Genetic value of animal (examples)

1. Calculate the additive genetic relationship matrix based on the following pedigree information (tabular method):

Animal	Father	Mother
A	-	-
B	-	-
C	A	B
D	A	C
E	D	B

	A	B	C	D	E
A					
B					
C					
D					
E					

Source: Schaeffer (2010)

To give you an understanding, we mention a procedure based on a simple tabular method which enables to evaluate relationship and inbreeding for large number of animals and is generally used in various methods for the estimation of breeding values.

The method is based on the assumption that if two individuals (X and Y) are related, then one or both parents of the individual Y should be related to X. Another prerequisite is the need to arrange the pedigree information from the oldest generation of animals to the youngest (last) one. The last assumption is that the initial parents are not the result of inbreeding.

Off-diagonal element of matrix (a_{XY}) is calculated as follows:

$$a_{XY} = 0{,}5.(a_{XYo} + a_{XYm})$$

a_{XYo} – relationship between the individual X anf father O of individual Y, a_{XYm} – relationship between individual X and mother M of individual Y.

Diagonal matrix elements are calculated by means of the following formula:

$$a_{XX} = (1 + F_X) \text{ a } a_{YY} = (1 + F_Y)$$

F_X and F_Y are the coefficients of inbreeding of individuals X and Y which are calculated as a half relationship of parents of an evaluated individual: $F_X = 0{,}5.a_{XoXm}$ a $F_Y = 0{,}5.a_{YoYm}$.

a_{XoXm} – relationship of parents of the individual X, a_{YoYm} – relationship between parents of the individual Y

If the parents of the evaluated individual are not related, the inbreeding coefficient is equal to 0 and the diagonal element of the evaluated individual is equal to 1. Diagonal elements of additive genetic relationship matrix which have a higher value than 1, point out the existence of inbreeding automatically. Table 12 shows a classic example of constructing the additive genetic relationship matrix for 5 evaluated individuals taking into consideration the inbreeding.

2. Calculate the additive genetic relationship matrix based on the following pedigree information (CFC software):

Animal	Father	Mother
A	-	-
B	-	-
C	A	B
D	A	C
E	D	B

	A	B	C	D	E
A					
B					
C					
D					
E					

3 Calculate the genomic relationship matrix based on the following information:

Animal genotypes

Animal	SNP1	SNP2	SNP3	SNP4
1	AA	Ct	GG	Ag
2	AA	Ct	Ga	AA
3	tt	CC	GG	AA

Source: Isik (2013)

The methods by taking into account the minor allele frequencies

$$G = \frac{\mathbf{Z}\mathbf{Z}'}{2\sum \mathbf{p_i}(\mathbf{1}-\mathbf{p_i})} \quad \text{(VanRaden, 2008)}$$

Z is the critical incidence matrix of markers (genomic information) for the calculation of the genomic relationship matrix G, Z' represents the transposed Z matrix, p_i - a minor allele frequency observed in the locus of all genotyped individuals regardless of inbreeding and selection of animals. In the case of the unknown minor allele frequencies in the base population, the same value of frequency p_i (0.5) can be used for all loci, or p_i may represent the average minor allele frequencies of the given locus in the genotyped population of animals.

For the purpose of calculating the genomic matrix, the genotypes must first be converted into a numerical form, which expresses the number of minor allele frequency for each animal and each locus. The MAF (Minor Allele Frequencies) matrix is being created. In terms of simplification of calculation procedures, the matrix M will be constructed in which each element of the M matrix = MAF - 1. Table 14 shows particular values of MAF matrix and M matrix in the representative example.

Table 14 Genomic relationship (MAF matrix and M matrix)

MAF						M			
Animal	SNP1	SNP2	SNP3	SNP4		SNP1	SNP2	SNP3	SNP4
1									
2									
3									

The next important step is to construct the P matrix, which indicates the frequency of alleles in the following formula: $P_i = 2 (p_i -0,5)$, where p_i represents the minor allele frequency in the locus i. P matrix and basic incidence Z matrix are constructed according to the used type of frequency. Using the representative example, we applied the following minor allele frequencies and formula to calculate the Z matrix :

Frequency	p_1	p_2	p_3	p_4	Z
observed					M - P
unknown					MAF - P
average					MAF - P

Table 15 Genomic relationship (P matrix and Z matrix, observed frequencies)

P						Z			
Animal	SNP1	SNP2	SNP3	SNP4		SNP1	SNP2	SNP3	SNP4
1									
2									
3									

Table 16 Genomic relationship (P matrix and Z matrix, unknown frequencies)

P						Z			
Animal	SNP1	SNP2	SNP3	SNP4		SNP1	SNP2	SNP3	SNP4
1									
2									
3									

Table 17 Genomic relationship (P matrix and Z matrix, average frequencies)

P						Z			
Animal	SNP1	SNP2	SNP3	SNP4		SNP1	SNP2	SNP3	SNP4
1									
2									
3									

Table 18 shows the final calculated values of the genomic relationship matrix G according to the various minor allele frequencies (basic formula, VanRaden, 2008).

Table 18 Genomic relationship matrix (G)

	G (frequencies observed			G (unknown frequencies)			G (average frequencies)		
Animal	1	2	3	1	2	3	1	2	3
1									
2									
3									