Using Pseudo-observations to combine Genomic and Conventional Data in the Dutch-Flemish National Evaluation

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Content

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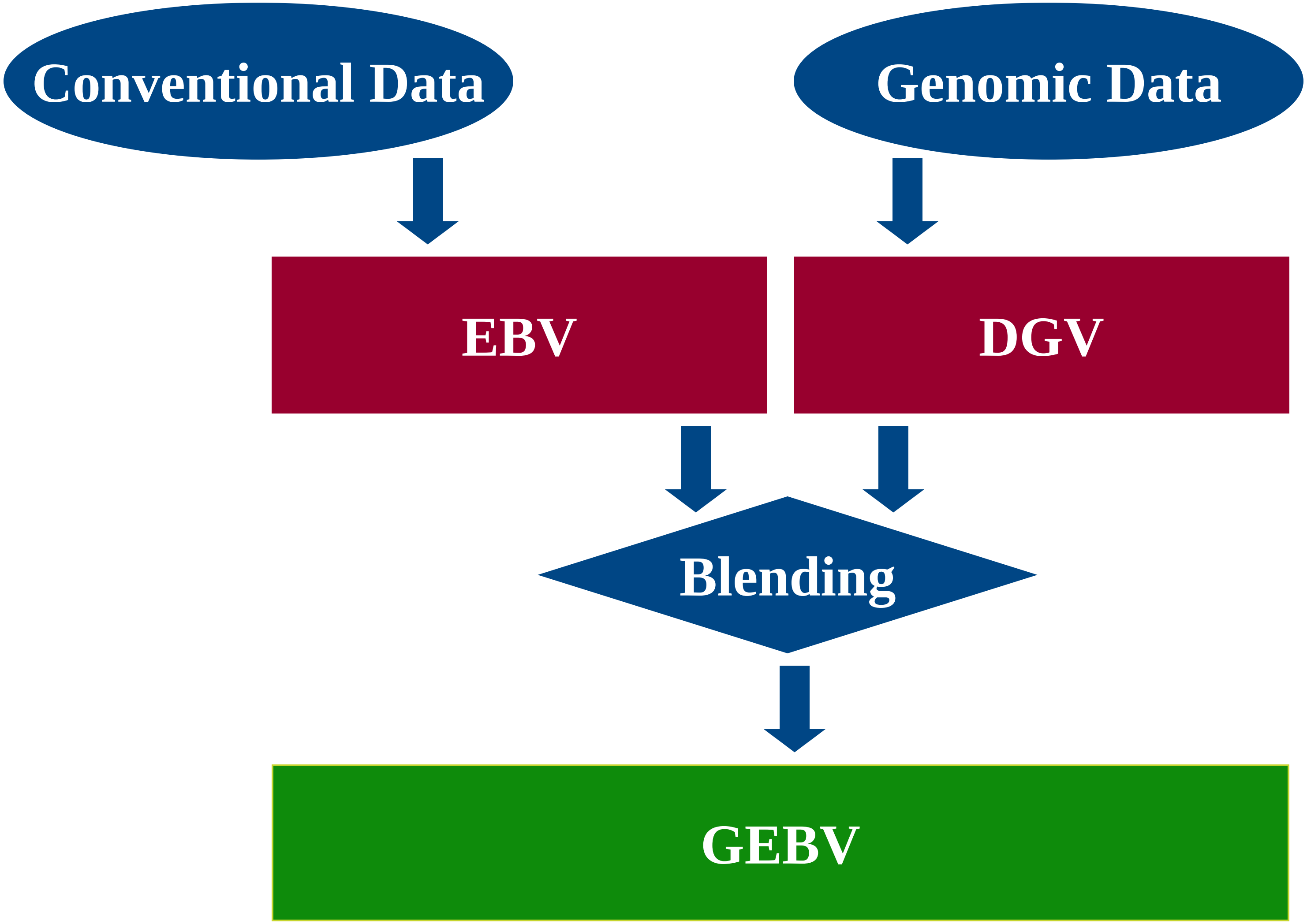
- Pseudo-Record Procedure
- Results for conformation:
  - Compare EBV vs. GEBV_{PSR}
  - Compare $\text{GEBV}_{\text{BLEND}}$ vs. GEBV_{PSR}
  - GEBV validation
- Conclusions


