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REVIEW OF METHODS FOR FERTILITY EVALUATION

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ABSTRACT

The purpose of this paper is to give the review of methods used for fertility evaluation and shortly describe theirs principles. There is not unified system of fertility evaluation over the world, even emphasis on particular fertility trait which should has described the fertility phenomenon vary from country to country as well as from particular fertility specialist.

INTRODUCTION

The quick world escalation of milk production is also connected with markedly decreasing reproductive efficiency of cows in last years. The most of studies discovered unfavorable genetic correlations between yield and fertility traits. Fertility traits are considered very important because of their impact on the economics of dairy cattle breeding.

REVIEW OF METHODS

Statistical models for fertility evaluation

The evaluation of fertility can be made by means of different measures; hence the choice of mathematical-statistical model must follow specialties and nature of every different measure of particular trait. On the other hand, because fertility is complex phenomenon the separate evaluation of one measure can't satisfactorily describe whole reality. On this account the construction of evaluating models sometimes consider more then one trait, hence it seems to be difficult to provide compact information about evaluation and properties of single trait as well as about results of its evaluation.

Fertility evaluation by means of interval measures

These traits can be evaluated in principle in the same way as every continues response in mixed linear regression model – animal model. The main difficulty is that they sometimes are not normally distributed and ignoring this fact can influence the results in a bad way.

Fertility evaluation by means of discrete measures

The Best linear unbiased prediction is extensively used for estimation of genetic merits for normally distributed traits, because it yields the maximum likelihood estimator of the best linear predictor.

Treshold models

There are some traits in animal breeding which are expressed phenotypicaly as being member of one of *m* categories, e.g. calving ease, pregnancy or disease. We can only assign an animal to one category; diseased animal or non-diseased animal or pregnant or non-pregnant. Categorical traits may be inherited in polygenic manner with a very large number of genes involved, so underlying susceptibility to e.g. disease trait may actually be continuous and may follow a normal distribution. On this underlying continuous *liability* scale is a threshold point t (or points in case of more ordinal categories, e.g. severity of disease) where above this threshold the animal expresses the disease phenotype, and below the threshold point the animal does not express the disease.

Longitudal data analysis for normal distributed traits

In the longitudinal regression we consider variables to be associated with a sequence of points in time in contrast to a cross-sectional regression model in which the explained and explanatory variables are associated with one period or point in time.

Longitudal data analysis and treshold model in evaluating subsequent inseminations

In addition to evaluation of result of first insemination we can reflect longitudinal nature of this trait by considering all subsequent inseminations in threshold model using random regression to model the additive genetic values on liability scale.

Multiple-trait models

Multivariate multiple-trait models, involving the modeling of two or more types of traits simultaneously, are important, particularly in selection situations in which the data are not necessary missing at random (censoring). Multiple-trait mixed models have been used as a tool to correct the resulting selection bias on estimation and prediction through the use of traits that might be measured on all or most individuals.

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