

# Bayesian Methods

Every variable in a linear model is a random variable derived from a distribution function. A fixed factor becomes a random variable with possibly a uniform distribution going from a lower limit to an upper limit. A component of variance is a random variable having a Gamma or Chi-square distribution with  $df$  degrees of freedom. In addition, the researcher may have information from previous experiments that strongly indicate the value that a variance component may have, and the Bayes approach allows the *a priori* information to be included in the analysis.

The Bayesian process is to

1. Specify distributions for each random variable of the model.
2. Combine the distributions into the joint posterior distribution.
3. Find the conditional marginal distributions from the joint posterior distribution.
4. Employ Markov Chain Monte Carlo (MCMC) methods to maximize the joint posterior distribution. Gibbs Sampling is a tool in MCMC methods for deriving estimates of parameters from the joint posterior distribution.

By determining conditional marginal distributions for each random variable of the model, then generating random samples from these distributions eventually converge to random samples from the joint posterior distribution. Computationally, any program that calculates solutions to Henderson's mixed model equations can be modified to implement Gibbs Sampling.

## 1 The Joint Posterior Distribution

Begin with a simple single trait animal model. That is,

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e}.$$

Let  $\theta$  be the vector of random variables and  $\mathbf{y}$  is the data vector, then

$$\begin{aligned} p(\theta, \mathbf{y}) &= p(\theta) p(\mathbf{y} | \theta) \\ &= p(\mathbf{y}) p(\theta | \mathbf{y}) \end{aligned}$$

Re-arranging gives

$$\begin{aligned} p(\theta | \mathbf{y}) &= \frac{p(\theta)p(\mathbf{y} | \theta)}{p(\mathbf{y})} \\ &= (\text{prior for } \theta) \frac{p(\mathbf{y} | \theta)}{p(\mathbf{y})} \\ &= \text{posterior probability function of } \theta \end{aligned}$$

In terms of the simple animal model,  $\theta$  includes  $\mathbf{b}$ ,  $\mathbf{a}$ ,  $\sigma_a^2$ , and  $\sigma_e^2$ .

## 1.1 Conditional Distribution of Data Vector

The conditional distribution of  $\mathbf{y}$  given  $\theta$  is

$$\mathbf{y} \mid \mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2 \sim N(\mathbf{Xb} + \mathbf{Za}, \mathbf{I}\sigma_e^2),$$

and

$$p(\mathbf{y} \mid \mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2) \propto (\sigma_e^2)^{(-N/2)} \exp \left[ -(\mathbf{y} - \mathbf{Xb} - \mathbf{Za})'(\mathbf{y} - \mathbf{Xb} - \mathbf{Za})/2\sigma_e^2 \right].$$

## 1.2 Prior Distributions of Random Variables

### 1.2.1 Fixed Effects Vector

There is little prior knowledge about the values in  $\mathbf{b}$  might have. This is represented by assuming

$$p(\mathbf{b}) \propto \text{constant}.$$

### 1.2.2 Random Effects and Variances

For  $\mathbf{a}$ , the vector of additive genetic values, quantitative genetics theory suggests that they follow a normal distribution, i.e.

$$\mathbf{a} \mid \mathbf{A}, \sigma_a^2 \sim N(\mathbf{0}, \mathbf{A}\sigma_a^2)$$

and

$$p(\mathbf{a}) \propto (\sigma_a^2)^{(-q/2)} \exp \left[ -\mathbf{a}'\mathbf{A}^{-1}\mathbf{a}/2\sigma_a^2 \right],$$

where  $q$  is the length of  $\mathbf{a}$ .

A natural estimator of  $\sigma_a^2$  is  $\mathbf{a}'\mathbf{A}^{-1}\mathbf{a}/q$ , call it  $S_a^2$ , where

$$S_a^2 \sim \chi_q^2 \sigma_a^2 / q.$$

Multiply both sides by  $q$  and divide by  $\chi_q^2$  to give

$$\sigma_a^2 \sim qS_a^2 / \chi_q^2$$

which is a scaled, inverted Chi-square distribution, written as

$$p(\sigma_a^2 \mid v_a, S_a^2) \propto (\sigma_a^2)^{-(\frac{v_a}{2}+1)} \exp \left( -\frac{v_a}{2} \frac{S_a^2}{\sigma_a^2} \right),$$

where  $v_a$  and  $S_a^2$  are hyperparameters with  $S_a^2$  being a prior guess about the value of  $\sigma_a^2$  and  $v_a$  being the degrees of belief in that prior value. Usually  $q$  is much larger than  $v_a$  and therefore, the data provide nearly all of the information about  $\sigma_a^2$ .

