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GEORGIA

College of Agricultural &
Environmental Sciences

Stability of breeding values in the genomic era

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Is stability important?

- Top bulls are priced according to their merit
- Stability means confidence in the evaluation system
- Industry was comfortable with BLUP EBV
 - Stable EBV for animals with no new data
 - Changes for animal with new data + relatives in pedigree
- Moving from traditional to genomic evaluation
 - $\text{Corr}(\text{EBV}, \text{GEBV}) = 0.60 \text{ to } 0.99$
 - GEBV were biased
 - Adjustments to give breeders confidence in genomics
 - “Unexpected” changes in subsequent evaluations

Are genomic evaluations less stable?

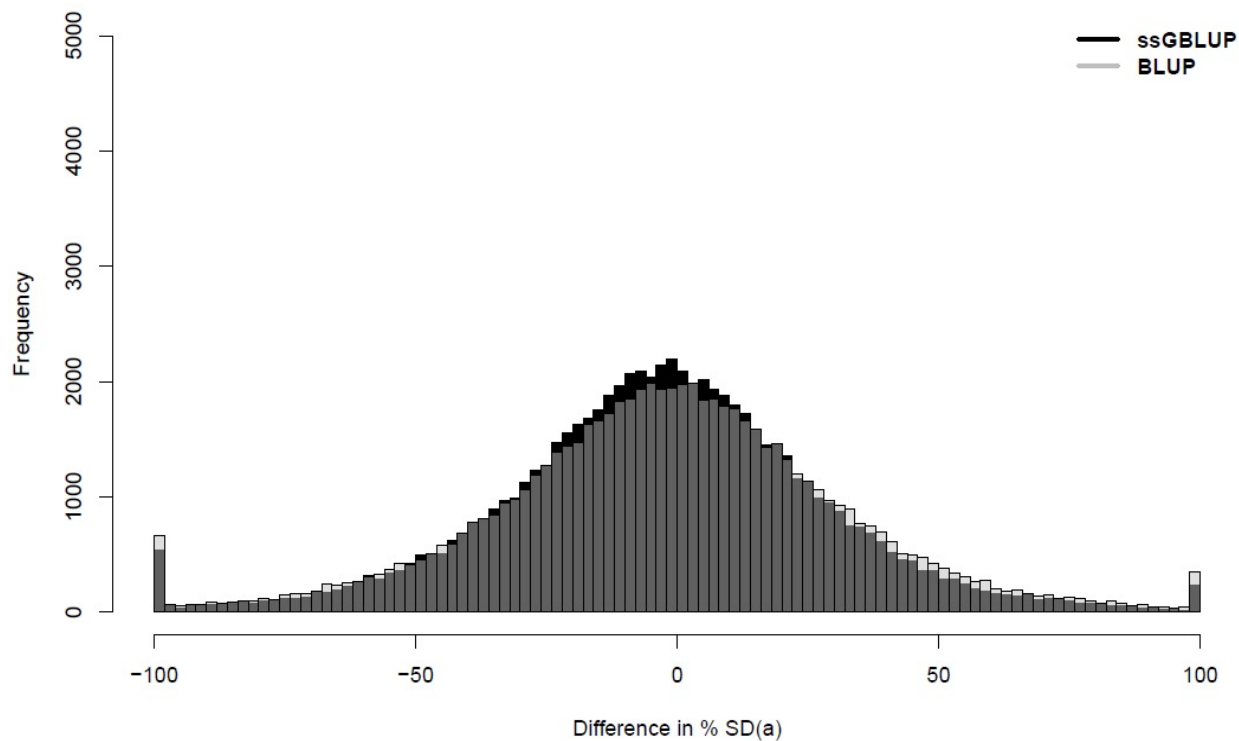
- 1) What happens with genomic evaluations when we add new data?
- 2) When small changes are made to the evaluation system?

