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Animal Production

Application of a single-step SNP BLUP random regression model to test-day yields and somatic cell scores in German Holsteins

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I) Genotype and phenotype data for the single-step evaluation

- Genotyped population of German Holsteins for routine genomic evaluation **April 2021**
  - 949,636 genotyped Holstein animals including young candidates and culled animals

- Phenotype data of national cows and international bulls for test-day yields and SCS
  - Full data set of national test-day with bull MACE data
    - 12,432,940 cows as in official conventional evaluation with 242,121,126 test-day records
    - 138,770 bulls with deregressed MACE EBV added (ΔEDC >0), → 12,571,710 cows and bulls

- Pedigree file for the single-step model evaluation
  - For youngest candidates 20 generations of ancestors selected
  - 20,461,400 animals in pedigree for the full evaluation and 177 phantom parent groups

I) A single-step SNP BLUP random regression model for test-day traits

- German multi-lactation random regression test-day model for national cow test-day data
  - Genetic effects modelled with 3 random regression coefficients (RRC) for each lactation
  - Official combined lactation EBV, a linear function of 3 x 3 = 9 RRC, submitted to MACE evaluation
  - Correlations of 9 coefficients with the combined lactation EBV (**MACE trait**) derived from national $\mathbf{G}_0$ matrix

- Deregressed MACE EBV for all bulls in Interbull evaluation as the **correlated MACE trait**
  - Weight as difference in (animal-model based) EDC between MACE and national evaluation
  - Adjustment in deregressed bull EBVs from national and MACE evaluation

- The ssSNPBLUP model with **30%** residual polygenic variance for all four test-day traits

- A special implementation of the ssSNPBLUP (Liu & Goddard) model in MiX99

I) The current multi-step genomic model

- **A mixed bull and cow reference population** for German Holsteins since 2019
- A single-trait genomic model on the combined lactation basis
- Data taken from **April 2021** genomic evaluation
  - 249,363 reference cows
  - 43,699 reference bulls
- Truncated data set for a genomic validation
  - Truncating cows or bulls using the current national conventional and MACE evaluations
  - Last 3 birth years of validation bulls (2014-2016) → 991 Holstein validation bulls
  - Last 2 years of cows plus daughters of the validation bulls removed

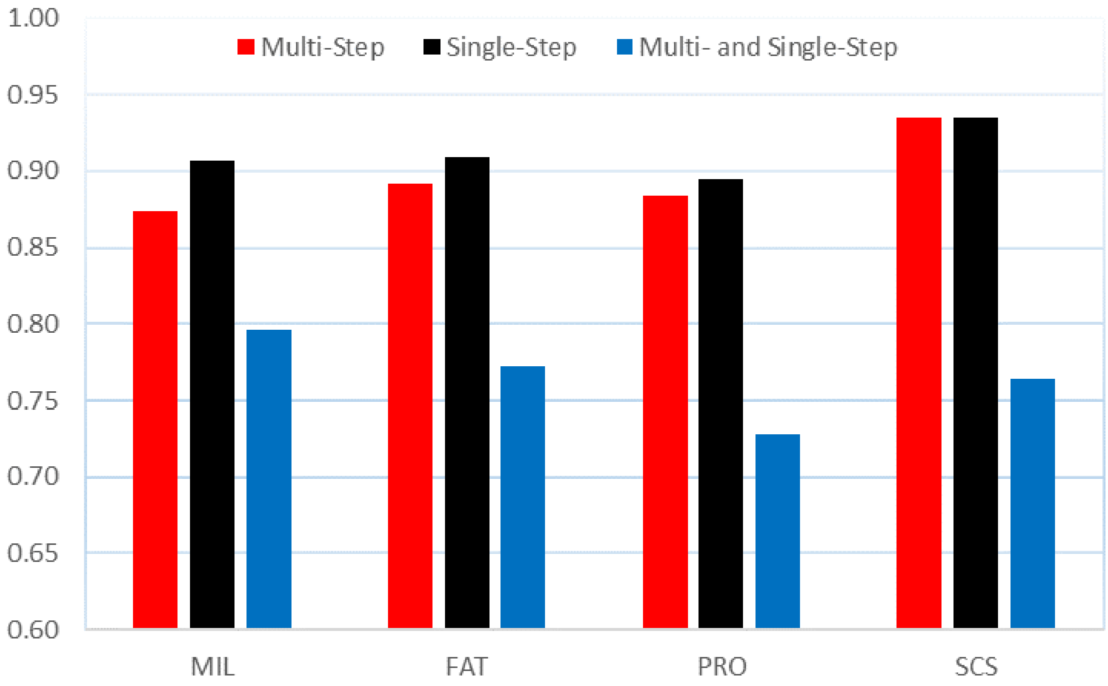
II) A genomic validation for the single-step model

