

# Estimation of variance components for clinical mastitis and somatic cell scores for the Nordic dairy cattle populations

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# Clinical mastitis

- Important disease affecting dairy cattle
  - Causing loss of production and early culling
  - Needing changes in management and treatment of cows
- Risk of infection differs
  - Early vs. late lactation
  - First vs. later lactations
- Clinical mastitis (**CM**) is binary trait
  - Difficult to estimate variance components
- Somatic cell scores (**SCS**) easier to measure
  - Related to CM

# Trait harmonization and evaluation

- EuroGenomics member countries agreed to trait harmonization for udder health traits
- Nordic Cattle Genetic Evaluation (NAV) upgrading evaluations to “golden standard”
- Important to determine genetic architecture of udder health traits
- Objectives were to estimate variance components
  1. CM at two risk stages (early and late lactation) and at three lactations
  2. SCS at three lactations

# Data

Breed	Cows	Sires	Lactation	CM – early	CM – late	SCS
Holstein (HOL)	68422	2159	1	68422	66594	597079
			2	44688	43576	423213
			3	26323	25398	245977
Jersey (JER)	64194	986	1	64194	63543	617847
			2	43626	42846	428453
			3	27512	27507	269072
Red dairy cattle (RDC)	71596	1258	1	71596	69546	612062
			2	46355	45408	423202
			3	27665	26817	244788



# CM incidence and mean SCS

Breed	Lactation	CM – early <sup>#</sup>	CM – late <sup>#</sup>	SCS*
HOL	1	3.50	5.11	4.04 (1.11)
	2	4.43	10.59	4.40 (1.20)
	3	7.05	13.29	4.70 (1.23)
JER	1	5.65	7.33	4.19 (1.04)
	2	7.23	12.32	4.32 (1.15)
	3	10.18	13.58	4.49 (1.21)
RDC	1	3.11	4.55	4.07 (1.12)
	2	3.83	8.88	4.41 (1.20)
	3	5.61	10.86	4.71 (1.23)

