

## Assignment 13

Please choose one project. At best the projects should be done in groups and involve extensive discussions.

### Project 1

1. Write a program that creates a 2 trait sire model using some values for variances.
2. Improve the simulation to an animal model. Define parts of the model such as the number of levels, number of sires + dams per generation, number of generations, variances, etc, in a module. Check with an estimation program that it works.
3. Rework the simulation program to include censored data; censor top 10-30% records for one trait. Estimate. Can thrigibbs1 handle censored data?
4. Write your own computer program to handle 2 effects and the animal model. The program can be based on lsq.f90 and may be using dense matrices initially.
  - a) make it work with a parameter file
  - b) rework it to be a gibbs sampler (one trait)
  - c) rework it to support censored models.

At every step, check whether your program works with sire and animal models.

### Project 2

As above but for threshold models; start with 2 categories and extend to 3.

### Project 3

The project below can be used for the following:

*Find accuracies of genomic selection assuming:  $n$  animals,  $m$  markers, and  $s$  markers as QTL. The results will be functions of many assumptions, perhaps the strongest being that all QTL are SNP markers.*

1. Write a simple genome simulation program for SNP markers. Make assumptions as needed. Initially simulate 1000 animals and 5000 SNP markers with only 200 markers having nonzero effects. Simulate only the base population. For every animal, output genotypes and breeding values.
2. Adapt lsqf90 to analyze that data. Find correlations of BV and EBV.
3. Create multiple generations by mating: hard!