- Validation bulls defined following Interbull GEBV test (Mäntysaari, Liu and VanRaden 2010)
  - Youngest bulls with daughters, born in 2013 through 2016
  - Daughters in at least 10 herds in Germany
  - EDC ≥ 20 → 1,655 Holstein validation bulls

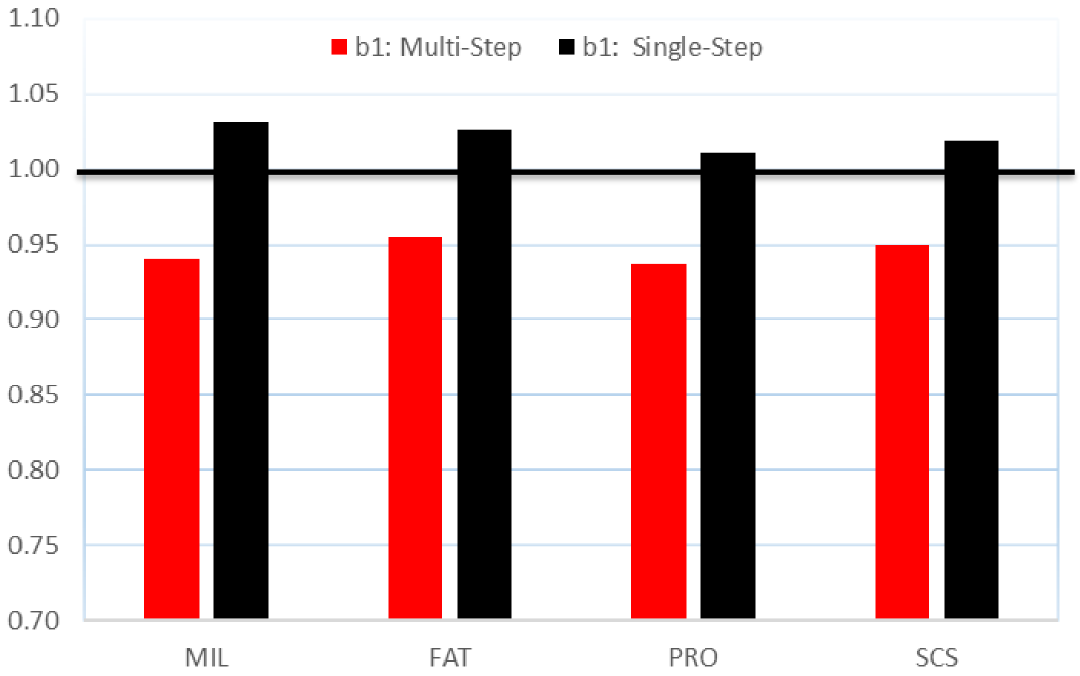
- Truncated phenotype data for single-step evaluation
  - Removing **last 4 years test-day records** of national cows
  - Deleting **last 4 birth years** of MACE bulls in current MACE evaluation
  - Additionally daughters of validation bulls removed
  - In total 10,903,891 cows with 222,634,210 test-day records
  - 128,504 bulls with deregressed MACE EBV, → 11,032,395 cows and bulls

