MCMC I Methods
Introduction

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Prior, likelihood, and posterior

- Let
  - $y = (y_1, \ldots, y_n)$: observed data
  - $f(y|\theta)$: model for the observed data, usually a probability distribution
  - θ: vector of unknown parameters, assumed a random quantity
  - $\pi(\theta)$: prior distribution of θ
- The posterior distribution for inference concerning θ is

$$f(\theta|y) = \frac{f(y|\theta)\pi(\theta)}{\int f(y|u)\pi(u)du}.$$

Posterior and marginal density of y

- The integral $\int f(y|u)\pi(u)du$, the marginal density of the data y, does not depend on θ.
- When the data y are fixed, then the integral can be regarded as a normalizing constant C.
- In high dimensional problems, the integral can be very difficult to evaluate.
- Evaluation of the complex integral $\int f(y|u)\pi(u)du$ was a focus of much Bayesian computation.

Advent of MCMC Methods

- With the advent of the use of Markov chain Monte Carlo (MCMC) methods,
  $\longrightarrow$ one could avoid evaluating the integral, making use of the unnormalized posterior density.

$$f(\theta|y) \propto f(y|\theta)\pi(\theta).$$

- Equivalently, if we denote the likelihood function or sampling distribution by $L(\theta)$, then

$$\begin{aligned} f(\theta|y) &\propto L(\theta)\pi(\theta). \\ \text{posterior} &\propto \text{likelihood} \times \text{prior} \end{aligned}$$

- We will show how this works.

Other Uses of MCMC Methods

- Can simplify otherwise difficult computations.
- Sometimes a likelihood would be easy to evaluate if some data had been observed that was not observed or is unobservable.
- Examples:
  - infection times,
  - time of clearing infection,
  - when someone is infectious,
  - chains of infection.
- MCMC methods can be used to augment the observed data to make estimation simpler.

Likehood and Data Transforms Prior to Posterior

- Likelihood and data take prior to posterior:

$$\text{Prior} \xrightarrow[\text{–Likelihood}\ \text{–Data}]{\text{Transformation}} \text{Posterior}$$

- Bayesian data analysis is a study of the transformation.

Transmission probability

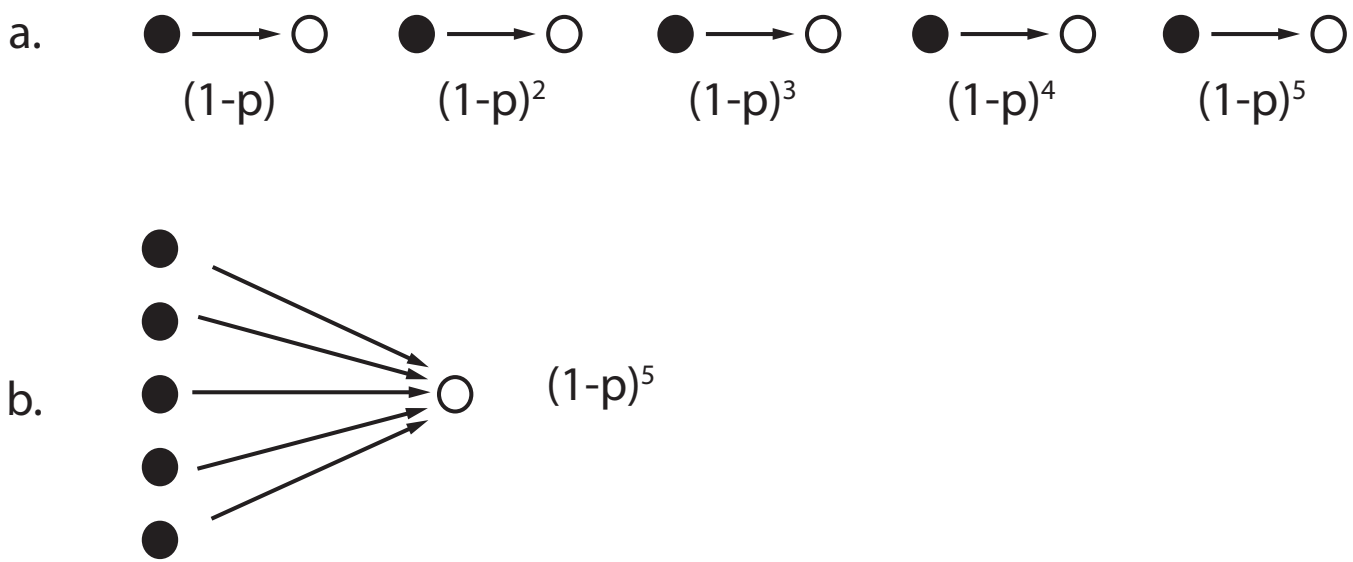
- p is the probability an infective infects a susceptible: transmission probability
- $q = 1 - p$ is the probability a susceptible escapes infection when exposed to an infective: escape probability
- Transmission versus escape ? which is the "success" and which the "failure" ?
- Given there are n exposures, and y infections, what is the estimate of the transmission probability?
- Given there are n exposures, and $n - y$ escapes, what is the estimate of the escape probability?

