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An optimized single-step SNP BLUP model for calf fitness in German Holstein

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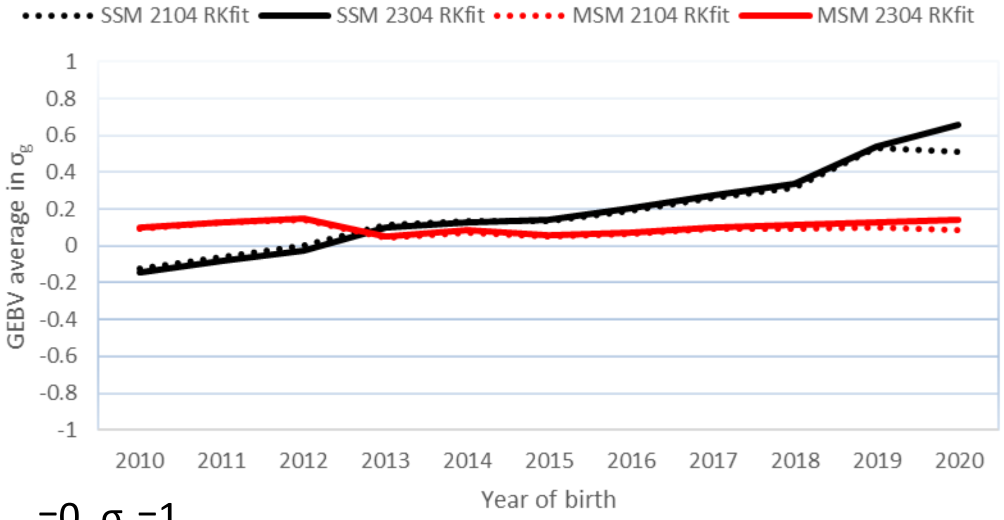
A single-step genomic model for calf fitness

- A multi-trait linear animal model for calf survival from day 3 to 15 months (Heise et al. 2016)
- Defined in 5 periods (days 3 to 14, 15-60, 61-120, 121-200, 201-458) as correlated traits
  - Calf fitness index, $h^2 = 0.014$
  - Only female calves considered
- A mixed reference population of the **multi-step model** for German Holstein
  - All genotyped female calves with own phenotypic records (deregressed EBV and ERC)
    - Dec 2024: 1,105,445 genotyped calves with phenotypic records
  - All genotyped sires of calves with phenotypic data (deregressed EBV and EDC):
    - Dec 2024: 13,212 genotyped bulls with calves
- A single-step SNP BLUP model officially implemented for DEU Holstein in April 2025
  - For all evaluated traits (Johannes Heise’s presentation)
  - Including **a new, optimized model for calf fitness**

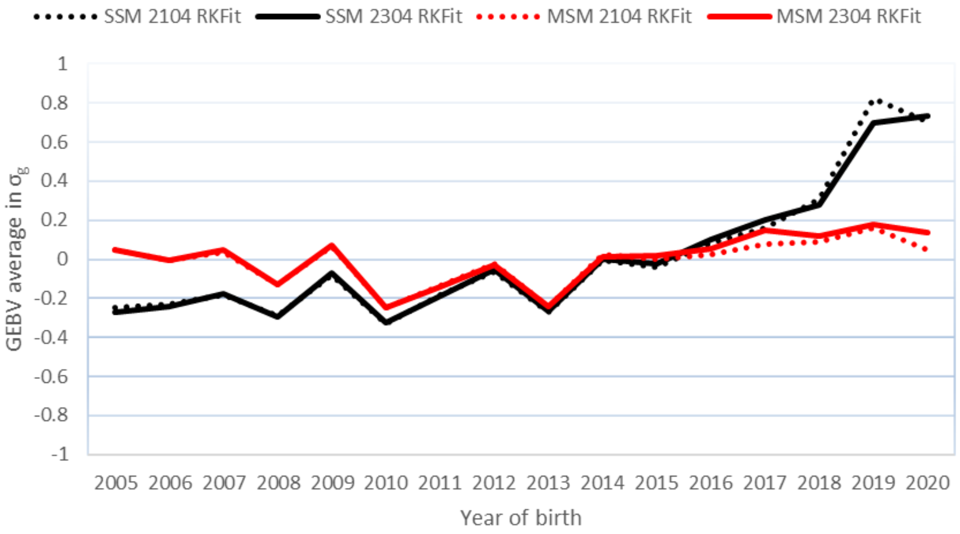
GEBV trend differences between the genomic models

