

Using SNP BLUP REL software for prediction reliability of DGV in Poland

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- ▶ The efficiency of the software regarding the size of the data
- ▶ CPU memory usage and time
- ▶ Differences with ~~currently~~ (before EG) used national methods
- ▶ Results using the attached test data set



The size of the data

Traits:

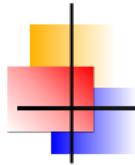
- ▶ Protein yield (PRO) – $h^2 = 0.29$
- ▶ Non return rate of heifers (HCO) – $h^2 = 0.02$

Animals:

- ▶ 31 968 individuals for PRO
- ▶ 29 458 individuals for HCO

Genotype:

- ▶ 46 267 SNPs after selection based on MAF > 1% and call rate > 95%



The size of the attached data

Animals:

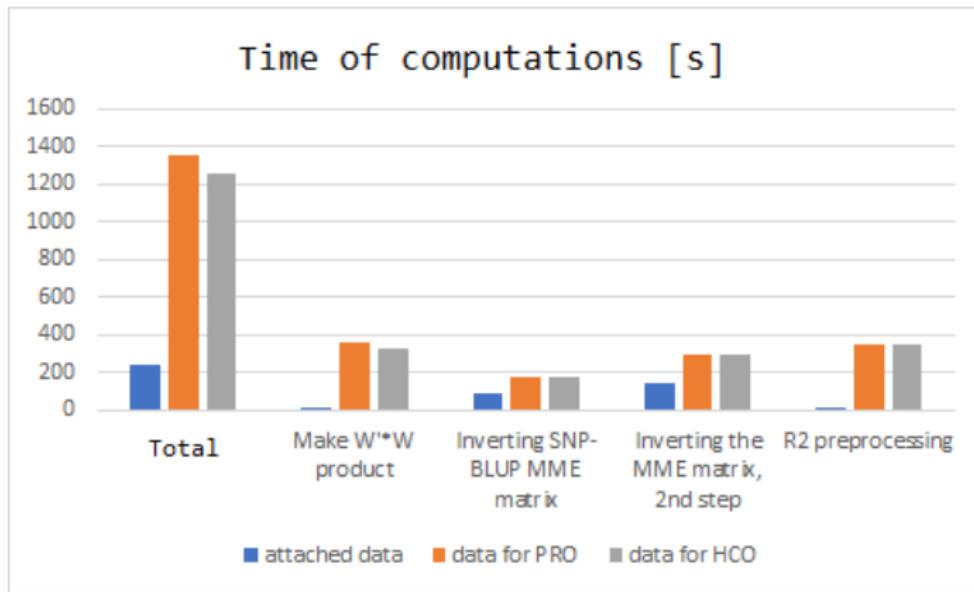
- ▶ 345 individuals

Genotype:

