

2. Inbreeding and relationships can be accounted for during simulation by including the Cholesky decomposition of the numerator relationship matrix in the calculation.

**Key Words:** Genetic Evaluation, Selection Index

**25 A bivariate quantitative genetic model for a linear Gaussian trait and a survival trait.** L. H. Damgaard\* and I. R. Korsgaard, *Research Centre Foulum, Dept. Genetics and Biotechnology, Bioinformatics and Statistical Genetics, Tjele, Denmark.*

A bivariate quantitative genetic model for a linear Gaussian and a survival trait genetically and environmentally correlated was derived and implemented. For the survival trait, we considered the Weibull log-normal animal frailty model. A Bayesian approach using Gibbs sampling was adopted. Model parameters were inferred from their marginal posterior distributions. The required fully conditional posterior distributions were derived and issues on implementation discussed. The two Weibull baseline parameters were updated jointly using a Metropolis-Hasting step. The remaining model parameters with non-normalized fully conditional distributions were updated univariately using adaptive rejection sampling. Simulation results showed that the estimated marginal posterior distributions covered well and placed high density to the true parameter values used in the simulation of data. All the true parameter values were within the 95% central posterior density regions defined by the 2.5% and 97.5% percentiles. In conclusion, the proposed method allows inferring additive genetic and environmental correlations between a linear Gaussian trait and a survival trait.

**Key Words:** Survival, Gaussian, Genetic Correlation

**26 Bivariate recursive and simultaneous models for milk yield and somatic cell scores.** G. de los Campos\*<sup>1</sup>, D. Gianola<sup>1</sup>, and B. Heringstad<sup>2</sup>, *<sup>1</sup>University of Wisconsin-Madison, Madison, <sup>2</sup>Norwegian University of Life Sciences, Aas, Norway.*

Diseases may affect production and vice versa. Standard linear model theory does not accommodate recursiveness or simultaneity of effects. Structural Equation Models (SEM), however, allow modeling such features. Using LISREL<sup>®</sup>, we compared four bivariate SEM for analysis of milk yield (MY) and somatic cell scores (SCS). Models were: MO (standard), M1 (SCS=>MY), M2 (SCS<=>MY), and M3 (SCS<=>MY); arrows indicate direction of effects. The data set had test-day MY and SCS, and clinical mastitis (CM) records of 33,453 first-lactation daughters of the 245 Norwegian Red (NRF) sires with a first progeny test in 1991 or 1992. First lactation was divided into five 60-day periods and a test-day was assigned to each period. Within-herd SCS and MY deviates were responses, and presence of CM within 15-days prior to test day, age at calving, and sire were 'exogenous' variables. The Bayesian Information Criterion (BIC) favored M1. SCS had a negative effect on MY both in M1 and M3 (in M1: -1.1 kg/day/SCS,  $p < .001$ ). The association between SCS and MY was mostly due to a negative effect of SCS on MY; 'dilution' effect (MY=>SCS) seems unlikely to exist. Using estimates from M1, an event of CM would be expected to increase SCC by 70,000 cells/ml in the following test day; through the recursive effect (SCS=>MY), MY would be reduced by 0.93 kg/day. Estimates may be biased downwards, because of false negative CM (cases outside of the 15-day period may affect SCS). For M1, phenotypic (additive genetic) variances of MY and SCS were 13.19 (1.74) and 1.19 (0.11) respectively. Phenotypic and genetic correlations between SCS and MY were -0.23 and 0.34 respectively. The phenotypic correlation was the most sensitive parameter to specification of recursive effects.