II) Comparison of SNP effect estimates

Observed correlations between SNP effects of the full and truncated data sets



Regression of SNP effects of the full on truncated data sets



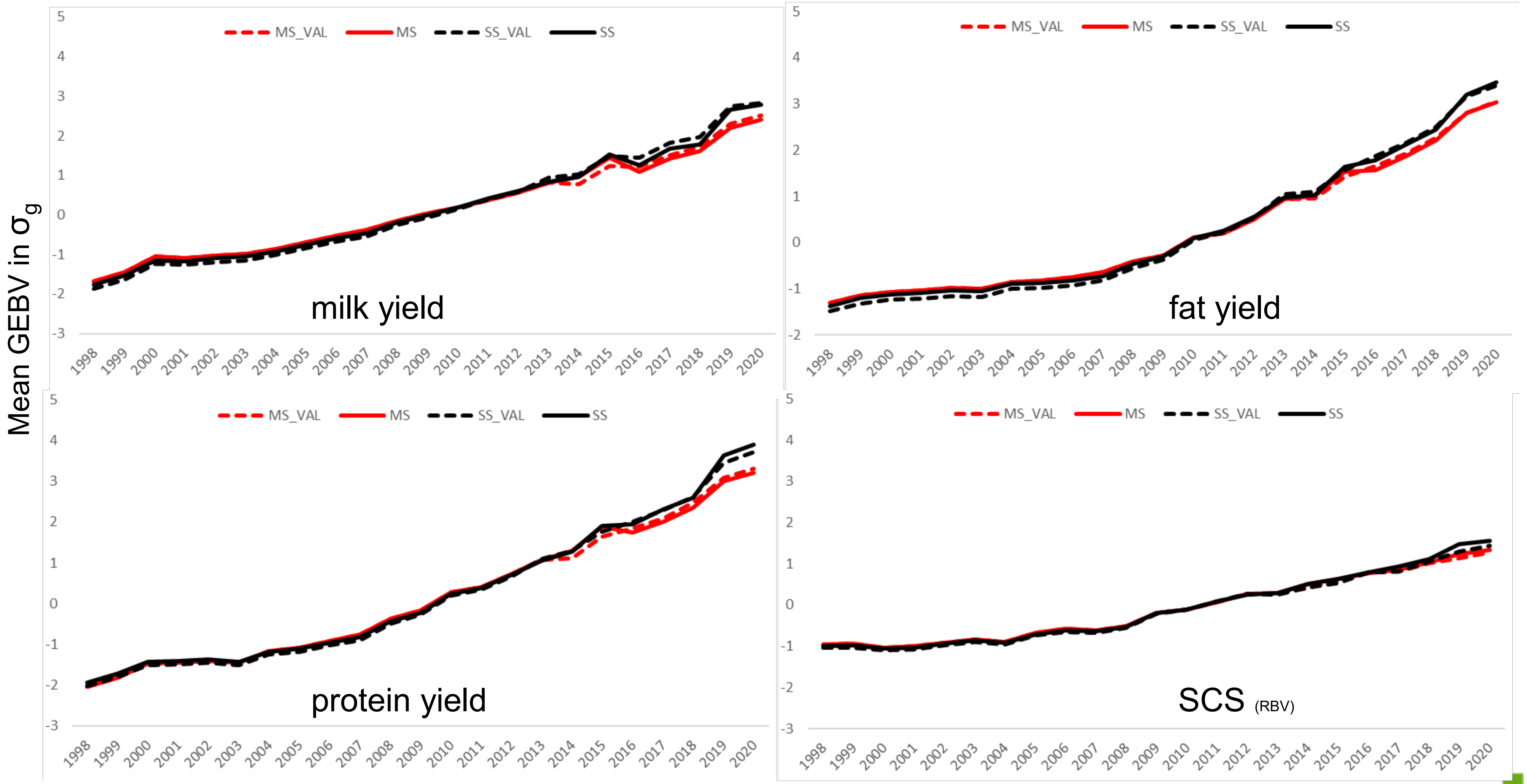
II) Regression of GEBV of the full on truncated evaluation: validation bulls

Single-step model	b_0	b_1	R^2
Milk yield	-103.17	1.02	0.81
Fat yield	-2.02	1.00	0.80
Protein yield	0.47	0.96	0.71
Somatic cell scores	0.02	0.99	0.78

Multi-step model	b_0	b_1	R^2
Milk yield	112.44	0.98	0.70
Fat yield	-4.91	1.12	0.76
Protein yield	-0.03	1.07	0.70
Somatic cell scores	-0.01	1.07	0.68