#%

\*log 1000 cells/mL

# Model

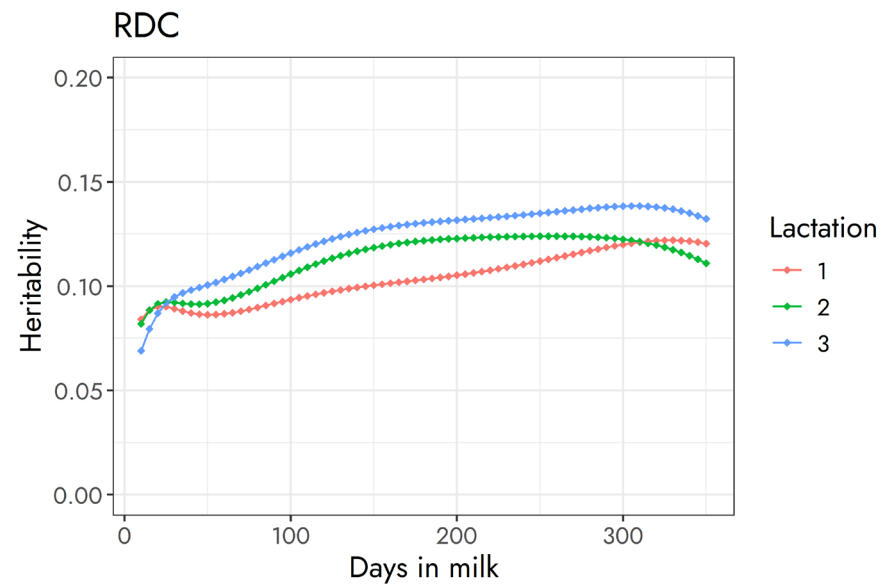
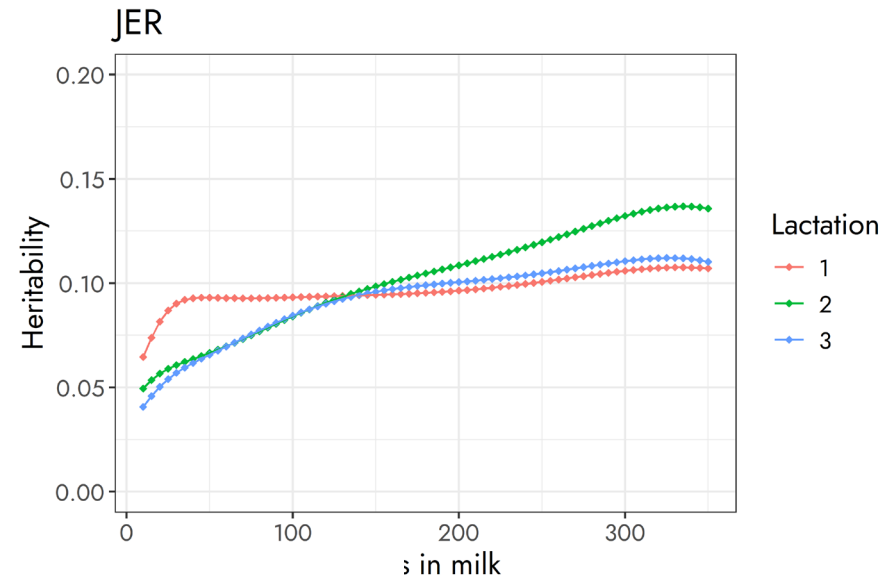
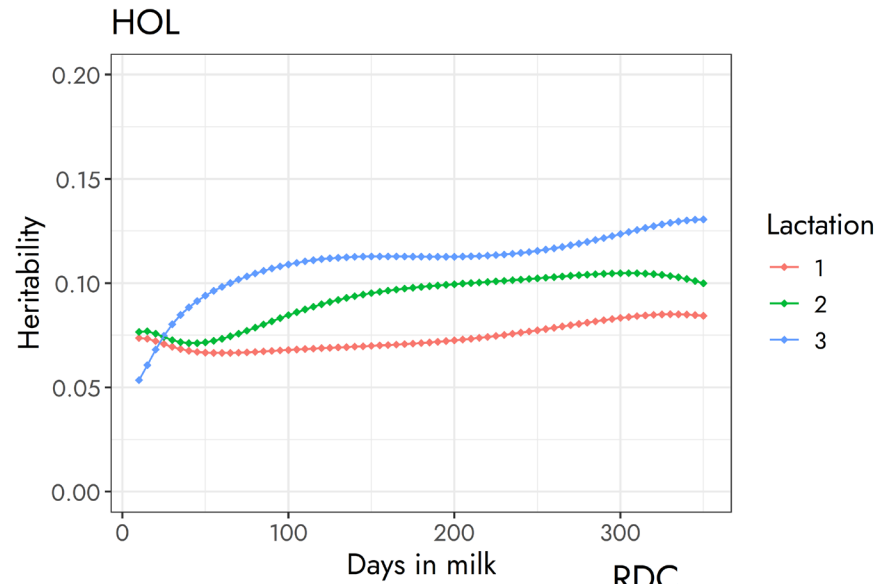
$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_c \mathbf{c} + \mathbf{Z}_u \mathbf{u} + \mathbf{e}$$

- Fixed effects ( $\boldsymbol{\beta}$ )
  - Herd-year, age, inbreeding, rec. loss, heterosis
- Permanent environmental effect ( $\mathbf{c}$ ) and sire ( $\mathbf{u}$ )
  - Random regression
  - CM (intercept)
  - SCS (intercept, linear, quadratic, exponential)
- Parameters estimated in MiX99
  - Monte Carlo (**MC**) Expectation-Maximization (**EM**) REML
  - Pedigree information

# CM – heritability (%)

Breed	Lactation 1		Lactation 2		Lactation 3	
	Early	Late	Early	Late	Early	Late
HOL	0.74	1.24	1.38	2.08	1.43	3.48
JER	1.11	1.22	1.38	2.32	1.51	2.82
RDC	1.62	1.13	1.29	2.61	1.61	3.39

