

## Single-step in a multi-breed population with crossbred animals

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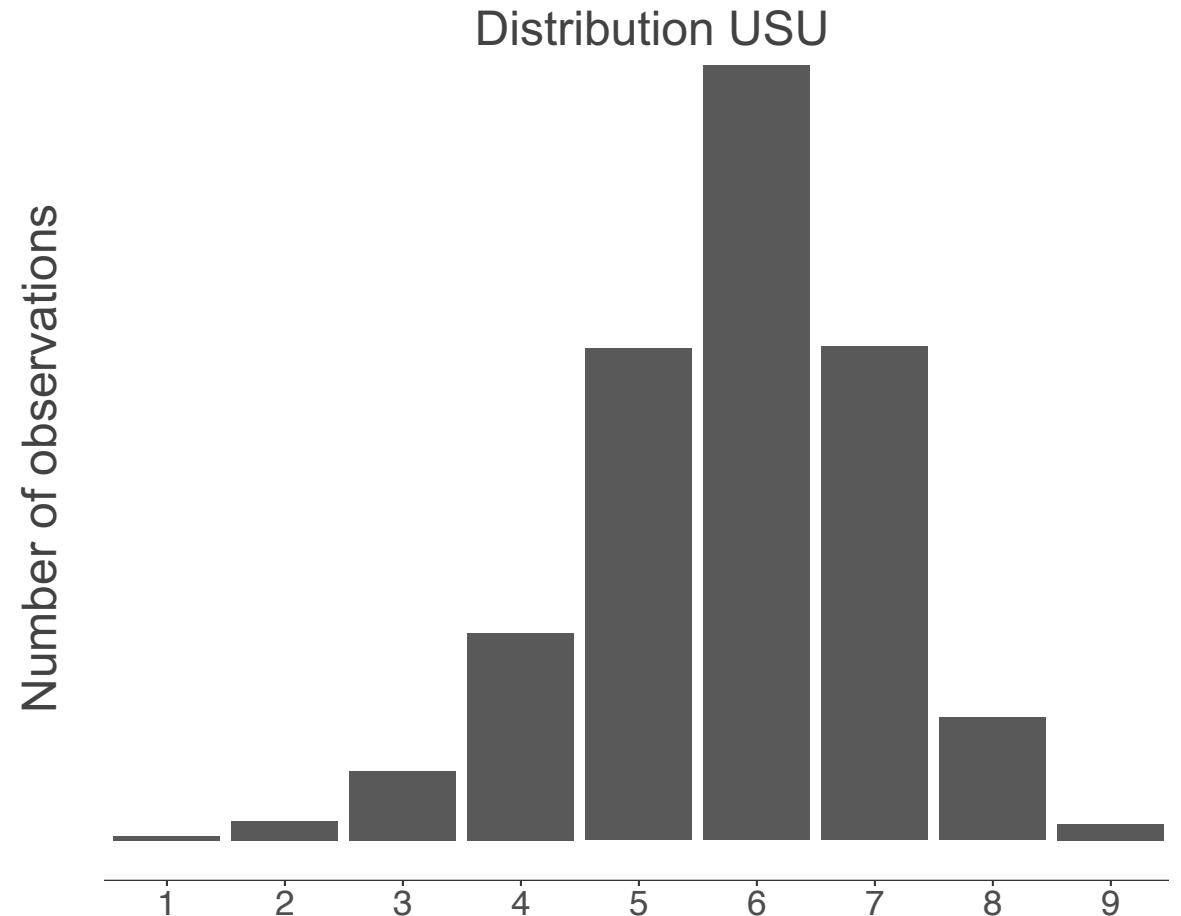
Interbull Meeting, Montréal

# Objective

Compare **traditional and genomic** breeding values estimation with inclusion of phenotypes and/or genotypes of **one or multiple breeds**.

