Incorporating external information as observations in Dutch/Flemish genetic evaluations

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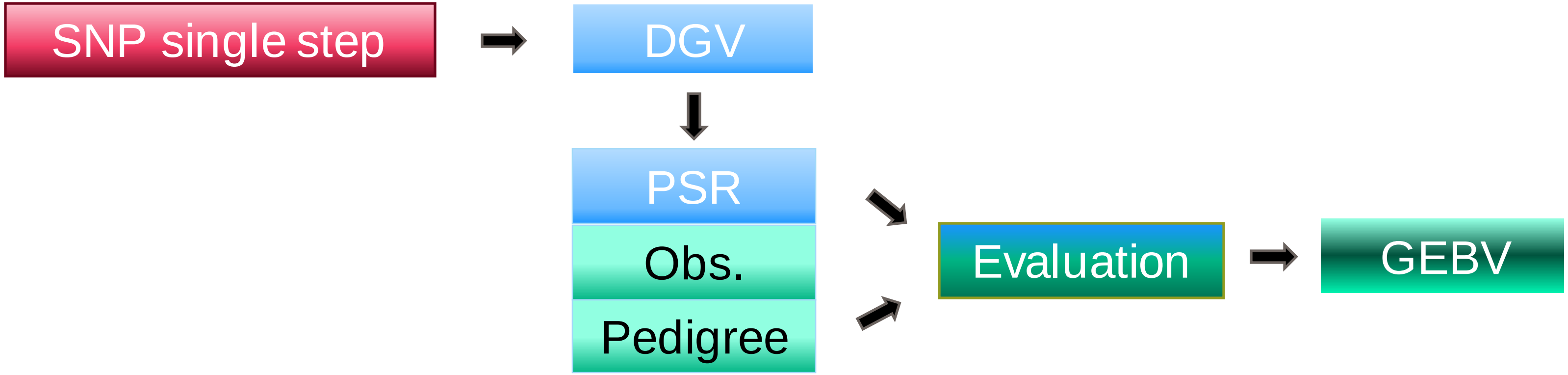
Introduction I

Introduction single step genomic evaluations
December 7, 2023

Pubished GEBV from pseudo-record system
DGV fitted as correlated traits



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Introduction II

Trigger

- Incorporate DGV information of underlying traits
  - – Without (increasing) number of correlated traits (runtime!)
  - – Improved transfer of DGV to official evaluations.

- Deregressed proofs as observations on actual traits
  - No extra correlated pseudo-traits necessary
  - Limiting run time evaluation (avoid fitting extra traits)

Challenges

1. Observations ➔ Breeding values
2. Number of repeat records ➔ Reliabilities

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Observations

Deriving observation records from GEBV

Two step process

1. Deregression
   – Linear deregression to remove national information from MACE proof

2. Transformation
   – Based on approach already in use.
   – Somewhat more formalized and simplified:

$$\mathbf{o} = \mathbf{Tb}$$

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Observation: Deregression

For a list of eurogenomics bulls

External BV	XBV
National BV	EBV

Observation: Deregression

For a list of eurogenomics bulls

External BV XBV => $DRP_x = PA + (XBV-PA)/r_x$; $EOCx = \alpha * r_x/(1-r_x)$

National BV EBV => $DRP_e = PA + (EBV-PA)/r_e$; $EOCe = \alpha * r_e/(1-r_e)$

EOC = Expected Own Contribution; expected number of observation records

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Observation: Deregression

For a list of eurogenomics bulls

External BV XBV => $DRP_x = PA + (XBV-PA)/r_x$; $EOCx = \alpha * r_x/(1-r_x)$

National BV EBV => $DRP_e = PA + (EBV-PA)/r_e$; $EOCe = \alpha * r_e/(1-r_e)$

EOC = Expected Own Contribution; expected number of observation records

Final result

EOC = (EOCx – EOCe)

DRP = [DRPx * EOCx – DRPe*EOCe] / EOC

(Pitkänen et al, 2019)

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Observations: Transformation

The function

- **b** is a vector with *n* input DRP
- **o** is a vector with *m* output observations
- **T** is a *m* x *n* transformation matrix

$$\mathbf{o} = \mathbf{T}\mathbf{b}$$

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Observations: Transformation

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The transformation matrix

Important to distinguish between:

- Input trait: Which traits have DRP records?
- Analyzed traits: Which traits are in the evaluation?
- Observed traits: Which traits have observations?