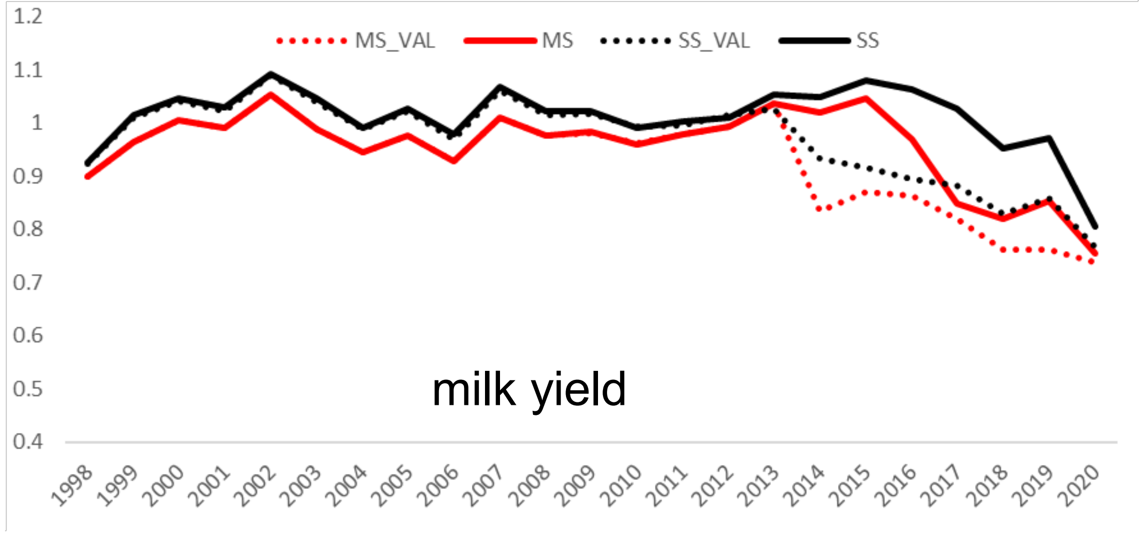
- Single-step: single step genomic model (four years data deleted, truncated national evaluation)
- Multi-step: multiple step genomic model (three years data deleted, no truncated national evaluation)

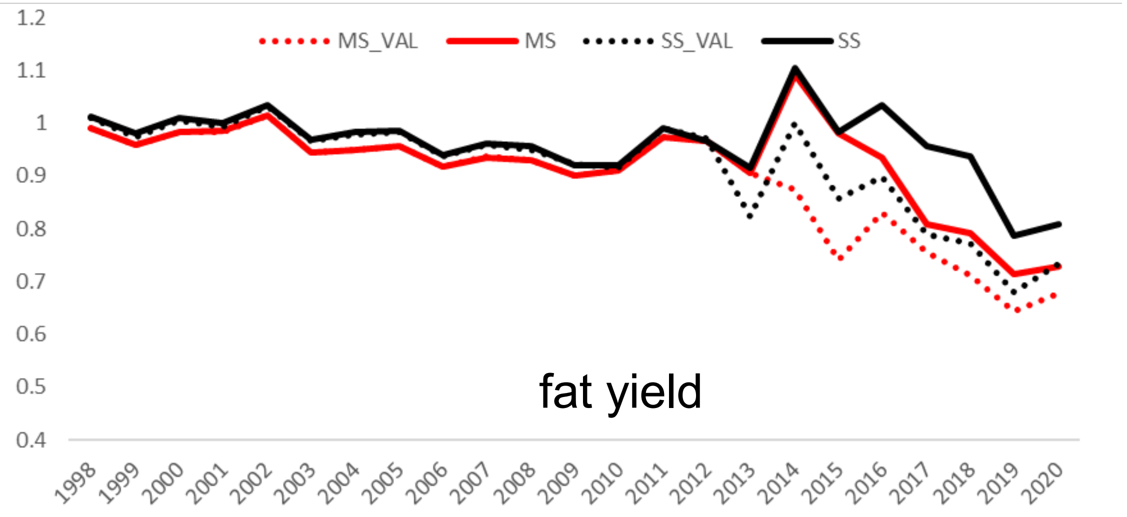
III) Genotyped German Holstein AI bulls: Genetic trends in GEBV