Changes with more data

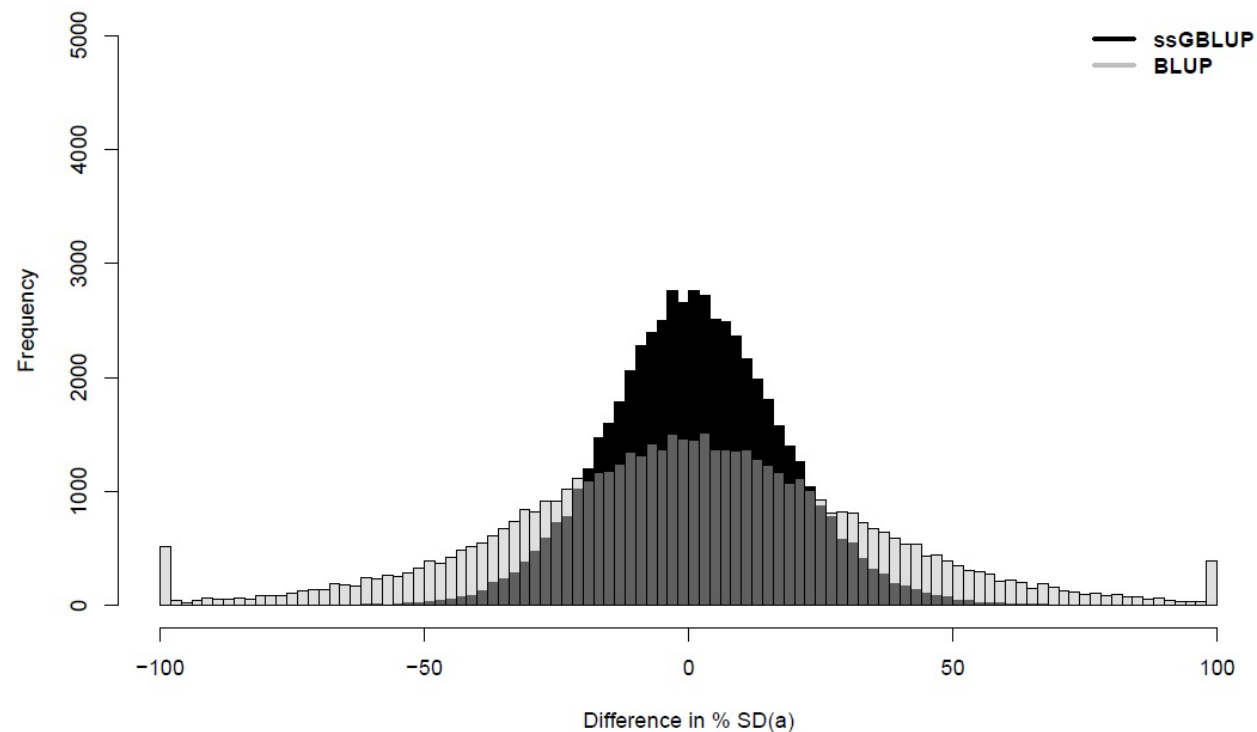
- American Angus data
 - 10.7 M pedigree
 - 509 K genotyped animals
 - Post-weaning gain
 - July/2017: 4.26 M
 - December/2017: 4.38 M
 - 125 K records
 - 55 K for genotyped
- Changes in EBV and GEBV
 - 10 M non-genotyped no new data
 - 454 K genotyped no new data
 - 70 K non-genotyped + new data
 - 55 K genotyped + new data

