

A Single-Step evaluation of functional longevity of cows including data from correlated traits

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= part of **Laure-Hélène Maugan's** PhD at INRAE / AgroParisTech

Contribution to the **UniGéno** project involving:



Lyon, France

August 26-27 2023

Interbull meeting

UniGéno : a generalization
of **single-step evaluations**
to all traits / all dairy and beef breeds

here :

Development of a Single-Step evaluation
of **functional longevity** of cows
including data from correlated traits



Montbéliarde

For a farmer, two major objectives for heifers « at birth »



- High production
- **Long functional life** (= independent from production)

- **Survival analysis** => « survival kit » software to evaluate **sires**
 - accounts for censored records (= information from animals still alive)
 - corrects for level of milk production
 - Main problem: not accurate when daughters are still young !

Implementation *before the genomic era*

1. linearize the survival analysis model

in order to get a **cow EBV for functional longevity**

(underlying idea: construct a **cow pseudo-record** for « **functional life** » **corrected for fixed effects** and such that an animal model BLUP evaluation of these pseudo-records leads to the same functional longevity breeding values of the sires)



at this stage, the pseudo-record y_i of cow i (**culled or still alive**)
can be written as: $y_i = \mu + a_i + \varepsilon_i$ where a_i is the breeding value of i
and $\text{var}(\varepsilon_i)$ is derived from the survival model

Implementation *before the genomic era*

2. Derive similar cow pseudo-records for **traits genetically correlated with functional longevity.**

(for example: conception rate, somatic cells score, clinical mastitis, etc.)



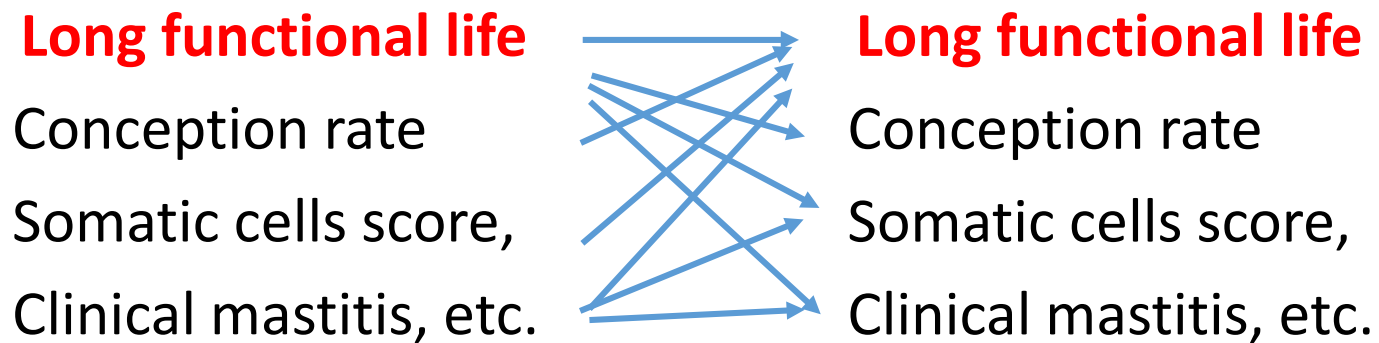
This is usually easier than for functional longevity because

breeding values come directly from an animal model

Again, the *pseudo-records* y_i of cow i can be written as $y_i = \mu + a_i + \varepsilon_i$

Implementation *before the genomic era*

3. Include these pseudo-records in a **multiple trait evaluation** together with cow records on **traits correlated with functional life**



combined evaluation = multiple trait evaluation of pseudo-records

Consequences : more accurate **functional longevity EBV of cows**

+ other functional traits + easy inclusion in Total Merit Index

Extension to single-step evaluations?