Alger Meekma

GEBV in NLD: Post-processing



Conventional Data

Genomic Data

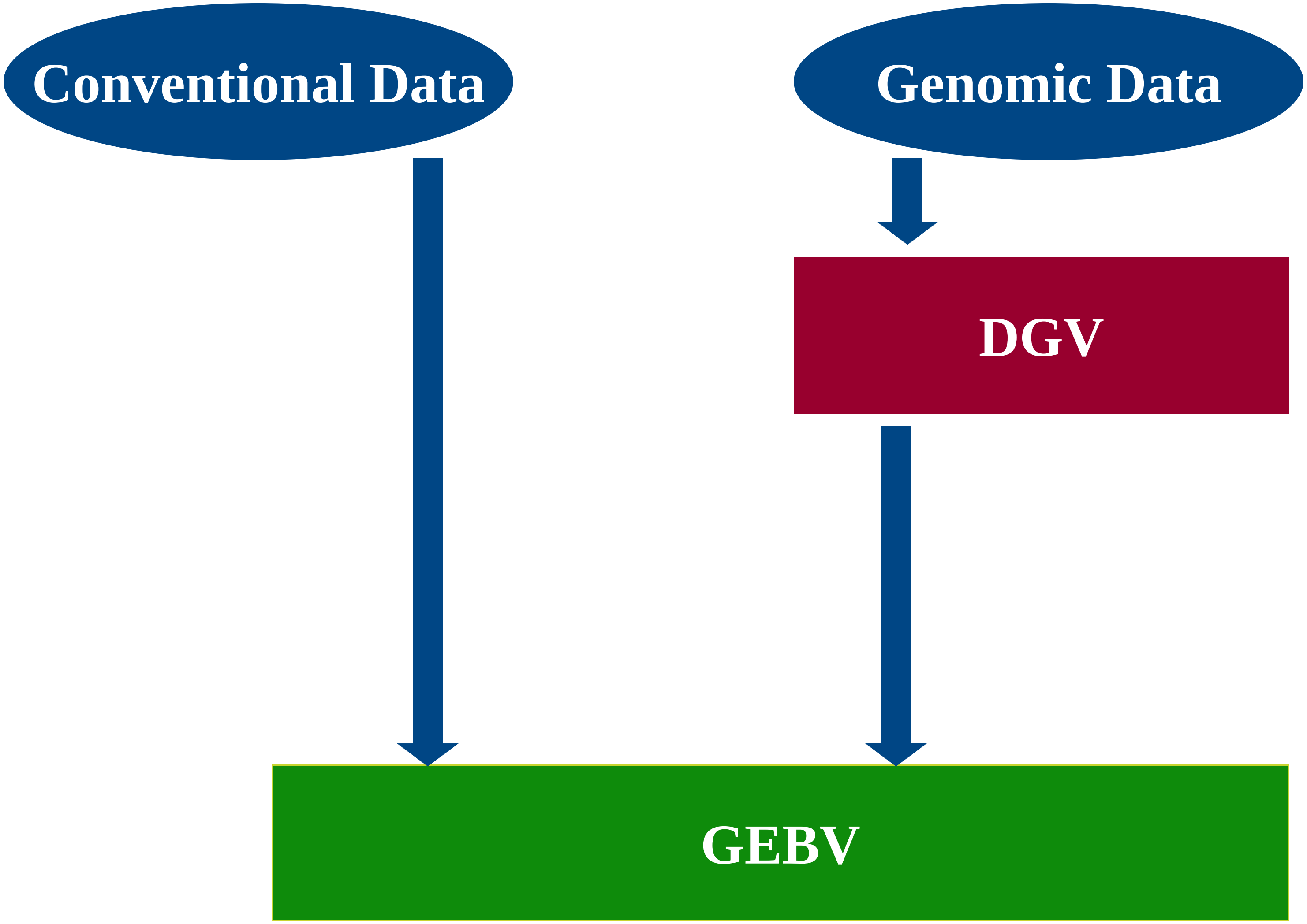
EBV

DGV

Blending

GEBV

GEBV in NLD: Pseudo-records