Usually 2 or all 3 categories are identical, but not always!

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Observations: Transformation matrix

$$\mathbf{o} = \mathbf{Tb}$$

Transformation matrix T can be obtained relatively easily

- Two 'phi'-matrices are needed that describe the relations between traits
  - Matrix **F** describes relation between input and analyzed traits
  - Matrix **D** describes relation between analyzed and output traits

- Additionally a genetic matrix **G** is needed (the one in the evaluation)

$$\mathbf{T} = (\mathbf{DGF'})(\mathbf{FGF'})^{-1}$$

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Observaties: Transformation matrix conformation

For evaluations like Conformation
Single observation (lactation), single DRP
Input, analyzed and observed traits are identical

$$\mathbf{o} = \mathbf{Tb}$$

- **F** = **I** (identity matrix)
- **D** = **I**

- Result: $\mathbf{T} = (\mathbf{DGF'})(\mathbf{FGF'})^{-1} = \mathbf{GG}^{-1} = \mathbf{I}$

$$\mathbf{o} = \mathbf{Tb} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \mathbf{b} = \mathbf{b}$$

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Observations: Transformation matrix index trait

For evaluations like Fertility, Udder health
Single GEBV/DRP; multiple underlying observed traits

$$\mathbf{o} = \mathbf{Tb}$$

- $\mathbf{F} = \mathbf{w}' = [\ 0.41\ 0.33\ 0.26\ ]$ ← lactation specific weights
- $\mathbf{D} = \mathbf{I}$

- Result: $\mathbf{T} = (\mathbf{DGF'})(\mathbf{FGF'})^{-1} = (\mathbf{Gw})(\mathbf{w'Gw})^{-1}$

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Observations: Transformation matrix index trait

For evaluations like Fertility, Udder health
Single GEBV/DRP; multiple underlying observed traits

o = Tb

- **F** = **w**' = [0.41 0.33 0.26] 🡐 lactation specific weights
- **D** = **I**

- Result: **T** = (**DGF'**)(**FGF'**)$^{-1}$ = **(Gw)(w'Gw)**$^{-1}$

- Example:

$$\mathbf{C} = \begin{bmatrix} 1 & 0.7 & 0.6 \\ 0.7 & 1 & 0.8 \\ 0.6 & 0.8 & 1 \end{bmatrix} \quad \mathbf{v} = \begin{bmatrix} 9 \\ 16 \\ 25 \end{bmatrix} \quad \rightarrow \mathbf{G} = \begin{bmatrix} 9 & 8.4 & 9.0 \\ 8.4 & 16 & 16 \\ 9.0 & 16 & 25 \end{bmatrix}$$

$$\mathbf{T} = \begin{bmatrix} 0.933 \\ 1.048 \\ 1.045 \end{bmatrix} \quad \mathbf{b} = [5.0] \quad \mathbf{o} = \mathbf{Tb} = \begin{bmatrix} 4.7 \\ 5.2 \\ 5.2 \end{bmatrix}$$

Observations: Transformation Matrix Test Day Model

For random regression evaluations like Fertility, Udder health
Production test day model is an example that needs both **F** and **D** matrix

– INPUT : DRP from cumulative 305 day breeding values
– ANALYZED : Legendre regression polynomes
– OUTPUT : Production on day 60 of lactation

Construction of matrices

- For **F** 305 day factors needed: **s** = [212.84 -102.16 -57.96 -1.12 32.48]'

- For **D** factors needed for day 60: **t** = [0.707 -0.900 0.491 0.206 -0.794]'

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Observations: Transformation matrix TDM

Example: Three lactations, 5 legendre regressions per lactations

$\mathbf{F} = \mathbf{s} \otimes \mathbf{I}_3 =$

212.8391	0	0	-102.156	0	0	-57.9619	0	0	-1.1099	0	0	32.4796	0	0
0	212.8391	0	0	-102.156	0	0	-57.9619	0	0	-1.1099	0	0	32.4796	0
0	0	212.8391	0	0	-102.156	0	0	-57.9619	0	0	-1.1099	0	0	32.4796

