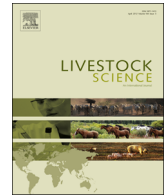




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# Avoiding double counting when deriving economic values through stochastic dairy herd simulation



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## ABSTRACT

It has been a challenge to avoid double counting when economic values (EV) of traits are derived for breeding goal traits when using stochastic herd simulation models. In this study multiple regression and model building with mediator variables representing other traits in the breeding goal were evaluated to avoid double counting. EV were derived from data simulated with the SimHerd dairy herd simulation model. Scenarios were simulated to represent dairy herds with low and high levels of metritis and cow mortality. The simulated data was analyzed statistically with the economic net return per cow-year as the dependent variable and either the incidences of metritis or the incidence of cow mortality as the independent variables. In the model with metritis we corrected for mediator variables representing the direct effects of metritis on milk yield, fertility and occurrence of other diseases. The EV was estimated as the marginal change in economic net return in response to a change in the trait of interest. To avoid the multiple regression models to correct the EV for structural herd effects (changes in distribution of parities and lactation stages) we used a single animal based indicator variable for each trait of interest, such as incidence rate of cow mortality 1–100 DIM in multiparous cows.

The EV value of improving the trait ‘incidence rate of metritis 1–100 DIM in multiparous cows’ by 0.01 was estimated to be €0.93. The importance of avoiding double counting was demonstrated as the EV of metritis was overestimated by 82% when no mediator variables were included in the multiple regression analysis. And by ignoring structural herd effects for the EV of metritis we demonstrated an underestimation in the order of 9%. Further pitfall of underestimation was demonstrated for EV of cow mortality.

The EV of improving the trait ‘incidence rate of cow mortality 1–100 DIM in multiparous cows’ by 0.01 was estimated to be €46.4. Correcting for the independent variation in mortality between simulation replicates within the individual scenarios was found to be important.

The results of this study suggests a new method for designing simulation experiments and analyzing simulated herd effects for estimation of EV of traits in a breeding goal. This deals with a number of previous and new concerns of how to correct for double counting and at the same time still include the structural herd effects.

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## 1. Introduction

The breeding goal defines which traits are to be improved, and how much weight is given to each trait (Groen et al., 1997). In dairy cattle breeding, the weighting factors are usually economic values (EV) that are retrieved from a model of a dairy herd

production system. To be applied in a breeding program, the EV and the breeding values for each trait are used to construct a total merit index as a function of breeding indexes and economic weights. The breeding indexes are the original breeding values multiplied by certain standardizing factors to provide breeding indexes all with the same variation. Accordingly, the EV are divided by these standardizing factors to provide the economic weights to be used in the total merit index. This way the EV are standardized taking into account the respective standard

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deviations.

The EV are marginal values, which means the EV of one unit improvement of the trait, while keeping the remaining traits constant. However, this is not straight-forward as relationships among traits exist as described by Kargo et al. (2014). To avoid double counting, the EV of a given trait should therefore not include its direct effects if those direct effects are included in the breeding goal as traits with EV of their own. For example, reduced milk production as a direct effect of metritis should not be included in the EV of metritis. Milk yield is a breeding goal trait of its own and therefore increased milk yield caused by reduced metritis should not be accounted for again. What to correct for when estimating an EV of a given trait, is therefore depending on which other traits are actually included in the breeding goal. The change in milk yield due to increased age of the herd, so-called structural effect, needs however always to be included (Wolfova and Wolf, 2013).

Relationships between longevity, functional traits and milk yield traits are especially difficult to handle because longevity is highly affected by improvements of these other traits. If improvement of a certain trait causes a decreased culling rate or enables another selection strategy of cows for culling, which are not traits in the total merit index, then this has a value to be accounted for by this trait. If structural effects are neglected in the derivation of EV of functional traits and milk yield, the EV of the functional traits and milk yield are underestimated, and the EV of longevity is overestimated when interpreting longevity as a residual longevity trait. Wolfova and Wolf (2013) suggest that relationships among traits should be taken into account when these relationships are structural such as those caused by changes in the age structure of the herd, but not when they are caused by genetic correlations between traits.

