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Livestock Science

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Short communication

Censored Bayesian models for genetic evaluation of age at first calving in Brazilian Brahman cattle

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ARTICLE INFO

Keywords:

Penalty method

Data augmentation

Threshold-liner model

ABSTRACT

We compared different Bayesian models to handle censored data for genetic parameters estimation of age at first calving (AFC) in Brazilian Brahman cattle. Data from females with AFC above 1825 days of age were assumed to have failed to calve and were considered as censored records. Data including information of 53,703 cows were analyzed through the following methods: conventional linear model method (LM), which consider only uncensored records; simulation method (SM), in which the data were augmented by drawing random samples from positive truncated normal distributions; penalty method (PM), in which a constant of 21 days was added to censored records; and the bivariate threshold-linear method (TLcens). The LM was the most suited for genetic evaluation of AFC in Brazilian Brahman cattle based on the predictive ability evaluation through cross-validation analysis. The similar results for LM and PM regarding Spearman correlations, and the higher percentages of selected animals in common, indicated that there was not relevant reranking of animals when censored records were used. In summary, the heritability estimates for AFC ranged from 0.09 (TLcens) to 0.20 (LM). Given its poor predictive performance, the SM is not recommended for handling censored records for genetic evaluation of AFC.

1. Introduction

One of the most relevant selection criteria for genetic improvement of female reproductive efficiency in beef cattle is the age at first calving (AFC). Despite easiness of AFC data recording, it might assume missing values due to non-occurrence and/or delay in the recording of calving information. Thus, this trait is widely referred as censored (Tarrés et al., 2006).

The simplest option to handle with this problem is omitting these observations (assuming as missing values). According to Guo et al. (2001) and Dias et al. (2004), this approach would lead to loss of information for genetic evaluation, and may affect the real variability of the trait by masking the true genetic differences between animals.

Another option is using suitable statistical methods to treat censored records in genetic evaluations. Different methods have been proposed. One approach is based on simulation of censored records from positive

truncated normal distributions taking into account the estimated effects (Donoghue et al., 2004a; Korsgaard et al., 2003). Another one is the penalty method (Johnston and Bunter, 1996), which consists in records imputation by adding a constant (number of days) to real data. For AFC, 21 days are often included as a constant based on the assumption that the heifer should be fertile in the subsequent estrous cycle. The bivariate linear-threshold approach considers the censoring status (threshold binary trait) as an additional trait aiming to improve the selection accuracy of the censored continuous traits. In this last method, it is assumed that the correlation between fertility traits (e.g., AFC) and the censoring status improves the prediction accuracy (Urioste et al., 2007a).

Studies on censored AFC data in Brahman cattle are scarce, and the comparisons involving the mentioned methods have been not exploited in literature. In this context, we aimed to compare these different methods by accessing predictive performance via cross-validation under a Bayesian framework; as well as to estimate genetic parameters

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<https://doi.org/10.1016/j.livsci.2018.11.014>

Received 23 February 2018; Received in revised form 7 November 2018; Accepted 26 November 2018

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for AFC in Brazilian Brahman cattle.

2. Materials and methods

Brahman fertility data were provided by Brazilian Association of Zebu Cattle Breeders (ABCZ). Age at first calving (AFC) was defined as the time interval (in days) between birth and first calving. The AFC records were obtained during the period of 1960 and 2014. Before data editing, there were 59,929 trait records available in the database.

The contemporary groups (CG) consisted of the combination of herd, year and birth season. Data editing was performed by removing: 1) animals with incomplete records (missing observations); 2) CG with less than seven records; 3) animals belonging to CG consisting of only non-calving heifers; 4) outliers based on three standard deviation within CG. After editing the data, there were 50,630 uncensored and 3,073 censored records available. Thus, a total of 53,703 AFC records were used in the analysis, with mean of $1,221.70 \pm 267.54$ days, ranging from 731 and 1825 days. Cows with AFC longer than 1825 days were excluded since heifers that did not become pregnant after the breeding season were excluded too. Thus, this practice was adopted to prevent possible recording errors. The pedigree file included a total of 64,322 animals.

