# 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

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

- $\mathbf{G^{-1} = A^{-1} \otimes G_0^{-1}}$ : inverse of additive genetic (co)variance matrix
- $\mathbf{y_I}$ : vector of internal observations
- $\hat{\boldsymbol{\beta}}_\mathbf{I}$ : vector of estimated internal fixed effects
- $\hat{\mathbf{u}}_\mathbf{I}$ : vector of internal EBV

# Assumption

✓ Prior distribution of $\mathbf{u_I}$

$$\mathbf{p}(\mathbf{u_I}) = MVN(\mathbf{0}, \mathbf{G}) \quad \longrightarrow \quad \mathbf{p}(\mathbf{u_I} | \mathbf{y_E}) = MVN(\hat{\mathbf{u}}_\mathbf{E}, \mathbf{D_E})$$

- $\mathbf{y_E}$ : unavailable vector of correlated external phenotypes
- $\hat{\mathbf{u}}_\mathbf{E}$ : vector of external EBV
- $\mathbf{D_E}$ : prediction error (co)variance matrix of $\hat{\mathbf{u}}_\mathbf{E}$

# Methods

✓ Integration of correlated external information

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

⬇

$$\begin{bmatrix} \mathbf{X'R^{-1}X} & \mathbf{X'R^{-1}Z} \\ \mathbf{Z'R^{-1}X} & \mathbf{Z'R^{-1}Z+}\boxed{\mathbf{D_E^{-1}}} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_\mathbf{I} \\ \hat{\mathbf{u}}_\mathbf{I} \end{bmatrix} = \begin{bmatrix} \mathbf{X'R^{-1}y_I} \\ \mathbf{Z'R^{-1}y_I}\boxed{\mathbf{+D_E^{-1}\hat{u}_E}} \end{bmatrix}$$

# Issue

✓ External information only available for external animals

➔ $\hat{\mathbf{u}}_{\mathbf{E}}$ and $\mathbf{D}_{\mathbf{E}}^{-1}$ : partially unknown

➔ Estimations for internal animals

# Estimation of $\hat{\mathbf{u}}_{\mathbf{E}}$

✓ Available

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

✓ Internal animals

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

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

➔ $\hat{\mathbf{u}}_{\mathbf{E}} = \left[\hat{\mathbf{u}}'_{\mathbf{E_E}} \quad \hat{\mathbf{u}}'_{\mathbf{E_I}}\right]'$

➔ Correct propagation of external information

# Estimation of $\mathbf{D}_{\mathbf{E}}^{-1}$

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

$$\mathbf{\Lambda}_{\mathrm{E}} = block\ diag\left(\mathbf{\Delta}_{\mathbf{j}}\mathbf{R}_{\mathbf{0}}^{-1}\mathbf{\Delta}_{\mathbf{j}}\right);\ j = 1,\ldots,n \text{ animals}$$

$$\begin{cases} \text{For external animals}: \mathbf{\Delta}_{\mathbf{j}} = diag\left(\sqrt{RE_k}\right); k = 1,\ldots,t \text{ traits} \\ \text{For internal animals}: \mathbf{\Delta}_{\mathbf{j}} = \mathbf{0} \end{cases}$$