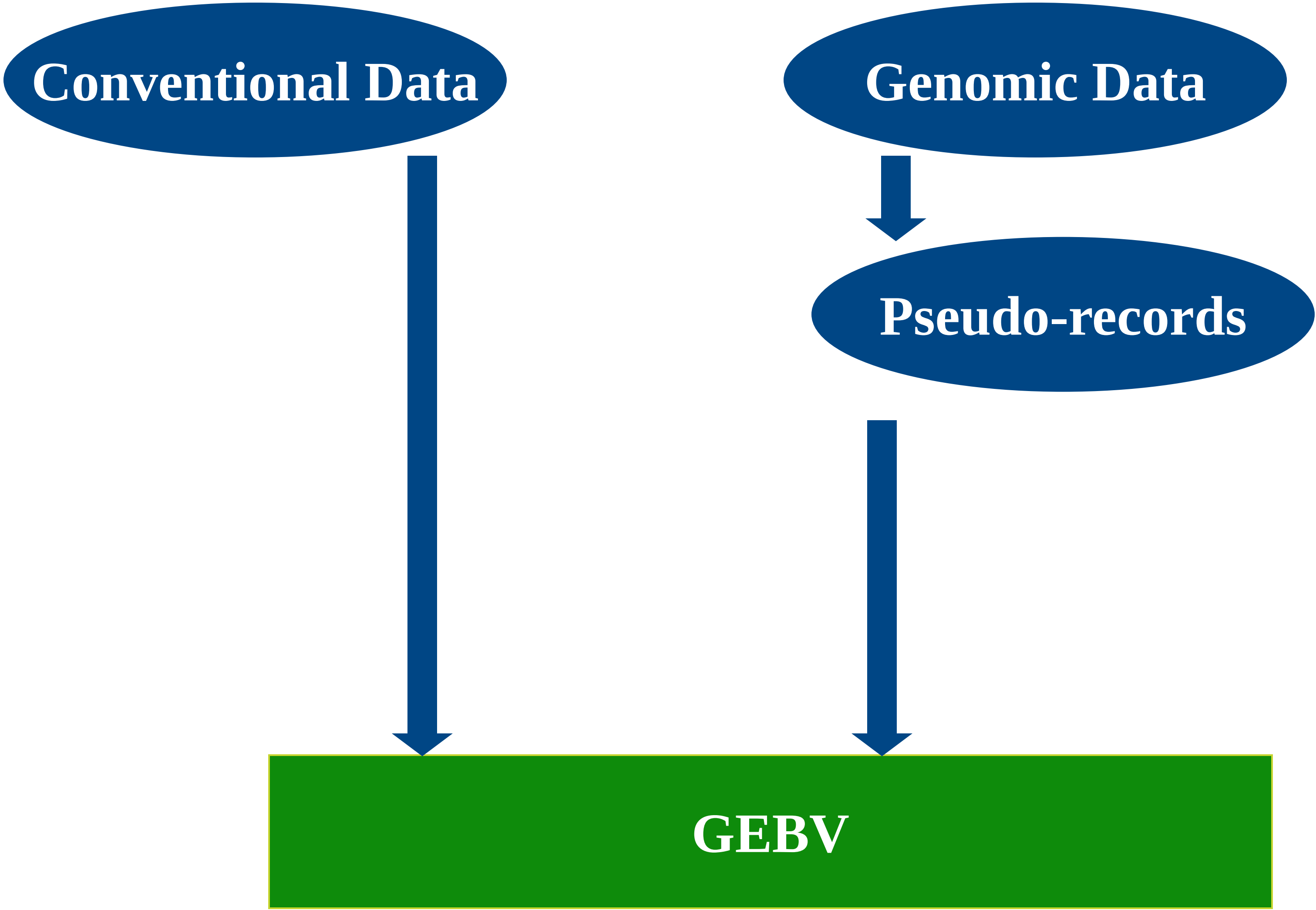
Conventional Data

Genomic Data

DGV

GEBV

GEBV in NLD: Pseudo-records



Conventional Data

Genomic Data

Pseudo-records

GEBV

PSR procedure: Mantysaari and Strandén (2010)

