

Bayesian approach integrating correlated foreign information into a multivariate genetic evaluation

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Introduction

- ✓ For some traits (e.g., fatty acids, dry matter intake)
 - ❑ Phenotypes are unavailable or difficult to collect internally

- ✓ Most situations
 - ❑ Low accuracy of internal evaluations
 - ❑ Accurate external evaluations for correlated traits (e.g., milk productions evaluations)

Introduction

- ✓ Multivariate genetic evaluations
 - ❑ Correlations among traits
 - ❑ Prediction of EBV of a trait for which phenotypes are unavailable or difficult to collect internally
 - ❑ Improvement of accuracy

Aim

- ✓ To develop and test a simultaneous combination of
 - pedigree
 - internal phenotypes
 - correlated external information (i.e. EBV and REL)
- with a multivariate evaluation using a Bayesian approach

Methods

✓ Regular mixed model equations

$$\begin{bmatrix} \mathbf{X}' \mathbf{R}^{-1} \mathbf{X} & \mathbf{X}' \mathbf{R}^{-1} \mathbf{Z} \\ \mathbf{Z}' \mathbf{R}^{-1} \mathbf{X} & \mathbf{Z}' \mathbf{R}^{-1} \mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_{\text{I}} \\ \hat{\mathbf{u}}_{\text{I}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}' \mathbf{R}^{-1} \mathbf{y}_{\text{I}} \\ \mathbf{Z}' \mathbf{R}^{-1} \mathbf{y}_{\text{I}} \end{bmatrix}$$

- $\mathbf{G}^{-1} = \mathbf{A}^{-1} \otimes \mathbf{G}_0^{-1}$: inverse of additive genetic (co)variance matrix
- \mathbf{y}_{I} : vector of internal observations
- $\hat{\boldsymbol{\beta}}_{\text{I}}$: vector of estimated internal fixed effects
- $\hat{\mathbf{u}}_{\text{I}}$: vector of internal EBV

Assumption

✓ Prior distribution of \mathbf{u}_I

$$p(\mathbf{u}_I) = MVN(\mathbf{0}, \mathbf{G}) \longrightarrow p(\mathbf{u}_I | \mathbf{y}_E) = MVN(\hat{\mathbf{u}}_E, \mathbf{D}_E)$$

- ❑ \mathbf{y}_E : unavailable vector of correlated external phenotypes
- ❑ $\hat{\mathbf{u}}_E$: vector of external EBV
- ❑ \mathbf{D}_E : prediction error (co)variance matrix of $\hat{\mathbf{u}}_E$

Methods

- ✓ Integration of correlated external information

$$\begin{bmatrix} \mathbf{X}' \mathbf{R}^{-1} \mathbf{X} & \mathbf{X}' \mathbf{R}^{-1} \mathbf{Z} \\ \mathbf{Z}' \mathbf{R}^{-1} \mathbf{X} & \mathbf{Z}' \mathbf{R}^{-1} \mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_I \\ \hat{\mathbf{u}}_I \end{bmatrix} = \begin{bmatrix} \mathbf{X}' \mathbf{R}^{-1} \mathbf{y}_I \\ \mathbf{Z}' \mathbf{R}^{-1} \mathbf{y}_I \end{bmatrix}$$



$$\begin{bmatrix} \mathbf{X}' \mathbf{R}^{-1} \mathbf{X} & \mathbf{X}' \mathbf{R}^{-1} \mathbf{Z} \\ \mathbf{Z}' \mathbf{R}^{-1} \mathbf{X} & \mathbf{Z}' \mathbf{R}^{-1} \mathbf{Z} + \mathbf{D}_E^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_I \\ \hat{\mathbf{u}}_I \end{bmatrix} = \begin{bmatrix} \mathbf{X}' \mathbf{R}^{-1} \mathbf{y}_I \\ \mathbf{Z}' \mathbf{R}^{-1} \mathbf{y}_I + \mathbf{D}_E^{-1} \hat{\mathbf{u}}_E \end{bmatrix}$$

Issue

✓ External information only available for external animals

→ $\hat{\mathbf{u}}_E$ and \mathbf{D}_E^{-1} : partially unknown

→ Estimations for internal animals

Estimation of $\hat{\mathbf{u}}_E$

✓ Available

□ External EBV of external animals ($\hat{\mathbf{u}}_{E_E}$)

✓ Internal animals

□ Prediction of external EBV ($\hat{\mathbf{u}}_{E_I}$)

$$p(\hat{\mathbf{u}}_{E_I} | \hat{\mathbf{u}}_{E_E}) = MVN(\mathbf{G}_{E_{IE}} \mathbf{G}_{E_{EE}}^{-1} \hat{\mathbf{u}}_{E_E}, (\mathbf{G}^{E_{II}})^{-1})$$

$$\rightarrow \hat{\mathbf{u}}_E = \begin{bmatrix} \hat{\mathbf{u}}'_{E_E} & \hat{\mathbf{u}}'_{E_I} \end{bmatrix}'$$