Chain-binomial model

- Assume independent households
- One person in each household introduces the infection into the household (index case).
- Infections occur within households in generations of infection (discrete time).
- p is the probability an infective infects a susceptible in a household in a generation
- $q = 1 - p$ is the probability a susceptible escapes infection when exposed to an infective in a household

Reed-Frost Chain Binomial Model

Figure : Independent exposures = independent Bernoulli trials



Chain Binomial Model

Table : Chain binomial probabilities in the Reed-Frost model in N households of size 3 with 1 initial infective and 2 susceptibles, $S_0 = 2, I_0 = 1$

Chain	Chain probability	Frequency	at p=0.4	at p=0.7	Final number infected
$1 \longrightarrow 0$	q^2	n_1	0.360	0.090	1
$1 \longrightarrow 1 \longrightarrow 0$	$2pq^2$	n_{11}	0.288	0.126	2
$1 \longrightarrow 1 \longrightarrow 1$	$2p^2q$	n_{111}	0.192	0.294	3
$1 \longrightarrow 2$	p^2	n_{12}	0.160	0.490	3
Total	1	N	1.00	1.00	

Chain binomial model

- Data: The observations are based on outbreaks of measles in Rhode Island 1929–1934.
- The analysis is restricted to $N = 334$ families with three susceptible individuals at the outset of the epidemic.
- Assume there is a single index case that introduces infection into the family.
- The actual chains are not observed, just how many are infected at the end of the epidemic.
- So the frequency of chains $1 \longrightarrow 1 \longrightarrow 1$ and $1 \longrightarrow 2$ are not observed.
- MCMC can be used to augment the missing data, and estimate the transmission probability p.

Chain Binomial Model

Table : Rhodes Island measles data: chain binomial probabilities in the Reed-Frost model in $N = 334$ households of size 3 with 1 initial infective and 2 susceptibles, $N_3 = n_{111} + n_{12} = 275$ is observed

Chain	Chain probability	Frequency	Observed frequency	Final number infected
$1 \longrightarrow 0$	q^2	n_1	34	1
$1 \longrightarrow 1 \longrightarrow 0$	$2pq^2$	n_{11}	25	2
$1 \longrightarrow 1 \longrightarrow 1$	$2p^2q$	n_{111}	not observed	3
$1 \longrightarrow 2$	p^2	n_{12}	not observed	3
Total	1	N	334	

General epidemic (SIR) model

- The population of N individuals
- Denote the numbers of susceptible, infective, and removed individuals at time t by $S(t)$, $I(t)$, and $R(t)$.
- The process can be represented by the compartmental diagram

$$S(t) \longrightarrow I(t) \longrightarrow R(t)$$

- Thus, $S(t) + I(t) + R(t) = N$ for all t.
- Initially, $(S(0), I(0), R(0)) = (N - 1, 1, 0)$

General epidemic model

- Each infectious individual remains so for a length of time $T_I \sim \exp(\gamma)$.
- During this time, infectious contacts occur with each susceptible according to a Poisson process of rate β/N
- Thus, the overall hazard of infection at time t is $\beta I(t)/N$
- The two model parameters of interest are β and γ

General epidemic model

- In a well-known smallpox data set, the removal times are observed. That is, when the people are no longer infectious for others.
- However, the infection times are not observed.
- Thus, estimating the two model parameters is difficult.
- The missing infection times are treated as latent variables.
- MCMC methods are used to augment the missing infection times and estimate the parameters β and γ.

