

# CGIL Summer Course - 2007

## 2. Animal Model, Genetic Evaluation, Parameter Estimation

1. Retrieve Fun3.d.(Pedigree file for large number of animals)
2. Create a data set according to the model,

$$y_{ijkm} = CG_i + Age_j + b(M_k) + a_m + e_{ijkm},$$

where  $CG_i$  is a random contemporary group effect,  $Age_j$  is an effect of age of the animal,  $b$  is a regression on  $M_k$  which is the marker genotype (-1, 0, or 1),  $a_m$  is the animal additive genetic effect, and  $e_{ijkm}$  is a random residual effect. Assume that the variances are 100 for contemporary group effects, 700 for residual effects, and 300 for additive genetic effects. Let  $b = 10$ . The number of contemporary groups should be 60, and the number of age groups should be 8. Allocate animals randomly to age groups, contemporary groups and marker genotypes.

- (a) Generate true breeding values for all animals.
  - (b) Generate 60 contemporary group effects.
  - (c) Let Age effects be (-25.0, -19.0, -14.0, -8.0, 3.0, 13.0, 17.0, 21.0).
  - (d) Allocate animals to contemporary groups.
  - (e) Allocate animals to age groups.
  - (f) Allocate marker genotype values (-1, 0, or 1) to each animal.
  - (g) Create the observation record, add to dataframe.
  - (h) Change observations on all animals with unknown parents to NA.
3. Apply iteration on data techniques to solve the mixed model equations for the data set just created.
    - (a) Compute means and variances of EBVs by year of birth for animals with observations.
    - (b) Plot means and variances by year of birth.
  4. Modify the iteration on data technique to do Gibbs sampling, and estimate the variances.
  5. Think about allowing animals to have more than one observation. Permanent environmental effects need to be added to the model. How would you assign contemporary groups, age effects, and regression on marker genotype?