MS2505: Bayesian Statistics Course Project

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1 Setup

1.1 Analysis problem

1.2 Data Selection

The dataset selected is a datasets containing a list of emails, as well as a label marking each email as "spam" or "ham" (spam or not spam). The first 10 rows of the dataset looks as follows:

Table 1

mail data.csv dataset first 10 rows

	dutuset hist to tows
Category	Message
ham	"Go until jurong point, crazy Available only in bugis n great
	world la e buffetCine there got amore wat"
ham	Ok larJoking wif u oni
spam	Free entry in 2 a wkly comp to win FA Cup final tkts 21st May
	2005. Text FA to 87121 to receive entry question (std txt rate)
	T&C's apply 08452810075over18's
ham	U dun say so early hoU c already then say
ham	"Nah I don't think he goes to usf, he lives around here though"
spam	"FreeMsg Hey there darling it's been 3 week's now and no word
	back! I'd like some fun you up for it still? Tb ok! XxX std chgs to
	send, £1.50 to rcv"
ham	Even my brother is not like to speak with me. They treat me like
	aids patent.
ham	As per your request 'Melle Melle (Oru Minnaminunginte Nurungu
	Vettam)' has been set as your callertune for all Callers. Press *9 to
	copy your friends Callertune
•••	

Then, using a Python script, the labels were converted to 1 if it was "spam" and 0 if it was "ham", for easier analysis.

1.3 Model

The model chosen was a binomial likelihood model with a beta prior. As the goal is to analyse the probability of an email being spam, the fallout will be binary (either it is spam or it is not). Hence, a binomial likelihood, where I want to find the parameter θ in a dataset of fixed size with a set number of "successes" and "fails" (spam and ham), is appropriate.

Additionally, as I do not have any prior knowledge in regards to this distribution, a non-informative prior is the most suited option, and as Beta(1,1) is a common prior used with binomial likelihood functions, I chose it for this problem.

2 Results

Table 2

Monte Carlo Posterior analysis data

Posterior Mean	0.1341994
Posterior SD	0.004576791
95% Credible Interval	[0.1252803, 0.1432051]

Table 3

Markov Chain Monte Carlo Posterior analysis data

Posterior Mean	0.1344085
Posterior SD	0.004670508
95% Credible Interval	[0.1254781, 0.1437142]

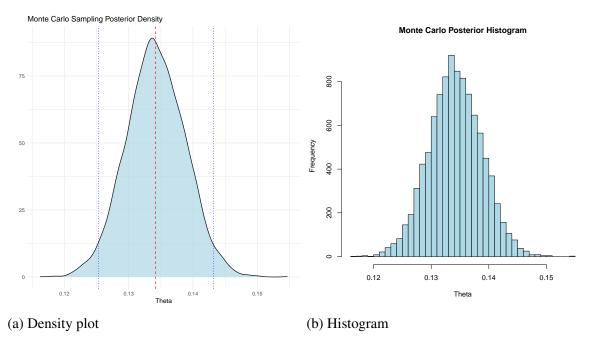


Figure 1

Posterior density plot for monte carlo sampling. As can be seen in the plot, the estimated θ is approximately 0.135, which corresponds to what was estimated in Table 2.

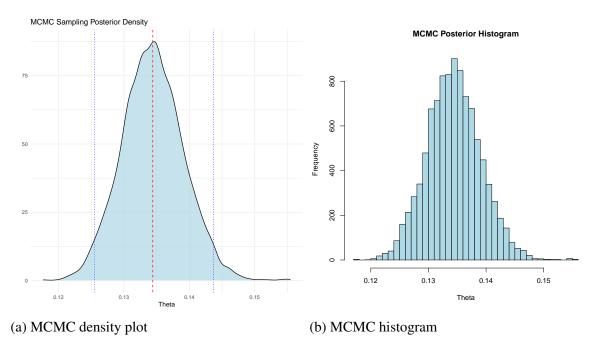


Figure 2 Posterior density plot for Markov Chain Monte Carlo sampling. Similarly to the results in Figure 1, the results show an expected value of 0.135, which follows what is estimated value in the corresponding Table 3