# Udder support

- Simple trait
- Score from 1 to 9
- Homogeneous data recording over time
- Almost normally distributed
- Trait shared through Interbull network



# Using ssGTBLUP as implemented in MiX99

- No inversion of the complete G matrix is needed and matrix size increase linearly with the number of genotyped animals (Stranden et al, 2018)
- Reliabilities were estimated in four step following Ben Zaabza et al. (EAAP 2020)

# Model

- Animal repeatability model including
  - Fixed effects: classifier-year, year-season, age at calving, lactation stage, heterosis, recombination loss, and description scheme
  - Random effects: herd, permanent environment, animal, residual
- Genetic groups modelled into  $A_{22}^{-1}$  and  $G^{-1}$  with QP transformation
  - Genetic groups divided by breed

$$\mathbf{H}_{AB}^{-1} = \mathbf{A}_A^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{B} & -\mathbf{BQ}_2 \\ \mathbf{0} & -\mathbf{Q}'_2\mathbf{B} & \mathbf{Q}'_2\mathbf{BQ}_2 \end{bmatrix}$$

(Matilainen et al., 2018)

# Three breeds

Holstein (HO)



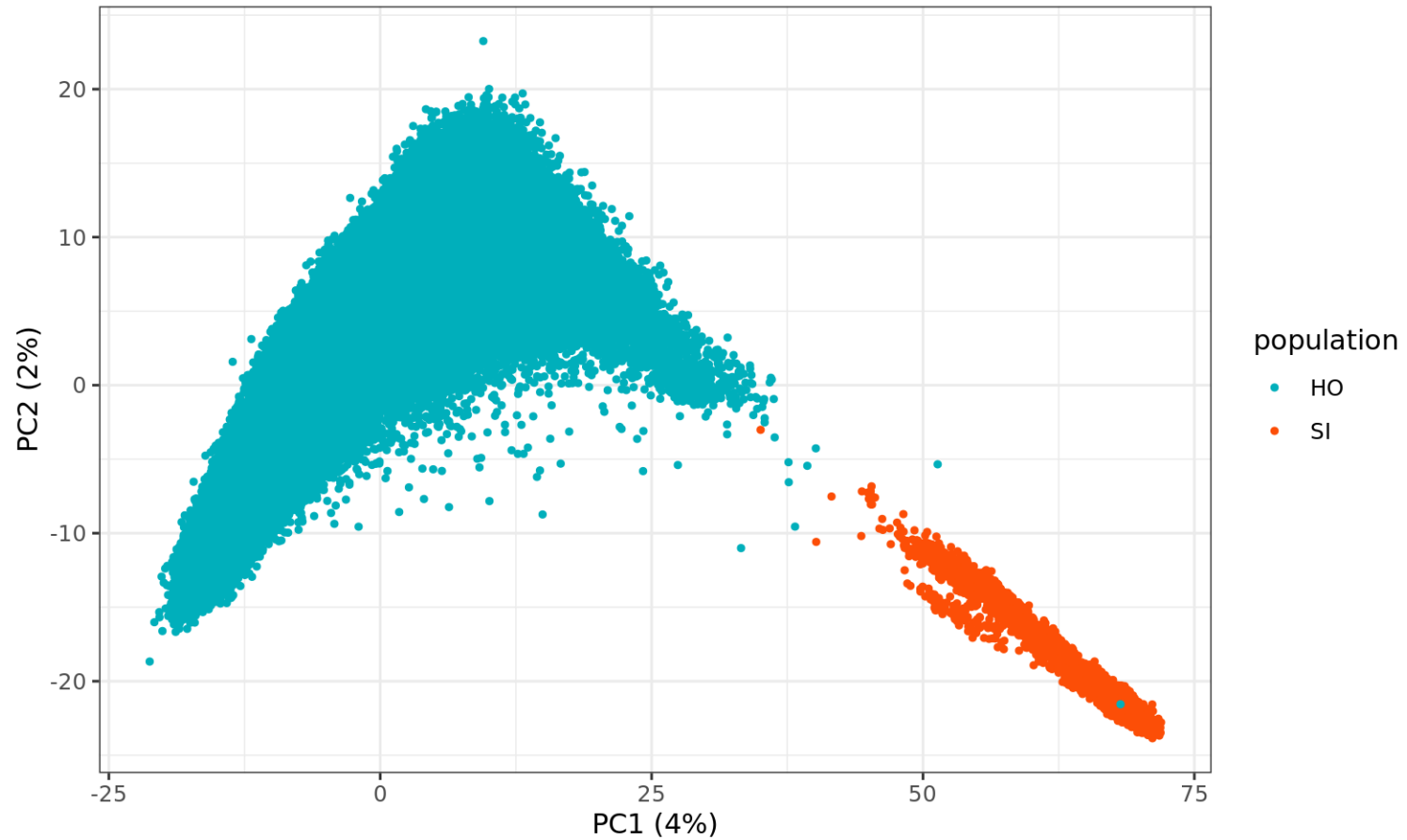
Swiss Fleckvieh (SF)

