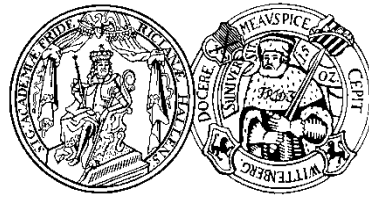




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# Estimating heritabilities for fertility disorders using on farm recorded health data

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# The objective of my work

- evaluation of on farm recorded health data and definition of traits for fertility disorders
- estimating variance components, heritability's and breeding values for the whole lactation, using single trait animal models
- consider the lactation in parts and fit random regression models for estimation
- calculate phenotypic and genetic correlations between parts



# data, data editing and trait definition

- raw data: 741,776 diagnoses from 01/01/2013 until 15/11/2015
  - 77,040 animals in 145 farms
- edited data: 24,593 lactations (20,534 animals)
  - 9,605 cows in 1<sup>st</sup>, 14,988 cows in 2<sup>nd</sup> and 3<sup>rd</sup> lactation
  - average of 647 lactations per herd (38)
  - calvings in 8 seasons
  - 553 sires
- calculation of incidence rates (inc) and number of new cases (nonc) per lactation for fertility disorders:
  - fertility disorders in general (GD)                      inc= 42.28%
  - sterility diagnoses (SD)                                      inc= 34.01%
  - disorders observed post-partum (DPP)                      inc= 16.49%

# models for overall lactation

- fixed effects with a significant effect on the traits were evaluated using the glimmix and the mixed procedure in SAS
- adding the additive genetic effect of the animal and a random effect for the permanent environment of the animal, in ASReml

$$y = Xb + Z1a + Z2pe + e \quad [+lin(DIM)]$$

with:

y = phenotypic observations;

X = matrix of fixed effects;

b = vector of fixed effects;

Z1 and Z2 = matrix for the random effect

a (add.-gen.) und pe (permanent environment);

a = genetic effect (random);

pe = permanent environment (random);

e = random error term;

lin(DIM) = linear regression of days in milk,  
only for nonc

# $h^2$ from models for overall lactation

| trait | model         |               |               |
|-------|---------------|---------------|---------------|
|       | inc (bin)     | inc (lin)     | nonc          |
| FD    | 0.041 (0.012) | x             | 0.034 (0.008) |
| SD    | 0.041 (0.013) | 0.018 (0.006) | 0.027 (0.007) |
| DPP   | 0.066 (0.014) | 0.026 (0.007) | 0.021 (0.006) |

(standard error)

# random regression - data and trait editing

- using the already selected 24,593 lactations
  - splitting up every lactation into 15 equal parts (368,895 records)
  - programing incidence for every part and disorder
- apply local regression to inspect parts of interest for all fertility disorder traits
  - herds with at least 1 diagnosis in every considered part
- FD: part 1 – 15 → 22 herds, 237,645 records
- SD: part 1 – 10 → 26 herds, 167,230 records
- DPP: part 1 – 5 → 3 herds, 26,145 records

# random regression - models

$$\text{Model: } y_{ijk} = \mu + la_i + \sum_{k=1}^4 h_j \cdot x_k + a_{0n} + a_{1n} \cdot x_1 + a_{2n} \cdot x_2 + pu_{0n} + pu_{1n} \cdot x_1 + e_{ijkn}$$