# Material

**Pedigree**

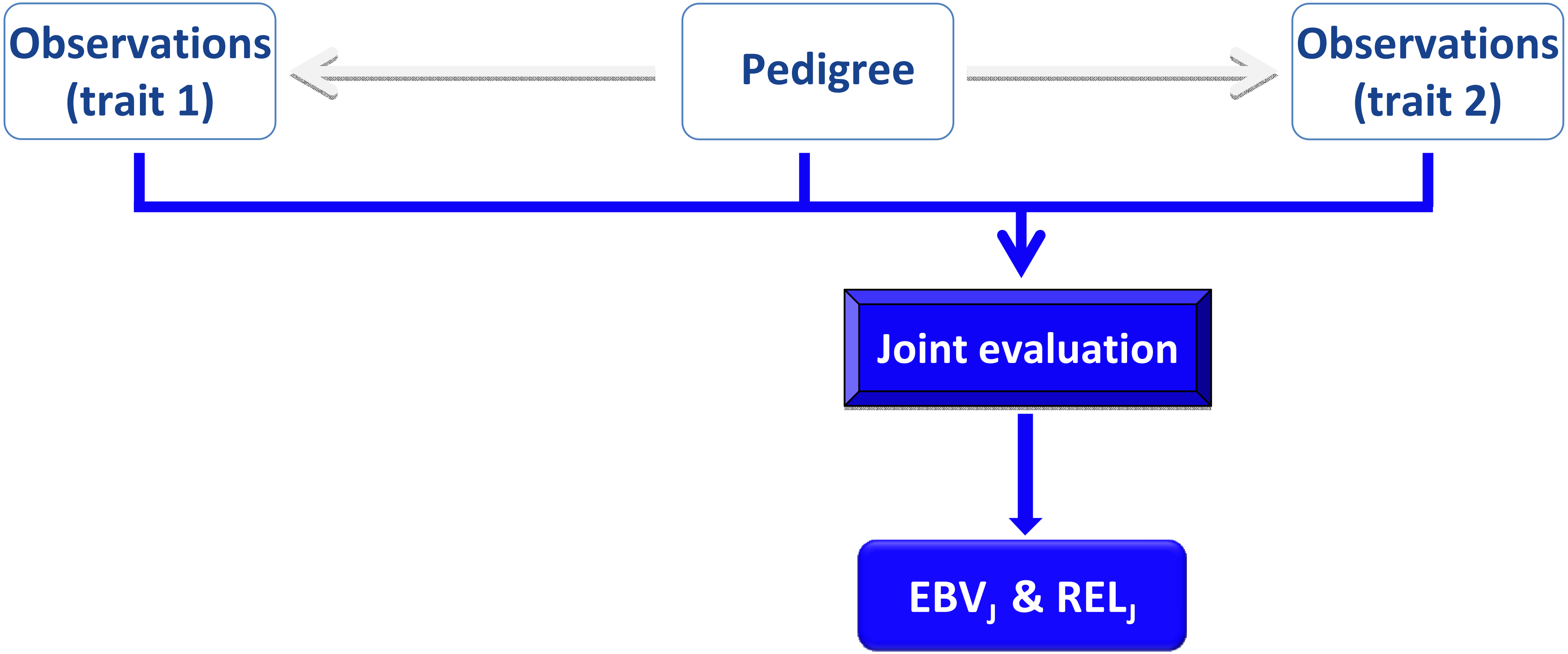
- **QMSim** (Sargolzaei and Schenkel, 2009)
  - **10 generations**
  - **2240 animals**
  - **Random selection and matings**