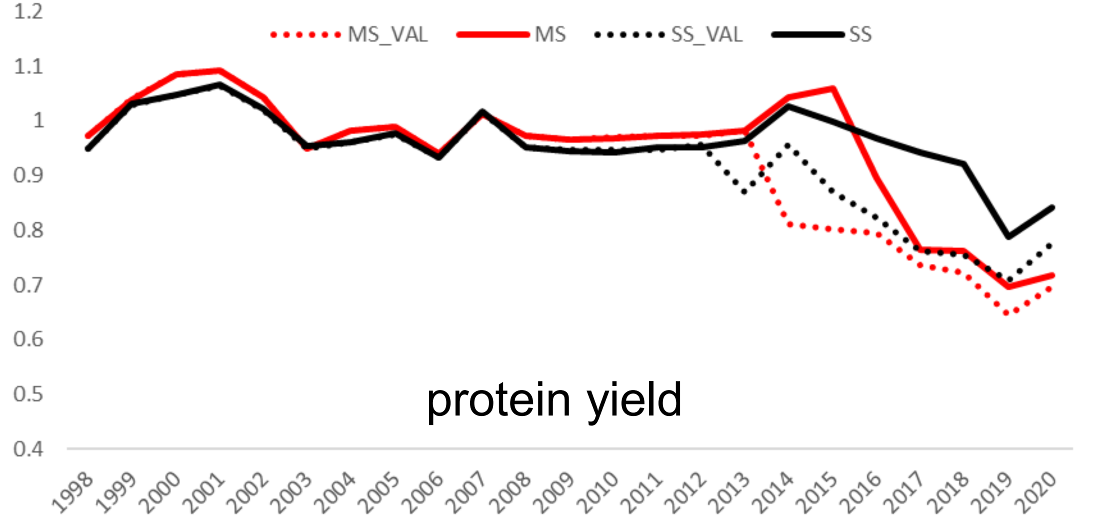


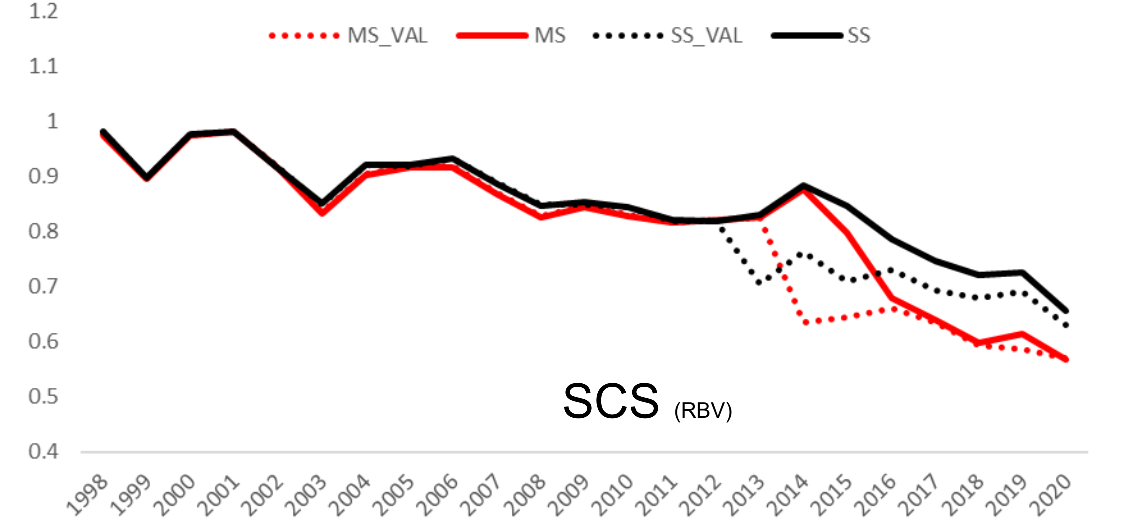
III) Genotyped German Holstein AI bulls: Standard deviations of GEBV