- Genomic part of the DGV ~ summation of SNP effects
- Observed variation explained by genetic makeup
- h^2 of 0.999

- DGV => pseudo-observation (PSR) on absolute scale for a pseudo-trait with $h^2 = 0.999$, and $\sigma_{g,psr} = \sigma_{g,original}$

$$y_{ij} = mu_{PSR} + animal_i + e_{ij}$$

- Multitrait setting with $r_{g\ (pseudo,original)}$ from DGV validation study

PSR procedure: r_g from DGV validation

- Historic run
- Validation cohort of 836 bulls
- Calculate Male Pedigree Index and DGV
- Correlate to realized daughter EBV: r_{pi} and r_{dgv}

R^2_{dgv} ~EDC_{dgv}, and R^2_{pi} ~ EDC_{pi}

$EDC_{add} = EDC_{dgv} – EDC_{pi}$

$EDC_{add} \sim R^2_{add}$

$r_{g\ (pseudo,original)} = (R^2_{add}/R^2_{val})^{1/2}$

Multi-trait analysis for Conformation

1. The genomic evaluation
    - Data of Eurogenomics consortium
    - ~ 24,000 bulls in the reference population for conformation traits.

2. The national evaluation
    - both conventional data (conformation scores of daughters) and DGV transformed to pseudo-observations
    - 5,411,754 records, incl. 27,373 pseudo-observations of males and females
    - 5,407,253 animals with pedigree

Compare EBV vs. GEBV$_{PSR}$: Expectations

- Only changes in Holstein & Holstein pedigrees

- No PSR & with dau : very small changes (due to pedigree)
- Own PSR & with dau : small changes (some extra data)
- Own PSR, no dau : some changes (from PA/PI -> GEBV)

