



# Implementation of single-step evaluations for fitness traits in the German and Austrian Fleckvieh and Brown Swiss populations

**ZuchtData**  
EDV-DIENSTLEISTUNGEN GMBH

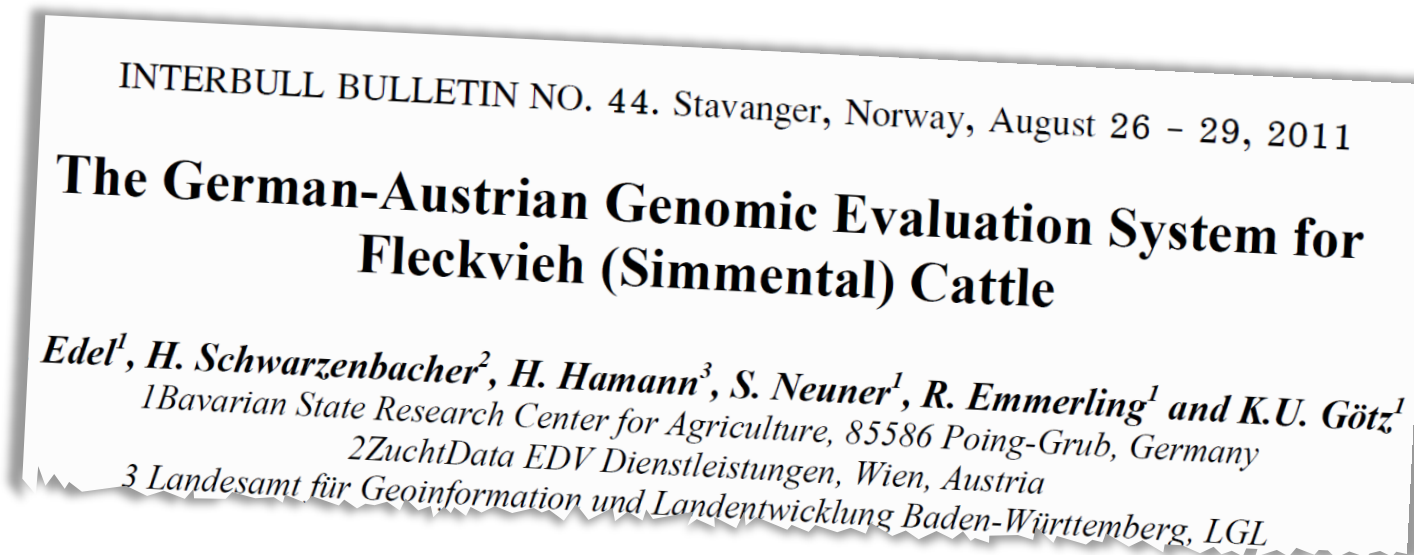
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ZuchtData

*Vienna, 30<sup>th</sup> April 2021*



# Introduction

10 years ago:



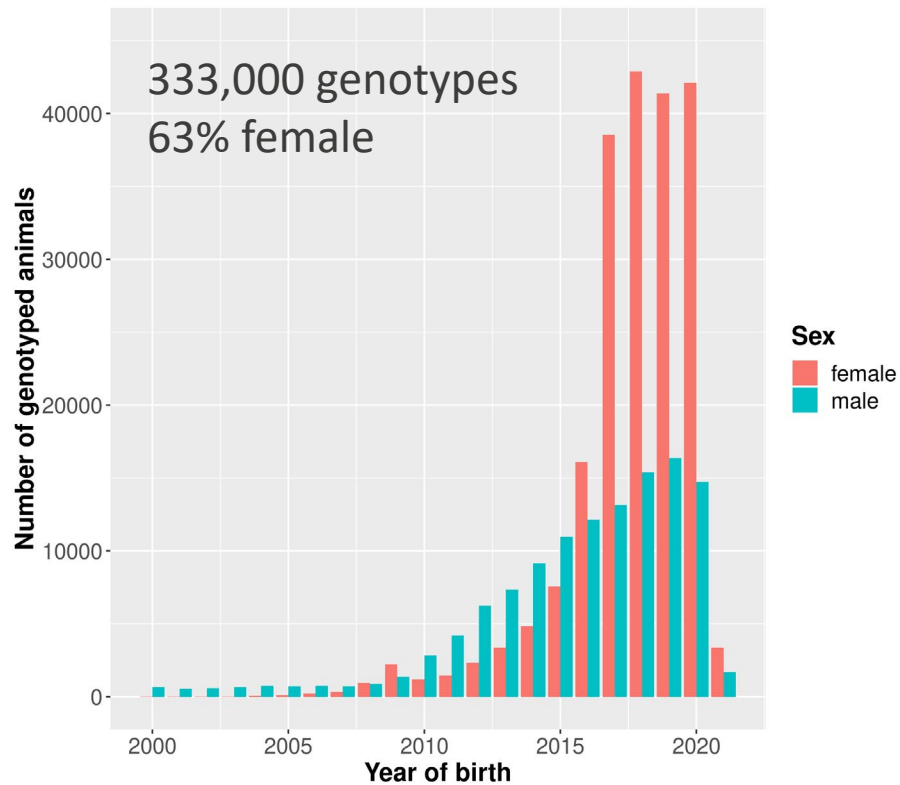
April 2021: official **single step** genomic breeding values



