Geneticgain_Multivariate_Description

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Target / Zweck

Informing how the genetic gain for carcass traits has been computed for two breeding scenarios.

Plan / Principle

Define the scenarios. Start from the result of the computations. Tell why the result is important and what the basic thoughts behind the computations are. Then explain the main equations.

Material

- Skript "Geneticgain_CarcassTraits_Multivariate"
- Skript "ResponseToSelection"
- Skript "02-matandmeth"

Implementation

Target

In this project breeding strategies should be evaluated in their effectiveness to improve early maturity. This evaluation requires certain tools, which help to characterize the breeding strategies. A particularly powerful tool is the value of genetic gain. This value provides information about a trait's or index's mean genetic improvement over a period of time in a population.

Two breeding strategies characterized by selection index theory

The estimated variance components have been used to predict the genetic gain (Q). In this thesis the genetic gain has been used to compare two breeding strategies for early maturity. Subsequently the strategies will be called scenarios to show that they are based on predictions. In both scenarios the breeding values of "calves" and "stirks" have been included. The first scenarium assumes a selection for only carcass fat and the second scenarium assumes a selection for an economically weighed combination of carcass fat, carcass conformation and carcass weight. The value of genetic gain predicts a trait's or aggregate genotype's improvement in a population over a period of time. For both scenarios this improvement is defined by an increase in the aggregate genotype H

$$H = \sum a_m u_m$$

where

a is an economic weight,

u is a true breeding value and

m indicates the breeding values CFa, CFc, CCa, CCc, CWa and CWc.

The aggregate genotype is designed to show the economic value of an animal when considering the carcass traits CFa, CFc, CCa, CCc, CWa and CWc. Therefore it is a useful tool to evaluate the effectiveness of the two breeding strategies in improving the desired trait early maturity. However, the true breeding value is impossible to compute, which also makes it impossible to compute H for an animal. Therefore H must be approximated using multiple regression with information sources which estimate the true breeding values. Here, the information sources are estimated breeding values û and do not have the same number for the two scenarios.

In the first scenario it is assumed that selection will base only on the estimated breeding values for carcass fat $\hat{u}_{aCF}$ and $\hat{u}_{cCF}$. This results in the index I_1

$$I_1 = b_{aCF}\hat{u}_{aCF} + b_{cCF}\hat{u}_{cCF}$$

where

b is a multiple regression coefficient chosen so as to make the correlation between H and I as large as possible.

b has been computed using the equation

$$b = P^{-1}Ga$$

where

P is the variance/covariance matrix of the estimated breeding values,

a is the vector of economic weights from the true breeding values in the aggregate genotype and

G is the covariance matrix between estimated breeding values and true breeding values.

The variances and covariances of P have been approximated through the values of the covariance matrix between true and estimated breeding values C. G was computed under the assumption, that BLUP-based estimated breeding values will be used by the breeders. This assumption allows the relationship

$$Cov(u, \hat{u}) = Var(\hat{u}) = Var(I)$$

which results the approximation using C as well. Nevertheless P and G do not have the same shape in this scenarium, because the information sources are not the same as the true breeding values in the aggregate genotype. They are expressed as

$$P = C_{aCF,cCF}$$
$$G = C[aCF, cCF]$$

where

$C_{aCF,cCF}$ is C only involving the traits aCF and cCF, which makes it a 2 x 2 matrix and

$C[aCF, cCF]$ are the columns of aCF and cCF of C, which makes them a 2 x 6 matrix.

In the second scenarium that selection will be based on all the economically weighed breeding values existing in the aggregate genotype. This results in the index

$$I_2 = \sum b_m \hat{u}_m$$

where

m are again all carcass breeding values.

Here all breeding values in the index are also present in the aggregate genotype. Recalling the definition of P and G, both result in the same matrix C in this scenarium. When

$$P = G = C$$

then

$$b = a$$

Genetic gain of the Index

For both scenarios the Genetic gain Q_I^* of their index has been computed by the equation

$$Q_I^* = \frac{\sum_{y=1}^{2} i_y r_y^* \sigma^*}{\sum_{y=1}^{2} L_y} \tag{1}$$

$$Q_I^* = \frac{\sum_{y=1}^{2} i_y r_y^* \sigma_H^*}{\sum_{y=1}^{2} L_y}$$

where

i is the selection intensity,

r^* is the asymptotic accuracy of the index I,

σ^* is the standard deviation of the aggregate genotype H,

L is the generation intervall,

y is the selection path and

$*$ indicates, that the value is corrected for the "Bulmer effect" [@Bulmer??].

For both scenarios L and i have the same values, but r^* and σ^* differ.\

The generation intervall and selection intensity have been derivated from the mean values of 1956 - 2014 in the populations of Swiss Limousin (LM) and Swiss Angus (AN) each [@Kunz2016].

In scenarium 1 σ^* has been computed using the equation

$$\sigma^* = \sqrt{Var(H)}$$

frac{}{} The breeding conditions are defined by the generation intervall L, the accuracy of the breeding value r, the genetic standard deviation of the trait σ_g and the selection intensity i. They are derived from the past breeding situation. The type of computation is derived from the approach of @Phocas1996.

There, the so-called Bulmer-Effect [@Bulmer??] is considered.

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2+5
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## [1] 7
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