Is production system important for survival times after first calving of dairy cows?

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Contents

Abstract

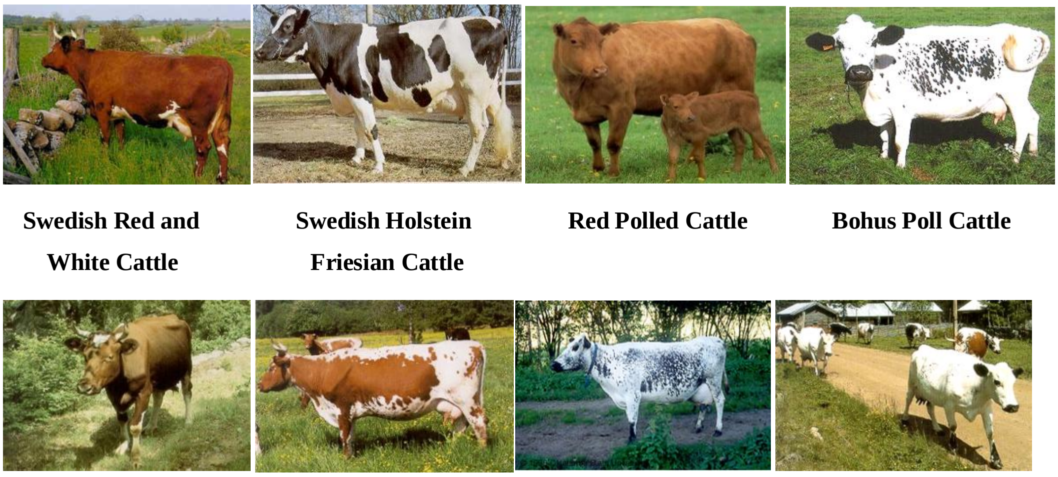
The survival times of dairy cows after first calving as a part of animal welfare has attracted broad attention. In this article the main objective is to find whether the difference of production systems can affect the survival times after first calving; the sub objective is to apply different methods to solve this problem. We solve this problem from two directions: Survival Analysis and a Generalized Linear model approach. The Survival Analysis includes both Cox proportional hazard model and a parametric survival model. Then “herd effect” is added as a random effect to all three models. After model regression the results of all models which are without or with random effect show the organic production system has a higher survival rate than the traditional production system. After adding the herd effect, the higher survival rate of organic production system becomes more significant in all three models. Modelling of individuals’ relationship is also discussed.

Key words: dairy cows, survival times after first calving, Survival Analysis, Cox proportional hazard model, parametric survival model, Generalized Linear model, random effect

1. Introduction

Dairy cows are domesticated animals bred to produce milk. A cow will produce large amounts of milk over its life after first calving which is a precondition of milking. Common gestation period of cows is about nine months, so most heifers (cows before first calving) give birth and become cows at about two years of age. There are many kinds of dairy cows. Certain breeds produce more milk than others; however, different breeds produce within a range of around 4,000 to over 10,000 kg of milk per annum. Production levels peak at around 40 to 60 days after calving. The cow is then bred. Production declines steadily afterwards, until, at about 305 days after calving, the cow is "dried off", and milking ceases. About sixty days later, one year after the birth of her previous calf (baby), a cow will calve again. High production cows are more difficult to breed at a one year interval. Many farms take the view that 13 or even 14 month cycles are more appropriate for this type of cow[1].

In Sweden **Swedish Red and White Cattle** are the most common dairy cows and the population of this breed is 60% of the total number. Besides this breed there are still seven breeds in Sweden shown below. **Swedish Holstein Friesian Cattle,** which are characterized by a high milk yield, are the second large breeds of dairy cows in Sweden. And also some breeds of small size groups such as **Swedish Red Polled Cattle**, **Bohus Poll Cattle**, **Ringamala Cattle**, **Vane Cattle**, **Fjall Cattle** and **Swedish Mountain Cattle**[2].



Swedish Red and White Cattle

Swedish Holstein Friesian Cattle

Red Polled Cattle

Bohus Poll Cattle

Ringamala Cattle

Vane Cattle

Fjall Cattle

Swedish Mountain Cattle

Figure 1 Breeds of dairy cows in Sweden.

The dairy sector is the most important sector in Swedish agriculture today. The main dairy products in Sweden are drinking milk, fermented milk, cream, cheese, butter and milk powder. In total, there are 15 dairy companies in Sweden. Seven of them are

[1] http://en.wikipedia.org/wiki/Dairy_cattle
[2] http://neurocad.lva.lt/Breeds/SwedishBreeds.htm

members of the industry organization “Swedish Dairy Association” and account for over 99 percents of the county’s production[3]. The others are dairy farms of varying size. With the scientific management and advanced rearing technique they provide the high-quality milk products to consumers in the daily life.

The total number of Swedish cows is declining (just under 400,000 cows in 2006, as compared with 1,200,000 in 1960), but at the same time, the yield is increasing somewhat[4]. It is strongly relative with the good health condition. Longevous and productive dairy cows are expected by the dairy farmers[5]. However, in fact, herd life is strongly correlated with production levels. Lower production cows live longer than high production cows, but less profitable all the same. One side is economic profit the other side is animal welfare, it needs widely study to find a balance solution.