**Key Words:** Diseases and Production, Structural Equation Model, Simultaneity

**27 Standard errors of solutions in large scale mixed models, application to linear and curvilinear effects of inbreeding on production traits.** N. Gengler\*<sup>1,2</sup> and C. Croquet<sup>1,2</sup>, *<sup>1</sup>National Fund for Scientific Research, Brussels, Belgium, <sup>2</sup>Gembloux Agriculture University, Gembloux, Belgium.*

Many approaches for using linear mixed models do not produce standard errors of solutions. However, knowing the standard errors allows for statistical tests. Even if exact estimation of standard errors is not feasible in large mixed models, there are methods to approximate them. We based this on Mixed Model Conjugate Normal Equations associated with a Preconditioned Conjugate Gradient (PCG) solver. The advantage of associating both methods is that the right hand side vector normally accumulated by PCG can be easily changed to a function of solutions vector  $\mathbf{k}$  allowing direct solution for  $\Phi = \mathbf{C}^{-1}\mathbf{k}$  using regular PCG solving programs. The square root of  $\mathbf{k}'\Phi = \mathbf{k}'\mathbf{C}^{-1}\mathbf{k}$  gives the standard error associated with the function of solutions described by  $\mathbf{k}$ . Often a block of  $\mathbf{C}^{-1}$  is needed. Its elements were obtained by computing linear functions of element of this block and by back-solving to obtain the needed elements. In matrix notation let  $\mathbf{K}$  be the coefficients of the linear functions and  $\mathbf{D}$  a matrix containing the values obtained by computing  $\mathbf{K}'\mathbf{C}^{-1}\mathbf{K}$ . The elements of the block were then obtained as  $(\mathbf{K}\mathbf{K}')^{-1}\mathbf{K}\mathbf{D}\mathbf{K}'(\mathbf{K}\mathbf{K}')^{-1}$ . This method was applied to study linearity of inbreeding depression on milk, fat and protein test-day yields. Inbreeding effects were estimated using linear, quadratic and cubic regressions on inbreeding coefficients inside breeds in a test-day model similar to the one used in the Walloon Region of Belgium. The pedigree contained 956,516 animals. A total of 5,596,038 first lactations test-day records from 660,407 cows were used. Results had contrasting behaviors, however evaluation of plotted inbreeding effect and the associated confidence interval showed that between 0 and 10% inbreeding differences among evaluations of inbreeding depression were small.

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**Key Words:** Standard Error, Inbreeding, Curvilinear

**28 Predictions of test day yields for milk production traits in cattle by partial least squares multiple regression.** N. P. P. Macciotta\*<sup>1</sup>, D. Vicario<sup>2</sup>, C. Dimauro<sup>1</sup>, N. Bacciu<sup>1</sup>, and A. Cappio-Borlino<sup>1</sup>, *<sup>1</sup>Università di Sassari, Sassari, Italia, <sup>2</sup>Italian Association of Simmental Cow breeders, Udine, Italia.*

The research of methods able to predict Test Day (TD) yields from a limited number of actual records available is an important challenge for the dairy cattle industry. Most of proposed methods deal with a univariate approach and can forecast only future TD in lactation in progress. On the other hand, multivariate approaches are theoretically and computationally heavy. The Partial Least Squares Regression (PLS) multivariate approach can represent a valid alternative, being able to handle plans characterised by the presence of missing data in different parts of the lactation. Moreover, the extraction of orthogonal latent factors enable the PLS to reduce problems of the collinearity among predictors and, at the same time, to exploit correlations between dependent and independent variables. The PLS prediction ability was tested on a data set of 31,356 lactations of Italian Simmental Cows of parity 1 to 3, with 8 test day records of milk production traits (milk, fat and protein yields) per lactation, arranged in a multivariate setting. Ten scenarios of missing TD records were simulated. Predictions were calculated separately for each parity class. Correlations among actual and predicted TD yields evaluated by cross validation methodology ranged from 0.60 to 0.90 for protein and from 0.55 to 0.80 for fat in the scenarios where also milk yield has to be predicted. Correlations increased up to 0.97 for protein and 0.88 for fat when all milk TD were available. Average correlations between actual and predicted TD for milk yield was 0.87. The analysis of Mean Square Error of Prediction confirm the higher accuracy of the PLS method and highlights a certain degree of imprecision mainly due to the random nature of individual variation. Results of the study indicate a good predictive ability of the PLS method that, in addition, is markedly flexible, does not require special computing capability and is easily transferable to the farm level.

**Key Words:** PLS, Prediction, Milk Test Day