

# Bayesian Methods

LRS

CGIL

July-Aug 2012

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# Bayes Approach

## Philosophy

Every variable in a linear model is a random variable having its own distribution function.

## Concept

Combine *a priori* information having  $df$  degrees of belief with  $N$  data points to obtain more informed estimates.

# Process

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.

# Gibbs Sampling (MCMC) Process

Random samples from the conditional marginal distributions for each random variable eventually converge to random samples from the joint posterior distribution.

# Joint Posterior Distribution

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

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

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

$$\mathbf{y} | \mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2 \sim N(\mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a}, \mathbf{I}\sigma_e^2)$$

$$p(\mathbf{y} | \mathbf{b}, \mathbf{a}, \sigma_a^2, \sigma_e^2) \propto (\sigma_e^2)^{(-N/2)} \exp \left[ -(\mathbf{y} - \mathbf{X}\mathbf{b} - \mathbf{Z}\mathbf{a})'(\mathbf{y} - \mathbf{X}\mathbf{b} - \mathbf{Z}\mathbf{a}) / 2\sigma_e^2 \right]$$

# Prior Distributions

**Fixed Effects Vector** - There is little prior knowledge about the values in  $\mathbf{b}$

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

**Random Effects** For  $\mathbf{a}$ ,

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

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  $\mathbf{a}$ .

# Prior Distributions

## Random Factor Variances

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

is a scaled, inverted Chi-square distribution

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

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.

## Residual Variance

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



# Combining Prior Distributions

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

which can be written as

$$\propto (\sigma_e^2)^{-\left(\frac{N+v_e}{2}+1\right)} \exp \left[ -\frac{1}{2\sigma_e^2} ((\mathbf{y} - \mathbf{Xb} - \mathbf{Za})'(\mathbf{y} - \mathbf{Xb} - \mathbf{Za}) + v_e S_e^2) \right]$$

$$(\sigma_a^2)^{-\left(\frac{q+v_a}{2}+1\right)} \exp \left[ -\frac{1}{2\sigma_a^2} (\mathbf{a}'\mathbf{A}^{-1}\mathbf{a} + v_a S_a^2) \right]$$

# Conditional Marginal Distributions

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

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  $k = \sigma_e^2 / \sigma_a^2$ .

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

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  $\mathbf{e} = \mathbf{y} - \mathbf{Xb} - \mathbf{Za}$ .

# Example

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

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

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

# Computations

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  $k = 14$ .

## Overall mean

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

# Computations

## Animal 1

$$\begin{aligned}\hat{a}_1 &= (38.5 - \mu - 7a_2 + 7a_3 + 14a_4)/29 \\ &= -.1349 \\ a_1 &= \hat{a}_1 + RND * (\sigma_e^2/29)^{.5} \\ &= -.1349 + (1.138)(1.794) \\ &= 1.9067\end{aligned}$$

Same calculations for animals 2 to 5.

# Computations

## Residual variance

$$e_1 = 38.5 - 42.41 - 1.9067 = -5.8167$$

$$e_2 = 48.9 - 42.41 + .2203 = 6.7103$$

$$e_3 = 64.3 - 42.41 + .8879 = 22.7779$$

$$e_4 = 50.5 - 42.41 + 1.3006 = 9.3906$$

$$e_5 = 36.0 - 42.41 + 2.0200 = -4.3900$$

$$\mathbf{e}'\mathbf{e} = 705.1503$$

A new sample value of the residual variance is

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

# Computations

## Additive genetic variance

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

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

A new sample value of the variance ratio becomes

$$k = 95.6382 / 8.0605 = 11.8650$$

Repeat many times, many samples.  
Chains.

# Save Samples

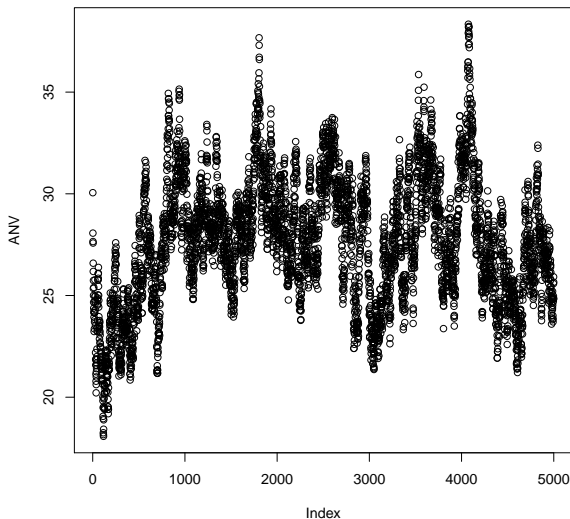
- $\sigma_e^2, \sigma_a^2, k, h^2$
- Determine burn-in period, number of samples that are not part of the joint posterior distribution. Plot samples on graph.
- Use samples after burn-in to calculate standard errors of estimates.