- The original single-step model for calf fitness used genotypes of 1.8 million animals
  - Genomic validation conducted between April 2023 and April 2021
- Full evaluation 2304 (solid line) vs truncated evaluation 2104 (dotted line)
  - Single-Step Model (**SSM**) vs Multi-Step Model (**MSM**)
  - For animals with phenotypes GEBV of **MSM** are nearly equal to conventional EBV

Genotyped B&W Holstein cows (N = 760,804)



Genotyped German Holstein AI bulls (N = 7,778)



GEBV: μ_{base}=0, σ_g=1

Earlier genomic validation results for calf fitness

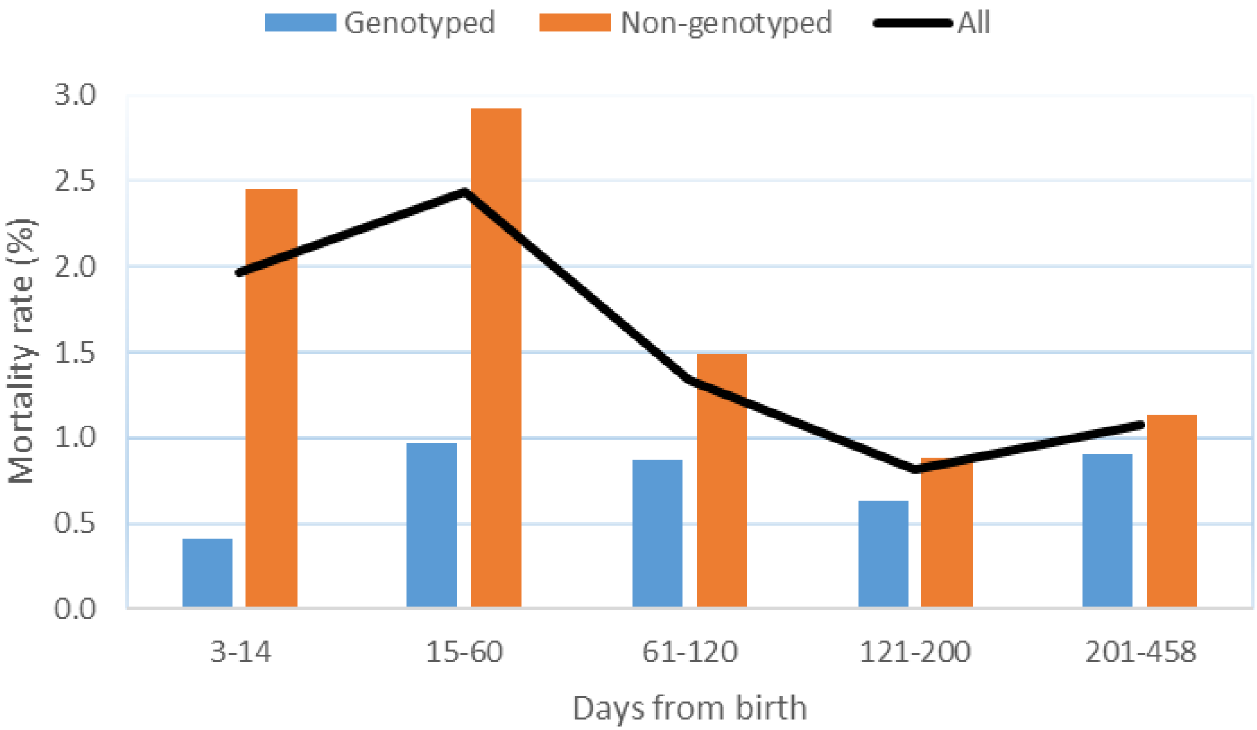
- Genomic validations for the multi-step and single-step genomic models
  - Based on full evaluation Apr 2023 and truncated evaluation Apr 2021
    - **2-year data truncation** due to the relatively short history of female genotyping
  - According to the LR test (Legarra and Reverter, 2018)
    - $u_{full} = b_0 + b_1 * u_{trunc} + e$
    - **GEBV as dependent variable**

Model	# validation bulls	R^2 value	b_1 value
Single-step	355	0.61	1.04
Multi-step	355	0.40	0.92

  - Validation bulls have lower reliabilities than most traits due to the low heritability
    - Between 0.5 and 0.6

Mortality rate of Holstein female calves born in 2022

- Holstein female calves in April 2025 single-step evaluation for calf fitness
  - 615,927 with own phenotype records
    - Genotyped: 148,427
    - Non-genotyped: 467,500



