Number of Inseminations to Conception in Holstein Cows Using Censored Records and Time-Dependent Covariates

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ABSTRACT

Three methodologies that accommodate censoring or time-dependent covariates were used to estimate variance components for number of inseminations to conception. Data included 80,071 lactation records and 143,927 artificial inseminations in 47,509 Spanish Holstein cows. Up to 4 inseminations to conception, along with their respective censoring information, were analyzed. An ordinal-censored threshold model (CTM), a sequential threshold model (STM), and a grouped survival analysis via a discrete proportional hazards model (DPH) were implemented. Sire variance estimates on the liability scale were 0.016 and 0.010 for CTM and STM, respectively, and 0.012 for DPH on the logarithmic scale. Heritability estimates on the liability scale were 0.050 and 0.038 with CTM and STM, respectively. All models led to similar rankings of sires, and the strong correlations (0.97 to 0.98) between methodologies suggested robustness in ranking of sires of cows. Service sire variance estimates were 0.021 for both CTM and STM; DPH led to an approximate service sire variance of 0.020. Rankings for service sires between methodologies ranged from 0.76 to 0.90. These lower values are most likely due to differences in the treatment of time-dependent covariates.

The STM had greater predictive ability of daughter fertility at first insemination than the other methodologies. However, the CTM predicted daughter fertility more accurately in subsequent inseminations. The DPH and STM had a similar predictive ability of daughter fertility in second and subsequent inseminations. (**Key words:** fertility, ordinal-censored threshold model, sequential threshold model, survival analysis)

Abbreviation key: CTM = ordinal-censored threshold model, DPH = discrete proportional hazard model, INS = inseminations per conception, STM = sequential threshold model.

INTRODUCTION

Fertility traits have been incorporated into national genetic evaluation systems of many leading dairy countries recently. Interval traits, such as days to first insemination, calving interval, or days open are most commonly used. However, the variation of these traits is highly dependent on management practices, such as estrus synchronization and differences in the voluntary waiting period (Wall et al., 2003). The number of inseminations to conception (INS) probably reflects actual variation of female fertility more closely, and it is one of the most important fertility traits from an economic point of view (González-Recio et al., 2004). The costs of semen, hormonal treatments, labor, and delayed subsequent calving increase rapidly as more inseminations are required for a cow to become pregnant. In addition, INS can reflect variation in both male and female fertility. An additional concern in the analysis of fertility is proper handling of cows that never become pregnant (i.e., censoring mechanisms). Furthermore, certain farmers may allocate cows to a natural service bull after several failed artificial inseminations and this leads to errors in services to conception data if such practice is not recorded. High quality reproductive data are needed to study this trait, but there are herds with missing or incomplete records in most dairy populations. Increasing the reliability of pregnancy check records could improve the quality of data from reproductive schemes. Therefore, it is necessary to develop suitable methods for analyzing INS data, to obtain accurate estimated breeding values and parameter estimates when using INS in a national genetic improvement program.

Three methods were developed and applied to field data on INS in Holstein cattle. First, an ordinal threshold model (Gianola, 1982; Gianola and Foulley, 1983) that accommodates censored records was implemented (CTM). Second, a sequential threshold model (STM), as described by Albert and Chib (2001), which can analyze categorical traits that occur in a sequential order, was applied. Third, a grouped survival model for discrete proportional hazard analysis (DPH), as developed by Prentice and Gloeckler (1978), was fitted. The STM

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and DPH models allow for time-dependent covariates, whereas CTM does not.

The objective of this research was to infer parameters of INS data with the aforementioned CTM, STM, and DPH models, and to assess their relative predictive abilities.