AFC data were analyzed using four different Bayesian methods to deal with censored phenotypic records.

The linear method (LM) was used to evaluate the scenario when censored records were not used. For this, the following standard animal model was fitted:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{W}\mathbf{c} + \mathbf{Z}\mathbf{a} + \mathbf{e}, \quad (1)$$

where: \mathbf{y} is the vector of AFC records; $\boldsymbol{\beta}$ is the vector of systematic effects (mean, registration class - pure by origin or in open book, and mating type - artificial insemination, embryo transfer, fertilization *in vitro* and natural mating); \mathbf{c} is the vector of CG (herd-year-season) effects; \mathbf{a} is the vector of additive genetic effects; \mathbf{e} is the vector of residual effects; and \mathbf{X} , \mathbf{W} and \mathbf{Z} are the incidence matrices associated with $\boldsymbol{\beta}$, \mathbf{c} and \mathbf{a} , respectively. It was assumed that: $\boldsymbol{\beta} \sim N(\mathbf{0}, \mathbf{I}\sigma_{\beta}^2)$, being σ_{β}^2 a known variance with value $1e + 10$ (large variance) to represent non-informative (vague) prior; $\mathbf{c} \sim N(\mathbf{0}, \mathbf{I}\sigma_c^2)$, $\mathbf{a} \sim N(\mathbf{0}, \mathbf{A}\sigma_a^2)$ and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$, being σ_c^2 the CG variance, σ_a^2 the additive genetic variance and σ_e^2 the residual variance; \mathbf{A} and \mathbf{I} are, respectively, the numerator relationship and the identity matrices.

The simulation method (SM) is based on the same model presented in Eq. [1]; however, a dataset including censored and uncensored data was used. The censored record was obtained through simulation. Thus, $\mathbf{y}' = [\mathbf{y}_{ur}, \mathbf{y}_{cr}]'$ is a vector in which \mathbf{y}_{ur} is the vector of uncensored records of AFC, and \mathbf{y}_{cr} is the vector of simulated values for censored records. Using Gibbs sampling approach (Sorensen et al., 1998; Guo et al., 2001), \mathbf{y}_{cr} values were sampled from their respective posterior predictive distribution. This distribution is the truncated Gaussian with lower limit defined by the maximum values of AFC within the corresponding CG. The predicted age at first calving for a censored record was between the truncation point and positive infinity. Thus, an animal with a censored record could not receive a simulated record that was smaller than a uncensored record within its contemporary group, and under this framework, the \mathbf{y}_{cr} values were updated within each Gibbs sampler iteration (Donoghue et al., 2004a; Korsgaard et al., 2003) until convergence was achieved.

The penalty method (PM) assigns penalties to each censored record within contemporary group. It is similar to SM, however the censored records were replaced by a set of augmented data, which is obtained by adding a constant of 21 days over the highest AFC value within each CG to provide imputed values for all censored records. The penalty suggests that the heifers failing to calve would conceive if they have another opportunity, as an extra estrous cycle (Donoghue et al., 2004b; Hou et al., 2009; Malhado et al., 2013).

The threshold-linear censored (TLcens) method is based on the bivariate model where one trait is continuous (AFC values) and the other one is a threshold binary trait (censored status). The binary records were associated to liability values which is given by a latent continuous variable (Sorensen and Gianola, 2002). At each MCMC (Markov Chain Monte Carlo) iteration, the binary records generate a liability value below or over a given threshold. This model considers $\mathbf{y}' = [\mathbf{y}_{ur}, \mathbf{y}_{cr}]'$, where \mathbf{y}_{cr} are the censored records added to a constant of 21 days over highest AFC value within each contemporary group. This model is given by:

