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Bavarian State Research Center
for Agriculture

Effects of different groups of cows in the reference population on genomic breeding values

Laura Plieschke, C Edel, ECG Pimentel, R Emmerling, K-U Götz

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27. August 2018

Background

- Simulation study: extending the reference population by genotyped cows

Plieschke *et al. Genet Sel Evol (2016) 48:73*
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GSE Genetics Selection Evolution

RESEARCH ARTICLE Open Access

Systematic genotyping of groups of cows to improve genomic estimated breeding values of selection candidates

Laura Plieschke[1*], Christian Edel[1], Eduardo C. G. Pimentel[1], Reiner Emmerling[1], Jörn Bennewitz[2] and Kay-Uwe Götz[1]

Background

- Effects of selected cow samples:

Scenario	N		Validation reliability (%)	b
	bulls	cows		
basic	4200	0	40	.99
--/50	4200	52,500	65	.95
--/50s	4200	52,500		

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Background

- Effects of selected cow samples:

Scenario	N		Validation reliability (%)	b
	bulls	cows		
basic	4200	0	40	.99
--/50	4200	52,500	65	.95
--/50s	4200	52,500	42	.76

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Background

- Extending the reference population by females **increases reliability** of genomic breeding values

- ~~Selected daughter sample~~
  - directional selection **decreases** benefits on validation reliability
  - leads to biased results
  - negative effects are hard to compensate for

Objective

- What changes do we find when looking at r**eal data**?

- What happens if we extend the reference population by cows now?
  - What changes can be detected?

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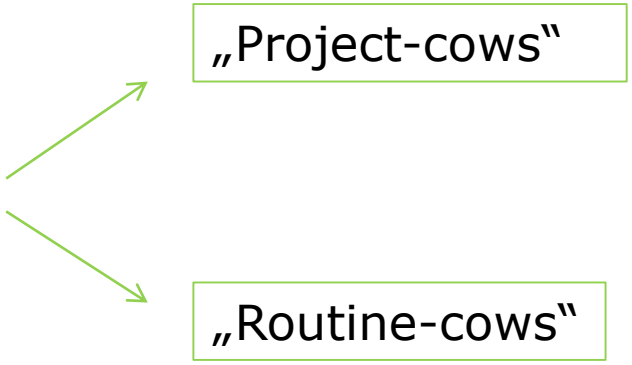
Objective

- When including cows: why not using **single-step**?
  - all cows are included
- In practice:
  - selection hardly to avoid
  - selection not only based on phenotype, but also on EBV
  - selection based on different trait
  - we do not know whether an animal is pre-selected or not

Material & Methods

- Stepwise procedure:
  - two-step GBLUP including blending
    - ✓ bulls
    - ✓ bulls and cows
    - ✓ bulls and different group of cows
  - single-step GBLUP
    - ✓ using DRP



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Material & Methods

- Fleckvieh data
- 3 traits: MY, FY, PY
- Number of genotyped females is small

Material & Methods

- Fleckvieh data
- 3 traits: MY, FY, PY
- Number of genotyped females is small
  - minus-4-year validation (m4y)
  - minus-2-year validation (m2y)
- Validation animals:
  - same animals for all sets
  - m4y: ca. 1600
  - m2y: ca. 775

Material & Methods

- Compared reference population

Set	Explanation	N			
		m4y		m2y	
		bulls	cows	bulls	cows
0	bulls	7085	0		
1	bulls + all cows	7085	4449		
1a	bulls + routine-cows	7085	673		
1b	bulls + project-cows	7085	3773		

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Material & Methods

- Compared reference population

Set	Explanation	N			
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		bulls	cows	bulls	cows
0	bulls	7085	0	8107	0
1	bulls + all cows	7085	4449	8107	6572
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Material & Methods

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1b	bulls + project-cows	7085	3773	8107	3942
1ss	single-step	>7085	>4449	>8107	>6572