### 1.2.3 Residual Effects

Similarly, for the residual variance,

$$p(\sigma_e^2 | v_e, S_e^2) \propto (\sigma_e^2)^{-(\frac{v_e}{2}+1)} \exp\left(-\frac{v_e}{2} \frac{S_e^2}{\sigma_e^2}\right).$$

### 1.2.4 Combining Prior Distributions

The joint posterior distribution is

$$p(\mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2 | \mathbf{y}) \propto p(\mathbf{b})p(\mathbf{a} | \sigma_a^2)p(\sigma_a^2)p(\sigma_e^2)p(\mathbf{y} | \mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2)$$

which can be written as

$$\begin{aligned} &\propto (\sigma_e^2)^{-(\frac{N+v_e}{2}+1)} \exp\left[-\frac{1}{2\sigma_e^2}((\mathbf{y} - \mathbf{X}\mathbf{b} - \mathbf{Z}\mathbf{a})'(\mathbf{y} - \mathbf{X}\mathbf{b} - \mathbf{Z}\mathbf{a}) + v_e S_e^2)\right] \\ &(\sigma_a^2)^{-(\frac{q+v_a}{2}+1)} \exp\left[-\frac{1}{2\sigma_a^2}(\mathbf{a}'\mathbf{A}^{-1}\mathbf{a} + v_a S_a^2)\right]. \end{aligned}$$

## 2 Fully Conditional Posterior Distributions

In order to implement Gibbs sampling, all of the fully conditional posterior distributions (one for each component of  $\theta$ ) need to be derived from the joint posterior distribution. The conditional posterior distribution is derived from the joint posterior distribution by picking out the parts that involve the unknown parameter in question.

### 2.1 Fixed and Random Effects of the Model

Let

$$\begin{aligned} \mathbf{W} &= (\mathbf{X} \ \mathbf{Z}), \\ \beta' &= (\mathbf{b}' \ \mathbf{a}'), \\ \Sigma &= \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{A}^{-1}k \end{pmatrix}, \\ \mathbf{C} &= \text{Henderson's Mixed Model Equations} \\ &= \mathbf{W}'\mathbf{W} + \Sigma \\ \mathbf{C}\hat{\beta} &= \mathbf{W}'\mathbf{y} \end{aligned}$$

A new notation is introduced, let

$$\beta' = (\beta_i \ \beta'_{-i}),$$

where  $\beta_i$  is a scalar representing just one element of the vector  $\beta$ , and  $\beta_{-i}$  is a vector representing all of the other elements except  $\beta_i$ . Similarly,  $\mathbf{C}$  and  $\mathbf{W}$  can be partitioned in the same manner as

$$\begin{aligned} \mathbf{W}' &= (\mathbf{W}_i \ \mathbf{W}_{-i})' \\ \mathbf{C} &= \begin{pmatrix} C_{i,i} & \mathbf{C}_{i,-i} \\ \mathbf{C}_{-i,i} & \mathbf{C}_{-i,-i} \end{pmatrix}. \end{aligned}$$

In general terms, the conditional posterior distribution of  $\beta$  is a normal distribution,

$$\beta_i \mid \beta_{-i}, \sigma_a^2, \sigma_e^2, \mathbf{y} \sim N(\hat{\beta}_i, C_{i,i}^{-1} \sigma_e^2)$$

where

$$C_{i,i} \hat{\beta}_i = (\mathbf{W}'_i \mathbf{y} - \mathbf{C}_{i,-i} \beta_{-i}).$$

Then

$$b_i \mid \mathbf{b}_{-i}, \mathbf{a}, \sigma_a^2, \sigma_e^2, \mathbf{y} \sim N(\hat{b}_i, C_{i,i}^{-1} \sigma_e^2),$$

for

$$C_{i,i} = \mathbf{x}'_i \mathbf{x}_i.$$

Also,

$$a_i \mid \mathbf{b}, \mathbf{a}_{-i}, \sigma_a^2, \sigma_e^2, \mathbf{y} \sim N(\hat{a}_i, C_{i,i}^{-1} \sigma_e^2),$$

where  $C_{i,i} = (\mathbf{z}'_i \mathbf{z}_i + A^{i,i} k)$ , for  $k = \sigma_e^2 / \sigma_a^2$ .

