

Model checking, hierarchical modeling and combined M-H and Gibbs

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Outline

- ▶ Chain binomial model for household outbreaks of measles
 - ▶ Bayesian analysis of incompletely observed data, using data augmentation (cf. the earlier lecture and computer lab)
 - ▶ Checking the model fit through comparison of predictive data with the observed data of the final number infected
- ▶ Model extension by allowing heterogeneity across households
→ a hierarchical model
- ▶ Implementation of posterior sampling in the hierarchical model by a combined Gibbs and Metropolis algorithm

The observed outbreak sizes

Recall the observed data in the chain binomial model:

Chain	Chain probability	Frequency	Observed frequency	Final number infected
1	q_j^2	n_1	34	1
1→1	$2q_j^2 p_j$	n_{11}	25	2
1→1→1	$2q_j p_j^2$	n_{111}	not observed	3
1→2	p_j^2	n_{12}	not observed	3
Total	1	N	334	

- ▶ If the final number infected is 1 or 2, the actual chain is observed
- ▶ If the final number infected is 3, the actual chain data are not observed
 - ▶ We still know that $N_3 \equiv n_{111} + n_{12} = 275$
- ▶ In the previous analysis, we assumed $q_j = q$ for $j = 1, \dots, 334$, i.e., for all 334 households

Prediction

- ▶ Recall that new (predictive) data y^{pred} can be generated by drawing from their posterior predictive distribution $f(y^{\text{pred}}|y)$
- ▶ Posterior predictive distribution because
 - ▶ conditioning on the observed data y
 - ▶ predicting a future observable y^{pred}
- ▶ Predictive data can be compared with the observed data to assess the fit of the model
- ▶ In this example, we compare the predictive and observed frequencies of chains 1 and $1 \rightarrow 1$

Posterior predictive distribution

- Denote the model parameters by θ . Then

$$\begin{aligned}f(y^{\text{pred}}|y) &= \int f(y^{\text{pred}}, \theta|y)d\theta = \int f(y^{\text{pred}}|\theta, y)f(\theta|y)d\theta \\ &= \int f(y^{\text{pred}}|\theta)f(\theta|y)d\theta\end{aligned}$$

- This means that samples from the posterior predictive distribution can be realised as follows:
 - [1] Draw an MCMC sample θ_k from the posterior $f(\theta|y)$ of the model parameters
 - [2] Given θ_k , draw a sample y_k^{pred} from $f(y^{\text{pred}}|\theta_k)$
 - [3] Repeat steps [1] and [2] K times ($k = 1, \dots, K$)

Model checking

- ▶ The posterior predictive distribution of the chain frequencies $(n_1, n_{11}, n_{111}, n_{12})$ is now

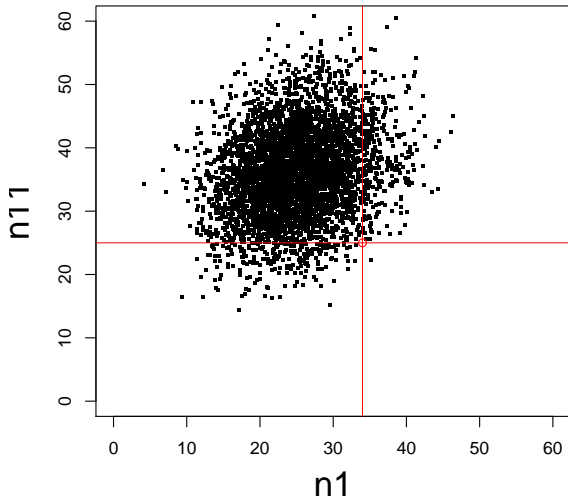
$$\begin{aligned} & f(n_1^{\text{pred}}, n_{11}^{\text{pred}}, n_{111}^{\text{pred}}, n_{12}^{\text{pred}} | n_1, n_{11}, N_3) \\ &= \int_0^1 f(n_1^{\text{pred}}, n_{11}^{\text{pred}}, n_{111}^{\text{pred}}, n_{12}^{\text{pred}} | q) f(q | n_1, n_{11}, N_3) dq \end{aligned}$$

- ▶ Samples from the posterior predictive distribution:
 - [1] Draw an MCMC sample $q^{(k)}$ from the posterior $f(q | n_1, n_{11}, N_3)$
 - [2] Draw a sample $(n_1^{(k)}, n_{11}^{(k)}, n_{111}^{(k)}, n_{12}^{(k)})$ from $\text{Multinomial}(334, (q^{(k)}, 2(q^{(k)})^2 p^{(k)}, 2q^{(k)}(p^{(k)})^2, p^{(k)}))$
 - [3] Repeat steps [1] and [2] K times ($k = 1, \dots, K$)