→ crossbreds

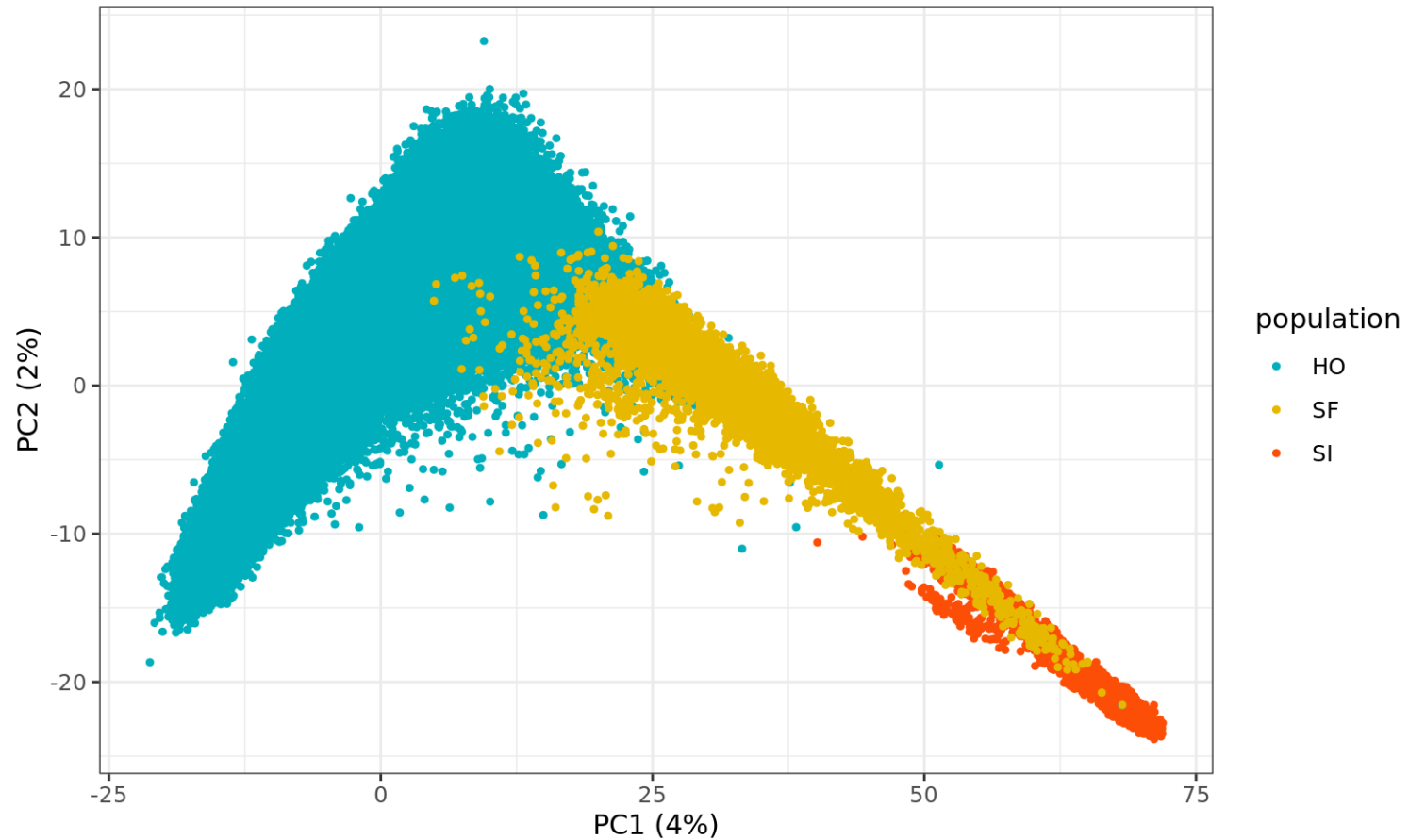
Simmental (SI)