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{l} \end{bmatrix} = \begin{bmatrix} \mathbf{X}_y \mathbf{0} \\ \mathbf{0X}_l \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}_y \\ \boldsymbol{\beta}_l \end{bmatrix} + \begin{bmatrix} \mathbf{W}_y \mathbf{0} \\ \mathbf{0W}_l \end{bmatrix} \begin{bmatrix} \mathbf{c}_y \\ \mathbf{c}_l \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_y \mathbf{0} \\ \mathbf{0Z}_l \end{bmatrix} \begin{bmatrix} \mathbf{a}_y \\ \mathbf{a}_l \end{bmatrix} + \begin{bmatrix} \mathbf{e}_y \\ \mathbf{e}_l \end{bmatrix}, \quad (2)$$

where: \mathbf{y} is the vector of AFC records; \mathbf{l} is the vector of liability generated from censored status; \mathbf{X} , $\boldsymbol{\beta}$, \mathbf{W} , \mathbf{Z} , \mathbf{c} , \mathbf{a} and \mathbf{e} are the same of model (1). The following prior distributions were assumed:

$$\begin{bmatrix} \boldsymbol{\beta}_y \\ \boldsymbol{\beta}_l \end{bmatrix} \sim N(\mathbf{0}, \Sigma_{\beta} \otimes \mathbf{I}), \quad \begin{bmatrix} \mathbf{c}_y \\ \mathbf{c}_l \end{bmatrix} \sim N(\mathbf{0}, \mathbf{C}_0 \otimes \mathbf{I}), \quad \begin{bmatrix} \mathbf{a}_y \\ \mathbf{a}_l \end{bmatrix} \sim N(\mathbf{0}, \mathbf{G}_0 \otimes \mathbf{A}),$$

$$\text{and } \begin{bmatrix} \mathbf{e}_y \\ \mathbf{e}_l \end{bmatrix} \sim N(\mathbf{0}, \mathbf{R}_0 \otimes \mathbf{I}),$$

where: \mathbf{C}_0 , \mathbf{G}_0 and \mathbf{R}_0 are the CG, additive genetic and residual (co) variance matrices, respectively; and Σ_{β} is a diagonal known matrix with values $1e + 10$ (large variances) to represent non-informative (vague) prior for systematic effects.

Inferences about all unknown parameters were done from the marginal posterior distributions through Gibbs sampling using the TM software (Legarra et al., 2008). More specifically, a unique MCMC process with 400,000 iterations was launched for each analysis, and the first 100,000 iterations were discarded as burn-in, keeping every 10th sample for inference of posterior features. The convergence of the MCMC chains was verified by graphical inspection and by Geweke (1992) criteria using the R package *boa* (Bayesian Output Analysis, Smith, 2007).

The predictive ability was accessed by cross-validation. The training dataset was composed by all censored records, and 70% of the uncensored records were randomly obtained within each CG. The validation dataset was defined by the remaining individuals. These two subsets (training and validation) were redefined 10 times, generating different datasets. The average of the correlation coefficients (considering the total of 10 replicates) between the predicted and observed phenotypes were calculated to measure the predictive ability of each method. The predicted phenotypes vector was calculated as $\hat{\mathbf{y}} = \mathbf{X}\hat{\boldsymbol{\beta}} + \mathbf{W}\hat{\mathbf{c}} + \mathbf{Z}\hat{\mathbf{a}}$. Thus, the solutions for the animals in the validation population were obtained based on the solutions of the training population. The mean square errors were also calculated and used in the methods comparison.

The breeding value accuracy for each animal i (r_i) was calculated as showed in Eq. [3]:

$$r_i = \sqrt{1 - \frac{(SD_i)^2}{\hat{\sigma}_a^2}}, \quad (3)$$

where: SD_i is the posterior standard deviation of the breeding value of animal i , and $\hat{\sigma}_a^2$ is the estimated (posterior mean) additive genetic variance.

