

## 12.1 Technology for breeding value estimation

In chapter 7 simple methods for calculation of the estimated breeding values were given. Only data with uniform relation were included. This is a very simple form of estimation of the breeding value and it demands very little computer power, as it is based on the calculation of a single weight factor. This weight factor is dependent on the heritability, the number of individuals in the group, their internal relations and how they are related to the candidate. With the introduction of modern computers, the basis for a better utilization of existing data for estimation of the breeding value has materialized. The more advanced methods are based on systems of linear equation, in which every observation is provided with its own equation. Thereby the creation of a system of equations for calculation of the weight factors for every observation is completed. The model includes all observations from related animal as well as observations from related to related. An example of related to related animals: The mother of an offspring, whose father is being evaluated. If the mother of the offspring is present in the model of the father's estimated breeding value, the preconditions for random mating does not have to be too strict, since the father's breeding value has been adjusted for deviations of the dam's from the population mean value.

The implied condition, that all observations must occur in the same environment, can also be taken more lightly, since for instance herd average can be taken into account in the models. To do this the model implies that more than one family per herd must be represented and that some of the sires in the herd should be used in other herds as well.

### **The most important methods for estimation of breeding value:**

1. Selection index (SI)
2. Best linear prediction (BLP)
3. Best linear unbiased prediction (BLUP)
4. Animal model (AM)
5. Genomic selection

The selection index was developed in the 1950's and was utilized before the computer age. The SI is at present mainly used for model calculation, as it is useful for the evaluation of the effect of multi trait selection. If a certain set of economic weight factors are used, each trait will get an expected delta G's. Before the computer age it was common to pre-correct data, as for instance for calving age or slaughter weight, since these traits had some biological variation. Pre-correction is still applied to some extent. With the production of faster computers, it has been possible to develop models, which calculate estimated breeding value for all animals in a population. When this is the case, it is easier to use all information from all the individuals, as these will give information on relations to all the others. BLP does not include environmental factors, which makes it less useful. The solutions obtained from a few animals are identical to the solutions obtained by SI. The BLUP and AM can simultaneously estimate environmental effects and the correction for them.

In the last three methods the relationship matrix is utilized at varying degrees. The relationship matrix is arranged according to the tabular method given in section 4.4. The solution of that many equations cannot be done explicitly, which have been taught when to solve two equations with two unknowns. The solutions are first based on guesses and then on recalculation until the solutions remain constant. This method is called iterative. It is possible, by means of this method, to estimate breeding values of millions of animals simultaneously. At present the AM method is used in the both Danish dairy and swine breeding work.

### **Genomic selection by Thomas Mark**

Genomic selection is a new technology in which breeding values are predicted from genome-wide markers in the form of single nucleotide polymorphisms SNP. The genetic maps are based on SNP and they enable us to divide the entire genome into thousands of relatively small chromosome segments. Then the effects of each chromosome segment are estimated simultaneously. Finally, the genomic breeding value equals the sum of all estimated chromosome segment effects. The chromosome segment effects can be estimated for a group of animals (ie a reference population); and for any remaining animal, only a blood or tissue sample is needed to determine its genomic breeding value. The chromosome segment effects apply to all animals in the population in which they were estimated, because markers are in linkage disequilibrium with the causal gene that they bracket.

Genome-wide information allows accurate selection of young animals provided that phenotypes from sufficiently many reference animals are available. This means that genomic breeding values are especially beneficial when traditional selection is difficult such as when phenotypic recording is restricted by sex and age (e.g. very beneficial for dairy cattle). However, conservative use of young animals without phenotypic information (relating to self or progeny) is advised to avoid potential negative side effects related to unfavourable mutations, unfavourable selection pressure on non-recorded breeding goal traits and high rates of inbreeding.