

Effect of cows in the reference population: First results in Swiss Brown Swiss

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Why genotype cows?

- Population level
 - Enlarging the reference population for increasing accuracy of genomic selection
 - ⇒ important for small breeds
 - Revealing the population structures (e.g. for imputation)
 - Finding new valuable families
 - Detecting genetic defects (e.g. BH2)
- Farm level
 - Selection at an early stage of life
 - Information for mating
 - Parentage verification
 - Detecting genetic defects

Including cows in the reference population: state of the art

- Only a few countries have included genotyped cows in the reference population:
 - US: HOL, BSW, JER
 - AUS: HOL, JER
 - NZL: ? ...
- Only a few investigations based on real data are published regarding the reliability gain:
 - Pryce et al. (2013)
 -

Motivation

- In **Switzerland available**: 1429♀ and 6309♂ BSW genotypes (without Intergenomics genotypes)
- How much is the **reliability gain** by including cows in our Swiss Brown Swiss population?
⇒ **step 1**
- **Which cows** should be genotyped?
⇒ **step 2**
- Does the origin of a cow have an influence on the accuracy gain? ⇒ **step 3**

Methods

- Estimating marker effects and direct genomic values (dgv):
 - Prediction of breeding values from genomic data:
Bayesian approach (BayesC), using the software GenSel (Fernando and Garrick, 2010)
 - Input ("phenotypic") data:
Deregressed proofs (Garrick et al., 2009)
- Validation: accuracy: $r_{dgv,ebv}$
- Computing the genomic relationship matrix (gmatrix):
VanRaden, 2008

Validation process

- Forward prediction
- Random sample from bull subset (birth year 05 - 08 = youngest sires) → validation set
old bulls + remaining part of the youngest sires → reference population
- one run cows included, one run without cows → comparison of the accuracies \cong 1 replication
- totally 120 replications

SNPs and number of genotyped cows

- 48194 SNP
 - Call rate ≥ 0.90

| | Requirements | Origin | n |
|--------------------|----------------------------|--|-------------|
| Bulls | Rel. production% ≥ 65 | Braunvieh Schweiz | 1650 |
| Bulls | Rel. production% ≥ 65 | bilateral exchange | 2435 |
| Bulls total | | | 4085 |
| Cows | Rel. production% ≥ 50 | Braunvieh Schweiz elite cow program | 264 |
| Cows | Rel. production% ≥ 50 | LIB project | 972 |
| Cows total | | | 1236 |
| Total | | | 5321 |

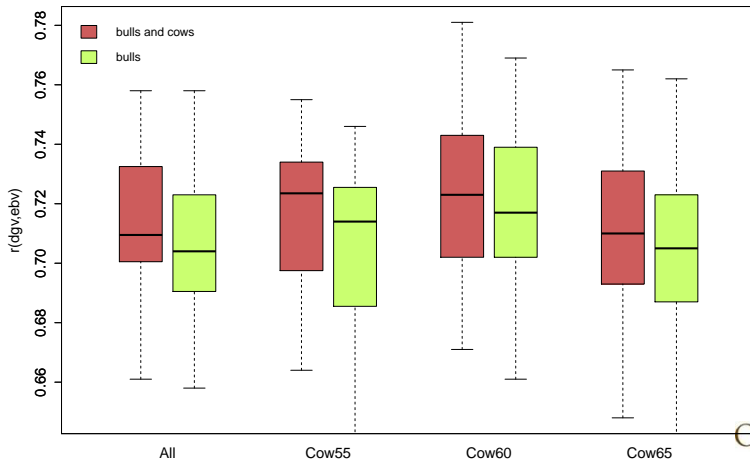
Step 1: Different Strategies

Composition of the reference populations

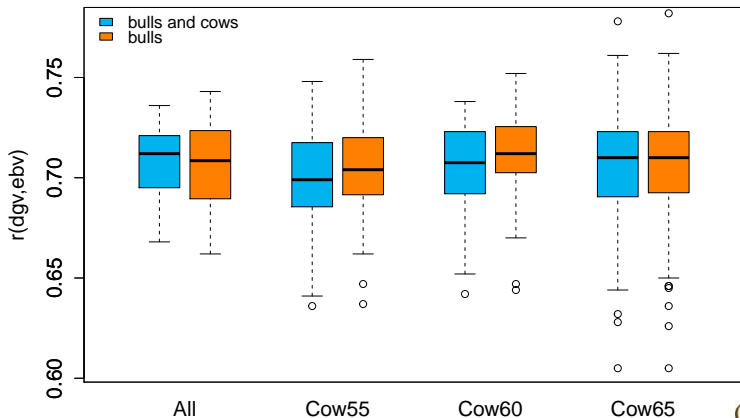
| Strategy | Reference population | Milk kg | | | Somatic cell count | | |
|--------------|---|------------|-----------|------------|--------------------|-----------|------------|
| | | Bulls n | Cows n | Total n | Bulls n | Cows n | Total n |
| All | Bulls Rel % ≥ 65 Cows Rel % ≥ 50 | 4085 | 1236 | 5321 | 3891 | 1162 | 5052 |
| Cow55 | Bulls Rel % ≥ 65 Cows Rel % ≥ 55 | 4085 | 1189 | 5274 | 3891 | 1014 | 4905 |
| Cow60 | Bulls Rel % ≥ 65 Cows Rel % ≥ 60 | 4085 | 1021 | 5106 | 3891 | 396 | 4287 |
| Cow65 | Bulls Rel % ≥ 65 Cows Rel % ≥ 65 | 4085 | 243 | 4328 | 3891 | 45 | 3936 |