- Main problem: Functional longevity **genomic** evaluations « alone » were among the **less accurate ones** ...
- **Predictor traits exist !** e.g., **Genetic correlation with functional longevity:**

| Conception rate for heifer | Conception rate for cow | Somatic cell score | Clinical mastitis | Udder development |
|----------------------------|-------------------------|--------------------|-------------------|-------------------|
| -0.12 | -0.45 | 0.60 | 0.63 | 0.60 |

(Rostellato et al. 2022)



- But **Multiple trait genomic evaluations** too complex, especially because based on very different models ...

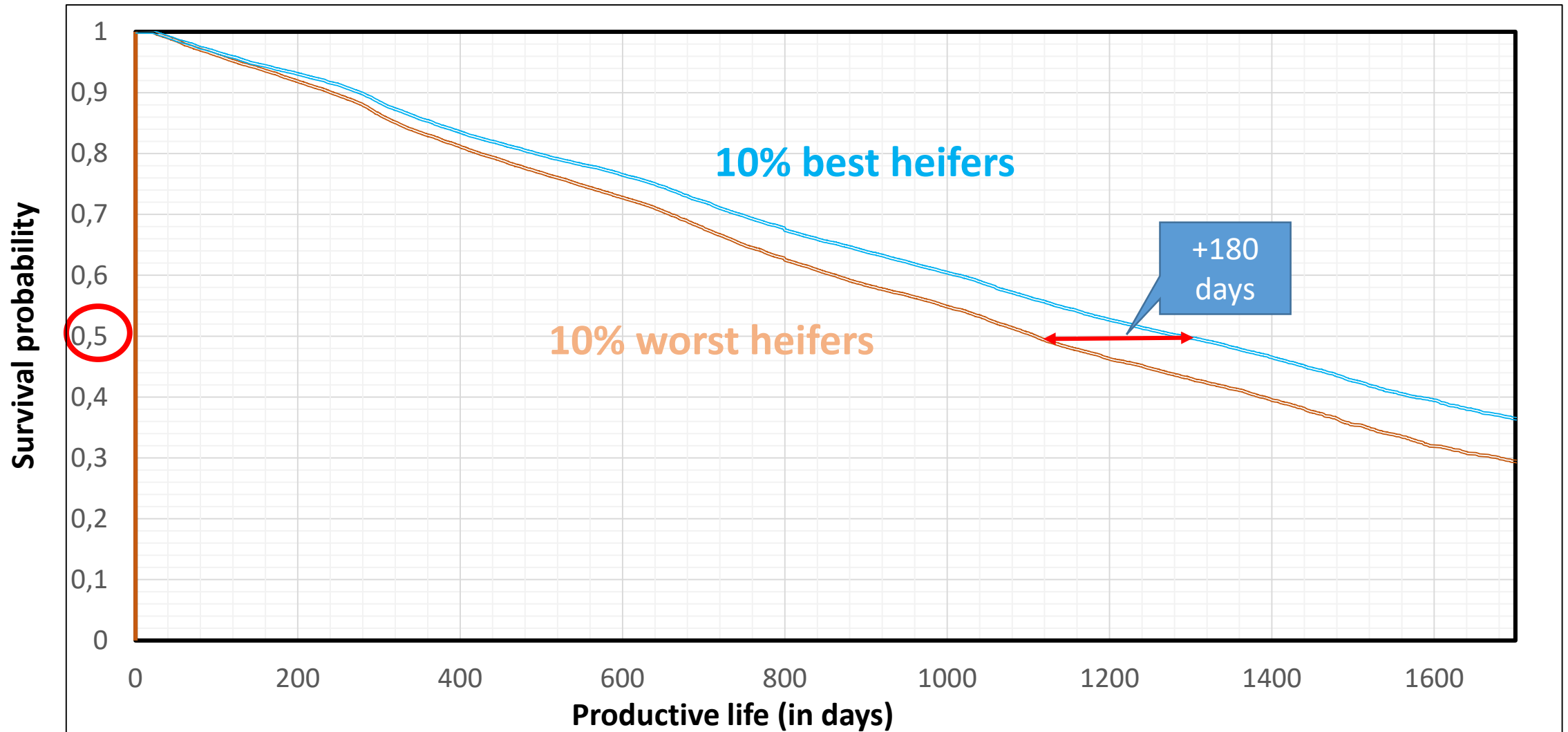