Changes for animals with new data

New data – Non-genotyped

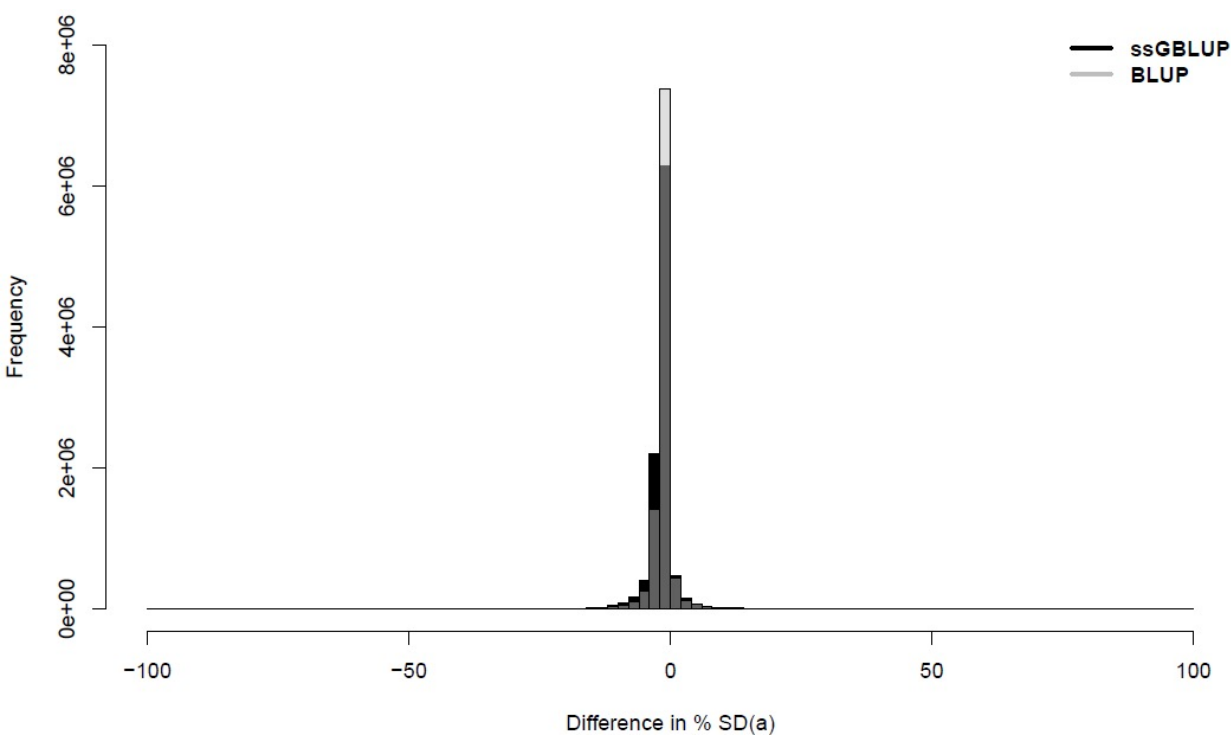


New data – Genotyped

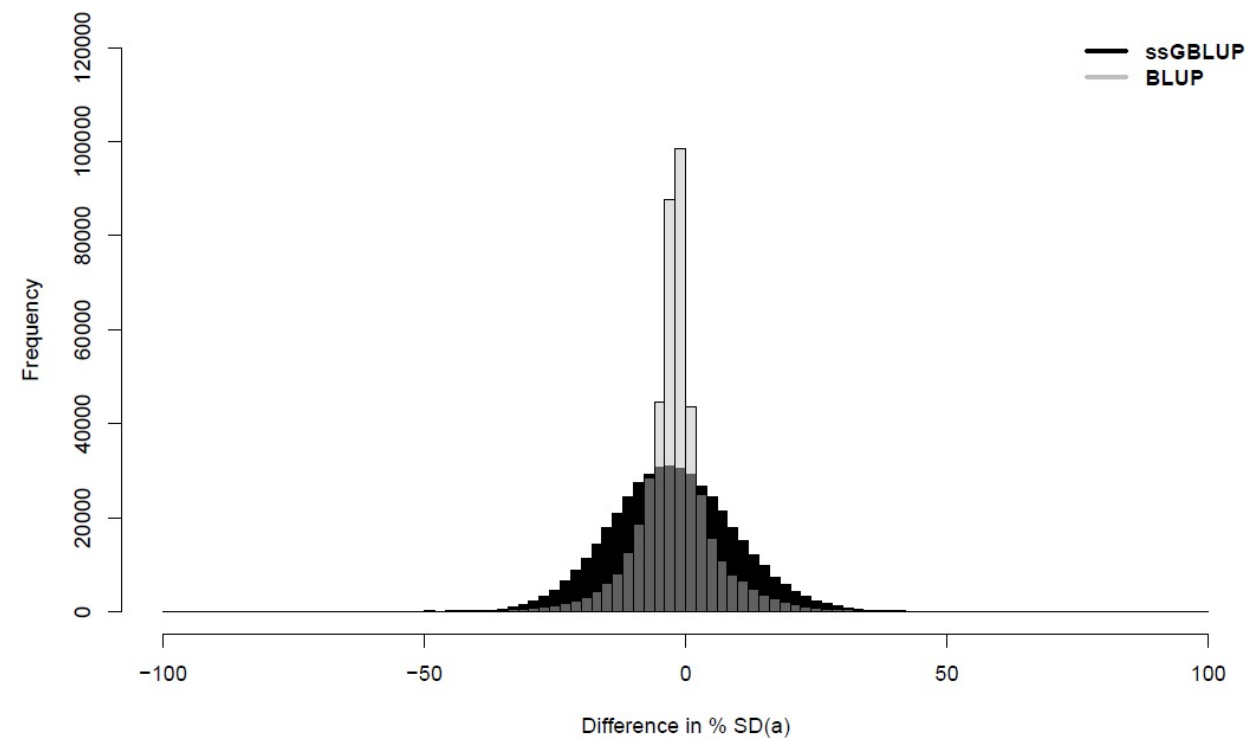


Changes for animals with NO new data

NO new data – Non-genotyped



NO new data – Genotyped

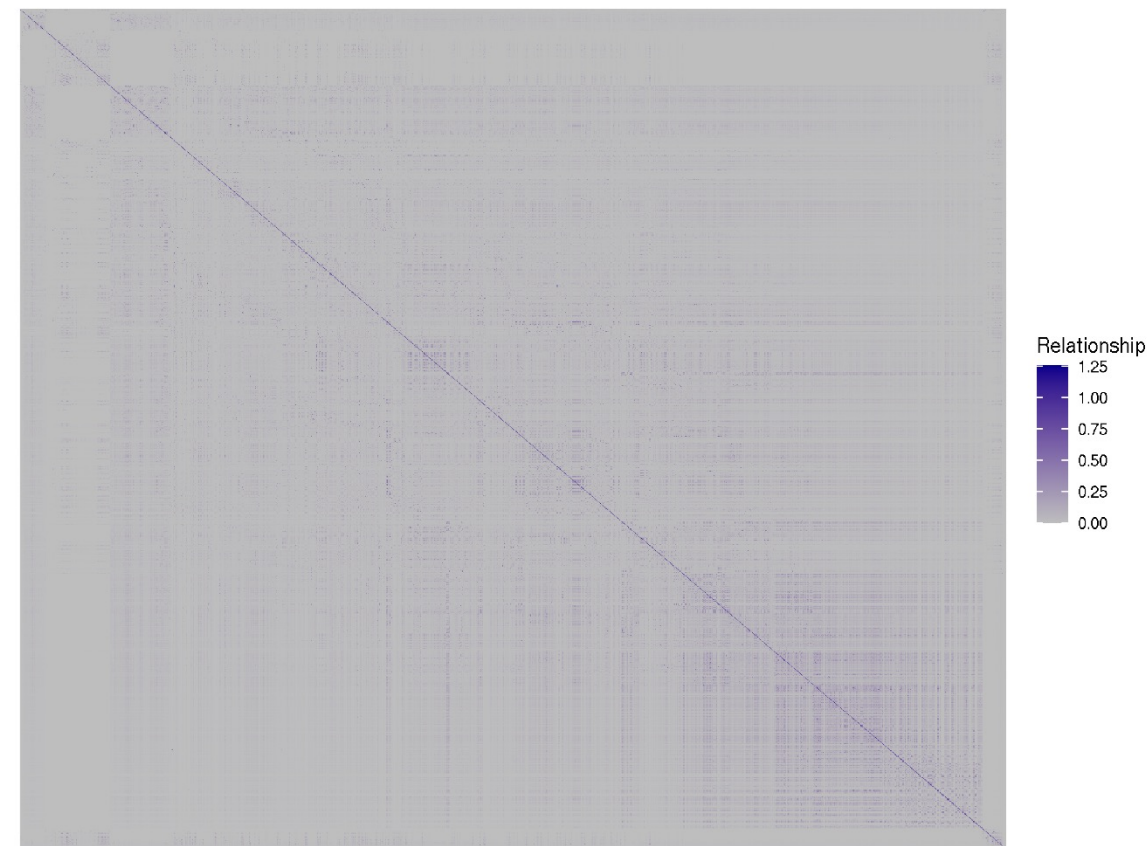


Why more changes for GEBV?



Genomic

$$u_i | u_1 + u_2 + u_3, \dots, u_{i-1} = \sum_{j=1}^{n-1} p_{ij} u_j + \varepsilon_i$$



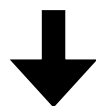
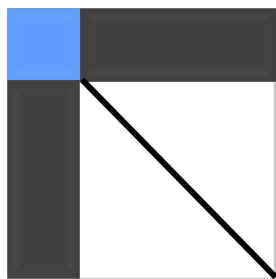
Pedigree

$$u_i = 0.5(u_{s_i} + u_{d_i}) + \varphi_i$$

Changes in the evaluation system

- Changing the core group in APY – efficient \mathbf{G}^{-1} (Misztal et al., 2014)
- Core sizes: 2k, 5k, for i in {10k..100k..10k}
- For each core size: 2 randomly sampled core sets
- Same amount of data

APY \mathbf{G}^{-1} core 1



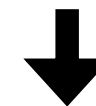
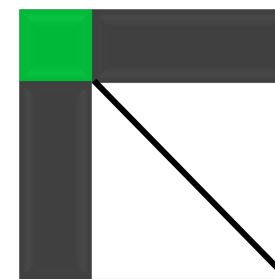
ssGBLUP



GEBV1

VS.