$y$  = vector of phenotypic observations

$\mu$  = population average

$la_i$  = fixed effect for i-th lactation

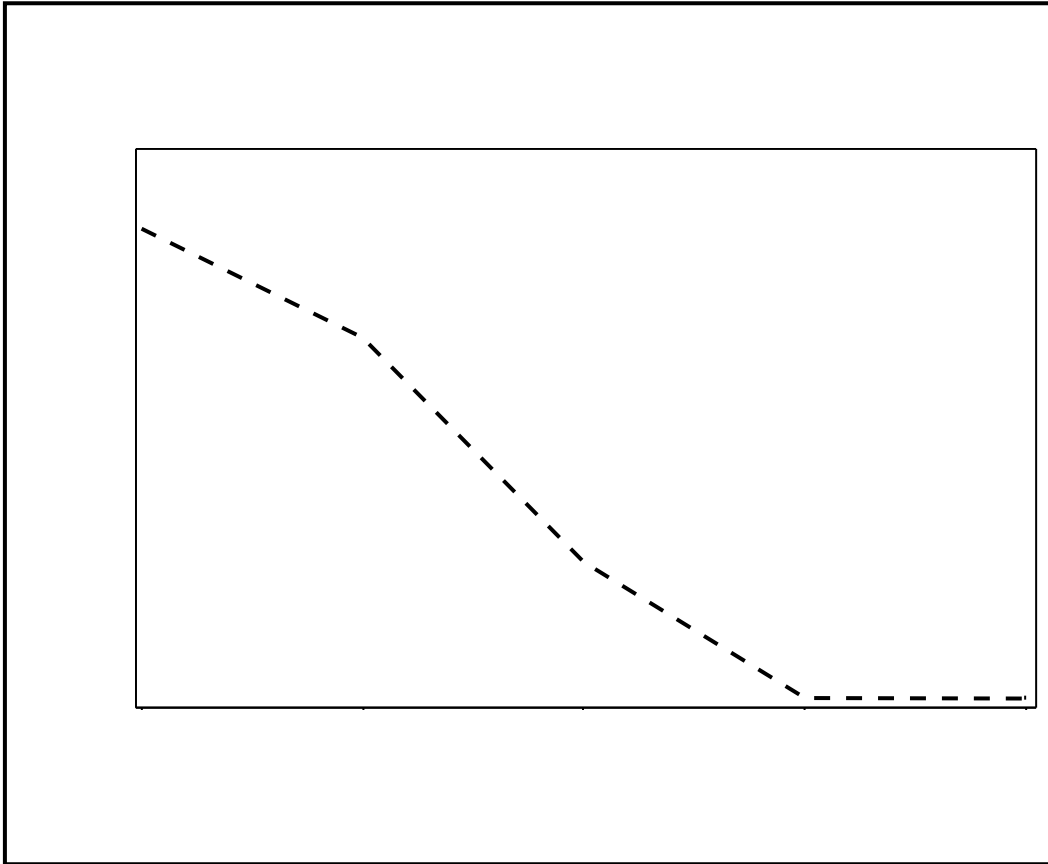
$h_j$  = fixed effect for j-th herd

$X_k, X_1 \dots X_4$  = Ali & Schäfer polynomials as regression coefficient for covariabls

$a_{1,2n}$  and  $pe_{1n}$  = regression coefficient for the random effect  $a$  (add.-gen.) und  $pe$  (permanent environment) for n-th animal,