## 2.2 Variances

The conditional posterior distributions for the variances are inverted Chi-square distributions,

$$\sigma_a^2 \mid \mathbf{b}, \mathbf{a}, \sigma_e^2, \mathbf{y} \sim \tilde{v}_a \tilde{S}_a^2 \chi_{\tilde{v}_a}^{-2}$$

for  $\tilde{v}_a = q + v_a$ , and  $\tilde{S}_a^2 = (\mathbf{a}' \mathbf{A}^{-1} \mathbf{a} + v_a S_a^2) / \tilde{v}_a$ , and

$$\sigma_e^2 \mid \mathbf{b}, \mathbf{a}, \sigma_a^2, \mathbf{y} \sim \tilde{v}_e \tilde{S}_e^2 \chi_{\tilde{v}_e}^{-2}$$

for  $\tilde{v}_e = N + v_e$ , and  $\tilde{S}_e^2 = (\mathbf{e}' \mathbf{e} + v_e S_e^2) / \tilde{v}_e$ , and  $\mathbf{e} = \mathbf{y} - \mathbf{Xb} - \mathbf{Za}$ .

## 3 Computational Scheme

Gibbs sampling is much like Gauss-Seidel iteration. When a new solution is calculated in the Mixed Model Equations for a level of a fixed or random factor, a random amount is added to the solution based upon its conditional posterior distribution variance before proceeding to the

next level of that factor or the next factor. After all equations have been processed, new values of the variances are calculated and a new variance ratio is determined prior to beginning the next round. The following MME for five animals will be used to illustrate the Gibbs sampling scheme:

$$\begin{pmatrix} 5 & 1 & 1 & 1 & 1 & 1 \\ 1 & 29 & 7 & -7 & -14 & 0 \\ 1 & 7 & 30 & -14 & 8 & -16 \\ 1 & -7 & -14 & 36 & -14 & 0 \\ 1 & -14 & 8 & -14 & 37 & -16 \\ 1 & 0 & -16 & 0 & -16 & 33 \end{pmatrix} \begin{pmatrix} \mu \\ a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \end{pmatrix} = \begin{pmatrix} 238.2 \\ 38.5 \\ 48.9 \\ 64.3 \\ 50.5 \\ 36.0 \end{pmatrix},$$

where  $k = \sigma_e^2/\sigma_a^2 = 14$ , and

$$\mathbf{A}^{-1} = \frac{1}{14} \begin{pmatrix} 28 & 7 & -7 & -14 & 0 \\ 7 & 29 & -14 & 8 & -16 \\ -7 & -14 & 35 & -14 & 0 \\ -14 & 8 & -14 & 36 & -16 \\ 0 & -16 & 0 & -16 & 32 \end{pmatrix}.$$

The starting values for  $\beta = (0 \ 0 \ 0 \ 0 \ 0 \ 0)$ , and for  $v_a = v_e = 10$ , and  $S_e^2 = 93\frac{1}{3}$  and  $S_a^2 = 6\frac{2}{3}$ , so that  $k = 14$ . Let *RND* represent a random normal deviate from a random normal deviate generator, and let *CHI(idf)* represent a random Chi-square variate from a random Chi-Square variate generator with *idf* degrees of freedom. Every time that *RND* and *CHI(idf)* appear, a different random number is generated for that expression.

To begin, let  $\sigma_e^2 = S_e^2$  and  $\sigma_a^2 = S_a^2$ . Below are descriptions of calculations in the first two rounds.

### 3.1 Round 1

#### 3.1.1 Fixed and Random Effects of Model

- Overall mean

$$\begin{aligned} \hat{\mu} &= (238.2 - a_1 - a_2 - a_3 - a_4 - a_5)/5 \\ &= 47.64 \\ \mu &= \hat{\mu} + RND * (\sigma_e^2/5)^{.5} \\ &= 47.64 + (-1.21) * (4.32) \\ &= 42.41 \end{aligned}$$

- Animal 1

$$\hat{a}_1 = (38.5 - \mu - 7a_2 + 7a_3 + 14a_4)/29$$

$$\begin{aligned}
&= -.1349 \\
a_1 &= \hat{a}_1 + RND * (\sigma_e^2/29)^{.5} \\
&= -.1349 + (1.138)(1.794) \\
&= 1.9067
\end{aligned}$$