→ Correct propagation of external information

Estimation of \mathbf{D}_E^{-1}

$$\mathbf{D}_E^{-1} = \mathbf{G}^{-1} + \mathbf{\Lambda}_E$$

$$\mathbf{\Lambda}_E = \text{block diag}(\Delta_j \mathbf{R}_0^{-1} \Delta_j); j = 1, \dots, n \text{ animals}$$

$$\left\{ \begin{array}{l} \text{For external animals : } \Delta_j = \text{diag}(\sqrt{RE_k}); k = 1, \dots, t \text{ traits} \\ \text{For internal animals : } \Delta_j = \mathbf{0} \end{array} \right.$$

Material

Pedigree

- **QMSim** (Sargolzaei and Schenkel, 2009)
 - **10 generations**
 - **2240 animals**
 - **Random selection and matings**

Material



➤ Observations

➤ 2 traits

➤ Only for females

➤ Fixed effect: herd effect (randomly attributed)

➤ Residual correlation: 0.00

➤ Genetic correlations: 0.10, 0.25, 0.50, 0.75 and 0.90

➤ Trait 1

➤ Trait of interest

➤ 2 herds

➤ $h^2 = 10\%$

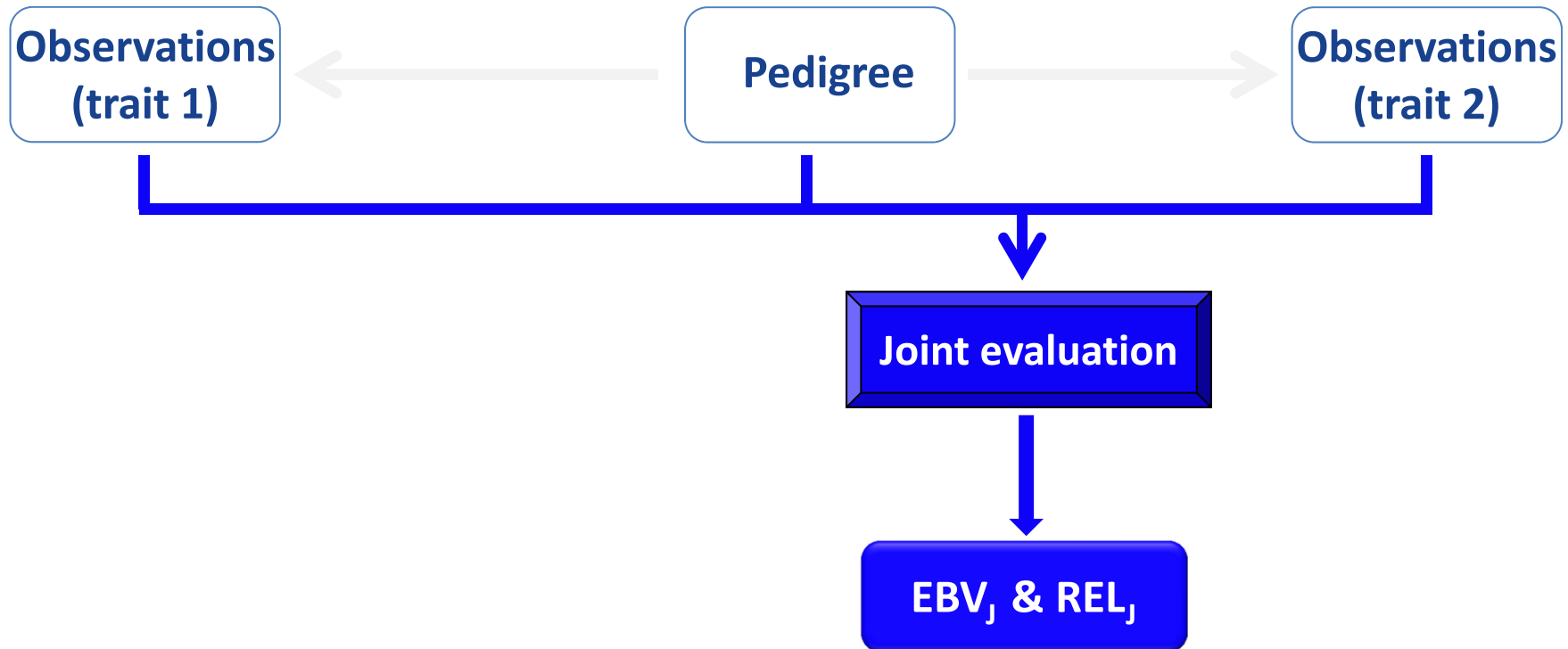
➤ Trait 2

➤ 3 herds

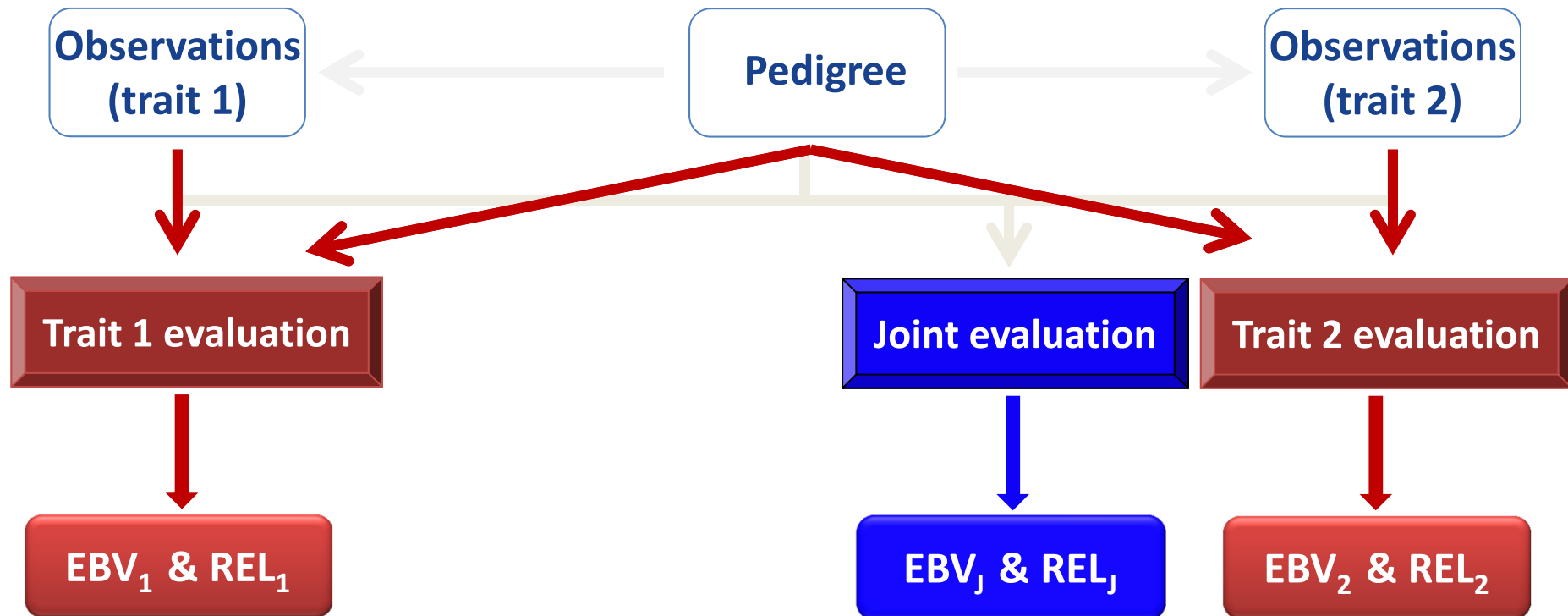
➤ $h^2 = 35\%$



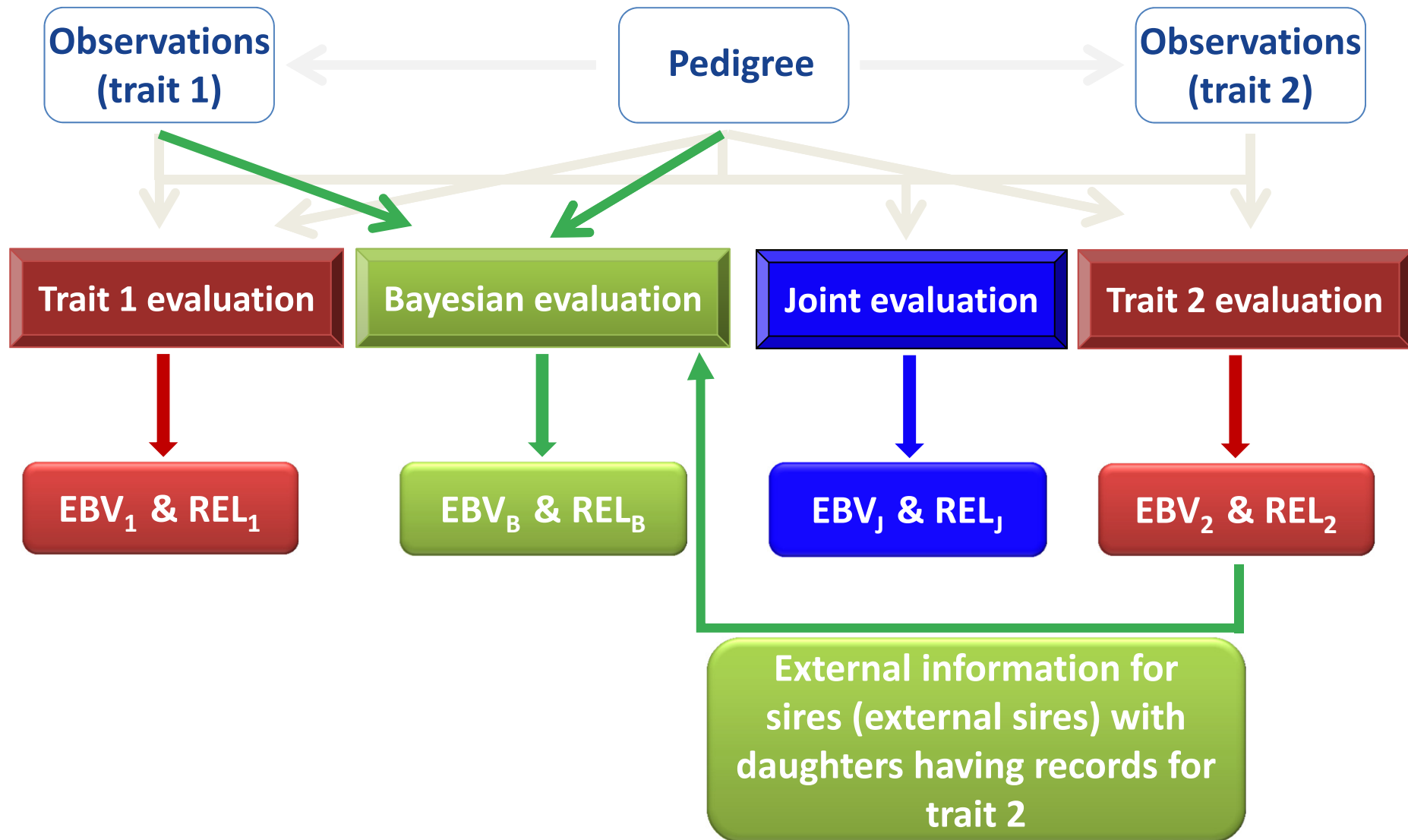
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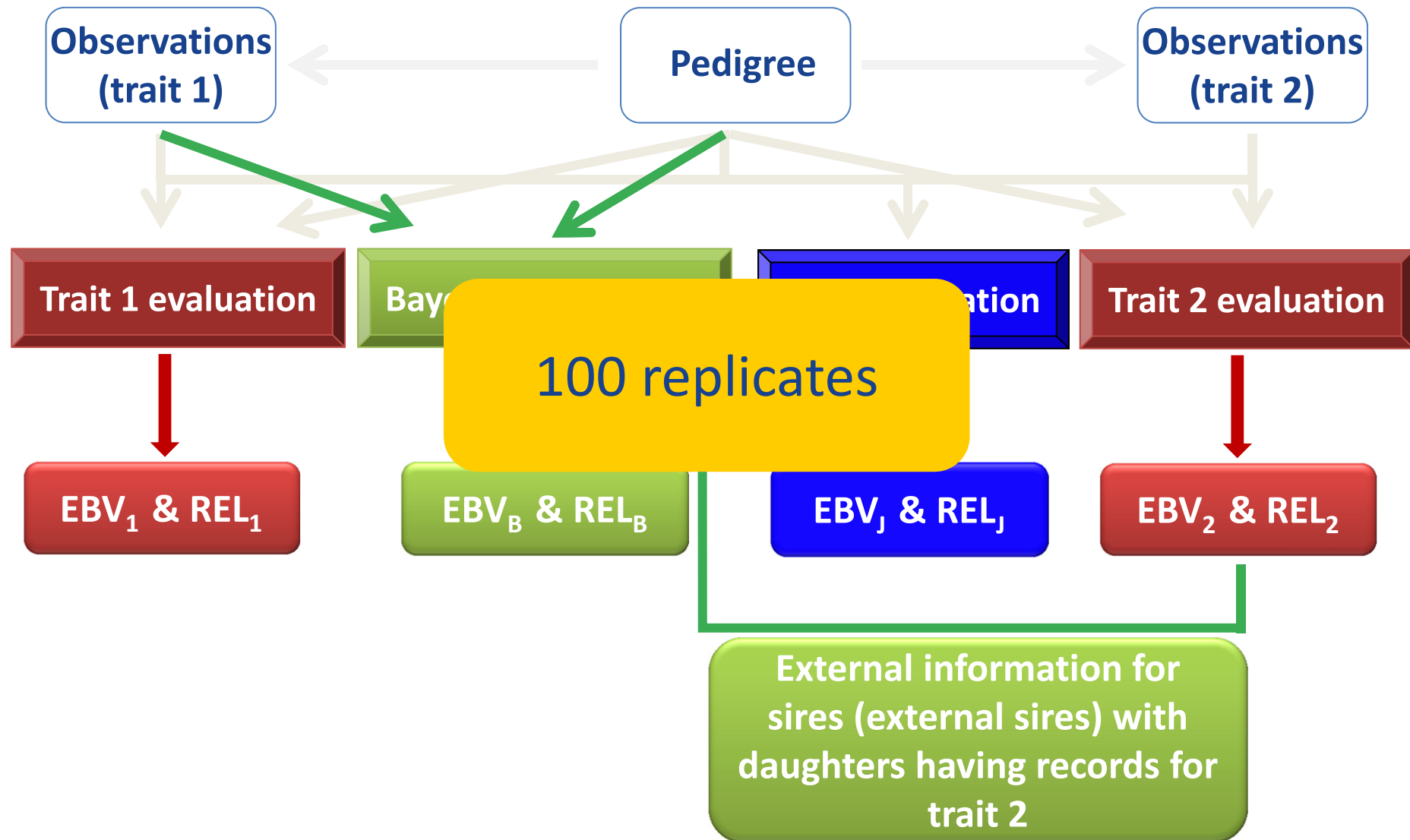
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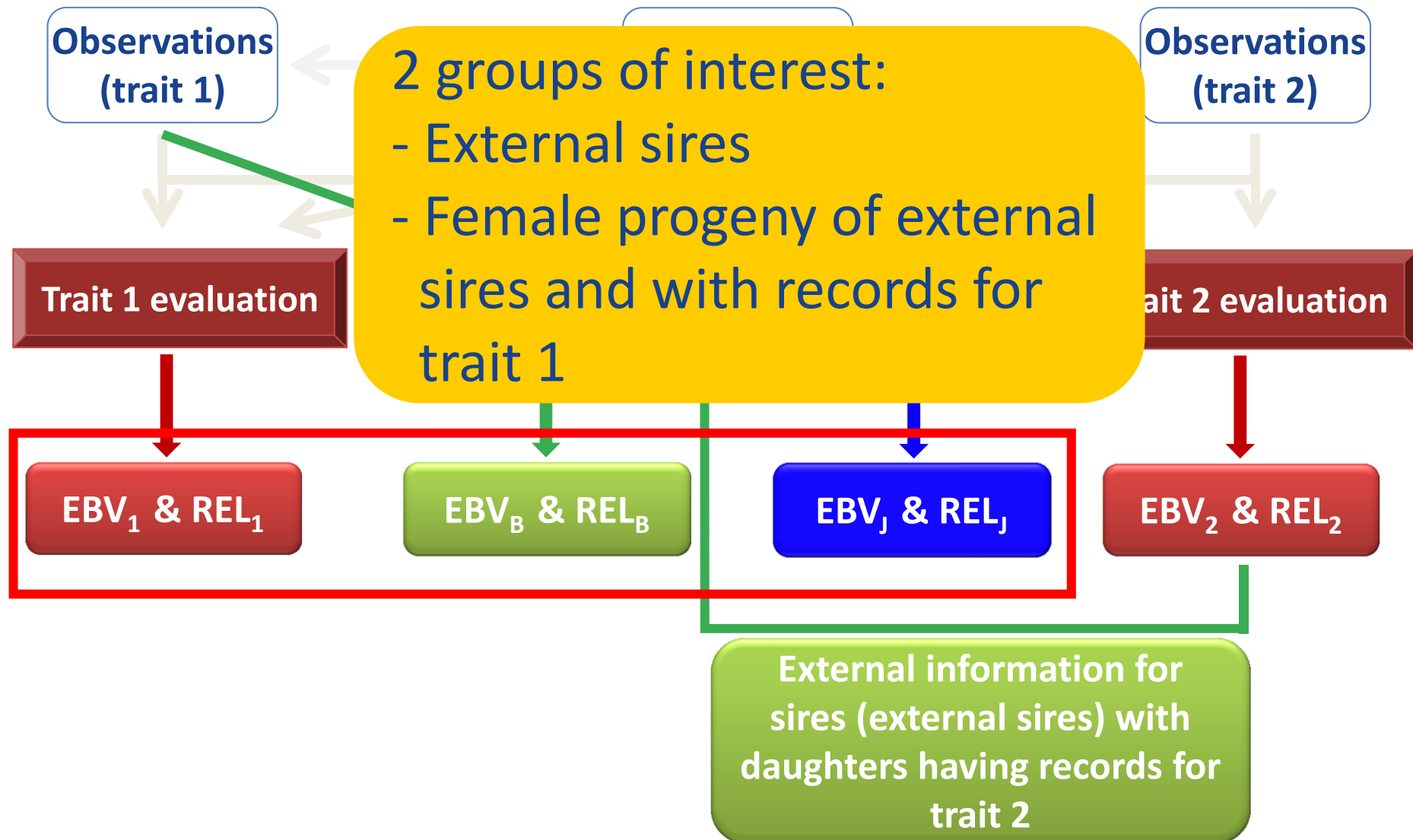
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Material