$e_{ijkn}$  = residual term

# random regression – heritabilities, phenotypic and genetic correlations for DPP

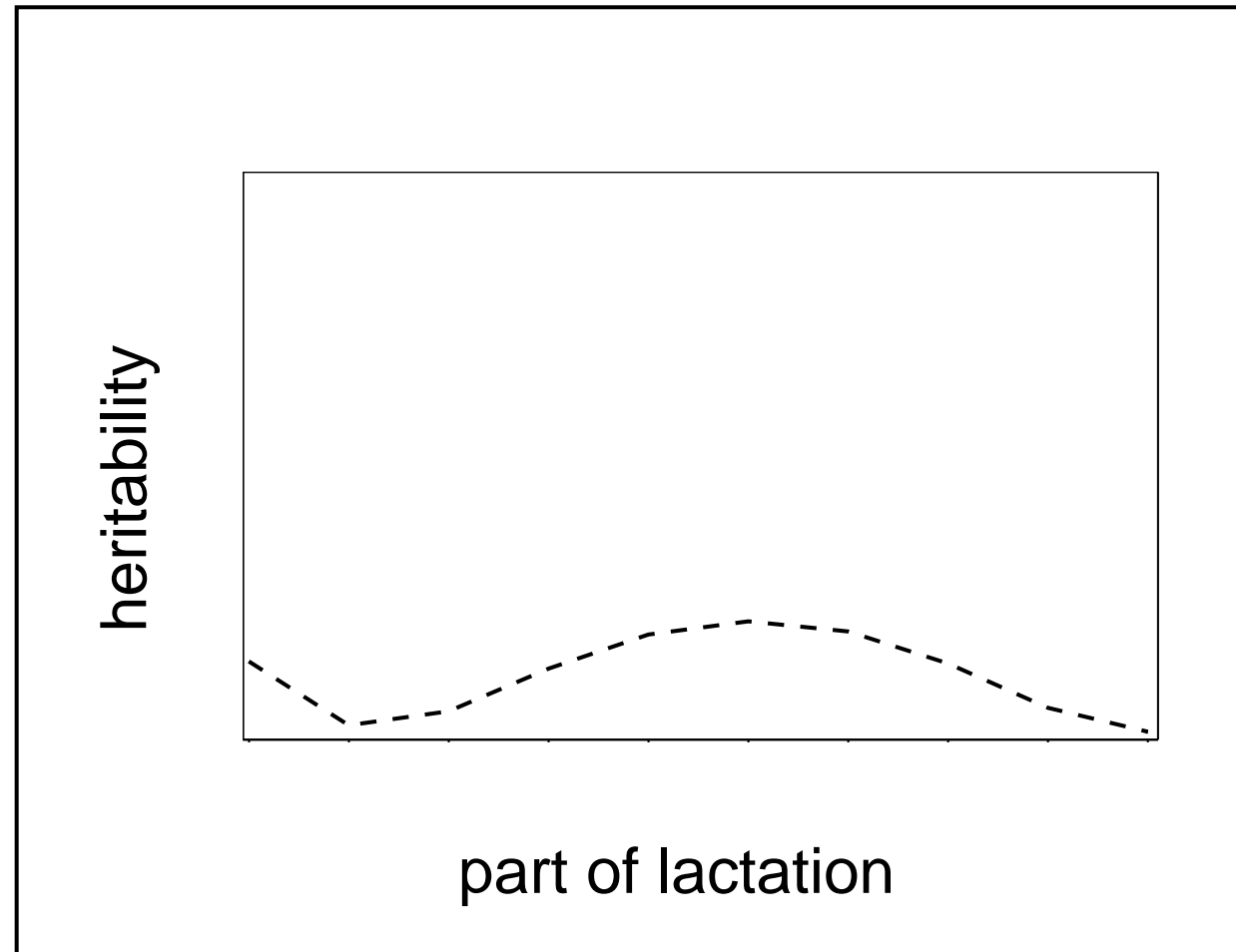


heritabilities, phenotypic and genetic correlations for DPP

| part | 1      | 2      | 3      | 4      | 5      |
|------|--------|--------|--------|--------|--------|
| 1    | 0.871  | 0.764  | 0.473  | 0.080  | -0.076 |
| 2    | 1.000  | 0.670  | 0.415  | 0.070  | -0.067 |
| 3    | 1.000  | 1.000  | 0.257  | 0.044  | -0.041 |
| 4    | 1.000  | 1.000  | 1.000  | 0.007  | -0.007 |
| 5    | -1.000 | -1.000 | -1.000 | -1.000 | 0.006  |



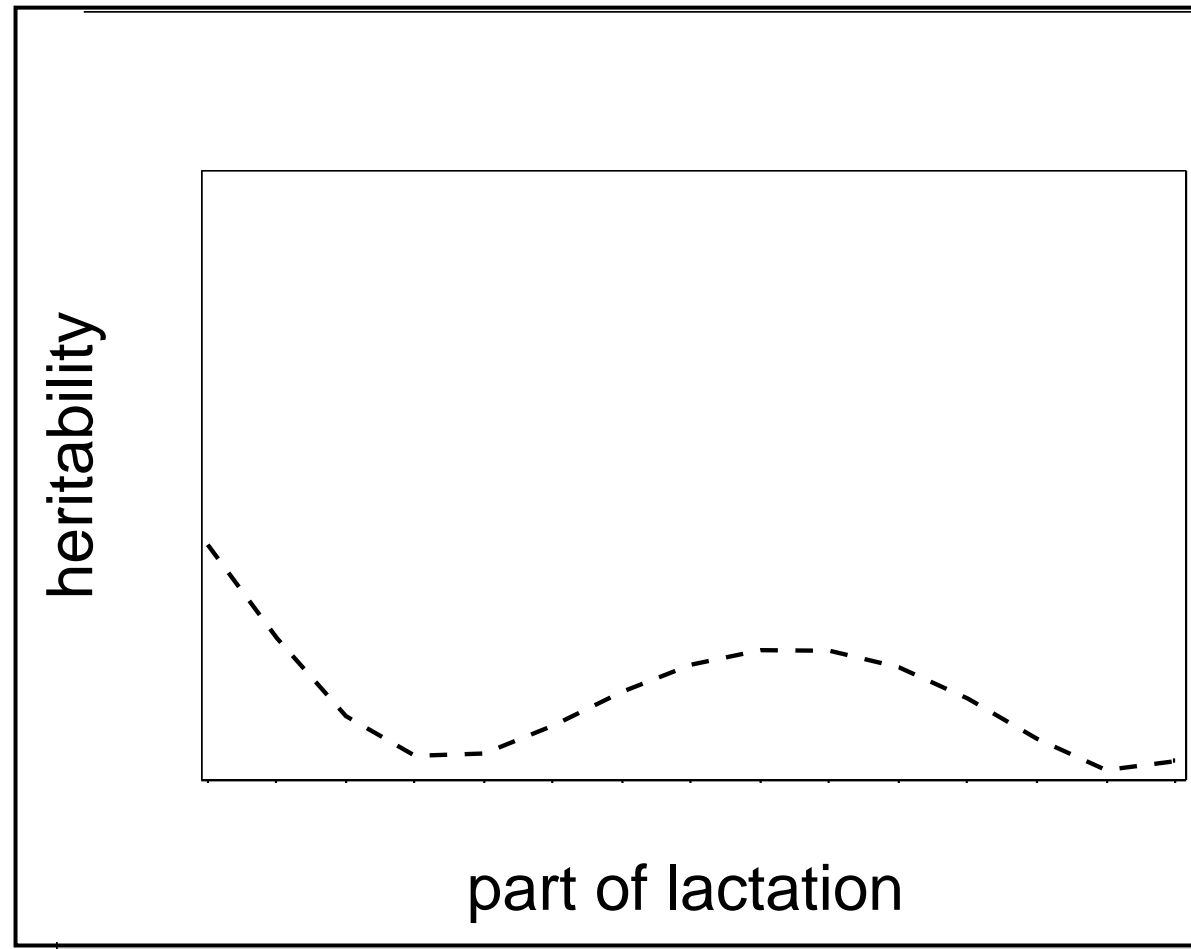
# random regression – heritabilities, phenotypic and genetic correlations for SD