MATERIALS AND METHODS

Data

Data were provided by the regional Holstein Associations from the Basque and Navarra Autonomous Regions of Spain. Milk yield and reproductive data from 1994 through 2004 were used in the analysis. Records from embryo transfers were omitted, and cows needed to have a minimum of 100 DIM before culling and at least 1000 kg of total lactation milk yield to be included in the analysis. In addition, calving interval had to range between 300 and 600 d, and records were omitted if days to first service were unknown, less than 25 d, or greater than 160 d. Cows with a first calving before 18 mo or after 40 mo of age were excluded. At least 5 uncensored records were required per herd and per service sire, and herds with an average INS less than 1.5 were removed. A record was considered censored at a particular service if no subsequent calving was recorded, if the next breeding event was a natural service mating, or if no pregnancy was achieved after the fourth insemination. Four values (1, 2, 3, or 4) were possible for INS, and an indicator variable tagged each cow as being either pregnant or censored. Hence, cows with a censored record after 4 inseminations were included into a fifth category that represented more than 4 inseminations. The edited data set contained 80,071 lactation records and 143,927 insemination events from 47,509 cows. A total of 3267 bulls were present in the pedigree file.

Ordinal-Censored Threshold Model

The ordinal threshold model (Gianola, 1982; Gianola and Foulley, 1983) was extended to accommodate censored records. The ordinal-censored threshold model (CTM) postulates an underlying latent liability (λ) for number of inseminations to conception.

The statistical model for liability was:

$$\lambda_{jklmno} = \mathbf{x}'\beta_{jklmno} + \mathbf{h}_m + \mathbf{ss}_n + \mathbf{u}_o + \mathbf{e}_{jklmno}$$

The systematic effects ($\mathbf{x}'\beta$) in the model were as follows: days to first service treated as a covariate; effect of number of lactation ($j = 1$ to 4 levels); effect of calendar month of calving ($k = 1$ to 12 levels), and effect of year-season of calving ($l = 1$ to 30 levels). The random effects

were: $\mathbf{h}_m$ = herd ($m = 1$ to 767 levels) distributed independently as $N(0, \mathbf{I}\sigma_h^2)$, where σ_h^2 is the variance among herds; $\mathbf{ss}_n$ = service sire for first insemination ($n = 1$ to 577 levels) distributed as $N(0, \mathbf{I}\sigma_{ss}^2)$, where σ_{ss}^2 is the variances among service sires; $\mathbf{u}_o$ = additive genetic effect of sire of cow ($o = 1$ to 3267 levels) distributed as $N(0, \mathbf{A}\sigma_u^2)$ where $\mathbf{A}$ is the additive relationship matrix between sires and σ_u^2 is the variances among sires of cows, and $\mathbf{e}_{jklmno}$ = random residual assumed independently distributed as $N(0, \mathbf{I}\sigma_e^2)$, where σ_e^2 is the residual variance, which was set equal to one. Service sires and sires of cows were assumed to be independently distributed.

When an observed response y_i falls into one of the possible known categories of INS, for example j , the liability of that observation is sampled from a truncated normal distribution between 2 given thresholds (T_{j-1} and T_j). Then, the conditional probability of the event can be written as:

$$\begin{aligned} \text{Prob}(y_i = j, \text{noncensored} | \beta, \mathbf{h}, \mathbf{ss}, \mathbf{u}, \mathbf{T}) = \\ \Phi[T_j - (\mathbf{x}'_i\beta + \mathbf{z}'_{h,i}\mathbf{h} + \mathbf{z}'_{ss,i}\mathbf{ss} + \mathbf{z}'_{u,i}\mathbf{u})] \\ - \Phi[T_{j-1} - (\mathbf{x}'_i\beta + \mathbf{z}'_{h,i}\mathbf{h} + \mathbf{z}'_{ss,i}\mathbf{ss} + \mathbf{z}'_{u,i}\mathbf{u})] \end{aligned}$$

where $j = 1, 2, 3, 4$ indexes the category to which the uncensored observation y_i belongs; $\Phi(\cdot)$ is the standard normal distribution function; $\mathbf{x}_i$, $\mathbf{z}_{h,i}$, $\mathbf{z}_{ss,i}$, $\mathbf{z}_{u,i}$ are the respective incidence vectors of systematic (β), herd ($\mathbf{h}$), first service sire ($\mathbf{ss}$), and sire of cow ($\mathbf{u}$) effects, and $\mathbf{T} = [T_1, T_2, T_3, T_4]'$ is the vector of unknown threshold parameters. The thresholds must satisfy the restrictions $T_1 \leq T_2 \leq T_3 \leq T_4$, such that the cumulative distribution function is strictly nondecreasing. Further, the first threshold T_1 is set to zero, because this parameter cannot be identified in a probit analysis; hence, only T_2 , T_3 , T_4 are unknown.

