

Practical: Hierarchical chain binomial model

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Background

In this computer class, we re-analyze the data about outbreaks of measles in households. The analysis is restricted to households with 3 susceptible individuals at the onset of the outbreak. We assume that there is a single index case that introduces infection to the household. The possible chains of infection then are 1 , $1 \rightarrow 1$, $1 \rightarrow 1 \rightarrow 1$, and $1 \rightarrow 2$.

In this example, the probabilities for a susceptible to escape infection when exposed to one infective in the household are allowed to be different in different households. These probabilities are denoted by q_j (and $p_j = 1 - q_j$), $j = 1, \dots, 334$. The following table expresses the chain probabilities in terms of the escape probability q_j . The observed frequency is the number of households with the respective chain.

chain	prob.	frequency	observed frequency
1	q_j^2	n_1	34
$1 \rightarrow 1$	$2q_j^2 p_j$	n_{11}	25
$1 \rightarrow 1 \rightarrow 1$	$2q_j p_j^2$	n_{111}	not observed
$1 \rightarrow 2$	p_j^2	n_{12}	not observed

The frequencies n_{111} and n_{12} have not been observed. Only their sum $N_3 = n_{111} + n_{12} = 275$ is known.

The hierarchical model was defined in the lecture notes. The joint distribution of parameters α and β , the household-specific escape probabilities and

the chain frequencies is

$$\prod_{j=1}^{334} \left(f(n_1^{(j)}, n_{11}^{(j)}, n_{111}^{(j)}, n_{12}^{(j)} | q_j) f(q_j | \alpha, \beta) \right) f(\alpha, \beta),$$

where

$$\begin{aligned} (n_1^{(j)}, n_{11}^{(j)}, n_{111}^{(j)}, n_{12}^{(j)}) | q_j &\sim \text{Multinomial}(1, (q_j^2, 2q_j^2 p_j, 2q_j p_j^2, p_j^2)), \\ q_j | \alpha, \beta &\sim \text{Beta}(\alpha, \beta), \\ (\alpha, \beta) &\propto (\alpha + \beta)^{-5/2}. \end{aligned}$$

N.B. The household-specific chain frequencies are vectors in which only one of the elements is 1, all other elements being 0. (In other words, each vector is a so called multinoulli random variable.)

N.B. The joint prior distribution of the parameters of the Beta distribution, α and β , is proportional to $(\alpha + \beta)^{-5/2}$. This is derived on the basis of assuming independent uniform priors for $\alpha/(\alpha + \beta)$ (the expectation of the Beta distribution) and $1/(\alpha + \beta)$ (an approximation to the the standard deviation of the Beta distribution). See Chapter 5.3 in Gelman et al.

We index the households with chain 1 as 1,...,34, and households with chain $1 \rightarrow 1$ as 35,...,59, and households with chain $1 \rightarrow 1 \rightarrow 1$ or $1 \rightarrow 2$ as 60,...,334. The model unknowns are α , β , indicators $n_{111}^{(j)}$ for $j = 60, \dots, 334$ (i.e., for all 275 households with the final number of infected 3), and q_j for $j = 1, \dots, 334$ (all households). There are altogether 611 (=2+275+334) model unknowns.

In this exercise we apply a combined Gibbs and Metropolis algorithm to draw samples from the posterior distribution of the model unknowns. Before that, we explore the fit of the simple model with $q_j = q$ for all j .

Exercises

1. The simple chain binomial model. Using R routine **chainGibbs.R** (or **mychainGibbs**), i.e., repeating the earlier exercise, realize an MCMC sample from the posterior distribution of the escape probability q in the simple model in which this probability is the same across all households.

2. Model checking (simple model). Based on the posterior sample of parameter q , draw samples from the posterior predictive distribution of frequencies (n_1, n_{11}) . Compare the sample to the actually observed value (34,25). The algorithm to do this is as follows:

(a) Discard a number of “burn-in” samples in the posterior sample of parameter q , as realised in exercise (1) above.

(b) When the size of the retained sample is K , reserve space for the $K \times 4$ matrix of predicted frequencies for n_1 , n_{11} , n_{111} and n_{12} .

(c) Based on the retained part of the posterior sample, take the k th sample $q^{(k)}$.

(d) Draw a sample of frequencies $(n_1^{(k)}, n_{11}^{(k)}, n_{111}^{(k)}, n_{12}^{(k)})$ from $\text{Multinomial}(334, ((q^{(k)})^2, 2(q^{(k)})^2 p^{(k)}, 2q^{(k)}(p^{(k)})^2, (p^{(k)})^2))$ using the `rmultinom()` function in R.

(e) Repeat steps (c) and (d) K times, storing the sample of frequencies after each step (d).

(f) Plot the samples of pairs $(n_1^{(k)}, n_{11}^{(k)})$, $k = 1, \dots, K$, and compare to the observed point (34,25).

The R routine covering steps (a)-(f) is provided in the script **checkmodel_reduced.R**, except for step (d). Complete step (d) and check the model fit:

```
mcmc.sample = chainGibbs(5000,1,1)
checkmodel_reduced(mcmc.sample,1000)
```

The complete R routine (**checkmodel.R**) will be provided once you have tried writing your own code.