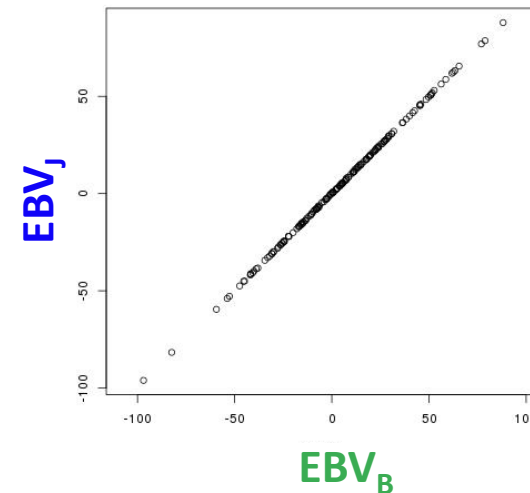
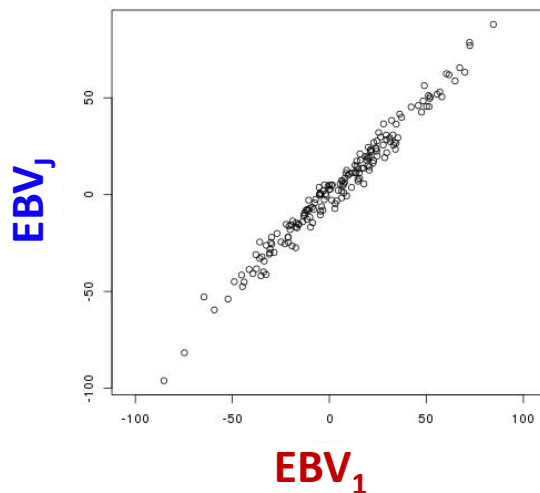
Material