# Material

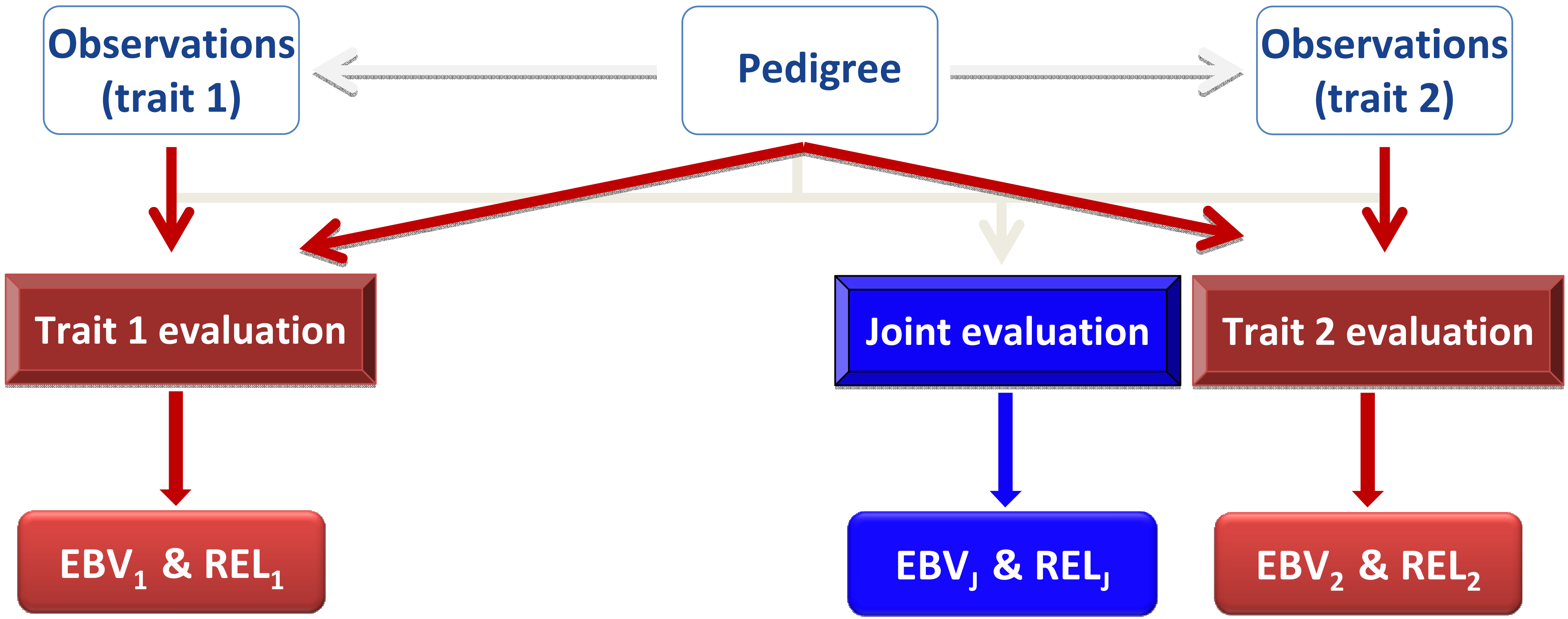
Observations (trait 1) ← Pedigree → Observations (trait 2)

