Predicting lifespan of dairy cows

Phenotypic and genetic change during life

Mathijs van Pelt

Gerben de Jong and Roel Veerkamp

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Introduction - Longevity

- Longevity = productive lifespan = days between 1st calving and last testdate
    - Available when cow is culled

- Current genetic evaluation in The Netherlands
    - Piecewice Weibull Model
    - Survival Kit software (Ducrocq & Sölkner)
    - Predictors included with selection index

Introduction - Longevity

- Problem:
  - Breeding values fluctuate too much
  - Especially from 1st to 2nd crop information

- Hypothesis:
  - Model is too simplistic in modelling the genetic variation in longevity
  - Assumes longevity is genetically same trait during life

Aim

Investigate the phenotypic and genetic (co-)variation of longevity

1. During total lifespan

2. Within and across lactations

Material and methods – Data

- National dataset available from CRV
  - Pedigree (20M), lactations (40M), movements (100M)
- Total dataset
  - Per cow one record for each month in productive life
  - Cows present in period 1988 - 2012
  - 370M records of 10M cows in total
- Dataset sized down
  - 27 herds
  - ~25K black & white cows (1-120 months in productive life)
  - ~600 sires
  - ~850K records

Material and methods – Genetic analysis

- Random regression model

$$\mathbf{Y = X\beta + Za + Zp + e}$$

Y = survival (1 – 120 months in productive life)

β = fixed effects

- Herd-year-season of calving
- Year-season of observation
- Parity-month in lactation
- Parity-year-season of calving
- Age at first calving (2nd order Legendre polynomial)
- Month in life (4th order Legendre polynomial)

a = additive genetic random effect

p = permanent environment random effect

➢ 2nd order Legendre polynomials for **a** and **p**

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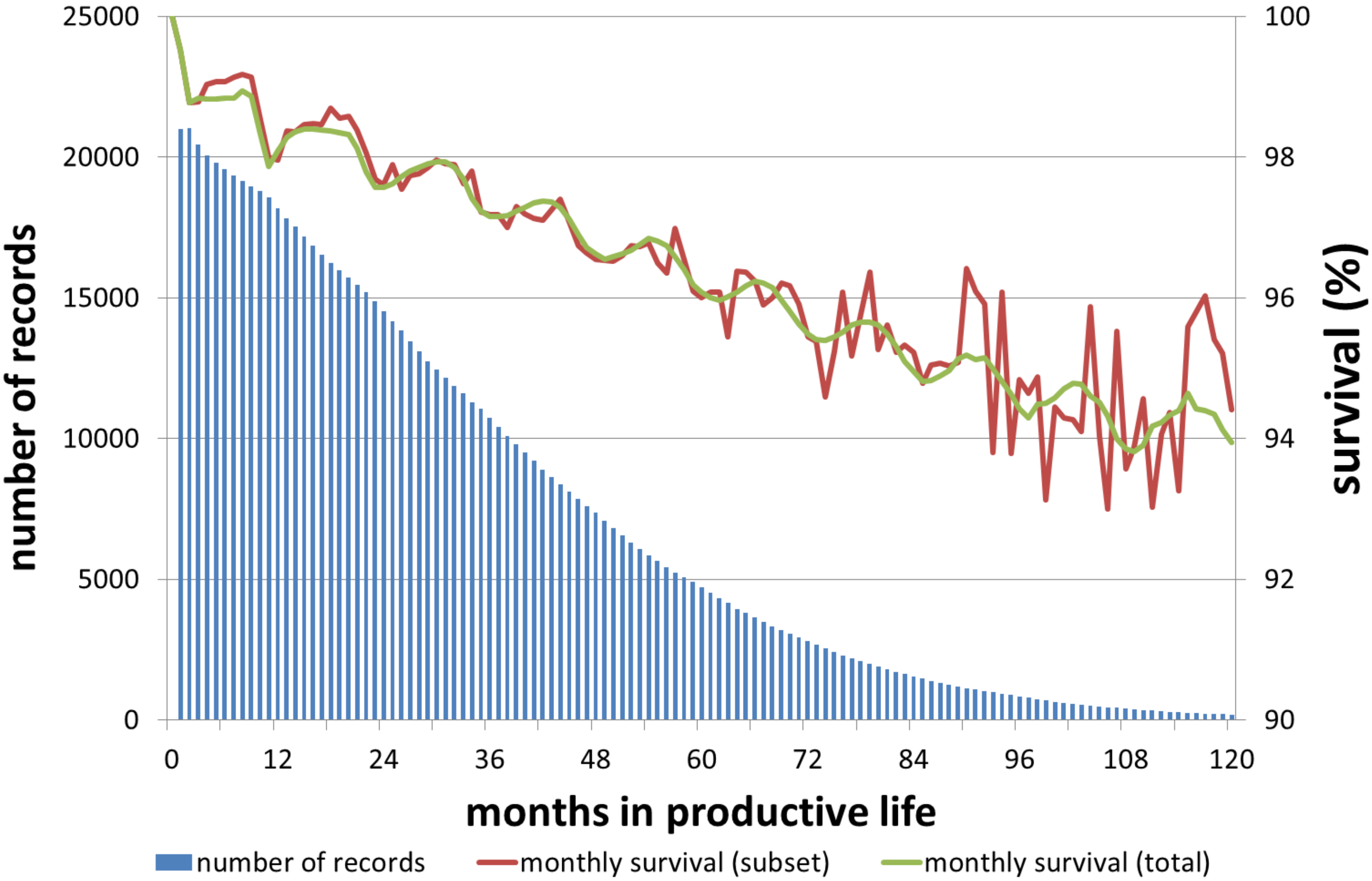
Material and methods – Genetic analysis

