Integration of MACE breeding values into domestic multi-trait test-day model evaluations

T.J. Pitkänen[1], M. Koivula[1], I. Strandén[1], G.P. Aamand[2], E.A. Mäntysaari[1]

[1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*

[2]*NAV Nordic Cattle Genetic Evaluation, 8200 Aarhus N, Denmark*

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Objective

The objective of this study was to develop practical approach to **integrate** (blend) **information** from Multiple Across Country Evaluation (**MACE**) to Nordic **test-day model**

This is very critical for

- **single-step evaluations**
- utilization of data from **EUROGENOMICS bull genotype exchange**

Nordic test-day model

- Nordic test-day model is a **multi-trait multi-parity** linear mixed effect model

- **9 traits**; **milk, protein** and **fat** in first **three lactations**

- Test-day records from **Finland, Denmark** and **Sweden (DFS)**

- Due to use of **rank reduction** and **covariance functions** **genetic lactation curves** for 9 traits are modelled using **15 random regression coefficients** per animal

Nordic evaluation model, genetic part

- **Breeding value a_i** is a vector of 15 regression coefficients

- The same a_i is used for all the traits, only the covariables change

$$\mathrm{var}(a_i) = I_{15}$$

  - i.e. each BV is independent and are assumed to have same variance

$$y_{i,m1,d} = \ldots + C_{m1,d}\,a_i + e$$
$$y_{i,m2,d} = \ldots + C_{m2,d}\,a_i + e$$
$$y_{i,m3,d} = \ldots + C_{m3,d}\,a_i + e$$
$$y_{i,p1,d} = \ldots + C_{p1,d}\,a_i + e$$
$$y_{i,p2,d} = \ldots + C_{p2,d}\,a_i + e$$
$$y_{i,p3d} = \ldots + C_{p3,d}\,a_i + e$$
$$y_{i,f1,d} = \ldots + C_{f1,d}\,a_i + e$$
$$y_{i,f2,d} = \ldots + C_{f2,d}\,a_i + e$$
$$y_{if3,d} = \ldots + C_{f3,d}\,a_i + e$$

Nordic evaluation model, genetic part

- **Genetic structure** is implemented using covariables C_{td} specific for each observation
- Covariables are varying according to biological trait, lactation and days in milk (DIM)

$$y_{i,m1,d} = \ldots + C_{m1,d}a_i + e$$
$$y_{i,m2,d} = \ldots + C_{m2,d}a_i + e$$
$$y_{i,m3,d} = \ldots + C_{m3,d}a_i + e$$
$$y_{i,p1,d} = \ldots + C_{p1,d}a_i + e$$
$$y_{i,p2,d} = \ldots + C_{p2,d}a_i + e$$
$$y_{i,p3d} = \ldots + C_{p3,d}a_i + e$$
$$y_{i,f1,d} = \ldots + C_{f1,d}a_i + e$$
$$y_{i,f2,d} = \ldots + C_{f2,d}a_i + e$$
$$y_{if3,d} = \ldots + C_{f3,d}a_i + e$$

For publising the EBVs are converted to 305d yield

- **305d EBVs** for animal $i,$ trait t and parity p are calculated as sum of genetic lactation curve over days in milk $8 - 312$

$$\widehat{EBV}_{itp} = \sum_{d=8}^{312} C_{tpd} \cdot \widehat{a}_i$$

- **3 Combined** EBVs are calculated as **weighted sum** of 305d EBVs

$$YI_{it}^{DFS} = 0.30\,\widehat{EBV}_{it1} + 0.25\,\widehat{EBV}_{it2} + 0.45\widehat{EBV}_{it3}$$

$$= (\sum_{d=8}^{312} 0.30 C_{t1d} + 0.25 C_{t2d} + 0.45 C_{t3d})\widehat{a}_i = m_t \widehat{a}_i$$

Interbull MACE

- After each official evaluation run YI_{it}^{DFS} and corresponding reliabilities $R2_{it}^{DFS}$ are submitted to Interbull

- After the MACE **Interbull returns** YI_{it}^{MACE} and $R2_{it}^{MACE}$ back us

- These MACE EBVs contain all available information for bulls:
    - ours
    - Eurogenomics countries
    - third countries

Choosing bulls to be blended

- We chose **external** bulls with additional information to be blended into our original test-day model.