My main objective in this paper is to find whether the difference of production systems has a significant influence to the survival times after first calving of dairy cows. And the sub objective is to search the different methods to solve this survival problem. The cows have the rights to get welfare during their lifetimes while they make a great contribution to human being. Now there are two different ways in the Swedish production systems, traditional and organic production systems.

To solve this problem, the more fundamental approach is Survival Analysis (Miller, 1981). It is a branch of statistics which provides special techniques to compare the risk for death (or some other event) associated with different treatments or groups, where the risk changes over time (Bewick, Cheek & Ball, 2004). The advantage of survival analysis is the capability of handing the problem of censoring which means that the survival times are not known for all individuals when the study is finished. All methods in survival analysis can handle censored data. The response value in this article is the survival times after first calving; moreover the most important explanatory variable is production system. To improve the analysis result I also select some other explanatory variables such as calving year, calving month and age at first calving in days. All of the above explanatory variables are called systematic factors.

However, the observations from the individuals studied in this article are not independent. Firstly dairy cows are bred herd-based, individuals from same herd (a group of cows that live in the same environment) always means the same growing condition. Secondly the reproduction of cows is artificial fertilization and a cow will give birth to many heifers (cows before first calving) during its life, as a result, dairy cows have high genetic relationship which means a high interdependence. The interdependence among dairy cows is very important so it should be included in the

[3] http://www.svenskmjolk.se/Default____13.aspx

[4] http://www.svenskmjolk.se/ImageVault/Images/id_916/scope_128/ImageVaultHandler.aspx

[5] http://en.wikipedia.org/wiki/Dairy_cattle

analysis. Both of them should be treated as random effects to improve survival models and make them have the ability of capturing the comovement of survival times among dairy cows. As we know Generalized Linear Model with random effect is commonly referred to as Generalize Linear Mixed Model (Fahrmeir & Tutz, 2001) in the statistical literature. And I also add random effect to the models of survival analysis and then compare the results of these different models.

All models have their own predominance. I will make a discussion after I apply them to the model regressions.

2. Data

The data in my article is provided by "Swedish Dairy Association" which belongs to the seven largest companies (jointly representing more than 99 percents of Swedish milk production), seven livestock cooperatives, two semen-producing companies, and nine breed societies. The work of this association covers ten different fields of expertise including "Nutrition & Gastronomy", "Milk Quality", "Environmental Issues", "Milk Police", "Milk Economy", "Management", "Cow Data", "Breeding", "Animal Welfare", "and Breeding". Today it has been a company with a well-established network of researchers, experts, decision-makers, and people who shape public opinions, in Sweden and abroad[6].

2.1 Data pretreatment

The complete data is recorded from January 1998 to September 2005. We select the individuals who had their first calving during year 1998 to year 1999. After this selection, there are 129760 individuals included in the dataset which come from 9295 different herds. In the methodology part "herd" will be treated as a random effect which has a $n \times n$ matrix form (here n=9295). It is too large to calculate for R software used in this article. To solve this problem I delete some observations to make the size of each herd more than or equal to 10 heads. Then the total number of herds reduced to 4769 (almost decreased 50%) which can be calculate by R in practice. At the same time the total number of observations is reduced to 109986 (almost decreased 15%) which is also large enough for modelling and analysis.

The dataset after selected by "herd" also incorporates information of individuals which consists some indirect and unnecessary information. So I must do some pre-treatments before I use them.

Firstly, delete unnecessary information. Table 1 is a typically sample of the rest information and their meaning after removing.

[6] http://www.svenskmjolk.se/Default____13.aspx

Table 1 Data after removing unnecessary information. (First three rows of observations.)

calvyr	calvmo	age	Utslagskod	utslagsdatum	Herd	Calvingdate	System
1998	1	809	3	15131	100	13896	0
1998	3	821	4	15472	100	13953	0
1999	8	894			107	14465	0

calvyr: year of first cavling	calvmo: month of first calving
age: age of cows at first calving in days	Utslagskod: reason of death
utslagsdatum: date of death	Herd: herd the cow belongs to
Calvingdate: data of first calving	System: traditional=0 organic=1

Secondly, calculate the survival times after first calving. There are pair wise missing values in date of death and death reason which means the cows are still alive until September 2005. Then I define a new group of data named “state” which have two values 1 and 0; 1 means the individual is dead and 0 means it is still alive after September 2005. The date of September 2005 is 16700 which I treat it as the date of death. The survival times of this kind of individuals are censored data[7].

Thirdly, make a final check. Survival times must be nonnegative in actual life but some values are negative in the dataset. So I delete them. After all of procedures I get the final dataset. Table 2 shows the final dataset after all above treatments.