- ▶ 35 573 SNPs

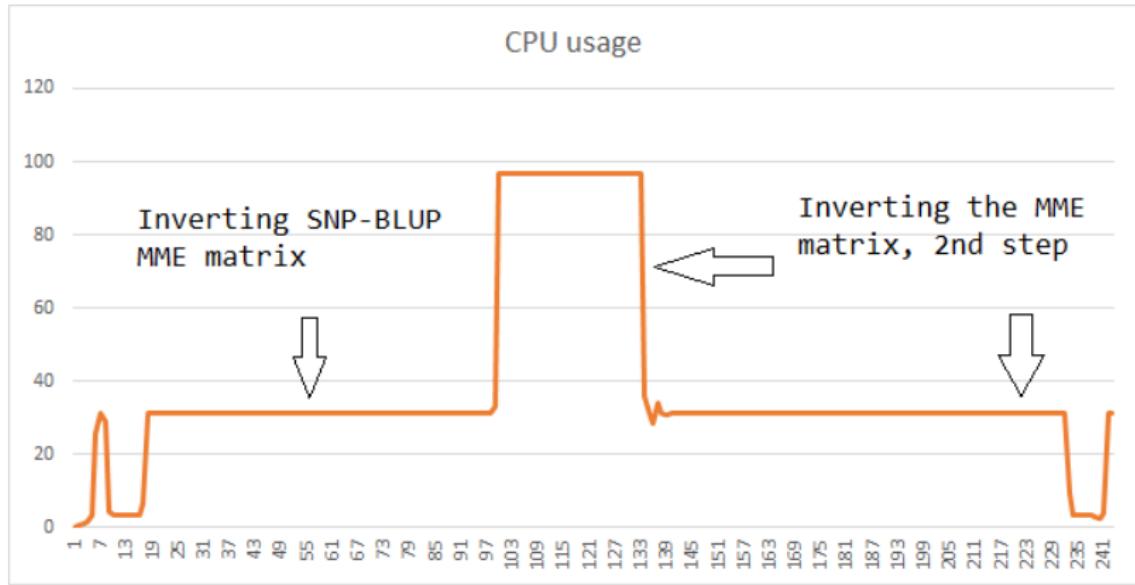


The efficiency of the software regarding the size of data - time

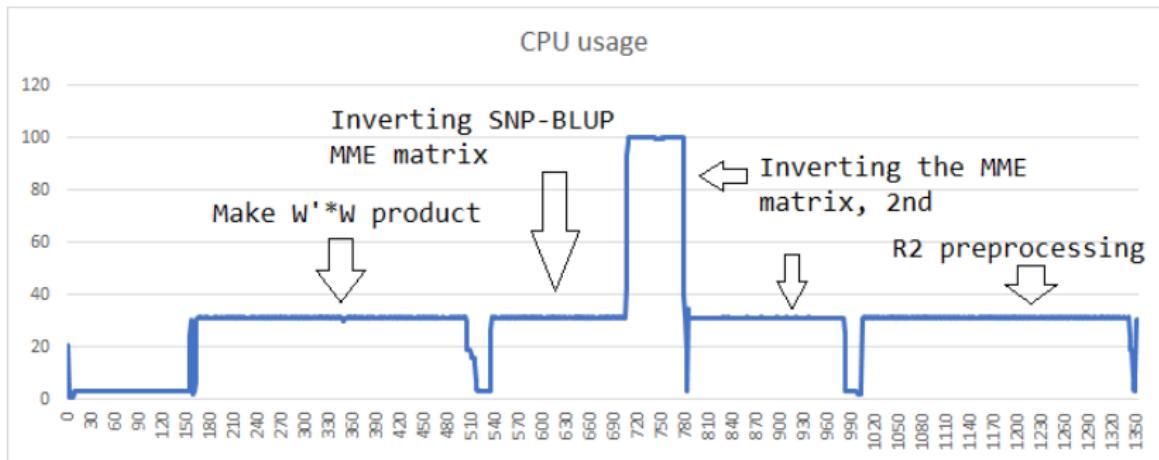




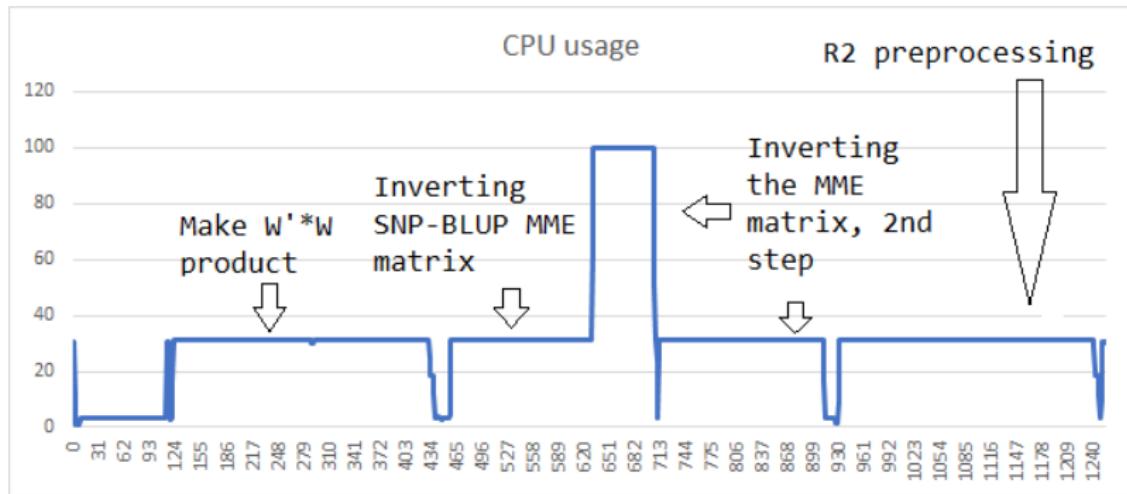
The efficiency of the software (attached data) - CPU