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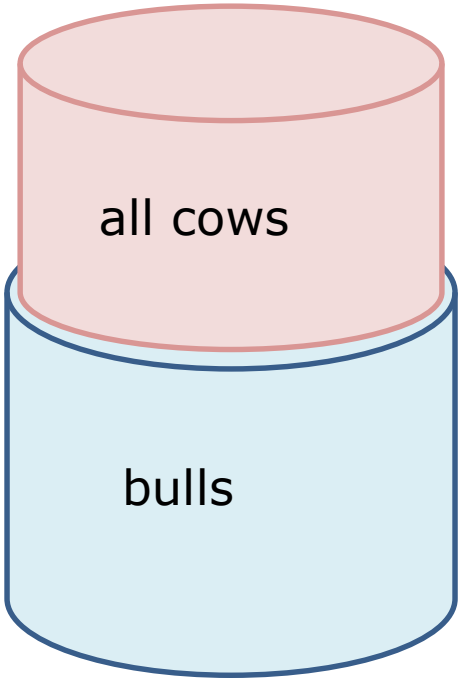
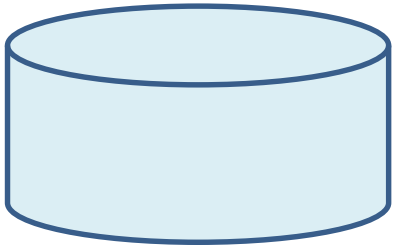
Material & Methods

- Reference animals



- Validation animals



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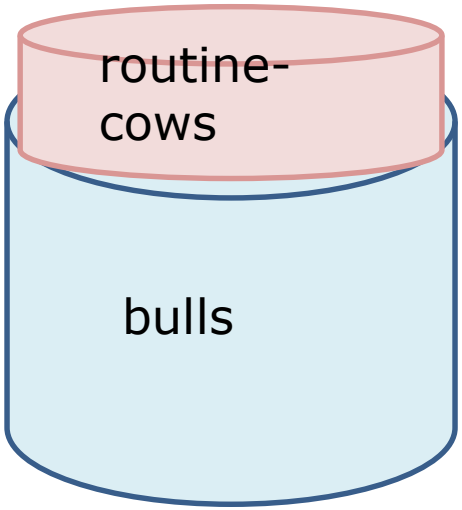
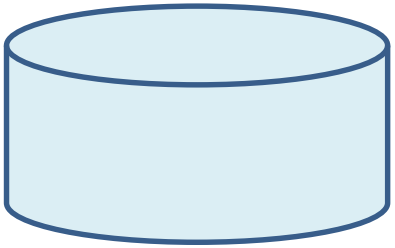
Material & Methods

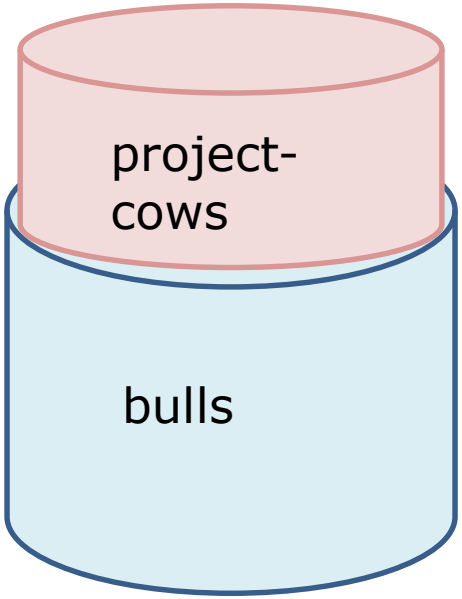
- Reference animals
- Validation animals





Material & Methods

- Reference animals



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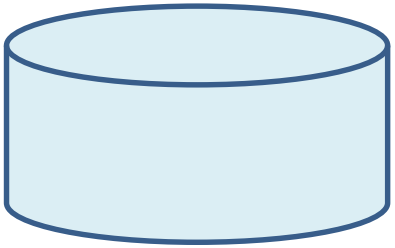