- 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%

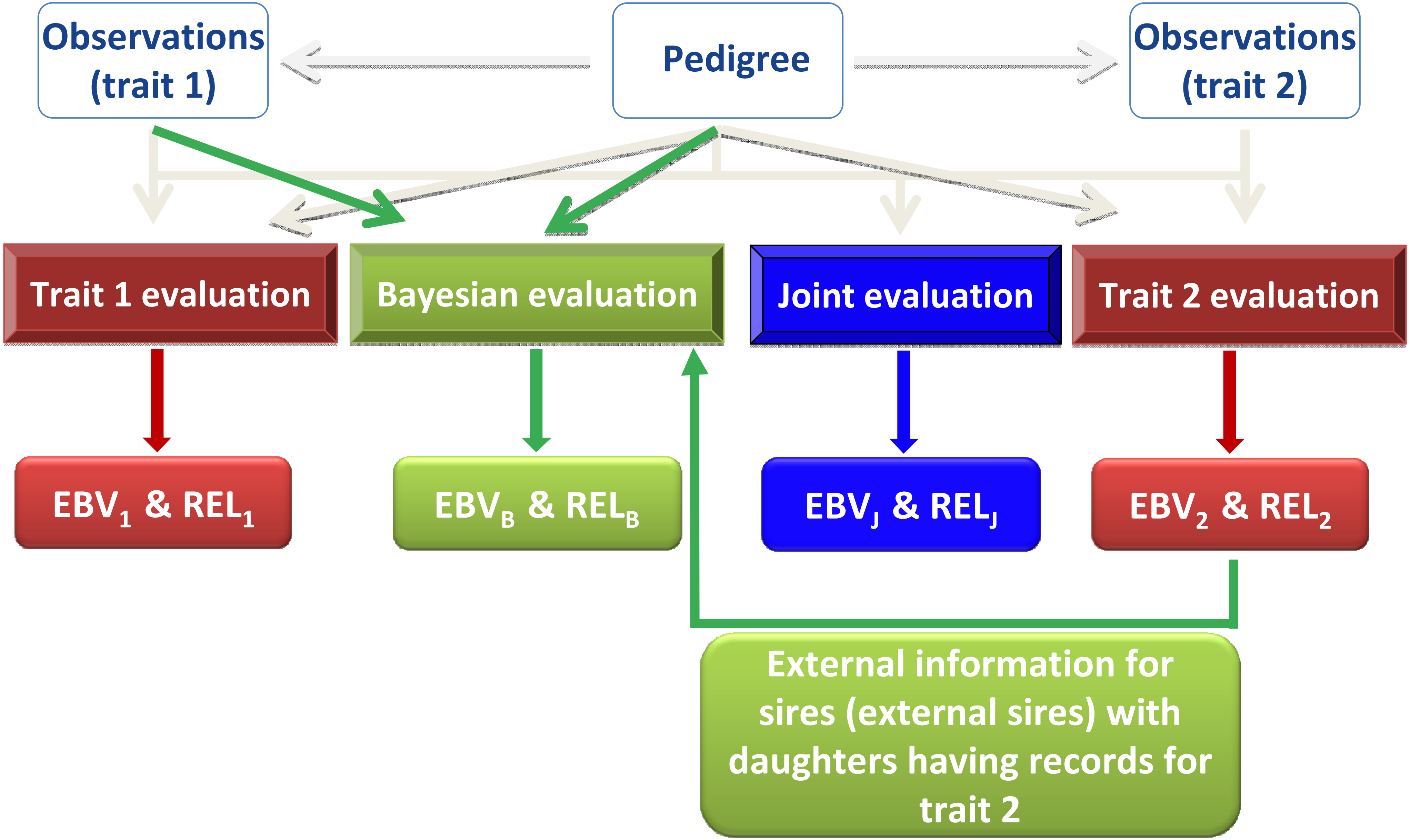
# Material


Observations (trait 1)
Pedigree
Observations (trait 2)
Joint evaluation
$EBV_J$ & $REL_J$

