

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

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Background

- Simulation study: extending the reference population by genotyped cows

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RESEARCH ARTICLE

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

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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		

Background

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basic	4200	0	40	.99
--/50	4200	52,500	65	.95
--/50s	4200	52,500	42	.76

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 **real data**?

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

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

„Project-cows“

„Routine-cows“

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		

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
1a	bulls + routine-cows	7085	673	8107	2630
1b	bulls + project-cows	7085	3773	8107	3942

Material & Methods

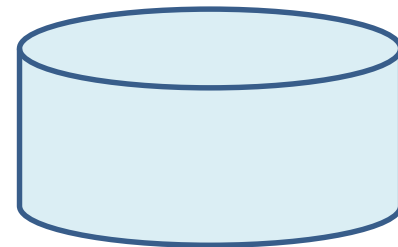
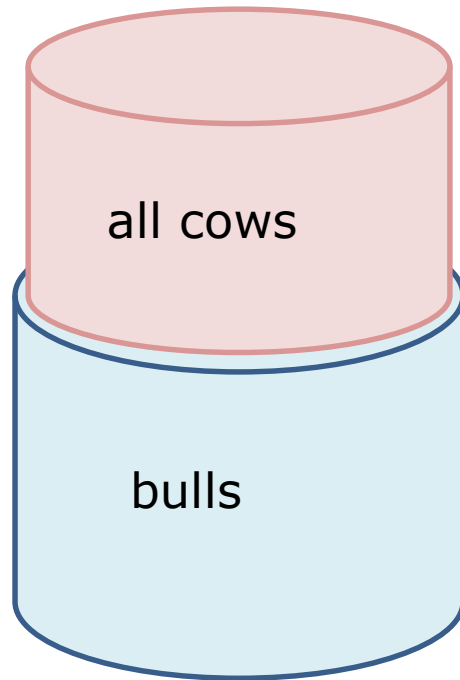
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1ss	single-step	>7085	>4449	>8107	>6572

Material & Methods

Reference animals

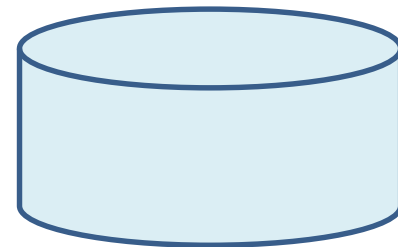
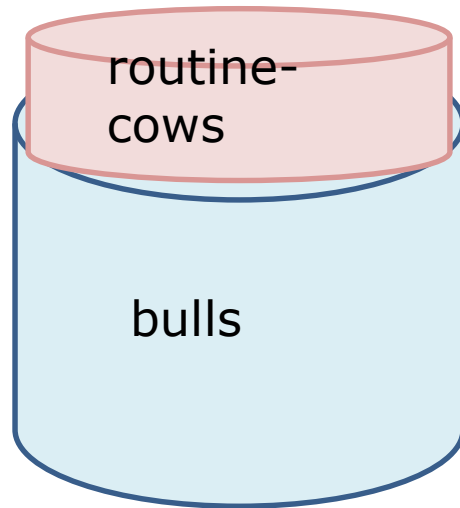
Validation animals



Material & Methods

Reference animals

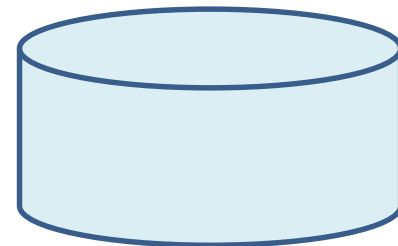
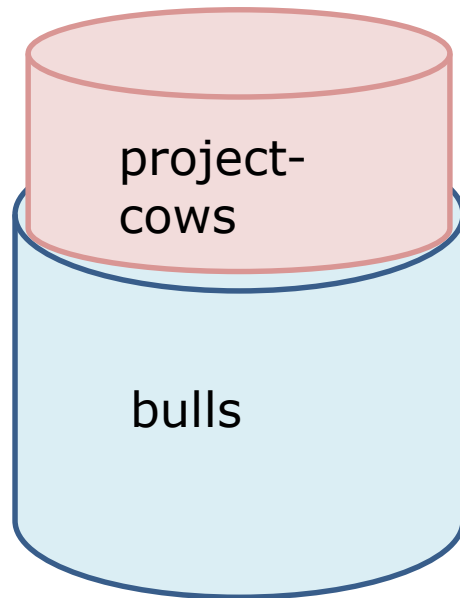
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Material & Methods