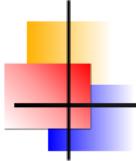


The efficiency of the software (PRO) - CPU

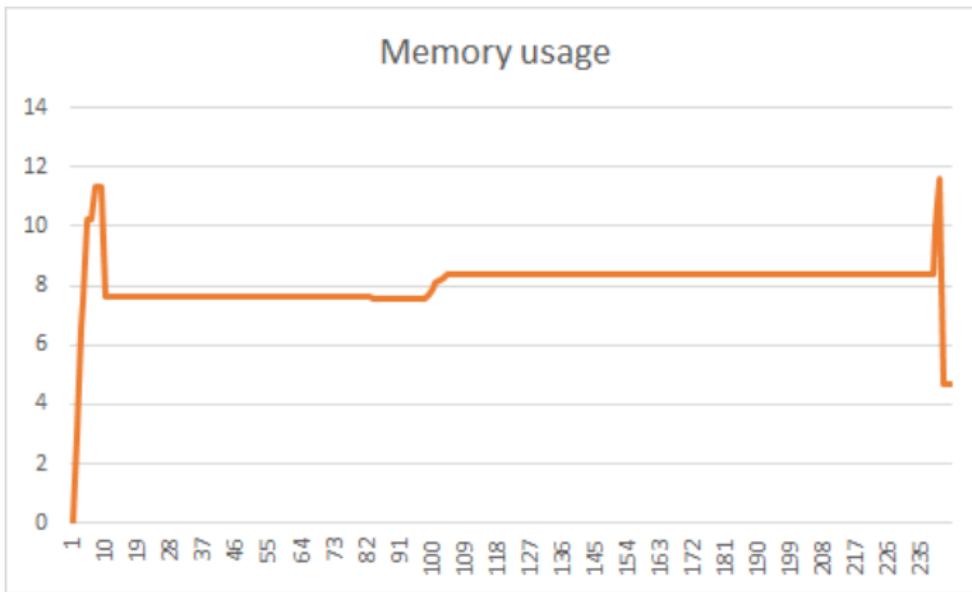


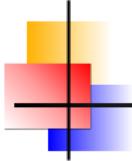
The efficiency of the software (HCO) - CPU