Spearman's correlation coefficients between predicted breeding values obtained from different methods were computed to infer differences in the ranking of the animals. In addition, the percentage of selected animals in common at different percentiles (TOP1% and TOP10%) were also used to evaluate similarities between methods.

Table 1

Average mean square error (MSE) and correlations between observed and predicted phenotypes from 10 fold cross-validation with respective standard deviation.

Method ¹	MSE	Correlation
LM	52,541.85 (643.26)	0.30 (0.006)
SM	81,104.72 (8,137.71)	0.19 (0.078)
PM	55,267.17 (1,320.13)	0.25 (0.008)
TLcens	56,660.74 (541.39)	0.22 (0.005)

¹ LM, SM, PM, TLcens: linear, simulation, penalty and threshold-linear censored methods, respectively.

Table 2

Spearman correlation between all animals (above diagonal), average accuracy of predicted breeding values for age at first calving (below diagonal); and percentage of animals in common between methods at 1% (above diagonal) and 10% (below diagonal) of selected individuals.

Method ¹	LM	SM	PM	TLcens
Spearman correlations and accuracy				
LM	-	0.82	0.97	0.95
SM	0.95	-	0.88	0.83
PM	0.98	0.96	-	0.95
TLcens	0.87	0.88	0.89	-
Percentage of animals in common				
LM	-	46.96	82.96	55.65
SM	61.23	-	52.17	32.70
PM	89.12	66.48	-	51.48
TLcens	81.70	59.48	78.33	-

¹ LM, SM, PM, TLcens: linear, simulation, penalty, threshold-linear censored methods, respectively.

3. Results and discussion

The predictive ability was performed through correlation coefficients between observed and predicted phenotypes through cross-validation analysis and mean square errors (Table 1). Higher correlation and lower MSE were found for LM, indicating that this method is recommended for AFC genetic evaluation with censored records in Brazilian Brahman cattle. Urioste et al. (2007a) using predictive ability on fertility traits (days to calving and calving success) of Uruguayan Aberdeen Angus cattle found similar correlations between training and validation dataset for PM and SM, and for PM and TLcens. However, Urioste et al. (2007b) commented that the main disadvantage of TLcens is the difficulty of implementation for large data sets in comparison to LM.

Spearman correlation coefficients, average accuracy of breeding values and percentage of selected animals in common are shown in Table 2. Concordance between the selected top 1% animals ranged from 32.70% (SM and TLcens) to 82.96% (LM and PM). For the top 10% of animals, these percentages were slightly higher than for top 1%,

Table 3

Posterior means, standard deviation and highest posterior density region (95%) for heritability and variance components for age at first calving in Brahman cattle provided by different censored Bayesian models.

Method ¹	h^2	σ_a^2	σ_c^2	σ_e^2
LM	0.20 (0.01) [0.18; 0.21]	11,887.01 (598.41) [10,765.13; 13,070.92]	5,780.80 (766.84) [4,331.42; 7,309.51]	43,205.65 (516.72) [42,198.82; 44,205.45]
SM	0.19 (0.01) [0.17; 0.21]	31,481.96 (1,378.36) [28,748.36; 34,210.96]	54,378.23 (6,188.77) [42,632.60; 66,547.76]	80,271.21 (1,110.02) [78,032.36; 82,409.43]
PM	0.18 (0.01) [0.16; 0.20]	14,354.36 (712.52) [13,014.01; 15,783.45]	17,560.54 (2,063.04) [13,715.58; 21,650.96]	46,658.04 (598.47) [45,494.81; 47,833.18]
TLcens	0.09 (0.006) [0.08; 0.10]	8,221.12 (518.38) [7,281.80; 9,261.24]	20,960.41 (2,476.74) [16,191.94; 25,910.80]	64,038.80 (503.09) [63,064.86; 64,972.09]

h^2 : heritability; σ_a^2 , σ_c^2 and σ_e^2 : additive genetic, contemporary group and residual variances, respectively; ¹LM, SM, PM, TLcens: linear, simulation, penalty, threshold-linear censored methods, respectively.