Compare EBV vs. GEBV$_{PSR}$

Difference in Breeding Value (GEBV – EBV) **~N (100, 4)**

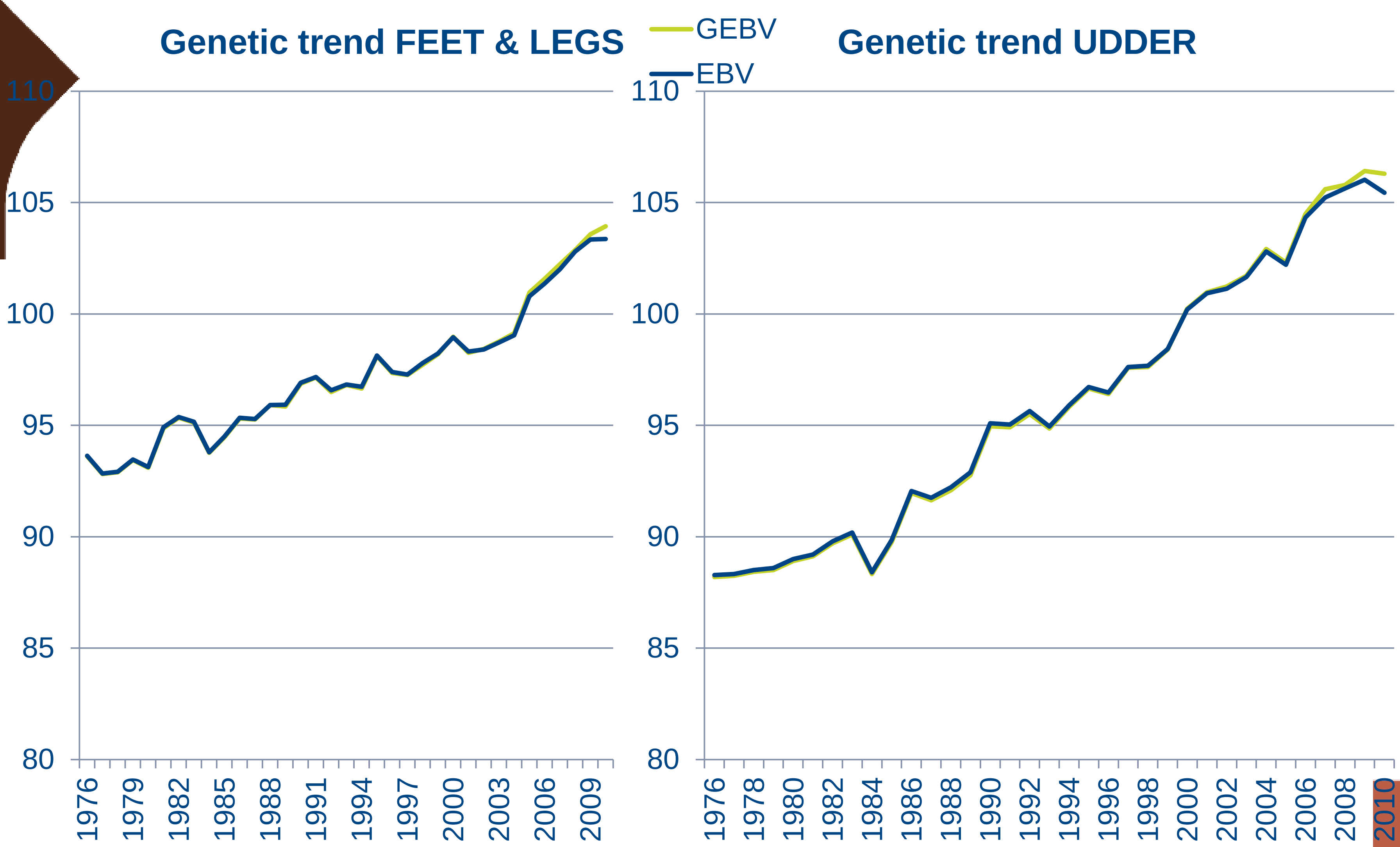
Trait	No PSR, > 10 dau (N=15.614)	PSR, >10 dau (N=4.720)	PSR, no dau (N=2.692)
Frame	-0.2	0.1	0.0
Dairy strength	0.5	0.0	0.0
Udder	0.0	0.1	0.5
Feet&Legs	-0.1	0.1	0.2
Correlation	**~ 1.00**	**~ 0.99**	**~ 0.90**

Compare EBV vs. GEBV$_{PSR}$

Difference in Reliability (GEBV – EBV)

Trait	No PSR, > 10 dau (N=15.614)	PSR, >10 dau (N=4.720)	PSR, no dau (N=2.692)
Frame	0	8	28
Dairy strength	0	9	23
Udder	0	6	29
Feet&Legs	0	6	20

Compare EBV vs. $GEBV_{PSR}$



Compare GEBV$_{BLEND}$ vs. GEBV$_{PSR}$: Expectations

- Only changes in Holstein & Holstein pedigrees

- Own PSR & with dau : very small changes (due to pedigree)
- Own PSR, no dau : small changes (due to pedigree)

Compare $GEBV_{BLEND}$ vs. $GEBV_{PSR}$

GEBV ~N (100, 4)

Trait	PSR	BLEND	diff	corr
Frame	104.0	103.6	0.4	0.86
Dairy strength	103.8	103.1	0.7	0.92
Udder	105.7	105.3	0.4	0.95
Feet&Legs	103.3	102.1	0.2	0.92