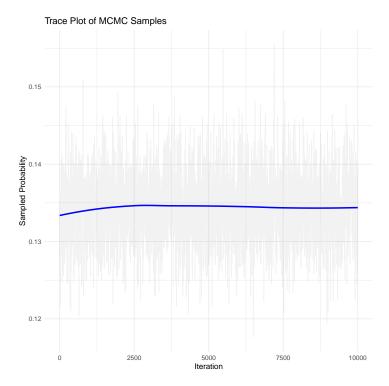


Figure 3Markov Chain Monte Carlo sampling trace plot

3 Discussion

A R Code

Listing 1 Project R code

```
# -----
  # Bayesian Analysis for Email Spam Classification
  # -----
  # Load Required Libraries
 required_packages <- c("ggplot2", "dplyr", "MCMCpack", "coda", "</pre>
    tidyr")
  installed_packages <- rownames(installed.packages())</pre>
  for (pkg in required_packages) {
   if (!pkg %in% installed_packages) install.packages(pkg)
   library(pkg, character.only = TRUE)
  }
11
12
  # Set a global random seed for reproducibility
13
 set.seed(123)
14
  # Output Logs
16
  if (!dir.exists("logs")) dir.create("logs")
17
  results_log_file <- "logs/combined_results.log"</pre>
18
19
  # -----
20
  # Load Data
  # -----
22
23
 data_path <- "data/mail_data_bin.csv"
24
  if (!file.exists(data_path)) stop("Data file not found!")
25
  mail_data <- read.csv(data_path)</pre>
26
  # Ensure the response variable is binary and properly coded
28
  if (!all(mail_data$Category %in% c(0, 1))) {
29
   stop("The response variable 'Category' must be binary (0 or 1).")
30
  }
31
32
  # Metadata
 spam_count <- sum(mail_data$Category == 1)</pre>
  ham_count <- sum(mail_data$Category == 0)</pre>
  total_emails <- nrow(mail_data)</pre>
36
37
38
  sink(results_log_file)
  cat("--- Data Metadata ---\n")
 cat("Spam Count:", spam_count, "\n")
41
cat("Ham Count:", ham_count, "\n")
43 cat("Total Emails:", total_emails, "\n")
```

```
sink()
  46
  # Beta Posterior Analysis
  48
  # Prior parameters
50
  |prior_alpha <- 1
51
 prior_beta <- 1
53
  # Posterior parameters
54
  posterior_alpha <- prior_alpha + spam_count</pre>
55
  posterior_beta <- prior_beta + ham_count</pre>
56
  # Monte Carlo Sampling
  n_samples <- 10000
59
  beta_samples <- rbeta(n_samples, posterior_alpha, posterior_beta)</pre>
60
61
  # Summary statistics
62
  |beta_mean <- mean(beta_samples)
  beta_sd <- sd(beta_samples)</pre>
  beta_ci <- quantile(beta_samples, c(0.025, 0.975))</pre>
65
66
  sink(results_log_file, append = TRUE)
67
  cat("\n--- Beta Posterior Analysis ---\n")
  cat("Posterior Mean:", beta_mean, "\n")
  cat("Posterior SD:", beta_sd, "\n")
  cat("95% Credible Interval:", beta_ci, "\n")
  sink()
72
73
  # MCMC Sampling
75
  76
77
  # Define log-posterior function
78
  log_posterior <- function(params) {</pre>
79
   theta <- params[1]
    log_prior <- dbeta(theta, 1, 1, log = TRUE)</pre>
81
    log_likelihood <- sum(dbinom(mail_data$Category,</pre>
82
                               size = 1,
83
                               prob = theta,
84
                               log = TRUE))
85
    return(log_prior + log_likelihood)
  }
87
  # Run MCMC sampling
89
 mcmc_results <- MCMCmetrop1R(</pre>
90
    fun = log_posterior,
91
   theta.init = 0.5,
   burnin = 1000,
93
  mcmc = n\_samples,
```

```