Results: external sires

- ✓ Average rank correlations of EBV_J with EBV_1 or EBV_B for external sires ($N = 181.0 \pm 1.1$)

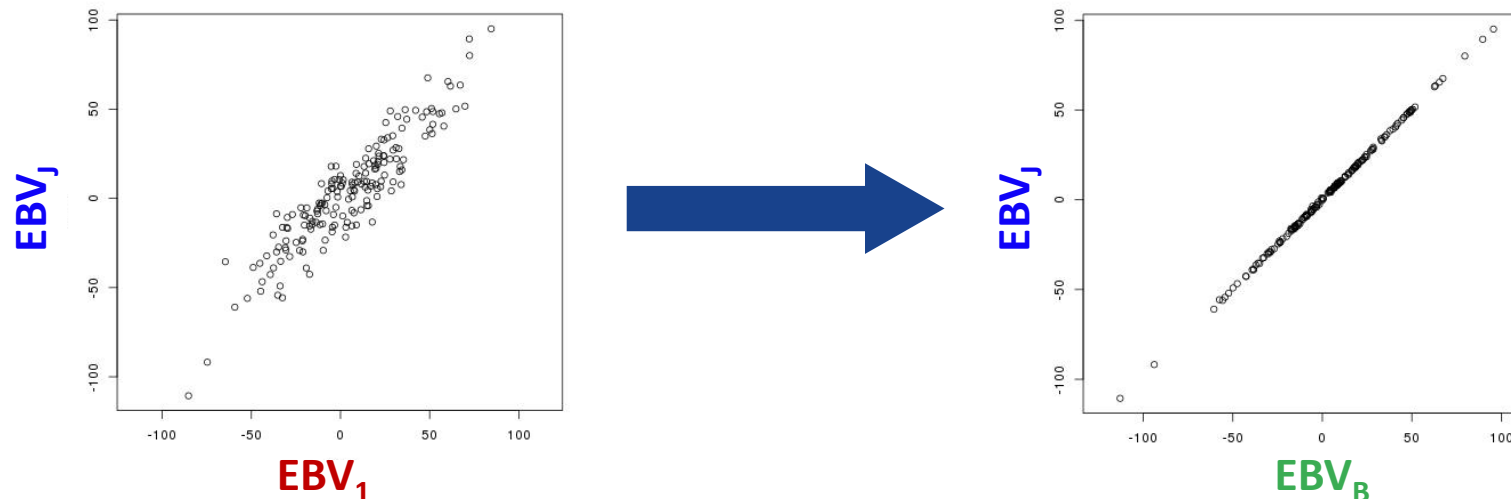
Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.987 (0.004)				
Bayesian	>0.999 (0.000)				