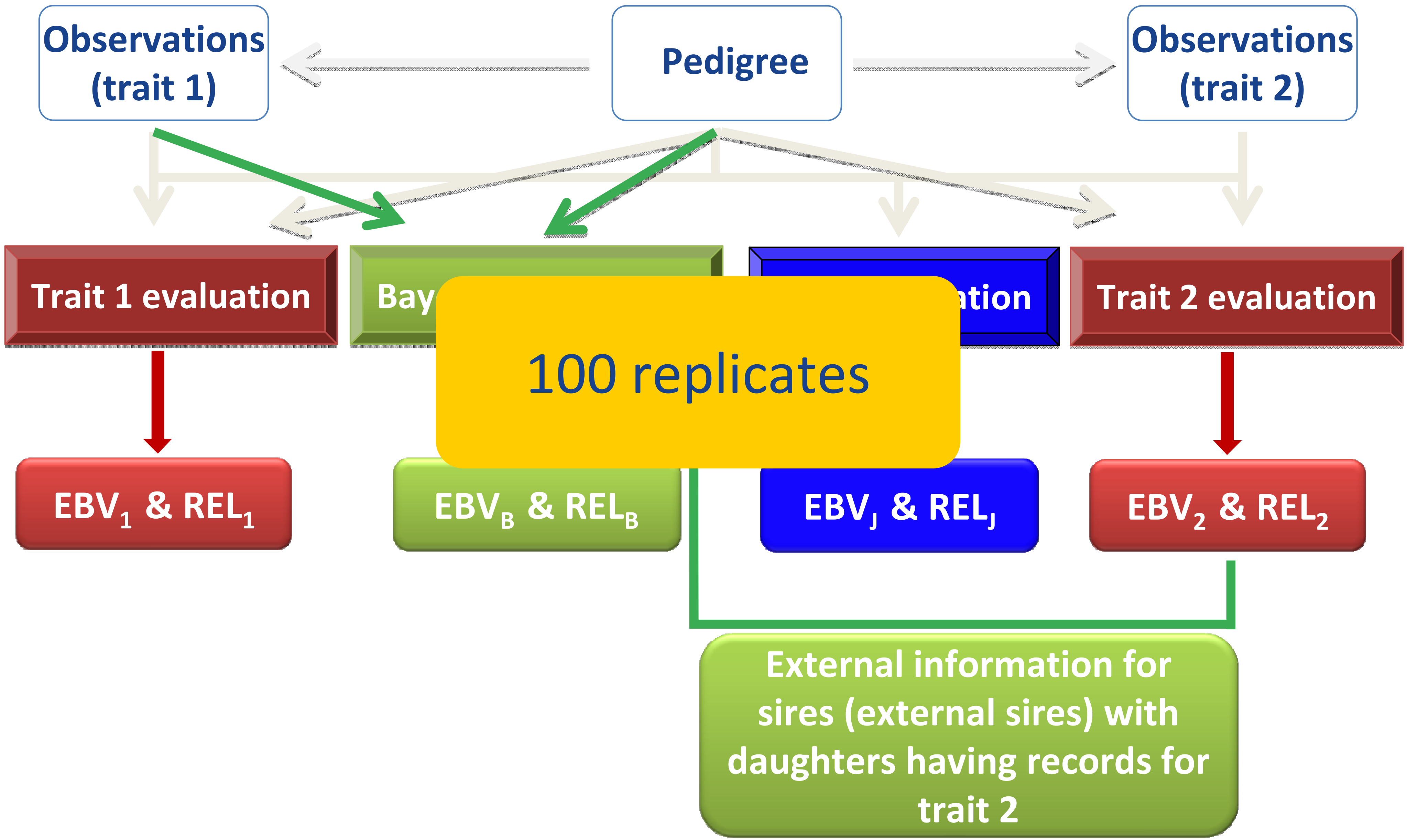
# Material


Observations (trait 1)
Pedigree
Observations (trait 2)
Trait 1 evaluation
Joint evaluation
Trait 2 evaluation
$EBV_1$ & $REL_1$
$EBV_J$ & $REL_J$
$EBV_2$ & $REL_2$