- Time covariables for **a** and **p** in random regression (RR)
    1. During total lifespan
        - RR on months in life (**MIL**)
    2. Within and across lactations
        - RR per parity on months in milk (**par x MIM**)
        - Parity 1, 2, 3+ with a maximum of 18 months in milk
- Use of uncorrelated residual classes
    1. **MIL**: 40 classes of 3 months
    2. **par x MIM**: 3 parity groups x 18 MIM classes
- Analysis with ASREML (Gilmour *et al.*, 2009)

Results – phenotypic means (**MIL**)



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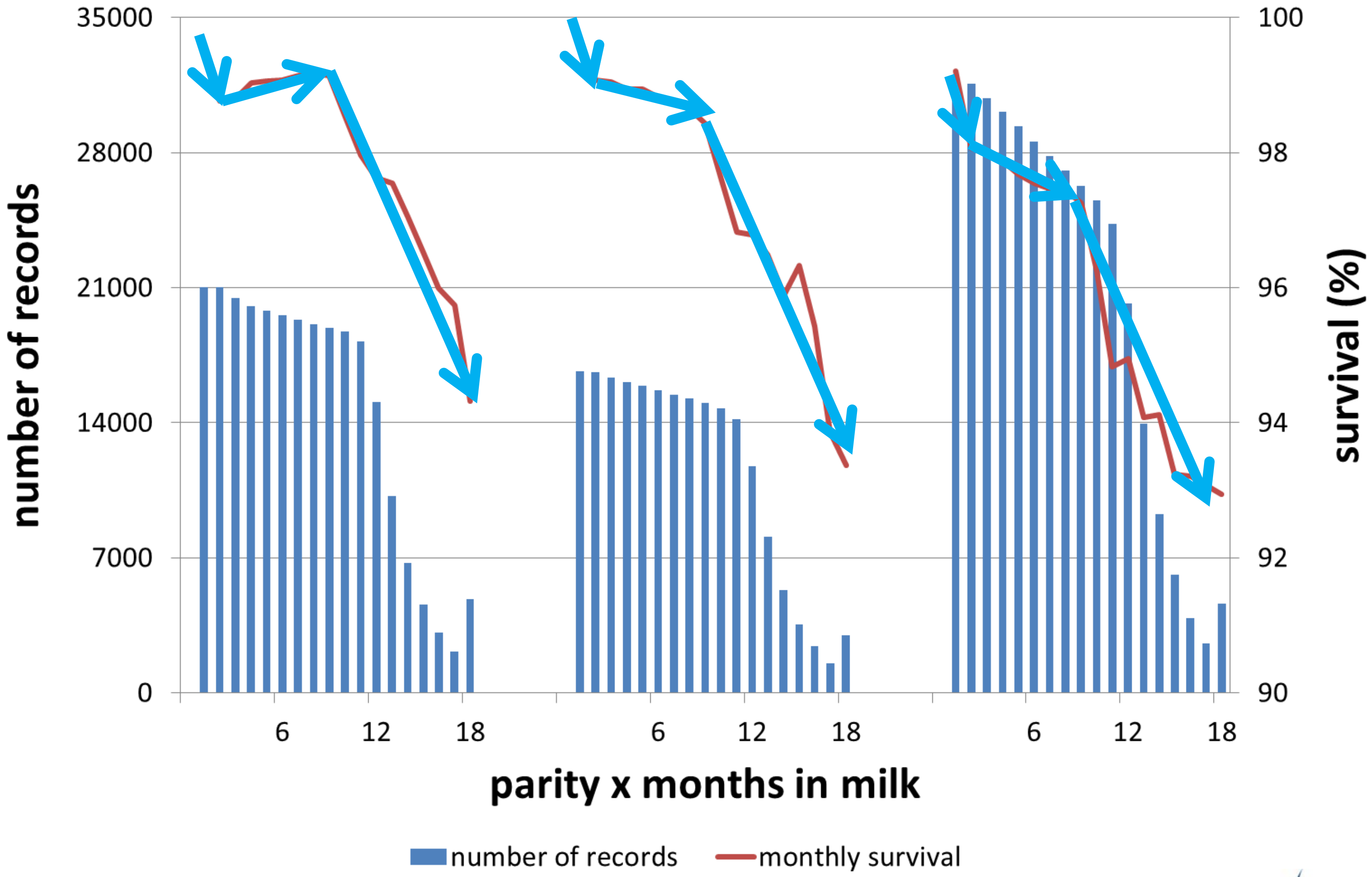
Results – phenotypic means (**par x MIM**)