APY \mathbf{G}^{-1} core 2



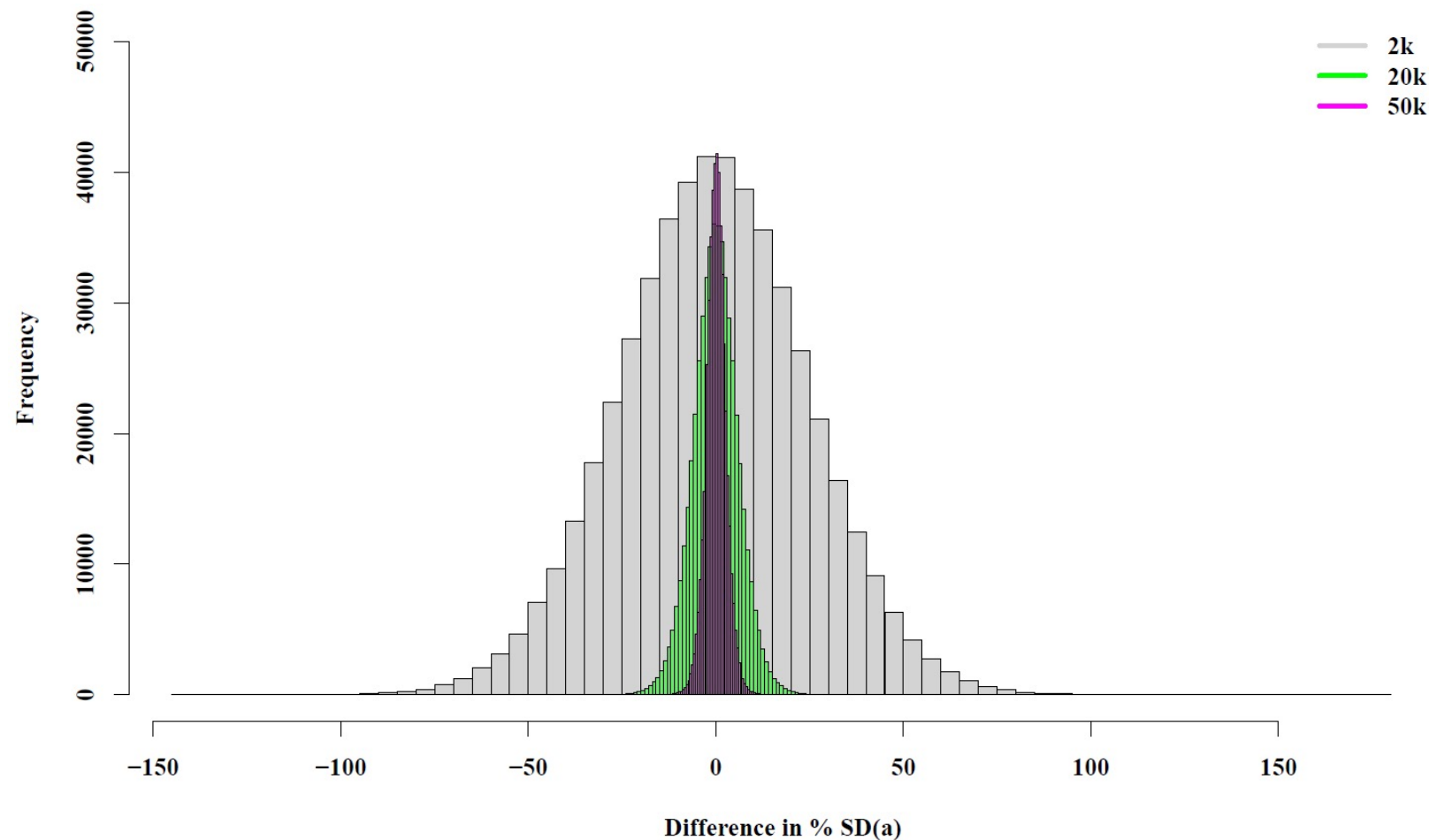
ssGBLUP



GEBV2

Changes in the evaluation system

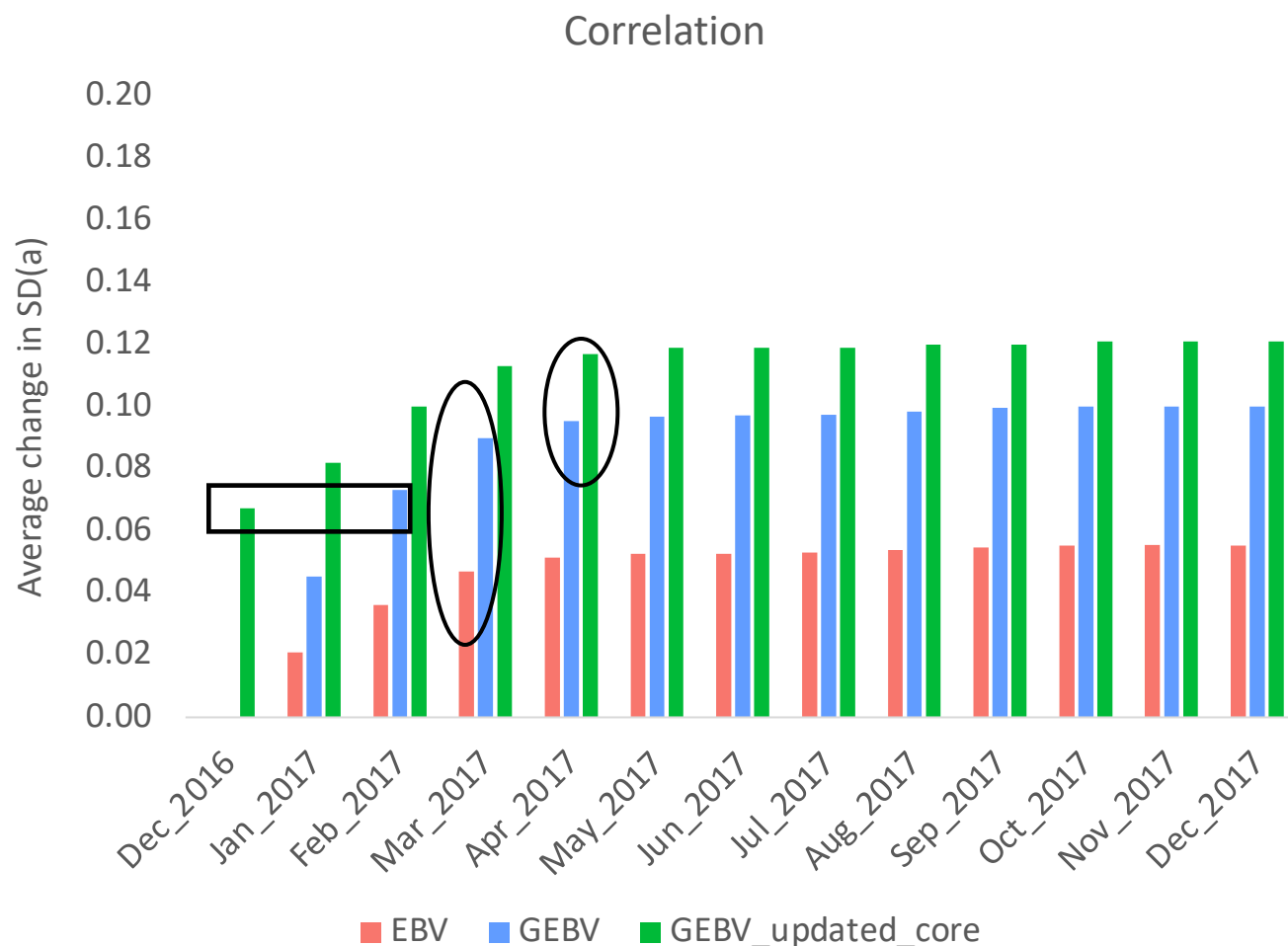
- Changing the core group in APY \mathbf{G}^{-1}



$$\mathbf{u}_n = \mathbf{P}_{nc} \mathbf{u}_c + \boldsymbol{\varepsilon}_n$$

Changes in the data + system

- Added genotypes, pedigree, phenotypes
 - Weaning weight in Angus
 - Added based on YOB
 - Jan/2017 to Dec/2017
 - Compared against Dec/2016
 - All genotyped animals
 - Born up to Dec/2016



Changes with and without genomics

- **Without genomics**

- New data
 - Recorded animals
 - Relatives through **A**

- Lower average change
- More extreme values

- **With genomics**

- New data
 - Recorded animals
 - Relatives through **G**
 - All animals are related though **G**
- New genotypes
- Changes in **G**

- Higher average change
- Less extreme values

Take home message

- **More changes with genomic information**
 - Better reflect accuracies of GEBV
 - Understand that genomic information connects more animals
 - New data will create many more changes
 - Part of the genomic system
- **How to minimize frequent changes**
 - Less frequent official evaluations and more interim evaluations
 - No changes in between official evaluations
 - More changes among official evaluations
 - APY: change the core group when adding more data