Model checking continues

- ▶ Comparison of a sample from the joint predictive posterior of $(n_1^{\text{pred}}, n_{11}^{\text{pred}})$ with the actually observed point (34,25) reveals a poor model fit (next page)
 - ▶ The prediction shows too few chains of size 1 and too many chains $1 \rightarrow 1$, so the estimated escape probability appears to be too small
- ▶ The model did not take into account possible heterogeneity across households in the escape probability
- ▶ Therefore, we'll next consider a model extension through allowing such heterogeneity

Model checking continues



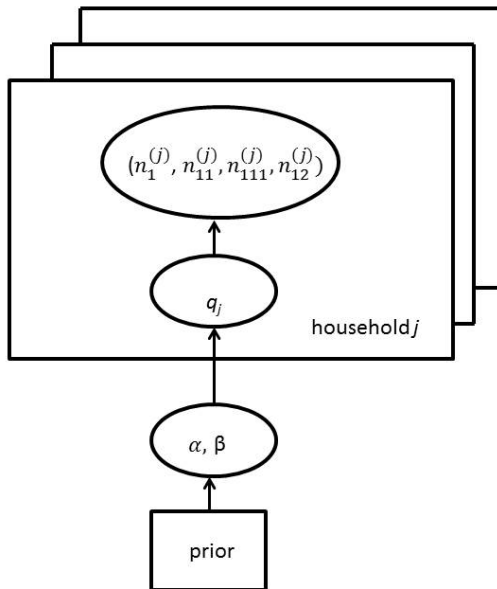
A hierarchical model

- ▶ In household j , let $(n_1^{(j)}, n_{11}^{(j)}, n_{111}^{(j)}, n_{12}^{(j)})$ follow a multinomial distribution with size 1 and probability vector $(q_j^2, 2q_j^2 p_j, 2q_j p_j^2, p_j^2)$, $j = 1, \dots, 334$
- ▶ Assume that the *household-specific* escape probabilities q_j follow a $\text{Beta}(\alpha, \beta)$ distribution
- ▶ Assuming an uninformative joint prior* for α and β , the hierarchical model becomes fully defined:

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

* The odd-looking joint prior distribution for α and β follows from assuming independent uniform prior distributions for $\alpha/(\alpha + \beta)$ (expectation of the Beta distribution) and $1/(\alpha + \beta)^{-1/2}$: see Chapter 5.3, Gelman et al.

A hierarchical model continues



The joint distribution

- ▶ The joint distribution of the parameters α and β , the household-specific escape probabilities q_j ($j = 1, \dots, 334$) and the chain frequencies is

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

- ▶ The model unknowns are parameters α and β , frequencies $n_{111}^{(j)}$ for all 275 households with outbreak size 3, as well as all 334 household-specific escape probabilities q_j

Sampling from the posterior cont.

- ▶ In each household, the full conditional (Beta) distribution of $q_j^{(k)}$ depends on the current iterates of the numbers of escapes ($e_j^{(k-1)}$) and infections ($d_j^{(k-1)}$) *in that household* and the prior parameters $\alpha^{(k-1)}$ and $\beta^{(k-1)}$
- ▶ So, $q_j^{(k)} \sim \text{Beta}(e_j^{(k-1)} + \alpha^{(k-1)}, d_j^{(k-1)} + \beta^{(k-1)})$
- ▶ The numbers of escapes and infections are given in the table below

Chain	Number of escapes $e_j^{(k-1)}$	Number of infections $d_j^{(k-1)}$
1	2	0
1→1	2	1
1→1→1	1	2
1→2	0	2

- ▶ Note that the unknown number of escapes in a household with outbreak size 3 (i.e. with either chain 1→1 or 1→2) is equal to $n_{111}^{(j,k-1)}$; this is useful in implementing the sampling routine (see computer lab)

Sampling from the posterior

- A sketch of the steps in k th iteration of the sampling algorithm:

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

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

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

$$n_{111}^{(j,k)} | q_j^{(k)} \sim \text{Binom}(1, 2q_j^{(k)} / (2q_j^{(k)} + 1)), j=60, \dots, 334$$

$$\alpha^{(k)} | \beta^{(k-1)}, q_1^{(k)}, \dots, q_{334}^{(k)} \text{ using a Metropolis-Hastings step}$$

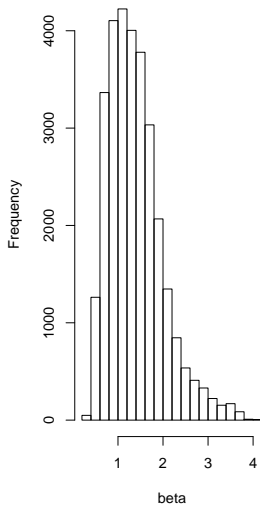
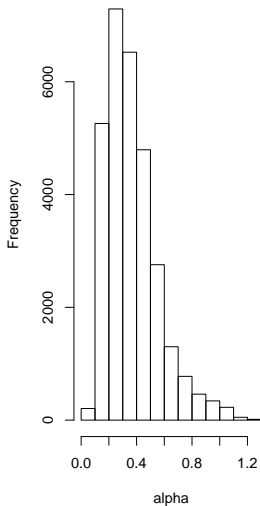
$$\beta^{(k)} | \alpha^{(k)}, q_1^{(k)}, \dots, q_{334}^{(k)} \text{ using a Metropolis-Hastings step}$$

Sampling from the posterior cont.