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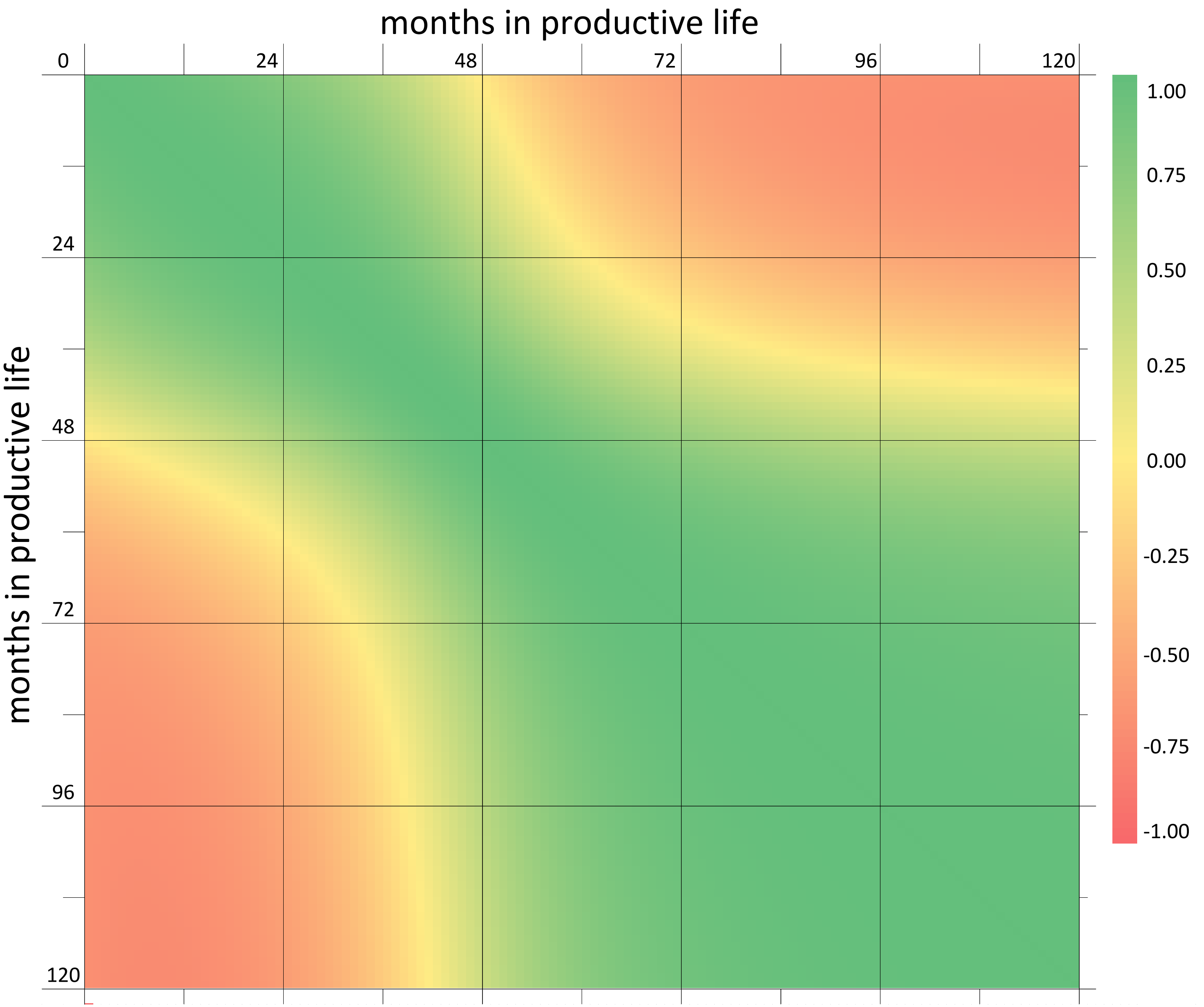
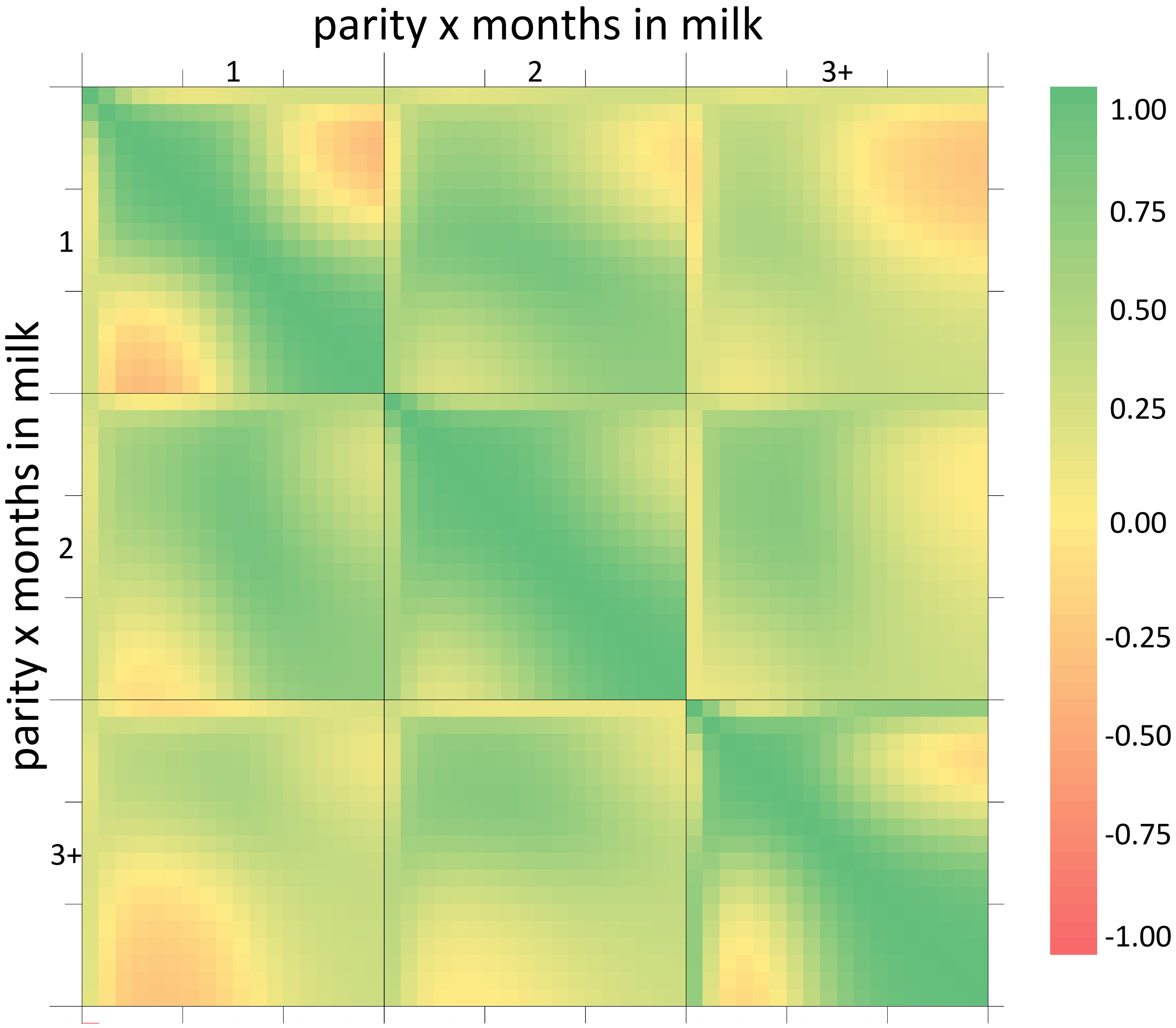
Results – Genetic parameters (**MIL**)

	variance					
months in life	genetic	permanent environment	residual	phenotypic	**h^2**	phenotypic mean (%)
2	7.3	5.5	90.6	97.9	**0.07**	98.77
20	6.4	4.8	142.2	148.5	**0.04**	98.58
40	5.2	3.9	271.1	276.3	**0.02**	97.20
60	12.4	9.3	352.8	365.3	**0.03**	96.00
80	48.4	36.3	385.8	434.2	**0.11**	95.26
100	…	…	…	…	…	94.45
118	…	…	…	…	…	95.41

Results – Genetic correlations (**MIL**)



Results – Genetic correlations (**par x MIM**)



Conclusions

- Survival is a different trait across and within lactations
    - Differences in phenotypic means
    - Genetic correlations < 0.90

- Modelling in a more complex way to get:
    - Better understanding of survival
    - More stable breeding values

Thank you for your attention

Questions?

Project is part of

BREED4FOOD

mathijs.vanpelt@wur.nl

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