    Require:
    $$R2_{it}^{MACE} - R2_{it}^{DFS} > 0.01$$

- Around 28,000 bulls were selected, some of them had daughters with records in DFS evaluation

- To avoid **double counting** Nordic information has to be removed from MACE EBVs before "blending" it to test-day model

Calculating pseudo-observation

- Multi-trait **ERC** and **DRP** for milk, protein and fat were calculated based on **MACE** and **DFS** combined EBVs and reliabilities for each bull i

- Amount of additional information is

$$ERC_{it}^{BL} = ERC_{it}^{MACE} - ERC_{it}^{DFS}$$

- **Pseudo-observation** was calculated as

$$DRP_{it}^{BL} = \frac{ERC_{it}^{MACE} \cdot DRP_{it}^{MACE} - ERC_{it}^{DFS} \cdot DRP_{it}^{DFS}}{ERC_{it}^{MACE} - ERC_{it}^{DFS}}$$

- DRP_{it}^{BL} was included in the model as observation using ERC_{it}^{BL} as weight

Inclusion of pseudo-observations into the Test Day model

- Model for pseudo-observations (**ERCs** as a weight) in test-day model

$$DRP_{i;milk}^{BL} = \mu_{milk} + \boldsymbol{m_{milk}a_i}$$
$$DRP_{i;prot}^{BL} = \mu_{prot} + \boldsymbol{m_{prot}a_i}$$
$$DRP_{i;fat}^{BL} = \mu_{fat} + \boldsymbol{m_{fat}a_i}$$

- **NOTE!** The vector $\boldsymbol{a_i}$ is used also for pseudo-observations!

Results, R2 for combined EBVs

R2 BEFORE BLENDING MILK
y= 0.76 + 0.196 x   corr= 0.45
sd(Y)= 0.05 sd(x)= 0.12 N= 27958
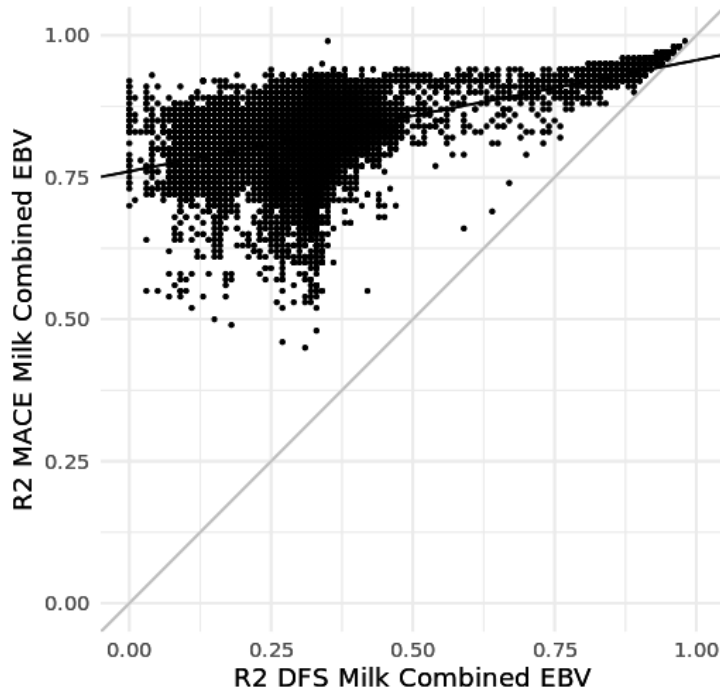
R2 AFTER BLENDING MILK
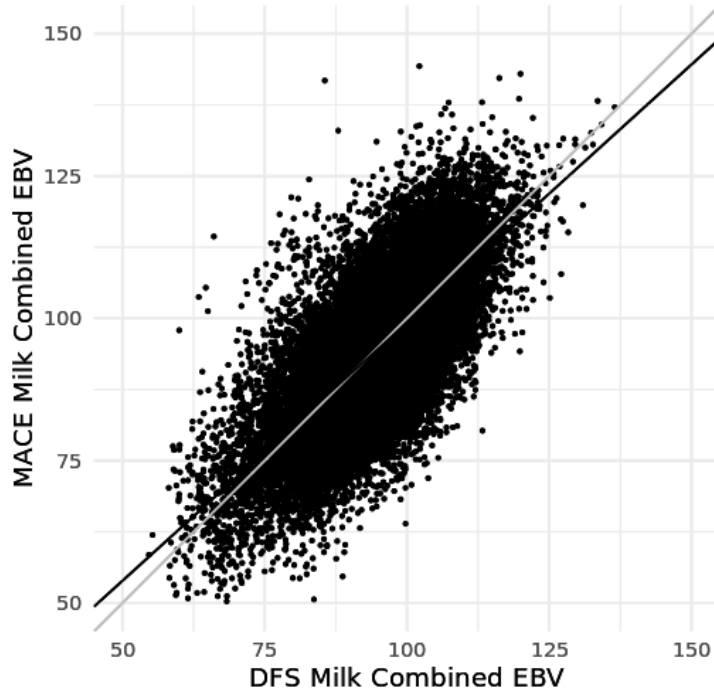y= -0.03 + 1.029 x   corr= 1
sd(Y)= 0.05 sd(x)= 0.05 N= 27958
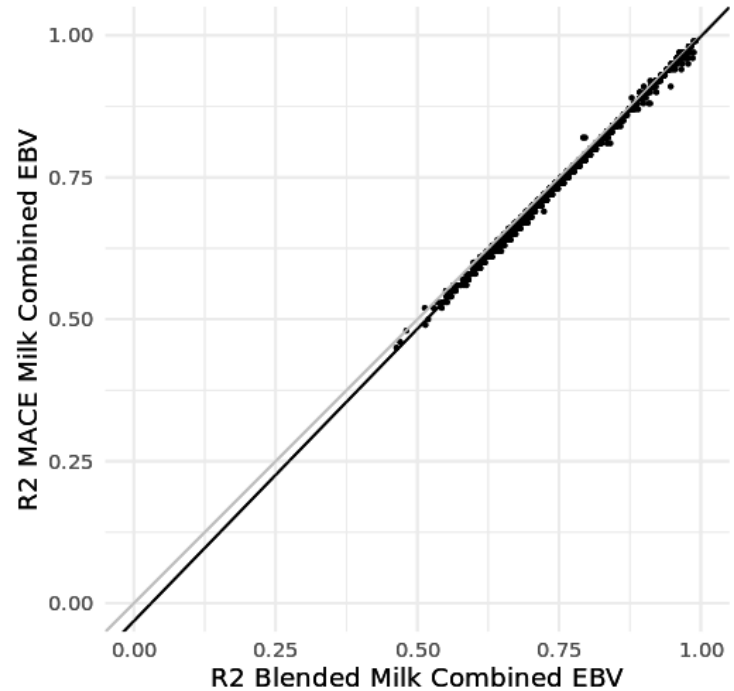
Results, Combined milk EBVs