A special single-step model for the early-measured trait

- Delayed genotyping seemed to have caused the wrong genetic trend
  - Some calves genotyped too late for first two periods
  - Genotyping not always done to dead or sick calves
- Sires have both survived and dead calves
  - Breeding values less impacted by the delayed or missing genotyping on the calves
- A special single-step model with **a sire genotype population**
  - Using only genotype data of sires of female calves with phenotypic records
    - No selection of the sires based on number of calves or herds
  - GEBV of all other genotyped animals / calves indirectly predicted as for weekly evaluation (Alkhoder et al. 2024)

Test runs: a full and truncated evaluation

- A full single-step evaluation with data from Aug 2024 (2408)
- A truncated single-step evaluation with data from Aug 2020 (2008t)
- Single-step evaluations **with all (incl. calves) genotypes**

  and **with only sire genotypes**
- Genotype data for animals born in 2005 or later

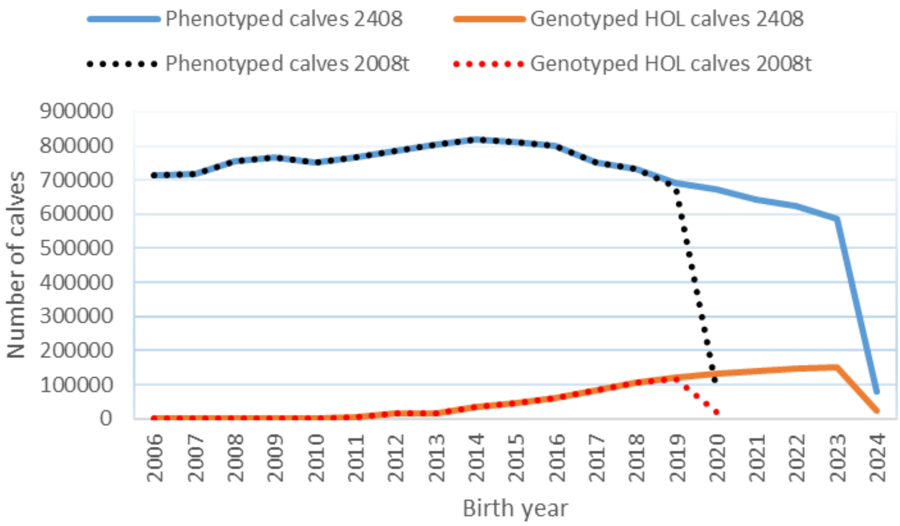
Evaluation	**Female calves with phenotypes**	**Genotyped Holstein female calves with phenotype**	**Genotyped Holstein sires**
Full: Aug 2024	13,273,996	1,075,268	36,325
Truncated: Aug 2020	10,733,873	501,653	26,578
Ratio	81%	47%	73%

- 93% Holstein female calves with phenotype born in 2022 have a genotyped sire

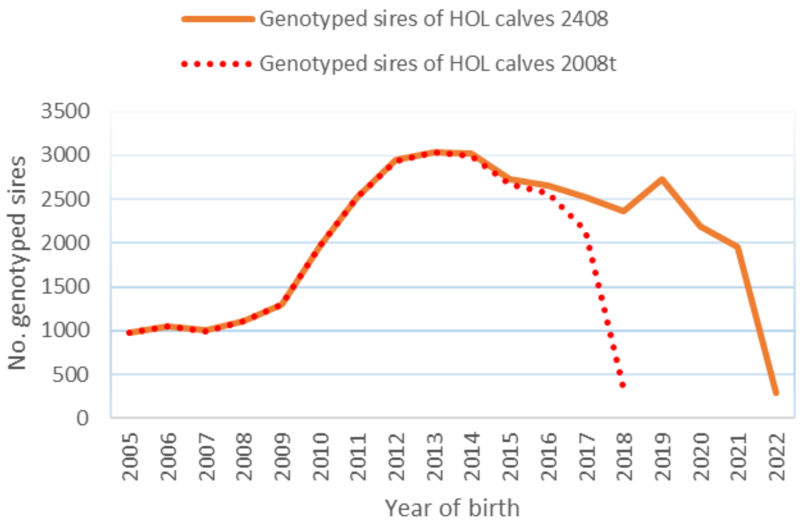
Two single-step models applied to both data sets

- Using genotypes of all animals / calves vs genotypes of sires of phenotyped calves
- Full evaluation 2408 vs truncated evaluation 2008t