If an observation is censored at the j th category, (e.g., a cow was not inseminated again beyond 2 services), then the liability is sampled from a left-truncated distribution. The truncation point is the threshold T_j corresponding to the last known insemination, and the probability can be written as:

$$\begin{aligned} \text{Prob}(y_i = j, \text{censored} | \beta, \mathbf{h}, \mathbf{ss}, \mathbf{u}, \mathbf{T}) = \\ 1 - \Phi[T_j - (\mathbf{x}'_i\beta + \mathbf{z}'_{h,i}\mathbf{h} + \mathbf{z}'_{ss,i}\mathbf{ss} + \mathbf{z}'_{u,i}\mathbf{u})]. \end{aligned}$$

Then, assuming conditional independence, the joint distribution of the noncensored and censored observations can be written as

$$L(\beta, \mathbf{h}, \mathbf{ss}, \mathbf{u}, \mathbf{T} | y)^\delta = \prod_{i=1}^N \{\Phi[T_{y_i} - (\mathbf{x}'_i\beta + \mathbf{z}'_{h,i}\mathbf{h} + \mathbf{z}'_{ss,i}\mathbf{ss} + \mathbf{z}'_{u,i}\mathbf{u})] - \Phi[T_{y_{i-1}} - (\mathbf{x}'_i\beta + \mathbf{z}'_{h,i}\mathbf{h} + \mathbf{z}'_{ss,i}\mathbf{ss} + \mathbf{z}'_{u,i}\mathbf{u})]\}^{1-\delta_i} \times \{1 - \Phi[T_{y_i} - (\mathbf{x}'_i\beta + \mathbf{z}'_{h,i}\mathbf{h} + \mathbf{z}'_{ss,i}\mathbf{ss} + \mathbf{z}'_{u,i}\mathbf{u})]\}^{\delta_i}$$

where $\delta_i = 1$ if an observation is censored observation, and 0 otherwise. Here, N is the total number of observations. Independent uniform priors were used for all elements of β , and the residual variance was set to one, as stated earlier. Normal priors were assumed for the herd, service sire, and sire of cow effects, and their distributions were as mentioned before. Independent scaled inverse χ^2 prior distributions with degrees of freedom equal to 3 and scale parameters equal to 0.1 were assigned to each of σ_h^2 , σ_{ss}^2 , and σ_u^2 .

The CTM was implemented via Markov chain Monte Carlo, as in Sorensen et al. (1995). Because thresholds have been shown to mix slowly in some cases (e.g., Kizilkaya et al., 2003), an efficient method proposed by Albert and Chib (1997) was adopted for sampling thresholds. With the first threshold set equal to zero, a logarithmic transformation was applied to the other 3 thresholds as:

$$\alpha_j = \log(T_j - T_{j-1}), \quad j = 2, 3, 4$$

Subsequently, a Metropolis algorithm was used to sample the thresholds with a normal proposal, instead of the multivariate-t process suggested by Albert and Chib (1997). The value from the previous iteration was used as the mean of the normal proposal distribution, and its standard deviation was set to 0.012, to attain a reasonable acceptance rate. In short, the proposed distribution had the form

$$\begin{pmatrix} \alpha_2 \\ \alpha_3 \\ \alpha_4 \end{pmatrix} \sim N(\tilde{\mathbf{a}}^*, \mathbf{I} \cdot 0.012^2),$$

where $\tilde{\mathbf{a}}^*$ is the value of the logarithmic transformation of the thresholds from the previous iteration. The α_1 value was set to zero.

Sequential Threshold Model

An STM described by Albert and Chib (2001) can be used to analyze an ordinal categorical trait that occurs in a sequential order, such as INS. This means that for an observation to be present at a given stage of the sequence, it must have passed through all previous

stages. For instance, a cow that is inseminated for a third time must have been inseminated and failed at both first and second AI. Therefore, a single latent variable can be used to represent the cow's propensity to pass from one category to the next. The response y_i can take the value j only after levels $1, \dots, j-1$ are reached, and then either a "success" (conception) or "failure" (no conception) in level j is observed. Hence, the probability of pregnancy at insemination j , conditionally on the event that the $(j-1)$ th insemination has been reached, is given by