Acknowledgements



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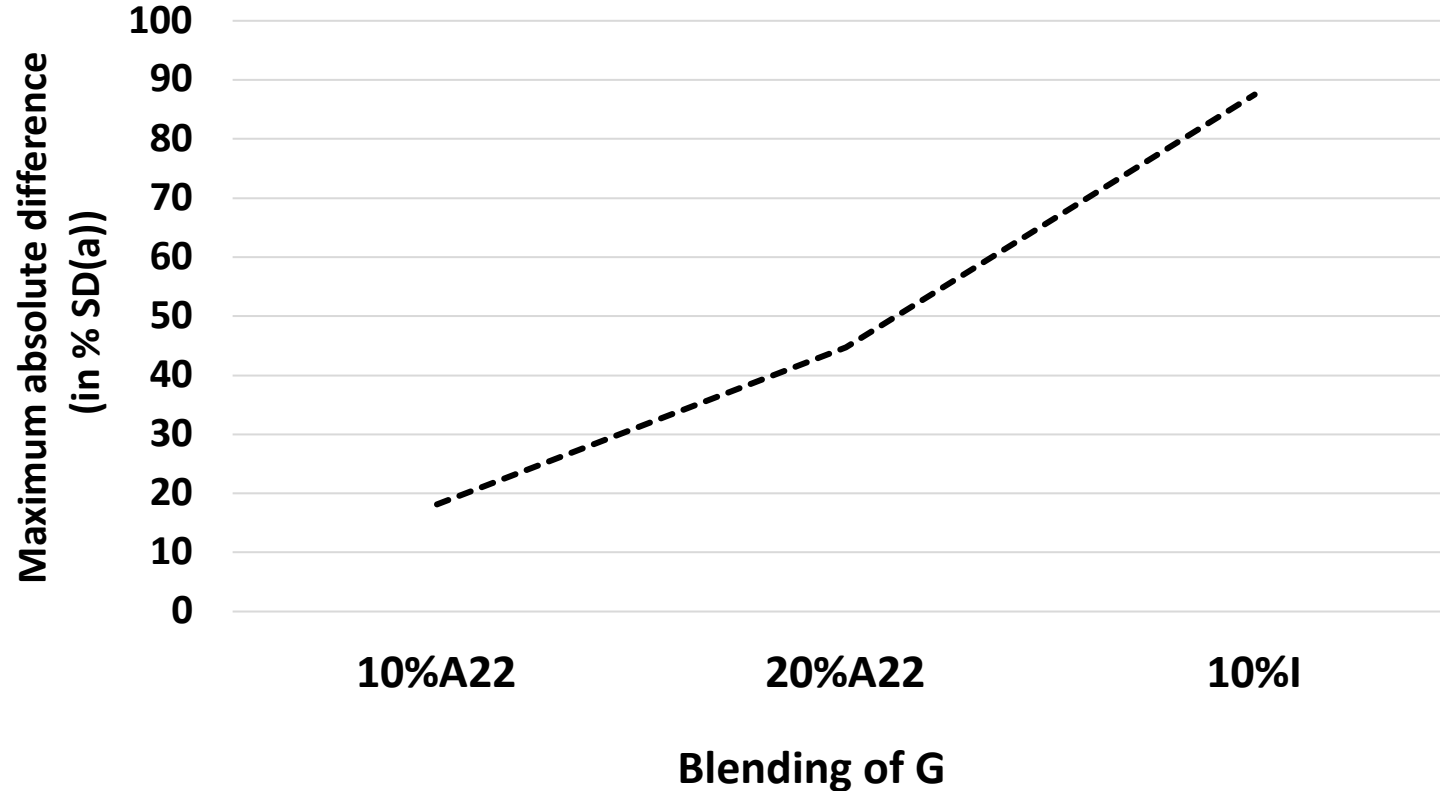
Extra slides