Table 2 Final model form (First three rows of observations.)

time	state	calvyr	calvmo	age	herd	system
1235	1	1998	1	809	100	0
1519	1	1998	3	821	100	0
2235	0	1999	8	894	107	0

time: survival time after first calving	state: dead=1 alive=0
calvyr: year of first cavling	calvmo: month of first calving
age: age of cows at first calving in days	herd: herd the cow belongs to
system: traditional=0 organic=1	

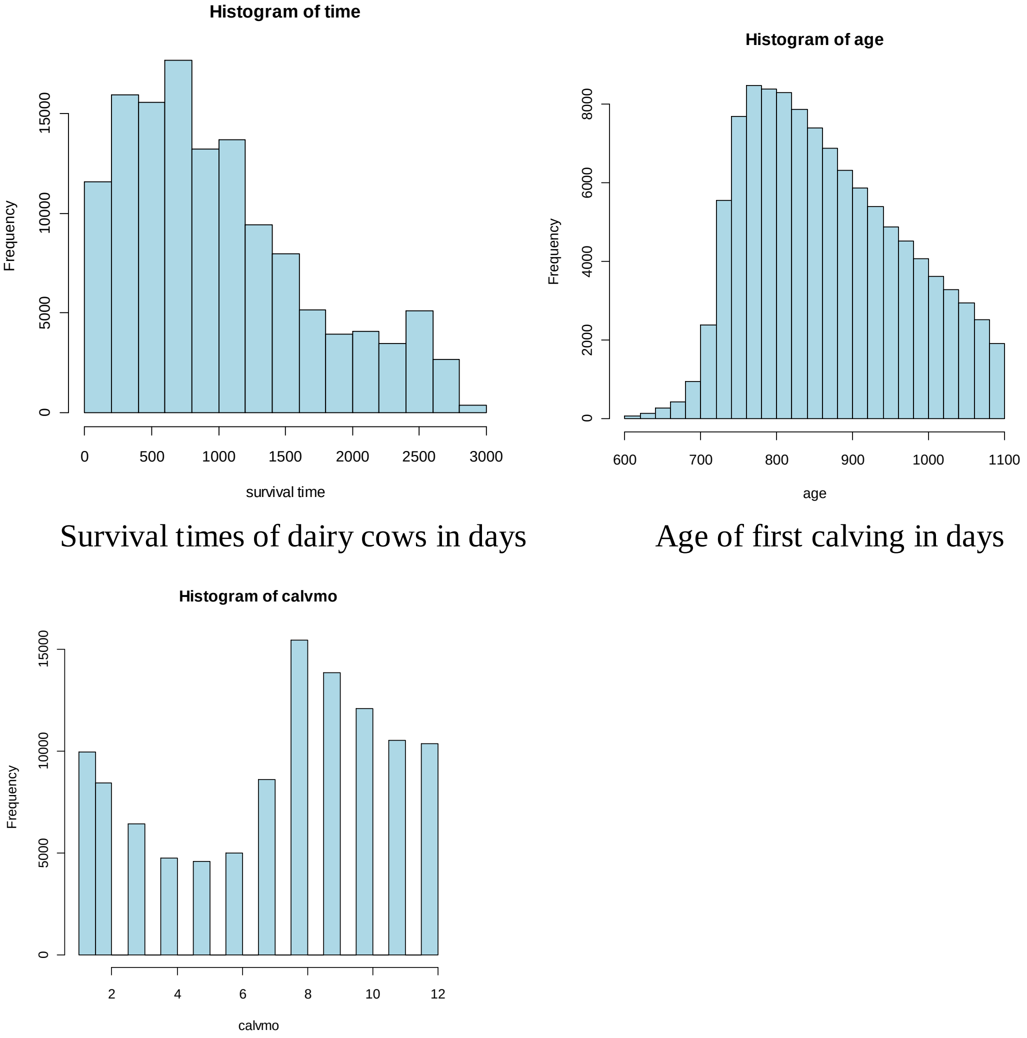
[7] http://en.wikipedia.org/wiki/Censoring_(statistics)

2.2 Data description

Table 3 shows the number of observations in each group of variables state, calving year and production system. Figure 2 shows the frequencies of survival times, calving age and calving month graphically.

Table 3 the number of observations in each group of variables state, calving year, and production system

variable	number of observations	
	(real)/(1998)/(traditional)	(censored)/(1999)/(organic)
state	101601	8385
calvyr	55293	54693
system	107310	2627



Survival times of dairy cows in days

Age of first calving in days

Month of first calving

Figure 2 Frequencies of survival times, calving age and calving month

3. Methodology

In this paper I will analysis the influence of the production system through two main directions: Survival Analysis (Miller, 1981) and a Generalized Linear Model (Fahrmeir & Tutz, 2001) approach. In the survival analysis section I will apply non-parametric survival model based on Cox proportional hazard model (Cox and Oakes, 1984) and parametric survival model based on Weibull distribution (Rodriguez, 2005). In the GLM section I will give a description of the use of GLM to fit Weibull distribution. Censored data are considered in all models.

3.1 Survival Analysis

Survival analysis is a classic methodology to analyze survival data. Of central importance in the analysis of survival time data are two functions used to describe their distribution, namely the survival function $S(t)$ and the hazard function $h(t)$ (Everitt & Hothorn, 2006).

Denote the density function for the survival times of cows after first calving with $f(t)$, and let the corresponding distribution function be $F(t)$. The survival function is defined as

$$S(t) = 1 - F(t),$$

which means the probability that the survival time, T, is greater than or equal to some times t, i.e., $S(t) = P(T \geq t)$.