Susceptible-infected-susceptible (SIS) model

- Background: Many infections are recurrent, occurring as an alternating series of presence and absence of infection
- Nasopharyngeal carriage of *Streptococcus pneumoniae* (Auranen et al 2000; Cauchemez et al; Melegaro et al)
- Nasopharyngeal carriage of *Neisseria meningitidis* (Trotter and Gay 2003)
- Malaria (Nagelkerke et al,)
- multi-resistant *Staphylococcus aureus* (Cooper et al)

Susceptible-infected-susceptible (SIS) model

- The population of N individuals
- Denote the numbers of susceptible and infected individuals at time t by $S(t)$ and $I(t)$.
- The process can be represented by the compartmental diagram

$$S(t) \leftrightarrow I(t)$$

- Thus, $S(t) + I(t) = N$ for all t.
- Acquisition and clearance times often remain unobserved
- Active sampling of the population to determine the current status of being infected or susceptible in individuals.

Susceptible-infected-susceptible (SIS) model

- Could be formulated as an infectious disease transmission process, as the general epidemic model.
- Too complicated for this introductory course
- We consider here the simple transition process, with rate parameters λ for acquisition and μ for clearance.
- The acquisition and clearance times are treated as latent variables.
- MCMC methods are used to augment the missing infection and clearance times, and estimate the parameters λ and μ.

Conjugate prior distribtions

- Conjugacy: the property that the posterior distribution follows that same parametric form as the prior distribution.
- Beta prior distribution is conjugate family for binomial likelihood: posterior distribution is Beta
- Gamma prior distribution is conjugate family for Poisson likelihood: posterior distribution is Gamma

Conjugate prior distributions

- Simply put, conjugate prior distributions in tandem with the appropriate sampling distribution for the data have the same distribution as the posterior distribution.
- Conjugate prior distributions have computational convenience.
- They can also be interpreted as additional data.
- They have the disadvantage of constraining the form of the prior distribution.

Nonconjugate prior distributions

- Nonconjugate prior distributions can be used when the shape of the prior knowledge or belief about the distribution of the parameters of interest does not correspond to the conjugate prior distribution.

- Noninformative prior distributions carry little population information and are generally supposed to play a minimal role in the posterior distribution.
  $\longrightarrow$They are also called diffuse, vague, or flat priors.

- Computationally nonconjugate distributions can be more demanding.

Data and Sampling Distribution

- Goal: Inference on the posterior distribution of the transmission probability

- Suppose that n people are exposed once to infection
  - y become infected ("successes")
  - $n - y$ escape infection ("failures")

- Let
  - $p =$ transmission probability
  - $1 - p = q =$ escape probability
- Binomial sampling distribution

$$L(y|p) = \text{Bin}(y|n, p) = \binom{n}{y} p^y (1-p)^{n-y} = \binom{n}{y} p^y q^{n-y}$$

Specify the Prior Distribution of p

- To perform Bayesian inference, we must specify a prior distribution for p.
- We specify a Beta prior distribution:

$$p \sim \text{Beta}(\alpha, \beta)$$

$$\text{Beta}(p|\alpha, \beta) = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} p^{\alpha-1}(1-p)^{\beta-1}, \alpha > 0, \beta > 0.$$

- Mean: $E(p|\alpha, \beta) = \frac{\alpha}{\alpha+\beta}$
- Variance: $\frac{\alpha\beta}{(\alpha+\beta)^2(\alpha+\beta+1)} = \frac{E(p|\alpha,\beta)[1-E(p|\alpha,\beta)]}{\alpha+\beta+1}$

Specify the Prior Distribution of p

- We specify a Beta prior distribution:

$$\begin{aligned} p &\sim \text{Beta}(\alpha, \beta) \\ \pi(p) &= \text{Beta}(p|\alpha, \beta) \\ \text{Beta} &\propto p^{\alpha-1}(1-p)^{\beta-1}. \end{aligned}$$

- Looks similar to binomial distribution
- $\alpha > 0$, $\beta > 0$, "prior sample sizes"

Posterior distribution of p

- The posterior distribution of the transmission probability p, $f(p|y)$:

$$\begin{aligned} f(p|y) &\propto p^y(1-p)^{n-y}p^{\alpha-1}(1-p)^{\beta-1} \\ \text{posterior} &\quad \text{likelihood} \times \textit{prior} \\ &= p^{y+\alpha-1}(1-p)^{n-y+\beta-1} \\ &= \text{Beta}(p|\alpha+y, \beta+n-y) \end{aligned}$$

- The role of α and β as prior sample sizes is clear.