# A multi-breed evaluation with crossbred animals



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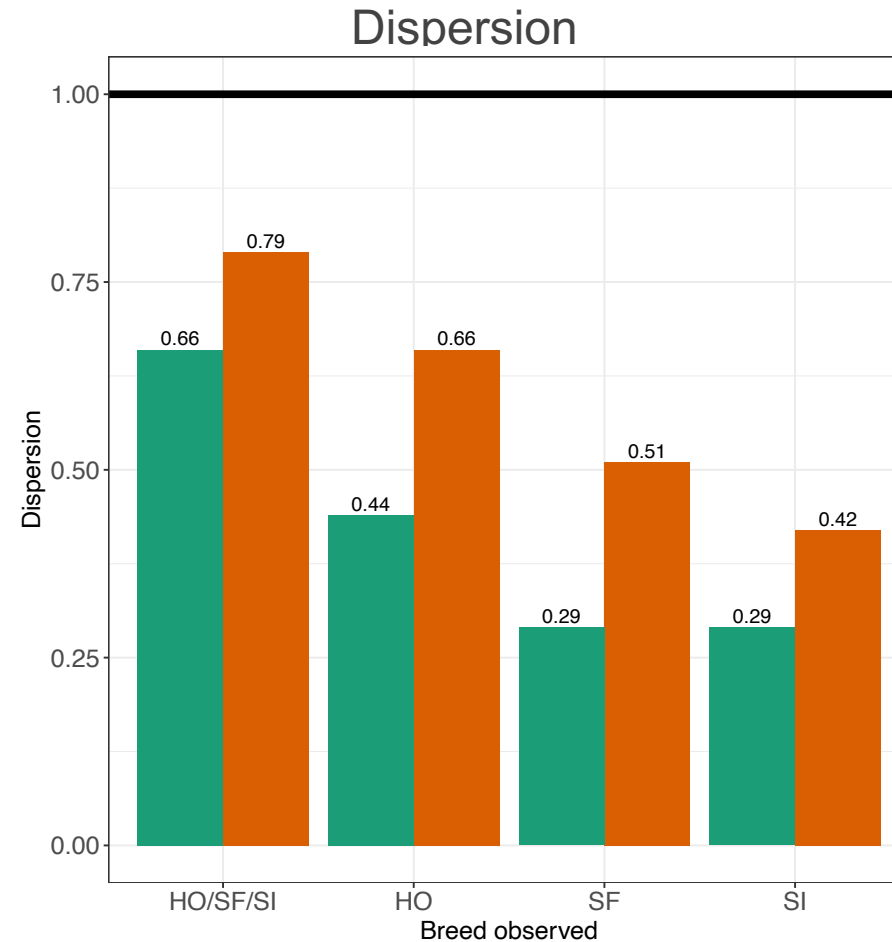
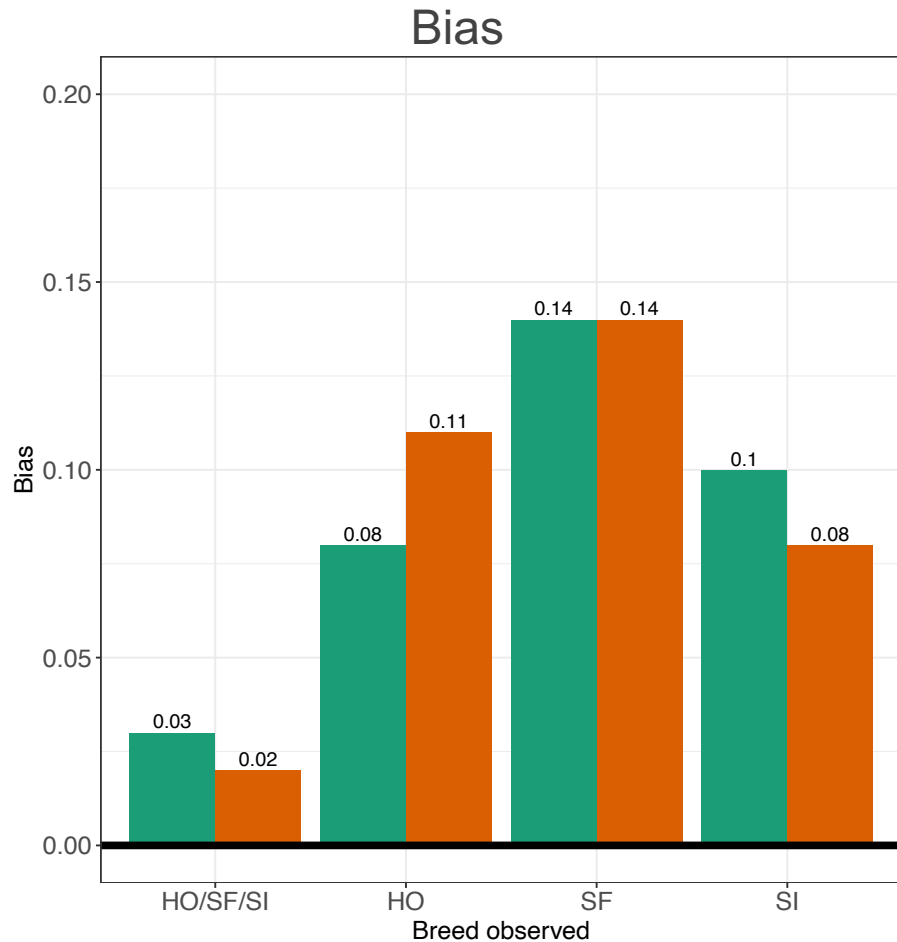