Std Dev in σ_g

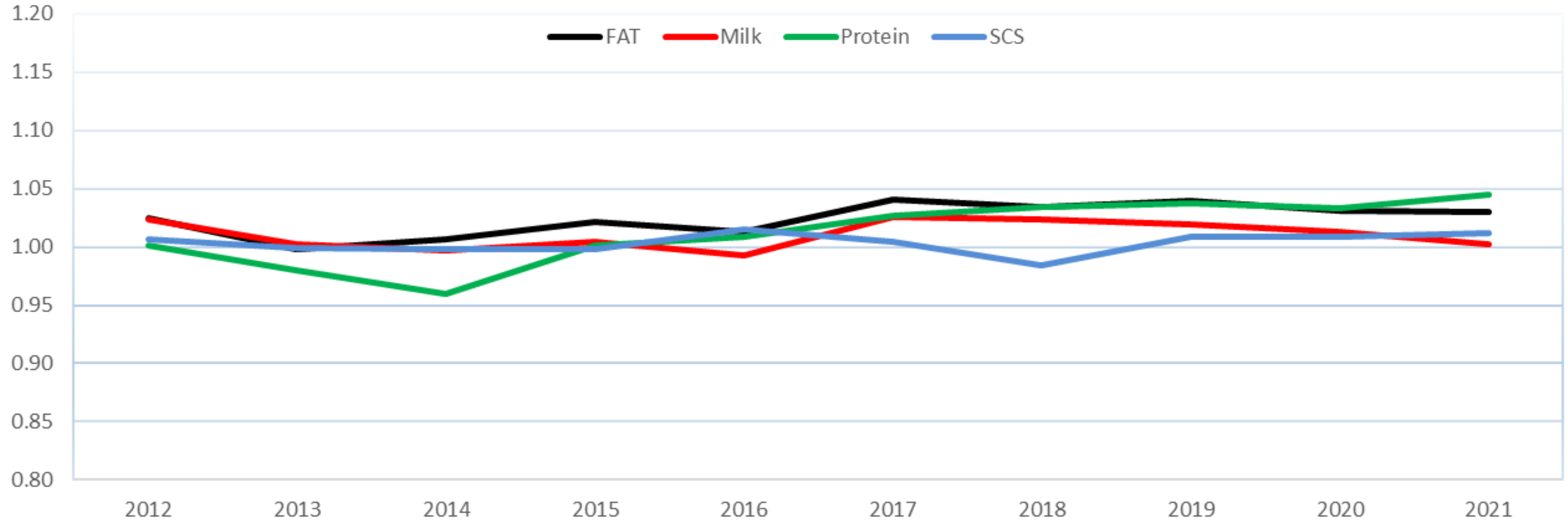




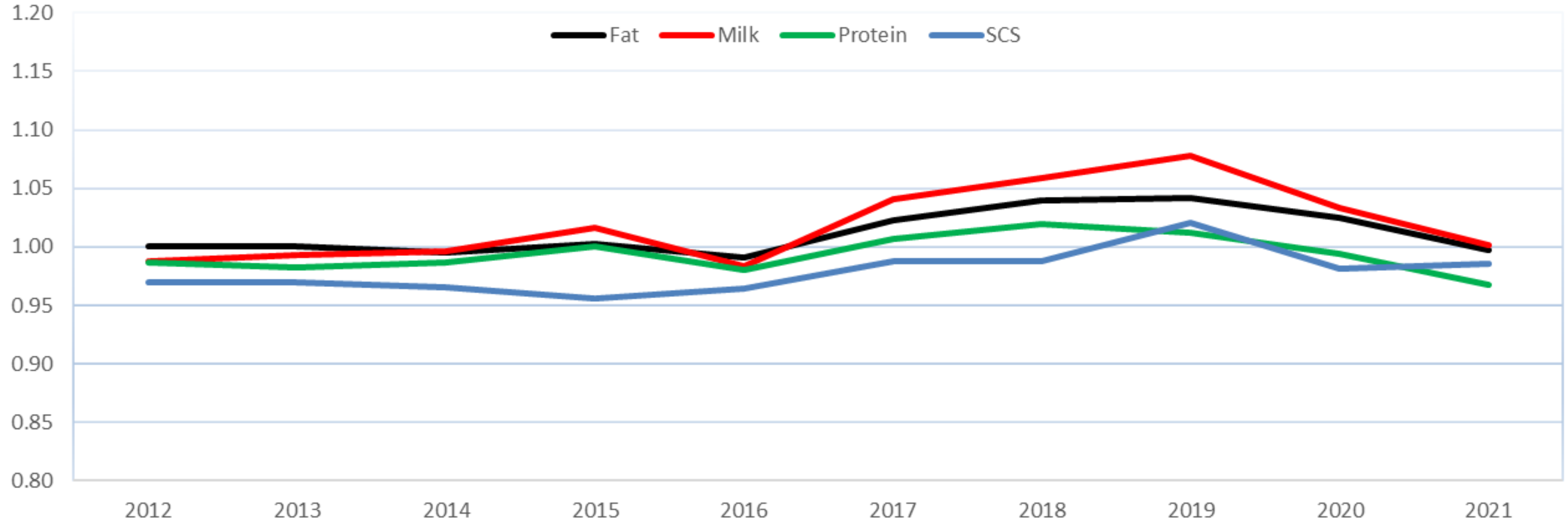




V) Regression of GEBV of the full on truncated evaluation for genotyped male candidates



single-step model



multi-step model

Summary and conclusions (1)