Reference animals

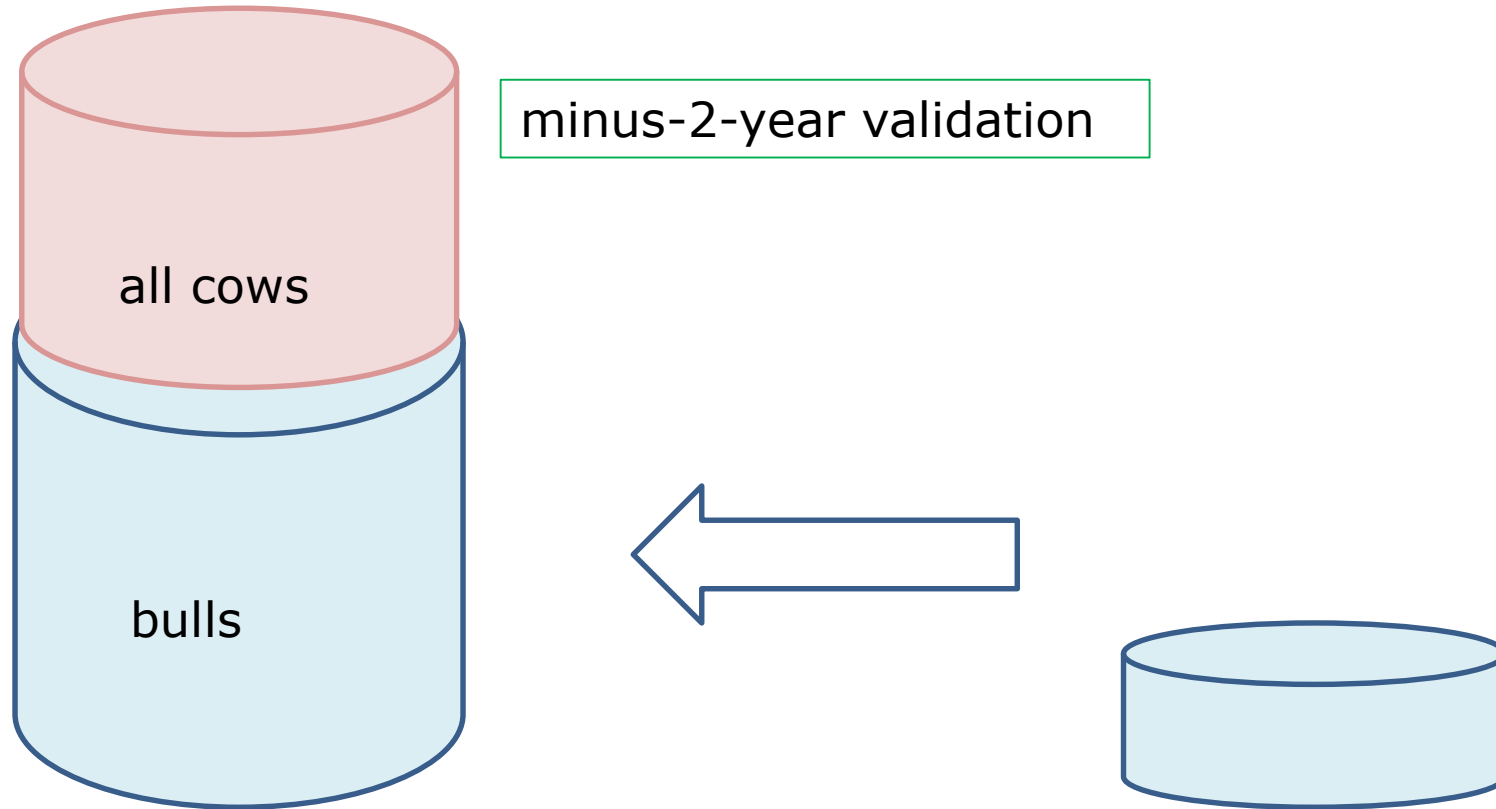
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Material & Methods