GEBV reliability

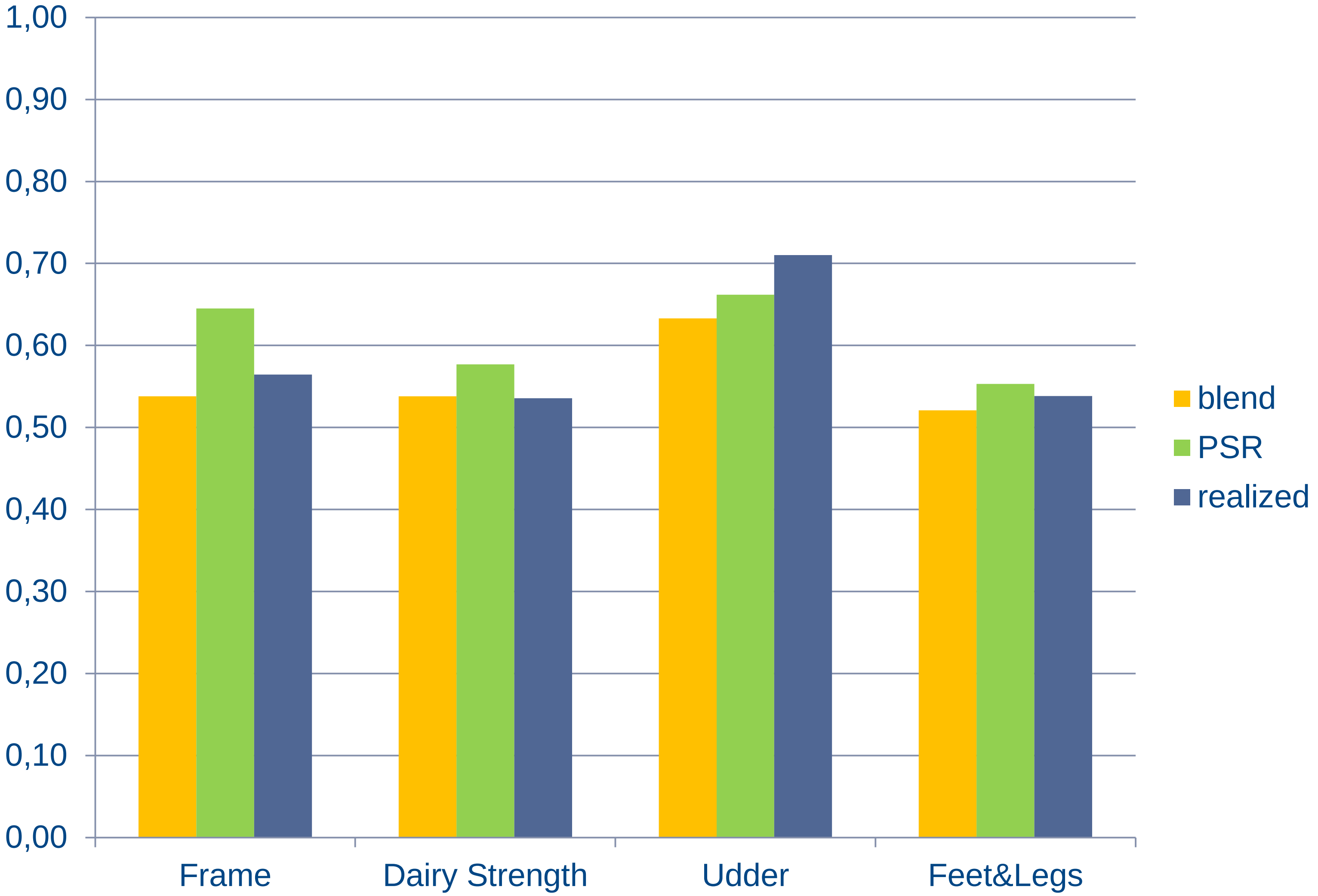
Trait	PSR	BLEND	diff
Frame	64.5	53.8	10.7
Dairy strength	57.7	53.8	3.9
Udder	66.2	63.3	2.9
Feet&Legs	55.3	52.1	3.2