Old model: using calf genotypes



New model: using sire genotypes



Results: Validation via the GEBV Test software

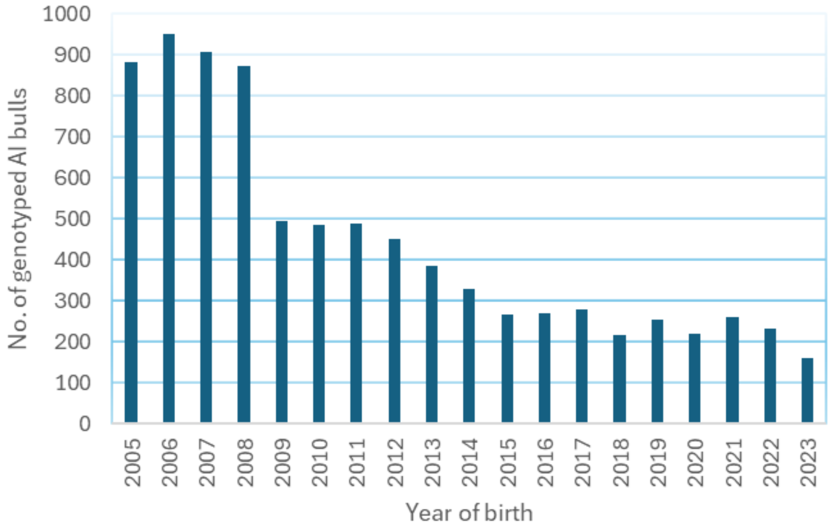
- Full single-step evaluation with genotype and phenotype data from August 2024
- Truncate phenotypic data in the last **4 years** (August 2000)
  - Participation in the October 2024 TMACE for all MACE traits
  - Evaluation also for national traits like calf fitness
- Genomic validation using Interbull's GEBV Test software (September 2024)
  - Two single-step models for calf fitness: using calf genotypes and sire genotypes only

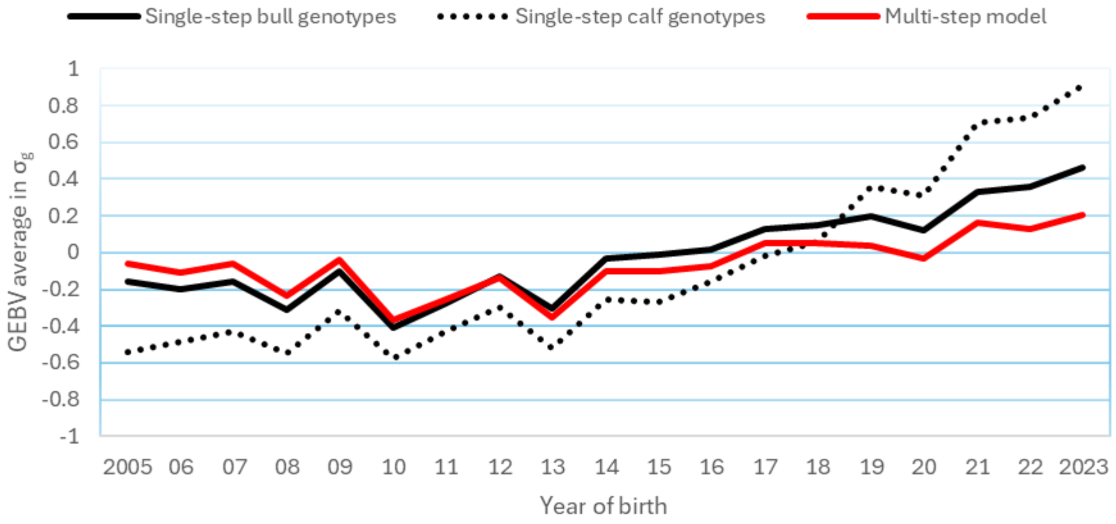
Deregressed GEBV as target	**# validation bulls**	**R^2 value**	**b_1 value**	**tests**	**Pass**
Using only sire genotypes	980	0.191	0.954	YYYY	PASS
Using all (incl. calf) genotypes	980	0.164	0.849	NYNY	FAIL

GEBV as target	**# validation bulls**	**R^2 value**	**b_1 value**	**tests**	**Pass**
Using only sire genotypes	980	0.444	0.963	YYYY	PASS
Using all (incl. calf) genotypes	980	0.436	0.933	YYYY	PASS

