



## Linear–threshold animal model for birth weight, gestation length and calving ease in United Kingdom Limousin beef cattle data

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### ABSTRACT

Breeding value evaluation for UK Limousin beef cattle data was carried out by multiple-trait linear–threshold animal model with variance components assumed to be known. Polychotomous calving ease with five categories was analysed with two continuous traits: birth weight and gestation length. Field data consisted of 220,799 animals with observations with every possible combination of traits, and 270,035 animals in the pedigree. The threshold model was solved either with Newton Raphson or Expectation Maximisation algorithm, and solutions were compared to evaluation by a linear model with original and normalised scores. There were insignificant differences in solutions between the two algorithms for threshold model analyses. Furthermore, solutions of the continuous traits were similar by the threshold and linear models. For the categorical trait, correlations for random effects from the threshold and linear models were high. In case of normalised scores (original scores case in brackets) correlations with solutions from the threshold and linear model were 0.97 (0.94) and 0.97 (0.93) for direct and maternal genetic effects and 0.95 (0.89) for permanent maternal effects. Even so, at least one third of the top 1% ranking of bulls differed between the linear and the threshold models. Predictive abilities as correlations between estimated breeding values and pedigree indices were almost equal between the linear and threshold models for both continuous and categorical traits. In conclusion, despite the higher computational demand, the linear–threshold animal model can be seen worthwhile in the genetic evaluation of the national UK beef cattle data set.

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### 1. Introduction

Current national evaluation of UK beef cattle consists of a multiple-trait linear model for eight traits. One of the traits is polychotomous calving ease that at present is evaluated as a linear trait, although the trait is strictly a categorical trait and a threshold model could be more appropriate. For single-trait models, Meijering and Gianola (1985) concluded that thresh-

old analysis was superior for binary traits with small frequencies and at least moderate heritability, while for polychotomous traits differences between the linear and threshold models were negligible. For UK beef cattle evaluation, advantages of the threshold model are unknown. Change of fully linear model to linear–threshold model can be studied for polychotomous calving ease and a subset of most important linear traits.

Many studies comparing multiple-trait linear and linear–threshold models have been published (for calving ease e.g. Varona et al. (1999), Ramirez-Valverde et al. (2001), Lee et al. (2002), and for clinical mastitis e.g. Vuori et al. (2007) and Negussie et al. (in press)). According to these studies, threshold models were slightly better than linear models when

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**Table 1**

Number of observations (N), mean value, standard deviation (SD), minimum value (Min) and maximum value (Max) of the traits birth weight (BW), gestation length (GL) and calving ease (CE).

Trait	N	Mean	SD	Min	Max
BW	178700	37.29	4.6	8.2	82.4
GL	69626	291.14	5.9	249.2	323.1
CE	85881	1.20	0.5	1	5

analysing categorical data. Advantages of the threshold model were clearer in bivariate models than in univariate models (for calving ease and birth weight e.g. Varona et al. (1999) and Ramirez-Valverde et al. (2001), for clinical mastitis and somatic cell score Negussie et al., (in press), and for ewe reproductive traits litter size and days to lambing Casellas et al. (2007)). According to a simulation study by Janss and Foulley (1993), a bivariate model improves the accuracy of evaluation for both continuous and categorical traits. Further, accuracies were higher when all information available was used, compared to discarding those discrete observations for which correlated continuous observation was missing.

Different techniques applied for evaluation of categorical data have been presented. Zhao (1987) used Expectation Maximisation (EM) algorithm when maximizing likelihood. Gianola and Foulley (1983), Janss and Foulley (1993) and Hoeschele et al. (1995) calculated Maximum a Posterior estimates with the Newton Raphson (NR) algorithm. Full Bayesian approach using Markov chain Monte Carlo (MCMC) has been tested by e.g. Wang et al. (1997) and Van Tassel et al. (1998). Two major disadvantages of the threshold models are computational demand and poor robustness (Meijering and Gianola, 1985). For example, MCMC is easy to implement even for advanced models, but impractical for large scale estimation due to large number of samples required for adequate convergence (Wang et al., 1997, Lee et al., 2002). In national evaluations, estimates from the full Bayesian inference for location and dispersion parameters can be used as starting values for numerically less demanding methods (Wang et al., 1997).

