K); Bhn[,,2] <- diag(0.1, K)
ahn <- rep(10, H); dhn <- rep(10, H)
an <- c(300, 700)
ELBOs <- rep(NA, S)
ELBOs[1] <- ELBO(rih = Rih, dhn = dhn, ahn = ahn, bhn = bhn,
    Bhn = Bhn, an = an)
epsilon <- 1e-5
for(s in 2:S){
  Rih <- VarParPsi(dhn = dhn, ahn = ahn, bhn = bhn, Bhn =
    Bhn, an = an)
  an <- VarParLambda(rih = Rih)
  bhn <- matrix(NA, K, H)
  Bhn <- array(NA, c(K, K, H))
  for(h in 1:H){
    EnsVarParBetah <- VarParBetah(ahn = ahn[h], dhn = dhn[h
    ], rh = Rih[,h])
    bhn[,h] <- EnsVarParBetah[["bhn"]]
    Bhn[,,h] <- EnsVarParBetah[["Bhn"]]
  }
  ahn <- rep(NA, H)
  dhn <- rep(NA, H)
  for(h in 1:H){
    EnsVarParSig2h <- VarParSigma2h(bhn = bhn[,h], Bhn = Bhn
    [,,h], rh = Rih[,h])
    ahn[h] <- EnsVarParSig2h[["ahn"]]
    dhn[h] <- EnsVarParSig2h[["dhn"]]
  }
  ELBOs[s] <- ELBO(rih = Rih, dhn = dhn, ahn = ahn, bhn =
    bhn, Bhn = Bhn, an = an)
  # Check if lower bound decreases
  if (ELBOs[s] < ELBOs[s - 1]) { message("Lower bound
    decreases!\n")}
  # Check for convergence
  if (ELBOs[s] - ELBOs[s - 1] < epsilon) { break }
  # Check if VB converged in the given maximum iterations
  if (s == S) {warning("VB did not converge!\n")}
}
plot(ELBOs[1:s], type = "l", main = "ELBO over iterations",
    ylab = "ELBO", xlab = "Iteration")
Sig21 <- MCMCpack::rinvgamma(S, ahn[1]/2, dhn[1]/2)
summary(coda::mcmc(Sig21))
Sig22 <- MCMCpack::rinvgamma(S, ahn[2]/2, dhn[2]/2)
summary(coda::mcmc(Sig22))
Beta1 <- MASS::mvrnorm(S, mu = bhn[,1], Sigma = Bhn[,,1])
summary(coda::mcmc(Beta1))
Beta2 <- MASS::mvrnorm(S, mu = bhn[,2], Sigma = Bhn[,,2])
summary(coda::mcmc(Beta2))
Lambda <- MCMCpack::rdirichlet(S, alpha = an)
summary(coda::mcmc(Lambda))
```

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Appendix

TABLE 14.1
Libraries and commands in BEsmarter GUI.

Univariate models			
Model	**Library**	**Command**	**Reference**
Normal	MCMCpack	MCMCregress	[26]
Logit	MCMCpack	MCMClogit	[26]
Probit	bayesm	rbprobitGibbs	[37]
Multinomial(Mixed) Probit	bayesm	rmnpGibbs	[37]
Multinomial(Mixed) Logit	bayesm	rmnlIndepMetrop	[37]
Ordered Probit	bayesm	rordprobitGibbs	[37]
Negative Binomial(Poisson)	bayesm	rnegbinRw	[37]
Tobit	MCMCpack	MCMCtobit	[26]
Quantile	MCMCpack	MCMCquantreg	[26]
Bayesian bootstrap	bayesboot	bayesboot	[2]
Multivariate models			
Model	**Library**	**Command**	**Reference**
Multivariate	bayesm	rmultireg	[37]
Seemingly Unrelated Regression	bayesm	rsurGibbs	[37]
Instrumental Variable	bayesm	rivGibbs	[37]
Bivariate Probit	bayesm	rmvpGibbs	[37]
Hierarchical longitudinal models			
Model	**Library**	**Command**	**Reference**
Normal	MCMCpack	MCMChregress	[26]
Logit	MCMCpack	MCMChlogit	[26]
Poisson	MCMCpack	MCMChpoisson	[26]
Bayesian model averaging			
Model	**Library**	**Command**	**Reference**
Normal (BIC)	BMA	bic.glm	[31]
Normal (MC^3)	BMA	MC3.REG	[31]
Normal (instrumental variables)	ivbma	ivbma	[24]
Logit (BIC)	BMA	bic.glm	[31]
Gamma (BIC)	BMA	bic.glm	[31]
Poisson (BIC)	BMA	bic.glm	[31]
Diagnostics			
Diagnostic	**Library**	**Command**	**Reference**
Trace plot	coda	traceplot	[28]
Autocorrelation plot	coda	autocorr.plot	[28]
Geweke test	coda	geweke.diag	[28]
Raftery & Lewis test	coda	raftery.diag	[28]
Heidelberger & Welch test	coda	heidel.diag	[28]

TABLE 14.2
Datasets 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 513SimNormalBMAivZ.csv	513SimNormalBMAiv.R
Logit (BIC)	52SimLogitBMA.csv	52SimLogitBMA.R
Gamma (BIC)	53SimGammaBMA.csv	53SimGammaBMA.R
Poisson (BIC)	53SimPoissonBMA.csv	53SimPoissonBMA.R

TABLE 14.3
Real 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 12ExportDiversificationHHIInstr.csv	avghhi and avglgdpcap
Logit (BIC)	13InternetMed.csv	internet
Gamma (BIC)	14ValueFootballPlayers.csv	log market value
Poisson (BIC)	15Fertile2.csv	ceb