The hazard function is defined as

$$h(t) = f(t)/S(t),$$

which means the probability that an individual died in a small interval, s, given that the individual has survived up to the beginning of the interval, when the size of the time interval approaches zero; it can be express as $h(t) = lim_{s \to 0} P(t \leq T \leq t + s|T \geq t)$. It is very useful to assess which periods have high or low chances of death among those still active at the time. At the same time high hazard rate means low survival.

3.1.1 Non-parametric survival model

3.1.1.1 Kaplan-Meier estimator

In non-parametric modeling, the survival function is not specified, but is estimated non-parametrically through the observed survival distribution. In the presence of censoring, the survival function is typically estimated using the Kaplan-Meier estimator (Kaplan & Meier, 1958). The Kaplan-Meier estimator is the non-parametric maximum likelihood estimate of $S(t)$ and it is defined as

$$\widehat{S_{KM}} = \prod_{t_i \leq t}(1 - n_i/N_i) \qquad \text{if } t \geq t_i$$
$$= 1 \qquad \text{if } t < t_i$$

where,
n_i means the number of the cows dead at time t
N_i means the number of cows who are at risk at time t.

In the study of cows the Kaplan-Meier method was used to estimate the survival function for all cows after first calving and by different production systems. The graph of $S(t)$ against t is called the survival curve. By comparing the estimated survival curves in different production systems, a rough idea about the survival rate between different production systems will be shown.

3.1.1.2 Log-rank test

Log-rank test is a statistical test to examine whether the difference of production systems is statistically significant. The log-rank test (Peto & Peto, 1972) is a hypothesis test to compare the survival function between two groups. The statistical hypothesis is

$$H_0: S_1(t)=S_2(t) \quad \text{for all } t \leq T \qquad (1)$$
$$H_1: S_1(t) \neq S_2(t) \quad \text{for some } t \leq T$$

And the formula for the test statistic is

$$Z = (O - E)/(Var(O))^{1/2}$$

where,
O is the number of observed event times from group 1
E is the expected number of event times from group 1 under H_0.

3.1.1.3 Cox proportional hazard model

Because of non-symmetric the censored survival time, we need special regression techniques for modeling the relationship of the response to explanatory variables. The most widely used procedure is that known as Cox proportional hazards model. Another most important reason is that the proportional hazards model is non-parametric in the sense that it depends only on the ranks of the survival times. The model is given as follows (Ivan Iachine, 2001)

$$h(t|x_1, \dots, x_q) = h_0(t)exp(\beta_1 x_1 + \cdots + \beta_q x_q)$$

Where,
$h_0(t)$ is the baseline hazard function
$\beta_1, \dots, \beta_q$ are the regression coefficients
$x_1, \dots, x_q$ are the covariates

Suppose β_{NP} is the coefficient of the production system. It means that
In group 1 (traditional) the hazard function is

$$h(t|x_j = 0) = h_0(t)exp(\beta_1 x_1 + \cdots + \beta_{NP} * 0 + \cdots + \beta_q x_q)$$

In group 2 (organic) the hazard function is

$$h(t|x_j = 1) = h_0(t)exp(\beta_1 x_1 + \cdots + \beta_{NP} * 1 + \cdots + \beta_q x_q)$$

The relative risk for group 2 vs. group 1 is

$$RR = \frac{h(t|x_j = 1)}{h(t|x_j = 0)} = \frac{h_0(t)exp(\beta_1 x_1 + \cdots + \beta_{NP} * 1 + \cdots + \beta_q x_q)}{h_0(t)exp(\beta_1 x_1 + \cdots + \beta_{NP} * 0 + \cdots + \beta_q x_q} = exp(\beta_{NP})$$

The parameters in this model can be estimated by maximizing a partial likelihood without knowing anything about baseline hazard function because it is a nuisance variable. Then the interpretation of $\widehat{\beta_{NP}}$ is that

$\widehat{\beta_{NP}} > 0: RR > 1 \text{ } and \text{ } h(t|x_j = 1) > h(t|x_j = 0)$

$\widehat{\beta_{NP}} = 0: RR = 1 \text{ } and \text{ } h(t|x_j = 1) = h(t|x_j = 0)$

$\widehat{\beta_{NP}}_j < 0: RR < 1 \text{ } and \text{ } h(t|x_j = 1) < h(t|x_j = 0)$

3.1.2 Parametric survival model

The parametric regression model can also be used to examine the relationship between the survival times and the explanatory variables. Generally any distribution defined for $t \in [0, \infty)$ can be treated as a survival distribution. Through a logarithm transform we get $log(t) \in (-\infty, +\infty)$ which is more suitable for modeling. In this paper I assumed the survival times has a Weibull distribution which is most commonly used in survival analysis. The general regression model is given below (German Rodriguez, 2005)

$$ln(t) = \alpha + \sigma w$$

Where $\alpha = -log(h(t))$ and w has a specific distribution.
For Weibull distribution,

$$ln(t) = u + \beta_1 x_1 + \cdots + \beta_q x_q + \sigma w$$

Where,
$x_1, \dots, x_q$ are explanatory variables
$\beta_1, \dots, \beta_q$ are regression coefficients
σ is a scale parameter
w has the extreme value distribution
u is an intercept

The regression parameters will be used to interpret the direction and strength of the relationship of each explanatory on the effect of the survival time. Positive value of $\widehat{\beta_P}$ is indicative of increased survival.

