Description of Model for Estimation of Breeding Values for Longevity

Trait definition

Functional herd life

- number of days between first calving and culling or first calving and actual date
- censored data = data of living cows; used for estimation of breeding values but with no contribution for reliability

Data

- Milk recording data used for evaluation.
- Cows with known date of birth and date of first calving.
- Cows with date of first calving since 1.1.1992.
- Age at first calving 500 1200 days.
- Sires: all bulls registered in herd book including domestic and foreign AI bulls without natural service bulls.
- Sire must be at least 19 months older than his daughter.

Breed

- there are two separate evaluations for Simmental (SIM) population and Holstein (HOL) population
- SIM: cows included with at least 51% of SIM breed and no more than 13% of HOL breed and no more than 49% of RED breed; sire must be registered in SIM herd book
- HOL: cow included with at least 75% of HOL breed; sire must be registered in HOL herd book

Model

ST S-MGS

(Single Trait Sire - Maternal Grandsire Model)

- Non-linear model with usage of hazard functions with Weibull distribution.
- Survival analysis used Survival Kit (Vincent Ducrocq, Johann Sölkner).
- Methodology: Vincent Ducrocq: Survival Analysis Applied to Animal Breeding and Epidemiology, 2007

Effects used in model

- no pre-corrections of data used

Age at first calving

- not a time dependent effect
- relation of production herd life and age at first calving was treated by classification into 6 classes

Class	Age	SIM breed	HOL breed
1	500 - 750	43 467	154 617
2	751 - 780	57 845	98 027
3	781 - 830	145 066	149 898
4	831 - 900	204 435	143 844
5	901 - 960	120 050	69 572
6	961 - 1200	144 185	75 216

Lactation number

- the most important time dependent effect
- 8 classes; classes 1 7 correspond with number of lactation, class 8 is for lactation 8 and higher

Herd*year*season

- time dependent effect
- three 4-month seasons: January April, May August, September December
- at least 2 cows within an effect
- if a cow is only 1 within an effect, only this particular record is excluded (not all data of this cow)

Yield within a herd

- time dependent effect
- -7 classes for milk, 7 classes for fat, 7 classes for protein; separately for cows on first lactation and cows on higher lactations
- bounds for these 7 classes:

herd average -1.28 * herd st. deviation herd average -0.84 * herd st. deviation herd average -0.39 * herd st. deviation herd average +0.39 * herd st. deviation herd average +0.84 * herd st. deviation herd average +1.28 * herd st. deviation

- determination of yield for classification: average whole-life performance per lactation after end of each lactation
- determination of average and standard deviation for herd: moving average of herd per last 12 months
- if cow hasn't got yet any lactation her yield for classification is average of her herd (8 classes to 4000 kg of milk, then step of 1000 kg of milk for each class, over 9000 kg of milk for last class)
- if average of herd is not known (e.g. due to low number of cows in herd): individual class is for such cows

Herd size

- time dependent effect
- 6 classes: to 20 cows, 21-50, 51-100, 101-200, 201-400, 401 and more

Sire of cow

- the only one random effect in model
- sire must have at least 5 daughters to be included into evaluation

- relationship between bulls is expressed by relationship between evaluated bull, his sire and maternal grand sire

Results

Breeding value

- Breeding value expresses risk of culling of daughter.
- Publication in form of relative breeding value RBV with standardization to average of 100 and standard deviation of 12 for bulls born in 1995 (base). Values above 100 are desirable and mean higher ability of daughters to alive in herd.

$$RBV = 100 - (BV - x_{95}) / s_{95} * 12$$

Reliability

$$R = N_n / (N_n + (4 - h^2) / h^2)$$

 N_n number of non-censored (culled) daughters h^2 heritability

Heritability

$$h^2 = 4 * Var(s) / (Var(s) + N / N_n)$$

Var(s) estimated genetic variation

- N number of all daughters used in model
- N_n number of non-censored (culled) daughters

Genetic parameters used

- SIM: $h^2 = 0,230202$, Var(s) = 0,07520
- HOL: $h^2 = 0.223463$, Var(s) = 0.07698