

Practical session:
Chain binomial model I: Gibbs sampler
June 6, 2011

Background

In this computer class, we apply Gibbs sampling to incompletely observed data in a chain binomial model. The observations are based on outbreaks of measles in Rhode Island during the years 1929–1934 [1]. We restrict the analysis to families with 3 susceptible individuals at the onset of the outbreak. This example is based on references [1]–[4].

We assume that there is a single index case that introduces infection to the family. Thus, possible epidemic chains are 1, $1 \rightarrow 1$, $1 \rightarrow 1 \rightarrow 1$ and $1 \rightarrow 2$. Denote the probability for a susceptible to escape infection when exposed to one infective in the family by q (and $p = 1 - q$). The following table lists chain probabilities, with the actually observed frequencies of the size of epidemic:

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

In this exercise, we assume that frequencies n_{111} and n_{12} have not been observed. Only their sum $N_3 = n_{111} + n_{12} = 275$ is known.

The estimation problem concerns the escape probability q , so that there is basically only one unknown parameter in the model. However, the fact that not all frequencies have been observed creates a computational problem that can be solved by Bayesian data augmentation and Gibbs sampling [2].

Marginal likelihood. The joint probability of the *complete data* $(n_1, n_{11}, N_3, n_{111})$ is proportional to a multinomial probability:

$$\begin{aligned} f(n_1, n_{11}, N_3, n_{111}|q) &= (q^2)^{n_1} (2q^2p)^{n_{11}} (2qp^2)^{n_{111}} (p^2)^{N_3-n_{111}} \\ &= \text{constant} \times q^{2n_1+2n_{11}+n_{111}} p^{n_{11}+2N_3}. \end{aligned} \quad (1)$$

The marginal likelihood $f(n_1, n_{11}, N_3|q)$ would be obtained by summing up expressions (1) with n_{111} running from 0 to N_3 .

The Bayesian approach. Instead of using the marginal likelihood, we will treat frequency n_{111} as a model unknown in addition to parameter q . The joint distribution of the observations (n_1, n_{11}, N_3) and the model unknowns (n_{111}, q) is

$$f(n_1, n_{11}, N_3, n_{111}, q) = f(n_1, n_{11}, N_3, n_{111}|q)f(q). \quad (2)$$

The first term in is the complete data likelihood (see (1)), based on the augmented data (i.e. the data are augmented with the unknown frequency n_{111}).

The second term is the prior density of probability q . We choose a Beta prior for parameter q : $q \sim \text{Beta}(\alpha, \beta)$ so that $f(q) \propto q^{\alpha-1}(1-q)^{\beta-1}$. With the choice $\alpha = \beta = 1$, this is uniform prior on $[0,1]$.

The joint posterior distribution of the model unknowns is $f(q, n_{111}|n_1, n_{11}, N_3)$.

Gibbs sampling. It was argued in the lectures that the joint posterior distribution of the model unknowns n_{111} and q can be investigated by Gibbs sampling. This means making a numerical sample from the posterior distribution by drawing samples of n_{111} and q in turn from their full conditional posterior distributions:

$$f(q|n_1, n_{11}, N_3, n_{111}) \quad \text{and} \quad f(n_{111}|n_1, n_{11}, N_3, q).$$

These were found to be

$$q|n_1, n_{11}, N_3, n_{111} \sim \text{Beta}(2n_1 + 2n_{11} + n_{111} + \alpha, n_{11} + 2N_3 + \beta). \quad (3)$$

and

$$n_{111}|n_1, n_{11}, N_3, q \sim \text{Binomial}(N_3, 2q/(2q+1)). \quad (4)$$

Exercises

1. **Gibbs sampling.** The R program (**chainGibbs.R**) contains a function `chainGibbs(M, α, β)` that draws samples from the joint posterior distribution of q and n_{111} . The function has this particular data set “hardwired” within the program. Using Gibbs sampling, the program draws samples in turn from distributions (3) and (4). Starting with the initial values $(q^{(1)}, n_{111}^{(1)}) = (0.5, 275 * (2 * 0.5)/(2 * 0.5 + 1))$, it iterates between sampling

$$q^{(i)}|n_1, n_{11}, N_3, n_{111}^{(i-1)} \quad \text{and}$$

$$n_{111}^{(i)}|n_1, n_{11}, N_3, q^{(i)}, \quad i = 2, \dots, M.$$

This creates a sample $(q^{(i)}, n_{111}^{(i)})$, $i = 1, \dots, M$.

2. **Write your own Gibbs sampler** Before running `chainGibbs.R`, you might like to try writing your own Gibbs sampler for the chain binomial problem. Assume you will run M iterations.
 - (a) Reserve space for the M-vector of q and n_{111} values.
 - (b) Initialize the model unknowns `q[1]` and `n111[1]` (round the `n111[1]`)
 - (c) Enter the data `n1`, `n11`, `N3`
 - (d) Draw the MCMC samples 2:M using the `rbeta()` and `rbinom()` functions
3. **Posterior inferences.** By discarding a number of "burn-in" samples, you can use the rest of the numerical sample to explore the posterior of escape probability q . It is enough to discard a few hundred first samples in this simple model.
 - (a) Make a histogram of the samples 500:M of `q` and `n111`.
 - (b) Use the `summary()` function to get summaries of later samples of `q` and `n111`.
4. **Writing a Gibbs sampler function** You can now convert your R program to a function that can be called. It could be similar to the function in (**chainGibbs.R**) `chainGibbs(M, α , β)`. However, you might prefer to write a function `mychainGibbs(n1, n11, N3, M, α , β)` that allows you to do inference on other data sets with observed (n_1, n_{11}, N_3) .
5. **Sensitivity to the choice of prior.** Assess how the choice of the prior distribution affects estimation of the escape probability. Use the $\text{Beta}(\alpha, \beta)$ prior with different values of α and β . Note that both parameters can be given as input to the function `chainGibbs(M, α , β)` in **chainGibbs.R** or hopefully your own new function.

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'Neill Ph. A tutorial introduction to Bayesian inference for stochastic epidemic models using Markov chain Monte Carlo methods. *Mathematical Biosciences* 2002; 180:103-114.