GEBV Validation of reliabilities

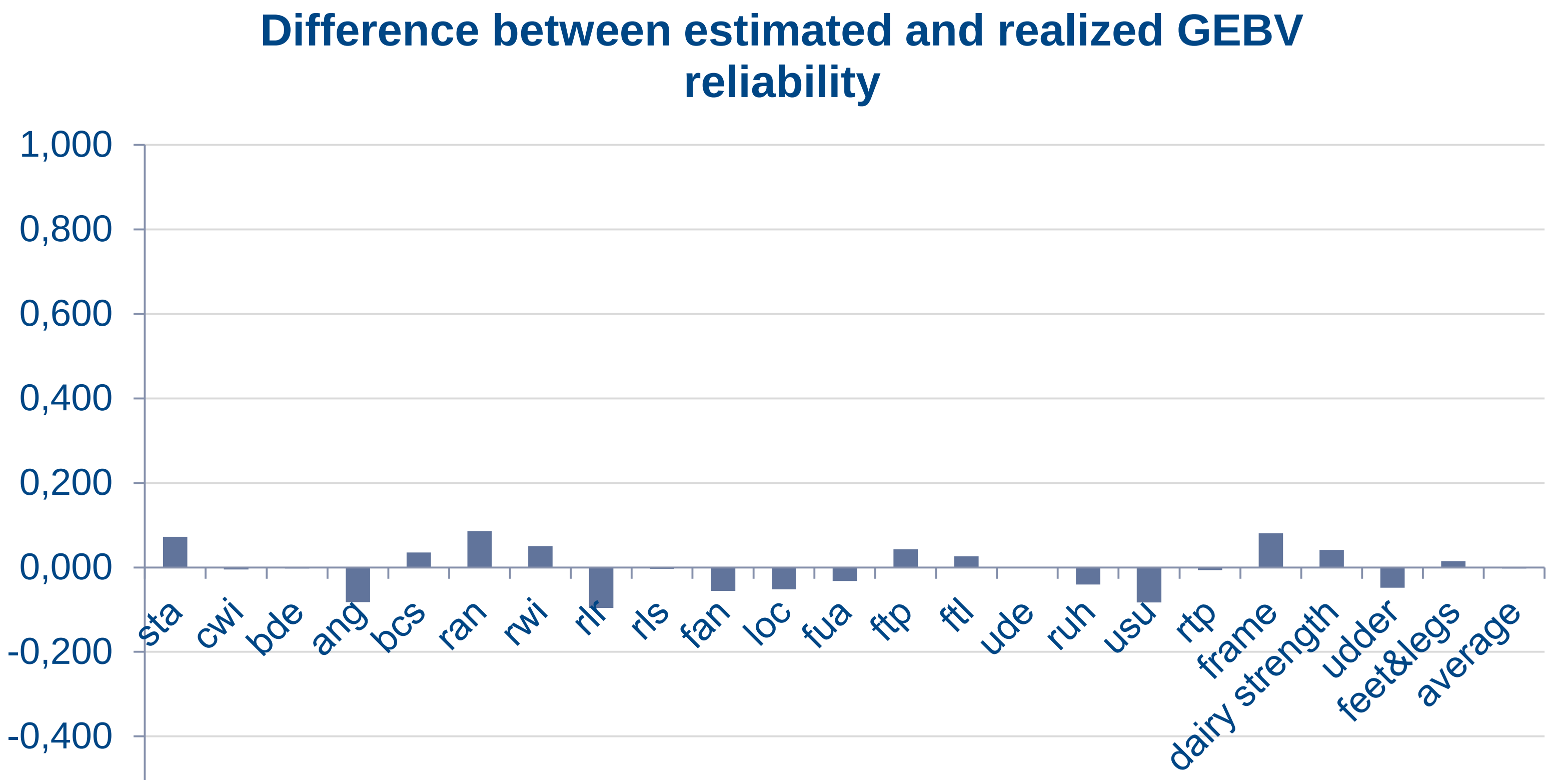
- Historic run
- Calculate Male Pedigree Index and DGV
- Calculate GEBV
- Correlate to realized daughter EBV ($r_{ebv,gebv}$)
- Compare R^2_{gebv} to realized reliability, based on R^2_{ebv} :

$$R^2_{gebv} = (r_{ebv,gebv} / \sqrt{R^2_{ebv}})^2$$

GEBV validation



GEBV validation



Conclusions

- Method of Mantysaari and Strandén (2010) seems to work well, results are according to expectations
- GEBV validation shows that increase in reliability (MT setting) compared to old blending method is correct
- Some BIAS left in CONF (and PROD) when using PA + PSR instead of PI + PSR
- Implementation planned for April 2014