- The Liu-Goddard ssSNPBLUP model applied to test-day traits with a random regression model
- Deregressed bull MACE EBV were integrated as a correlated trait to national RRCs
- All genotyped animals evaluated including culled male candidates, young animals without phenotype
  - Jointly with phenotyped animals, no approximation in genomic information
- Genomic validation results of the ssSNPBLUP model, compared to the multi-step genomic model
  - Higher accuracy and genetic trends, greater GEBV variance
  - Regression of GEBV of the full on truncated evaluation close to 1, at least 0.96
  - No indication of inflation of genomic prediction for young animals
- For highly selected youngest genomic AI bulls GEBV correlation
  - Between truncated and full single-step evaluation: 0.95 across traits
  - Between the single-step and multi-step models: 0.93 on average

Summary and conclusions (2)

- Effect of genotype edit: removal of genotype data of bulls born before 2005
    - Average Mendelian sampling effects of genotyped female animals more closer to 0
    - Reduced by half in protein yield
- Presentations on impact of selection of bull MACE phenotype
    - Alkhoder et al. **EAAP** session 14, oral presentation; Liu et al. **WCGALP** session 2, poster
- No post-processing of genotyped young animals, e.g. genomic AI bulls, seems to be necessary
- Interbull genomic reliability method is being tested for the single-step model
- Interim weekly genomic evaluation is under development
- Integration of MACE SNP effects in future

Thank you for your attention!

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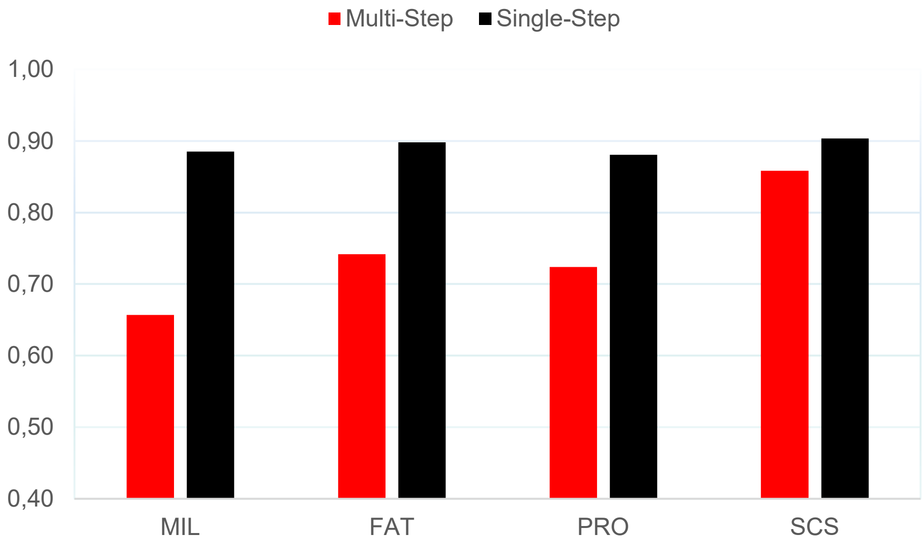
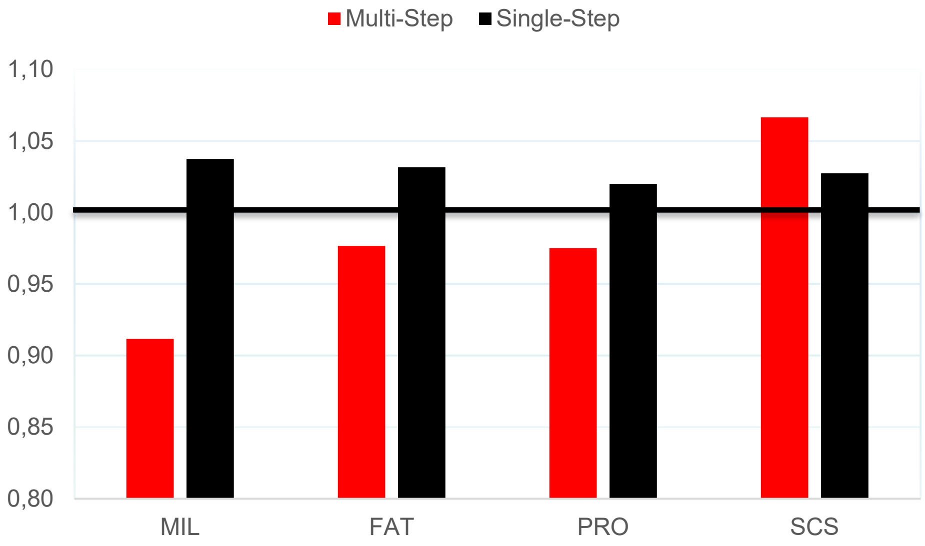
II) Regression of GEBV of the full on truncated evaluation: validation cows