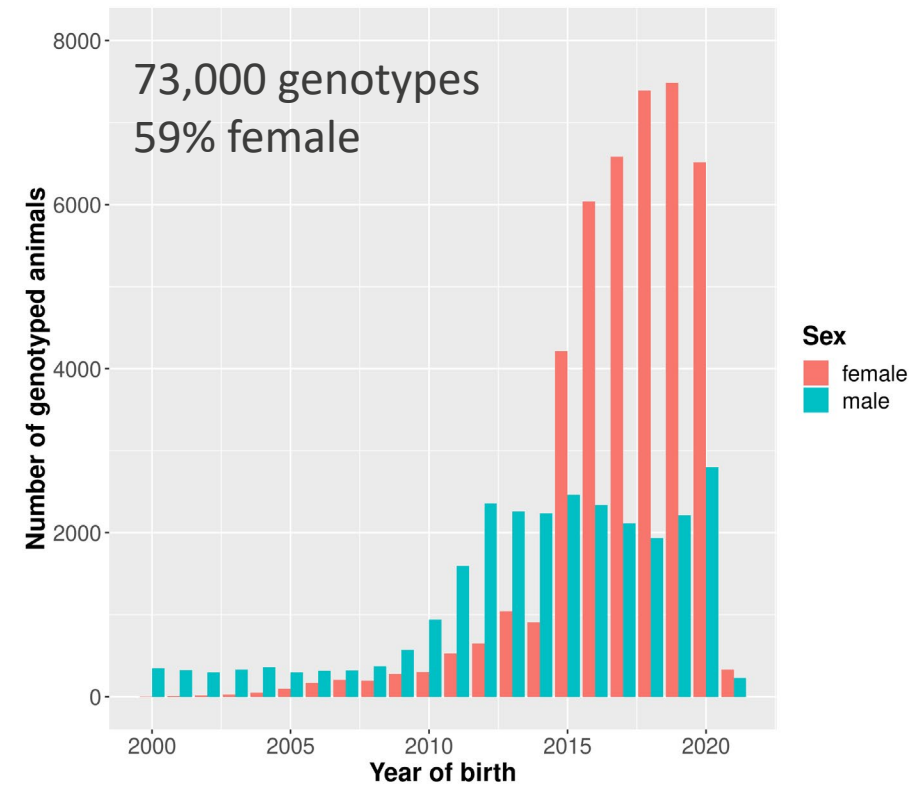
# Quick look at genotypes

(April 2021)

## Fleckvieh



## Brown Swiss



around 10% of heifers and young cows in the Austrian breeding population are genotyped



# Quick look at traits

Animals/Observations in the **training sample** of Single-Step:

(Fleckvieh, April 2021)

Trait	Bulls	
longevity	21,087	+99%
fertility	21,718	+87%
calving ease	27,535	+84%
rearing losses	27,855	+111%
mastitis	11,122	New!
early fertility disorders	17,488	New!
cystic ovaries	11,090	New!

Trait	longevity	fertility	calving ease	rearing losses	mastitis	fertility disorders	cysts
<b>h2</b>	<b>11%</b>	<b>3%</b>	<b>6%</b>	<b>2%</b>	<b>2%</b>	<b>2%</b>	<b>2%</b>



# Validation of Single-Step GEBVs

## GEBV Test

- **full** and **reduced** Dataset (minus 4 years)
- **Validation group:**
  - young bulls
- Validation based on DYDs or deregressed proofs  
(→ **Deregression** of EBVs necessary)

## LR-Method (*Legarra and Reverter (2018)*: Linear Regression method)

- **full** and **reduced** Dataset (minus 4 years)
- **Validation groups:**
  - several groups possible
  - large groups of animals
  - groups of female animals
- Validation based on EBVs  
→ genotypes are considered in the full dataset  
→ no **Deregression** needed (easier for traits with low  $h^2$ )