A **combined** single-step evaluation

- Step 1: Run a **sire genetic** analysis of functional longevity and derive **pseudo records** for functional longevity of **cows**
- Step 2: Run a **univariate animal model single-step evaluation** of each **predictor trait** of all animals with a least one record on one trait and derive the corresponding **pseudo-records** and their associated weight
- Step 3: Combine these results into a **multiple-trait single-step evaluation** of all animals with a pseudo-record and their ancestors (easy!)
- (Step 4: Combine into a total merit index)

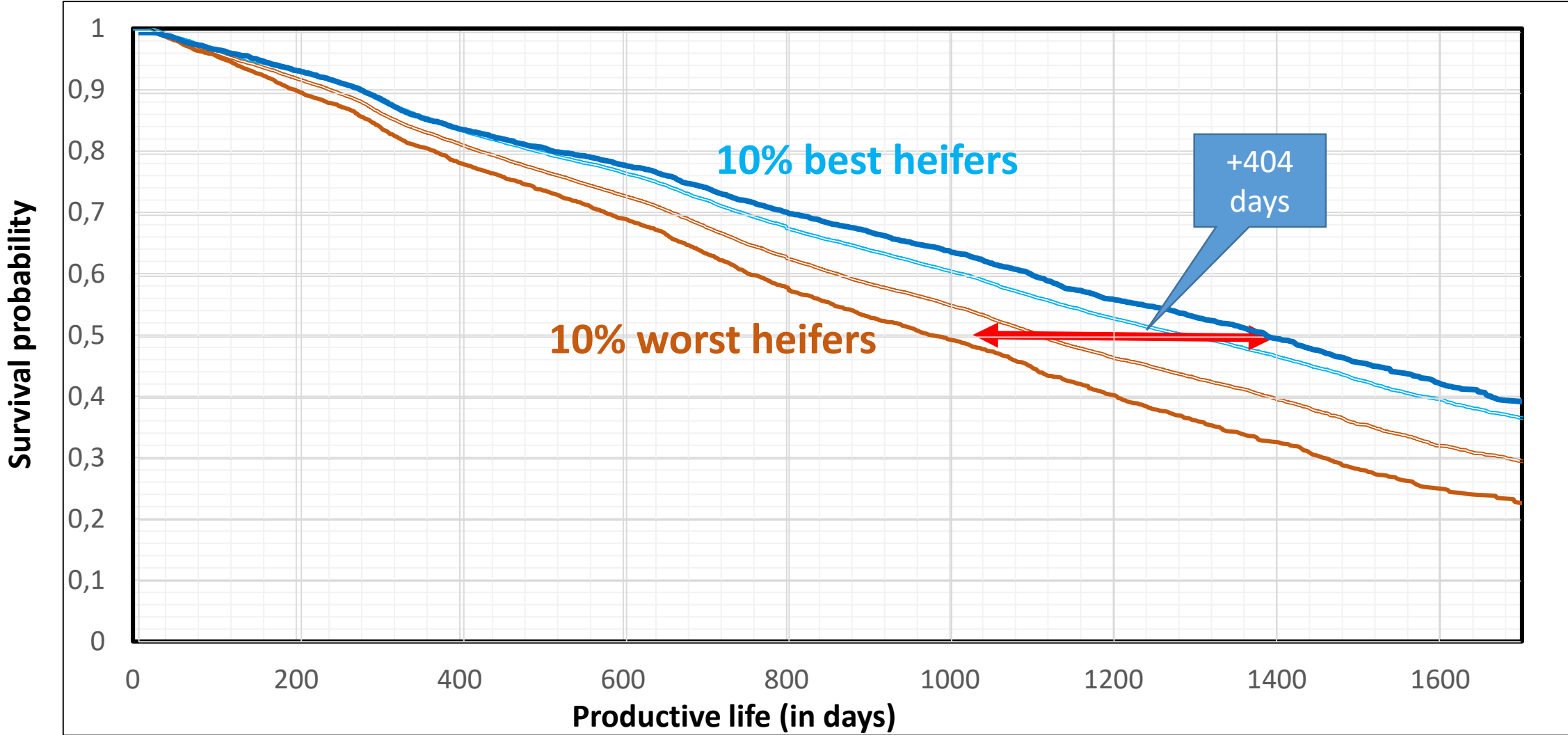
An example of combined single-step evaluation