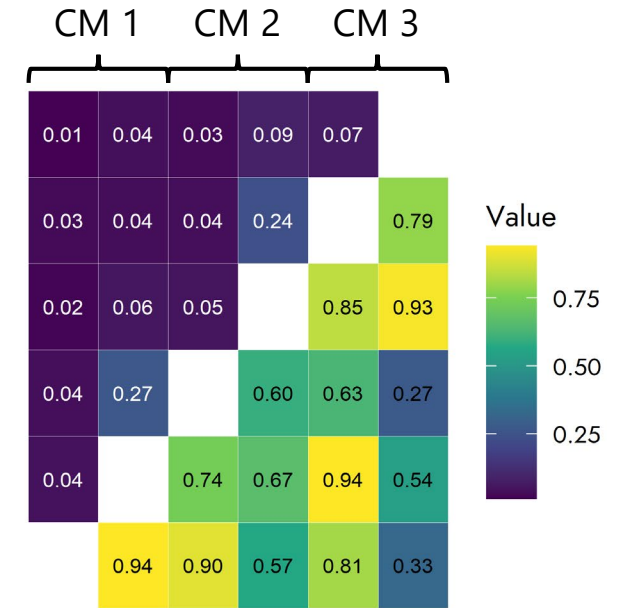
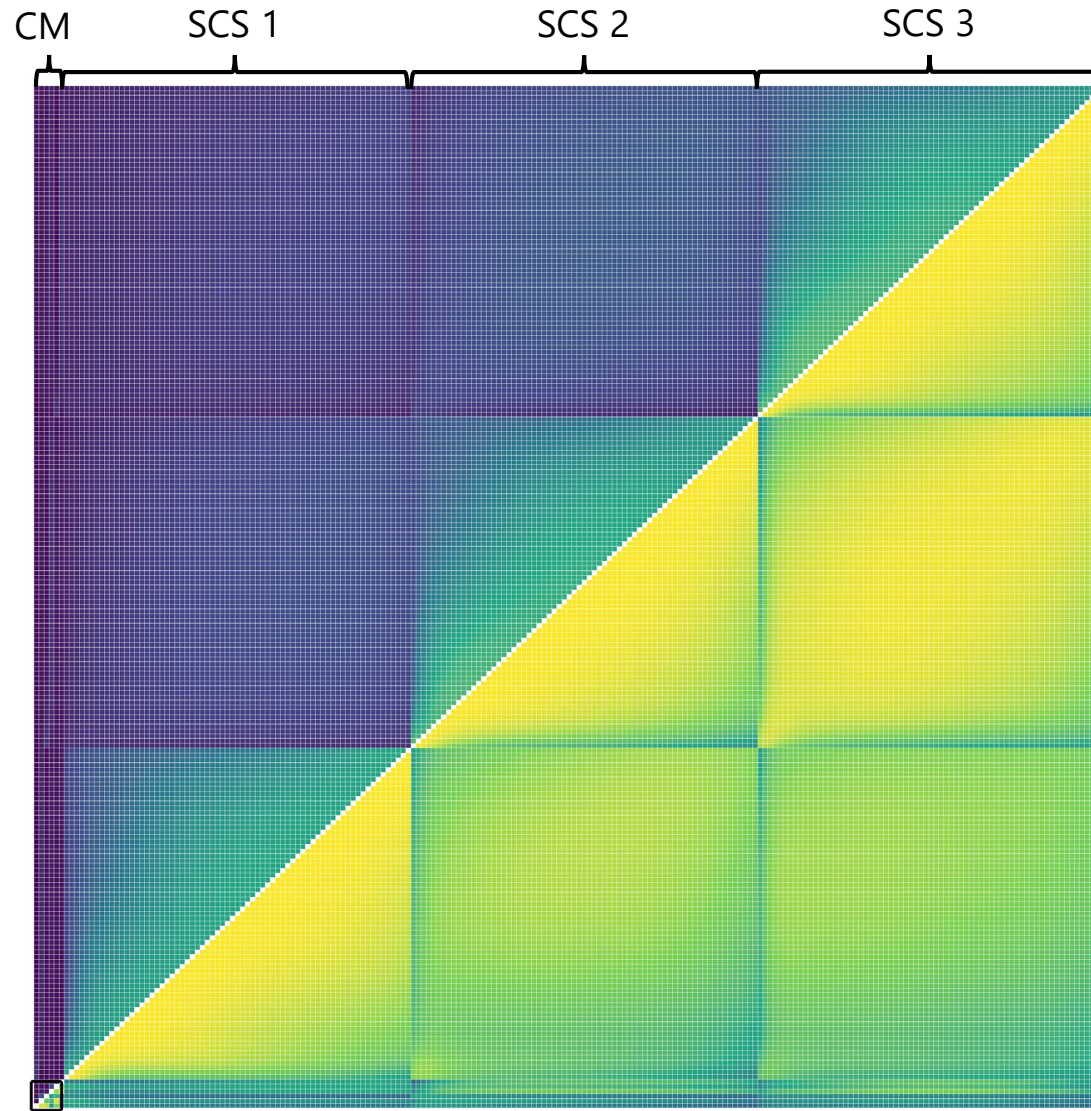
# SCS heritability





