Chapter 8.10: Best Linear Unbiased Prediction

The Animal model is about utilising alternative information sources through their additive genetic relationship with the animal you want to estimate the breeding value for. Estimating breeding values is about optimising the estimation of the regression coefficient, but also about optimising the phenotypic information. There is a method that combines these two important factors: it simultaneously corrects the phenotypes for systematic effects, and it estimates breeding values while making use of the additive genetic relationships between the animals. The result is an unbiased estimate of the breeding value. This method is the Best Linear Unbiased Prediction, or in short: BLUP.

It is a method that makes use of matrix algebra. We will not go into details here, but we will try to give the main idea. In formula it would look like this:

\[ Y = Xb + Za + e \]

The \( Y \) is the phenotypic information, the \( Xb \) corrects the phenotypic superiorities for the systematic effects, and the \( Za \) links the phenotypic superiorities to the additive genetic relationships to estimate the EBV. The \( e \) indicates the error variance. In a way BLUP does follow the simple model \( P = E + G \), but also provides estimates of \( G \) and \( E \).

For example, if animals on one farm are fed much better than on another farm, then ranking animals based on their weight would benefit the animals from the farm with the better nutrition. However, genetically the animals on both farms may be similar. Without taking this systematic influence of farm of origin into account it is likely that the top ranking animals would mainly originate from the farm with the better feed. To be able to compare the performance of the animals more on their genetic potential it is important to take this farm effect into account, and this is what BLUP does (if you provide the information about on which farm each animal was housed). The principle of BLUP is to determine the average weight of the animals on each farm and subtract the difference from the animals on the farm with the highest weight. If animals on farm 1 weigh 100 kg, and on farm 2 they weigh 120 kg, then you ‘punish’ the animals of farm 2 by subtracting 20 kg from their weight.

Critical issue in correcting for systematic effects is that it only works well if genotypes are sufficiently spread across systematic environmental influences. So the animals on both farms need to be related, for example because the same fathers were used, or because the fathers used on each farm were brothers. If the animals on both farms are unrelated, then part of the reason of the difference in weight may be a difference in genetic potential. And that is what you want to estimate so you don’t want to lose that by correcting the weight. Artificial insemination allows for genetic links between farms because the same sires are used in many farms. In farm animal species where natural mating is common practice, such as in beef cattle and sheep, it often is not possible to estimate systematic farm effects accurately because lack of exchange of animals between farms results in poor genetic links between farms. In species where the sires are brought to their mates on various locations, as can be the case in horse or dog breeding, genetic links will not be a limiting factor. Provided the sires are used often enough.

Thus:

With BLUP it is possible to estimate breeding values using information on relatives and correcting phenotypes for systematic influences.

Critical point is that sufficient genetic links between environments are required to estimate systematic effects of those environments (e.g. farms).