- consider all data collected of **Montbéliade cows born since 1998**
 - mimic a single-step **functional longevity evaluation alone** vs **combined** in **2016** of **genotyped** and **non genotyped** cows
- ➔ Compare true functional longevity (survival curves) of **groups** of **genotyped** and **non-genotyped cows** born in 2014/2015 as observed **in 2021** (deciles: top 10%, next 20%, etc..)

Survivor curves of *non genotyped* heifers

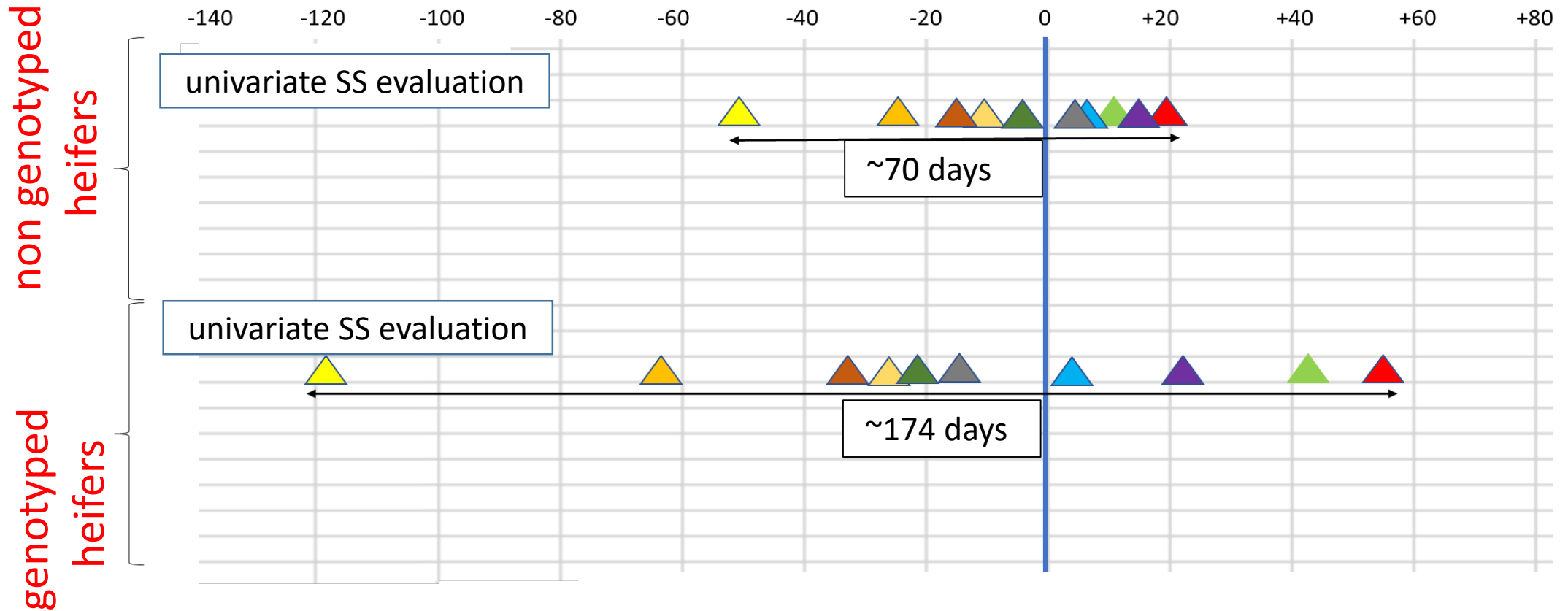


Survivor curves of *genotyped heifers*



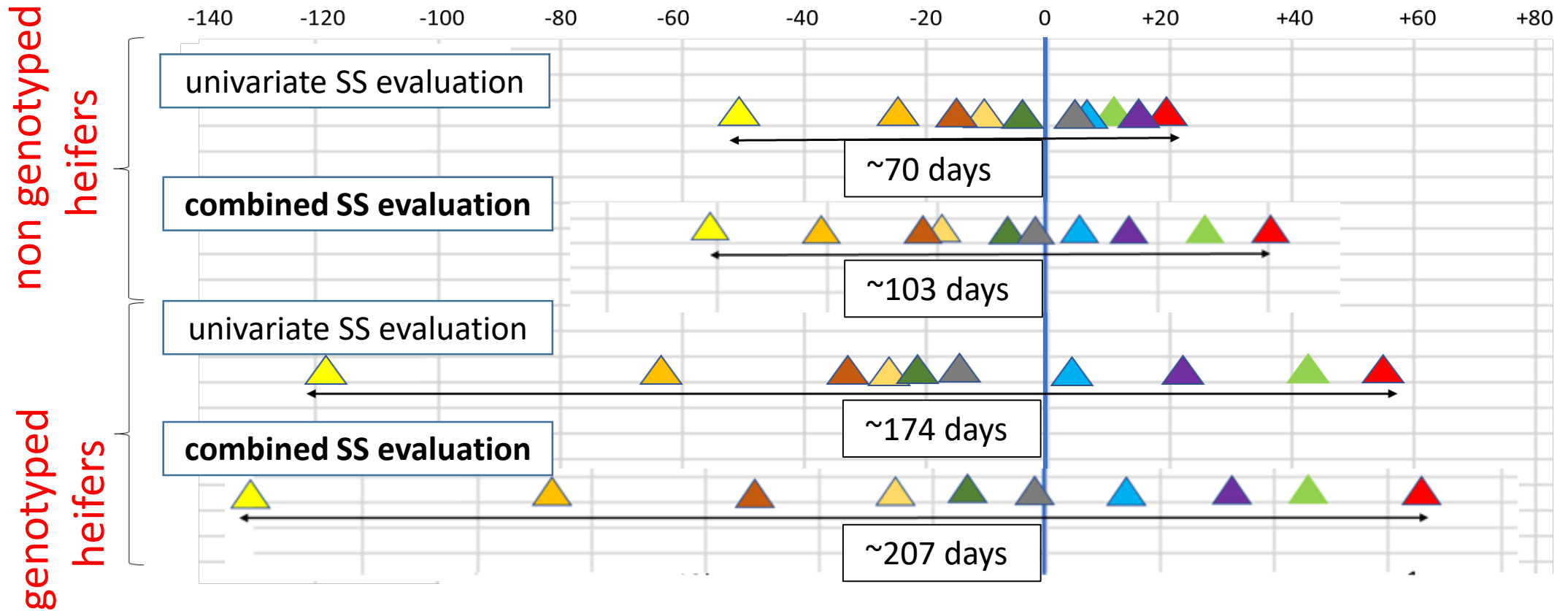
Variation in **functional life expectancy** at birth (expressed in days)

Average productive life (as a deviation from the mean)