ranging from 59.48% (SM and TLcens) to 89.12% (LM and PM). Similarly to the results reported by Donoghue et al. (2004a), we observed that accuracies (Table 2) based on the uncensored data were slightly higher than the censored data. The Spearman correlation between LM and SM was lower than other methods (0.82) because the SM presented higher variation due to the generation data process whereas the LM is most consistent since only uncensored observation have been considered for the analysis. This result is similar to Donoghue et al. (2004b) that studied days to calving in Australian Angus cattle (0.81). The percentages of selected animals in common (Table 2) were higher between LM and PM, indicating no relevant reranking of animals when censored records are used. These percentages were smaller when TOP1% of the animals was considered. Similarly to the present study, Garcia et al. (2016) studying Nelore cattle found higher coincidence in sire ranking using linear models.

The inclusion of heifers that did not calve in the analysis of the data did not change the correlations between the studied methods (Tables 1 and 2). Thus, if removing the heifers that did not conceive after the breeding season from the analysis, there are no effective changes in the genetic evaluation.

Posterior means with respective standard deviation and HPD95% region for variance components and heritability from different methods are presented in Table 3. Since LM presented the best predictive ability, it was considered as reference in the latter comparisons. LM and PM resulted in similar additive genetic and residual variance estimates (Table 3), indicating some correspondence between these methods. When using either LM or PM to handle censored AFC records, a small impact on variance components estimation would be expected. Similarly, Forni and Albuquerque (2003) reported that imputation of censored data did not improve the identification of genetic differences between animals. These highest variance components values reported for the SM (Table 3) suggests that the simulated records for all censored records can result in overestimation of all variance components. The estimates from TLcens method presented the lowest additive variance estimated. Differently from our study, Urioste et al. (2007b) found similar additive genetic and residual variance estimates for SM and PM considering days to calving in Angus cattle. Probably, the correlation generated by the multi-trait analysis (three calving intervals) performed by these authors might have affected the variance components estimates. Since the SM method was based on simulated random numbers, it might insert some source of variation in the data as previously mentioned.

The heritability estimates ranged from 0.09 (TLcens) to 0.20 (LM). The LM, SM and PM provided similar estimates, which were higher than TLcens (Table 3). All methods showed moderate heritabilities (Table 3) for AFC (0.18 to 0.20); with the exception of the TLcens (0.09). In general, heritability estimates for AFC reported in the literature oscillated such as in the present study, ranging from 0.10 to 0.37 in Brazilian Zebu cattle (Boligon and Albuquerque, 2011; Barrozo et al., 2012; Moreira et al., 2015; Oliveira et al., 2017). Variation in

heritability estimates from literature may reflect differences in populations, trait definition and data structure (Oliveira et al., 2017).

Donoghue et al. (2004a) and Donoghue et al. (2004b) using simulated and real data of days to calving, reported heritability estimates similar to our study when using penalty (PM) and simulation (SM) methods. On the other hand, the heritability estimates for TLcens diverged from some authors (Johnston and Bunter, 1996; Morris et al., 2000; Phocas and Sapa, 2004) that reported high heritability estimates using TLcens when compared to the present study.

4. Conclusion

The LM using only uncensored data was the most indicated for genetic evaluation of AFC in Brazilian Brahman cattle based on predictive ability via cross-validation analysis.

The similar results of LM and PM regarding Spearman correlations and the higher percentages of selected animals in common, indicated that there was not relevant reranking of animals when censored records were used. Therefore, the LM model could be recommended to perform genetic evaluation of age at first calving in this Brahman population.

Conflict of interest

This paper does not cause any conflict of interest including financial, personal or other relationships with other people or organizations.

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