# Numbers

# Records	Holstein	Swiss Fleckvieh	Simmental
Phenotypes	850'951 (79%)	195'637 (18%)	34'025 (3%)
Genotypes	343'233 (94%)	8'656 (2%)	12'565 (4%)
Both	22'164 (84%)	2'647 (10%)	1'601 (6%)

- Genotypes imputed together (one reference population) to 125K SNP
- Pedigree build for all phenotyped and/or genotyped animals and pruned to 2 generations

# Multi-breed evaluation results

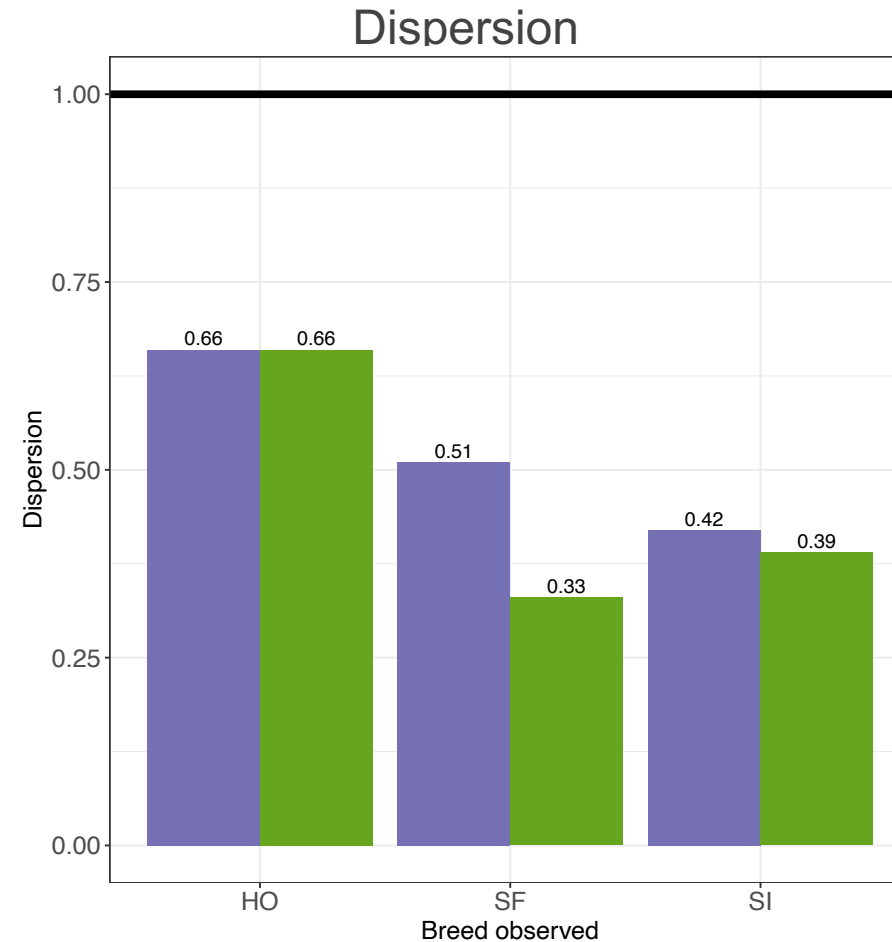
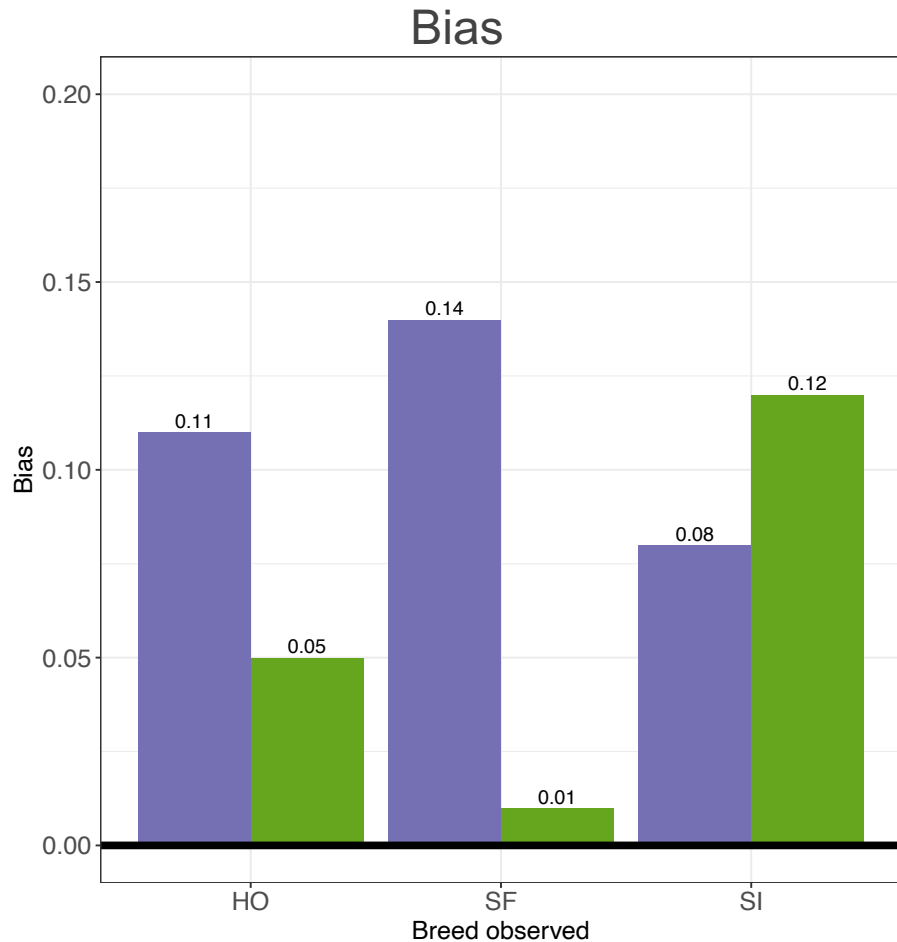


Evaluation

- PBLUP
- ssGTBLUP

Validation bulls:  
edc 0 in partial  
edc >10 in whole

# Multi-breed vs single-breed



### Dataset

- Multi-breed
- Single-breed

Validation bulls:  
edc 0 in partial  
edc >10 in whole

# Conclusions

- Change from PBLUP to ssGTBLUP evaluation reduces bias and improve dispersion
  - Lower bias and better dispersion are reached with the complete multi-breed dataset
- ➔ Multi-breed ssGTBLUP evaluation seems to be the best option so far

**BUT**

Results of multi-breed ssGTBLUP for HO validation animals are not always the best

# Next steps

- HO dataset comprised the most non-selected candidates:
  - Test the effect of **removing genotypes of unselected candidates**
- HO validation bulls are the furthest from the proven bulls:
  - Test the effect of increasing/decreasing the **proportion of residual polygenic variance**

# Acknowledgements



# ASR

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Communauté de travail des éleveurs bovins suisses

SWISS   
**herdbook**



# Thank you for your attention



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Credit: Mirjam Spengeler