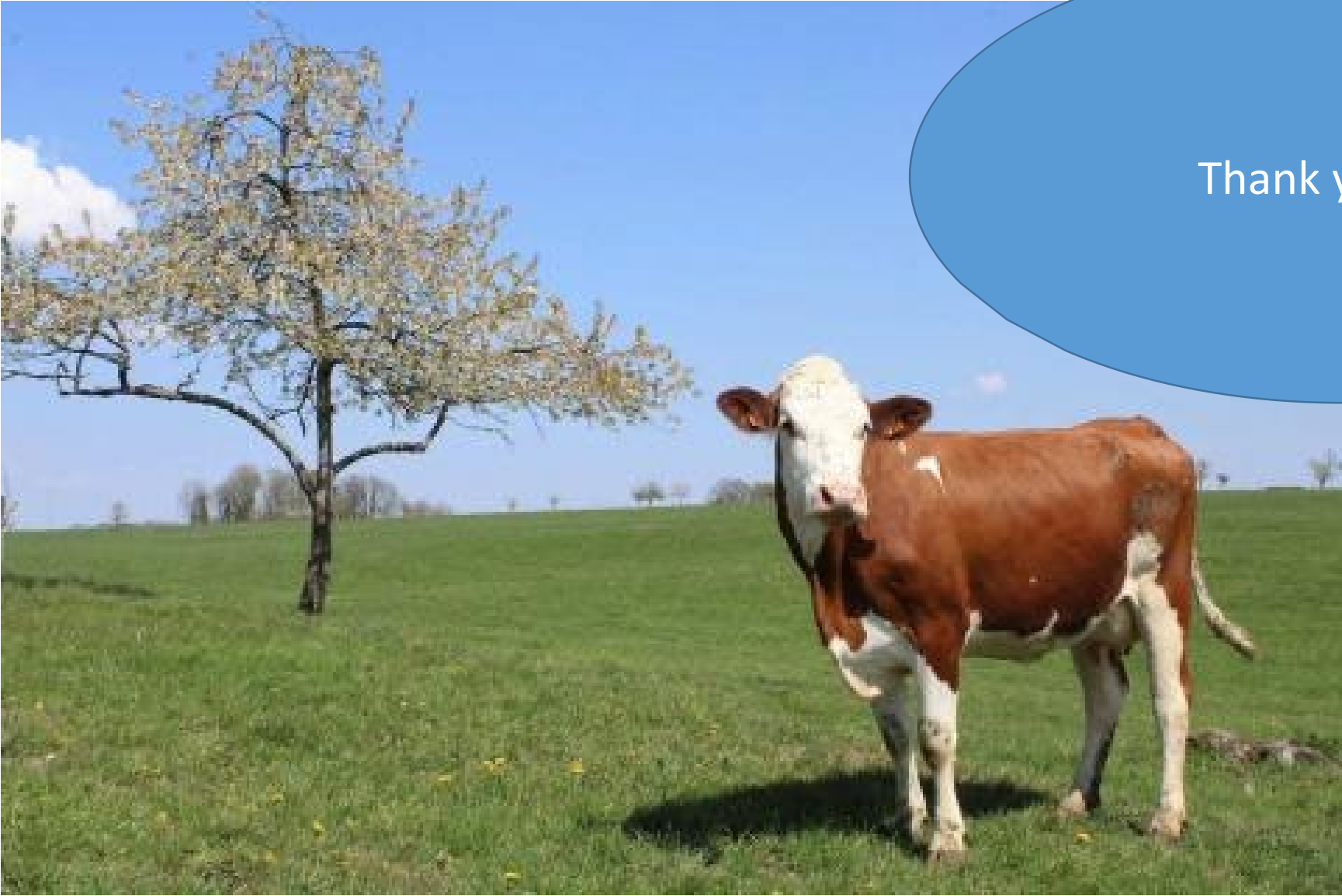
Variation in **functional life expectancy** at birth (expressed in days)

Average productive life (as a deviation from the mean)



Conclusion: The Single-step evaluations
of functional longevity of Montbéliarde heifers
are good predictors of their « future stayability in the herd »

- As expected, **Single-Step breeding values of functional longevity** lead to more accurate predictions for **genotyped heifers** than for **ungenotyped ones**
- The **Single-Step breeding values** of young heifers combining information on traits correlated with survival can inform the farmer about **which are the ones that are more likely to be culled early**



Thank you ! 😊