# Validation: LR-Method

*(April 2021 (\*December 2020), Trait: longevity, Breed: Fleckvieh)*

		Dispersion	Accuracy
Group of animals	N		



# G-Matrix: Scaling

## G-Matrix:

- VanRaden's method one G: 
$$G = \frac{ZZ'}{2 \sum p_i q_i}$$
- Base allele frequencies estimated based on bulls with progeny
- inverted with algorithm for “parents (core)” and “young (noncore)” (APY) (*Misztal et al., 2015*)
- Core: male animals with progeny (FV: 30,660 / BS: 12,980)

## Scaling G:

$$G_{SC} = \beta G_{vR} + \alpha$$

- $\alpha$  and  $\beta$  derived by applying *O. F. Christensen et al. (2012)* on the core animals
- $\alpha \approx 0.00520$
- $\beta \approx 1.00957$



# G-Matrix: Effects of Scaling

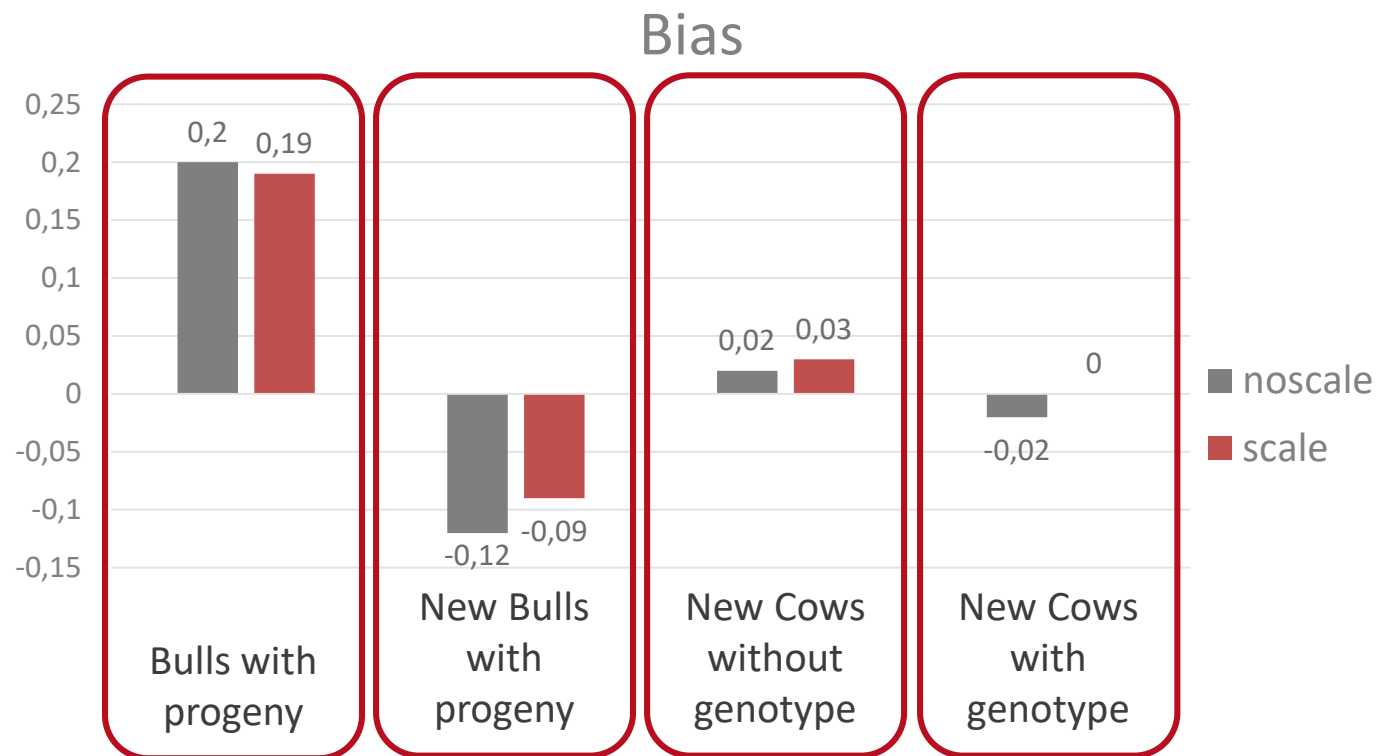
(December 2020, Breed: Fleckvieh)

## Statistics of $G_{VR}$ :

- Mean Diagonal: 1.016 (0.0235); [0.943; 1.298]

## Statistics of $G_{sc}$ :

- Mean Diagonal: 1.030 (0.0237); [0.957; 1.315]