• **Animal 2**

$$\begin{aligned}
\hat{a}_2 &= (48.9 - \mu - 7a_1 + 14a_3 - 8a_4 + 16a_5)/30 \\
&= -6.8591/30 = -.2286 \\
a_2 &= \hat{a}_2 + RND * (\sigma_e^2/30)^{.5} \\
&= -.2286 + (.0047)(1.7638) \\
&= -.2203
\end{aligned}$$

• **Animal 3**

$$\begin{aligned}
\hat{a}_3 &= (64.3 - \mu + 7a_1 + 14a_2 + 14a_4)/36 \\
&= .8931 \\
a_3 &= \hat{a}_3 + RND * (\sigma_e^2/36)^{.5} \\
&= .8931 + (-1.1061)(1.6102) \\
&= -.8879
\end{aligned}$$

• **Animal 4**

$$\begin{aligned}
\hat{a}_4 &= (50.5 - \mu + 14a_1 - 8a_2 + 14a_3 + 16a_5)/37 \\
&= .6518 \\
a_4 &= \hat{a}_4 + RND * (\sigma_e^2/37)^{.5} \\
&= .6518 + (-1.2293)(1.5882) \\
&= -1.3006
\end{aligned}$$

• **Animal 5**

$$\begin{aligned}
\hat{a}_5 &= (36.0 - \mu + 16a_2 + 16a_4)/33 \\
&= -.9316 \\
a_5 &= \hat{a}_5 + RND * (\sigma_e^2/33)^{.5} \\
&= -.9316 + (-.6472)(1.6817) \\
&= -2.0200
\end{aligned}$$

### 3.1.2 Residual Variance

Calculate the residuals and their sum of squares in order to obtain a new residual variance.

$$\begin{aligned}
 e_1 &= 38.5 - 42.41 - 1.9067 = -5.8167 \\
 e_2 &= 48.9 - 42.41 + .2203 = 6.7103 \\
 e_3 &= 64.3 - 42.41 + .8879 = 22.7779 \\
 e_4 &= 50.5 - 42.41 + 1.3006 = 9.3906 \\
 e_5 &= 36.0 - 42.41 + 2.0200 = -4.3900 \\
 \mathbf{e}'\mathbf{e} &= 705.1503
 \end{aligned}$$

A new sample value of the residual variance is

$$\begin{aligned}
 \sigma_e^2 &= (\mathbf{e}'\mathbf{e} + v_e S_e^2) / CHI(15) \\
 &= (705.1503 + (10)(93.3333)) / 17.1321 \\
 &= 95.6382.
 \end{aligned}$$

### 3.1.3 Additive Genetic Variance

The additive genetic variance requires calculation of  $\mathbf{a}'\mathbf{A}^{-1}\mathbf{a}$  using the  $a$ -values obtained above, which gives

$$\mathbf{a}'\mathbf{A}^{-1}\mathbf{a} = 19.85586.$$

Then

$$\begin{aligned}
 \sigma_a^2 &= (\mathbf{a}'\mathbf{A}^{-1}\mathbf{a} + v_a S_a^2) / CHI(15) \\
 &= (19.85586 + (10)(6.66667)) / 10.7341 \\
 &= 8.0605.
 \end{aligned}$$

A new sample value of the variance ratio becomes

$$k = 95.6382 / 8.0605 = 11.8650.$$

## 3.2 Round 2

Round 2 begins by re-forming the MME using the new variance ratio. The equations change to

$$\begin{pmatrix} 5 & 1 & 1 & 1 & 1 & 1 \\ 1 & 24.73 & 5.93 & -5.93 & -11.86 & 0 \\ 1 & 5.93 & 25.58 & -11.86 & 6.78 & -13.56 \\ 1 & -5.93 & -11.86 & 30.66 & -11.86 & 0 \\ 1 & -11.86 & 6.78 & -11.86 & 31.51 & -13.56 \\ 1 & 0 & -13.56 & 0 & -13.56 & 28.12 \end{pmatrix} \begin{pmatrix} \mu \\ a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \end{pmatrix} = \begin{pmatrix} 238.2 \\ 38.5 \\ 48.9 \\ 64.3 \\ 50.5 \\ 36.0 \end{pmatrix}.$$

### 3.2.1 Fixed and Random Effects of Model

The process is repeated using the last values of  $\mu$  and  $\mathbf{a}$  and  $\sigma_e^2$ .