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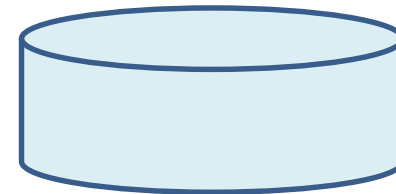
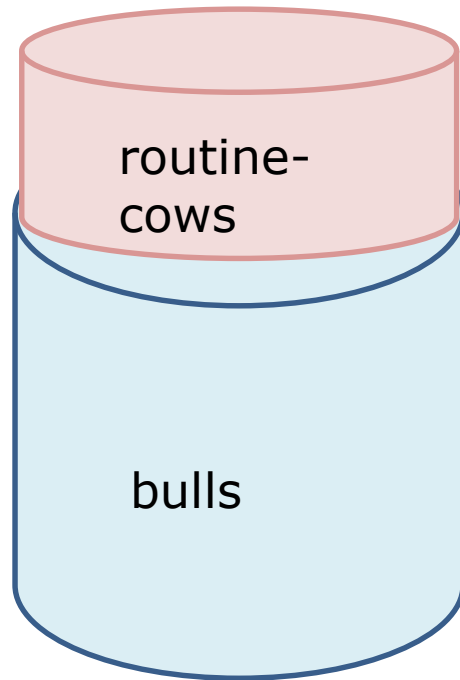
☐ Validation animals



Material & Methods

Reference animals

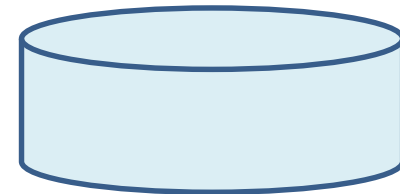
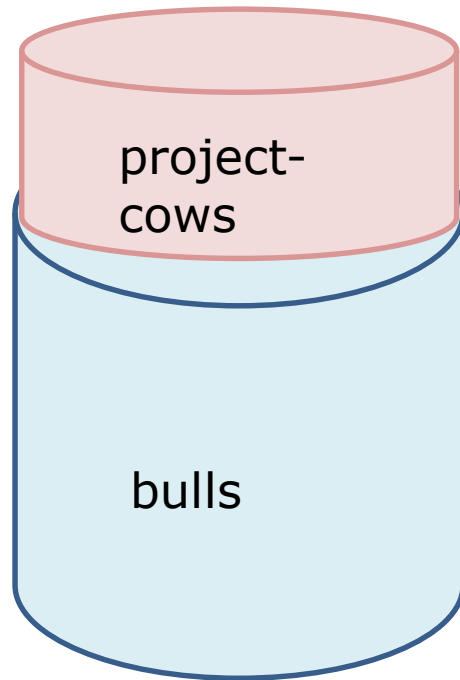
Validation animals



Material & Methods

Reference animals

Validation animals



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

Results

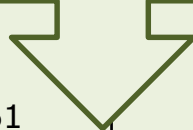
Set	Explanation	b					
		m4y			m2y		
		MY	FY	PY	MY	FY	PY
0	bulls	.96	.94	1.03	.90	.88	.95
1	bulls + all cows	.98	.96	1.04	.91	.91	.94
1a	bulls + routine-cows						
1b	bulls + project-cows						
1ss	Single-step						

Slightly higher b when including cows

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						

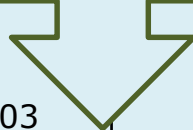
Very similar,
but project-cows seem to have a slightly
more positive effect



Results

Set	Explanation	b					
		m4y			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						

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but project-cows seem to have a slightly
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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

Results

Set	Explanation	b					
		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	.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

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

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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