- ▶ Parameters α and β require a Metropolis-Hastings step
- ▶ For example, for parameter α , if the current iterate is $\alpha^{(k-1)}$, a new value $\bar{\alpha}$ is first proposed (e.g.) uniformly about the current iterate (this is a symmetric proposal)
- ▶ The proposal is then accepted, i.e., $\alpha^{(k)} := \bar{\alpha}$, with probability

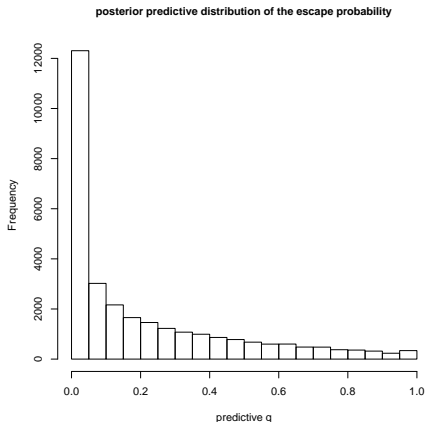
$$\min\left\{1, \frac{\prod_{j=1}^{334} f(q_j^{(k)} | \bar{\alpha}, \beta^{(k-1)}) f(\bar{\alpha}, \beta^{(k-1)})}{\prod_{j=1}^{334} f(q_j^{(k)} | \alpha^{(k-1)}, \beta^{(k-1)}) f(\alpha^{(k-1)}, \beta^{(k-1)})}\right\}$$

Posterior distributions of α and β

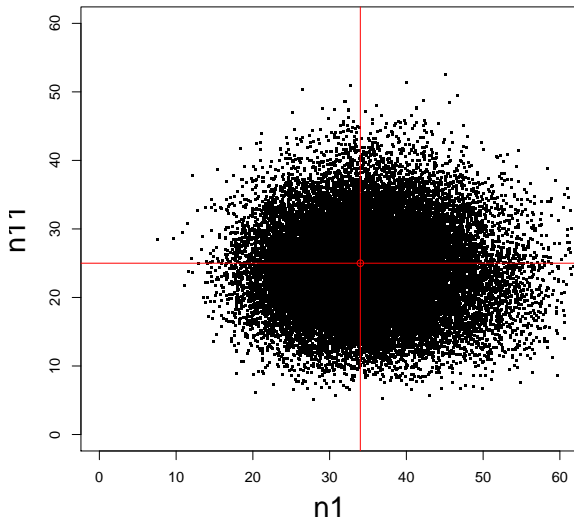


Predictive distribution of the household-specific escape probability

- Posterior predictive distribution of the household-specific escape probability, $\int f(q_{335}|\alpha, \beta)f(\alpha, \beta|n_1, n_{11}, N_3)d\alpha d\beta$



Checking the hierarchical model



An alternative approach

- ▶ In this example, it is actually possible to marginalise q_j over its prior distribution
- ▶ This means calculating the chain probabilities as expectations of the probabilities given in the Table on page 3 with respect to $\text{Beta}(\tilde{q}/z, (1 - \tilde{q})/z)$
 - ▶ Note that the Beta distribution is now parameterised differently: $\tilde{q} = \alpha/(\alpha + \beta)$, $z = 1/(\alpha + \beta)$

Chain	Chain probability	Frequency	Observed frequency	Final number infected
1	$\tilde{q}(\tilde{q} + z)/(1 + z)$	n_1	34	1
1→1	$2\tilde{p}\tilde{q}(\tilde{q} + z)/((1 + z)(1 + 2z))$	n_{11}	25	2
1→1→1	$2\tilde{p}\tilde{q}(\tilde{p} + z)/((1 + z)(1 + 2z))$	n_{111}	missing	3
1→2	$\tilde{p}(\tilde{p} + z)/(1 + z)$	n_{12}	missing	3

Alternative approach continues

- ▶ The following identity helps to calculate the expectations:

$$E(p_j^u q_j^v) = \frac{\tilde{q}(\tilde{q} + z) \dots (\tilde{q} + z(u - 1)) \tilde{p}(\tilde{p} + z) \dots (\tilde{p} + z(v - 1))}{(1 + z) \dots (1 + z(u + v - 1))}$$

- ▶ Using the probabilities as given in the table, it is straightforward to implement a Metropolis-Hastings algorithm to draw samples from the posterior of parameters \tilde{q} and z
- ▶ A suitable prior for \tilde{q} and z is of course needed

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, 1999; 162: 121–129.
- [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.
- [5] Gelman, Carlin, Stern, Rubin: Bayesian Data Analysis, Chapman and Hall, 2004; see Chapter 5.3.