Changes in the evaluation system

- Changing the blending of **G**

$$\mathbf{G} = \alpha \mathbf{G} + (1-\alpha) \mathbf{A}_{22}$$

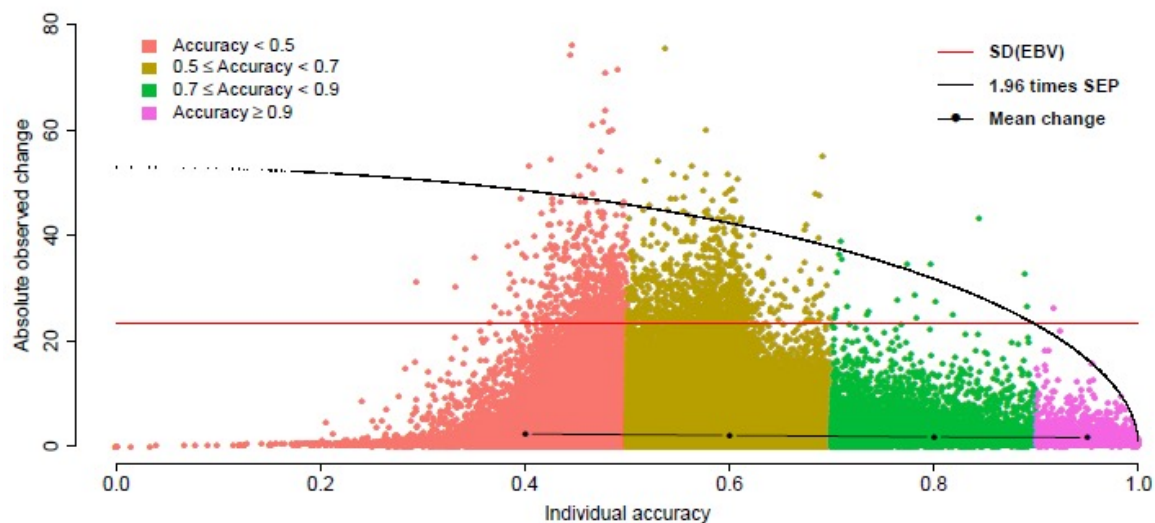
$$\mathbf{G} = \alpha \mathbf{G} + (1-\alpha) \mathbf{I}$$



SD (a) = 39

Changes as a function of accuracy

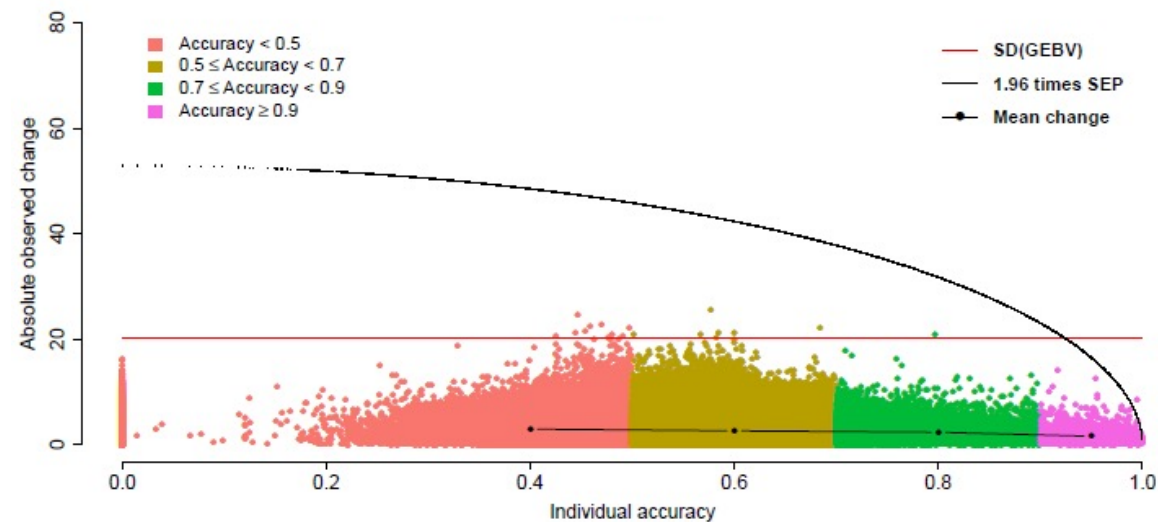
EBV



- Changes in % σ_a
 - Mean = 8
 - Min = 0
 - Max = 281

$$\sigma_a = 27$$

GEBV



- Changes in % σ_a
 - Mean = 10
 - Min = 0
 - Max = 95

Changes for animals with NO new data

NO new data – All animals

		Average	SD	Correlation
EBV	Jul	47.8	32.7	0.99
	Dec	47.4	32.6	
GEBV	Jul	54.8	33.6	0.99
	Dec	54.3	33.5	

Changes for animals with new data

New data – All animals

		Average	SD	Correlation
EBV	Jul	91.3	15.7	0.85
	Dec	91.0	18.2	
GEBV	Jul	98.6	18.5	0.93
	Dec	98.3	19.7	