Simultaneous de-regression of cow and bull breeding values

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Introduction

Accuracy of genomic prediction depends on size of the reference population (RP)

RP have been extended by:

- Genotyping all bulls with EBV (nationally)
- Exchanging genotypes of bulls (internationally)

Further extension is possible by including cows

• How should cow information be included properly?





Introduction

- Genomic prediction models use deregressed proofs (DRP)
- (Approximate) de-regression procedures used for bulls may not be appropriate for cows
 - Reliability Cow EBV << Reliability Bull EBV
- Objective is to test alternative approach to de-regress
 - EBV (=DRP)
 - EDC (i.e. appropriate weights of de-regressed EBV)





"De-regression" of EDC

Obtain weights for DRP, i.e. "dEDC" for all animals:

1. Initialize dEDC = EDC_{EBV}

For each animal:

- 2. Compute EDC due to information in the RP (i.e. EDC_{RP})
- 3. Compute $EDC_{DRP} = EDC_{EBV} EDC_{RP}$
- 4. Repeat 2 & 3 until convergence

Per iteration (where EDC_{DRP} are computed for all animals):

- Set up and invert coefficient matrix of MME for RP once
- Per animal: adjust inverse to compute its EDC_{RP}





De-regression of EBV

Matrix de-regression:

$$\begin{bmatrix} \mathbf{X}' R^{-1} \mathbf{X} & X' R^{-1} \mathbf{Z} \\ Z' R^{-1} \mathbf{X} & \mathbf{Z}' R^{-1} \mathbf{Z} + A^{-1} \frac{\sigma_e^2}{\sigma_A^2} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\mu}} \\ \hat{\boldsymbol{\alpha}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}' R^{-1} \mathbf{y} \\ \mathbf{Z}' R^{-1} \mathbf{y} \end{bmatrix}$$

- Iteratively compute *DRPs* and $\hat{\mu}$ to account for mean EBV
- Using de-regressed EDC (*R*⁻¹)





Procedure to test de-regression method

- 1. Compute EBV
- 2. For animals in RP:
 - a) "De-regress" EDC (=dEDC)
 - b) De-regress EBV (=DRP)
 - c) Compute EBV using dEDC and DRP

Expectations:

EBV (2c) = EBV (1)

- For bulls: EDC (2a) = EDC from daughters outside RP
- For cows: EDC (2a) = EDC from own records





Data used

- 15,252 animals in RP
 - 1,532 bulls & 13,720 cows
- Phenotypes were simulated:
 - Such that "true" weights (EDC) were known
 - 50-200 daughters (with 1 record) per sire (outside RP)
 - 1-5 records per cow in the data





"De-regressed" EDC bulls (after 5 iterations)



"De-regressed" EDC cows (after 5 iterations)



Original vs. final EBV



Reliability original vs. final EBV



Conclusions

- "De-regressed" EDC overestimate true EDC
 - Especially for bulls with many (grand)daughters in RP
- Final and initial EBV matched very well
- Similar results were obtained with 1 iteration to deregress EDCs (not shown)



