



Combining co-variance components from different models using iterative summing of expanded part matrices: Udder health traits

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Background

Genetic evaluation of udder health by a meta-model combines longitudinal test-day somatic cell score (TDSCS) and non-longitudinal traits such as clinical mastitis (CM) and udder type traits (UA & UD). This requires reliable estimates of co-variance (VCV) components. However, direct estimation of VCV fitting multi-trait random regression model (mt-RRM) is time consuming and convergence may not be guaranteed.

Objectives

- ◆ Estimate genetic correlations between TDSCS, CM & two udder type traits involving later lactations
- ◆ Compare two approaches of estimating co-variance components fitting mt-RRM

Methods

Data - 17,500 Danish Holsteins

Traits - First three lactations TDSCS & CM traits and two first lactation udder type traits, UA & UD

Two methods of estimating VCV components for a meta-model BLUP

Direct estimate fitting mtRRM REML

$$\begin{bmatrix} \text{TDSCS1} \\ \text{TDSCS2} \\ \text{TDSCS3} \\ \text{CM11} \\ \text{CM12} \\ \text{CM2} \\ \text{CM3} \\ \text{UA} \\ \text{UD} \end{bmatrix} = \text{hy3} + \text{ym} + \text{age} + \underbrace{\begin{bmatrix} \sum_{d=0}^1 \phi(d), b \\ 0 \\ \vdots \\ 0 \end{bmatrix}}_{\text{fixed}} + \underbrace{\begin{bmatrix} \text{htd} \\ \text{hy1} \\ \vdots \\ \text{pe} \end{bmatrix} + \underbrace{\begin{bmatrix} \sum_{d=0}^1 \phi(d), \text{pe} \\ \vdots \\ \text{pe} \end{bmatrix}}_{\text{random}} + \underbrace{\begin{bmatrix} \sum_{d=0}^1 \phi(d), a \\ \vdots \\ a \end{bmatrix}}_{\text{random}} + e$$

1000 rounds of iteration ~6-8 wks

$$\mathbf{K}_{\text{mtRRM}} = \begin{bmatrix} \Phi_{\text{TDSCS1}} & \Phi_{\text{TDSCS2}} & \Phi_{\text{TDSCS3}} & \text{symm.} & & & & & \\ & \text{symm.} & & & & & & & \\ & & \text{CM11} & \text{CM12} & \text{CM2} & \text{CM3} & \text{UA} & \text{UD} \\ & & & \text{symm.} & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \end{bmatrix}$$

Combining estimates from non-longitudinal model with mtRRM (using iterative summing of expanded part matrices)

$$\begin{bmatrix} \text{CM11} \\ \text{CM12} \\ \text{CM2} \\ \text{CM3} \\ \text{UA} \\ \text{UD} \end{bmatrix} = \underbrace{\text{hy3} + \text{ym} + \text{age}}_{\text{fixed}} + \underbrace{\text{hy1} + \text{pe} + a + e}_{\text{random}}$$

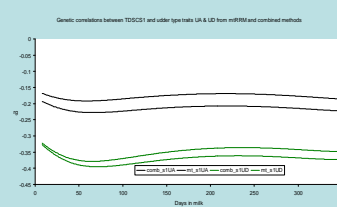
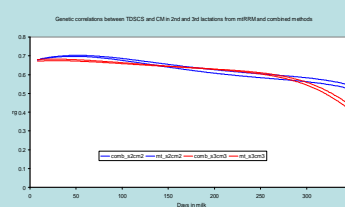
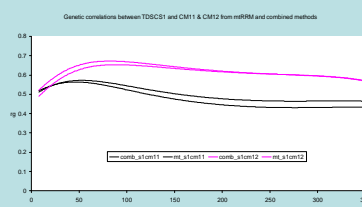
$$\begin{bmatrix} \text{TDSCS1} \\ \text{TDSCS2} \\ \text{TDSCS3} \\ \text{CM11} \\ \text{CM12} \\ \text{CM2} \\ \text{CM3} \\ \text{UA} \\ \text{UD} \end{bmatrix} = \text{hy3} + \text{ym} + \text{age} + \underbrace{\begin{bmatrix} \sum_{d=0}^1 \phi(d), b \\ 0 \\ \vdots \\ 0 \end{bmatrix}}_{\text{fixed}} + \underbrace{\begin{bmatrix} \text{htd} \\ \text{hy1} \\ \vdots \\ \text{pe} \end{bmatrix} + \underbrace{\begin{bmatrix} \sum_{d=0}^1 \phi(d), \text{pe} \\ \vdots \\ \text{pe} \end{bmatrix}}_{\text{random}} + \underbrace{\begin{bmatrix} \sum_{d=0}^1 \phi(d), a \\ \vdots \\ a \end{bmatrix}}_{\text{random}} + e$$

$$\mathbf{G}_{\text{non}} = \begin{bmatrix} 0 & & & & & & & & \\ & 0 & & & & & & & \\ & & \text{CM11} & & & & & & \\ & & & \text{CM12} & & & & & \\ & & & & \text{CM2} & & & & \\ & & & & & \text{CM3} & & & \\ & & & & & & \text{UA} & & \\ & & & & & & & \text{UD} \end{bmatrix}$$

Iterative summing of expanded part matrices approach

Results

a) Genetic correlations between TDSCS & CM and udder type traits



b) Comparison between two approaches (mtRRM Vs. combined) of estimating VCV for a meta-model BLUP

Method	Comparison between parameters estimated by the two approaches (mtRRM Vs. combined) in terms of	
	Corr. between EBVs (~50 daughters)	Computational time
mtRRM	0.98 - 0.99	6-8 wks
Combined		1 wk

Conclusions

Combining co-variance components estimated by different models using iterative summing of expanded part matrices offer a quick and reliable method to estimate parameters for a meta-model udder health genetic evaluation.