Results: Trends in genotyped Holstein AI bulls

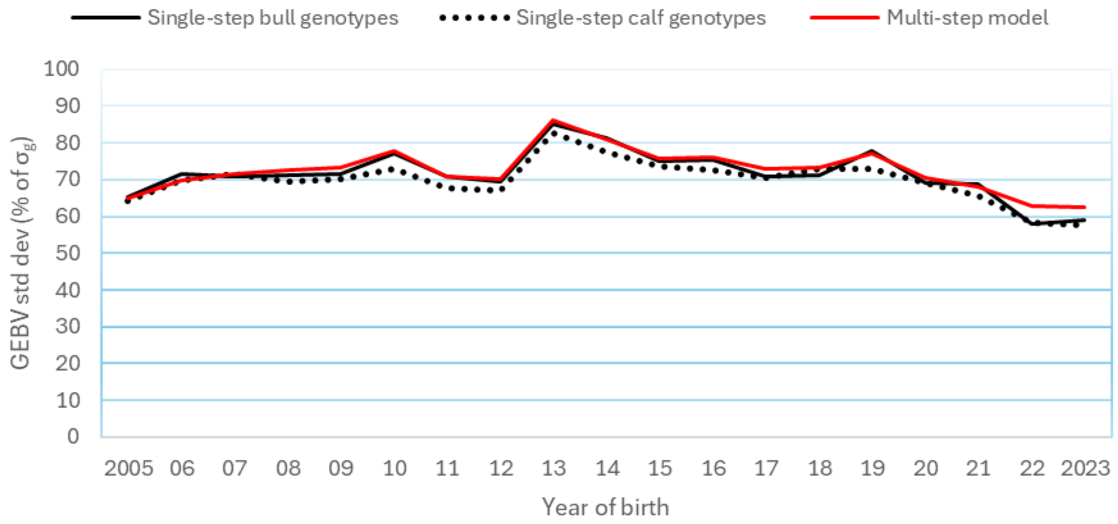
- 8,391 genotyped Holstein AI bulls owned by German AI studs born in 2005 to 2023
- **Single-step** evaluations with all (incl. calf) genotypes versus sire genotypes
- **Multi-step** evaluation with a mixed reference population of calves and bulls