Material & Methods

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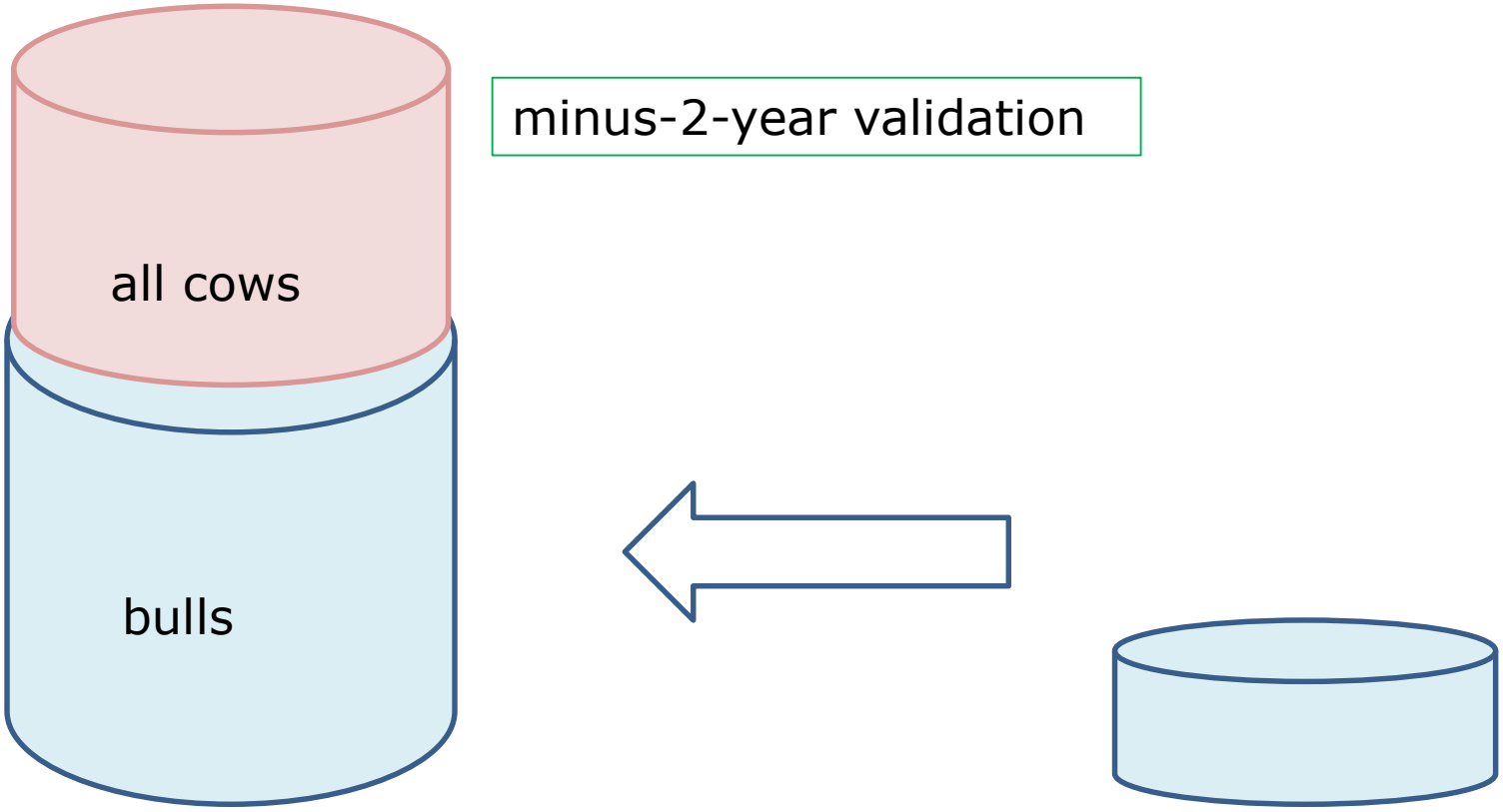

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Material & Methods

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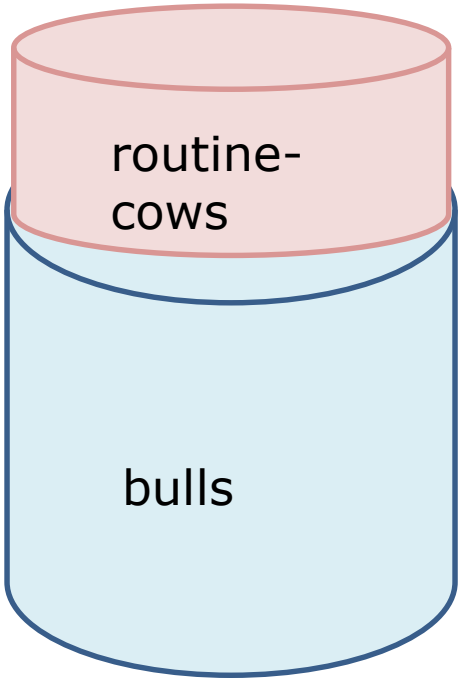

