

# CGIL Summer Course - 2007

## 4. Multiple Traits Genetic Evaluation and Parameter Estimation

1. Retrieve Fun3.d.(Pedigree file for large number of animals)
2. Create a data set having up to 4 traits per animal, where each trait follows the model,

$$y_{tijk} = CG_{ti} + Age_{tj} + a_{tk} + e_{tijk},$$

where  $CG_{ti}$  is a contemporary group effect(200 groups),  $Age_{tj}$  is a fixed age effect (12 groups),  $a_{tk}$  is the animal additive genetic effect (direct), and  $e_{tijk}$  is a random residual effect. Assume the following covariance matrices:

$$\mathbf{G}_{cg} = \begin{pmatrix} 1200 & 400 & 200 & 20 \\ 400 & 600 & 80 & -10 \\ 200 & 80 & 100 & -5 \\ 20 & -10 & -5 & 16 \end{pmatrix},$$

$$\mathbf{G}_a = \begin{pmatrix} 4500 & -1099 & -1055 & 505 \\ -1099 & 2300 & -1025 & 1008 \\ -1055 & -1025 & 370 & 110 \\ 505 & 1008 & 110 & 63 \end{pmatrix},$$

and

$$\mathbf{R} = \begin{pmatrix} 8400 & 3200 & 1600 & 160 \\ 3200 & 4200 & 640 & -100 \\ 1600 & 640 & 700 & -40 \\ 160 & -100 & -40 & 130 \end{pmatrix}.$$

- (a) Check that covariance matrices are positive definite. If they are not, then make them positive definite.
- (b) Generate true breeding values for all animals and traits.
- (c) Generate effects for 200 contemporary group effects and 4 traits each.
- (d) Allocate animals to contemporary groups.
- (e) Generate age effects for each trait (plus the overall means of 1000, 500, 50, and 0 for traits 1 to 4, respectively).
- (f) Create the observation records.
- (g) With probability 0.13, randomly change observations to NA (missing). For each animal and trait within animal, generate a random uniform variate, and if it is below 0.13, then change it to NA.

3. Apply iteration on data techniques to solve the mixed model equations for the data set just created.
  - (a) Plot EBVs of trait  $a$  versus trait  $b$ .
  - (b) Compute an index using weights ( 1, -2, 0, 20.).
  - (c) Plot index values against each trait.
4. Estimate the covariance matrices.
5. Think about a multiple trait model with a different model for each trait, and perhaps one trait has maternal genetic effects. Make up the necessary covariance matrices.