$$\begin{aligned}\hat{\mu} &= (238.2 - a_1 - a_2 - a_3 - a_4 - a_5)/5 \\ &= 48.14 \\ \mu &= \hat{\mu} + RND * (\sigma_e^2/5)^{.5} \\ &= 48.14 + (.7465) * (4.3735) \\ &= 51.41\end{aligned}$$

$$\begin{aligned}\hat{a}_1 &= (38.5 - \mu - 5.93a_2 + 5.93a_3 + 11.86a_4)/24.73 \\ &= -1.3059 \\ a_1 &= \hat{a}_1 + RND * (\sigma_e^2/24.73)^{.5} \\ &= -1.3059 + (-.0478)(1.9665) \\ &= -1.3999\end{aligned}$$

$$\begin{aligned}\hat{a}_2 &= (48.9 - \mu - 5.93a_1 + 11.86a_3 - 6.78a_4 + 13.56a_5)/25.58 \\ &= -.9113 \\ a_2 &= \hat{a}_2 + RND * (\sigma_e^2/25.58)^{.5} \\ &= -.9113 + (.8386)(1.9336) \\ &= .7102\end{aligned}$$

$$\begin{aligned}\hat{a}_3 &= -2.41355/30.66 \\ &= -.0787 \\ a_3 &= \hat{a}_3 + RND * (\sigma_e^2/30.66)^{.5} \\ &= -.0787 + (-1.8414)(1.7662) \\ &= -3.3309\end{aligned}$$

$$\begin{aligned}\hat{a}_4 &= -89.2236/31.51 = -2.8316 \\ a_4 &= -2.8316 + (-1.2549)(1.7422) \\ &= -5.0179\end{aligned}$$

$$\begin{aligned}\hat{a}_5 &= -73.8224/28.12 = -2.6253 \\ a_5 &= -2.6253 + (.8184)(1.8442) \\ &= -1.1160\end{aligned}$$

### 3.2.2 Residual Variance

The residuals and their sum of squares are

$$\begin{aligned}e_1 &= 38.5 - 51.41 + 1.3999 = -11.5101 \\e_2 &= 48.9 - 51.41 - .7102 = -3.2202 \\e_3 &= 64.3 - 51.41 + 3.3309 = 16.2209 \\e_4 &= 50.5 - 51.41 + 5.0179 = 4.1079 \\e_5 &= 36.0 - 51.41 + 1.1160 = -14.2940 \\e'e &= 627.1630\end{aligned}$$

The new sample value of the residual variance is

$$\begin{aligned}\sigma_e^2 &= (e'e + v_e S_e^2)/CHI(15) \\&= (627.1630 + (10)(93.3333))/20.4957 \\&= 76.1377.\end{aligned}$$

### 3.2.3 Additive Genetic Variance

The new sample value of the additive genetic variance is

$$\begin{aligned}\sigma_a^2 &= (\mathbf{a}'\mathbf{A}^{-1}\mathbf{a} + v_a S_a^2)/CHI(15) \\&= (36.8306 + (10)(6.66667))/16.6012 \\&= 6.2343.\end{aligned}$$

The new variance ratio becomes

$$k = 76.1377/6.2343 = 12.2127.$$

Continue taking samples for thousands of rounds.

## 3.3 Burn-In Periods

The samples do not immediately represent samples from the joint posterior distribution. Generally, this takes anywhere from 100 to 10,000 samples depending on the model and amount of data. This period is known as the *burn-in period*. Samples from the burn-in period are discarded. The length of the burn-in period (i.e. number of samples) is usually judged by visually inspecting a plot of sample values across rounds.

A less subjective approach to determine convergence to the joint posterior distribution is to run two chains at the same time, both beginning with the same random number seed. However, the starting values (in variances) for each chain are usually greatly different, e.g. one set is greatly above the expected outcome and the other set is greatly below the expected outcome. When the two chains essentially become one chain, i.e. the squared difference between variance estimates is less than a specified value (like  $10^{-5}$ ), then convergence to the joint posterior distribution has occurred. All previous samples are considered to be part of the burn-in period and are discarded.