Results: external sires

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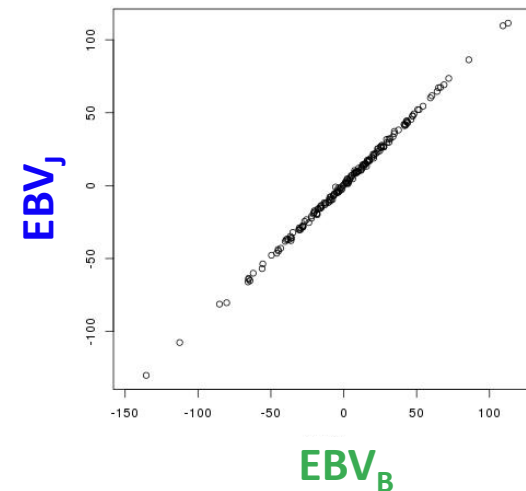
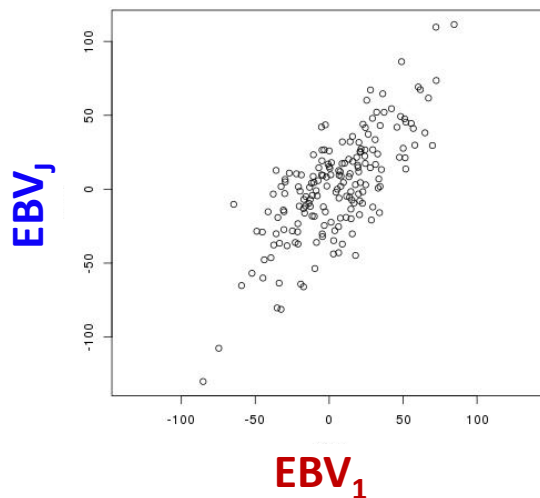
Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.987 (0.004)	0.927 (0.020)			
Bayesian	>0.999 (0.000)	>0.999 (0.000)			



Results: external sires

- ✓ Average rank correlations of EBV_J with EBV_1 or EBV_B for external sires ($N = 181.0 \pm 1.1$)

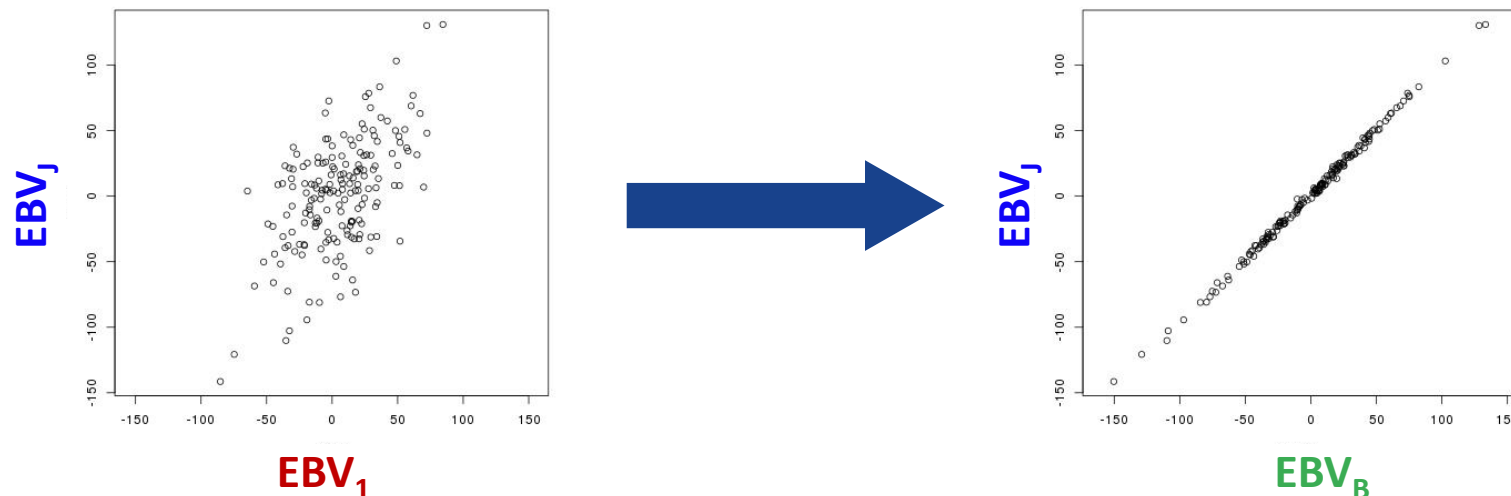
Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.987 (0.004)	0.927 (0.020)	0.777 (0.053)		
Bayesian	>0.999 (0.000)	>0.999 (0.000)	0.999 (0.000)		



Results: external sires

- ✓ Average rank correlations of EBV_J with EBV_1 or EBV_B for external sires ($N = 181.0 \pm 1.1$)