(Trait: longevity)



# G-Matrix: Effects of Scaling

(April 2021, Breed: Fleckvieh)

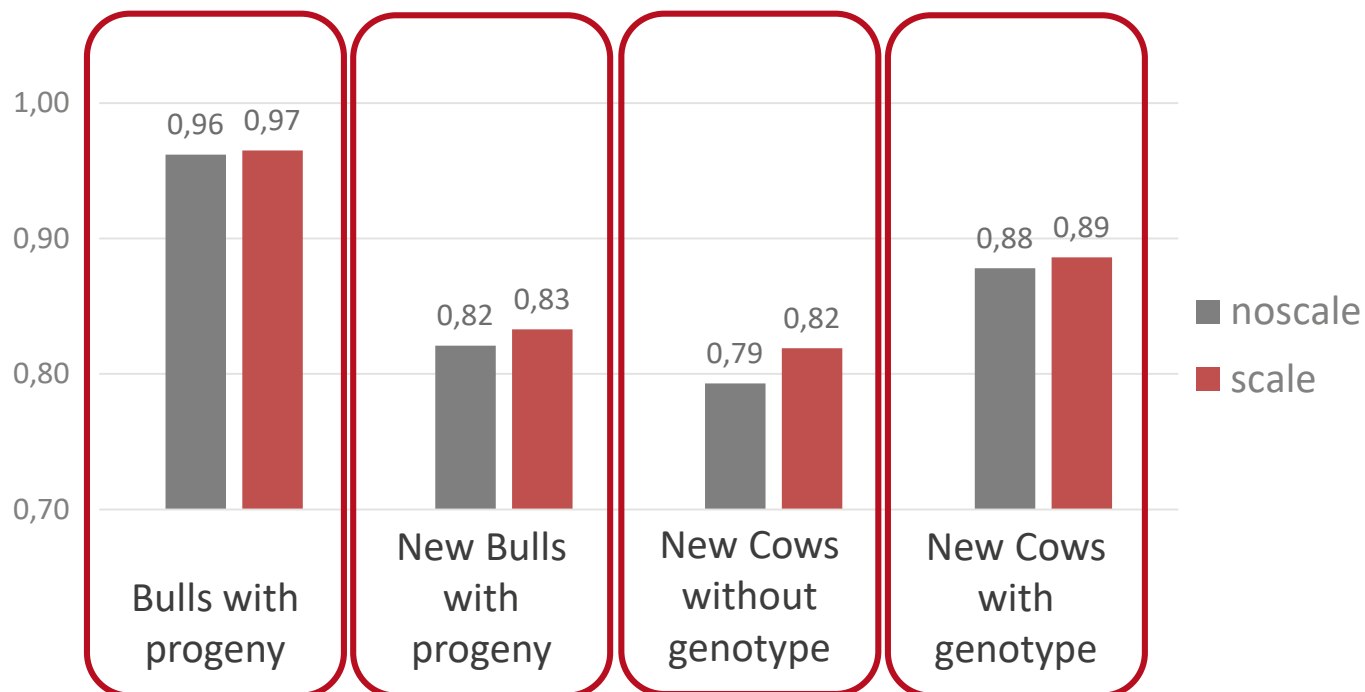
## Statistics of $G_{VR}$ :

- Mean Diagonal: 1.015 (2.360); [0.942; 1.297]

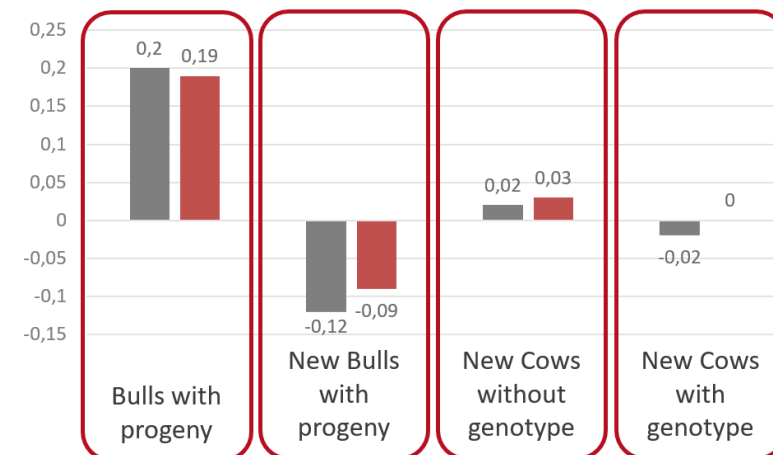
## Statistics of $G_{SC}$ :