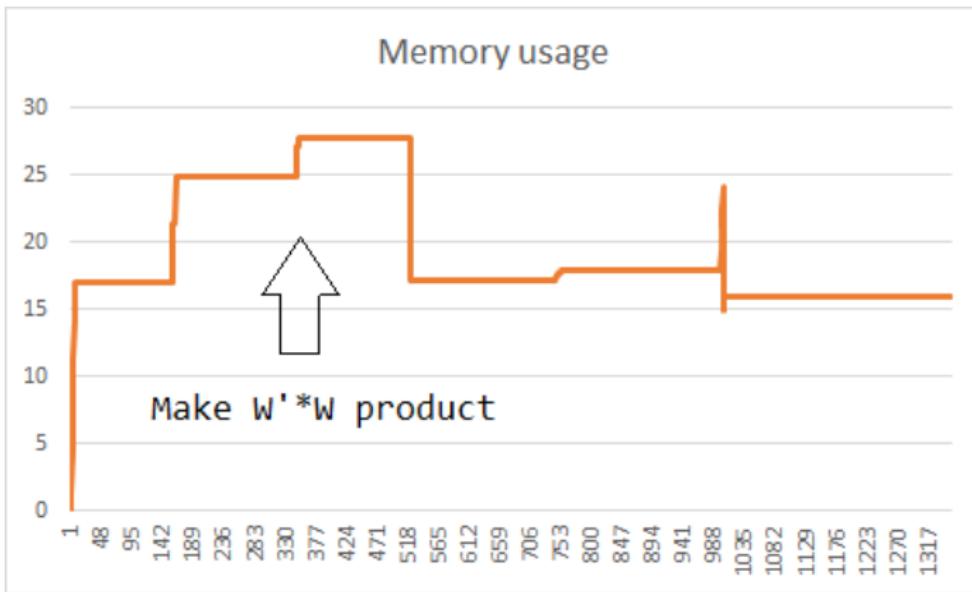


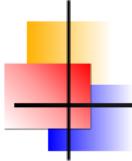
The efficiency of the software (attached data) - MEM



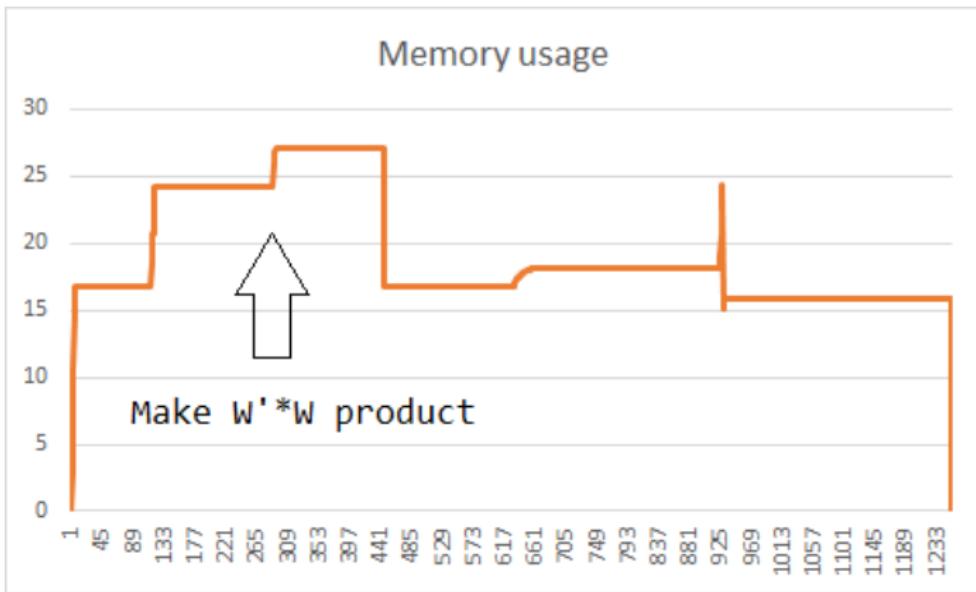


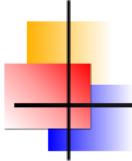
The efficiency of the software (PRO) - MEM