$$\Pr(Y_i = j, | Y_i \geq j-1, \gamma, \beta, \mathbf{h}, \mathbf{ss}, \mathbf{u}) = \Phi[\gamma_j - (\mathbf{x}'_{ij}\beta + \mathbf{z}'_{h,ij}\mathbf{h} + \mathbf{z}'_{ss,ij}\mathbf{ss} + \mathbf{z}'_{u,ij}\mathbf{u})]$$

where β now represents the systematic effects of DFS as covariate, number of lactation (4 levels), calendar month of calving (12 levels), and year-season of calving (30 levels), and $\mathbf{x}_i$ is the corresponding incidence vector. As before, $\mathbf{h}$, $\mathbf{ss}$, and $\mathbf{u}$ represent random effects of herds (767 levels), service sire (641 levels), and sire of cow (3267 levels), respectively, with their corresponding incidence vectors ($\mathbf{z}_{h,i}$, $\mathbf{z}_{ss,i}$, $\mathbf{z}_{u,i}$). Further, the vector $\gamma = (\gamma_1, \gamma_2, \gamma_3, \gamma_4)$ represents unordered cutpoints; these cutpoints do not need to be ordered as in the case of an ordinal threshold model (Albert and Chib, 2001).

This model can also be formulated in terms of latent variables expressing the propensity of a cow to receive an additional insemination. Corresponding to the j th insemination, define latent variables $\{w_{ij}\}$, where $w_{ij} = \mathbf{x}'_{ij}\beta + \mathbf{z}'_{h,ij}\mathbf{h} + \mathbf{z}'_{ss,ij}\mathbf{ss} + \mathbf{z}'_{s,i}\mathbf{u} + e_{ij}$, where $e_{ij} \sim \text{NIID}(0,1)$. We observe $y_i = 1$ if $w_{i1} \leq \gamma_1$, and we observe $y_i = 2$ if the first latent variable $w_{i1} > \gamma_1$ and the second latent variable $w_{i2} \leq \gamma_2$. In general:

$$y_i = \begin{cases} 1 & \text{if } w_{i1} \leq \gamma_1 \\ 2 & \text{if } w_{i1} > \gamma_1, w_{i2} \leq \gamma_2 \\ 3 & \text{if } w_{i1} > \gamma_1, w_{i2} > \gamma_2, w_{i3} \leq \gamma_3 \\ 4 & \text{if } w_{i1} > \gamma_1, w_{i2} > \gamma_2, w_{i3} > \gamma_3, w_{i4} \leq \gamma_4 \end{cases}$$

These latent variables can be incorporated into a Markov chain Monte Carlo sampling scheme. The latent variable representation can be simplified by incorporating the cutpoints $\{\gamma_i\}$ into the mean function and fixing one of the cutpoints, usually $\gamma_1 = 0$. In general, each latent variable can have different explanatory variables. Thus, a binary-threshold model can be fitted for each insemination event, including the vector of cutpoints in the model, and with the response being: "fail" (pass to next insemination) = 1, or "pregnancy" = 0.

The likelihood function takes the form

$$L(\gamma, \beta, \mathbf{h}, \mathbf{ss}, \mathbf{u} | \mathbf{y})^\delta = \prod_{i=1}^N \left[\Phi[\gamma_{y_i} - (\mathbf{x}'_i \beta + \mathbf{z}'_{h,i} \mathbf{h} + \mathbf{z}'_{ss,i,j} \mathbf{ss} + \mathbf{z}'_{u,i} \mathbf{u})] \right]^{1-\delta_i} \times \left[\prod_{j=1}^{y_i} \{1 - \Phi[\gamma_j - (\mathbf{x}'_i \beta + \mathbf{z}'_{h,i} \mathbf{h} + \mathbf{z}'_{ss,i,j} \mathbf{ss} + \mathbf{z}'_{u,i} \mathbf{u})]\} \right]^{\delta_i}$$

where $\delta_i = 1$ if the observation is censored, and 0 otherwise.

As before, uniform priors were used for location parameters other than $\mathbf{h}$, $\mathbf{ss}$, and $\mathbf{u}$. The residual variance was fixed to one and, for simplicity, it was assumed constant at each step of the sequence. Priors for the random effects and for the variance components were as in the CTM.