$\mathbf{D} = \mathbf{t} \otimes \mathbf{I}_3 =$

0,70711	0	0	-0,90011	0	0	0,49048	0	0	0,20577	0	0	-0,79362	0	0
0	0,70711	0	0	-0,90011	0	0	0,49048	0	0	0,20577	0	0	-0,79362	0
0	0	0,70711	0	0	-0,90011	0	0	0,49048	0	0	0,20577	0	0	-0,79362

Observations: Transformation matrix TDM

Application example: Three lactations of milk production in kg

$$\mathbf{T} = (\mathbf{DGF'})(\mathbf{FGF'})^{-1}$$

$$\mathbf{T} = \begin{bmatrix} 3.55\times10^{-3} & -3.59\times10^{-4} & -1.92\times10^{-4} \\ 6.01\times10^{-5} & 3.52\times10^{-3} & -5.07\times10^{-4} \\ 4.50\times10^{-4} & -1.33\times10^{-4} & 2.85\times10^{-3} \end{bmatrix}$$

$$\mathbf{b} = \begin{bmatrix} +1100 \\ +1300 \\ +1400 \end{bmatrix} \quad \Rightarrow \quad \mathbf{o} = \mathbf{Tb} = \begin{bmatrix} +3.2 \\ +3.9 \\ +4.3 \end{bmatrix}$$

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Observations

Transformation for every animal with DRP with a simple function

Transformation matrix **T** is a constant, needs to be constructed only once.

Accounts for genetic correlations among traits

Applicable to a variety of models, input DRP

Repeat records

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Repeat records

Number of repeat records determines reliability of DRP information in genetic evaluations

At a reliability *r* of DRP we can calculate *expected own contributions* (EOC)

$$\mathrm{EOC} = \frac{1-h^2}{h^2} \times \frac{r}{1-r}$$

Example: If h^2 = 0.20 and r = 0.75 then EOC = 3 ➔ Number of repeat records

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But…
Calculated this way, the EOC is valid for single trait analysis only.

- Does not account for correlations between traits in MT evaluations

Determining number of repeat records

- Reliability is a function **r** = *rel_liu* (**G**, **F**, **Y**)
  - **G** is the genetic covariance matrix
  - **F** is a ‘phi’ – matrix comparable to before (for TDM: 305 day matrix)
  - **Y** is a MT-EDC matrix following Liu *et al*. (2001)
    - But **Y** is enumerated using **D** (for TDM: day 60 matrix)

The objective is to find a $\mathbf{Y}_{est}$ such that $\mathbf{r}_{est} \approx \mathbf{r}_{DRP}$

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The objective is to find a $\mathbf{Y}_{est}$ such that $\mathbf{r}_{est} \approx \mathbf{r}_{DRP}$

$$\mathbf{Y} = 4\mathbf{O}\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}$$

- **Z** is a genetic effect matrix comparable to **D** (day 60 matrix) in the previous
- **R** is the residual covariance matrix (the one used in analysis)
- **O** is a diagonal matrix with number of repeats per trait

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Repeat records: Iterative approach

Goal: To optimize the matrix **O** such that $\mathbf{r}_{est} \approx \mathbf{r}_{DRP}$

Start: Let **O** = **E** (single trait EOC of input traits, DRP)

1. Calculate $\mathbf{Y} = 4(\mathbf{OZ})'\mathbf{R}^{-1}\mathbf{Z}$
2. Calculate $\mathbf{r}_{est}$ = *rel_liu*(**G**, **F**, **Y**)
3. Compare $\mathbf{r}_{est}$ with $\mathbf{r}_{DRP}$
   a. If $\mathbf{r}(i)_{est} > \mathbf{r}(i)_{DRP}$ ➔ $\mathbf{O}(i,i) = \mathbf{O}(i,i) - 1$ (minimum value 0)
   b. If $\mathbf{r}(i)_{est} < \mathbf{r}(i)_{DRP}$ ➔ $\mathbf{O}(i,i) = \mathbf{O}(i,i) + 1$
4. Repeat until convergence or until **O** stops changing.

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Final remarks

Method provides capability to use DRP as observations on existing traits

Unified approach, valid for all types of models, DRP

- Single trait, indices, random regressions

No additional correlated traits

- No need for additional software
- Same statistical model, parameters and matrices
- Same output format

Approach is being implemented

Application to all test day model traits and claw health traits

Further implementation for all evaluations planned for later this year

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