### 3.4 Post Burn-In Analysis

After burn-in, each round of Gibbs sampling is dependent on the results of the previous round. Depending on the total number of observations and parameters, one round may be positively correlated with the next twenty to three hundred rounds. The user can determine the effective number of samples by calculating lag correlations, i.e. the correlation of estimates between rounds, between every other round, between every third round, etc. Determine the number of rounds between two samples such that the correlation is zero. Divide the total number of samples (after burn-in) by the interval that gives a zero correlation, and that gives the effective number of samples. Suppose a total of 12,000 samples (after removing the burn-in rounds) and an interval of 240 rounds gives a zero correlation between samples, then the effective number of samples is 12,000 divided by 240 or 50 samples. There is no minimum number of independent samples that are required, just the need to know how many there actually were.

An overall estimate of a parameter can be obtained by averaging all of the 12,000 samples (after the burn-in). However, to derive a confidence interval or to plot the distribution of the samples or to calculate the standard deviation of the sample values, the variance of the independent samples should be used.

The final estimates are therefore, an average of the sample estimates. Some research has shown that the mode of the estimates might be a better estimate, which indicates that the distribution of sample estimates is skewed. One could report both the mean and mode of the samples, however, the mode should be based on the independent samples only.

### 3.5 Influence of the Priors

In the small example,  $v_a = v_e = 10$  whereas  $N$  was only 5. Thus, the prior values of the variances received more weight than information coming from the data. This is probably appropriate for this small example, but if  $N$  were 5,000,000, then the influence of the priors would be next to nothing. The amount of influence of the priors is not directly determined by the ratio of  $v_i$  to  $N$ . In the small example, even though  $v_a/(N + v_a) = \frac{2}{3}$ , the influence of  $S_a^2$  could be greater than  $\frac{2}{3}$ . When  $N$  is large there may be no need for  $v_a$  or  $v_e$  at all, or at least very small values would suffice.

### 3.6 Long Chain or Many Chains?

Early papers on MCMC (Monte Carlo Markov Chain) methods recommended running many chains of samples and then averaging the final values from each chain. This was to insure independence of the samples. Another philosophy recommends one single long chain. For animal breeding applications this could mean 100,000 samples or more. If a month is needed to run 50,000 samples, then maybe three chains of 50,000 would be preferable, all running simultaneously on a network of computers. If only an hour is needed for 50,000 samples, then 1,000,000 samples would not be difficult to run.

Two chains that utilize the same sequence of random numbers, but which use different starting variances, are recommended for determining the burn-in period, after which enough samples need to be run to generate a sufficient number of independent samples for obtaining standard deviations of the samples. A sufficient number of independent samples may be 100 or more depending on the amount of time needed to generate samples.

### 3.7 Heritabilities and Correlations

The Gibbs sampling process gives samples of variances, and usually each sample is saved (or every  $m^{th}$  sample). Thus, for each saved sample of variances, the heritability (or genetic correlation) could be calculated or the ratio of residual to additive variance, or any other quantity that may be of interest to the user. Then those values could be averaged and the variance of the samples calculated to give a standard error of the overall heritability estimate. This gives the user a good idea of the variability in these ratios.

### 3.8 Estimated Breeding Values

Although not common, Gibbs sampling can be used to get Estimated Breeding Values (EBV) of animals and their standard errors of prediction (across samples). The standard errors of prediction could then be converted to a reliability of the EBV rather than deriving an approximation for reliability. Only 100 to 500 additional rounds of Gibbs sampling are needed for this purpose.

## 4 EXERCISES

Below are data on progeny of 4 sires. Sires are assumed to be unrelated. Each number is an observation on one progeny.

**Data For Assignment.**

Sire	Contemporary Groups		
	1	2	3
1	13, 9	3, 9	12, 18
2	3	8, 13	6
3	-	18, 10	15
4	6, 8	-	9

Assume the model equation

$$y_{ijk} = c_i + s_j + e_{ijk},$$

where  $c_i$  is a fixed contemporary group effect,  $s_j$  is a random sire effect, and  $e_{ijk}$  is a random residual effect.

1. Set up the MME. Assume that  $\sigma_e^2/\sigma_s^2 = 10$ .
2. Apply REML EM to the model (Just one iteration) to estimate the sire and residual variances. Calculate an estimate of heritability.
3. Perform many rounds of Gibbs sampling on the MME solutions and on the variances. The MME solutions have normal conditional posterior distributions, and the variances have inverted Chi-square distributions. Assume degrees of belief equal to the number of observations, and prior values equal to the estimates from the previous question.
4. Plot the sample values of the variances.
5. Calculate an estimate of heritability for each Gibbs sample, and compute the mean and variance of the sample heritability values.