Posterior distributions of the parameters were estimated using a Gibbs sampling algorithm for STM, and a Gibbs/Metropolis combination for CTM (Gelfand and Smith, 1990; Sorensen et al., 1995; Sorensen and Gianola, 2002). The analyses were based on a single chain of 200,000 iterations, with the first 50,000 samples discarded. Monte Carlo standard errors (Geyer, 1992) were calculated for the posterior means of herd, service sire, and sire variances. Heritability in the liability scale was calculated for CTM and STM as:

$$h^2 = \frac{4\sigma_u^2}{\sigma_u^2 + \sigma_h^2 + \sigma_{ss}^2 + \sigma_e^2}$$

and samples from its posterior distribution were obtained from the draws for the variance components.

Grouped Survival Model

Survival analysis is widely used for analysis of time-to-event traits, and this methodology can deal with censored records more flexibly than most other approaches. Here, the “grouped” survival model developed by Prentice and Gloeckler (1978) was applied to INS, using a DPH model. Services that occur during lactation can be treated as grouped intervals of time to conception; in the absence of known conception, the event is treated as a censored record in the last known insemination. This model was extended by Ducrocq (1999) to accommodate random effects. In the DPH model, the hazard function at insemination q_i is defined as the conditional probability of pregnancy at q_i given that the cow was inseminated at such time. The hazard function can be expressed as:

$$h_{klmnopq}(t) = 1 - \exp\{-\exp(\alpha DFS_{klmnopq} + \mathbf{L}_k + \mathbf{M}_l + \mathbf{YS}_m(t) + \mathbf{h}_n + \mathbf{ss}_o(t) + \mathbf{u}_p + \xi_q)\}$$

where

$h_{klmnopq}(t)$ = hazard function (instantaneous probability of conceiving) for a given cow at insemination t ;

α = regression coefficient;

$DFS_{klmnopq}$ = continuous covariate for days to first service;

$\mathbf{L}_k$ = time-independent fixed effect of lactation number ($k = 1$ to 4);

$\mathbf{M}_l$ = time-independent fixed effect of calendar month of calving ($l = 1$ to 12);

$\mathbf{YS}_m(t)$ = time-dependent fixed effect of year-season of insemination ($m = 1$ to 30);

$\mathbf{h}_n$ = time-independent random effect of herd ($n = 1$ to 767), assumed to be independently distributed as log-gamma with shape parameter γ_h .

$\mathbf{ss}_o(t)$ = time-dependent random effect of service sire ($o = 1$ to 641), assumed to be independently distributed as log-gamma with shape parameter γ_{ss} ;

$\mathbf{u}_p$ = time-independent random effect of sire of cow ($p = 1$ to 3267) assumed to be distributed as multivariate normal with mean 0 and covariance matrix $\mathbf{A}\sigma_u^2$, where $\mathbf{A}$ is the additive relationship matrix between sires, and σ_u^2 is the sire of cow variance;

$\xi_q = \log(-\log \alpha_q)$;

$\alpha_q = \exp\left\{-\int_{\tau_{q-1}}^{\tau_q} h_0(\omega) d\omega\right\}$, where h_0 is the baseline hazard function and τ_q is insemination q .

The ρ parameter of the Weibull distribution is fixed to one in the grouped survival model.

The analysis was implemented using the Survival Kit, version 3.12 (Ducrocq and Solkner, 1998). The herd and service sire variances were evaluated by the trigamma function at the corresponding estimated gamma shape parameter.

Comparison Among Models

Spearman rank correlation coefficients among the methods for either sire of cow and service sire solutions (posterior means used in CTM and STM were calculated for each model). In addition, a cross-validation analysis was carried out as follows: predictability of the 3 methodologies was compared by taking 2 random samples