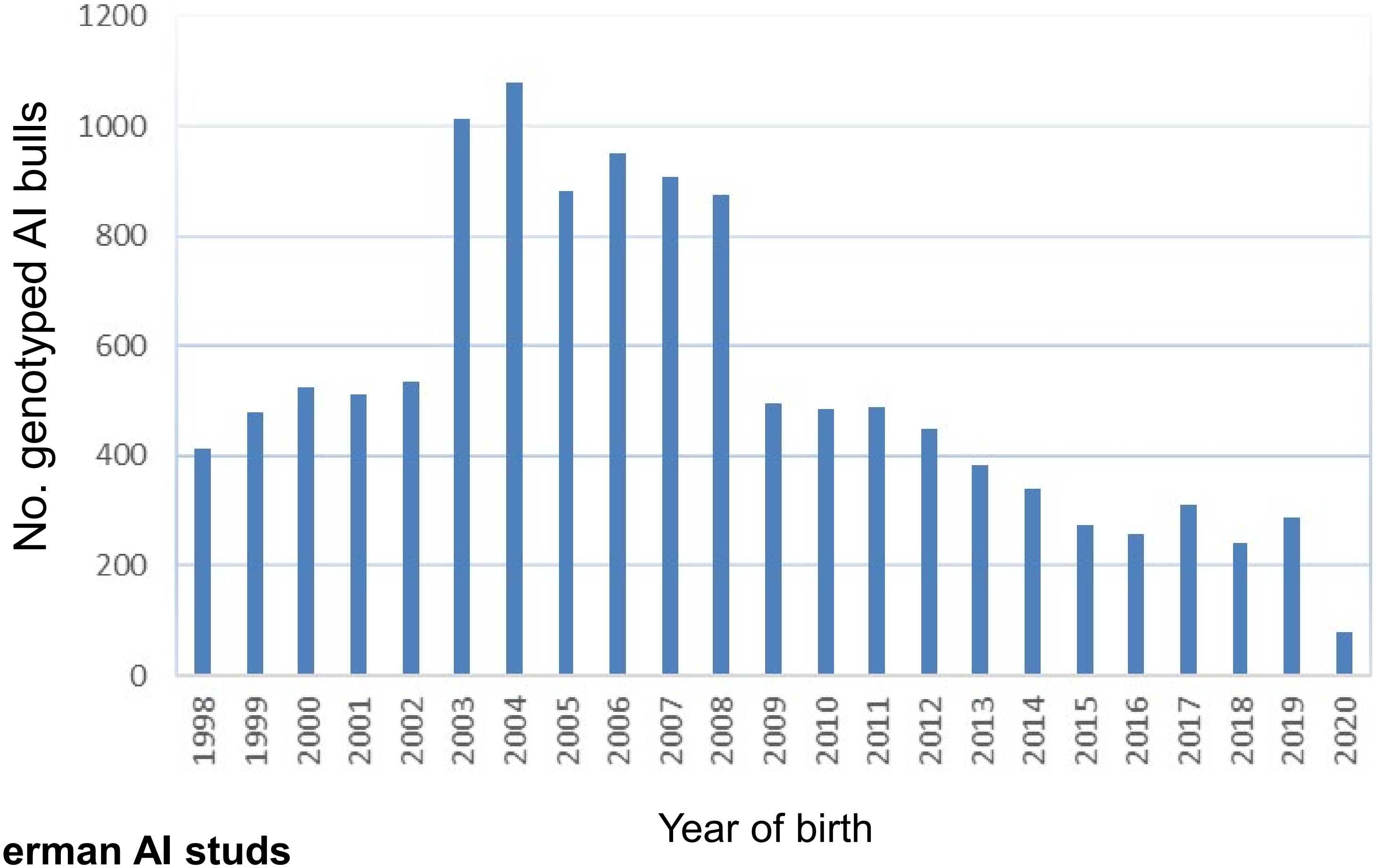
R^2 value by trait



b_1 value by trait



III) Genotyped German Holstein AI bulls



Bulls owned only by German AI studs

IV) Genotyped females: observed GEBV correlations between the full and truncated evaluations