Posterior mean of θ

- Posterior mean of p
  $\longrightarrow$ posterior probability of success (transmission) for a future draw from the population:

$$E(p|y) = \frac{\alpha + y}{\alpha + \beta + n}$$

- posterior mean always lies between the prior mean $\alpha/(\alpha + \beta)$ and the sample mean y/n.
- Posterior variance of p:

$$\text{var}(p|y) = \frac{E(p|y)[1 - E(p|y)]}{\alpha + \beta + n + 1}$$

Uniform prior distribution

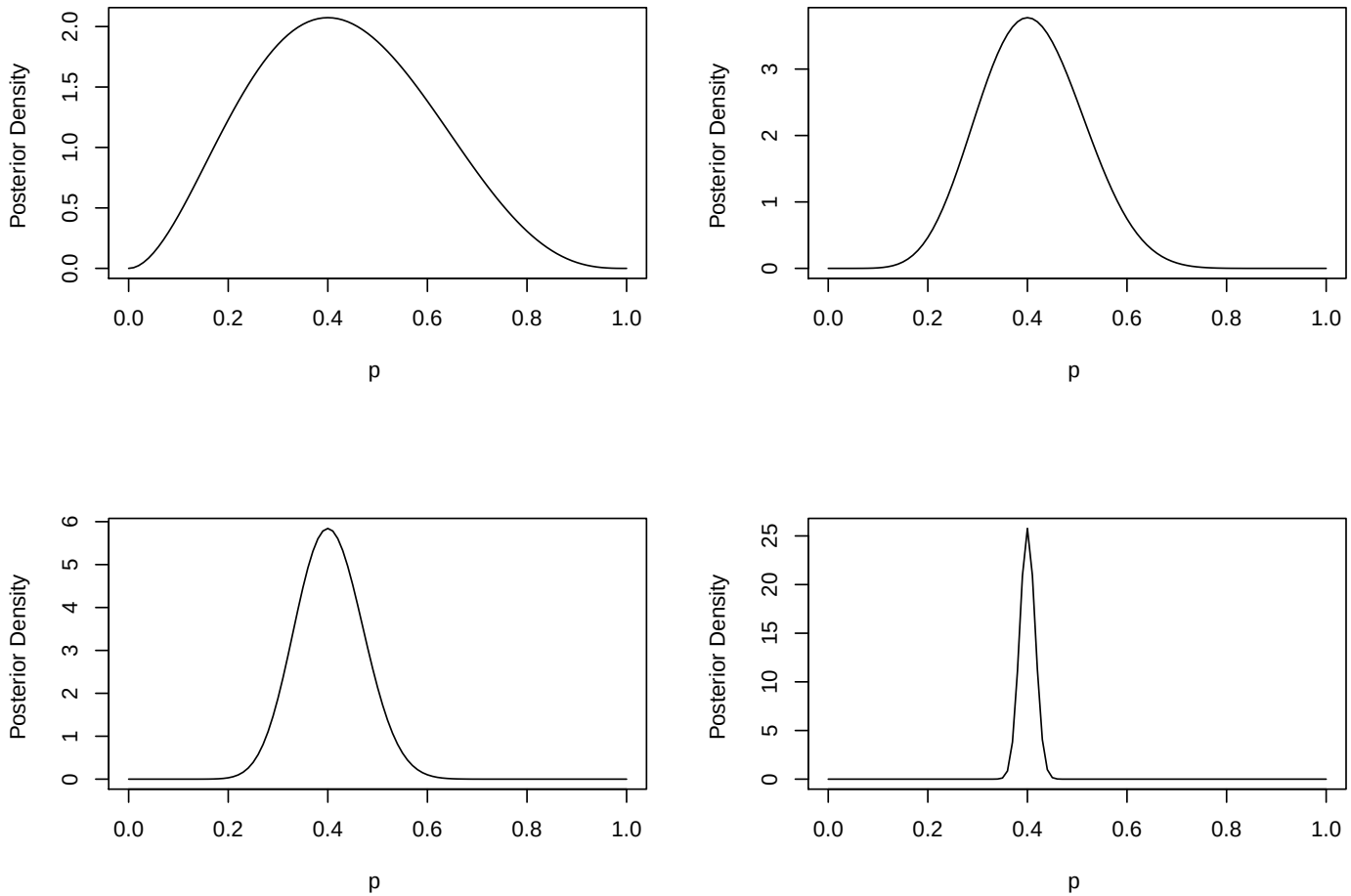
- The uniform prior distribution on [0,1] corresponds to $\alpha = 1$, $\beta = 1$. Essentially no prior information on p.

