Practical Tuesday 20 October morning

Part 1. Standard error of the genetic correlation

Use for this exercise the R-code se_rg.R based on Bijma and Bastiaansen. It is made for looping across different parameters. The program was made for the standard error of the genetic correlation between purebred and crossbred performance. For this practical, you can read purebred and crossbred as environment 1 and environment 2.

1. Make a plot of the standard error of the genetic correlation as a function of the heritability when the genetic correlation is 0.8, the number of half-sib families is 100 (one offspring per dam; 100 sires) and number of offspring per environment is 50. Ignore the common environmental effect (c^2=0).

2. Make a plot of the standard error of the genetic correlation as a function of the number of offspring per environment when the genetic correlation is 0.8, the number of half-sib families is 100 (one offspring per dam; 100 sires) and the heritability is 0.1, 0.3 or 0.5. Ignore the common environmental effect (c^2=0).

3. Make a plot of the standard error of the genetic correlation as a function of the number of families when the genetic correlation is 0.8, the number of offspring per environment is 50 and the heritability is 0.1, 0.3 and 0.5. Ignore the common environmental effect (c^2=0).

4. Let's consider a trait with quite large common environmental effects such as harvest weight in fish. Typically, because of their small size as fingerlings, families are kept together for quite some time in family tanks. Make a plot of the standard error of the genetic correlation as a function of c^2, the ratio of common environmental variance to the phenotypic variance, when the genetic correlation is 0.8, the heritability is 0.3, the number of sires is 100 and the number of dams mated to each sire is 2. Each dam has 50 offspring in one environment.

5. (challenging) Adapt the R-code in which the total number of animals per environment is constant and vary the number of families and family size and determine whether there is an optimum. Vary the heritability. Ignore the common environmental effect (c^2=0). Set the number of animals per environment equal to 2000. Assume as in question 4 that each sire is mated to 2 dams for each environment.

Part 2. Bivariate and reaction norm models in ASREML

The aim of this exercise is to work with ASReml to estimate a genetic correlation between two environments in a bivariate analysis and to analyse a data set using a reaction norm model. In both cases, you will use simulated in both cases. The focus is on interpreting the output from ASReml. For the bivariate model (bivariate.zip), the used simulated dataset cows.dat contains 10,000 cows, from which 4900 are in environment 1 and 5100 in environment 2. The 10,000 cows are daughters from 100 sires, each with 100 daughters. Each sire has approximately half of the daughters in each environment. For the reaction norm model (RN.zip), the used dataset is cows_asreml.dat. The dataset is slightly different than the previous one, but has the same structure with 100 sires each with 100 daughters.

1. Look at the biv.as file and the cows.dat file to understand the analysis.

2. Run the biv.as and the pin-file in ASREMLW. Study the output in biv.asr and in biv.pvc. How do you interpret the genetic correlation and its standard error?

3. Is the standard error according to your expectation, e.g. when comparing to the program se_rg.R?

4. Open now the RN.zip and study the RN.as and the datafile cows_asreml.dat.

5. Run ASReml and run the pin-file. Study the output in RN.asr and RN.pvc. what is you conclusion with respect to GxE?

6. Plot the genetic correlation and its standard error between different pairs of environments using the provided r-code standard error rg.R.

6. Change the intercept of the reaction norm by subtracting/adding a certain value to x, e.g. (-1, -2, +1, +2). Write down the REML likelihood and the estimated variance components. What is your conclusion?

8. If time permits you may want to try Legendre polynomials by using leg(x,1).animal. You can see in the .res file the polynomial coefficients.