Step 1: Gain of accuracy

Milk kg

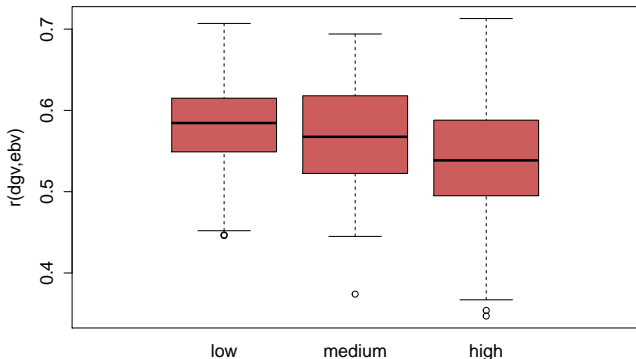


Step 1: Gain of accuracy Somatic cell score



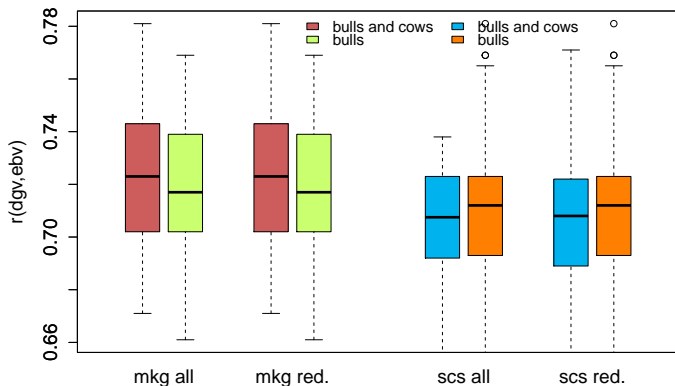
Step 2: Accuracy by different relationships of the bull- and cows subset in the reference population

- 3 levels of relationship: low, medium and high



Step 3: Influence of different origins of cow groups?

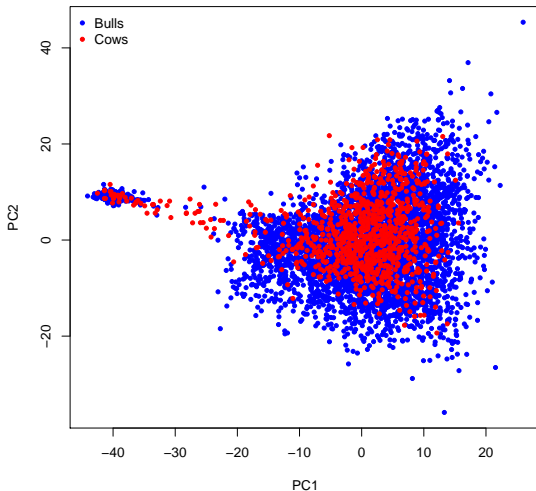
- **mkg all:** milk kg, all cows
- **mkg red.:** milk kg, without elite cows
- **scs all:** scs, all cows
- **scs red.:** scs, without elite cows



Discussion and outlook I

- The effect of including 1000 cows in the existing CHE BSW reference population (about 4100 bulls) is small
 - not enough cows
 - Pryce et al. (2013): 3000 HOL bulls + 10000 HOL cows in AUS → +4-8% reliability gain
- Trait dependent
- Composition of the bull and cow set in the reference population seems to have an influence
 - important to genotype/include the appropriate cows
- Covering the whole genetic diversity of the population (Pszczola et al., 2012)
 - see next figure

Composition of the reference population



Discussion and outlook II

- For us: Including cows in the reference population → Reducing bias of cows dgvs/gebvs?
applying approach Wiggans et al.(2011, 2012)
- Genotyping cows must go on 😊
(cost/benefit)
 - The number of bulls with accurate ebvs is limited
 - Exploring female specific traits
 - ...see introduction
- Exchange cow genotypes (phenotypes: cow ebv exchange)
- Vision: Genotyping should be so cheap that herdbook registration requires a valid genotype

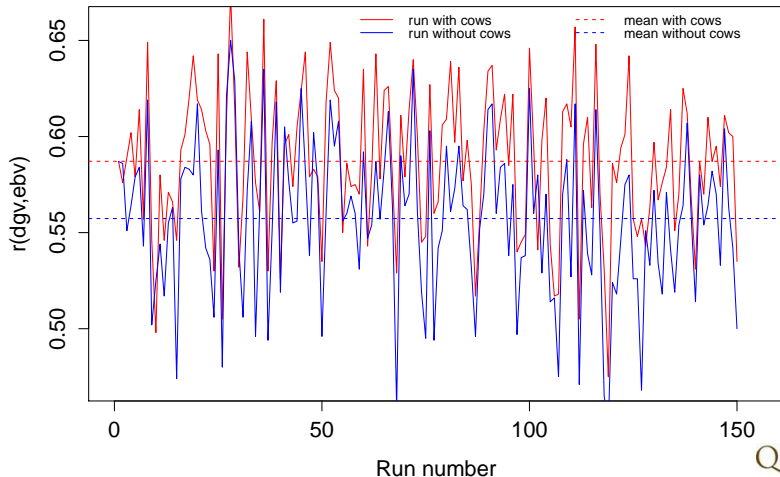
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Questions?



Introduction: Example of validation process



Validation process