$$f(p|y) = \text{Beta}(p|y+1, n-y+1)$$

- Let's see how the posterior distribution of the transmission probability depends on the amount of data given a uniform prior distribution (Sample mean $y/n = 0.40$).

n, number exposed	y, number infected
5	2
20	8
50	20
1000	400

Figure : R program: Posterior distribution with differing amounts of data. Uniform Beta prior, Binomial sampling distribution.



Prediction

- After the data have been observed, we can predict a future unknown observable y_{n+1}.
- For example, we may observe n people who were exposed to infection, and whether they became infected.
- We may want to predict the probability that the next person to be observed would become infected.
- Posterior predictive distribution:
  $\longrightarrow$ posterior because conditional on the observed y
  $\longrightarrow$ predictive because it is a prediction for an observable y_{n+1}.

Prediction

- **Posterior predictive distribution of unknown observable** y_{n+1}:

$$\begin{aligned} f(y_{n+1}|y) &= \int f(y_{n+1}, p|y)dp \\ &= \int f(y_{n+1}|p, y)f(p|y)dp \\ &= \int f(y_{n+1}|p)f(p|y)dp \end{aligned}$$

- The last line follows because y and y_{n+1} are conditionally independent given p in this model.

- Useful in model checking.

References

- Gelman, A, Carlin, JB, Stern, HS, Dunson, DB, Vehtari, A, Rubin, DB. *Bayesian Data Analysis*, Chapman and Hall/CRC, third edition, 2014.
- Carlin, BP and Louis, TA. *Bayesian Methods for Data Analysis*, CRC Press, third edition, 2008.

Chain Binomial Model

Table : Rhodes Island measles data: chain binomial probabilities in the Reed-Frost model in $N = 334$ households of size 3 with 1 initial infective and 2 susceptibles, $N_3 = n_{111} + n_{12} = 275$ is observed

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Complete data likelihood for q

- The multinomial complete data likelihood for q:

$$
\begin{aligned}
& f(n_1, n_{11}, N_3, n_{111}|q) \\
= & \binom{334}{n_1, n_{11}, n_{111}, N_3 - n_{111}} (q^2)^{n_1} (2q^2p)^{n_{11}} (2qp^2)^{n_{111}} (p^2)^{N_3 - n_{111}} \\
= & \text{ constant } \times q^{2n_1 + 2n_{11} + n_{111}} p^{n_{11} + 2N_3}
\end{aligned}
$$

- The observed data are (n_1, n_{11}, N_3), but we do not observe n_{111}.
- We could estimate q using a marginal model, but won't.

Gibbs sampler for chain binomial model

- The general idea of the Gibbs sampler is to sample the model unknowns from a sequence of full conditional distributions and to loop iteratively through the sequence.
- To sample one draw from each full conditional distribution at each iteration, it is assumed that all of the other model quantities are known at that iteration.
- In the theoretical lectures, it will be shown that that the Gibbs sampler converges to the posterior distribution of the model unknowns.
- In the Rhode Island measles data, we are interested in augmenting the missing data n_{111} and estimating the posterior distribution of q, the escape probability.

