GENOMIC SELECTION

Problems

6-1. Calculation of the genomic matrix ***G***. In the example of section 6.2.2, we assign the values 2, 1, 0 to the allele with the highest frequency in each SNP. However, it is more common to consider the lowest frequency allele for the 2,1,0 assignment, for practical reasons in file management (to debug low frequency SNPs). Repeat the analysis assigning 2,1,0 to the lowest frequency allele.

6-2. Starting from the four genotyped and phenotyped animals, where the first column is the phenotypes and each of the following six columns the values of the SNPs, predict the additive values of the four animals that do not have data

		SNP1	SNP2	SNP3	SNP4	SNP5	SNP6
Animal 1	100.2	1	1	1	1	0	1
Animal 2	102.3	1	2	1	1	2	2
Animal 3	108.7	1	0	2	2	2	0
Animal 4	99.0	0	1	1	2	2	0

	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6
Animal 5	0	1	2	1	1	2
Animal 6	0	2	1	0	0	0
Animal 7	1	1	2	2	1	1
Animal 8	1	1	1	0	1	1

The heritability is $h^2 = 0.3$. The phenotypic variance is 1. Calculate the prior variance σ^2_α of each marker as the additive variance divided by the number of markers (see section 6.2.1).

6-3. If we have the individual effect of each SNP, could we select animals having all the favorable versions without the need of recalculating the prediction equations every few generations?

6-4. If we detect large and medium effect genes by GWAS, can we keep the favorable versions of all these genes?

6-5. Genomic selection adds more information to the classic BLUP, for example by better specifying the relationship matrix. Why is genomic selection not used in all species?

Self-assessment questions (True or False)

1. Genomic selection with chips of 50,000 SNPs is much more efficient than with chips of 3,000 SNPs
2. Genomic selection with 1,200,000 SNP chips is much more efficient than with 50,000 SNP chips.
3. Genomic selection, if the whole genome sequence were readily available, would be much more efficient than current selection with chips of 50,000 SNPs.
4. The effects of the SNPs are the effects of the genes involved in the trait.
5. A SNP always has the same effect, whether the analysis is done with chips of 50,000 SNPs or with chips of 850,000 SNPs.
6. The variance of the SNP describes our a priori uncertainty about the effect of the SNP.
7. In Bayes B, we give *a priori* value zero to SNPs with a given probability, so we cannot ensure *a priori* that some specific SNPs have zero value.
8. The efficiency of genomic selection is expected to be similar in dairy cattle, pigs or poultry.

9. Genomic selection is a new paradigm in selection, and selection methods have radically changed since SNPs are used.
10. Genomic selection has contributed to an overall increase of the response to selection in poultry and pigs by around 20% - 30%.