Large scale implementations are commonly based on iteration on data (IOD), which implies that coefficients of the mixed model equations (MME) are recreated on each iteration round. This in principal makes the NR algorithm more competitive compared to the EM algorithm, where the coefficients of the iteration equations remain unchanged. The most efficient solving method with IOD is preconditioned conjugate gradient (PCG) (Strandén and Lidauer, 1999). However, it is unknown how suitable PCG is for iterative threshold model analyses. Although the EM algorithm tends to be slower than the NR algorithm, difference in convergence may diminish in analysis of large field data set (Wang et al., 1997). Also, the EM algorithm is expected to be more stable than the NR algorithm.

The aim of this study was to verify the feasibility of an animal threshold model with correlated continuous traits applied to the large UK beef cattle data in evaluation of calving ease, birth weight and gestation length. Breeding value estimation for categorical trait was implemented into MiX99 (Strandén and Lidauer, 1999, Vuori et al., 2006), an IOD and PCG program, which is extensively used for solving linear mixed effects models. Both NR and EM algorithms were implemented. The changes in breeding values and efficiency of these two

methods were compared with evaluations by a linear model with original and normalised scores.

## 2. Material and methods

### 2.1. Data and model

Limousin beef cattle data from the UK national evaluations was used. There were 220,799 animals with observations. All records having at least one of the traits birth weight (BW), gestation length (GL) or calving ease (CE) were included in the data. Calving ease was recorded by five categories from 1 to 5 (1 for no assistance needed to 5 for most difficult calving). In the linear model evaluations, original or normalised categories were used. Normalised categories were scored to  $-0.2, 1.4, 1.8, 2.1$  and  $2.6$  according to their frequencies in the data 83.3%, 14.5%, 1.1%, 0.7% and 0.4%, respectively. Statistics of the traits are listed in Table 1. Traits were observed with every possible combination, and e.g. 29% of calving ease records had no correlated continuous traits observed. Numbers of animals with one trait or two traits recorded are in Table 2. For 15,446 animals, all three birth records were observed. The pedigree consisted of 270,035 animals.

The multiple-trait animal model was

$$y = X\beta + Z_1p + Z_2a + Z_3m + e,$$

where  $y$  contained BW, GL and CE records in the linear model or liability of CE in the threshold model. Fixed effects  $\beta$  included birth month, pregnancy type, birth type, breed of dam, percent of primary breed, and contemporary group as herd-birth year separately for all three traits. Furthermore, for continuous traits BW and GL,  $\beta$  included fixed effects of sex and fixed second order regression of dam age, while for CE, parity of dam within sex of calf was fitted. Although none of the fixed effects included an extreme category problem (Miszta et al., 1989), contemporary group of CE had 10% of classes with only two observations.

Random effects in the model were maternal permanent environment  $p$ , direct genetic  $a$ , maternal genetic  $m$  and residual  $e$ . The random effects were assumed to be Normally distributed:  $p \sim N(0, \mathbf{P}_0 \otimes \mathbf{I})$ ,  $(a, m) \sim N(0, \mathbf{G}_0 \otimes \mathbf{A})$  and  $e \sim N(0, \mathbf{R}_0 \otimes \mathbf{I})$ , where  $\mathbf{P}_0$ ,  $\mathbf{G}_0$  and  $\mathbf{R}_0$  are variance–covariance matrices for random effects,  $\mathbf{I}$  is an identity matrix and  $\mathbf{A}$  is the numerator relationship matrix. The design matrices  $\mathbf{X}$ ,  $\mathbf{Z}_1$ ,  $\mathbf{Z}_2$  and  $\mathbf{Z}_3$  were for fixed, random maternal permanent environment, direct genetic and maternal genetic effects, respectively.

The same underlying linear model was used when calving ease was considered either linear or a categorical trait. However, variance and covariance components with calving ease were different. Covariance components used in the UK national

**Table 2**

Number of animals with one trait (birth weight (BW), gestation length (GL) or calving ease (CE)) recorded (in the diagonal), and number of animals with two traits recorded by each trait combination (below the diagonal).

	BW	GL	CE
BW	86546		
GL	37181	11191	
CE	39536	5808	25091

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