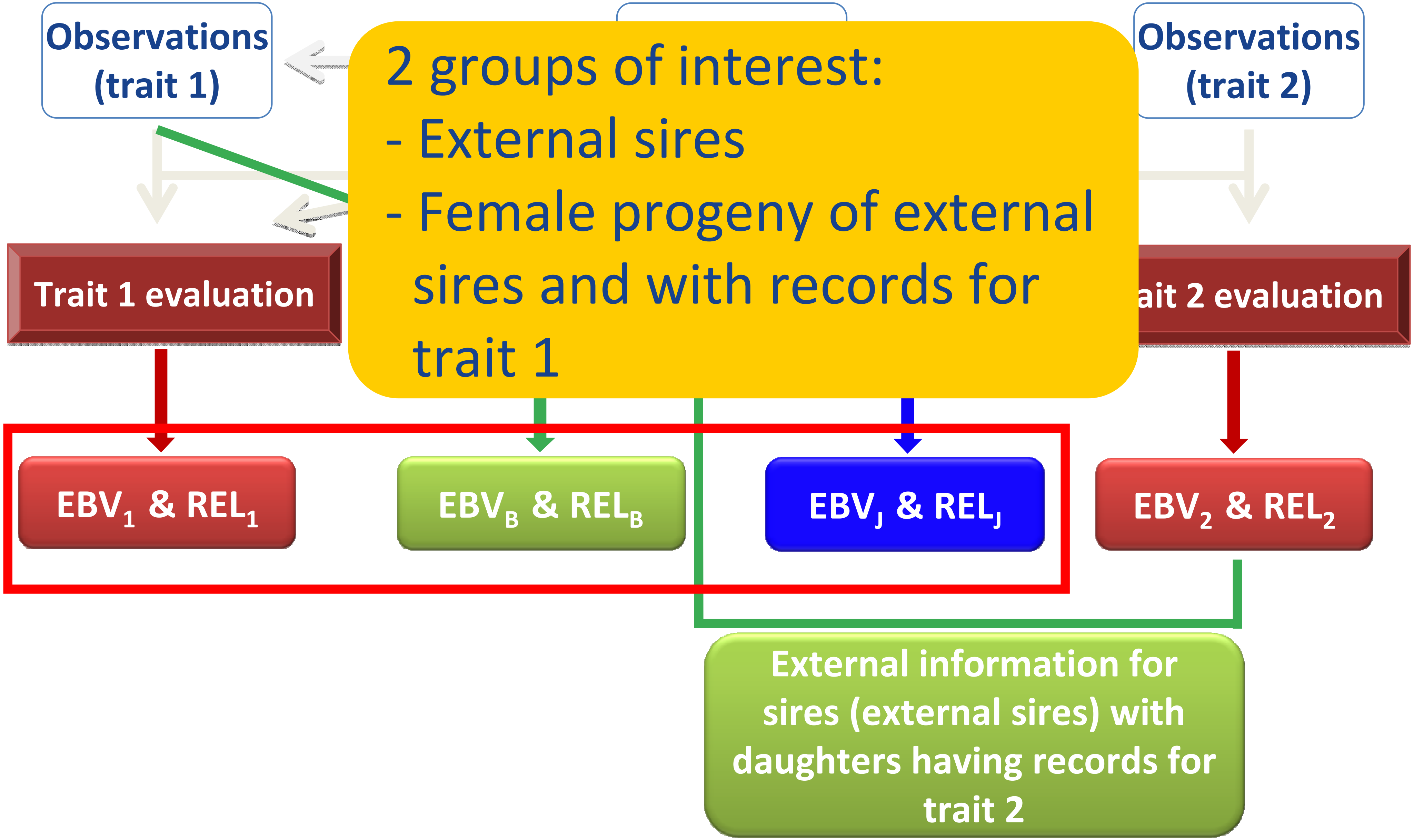
# Material


Observations (trait 1)
Pedigree
Observations (trait 2)
Trait 1 evaluation
Bayesian evaluation
Joint evaluation
Trait 2 evaluation
$EBV_1$ & $REL_1$
$EBV_B$ & $REL_B$
$EBV_J$ & $REL_J$
$EBV_2$ & $REL_2$
External information for sires (external sires) with daughters having records for trait 2

# Material


Observations (trait 1)
Pedigree
Observations (trait 2)
Trait 1 evaluation
Bay
ation
Trait 2 evaluation
100 replicates
EBV$_1$ & REL$_1$
EBV$_B$ & REL$_B$
EBV$_J$ & REL$_J$
EBV$_2$ & REL$_2$
External information for sires (external sires) with daughters having records for trait 2

