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Comparison of two software to estimate breeding value in cattle by single-step approach

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Conclusions

- Top 50 rankings of EBV between both programs have significant overlap.
 - Top 50 rankings of EBV between cores for both programs have significant overlap.
- Correlations between both data sets are equally high regarding to the core and to the program.

Data

Introduction

Currently many countries implement single-step models in the national routine evaluation of cattle. Because of complexity of the models used in this proceduree there is a demand to reliable, and efficient software to perform such operations.

Right now the two most popular programs to perform single-step genomic evaluation MixBlup by Ten Napel et al., and BLUP90io3 by Misztal et al.

Our aim was to conduct single-step genomic evaluation for highly heritable trait based on data used in polish routine evaluation and compare the results obtained by both software.

Methods

- Data used during Polish national genetic evaluation for stature trait ($h^2 = 0.54$).
- 89 242 genotypes (42134 F, 47108 M).
- 1 240 088 phenotypes for the full data set.
- 1 136 020 phenotypes for validation.
- APY approach with three different cores. Model

y = Xb + Wa + e

- y vector of phenotypes.
 - b vector of fixed effects (calving, herd and lactation phase ,phantom codes of the fixed effects).
- **a** individuals breeding values.
- e residuals.

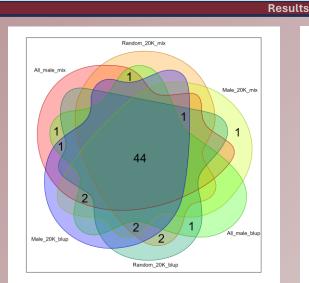


Fig 1. Ranking of top 50 bulls for the whole data set

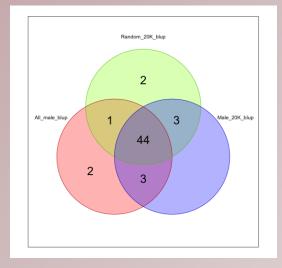
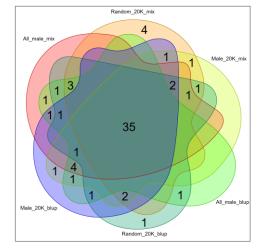
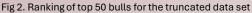


Fig 3. Ranking of top 50 bulls for each core in blupiod3





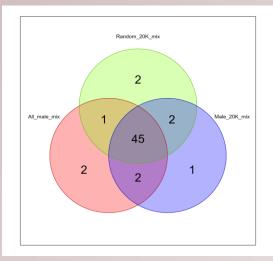


Fig 4. Ranking of top 50 bulls for each core in mixplup

Scenarios	Correlation between validation bulls		
	(full and truncated data set)		
	Mixblup	BLUPF90	
20K_male	0.90	0.90	Tab 1. Correlation for bulls 2013- 2017 with EDC > 20, bulls with daughters in Poland
20K_random	0.90	0.90	
All_male	0.90	0.90	