BEFORE BLENDING MILK
y= 8.54 + 0.907 x   corr= 0.72
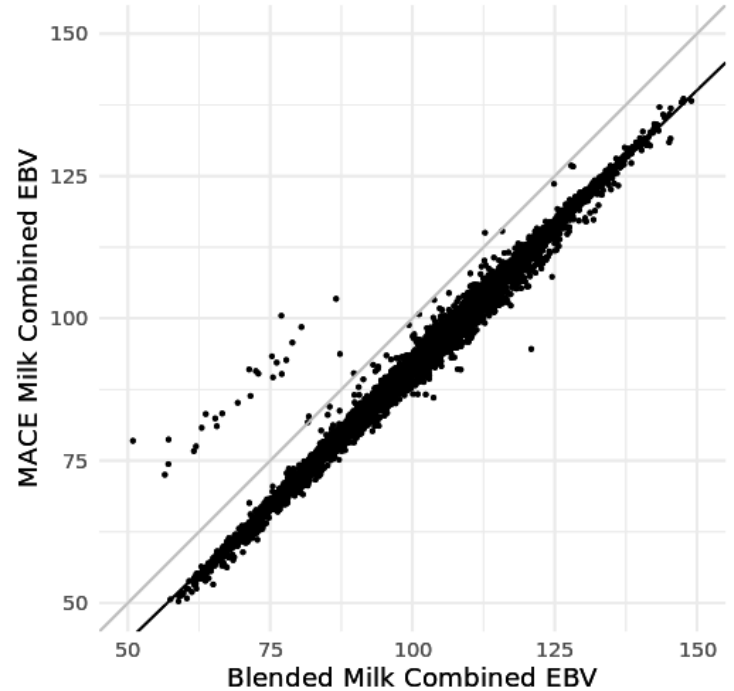sd(Y)= 12 sd(x)= 10 N= 27958

AFTER BLENDING MILK
y= -5.05 + 0.967 x   corr= 0.99
sd(Y)= 12 sd(x)= 13 N= 27958

Conclusions

- Blending of information from MACE EBVs to test-day model works very well
  - Each pseudo-observation is modelled by all **15 BV coefficients**
- Correlations between MACE and Blended combined EBVs was 0.99 for all three traits
- Also correlations between R2s were > 0.99
- Blending procedure has multiple steps which depend on the evaluation model

Thank you!