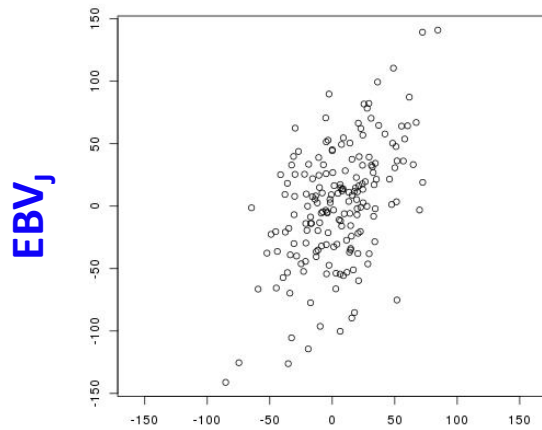
Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.987 (0.004)	0.927 (0.020)	0.777 (0.053)	0.634 (0.079)	
Bayesian	>0.999 (0.000)	>0.999 (0.000)	0.999 (0.000)	0.999 (0.000)	



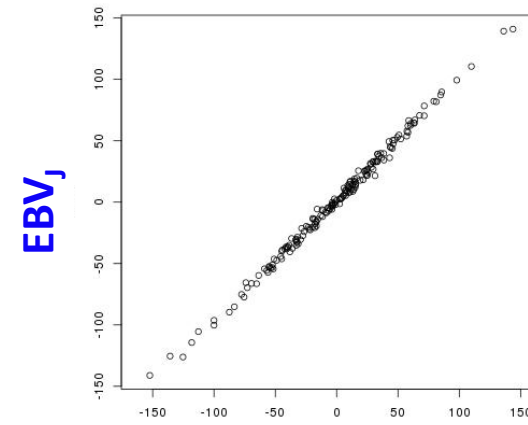
Results: external sires

- ✓ Average rank correlations of EBV_J with EBV_1 or EBV_B for external sires ($N = 181.0 \pm 1.1$)

Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.987 (0.004)	0.927 (0.020)	0.777 (0.053)	0.634 (0.079)	0.563 (0.091)
Bayesian	>0.999 (0.000)	>0.999 (0.000)	0.999 (0.000)	0.999 (0.000)	0.998 (0.000)



EBV_1



EBV_B



Results: external sires

- ✓ Average rank correlations of EBV_j with EBV_1 or EBV_B for external sires ($N = 181.0 \pm 1.1$)

Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.987 (0.004)	0.927 (0.020)	0.777 (0.053)	0.634 (0.079)	0.563 (0.091)
Bayesian	>0.999 (0.000)	>0.999 (0.000)	0.999 (0.000)	0.999 (0.000)	0.998 (0.000)

- ➔ Rankings of Bayesian evaluations similar to rankings of joint evaluations

Results: external sires

✓ Average REL

Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.10 (0.00)	0.10 (0.00)	0.10 (0.00)	0.10 (0.00)	0.10 (0.00)
Bayesian	0.10 (0.00)	0.12 (0.00)	0.17 (0.00)	0.26 (0.00)	0.34 (0.00)
Joint	0.10 (0.00)	0.12 (0.00)	0.17 (0.00)	0.26 (0.00)	0.33 (0.00)

➔ Retrieving almost all correlated information

➔ Still some double counting



Results: female progeny

- ✓ Average rank correlations of EBV_J with EBV_1 or EBV_B for female progeny ($N = 241.2 \pm 47.1$) of external sires

Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.992 (0.002)	0.954 (0.009)	0.844 (0.029)	0.721 (0.048)	0.652 (0.057)
Bayesian	0.997 (0.001)	0.983 (0.003)	0.946 (0.010)	0.910 (0.017)	0.892 (0.021)

- ➔ Rankings of Bayesian evaluations more similar to rankings of joint evaluations

Results: female progeny

✓ Average REL

Evaluations	Genetic correlations				
	0.10	0.25	0.50	0.75	0.90
Trait 1	0.14 (0.00)	0.14 (0.00)	0.14 (0.00)	0.14 (0.00)	0.14 (0.00)
Bayesian	0.14 (0.00)	0.14 (0.00)	0.15 (0.00)	0.18 (0.00)	0.20 (0.00)
Joint	0.14 (0.00)	0.14 (0.00)	0.17 (0.00)	0.21 (0.00)	0.25 (0.00)

➔ Propagation of sires' external information to progeny



Perspectives

- ✓ Combination of information for traits having different
 - variance components – heritabilities
 - Milk yields in different countries
 - units of measurement
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 - Milk yields in different countries
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 - models
 - Random regressions test-day or lactation models

Perspectives

- ✓ Combination of information for traits having different
 - ❑ variance components – heritabilities
 - ❑ Milk yields in different countries
 - ❑ units of measurement
 - ❑ Milk yields expressed in kg or lb
 - ❑ models
 - ❑ Random regressions test-day or lactation models
 - ❑ genotype by environment interactions

Conclusions

- ✓ Good integration of correlated external information
 - even with low genetic correlations
- ✓ Rankings of the Bayesian evaluations more similar to rankings of the joint evaluations
 - for animals with external information
 - for their progeny
- ✓ Numerous possible applications

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