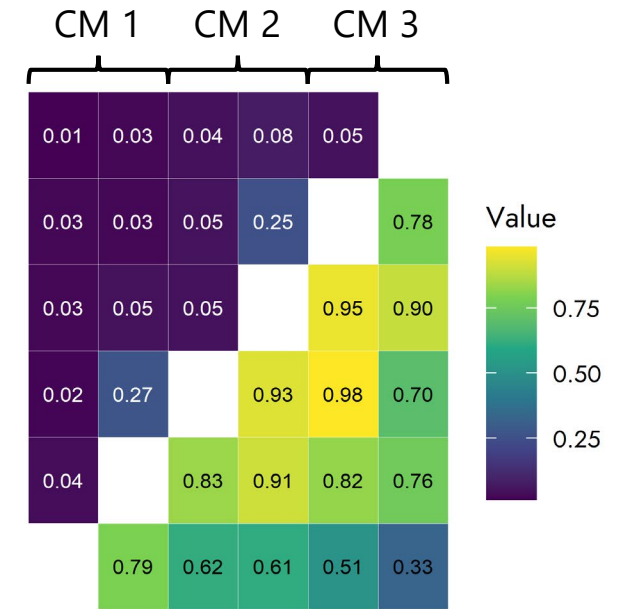
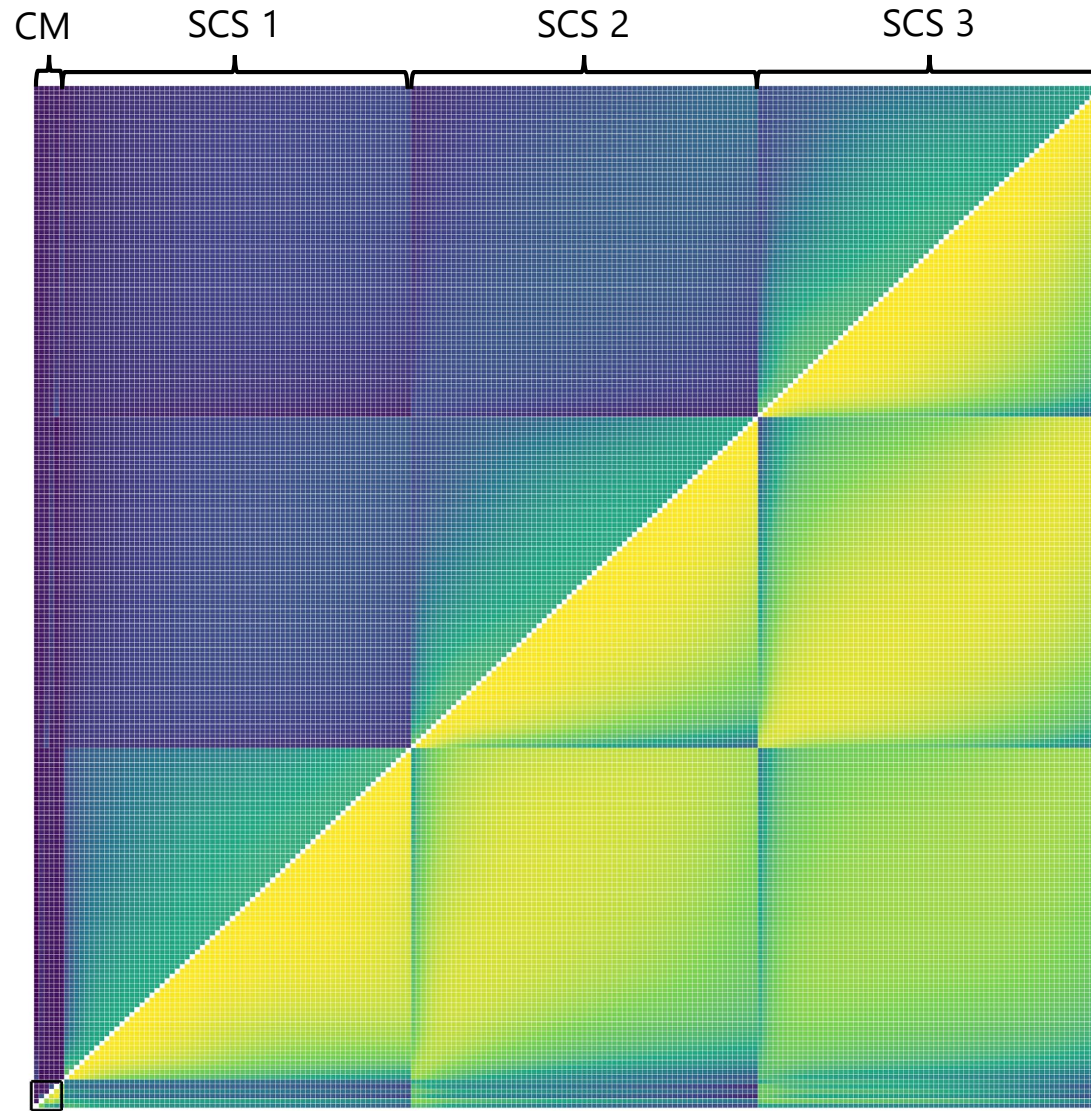
# CM and SCS - HOL