thin = 1,
     verbose = 0
   )
97
98
   # Extract posterior samples
99
  mcmc_samples <- as.vector(mcmc_results)</pre>
100
   mcmc_mean <- mean(mcmc_samples)</pre>
101
   mcmc_sd <- sd(mcmc_samples)</pre>
102
  mcmc_ci <- quantile(mcmc_samples, c(0.025, 0.975))</pre>
103
104
   sink(results_log_file, append = TRUE)
105
   cat("\n--- MCMC Sampling Analysis ---\n")
106
   cat("Posterior Mean:", mcmc_mean, "\n")
107
   cat("Posterior SD:", mcmc_sd, "\n")
108
   cat("95% Credible Interval:", mcmc_ci, "\n")
   sink()
110
111
   112
113
   # Diagnostics and Visualization
   114
115
   if (!dir.exists("figures")) dir.create("figures")
116
117
   # 1. Beta Density Plot
118
   pdf("figures/beta_posterior_density_plot.pdf")
119
   ggplot(data = data.frame(samples = beta_samples), aes(x = samples))
120
     +
     geom_density(fill = "lightblue", alpha = 0.7) +
121
     geom_vline(xintercept = beta_mean, color = "red", linetype = "
122
        dashed") +
     geom_vline(xintercept = beta_ci, color = "blue", linetype = "
123
        dotted") +
     labs(title = "Monte Carlo Sampling Posterior Density", x = "Theta
124
        ", y = "") +
     theme_minimal()
125
   dev.off()
126
127
   # 2. MCMC Density Plot
128
   pdf("figures/mcmc_posterior_density_plot.pdf")
129
   qqplot(data = data.frame(samples = mcmc_samples), aes(x = samples))
130
     geom_density(fill = "lightblue", alpha = 0.7) +
131
     geom_vline(xintercept = mcmc_mean, color = "red", linetype = "
132
        dashed") +
     geom_vline(xintercept = mcmc_ci, color = "blue", linetype = "
133
        dotted") +
     labs(title = "MCMC Sampling Posterior Density", x = "Theta", y =
134
        "") +
     theme_minimal()
   dev.off()
136
137
```

```
# 3. Beta Posterior Histogram
  pdf("figures/beta_posterior_histogram.pdf")
  hist (beta_samples,
140
   breaks = 30, col = "lightblue", border = "black",
141
    xlab = "Theta", main = "Monte Carlo Posterior Histogram"
142
143
  dev.off()
144
145
  # 4. MCMC Posterior Histogram
146
  pdf("figures/mcmc_posterior_histogram.pdf")
147
  hist (mcmc_samples,
148
    breaks = 30, col = "lightblue", border = "black",
149
    xlab = "Theta", main = "MCMC Posterior Histogram"
150
151
  dev.off()
152
153
  # 5. Trace Plot for MCMC
154
  pdf("figures/mcmc_trace_plot.pdf")
155
  ggplot (
156
    data.frame(Iteration = 1:n_samples, Sample = mcmc_samples),
157
    aes(x = Iteration, y = Sample)
158
  ) +
159
    geom_line(alpha = 0.2, color = "gray") +
160
    geom_smooth(color = "blue", method = "loess", se = FALSE) +
161
    labs(title = "Trace Plot of MCMC Samples",
162
         x = "Iteration",
163
         y = "Sampled Probability") +
164
    theme_minimal()
165
  dev.off()
166
167
   # ______
168
  # Completion
  170
171
  cat ("Analysis complete. Check 'logs' and 'figures' directories for
172
     results.\n")
```