BAYESIAN INFERENCE

Problems

Find out the difference between the additive values of two bulls in quantity of milk in kg. The relevant value of the difference is estimated at 100 kg. The actual chains for estimating the additive value of the bulls have hundreds of thousands of samples, but in our example we will take two chains of only five samples. The chains for the bulls are:

$$\text{Bull 1:}\quad 110 \quad 50 \quad 20 \quad 120 \quad -50$$

$$\text{Bull 2:}\ -110 \quad -50 \quad -20 \quad -120 \quad 50$$

5-1. Predict the difference between bulls with a MEAN and with a MEDIAN.

5-2. Probability that bull 1 has a higher additive value than bull 2.

5-3. Probability P_R that the difference between bulls is equal to or greater than the relevant value (100 kg). Probability of similarity P_S between bulls (probability that there is no difference between them, for practical purposes).

5-4. Minimum value of the difference that can be guaranteed with an 80% probability.

5-5. Shorter confidence interval with 80% probability (HPD80%).

Self-assessment questions (True or False)

1. The prior probability is usually an arbitrary value.
2. The prior probability is usually a constant or a mathematical artefact (a function) that does not capture the true prior probability.
3. When the a priori probability it is a mathematical artefact, has little influence on the results, so that the results are essentially based on the data.
4. When the prior probability is a constant, the maximum likelihood results and those from the posterior marginal distributions are the same.
5. Using the data augmentation method, data are generated and used in the parameter estimation process, but this does not affect the result.
6. The Bayesian method for estimating genetic parameters is the Monte Carlo Markov chains (MCMC).
7. Marginalization takes into account the errors made when estimating the parameters that are marginalized; thus, when estimating the additive values, the estimation errors of the additive and residual variances have been taken into account.
8. BLUP can be interpreted as a Bayesian method.
9. REML gives the same result as the Bayesian estimate based in marginal posterior distributions.
10. By increasing the length of the MCMC chain (that is, the number of samples in the chain) we increase the precision of the estimation.