

Developing the Method of Estimating Genetic Similarity between Populations

Mohammad A. Nilforooshan

Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

Mohammad.Nilforooshan@hgen.slu.se



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BACKGROUND

Genetic similarity is the extent of genetic exchange or the amount of the genetic material that is shared between the gene pools of two populations, which is an indicator of genetic connectedness.

Genetic correlations and the number of exchanged individuals have been used traditionally as indicators of genetic connectedness. However, genetic correlations are trait-dependent and under the influence of genotype by environment interaction and the number of exchanged individuals do not show the extent of spreading genes from exchanged individuals into two populations.

AIM

Improving an existing method for measuring genetic similarity to include information from ancestors.

METHODOLOGY

The base method as proposed by Rekaya *et al.* (1999):

We can show the above equation as:

$$GS_{ij} = \frac{N = \sum_i \sum_j (A_i \cap A_j)}{\sum_i \sum_j (A_i \cup A_j)}$$

$$GS_{ij} = \frac{\sum_{k=1}^{N_{ij}} (n_{ik} + n_{jk})}{\sum_{k=1}^{N_i} n_{ik} + \sum_{k=1}^{N_j} n_{jk}}$$

Number of progeny from common bulls

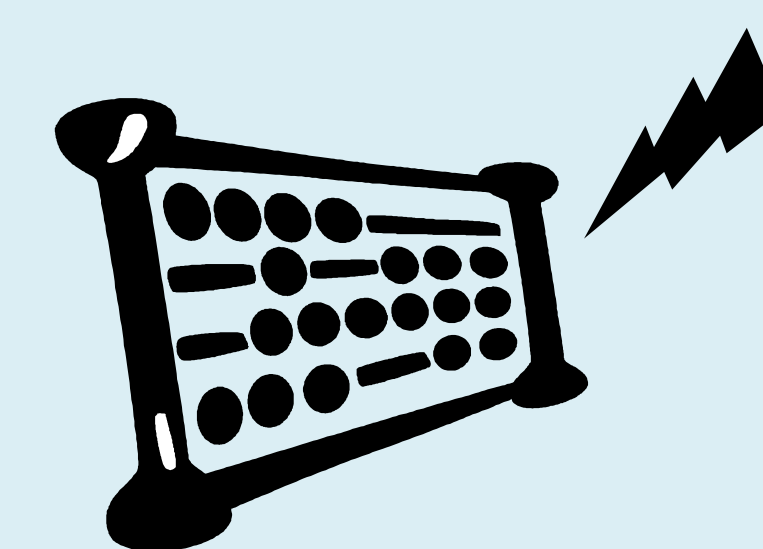
Total number of progeny in both populations

However, there are more intersections to consider:

Σ_i : number of progeny in country i ; Σ_j : number of progeny in country j
 A : bull population; B : sire population; C : maternal grandsire population

$$N = \begin{bmatrix} \sum_i \sum_j (A_i \cap A_j) & \frac{1}{2} \sum_i \sum_j (B_i \cap A_j) & \frac{1}{4} \sum_i \sum_j (C_i \cap A_j) \\ \frac{1}{2} \sum_i \sum_j (A_i \cap B_j) & \frac{1}{4} \sum_i \sum_j (B_i \cap B_j) & \frac{1}{8} \sum_i \sum_j (C_i \cap B_j) \\ \frac{1}{4} \sum_i \sum_j (A_i \cap C_j) & \frac{1}{8} \sum_i \sum_j (B_i \cap C_j) & \frac{1}{16} \sum_i \sum_j (C_i \cap C_j) \end{bmatrix}$$

After a few steps of removing over-counted number of progeny:



$$N = \begin{bmatrix} \frac{11}{16} \sum_i \sum_j (A_i \cap A_j) & \frac{1}{2} \sum_i (B_i \cap A_j \cap B'_j) + \frac{1}{2} \sum_j (B_i \cap A_j \cap A'_i) & \frac{1}{4} \sum_i (C_i \cap A_j \cap C'_j) + \frac{1}{4} \sum_j (C_i \cap A_j \cap A'_i) \\ \frac{1}{2} \sum_j (A_i \cap B_j \cap B'_i) + \frac{1}{2} \sum_i (A_i \cap B_j \cap A'_i) & \frac{1}{4} \sum_i \sum_j (B_i \cap B_j) & \frac{1}{8} \sum_i (C_i \cap B_j \cap C'_j) + \frac{1}{8} \sum_j (C_i \cap B_j \cap B'_i) \\ \frac{1}{4} \sum_j (A_i \cap C_j \cap C'_i) + \frac{1}{4} \sum_i (A_i \cap C_j \cap A'_i) & \frac{1}{8} \sum_j (B_i \cap C_j \cap C'_i) + \frac{1}{8} \sum_i (B_i \cap C_j \cap B'_i) & \frac{1}{16} \sum_i \sum_j (C_i \cap C_j) \end{bmatrix}$$

$$GS_{ij} = \frac{1'N1}{\sum_i \sum_j (A_i \cup A_j)}$$

RESULTS

Using data on two populations from Denmark-Finland-Sweden and Canada, submitted to Interbull Centre for the international evaluation of production traits in April 2009, the estimate of genetic similarity improved from 27.7% with the former method to 48.2% with this method.

This method is also further developed for sire-dam pedigree, which is going to be used at Interbull Centre.