of herds from the data set. Sample A contained 396 herds and 38,385 records, whereas sample B contained 371 herds and 41,672 records. The PTA for sires in both samples were calculated with the DPH (PTA_{DPH-A} and PTA_{DPH-B}, respectively) using parameters and variances estimated from the entire data set. Also, PTA for INS were obtained in both samples with the CTM (PTA_{CTM-A} and PTA_{CTM-B}, respectively) and the STM (PTA_{STM-A} and PTA_{STM-B}, respectively) using the corresponding model and variance components estimated from the whole data. Using logistic regression, sire PTA were converted into daughters' probability of conception at each insemination by regressing binary indicators of pregnancy at each of first, second, third, and fourth inseminations for cows in data subset A (among daughters that had an opportunity to be inseminated at each time) on PTA_{DPH-A}, PTA_{CTM-A}, and PTA_{STM-A}. Next, the expected number of daughters conceiving at each insemination in subset B was calculated as the probability of conception from data subset A, times the total number of daughters in subset B. The observed number of daughters that conceived or failed at each insemination in subset B was calculated for each sire (among daughters that had the opportunity to be inseminated at each time). The observed and expected number of conceptions and failures were compared using the sum across sires of χ^2 statistics as follows:

$$\text{Sum of } \chi^2 = \sum_{i=1}^n \left[\frac{(\text{Observed conceptions}_i - \text{Expected conceptions}_i)^2}{\text{Expected conceptions}_i} + \frac{(\text{Observed failures}_i - \text{Expected failures}_i)^2}{\text{Expected failures}_i} \right]$$

where n is the number of sires with daughters in each insemination and subset. The model producing the smallest sum of χ^2 was viewed as the most accurate predictor of female fertility. Reciprocal analyses were computed using conception probabilities calculated from subset B to predict daughters' fertility in subset A.

RESULTS AND DISCUSSION

Data used are summarized in Table 1. The data set contained 35.8% right-censored records. First inseminations occurred an average of 85 d after calving; the average "failure time" (mean of uncensored records of INS) was 1.68, and the average "censoring time" (last INS of censored records) was 2.11.

Ordinal-Censored Threshold Model

Estimates of variance components are shown in Table 2. The largest source of variation was herd, followed by service sire. The estimated herd variance using the

CTM was 0.104, and the first service sire variance was 0.021. Tempelman and Gianola (1999) used negative binomial models and estimated first service sire variances ranging from 0.011 to 0.057, but in a different scale. Andersen-Ranberg et al. (2003) found values ranging from 4.3×10^{-4} to 4.8×10^{-4} for the service sire variance of nonreturn rate with 3 different linear models, and Averill et al. (2004) estimated a service sire variance of 0.009 using a longitudinal Bayesian threshold analysis of the first 3 insemination events. A service sire variance of 0.013 was estimated with a threshold model for conception rate in French Holsteins by Boichard and Manfredi (1994). Nadarajah et al. (1988) found that service sire variance was 10% of the residual variance for nonreturn rate. Most of these estimates are not comparable because different traits, models, and methodologies are involved.

The sire variance on the liability scale was estimated at 0.014, with a posterior standard deviation of 0.0019. The corresponding heritability estimate was 0.05 ± 0.01 . Weller and Ezra (1997) reported a heritability of 0.035 for the inverse of the number of inseminations to conception in first parity, using a linear model and replacing censored records by contrived expectations. Veerkamp et al. (2001) reported a heritability of 0.034 for number of services to conception. Our estimate is probably larger due to the use of a threshold model, which tends to capture more additive genetic variation (Dempster and Lerner, 1950).

Sequential Threshold Model

The estimated service sire variance was as in the CTM (0.021), but estimates of herd and sire variances (0.084 and 0.010, respectively) were lower. Although estimates of the service sire were about the same in both models, the STM accounts for a different service sire in each insemination event, which CTM does not do. The STM model gave a lower heritability estimate (0.038) than the 0.05 estimated with the CTM. Smaller posterior standard deviations were obtained for all genetic parameters (Table 2), although the posterior coefficients of variation were about the same; e.g., 13.5 and 14% in CMT and STM, respectively, for σ_u^2 . The heritability estimate (0.038) from STM was similar to that of Veerkamp et al. (2001), studying number of services per lactation using a sire model, but higher than that of Kadarmideen et al. (2003) who found a heritability of 0.016 using a linear animal model for number of services per conception.

The ability to accommodate time-dependent explanatory variables is an advantage of the STM over the CTM when evaluating male and female fertility simultaneously. Also, heterogeneous sire and service sire vari-

Table 1. Number of inseminations, sires, service sires, and cows that reached each insemination; and number of successful inseminations, number of censored records, and baseline survivor function estimated by survival analysis at each insemination (1 through 4).