Often the structural effects as they exist in real dairy herds can be taken into account when EV are derived using mechanistic, dynamic and stochastic dairy herd models that simulate the production and state changes of the cows and the young stock. However, phenotypic correlations and thereby genetic correlations are also inherent in this type of model, where they typically are modeled as direct effects between traits. Therefore, when using herd simulation models it is problematic to keep all other traits constant when one trait (the trait of interest) is changed without violating the mechanistic and dynamic modeling of the structural effects as they exist in the model as in real herds. The direct effects of a certain trait on another trait, representing phenotypic (environmental and genetic) correlations, are providing indirect pathways from the trait of interest to the outcome (herd economics) in such a model. When estimating EV, according to Wolfova and Wolf (2013) these indirect pathways, also called mediating relationships, need to be adjusted for, while at the same time not adjusting for the structural effects. By doing this, double counting can be avoided in a proper way. A proposed method for correcting for these mediator effects in the simulated output, while keeping the structural effects in the simulation model, is to use multiple regressions including mediator variables (Fairchild and Mackinnon, 2009). To apply this method in this study we applied the existing SimHerd model, which is a dynamic, stochastic and mechanistic bio-economic simulation model with detailed representation of herd effects caused by between animal interactions and management decisions. The SimHerd model simulates the production and state changes of a dairy herd including young stock and has in previous studies been used to: (1) study various herd management tasks (Østergaard et al., 2003; Kristensen et al., 2008), (2) study the implication of genetic trend for the effect of reproduction management (Ettema et al., 2011), and (3) study the derivation of EV of production and functional traits (Nielsen et al., 2006).

Based on this background information, we want to demonstrate the merit in using multiple regression including mediator variables to avoid double counting and at the same time still include the structural herd effects when economic values are derived using stochastic herd simulation. This will be illustrated using metritis and cow mortality as two different model traits of interest to be included in a breeding goal and total merit index of dairy cows.

## 2. Materials and methods

### 2.1. General design of the study

The method developed in this study is exemplified on two traits: clinical metritis and cow mortality, but can be expanded to other traits. Metritis was chosen because it causes various effects on milk production, reproduction, culling risk and veterinary treatments in the affected cow. Cow mortality was chosen as its effect on the individual cow is very simple. For the two traits we simulated seven scenarios and analyzed these simulated data with various statistical models to demonstrate alternative methods to derive the EV.

A metritis case in this study was a clinical case of metritis that was treated with antibiotics. A cow mortality case in this study was a cow dying accidentally with no direct associations to other modeled health problems. A dead cow is attributed a cost for handling the dead body. Derivation the EV of these traits including their structural herd effects and correcting for double counting was done in two steps. First, we used the method of stochastic, dynamic and mechanistic herd simulation modeling to simulate different levels of the traits in a herd in order to estimate the joint contribution of structural effects and mediator variables. Secondly, we performed a statistical analysis to correct for double counting.

### 2.2. Model structure

In SimHerd, the state of an animal is defined by age, parity, lactation stage, actual milk yield, BW, culling status, reproductive status, SCC, disease status and a permanent component of milk yield potential. The permanent component of milk yield potential contains both genetic and environmental factors. The permanent component (the repeatability) accounted for 50% of the total variance (Kristensen et al., 2008), as a heritability of 0.35 was used and the permanent environment accounted for 15% of the total variance. Even though a heritability of 0.35 was assumed, this component of milk yield potential was not passed on from mother to daughter in the existing SimHerd, but only set in a way that resulted in a repeatability of 0.50. Repeatability was also represented indirectly in the model through events that is associated with the inherent milk yield capacity of the individual cow. This include higher disease in cows with higher milk yield within a herd as found by Ingvarsten et al. (2003). Finally, disease recurrence as found by Østergaard and Sørensen (1998), is also included in the simulation model as disease specific repeatability risks to represent permanent effect of environment.

The prediction of each state in the model is made week-by-week for each cow and heifer in the herd. The state of the individual animal is updated, and production and input consumption is calculated for each animal separately, and for the whole herd. Drawing random numbers from relevant probability distributions trigger individual and lactational (within individual) milk yield potential and discrete events, such as estrus, heat detection, conception, abortion, sex and viability of the calf, diseases, involuntary culling and death. The production and the development within the herd are, thus, determined indirectly by

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