3.2 Generalized Linear Model

Generalized linear model is proposed as a way of unifying various other statistical models, including linear regression, logistic regression and Poisson regression, under on framework. It is not common used in the survival analysis but no doubt it will be an interesting attempt to solve the survival problem with GLM (Aitkin & Clayton, 1979).

3.2.1 Maximum Likelihood Estimation

The hazard function is assumed to involve the explanatory variables through a log-linear (proportional hazards) model:

$$h(t_i) = \lambda(t_i)ex\,p\left(\sum_j \beta_j x_{ij}\right) = \lambda(t_i)exp(\boldsymbol{\beta}'\boldsymbol{x_i})$$

where,
$t_1, \dots, t_n$ are the survival times of n individuals
x_{ij} for $i = 1, \dots, n$, and $j = 0, 1, \dots, k$ is the explanatory variables with $x_{io} \equiv 1$
β_j is the regression parameter

Since $h(t) = f(t)/S(t)$, the density function $f(t)$ is assumed to be of the form $f(t) = \lambda(t)exp(\boldsymbol{\beta}'\boldsymbol{x} - \boldsymbol{\Lambda}(t)e^{\boldsymbol{\beta}'\boldsymbol{x}})$, and hence $S(t) = exp(-\boldsymbol{\Lambda}(t)e^{\boldsymbol{\beta}'\boldsymbol{x}})$, where

$$\boldsymbol{\Lambda}(t) = \int_{-\infty}^{t} \lambda\,(u)d_u$$

Let w be an indicator variable taking the value 1 for uncensored observation and 0 for censored observations. Under the usual assumption that the censoring mechanism is independent of the explanatory variables, the likelihood function is

$$L = \prod_{i=1}^{n} [f(t_i)]^{w_i}[S(t)]^{1-w_i}$$

$$= \prod_i [\lambda(t_i)exp(\boldsymbol{\beta}'\boldsymbol{x_i})]^{w_i}\, exp(-\boldsymbol{\Lambda}(t)e^{\boldsymbol{\beta}'\boldsymbol{x}})$$

$$= \prod_i [{u_i}^{w_i}e^{-u_i}]\,[\lambda(t_i)/\boldsymbol{\Lambda}(t_i)]^{w_i}$$

where $u_i = \boldsymbol{\Lambda}(t_i)exp(\boldsymbol{\beta}'\boldsymbol{x_i})$.

The first term in the likelihood function is the kernel of the likelihood function for n independent "Poisson variates" w_i with mean u_i. The second term does not involve the parameter vector β, but may depend on other unknow parameters. The log-linear model for the hazard function implies a log-linear model for the "Poisson mean"

$$log(u_i) = log\boldsymbol{\Lambda}(t_i) + \boldsymbol{\beta}'\boldsymbol{x_i}$$

Then a simple iterative maximization of the log-likelihood function is now possible in

GLM. Given initial estimates of the unknown parameters in $\boldsymbol{\Lambda}(t)$, the maximum likelihood estimate (MLE) of $\boldsymbol{\beta}$ is obtained for the Poisson model in GLM with log$\boldsymbol{\Lambda}(t_i)$ as a known function (an offset) incorporated in the log-linear model. For this estimate of $\boldsymbol{\beta}$, the MLE of the unknown parameters in $\boldsymbol{\Lambda}(t)$ may be obtained from the likelihood equations for these parameters., and this sequence of steps continued until convergence.

3.2.2 Weibull distribution

By assuming $t \geq 0$ and $\boldsymbol{\Lambda}(t) = t^{\alpha}$, we obtain Weibull density

$$f(t) = \alpha t^{\alpha-1} exp(\boldsymbol{\beta}'\boldsymbol{x} - t^{\alpha} e^{\boldsymbol{\beta}'\boldsymbol{x}}), (t \geq 0, \alpha > 0),$$

with $E(t) = \Gamma(1 + \alpha^{-1}) exp(-\boldsymbol{\beta}'\boldsymbol{x}/\alpha)$. In this case $\lambda(t)/\boldsymbol{\Lambda}(t) = \alpha/t$ will depend on the unknown shape parameter α. The kernel of the log-likelihood function is

$$logL = nlog\alpha + \sum_i (w_i log\, u_i - u_i),$$

where $i = 1, \ldots, n$ and $log\, u_i = \alpha log(t_i) + \boldsymbol{\beta}'\boldsymbol{x_i}$. The likelihood equations are

$$\frac{\partial logL}{\partial \beta_j} = \sum_i (w_i - u_i) x_{ij} = 0$$

$$\frac{\partial logL}{\partial \alpha} = n/\alpha + \sum_i (w_i - u_i) logt_i = 0$$

and the maximum likelihood estimate (MLE) of α satisfies

$$\hat{\alpha} = (\textstyle\sum_i (\hat{u_i} - w_i) logt_i / n)^{-1} \quad (1)$$

The iterative procedure begins by setting $\alpha_0 = 1$ (i.e. an exponential model is fitted). The Poisson model is fitted with offset $\alpha_0 log(t)$, and the fitted values ${u_i}^{(0)}$ are used to re-estimate $\widehat{\alpha_0}$ from (1). A new estimate

$$\alpha_1 = (\alpha_0 + \widehat{\alpha_0})/2$$

is then used to define a new offset $\alpha_1 log(t)$ for the Poisson model, and the process is continued until convergence.