3. A hierarchical chain binomial model. Samples from the joint posterior distribution of the unknowns in the hierarchical (beta-binomial) chain model can be sampled using the following algorithm, applying both Gibbs and Metropolis-Hastings updating steps (superscript k refers to the k th MCMC step):

(a) Reserve space for all model unknowns (parameters α and β as well as the 275 unknown frequencies $n_{111}^{(j)}$).

(b) Initialize the model unknowns.

(c) Update all household-specific escape probabilities from their full conditionals:

$$q_j^{(k)} | \alpha^{(k-1)}, \beta^{(k-1)} \sim \text{Beta}(2 + \alpha^{(k-1)}, \beta^{(k-1)}), \quad j = 1, \dots, 34$$

$$q_j^{(k)} | \alpha^{(k-1)}, \beta^{(k-1)} \sim \text{Beta}(2 + \alpha^{(k-1)}, 1 + \beta^{(k-1)}), \quad j = 35, \dots, 59$$

$$q_j^{(k)} | \alpha^{(k-1)}, \beta^{(k-1)}, n_{111}^{(j,k-1)} \sim \text{Beta}(n_{111}^{(j,k-1)} + \alpha^{(k-1)}, 2 + \beta^{(k-1)}), \quad j = 60, \dots, 334$$

(d) Update the unknown binary variables $n_{111}^{(j)}$ ($j = 60, \dots, 334$) from their full conditionals:

$$n_{111}^{(j,k)} | q_j^{(k)} \sim \text{Binomial}(1, 2q_j^{(k)} / (2q_j^{(k)} + 1))$$

(e) Sample $\alpha^{(k)}$ using a Metropolis-Hastings step (see the program code)

(f) Sample $\beta^{(k)}$ using a Metropolis-Hastings step (see the program code)

(g) Repeat steps (b)–(f) K times (in the R code, $K = \text{mcmc.size}$).

The above algorithm is written in the R script **chain_hierarchical_reduced.R**, except for parts of step (c). Complete the code and draw a posterior sample of all model unknowns. Note that the data set and the prior distributions are hardwired within the given program code.

The complete routine (**chain_hierarchical.R**) will be provided once you have tried your own solution.

4. Posterior inferences. Plot the marginal posterior distributions of the parameters α and β . You can also check how their joint posterior distribution looks like. Draw a histogram of the posterior distribution of $\alpha/(\alpha + \beta)$, the expected escape probability (= the expectation of the Beta distribution). Using output from program **chain_hierarchical.R**, the above plots can be done as follows (based on 2000 samples with the first 500 as burn-in samples):

```
mcmc.size = 50000
mcmc.sample = chain_hierarchical(mcmc.size)
mcmc.al = mcmc.sample$al
mcmc.be = mcmc.sample$be

burn.in = 10000
mcmc.al = mcmc.al[(burn.in+1):mcmc.size]
mcmc.be = mcmc.be[(burn.in+1):mcmc.size]

# Plot the sample paths of parameters alpha and beta
par(mfrow=c(1,2))
plot(mcmc.al,type='l',xlab="alpha")
plot(mcmc.be,type='l',xlab="beta")

# The marginal posterior distributions of parameters alpha and beta
par(mfrow=c(1,2))
hist(mcmc.al,xlab='alpha',main='')
hist(mcmc.be,xlab='beta',main='')

# The joint posterior distribution of alpha and beta
par(mfrow=c(1,1))
plot(mcmc.al,mcmc.be,xlab='alpha',ylab='beta')

# The posterior distribution of the expected escape probability
hist(mcmc.al/(mcmc.al+ mcmc.be),breaks=20,
     xlab='expected escape probability',main='',xlim=c(0.1,0.35))
```

You can also plot the posterior predictive distribution of the escape probability: see the programme code.

```
qpost = rbeta((mcmc.size-burn.in),mcmc.al,mcmc.be)
hist(qpost,main="posterior predictive distribution of the escape probability",
     cex.main=1,xlab="predictive q",breaks=20)
```

5. Model checking (hierarchical model). Check the fit of the hierarchical model with the R program **check_hierarchical.R**. The program draws samples from the posterior predictive distribution of the chain frequencies and plots these samples for frequencies n_1 and n_{11} with the actually observed point (34,25).

```
check_hierarchical(mcmc.sample,mcmc.burnin=500)
```

N.B. Unlike we pretended in the preceding exercises, the original data actually record the frequencies $n_{12} = 239$ and $n_{111} = 36$. You can now check the model fit with respect to these frequencies.

References:

- [1] Bailey T.J.N. “The Mathematical Theory of Infectious Diseases”, Charles Griffiths and Company, London 1975.
- [2] O’Neill Ph. and Roberts G. “Bayesian inference for partially observed stochastic processes”, Journal of the Royal Statistical Society, Series A, **162**, 121–129 (1999).
- [3] Becker N. Analysis of infectious disease data. Chapman and Hall, New York 1989.
- [4] O’Neil Ph. A tutorial introduction to Bayesian inference for stochastic epidemic models using Markov chain Monte Carlo methods. Mathematical Biosciences 2002; 180:103-114.
- [5] Gelman, Carlin, Stern, Rubin. Bayesian Data Analysis, Chapman and Hall, London 2004.