# random regression – heritabilities, phenotypic and genetic correlations for SD

| part | 1      | 2      | 3      | 4      | 5      | 6      | 7      | 8      | 9     | 10    |
|------|--------|--------|--------|--------|--------|--------|--------|--------|-------|-------|
| 1    | 0.131  | 0.384  | 0.297  | 0.227  | 0.184  | 0.168  | 0.177  | 0.212  | 0.275 | 0.358 |
| 2    | 0.729  | 0.016  | 0.369  | 0.343  | 0.324  | 0.316  | 0.319  | 0.334  | 0.357 | 0.377 |
| 3    | -0.680 | 0.006  | 0.041  | 0.417  | 0.418  | 0.417  | 0.416  | 0.413  | 0.402 | 0.369 |
| 4    | -0.847 | -0.252 | 0.966  | 0.118  | 0.469  | 0.472  | 0.469  | 0.454  | 0.421 | 0.352 |
| 5    | -0.887 | -0.330 | 0.942  | 0.997  | 0.180  | 0.498  | 0.493  | 0.472  | 0.426 | 0.339 |
| 6    | -0.904 | -0.366 | 0.928  | 0.993  | 0.999  | 0.204  | 0.500  | 0.478  | 0.427 | 0.334 |
| 7    | -0.912 | -0.387 | 0.919  | 0.989  | 0.998  | 1.000  | 0.186  | 0.474  | 0.427 | 0.338 |
| 8    | -0.915 | -0.398 | 0.911  | 0.985  | 0.995  | 0.998  | 0.999  | 0.128  | 0.423 | 0.352 |
| 9    | -0.900 | -0.396 | 0.892  | 0.966  | 0.978  | 0.982  | 0.986  | 0.992  | 0.047 | 0.370 |
| 10   | 0.198  | 0.113  | -0.160 | -0.178 | -0.175 | -0.165 | -0.146 | -0.107 | 0.016 | 0.004 |

# random regression – heritabilities for FD



# models for overall lactation- random regression models, comparison

|       | heritability from model      |                              |   |
|-------|------------------------------|------------------------------|---|
| trait | whole lactation<br>(inc bin) | random regression<br>(means) | random regression<br>(selected h <sup>2</sup> ) |
| FD    | 0.041 (0.012)                | 0.133 (0.103)                | 0.031 (part 4)                                  |
| SD    | 0.041 (0.013)                | 0.106 (0.074)                | 0.016 (part 2)                                  |
| DPP   | 0.066 (0.014)                | 0.362 (0.393)                | x   |

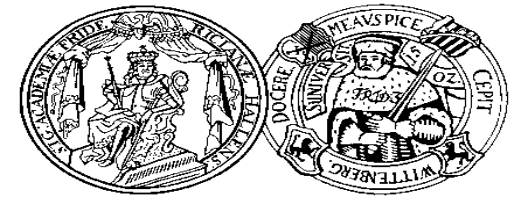
(standard error)

# conclusion and outlook

- heritabilities for fertility disorders from models for the whole lactation are in same range as in the literature
- estimates from random regression models for selected parts of the lactation seem to be higher
- correlations indicate that there are differences in traits for fertility disorders over the lactation
- traits should be defined as specific as possible
- results from random regression animal models demand a cautious interpretation
- confirm the results on a bigger data set



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# Thank you for your attention!



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