3.3 Adding random effect

In the above models we assume that the population of cows we study is homogenous. However, in fact, the breeding administration and environment of herds are different. It leads to a heterogeneous sample, i.e. a mixture of individuals with different hazards[8]. The herd effect is an unobserved effect. As an extension of above models, we consider it as a random effect and add it into all above models. In statistics there are two specific names: with random effect, Cox proportional hazard model is called frailty model; with random effect, Generalized Linear Model is called Generalized Linear Mixed Model (GLMM).

[8] http://www.demogr.mpg.de/papers/working/wp-2003-032.pdf

Herd effect is a simple random effect; I will add it directly into above models without repeated description of the basic models. Table 4 shows the new models with random effect. The interpretations of the coefficients of the production system in different models are also similar with coefficients in models without random effect. I compare them in the next section.

Table 4 Survival models and GLM with random effect

Z is the random effect term (herd effect), α is the coefficient of Z.

Models with random effect	Model form
Frailty model	$h(t\|x,Z) = (Z\alpha)h_0(t)exp(\boldsymbol{\beta}'\boldsymbol{x})$
Parametric survival model with random effect	$ln(t) = u + \beta_1 x_1 + \cdots + \beta_q x_q + \sigma w + Z\alpha$
GLMM	$log\, u_i = \alpha\, log(t_i) + \boldsymbol{\beta}'\boldsymbol{x_i} + Z\alpha$

4. Result

4.1 Kaplan-Meier estimator and log-rank test

We begin with a short discussion about the survival curves of the organic and traditional production systems, given in Figure 3. From the estimate curves we can get a rough idea that the survival rate of the organic production systems is higher than the traditional one.

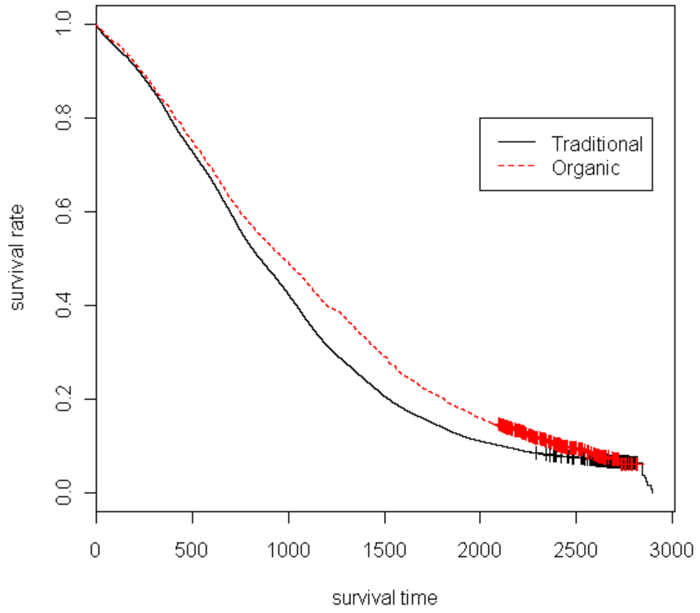


Figure 3 Survival curves of the production systems

However it is not the scientific evidence for us to make a conclusion. We use log-rank test to examine whether the difference between traditional and organic production systems is significant. The result is given in Table 5, where a significant value 10% is used. The p-value is small enough to reject the null hypothesis (1). The survival rates of the different production systems are statistically significant.

Table 5 Result of log-rank test

Strata	Chi-Square Statistic	P-value
System	65.3	6.66e-16

4.2 Cox proportional hazard model and frailty model

Based on the methodology in section 3.1.1.3 and 3.3, the estimation of the Cox proportional hazard model (denoted as model 1) and frailty model (denoted as model 2) are listed in Table 6.

Table 6 Estimation results of Cox proportional hazard model and frailty model

	model 1		model 2	
Variable	exp(coef)	p-value	exp(coef)	p-value
System	0.9440	<2e-16	0.940	0.000014
calvyr:1999	1.112	<2e-16	1.101	0.0
age	1.0000	0.008610	1.000	0.0
calvmo:2	1.012	0.444636	1.031	0.054
calvmo:3	1.013	0.422877	1.023	0.20
calvmo:4	1.049	0.008958	1.075	0.00018
calvmo:5	1.071	0.000211	1.076	0.00020
calvmo:6	1.060	0.001324	1.066	0.00084
calvmo:7	1.030	0.054136	1.015	0.35
calvmo:8	0.9925	0.576333	0.993	0.61
calvmo:9	0.9623	0.005180	0.958	0.0025
calvmo:10	0.9930	0.616514	0.999	0.93
calvmo:11	1.022	0.1432270	1.019	0.21
calvmo:12	1.041	0.005472	1.045	0.0036
herd	--------------	------------	---------------	0.0

Clearly in both of the models, the effect of production system is significant. In the Cox proportional hazard model the relative risk, RR=0.9440<1, means the hazard of organic production system is less than the traditional production system. In the frailty model the relative risk, RR=0.940<1, also means hazard of organic production system is less than the traditional production system. And the effect of herd is significant, test through the p-value.