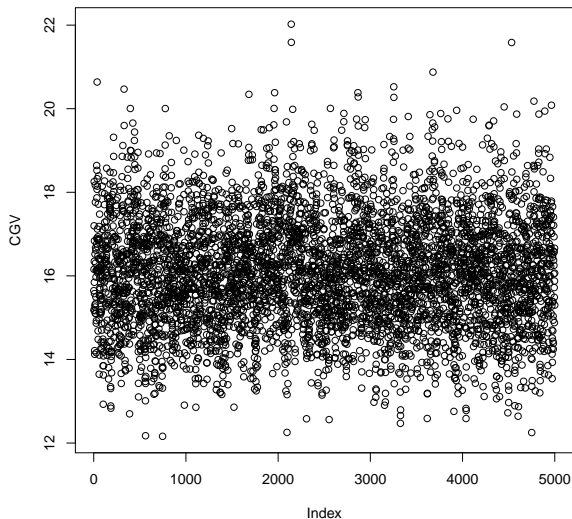
# Changes to Iteration Program

To incorporate Gibbs sampling, and saving samples.

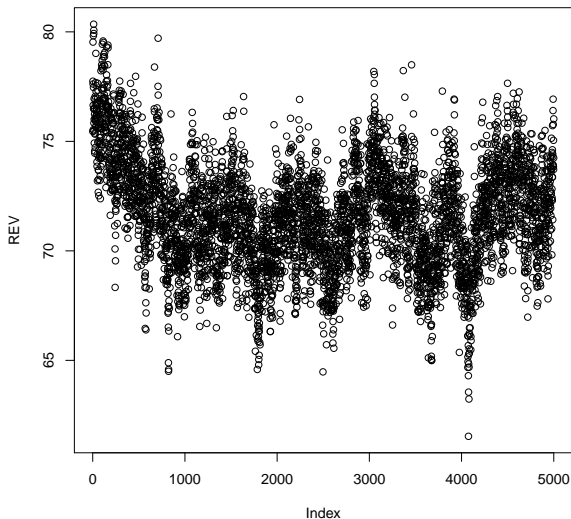
# Additive Genetic Component



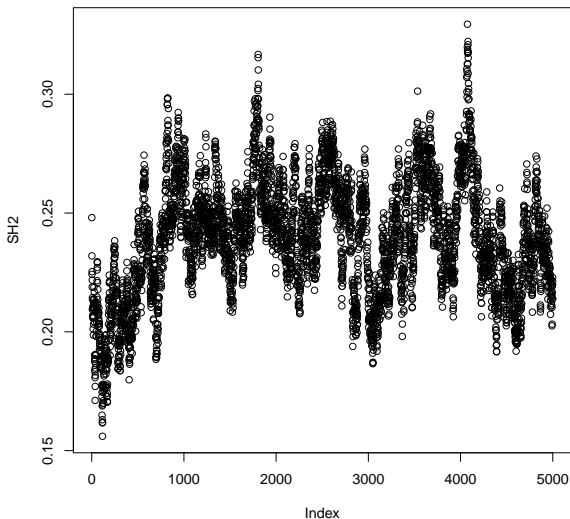
# Contemporary Group Component



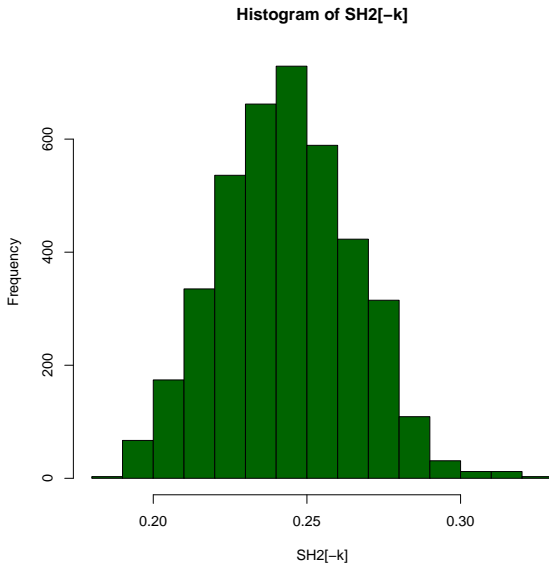
# Residual Component



# Heritability



# Heritability



# Summary

- Use REML or Bayes methods only.
- Estimating variances and covariances is more difficult than EBVs.
- Takes more computing time and effort.
- Should be re-done every 5-10 years in routine systems of evaluation.
- Covariance estimates have higher SE than EBVs.

# Properties of $\mathbf{A}$ matrix

- $\mathbf{A}^{-1} = \mathbf{T}'^{-1}\mathbf{D}^{-2}\mathbf{T}^{-1}$  thus,  $\mathbf{T}^{-1}$  specifies every mating (parents of each animal). Thus,  $\mathbf{A}^{-1}$  accounts for non-random matings.
- Progeny are expected to be random samples of potential progeny.
- Use of  $\mathbf{A}^{-1}$  in VC estimation gives an estimate of the **base** population genetic variance.
- Use of  $\mathbf{A}^{-1}$  accounts for reduction in genetic variance due to inbreeding, and due to selective matings, but not due to culling of animals.
- Abilities of  $\mathbf{A}$  depend on completeness of pedigrees, depth of pedigrees, and accuracy of parent identification.



# Tomorrow

- Cumulative PE effects model
- 11:00 AM, Go to Room 141, Affymetrix Presentation
- Lunch
- Maternal genetic effects model in PM.