60 DIM (10, 15, ..., 305)



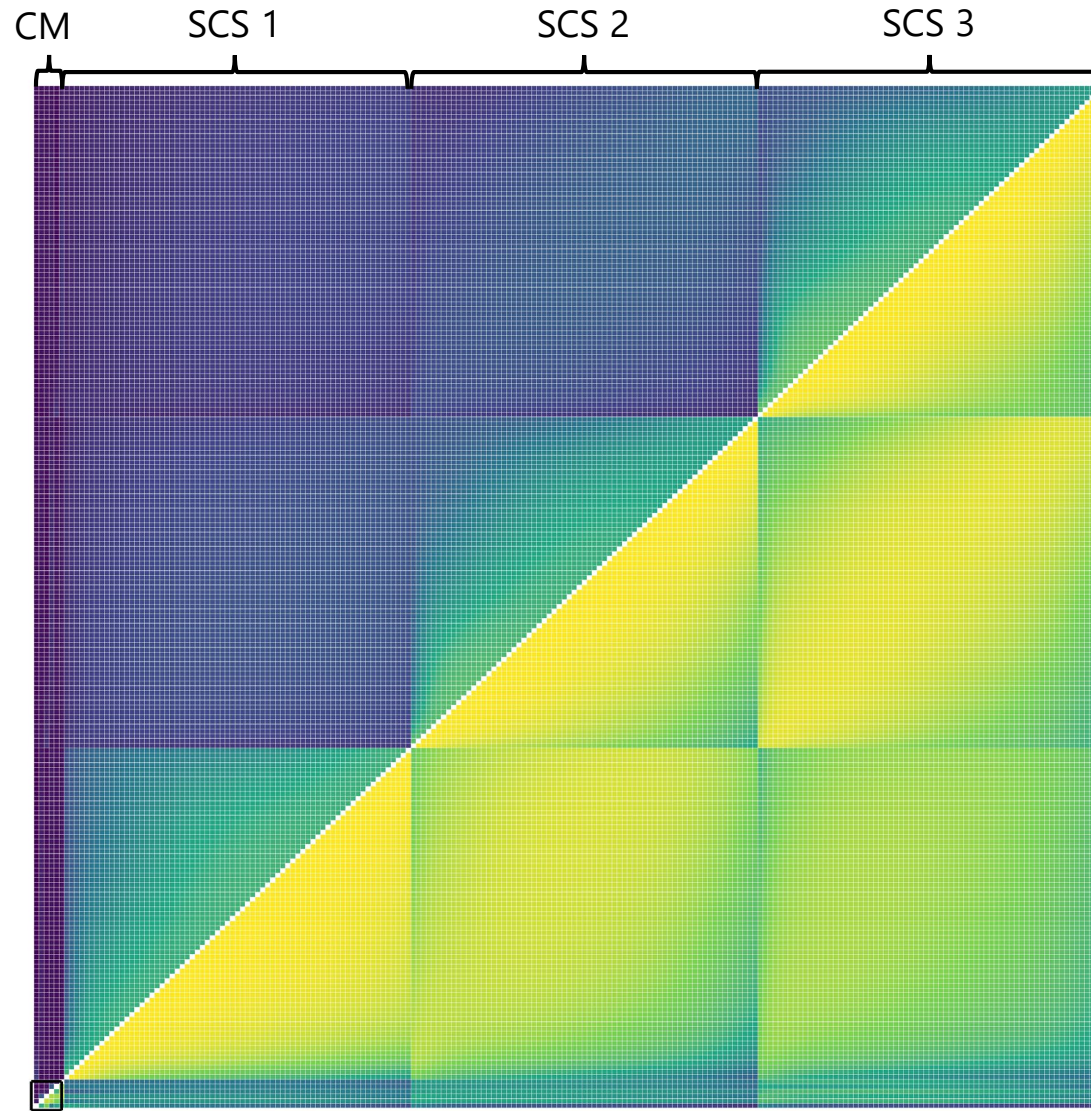
# CM and SCS – JER

60 DIM (10, 15, ..., 305)

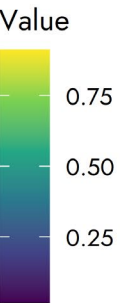


# CM and SCS - RDC

60 DIM (10, 15, ..., 305)



	CM 1	CM 2	CM 3
CM 1	0.03	0.05	0.03
CM 2	0.02	0.03	0.04
CM 3	0.03	0.07	0.08
SCS 1	0.05	0.30	
SCS 2	0.07		0.91
SCS 3	0.63	0.79	0.45



# Combined heritability and correlations

Breed	Trait*	CM	SCS 1	SCS 2	SCS 3
HOL	CM	<b>0.058</b>	0.147	0.191	0.208
	SCS 1	0.614	<b>0.146</b>	0.404	0.321
	SCS 2	0.733	0.861	<b>0.172</b>	0.478
	SCS 3	0.736	0.836	0.982	<b>0.198</b>
JER	CM	<b>0.061</b>	0.108	0.182	0.227
	SCS 1	0.433	<b>0.179</b>	0.408	0.328
	SCS 2	0.486	0.911	<b>0.188</b>	0.488
	SCS 3	0.627	0.851	0.952	<b>0.169</b>
RDC	CM	<b>0.064</b>	0.128	0.175	0.191
	SCS 1	0.474	<b>0.182</b>	0.443	0.336
	SCS 2	0.564	0.913	<b>0.201</b>	0.506
	SCS 3	0.632	0.845	0.960	<b>0.215</b>

\*CM heritability combined across periods and lactations  
305-d heritability for SCS

# Summary

- Greater incidence of CM in latter lactations
  - Higher for Jersey and lower for RDC
- Low heritability for CM
  - High correlations between consecutive CM events
- Moderately low heritability for SCS
  - Very high correlations among SCS
- CM and SCS moderately (highly) correlated
  - Larger correlations for latter lactations (higher CM incidence)

# Thank you!

# Questions?



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