- Mean Diagonal: 1.030 (2.384); [0.956; 1.315]

### Dispersion



### Bias



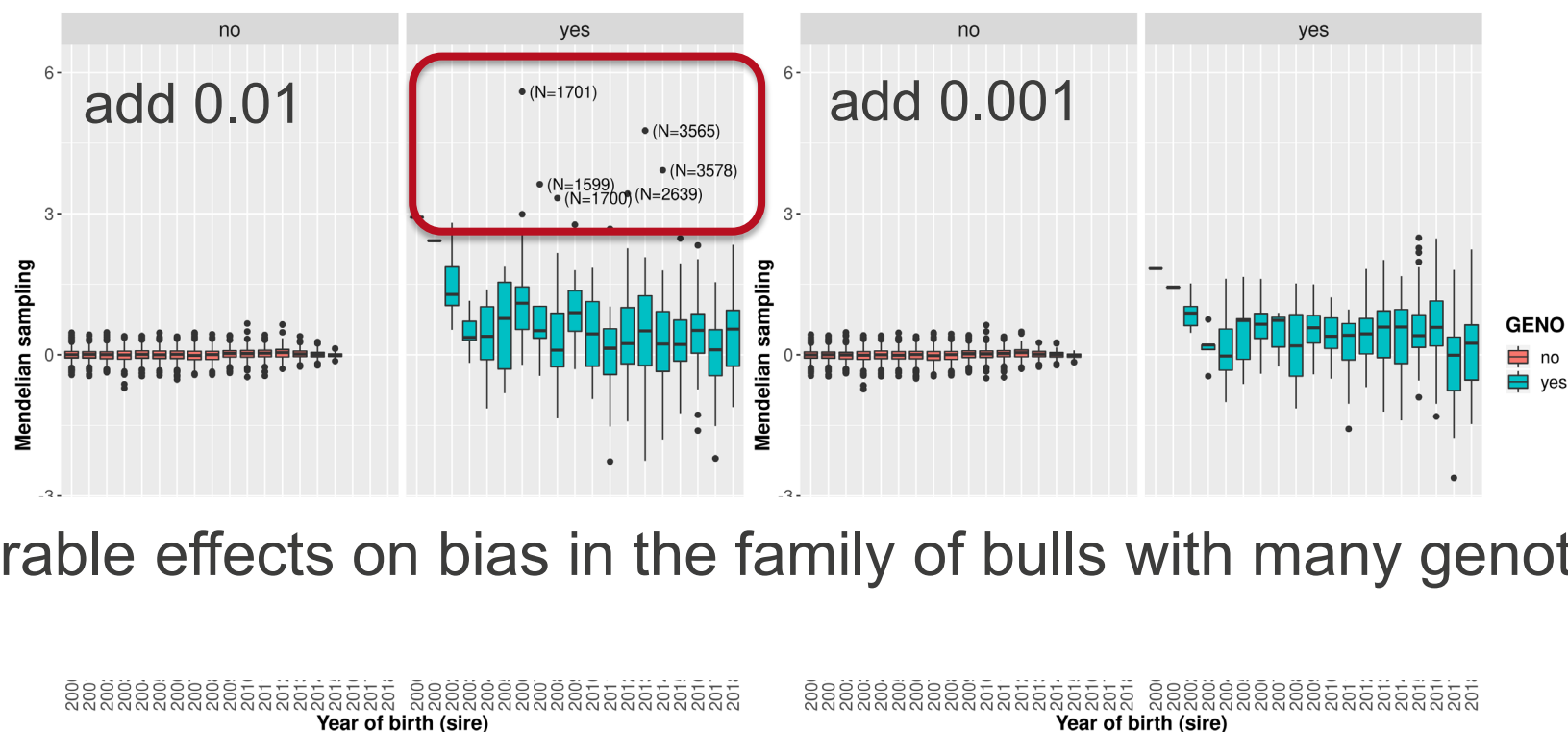
(Trait: longevity)

# G-Matrix: Singularity-prevention

add a small value on diagonal of G

- makes G invertible
- improves convergence behaviour

→ high correlations of breeding values:  $>0.99$  (add=0.01 vs. add=0.001)



→ Considerable effects on bias in the family of bulls with many genotyped progeny



# Summary and Outlook

## Validation using LR-method:

- possibility to consider female animals in validation
- quite easy to compute

## Scaling of G-Matrix:

- scaling to fit G to NRM
- small scaling has noticeable effects

## Singularity prevention:

- inconsistencies due to manipulation of the diagonal
- → MS-Bias in bull families with many genotyped progeny



THANK YOU FOR YOUR ATTENTION