As shown in the methodology part when relative risk equals to 1, traditional and organic production systems have the same hazard rate. After adding the random effect (herd effect) the relative risk is declined, relative risk of Cox proportional hazard model has a longer distance to 1 than relative risk of frailty model. It means the influence of the production system to the survival times is strengthened after adding the random effect.

4.3 Parametric survival model (with and without random effect)

Based on the methodology in section 3.1.2 and 3.3, the estimation of the parametric survival model without random effect (denoted as model 1) and with random effect (denoted as model 2) are listed in Table 7.

Table 7 Estimation results of parametric survival models (with and without random effect)

	model 1		model 2	
Variable	coef	p-value	coef	p-value
System	0.0435	1.98e-16	0.043692	0.0000248
calvyr:1999	-0.105	1.81e-104	-0.080625	1.73e-68
age	-0.0000572	0.0174	-0.000284	5.00e-26
calvmo:2	-0.00817	0.491	-0.021875	0.0532
calvmo:3	-0.0105	0.415	-0.017179	0.167
calvmo:4	-0.0406	0.00421	-0.055006	0.0000614
calvmo:5	-0.0616	0.0000158	-0.057613	0.0000322
calvmo:6	-0.0524	0.00016	-0.050666	0.000172
calvmo:7	-0.0351	0.00293	-0.018782	0.0997
calvmo:8	-0.0071	0.493	-0.004184	0.675
calvmo:9	0.0163	0.123	0.021578	0.0335
calvmo:10	-0.00908	0.403	-0.009261	0.373
calvmo:11	-0.0324	0.00379	-0.024202	0.0232
calvmo:12	-0/0474	0.0000247	-0.041617	0.0000972

The p-values in model 1 and model 2 are small enough so that the influence of production system is significant in both of models. Both of the coefficients of production system are positive, it means the organic production system has a positive effect for survival times. After adding the random effect (herd effect) the coefficient get bigger than before, which means the relationship of production system on the effect of the survival times is strengthened.

4.4 GLM and GLMM

Based on the methodology in section 3.2 and 3.3, the estimation of generalized linear model (denoted as model 1) and generalized linear mixed model (denoted as model 2) are listed in Table 8.

Table 8 Estimation results of GLM and GLMM

	model 1		model 2	
Variable	coef	p-value	coef	p-value
System	-0.058988	< 2e-16	-0.065698	1.66e-05
calvyr:1999	0.145285	< 2e-16	0.120163	< 2e-16
calvmo:2	0.011974	0.437595	0.035536	0.02708
calvmo:3	0.016341	0.327524	0.034012	0.05420
calvmo:4	0.056984	0.001941	0.092371	2.15e-06
calvmo:5	0.086254	3.19e-06	0.097124	7.99e-07
calvmo:6	0.074617	3.44e-05	0.089567	2.87e-06
calvmo:7	0.052831	0.000548	0.045797	0.00457
calvmo:8	0.015502	0.246675	0.025819	0.06705
calvmo:9	-0.016353	0.232801	-0.016204	0.25961
calvmo:10	0.016368	0.245563	0.023161	0.11630
calvmo:11	0.047126	0.001195	0.041536	0.00611
calvmo:12	0.067273	4.12e-06	0.064734	1.98e-05

The effects of production system in both models are significant no doubt because of the small p-values. From Table 8 the coefficients of the production system in both models are negative. The regression model of GLM is

$$log\, u_i = \alpha\, log(t_i) + \boldsymbol{\beta}'\boldsymbol{x_i}$$

where α is positive which have been calculated during the iterative process. The survival times t and the explanatory variables are in the same side of the formula, the we do a change to this formula

$$\alpha\, log(t_i) = log\, u_i - \boldsymbol{\beta}'\boldsymbol{x_i}$$

After this simple change, the effect of production system to survival times is positive which means the survival times of observations in organic production system is significant longer than the traditional one. The same change and result will be occurred in the GLMM. And also after adding the random effect the relationship of production system on the effect of the survival times is strengthened.

5. Conclusion

According to the results and analysis of all models above, the effect of production system to the survival times is significant. The organic production system leads to a high survival rate. After adding the random effect (herd effect), the effect of production system to the survival times is strengthened in all models. The conclusions of all these models are similar. It is interesting that the Cox proportional hazard model, parametric survival model and Generalized Linear Model can be used in the data.

6. Discussion

In this article we only consider the herd effect as a random effect. As we referred in the introduction section, high genetic relationship exists among dairy cows. If adding the genetic relationship of cows as the other random effect in above models, it will be more scientific than only with herd effect. Adding individual effect as a random effect needs complex technique, we will make a short introduction of the methodology shown by Yudi Pawitan (Pawitan, 2001).

The process of adding genetic relationship as a random effect is similar as adding herd effect. The most difficult part is making the relationship matrix which we denote it as R here. R is a $n \times n$ matrix where n is the total number of individuals included in the dataset we apply in this article. There is a specific dataset providing the basic relationships among dairy cows called pedigree. Table 9 shows the recording form of the pedigree dataset which is also a simple example. In the simple example animal 1, 2 and 6 have unknown parents; 3 is the offspring of 1 and 2; 4 has a known sire 1, but unknown dam; 5 has known parents 3 and 4; 7 has known parents 5 and 6.