Gibbs sampler for chain binomial model

- The joint distribution of the observations (n_1, n_{11}, N_3) and the model unknowns (n_{111}, q) is

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

complete data likelihood $\times$ prior

- We want to make inference about the joint posterior distribution of the model unknowns

$$f(n_{111}, q|n_1, n_{11}, N_3)$$

- This is possible by sampling from the full conditionals (Gibbs sampling): $f(q|n_1, n_{11}, N_3, n_{111})$ and $f(n_{111}|n_1, n_{11}, N_3, q)$

Algorithm for Gibbs sampler for chain binomial model

1. Start with some initial values $(q^{(0)}, n_{111}^{(0)})$
2. For $t = 0$ to M do
3. Sample $q^{(t+1)} \sim f(q|n_1, n_{11}, N_3, n_{111}^{(t)})$
4. Sample $n_{111}^{(t+1)} \sim f(n_{111}|n_1, n_{11}, N_3, q^{(t+1)})$
5. end for
6. How to get the two full conditionals in this model?

Full conditional of chain $1 \longrightarrow 1 \longrightarrow 1$

- Assume q is known
- Compute the conditional probability of chain $1 \to 1 \to 1$ when outbreak size is $N = 3$:

$$\Pr(1 \to 1 \to 1 | N = 3, q) = \frac{\Pr(N = 3, 1 \to 1 \to 1 | q)}{\Pr(N = 3 | q)}$$

$$= \frac{\Pr(N = 3 | 1 \to 1 \to 1, q) \Pr(1 \to 1 \to 1 | q)}{\Pr(N = 3 | 1 \to 1 \to 1, q) \Pr(1 \to 1 \to 1 | q) + \Pr(N = 3 | 1 \to 2, q) \Pr(1 \to 2 | q)}$$

$$= \frac{2p^2 q}{2p^2 q + p^2} = \frac{2q}{2q + 1}, \quad (0 \leq q < 1)$$

The full conditional of n_{111}

- We have found that

$$\Pr(1 \to 1 \to 1 | N = 3, q) = \frac{2q}{2q+1}$$

- So the full conditional distribution of n_{111} is

$$n_{111} | (n_1, n_{11}, N_3, q) \sim \text{Binomial}(275, 2q/(2q+1))$$

The full conditional of q

- Assume that n_{111} is known, that is, assume we know the complete data $(n_1, n_{11}, N_3, n_{111})$
- Assume a prior distribution for q: $q \sim \text{Beta}(\alpha, \beta)$,

$$f(q) \equiv f(q|\alpha, \beta) \propto q^{\alpha-1}(1-q)^{\beta-1}$$

- The full conditional distribution of q :

$$f(q|n_1, n_{11}, N_3, n_{111}, \alpha, \beta) \propto f(n_1, n_{11}, N_3, n_{111}|q, \alpha, \beta) f(q|\alpha, \beta)$$

$$\propto \underbrace{q^{2n_1+2n_{11}+n_{111}} p^{n_{11}+2N_3}}_{\text{complete data likelihood}} \times \underbrace{q^{\alpha-1}(1-q)^{\beta-1}}_{\times \text{ prior}}$$

The full conditional of q

- The full conditional distribution of q is thus a Beta distribution

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

- A uniform prior on q corresponds to $\alpha = 1$, $\beta = 1$.

- With the complete data, a natural point estimate of the escape probability would be the mean of the Beta distribution, i.e., the proportion of "escapes" out of all exposures:

$$\frac{2n_1 + 2n_{11} + n_{111} + \alpha}{2n_1 + 3n_{11} + 3n_{111} + 2n_{12} + \alpha + \beta}$$

Algorithm for Gibbs sampler for chain binomial model

1. Start with some initial values $(q^{(0)}, n_{111}^{(0)})$
2. For $t = 0$ to M do
3. Sample $q^{(t+1)} \sim \text{Beta}(2n_1 + 2n_{11} + n_{111}^{(t)} + \alpha, n_{11} + 2N_3 + \beta)$
4. Sample $n_{111}^{(t+1)} \sim \text{Binomial}(275, 2q^{(t+1)}/(2q^{(t+1)} + 1))$
5. end for
6. Get summaries of the marginal posterior distributions.

Posterior distributions of q *and* n_{111}