Insemination event	Cows	Sires	Service sires	Number of inseminations ¹	Successful insemination events	Censored records	Baseline survivor function
First	47,509	2636	577	80,071	28,324	13,159	0.50
Second	28,874	2069	611	38,588	13,994	5929	0.23
Third	15,715	1569	560	18,665	6321	3041	0.11
Fourth	8079	1139	550	9303	2711	6592	0.06

¹For example, the 80,071 first AI is the sum of pregnant (28,324), censored (13,159), and cows that receive a second insemination (38,588).

ances at different inseminations can be fitted with this model, but this option was not pursued, for simplicity.

Grouped Survival Model

The estimated baseline survivor function is shown in Table 1. At first insemination it was 0.5, which is the fraction of cows that had an opportunity to be inseminated at least twice. As expected, this fraction decreased as INS increased and, after 4 inseminations, only 6% of cows were not censored or had not yet achieved pregnancy.

Table 2 (bottom) shows estimated parameters of the log-gamma distributions of herd and service sire as well as their approximate variances obtained with the DPH. Gamma parameters for herd and service sire were 8.14 and 49.46, respectively, and their approximated variance functions were 0.13 and 0.02, respectively. The

Table 2. Estimated variances for sire of cow (σ_u^2), herd (σ_h^2), and service sire (σ_{ss}^2) and heritability (h^2) from the ordinal censored threshold model and the sequential threshold models. For the discrete proportional hazard model, sire variance (σ_u^2) in the log-scale, shape gamma parameters for herd (γ_h), and service sire (γ_{ss}) and their respective approximate variances ψ_h and ψ_{ss} are shown.

Ordinal-censored threshold model					
	σ_u^2	σ_h^2	σ_{ss}^2 ¹	h ²	
Posterior mean	0.014	0.104	0.021	0.050	
Posterior SD	0.0019	0.0074	0.0025	0.0065	
Monte Carlo error	<0.001	<0.001	<0.001	<0.001	
Sequential threshold model					
	σ_u^2	σ_h^2	σ_{ss}^2	h ²	
Posterior mean	0.010	0.084	0.021	0.038	
Posterior SD	0.0014	0.0060	0.0024	0.0051	
Monte Carlo error	<0.001	<0.001	<0.001	<0.001	
Discrete proportional hazard model					
	σ_u^2	γ_h	ψ_h	γ_{ss}	ψ_{ss}
	0.011	8.135	0.131	49.463	0.0204

¹First service sire variance for ordinal-censored threshold model.

estimated sire variance was 0.011 on the log scale. Schneider et al. (2005) found sire variance estimates ranging from 0.012 to 0.019, using different baseline hazard functions, for interval between calving and last insemination. There are no similar estimates reported elsewhere using discrete proportional hazard models.

Comparison of Models

Strong Spearman correlations (0.97 to 0.98 in absolute value), among sire PTA with the 3 models were obtained (upper diagonal, Table 3). The correlations of DPH with the other 2 models were negative because of different orientation of scale. A high PTA estimate in DPH indicates a higher probability of conception, whereas larger PTA values in CTM and STM mean larger number of inseminations to conception. The 3 methodologies would result in very similar sire rankings in a routine genetic evaluation.

Spearman correlations for service sires were lower than for sire of cow effects (lower diagonal, Table 3). The estimated correlation between CTM and STM was 0.79. Recall that CTM considers only service sire effects on the first insemination, whereas STM takes into account the service sire effect at each insemination, which is expected to lead to more accurate estimates of male fertility. Correlations of service sire solutions between DPH and CTM (−0.87) or DPH and STM (−0.73) are more difficult to interpret. A stronger correlation between DPH and STM was expected, because of the ability of both methods to handle time-dependent covari-

Table 3. Spearman correlations for sire PTA (above diagonal) and service sire solutions (below diagonal) among the discrete proportional hazard model (DPH), the ordinal-censored threshold model (CTM), and the sequential threshold model (STM).¹

	DPH	CTM	STM
DPH	—	−0.97	−0.98
CTM	−0.87	—	0.98
STM	−0.73	0.79	—

¹Standard errors < 0.0001.