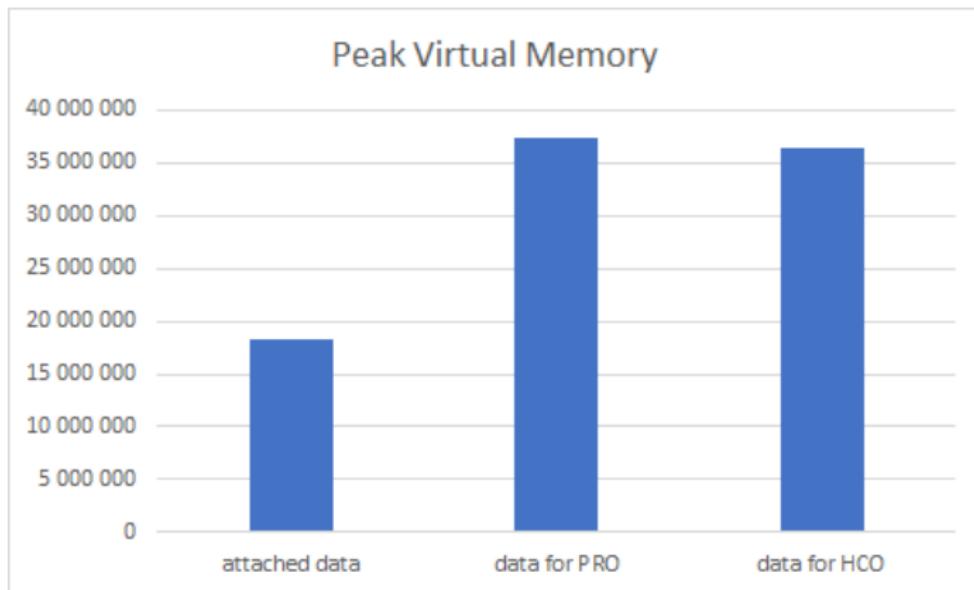


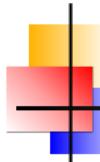
The efficiency of the software (HCO) - MEM





The efficiency of the software - VMEM



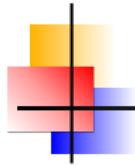


SNP effect estimation:

$$y = \mu + Zq + \epsilon,$$

- ▶ y - deregressed EBV
- ▶ μ - overall mean
- ▶ q - random SNP effect $\sim \mathcal{N}(0, I \cdot \frac{\hat{\sigma}_\alpha^2}{N_{SNP}})$
- ▶ $N_{SNP} = 46\ 267$
- ▶ $Z = \{-1, 0, 1\}$
- ▶ ϵ - error term $\sim \mathcal{N}(0, D \cdot \hat{\sigma}_\epsilon^2)$

$$\widehat{DGV} = \widehat{\mu} + \mathbf{Z} \cdot \widehat{\mathbf{q}}$$

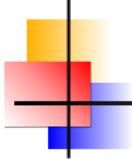


DGV reliability

Calculation of reliability:

$$Rel = \text{diag} \left\{ \left(Q - \frac{\widehat{\sigma}_\epsilon^2}{\widehat{\sigma}_\alpha^2} C^{22} \right) Q^{-1} \right\},$$

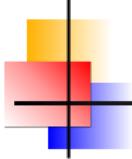
- ▶ C^{22} - inverse of coefficient matrix for MME
- ▶ $Q = ZZ^T \frac{1}{p_{het}^b}$
- ▶ p_{het}^b - sum over all SNP of heterozygous genotype frequencies in base population



Reliability comparison - reference bulls

PRO	Common Animals		3 687
	New method	Previous method	
mean	0.6552	0.8700	
sd	0.0178	0.1187	
min	0.6118	0.4290	
max	0.7309	0.9990	

HCO	Common Animals		3 582
	New method	Previous method	
mean	0.2261	0.5532	
sd	0.0179	0.1269	
min	0.1716	0.2590	
max	0.5723	0.9750	



Reliability comparison - candidates

PRO	Common Animals		659
	New method	Previous method	
mean	0.6256	0.6004	
sd	0.0097	0.0563	
min	0.5852	0.2384	
max	0.6550	0.8461	

HCO	Common Animals		694
	New method	Previous method	
mean	0.2234	0.3838	
sd	0.0143	0.0594	
min	0.1882	0.2569	
max	0.3095	0.7666	



Thank you for your attention!