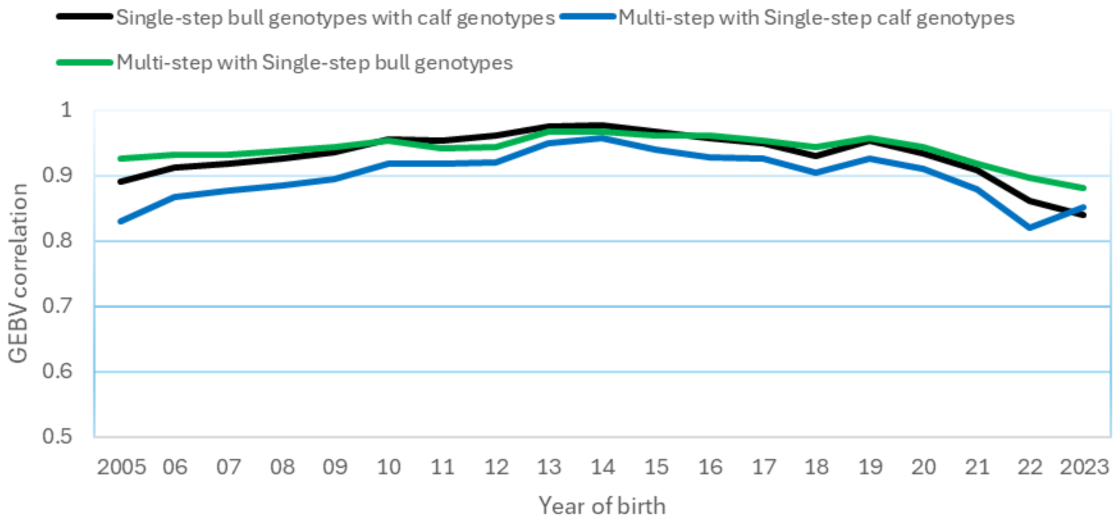




Results: GEBV variance and correlation for DEU Holstein AI bulls

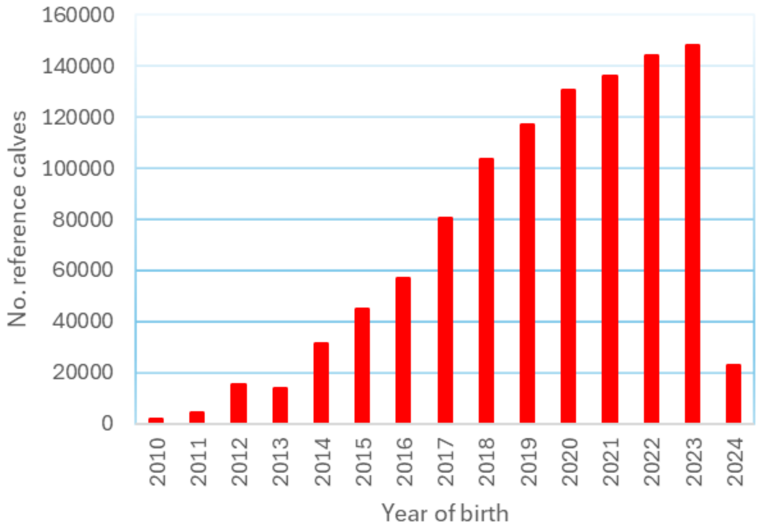
- Standard deviations of GEBV of the single-step and multi-step models
- GEBV correlations between the models

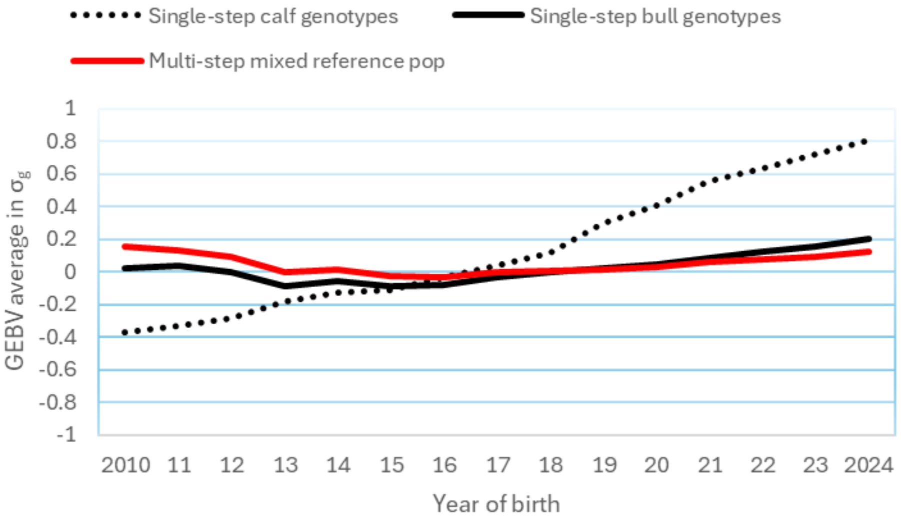




Results: Trend in genotyped Holstein female calves

- 1,072,492 genotyped Holstein female calves with phenotypes born >= 2010
- **Single-step** evaluations with all (incl. calf) genotypes versus sire genotypes
- **Multi-step** evaluation with a mixed reference population of calves and bulls





Summary and Conclusions

- Single-step model using all genotype data may give biased GEBV for early-measured traits
  - Like calf fitness
  - With delayed genotyping or limited genotyping of dead calves
    - Even for the whole-herd genotyping scheme
- A solution to the biased single-step evaluation was to use only genotypes of sires
- Genomic validation of the new German single-step model for calf fitness
  - Via the new Interbull GEBV test software (deregressed GEBV as dependent variable)
  - Slightly higher R^2 value: 0.19 with sire genotypes versus 0.16 with all genotypes
  - Nearly unbiased: b_1=0.95 with sire genotypes versus b_1=0.85 with all genotypes
- Reasonable and realistic genetic trends of the new single-step model
  - For genotyped AI bulls and female calves

Summary and Conclusions

- Genomic validation for the low heritability trait
  - Dependent variable: Deregressed GEBV clearly more appropriate than GEBV
  - 4-year data truncation preferred to 2-year data cut
    - In case of enough reference animals for the truncated evaluation
- Single-step evaluation bias in early-measured traits caused by genotyping
  - Removing SNP markers whose allele frequencies significantly changed
    - Reduced genetic trend of youngstock survival in Nordic evaluation (Nielsen et al., EuroGenetics 2025)
  - Calving trait Stillbirth using only sire genotypes
    - Implemented in the NLD single-step evaluation (Eding et al., EuroGenetics Nov 2024)
    - Sire reference population did not improve b_1 (Alkhoder et al. 2022, EAAP)

Colleagues of Nordic Evaluation Center (NAV) are greatly acknowledged for a video meeting on 26th Sep 2024 on youngstock survival evaluation

Vielen Dank!

Thanks for your attention!