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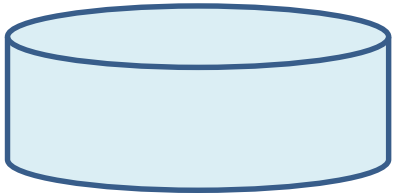

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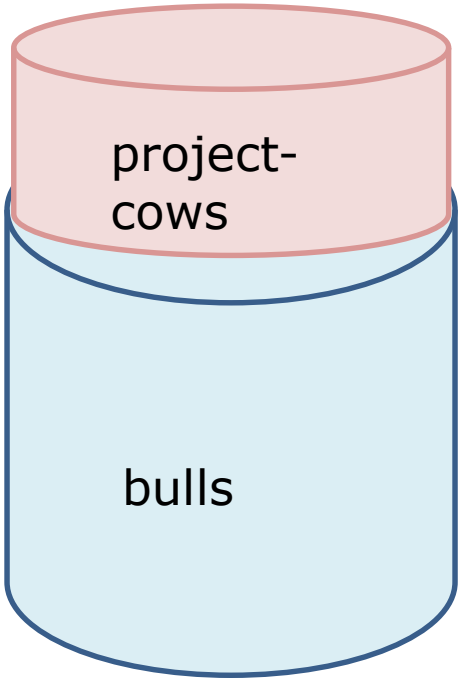

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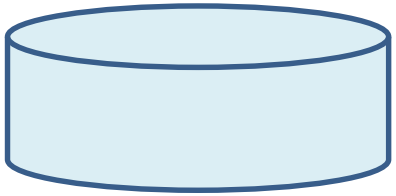

Results

Set	Explanation	Realized reliability (%)					
		m4y			m2y		
		MY	FY	PY	MY	FY	PY
0	bulls	62	61	60	69	59	65
1	bulls + all cows	64	62	61	72	62	67
1a	bulls + routine-cows						
1b	bulls + project-cows						
1ss	Single-step						

Higher reliabilities when extending the reference population by cow genotypes

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Results

b

Set	Explanation	m4y			m2y		
		MY	FY	PY	MY	FY	PY
0	bulls	.96	.94	1.03	.90	.88	.95
1	bulls + all cows	.98	.96	1.04	.91	.91	.94
1a	bulls + routine-cows						
1b	bulls + project-cows						
1ss	Single-step						

Slightly higher b when including cows

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Results

Set	Explanation	Realized reliability (%)					
		m4y			m2y		
0	bulls						
1	bulls + all cows						
1a	bulls + routine-cows	62	61	61	69	59	66
1b	bulls + project-cows	64	62	62	70	60	66
1ss	Single-step						

Very similar,
but project-cows seem to have a slightly more positive effect

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Results

Set	Explanation	m4y		b	m2y		
0	bulls						
1	bulls + all cows						
1a	bulls + routine-cows	.96	.94	1.03	.90	.89	.95
1b	bulls + project-cows	.98	.95	1.04	.90	.90	.96
1ss	Single-step						

Very similar,
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1a	bulls + routine-cows	62	61	61	69	59	66
1b	bulls + project-cows	64	62	62	70	60	66
1ss	Single-step	66	63	60	74	64	68

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Results

b

Set	Explanation	m4y			m2y		
		MY	FY	PY	MY	FY	PY
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1a	bulls + routine-cows	.96	.94	1.03	.90	.89	.95
1b	bulls + project-cows	.98	.95	1.04	.90	.90	.96
1ss	Single-step	.89	. 91	.92	.85	.89	.88

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Discussion

- Effects on validation statistics were small
- Effects on validation statistics in simulation study were large
  - 4200 + 52,500 bulls & cows vs. 8107 + 6572 bulls & cows
  - selected vs. unselected sample in real data
    - ✓ no pre-selection in routine-cows
    - ✓ selection was based on a different trait
- BUT: slight differences can be found

Conclusions

- Extending the reference population by females **increases reliability** of genomic breeding values also in real data
- Differences between groups were very small
  - number of females is still low
  - different size of groups
  - however small tendencies can be found, that should be further observed in the future

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Conclusions

- Replace two-step GBLUP with single-step GBLUP:
  - extends the reference population indirectly
  - results in higher realized reliabilities
  - with slightly higher inflation

Thank you for your attention

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