Table 4. Sum of χ^2 statistics, averaged over sires, based on comparing predicted vs. observed number of conceptions at first, second, third, and fourth insemination among daughters that had the opportunity to have such inseminations, by data subset A or B. Smaller values indicate more accurate predictions of daughter fertility.¹

Conception at insemination	Number of sires	Discrete proportional hazard model	Censored threshold model	Sequential threshold model
In data subset B from sire PTA calculated in subset A				
First	930	46.59	61.33	46.73
Second	783	15.24	13.99	15.50
Third	631	7.61	7.23	7.70
Fourth	485	4.27	4.21	4.31
In data subset A from sire PTA calculated in subset B				
First	930	40.99	41.71	40.89
Second	783	17.14	16.59	16.87
Third	631	7.31	7.10	7.26
Fourth	485	3.13	2.80	3.03

¹Smallest sum of χ^2 statistics for each insemination is in bold.

ates. However, some strong assumptions in the grouped survival model may generate numerical problems with random effects (Ducrocq, 1999). Further comparisons among models in terms of estimates of random time-dependent effects should be carried out in the future.

The STM seems to be a useful approach for dealing with time-dependent effects on discrete responses, and it should be studied more intensively. The performance of STM may be improved by allowing the random effect variances to change from one service to the next. Also, the STM can consider “clustering” of insemination events between and within lactations for individual cows by including a residual covariance between liabilities of different inseminations. Implementation of a genetic effect for service sire could be studied as well, as this would be of interest to AI companies selecting for male fertility. A conceptual appeal of the CTM and STM is that parameters are easier to interpret; for example, heritability pertains to a linear, Gaussian scale of liability. This means that all the machinery of the infinitesimal model holds on the liability scale. This is not the case with the DPH model.

The sums of χ^2 statistics for each method and data subset are shown in Table 4. The DPH and STM provided more accurate predictions for success in first insemination than did the CTM. However, CTM predicted probability of conception more accurately in subsequent inseminations. These results are surprising, because both STM and DPH were expected to deal more properly with time-to-event traits, time-dependent covariates, and with censoring. However, due to the categorical nature of INS, the DPH might not be a proper specification, as it assumes continuously recorded values that are grouped into categories. Further, heterogeneity of

variance (due to hormonal treatments, voluntary waiting period between inseminations, and other management decisions) could decrease the accuracy of DPH, which originally postulates fixed time intervals. Time to third and fourth insemination can differ widely between cows. Also, assuming a constant baseline hazard in pregnancy for all inseminations ($\rho = 1$) may not be suitable for INS: intervals (from INS n to $n+1$) usually differ in length and cows with silent heats or early embryonic mortality are usually less fertile at the next insemination. The assumptions made on CTM are less strong in this sense. The STM had a similar but somewhat lower predictive ability than DPH in the data subset B, but STM was slightly better in subset A. In summary, the CTM tended to produce better predictions of conception to insemination than either DPH or STM, perhaps due to higher robustness.

CONCLUSIONS

Three new methodologies for analyzing INS of dairy cattle were tested, leading to generally similar results. Estimated sire variances for INS were low, and heritabilities ranged from 0.038 to 0.050. All 3 models led to similar ranking for sires, with strong correlation between methods. The STM and DPH had a better performance for predicting success at first AI. The CTM was slightly better at second and subsequent inseminations, probably because of the assumptions made in DPH and STM. Because the sampling distributions of the χ^2 statistic used are unknown, there are no tests available to assess their significance. Bootstrapping is computationally unfeasible for this data set.

The results in this study suggest that STM may be better, globally, than DPH, and its interpretation is easier. Further, STM can be extended to allow for different variance components by insemination. The CTM provided satisfactory results, and is straightforward to program; however, it cannot deal with time-dependent covariates. Future studies could fit a genetic effect for service sires (via the relationship matrix) in DPH and STM; this would lead to genetic evaluations of male and female fertility, simultaneously. Bivariate analyses of INS and other fertility traits could also be of interest to estimate genetic correlations more accurately in the presence of censoring. This could slow down the rate of genetic degradation for fertility in field populations.

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