Table 9 Example of the dataset of pedigree

Values in the dataset mean ID numbers of each animal. Here we denote it as 1 2 3 … for short.

Animal	Sire	Dam
1	---	---
2	---	---
3	1	2
4	1	---
5	4	3
6	---	---
7	5	6

Sire: father of the animal   Dam: mother of the animal
“---“ means unknown

Then we introduce the methodology of the relationship matrix designing. Let r_{ij} be the element of R; the value of r_{ij} as a function of the pedigree data is defined by

1. For diagonal elements:

$$r_{ij} = 1 + \frac{1}{2} r_{sire,dam}$$

where “sire” and “dam” are those of the i’th dairy cow. The second term on the right-hand side takes account of inbreeding; if there is no inbreeding then $r_{ii} = 1$, and R is a correlation matrix.

2. For off-diagonal element r_{ij}, where j is of an older generation compared with i and

(1) both parents of i are known

$$r_{ij} = \frac{1}{2}(r_{j,sire} + r_{j,dam})$$

(2) only one parent of i is known

$$r_{ij} = \frac{1}{2}r_{j,sire}$$

or

$$r_{ij} = \frac{1}{2}r_{j,dam}$$

(3) both parents of i are unknown

$$r_{ij} = 0$$

By definition of $r_{ij} = r_{ji}$, R is a symmetric matrix. Then this relationship matrix can be added as a random effect same as herd effect done. Table 10 shows the new models with individuals' relationship effect.

Table 10 Survival models and GLM with individuals' relationship effect (random effect)

R is the relationship matrix (individuals' relationship effect), α is coefficient of R.

Models with random effect	Model form
Frailty model	$h(t\|x,R) = (R\alpha)h_0(t)exp(\boldsymbol{\beta}'\boldsymbol{x})$
Parametric survival model with random effect	$ln(t) = u + \beta_1 x_1 + \cdots + \beta_q x_q + \sigma w + R\alpha$
GLMM	$log\, u_i = \alpha\, log(t_i) + \boldsymbol{\beta}'\boldsymbol{x_i} + R\alpha$

The processes of model regression and model analysis are similar with processes of adding herd effect. We believe it will be a nice direction for further research on this topic.

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Appendix

```
#####load data
data<-read.table("D:/cows.txt",header=T)
attach(data)
names(data)

#####data description
length(state[state>0])
length(state[state<1])
length(calvyr[calvyr>1998])
length(calvyr[calvyr<1999])
length(system[system>1])
length(system[system<0])
hist(time,col="light blue",xlab="survival time")
hist(age,col="light blue")
hist(calvmo,col="light blue")

#####Survival Analysis
###load package
library(splines)
library(survival)
Surv(time,state==1)

###K-M method
surv.bysystem<-survfit(Surv(time,state==1)~system)
surv.bysystem
plot(surv.bysystem,xlab="survival time",ylab="survival rate",lty=1:2,col=1:2)
legend(2000,0.8,c("Organic","Traditional"),lty=1:2,col=1:2)

###Log-rank test
survdiff(Surv(time,state==1)~system)

###Cox proportional hazard model
summary(coxph(Surv(time,state==1)~system+factor(calvyr)+factor(calvmo)+age))

###frailty model (Cox proportional hazard model with random effect)
summary(coxph(Surv(time,state==1)~system+factor(calvyr)+factor(calvmo)+age+fra
ilty(herd,dist="gauss")))

###parametric survival model
g<-survreg(Surv(time,state==1)[time>0]~system[time>0]+factor(calvyr[time>0])+fac
tor(calvmo[time>0])+age[time>0],dist="weibull")
summary(g)
```

```
### parametric survival model with random effect
g1<-survreg(Surv(time,state==1)[time>0]~system[time>0]+factor(calvyr[time>0])+factor(calvmo[time>0])+age[time>0]+frailty(herd[time>0],dist="gauss"),dist="weibull")
summary(g1)

#####Generalized linear model
###GLM
a<-1
for(j in 1:20){
alpha.logt<-a*log(time[time>0])
g<-glm(state[time>0]~system[time>0]+factor(calvyr[time>0])+factor(calvmo[time>0])+age[time>0]),family=poisson(link=log),offset=alpha.logt,data=data)
u.hat<-g$fitted.values
alpha.hat<-((sum((u.hat-state[time>0])*log(time[time>0])))/length(time[time>0]))^(-1)
alpha.new<-(alpha.hat+a)/2
a.old<-a
a<-alpha.new
}
print(abs(alpha.new-a.old))
print(summary(g))


#GLMM (GLM with random effect)
library(Matrix)
library(lattice)
library(lme4)
a<-1
for(j in 1:20){
alpha.logt<-a*log(time[time>0])
g1<-lmer(state[time>0]~system[time>0]+factor(calvyr[time>0])+factor(calvmo[time>0])+age[time>0]+(1|herd[time>0]),family=poisson(link=log),offset=alpha.logt,data=data1)
u.hat<-fitted(g1)
alpha.hat<-((sum((u.hat-state[time>0])*log(time[time>0])))/length(time[time>0]))^(-1)
alpha.new<-(alpha.hat+a)/2
a.old<-a
a<-alpha.new
}
print(abs(alpha.new-a.old))
print(summary(g1))
```