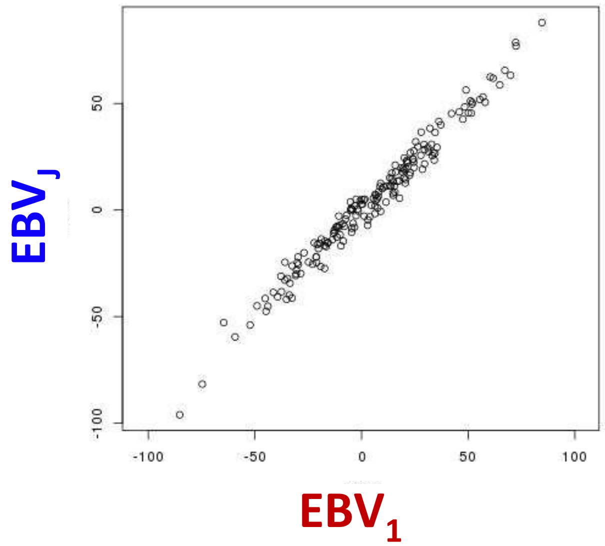
# Material

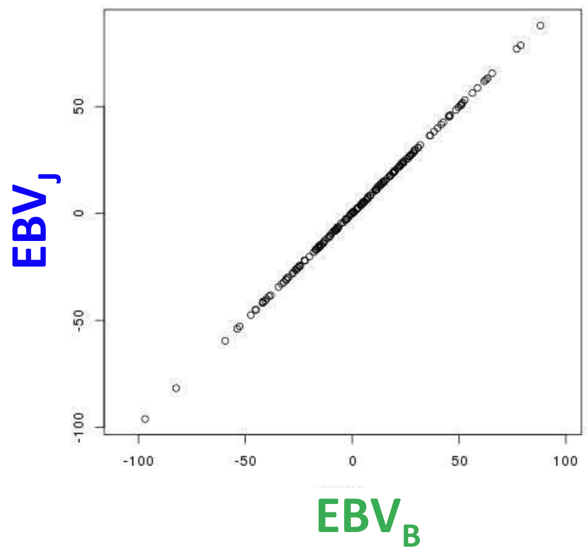

Observations (trait 1)
Observations (trait 2)
2 groups of interest:
- External sires
- Female progeny of external sires and with records for trait 1
Trait 1 evaluation
ait 2 evaluation
$EBV_1$ & $REL_1$
$EBV_B$ & $REL_B$
$EBV_J$ & $REL_J$
$EBV_2$ & $REL_2$
External information for sires (external sires) with daughters having records for trait 2

# Results: external sires

✓ Average rank correlations of $EBV_J$ with $EBV_1$ or $EBV_B$ for external sires (N = 181.0 ± 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) | | | | |



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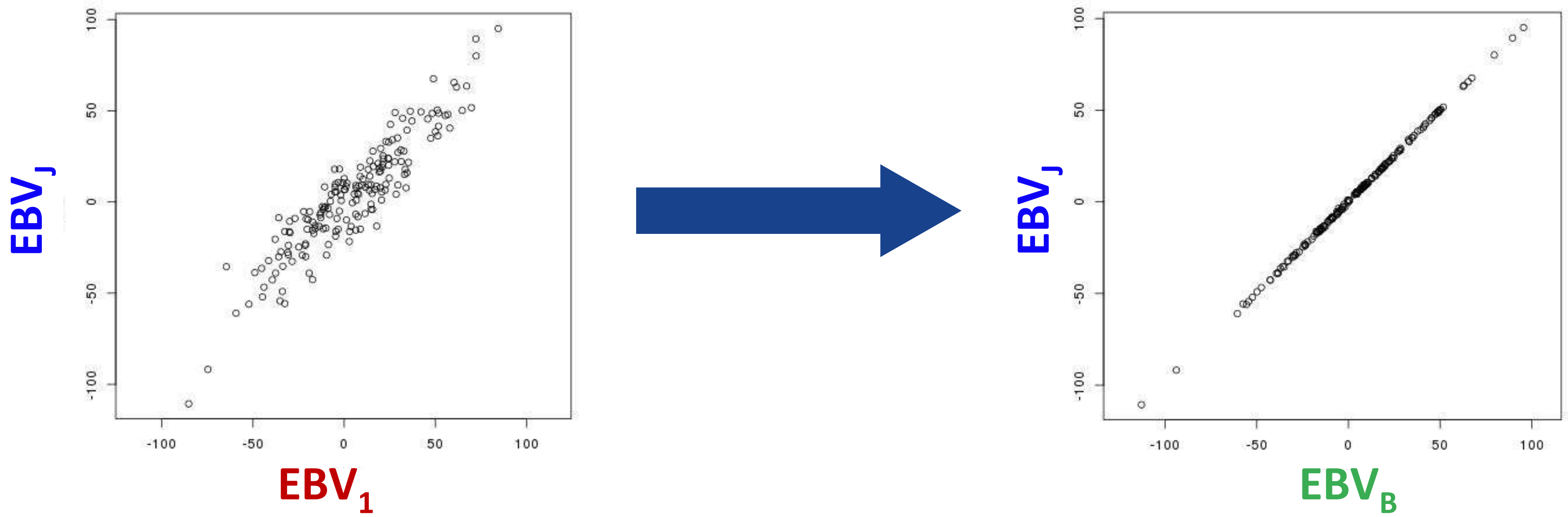
|---|---|---|---|---|---|
| | **0.10** | **0.25** | **0.50** | **0.75** | **0.90** |
| **Trait 1** | **0.987** (0.004) | **0.927** (0.020) | | | |
| **Bayesian** | **>0.999** (0.000) | **>0.999** (0.000) | | | |



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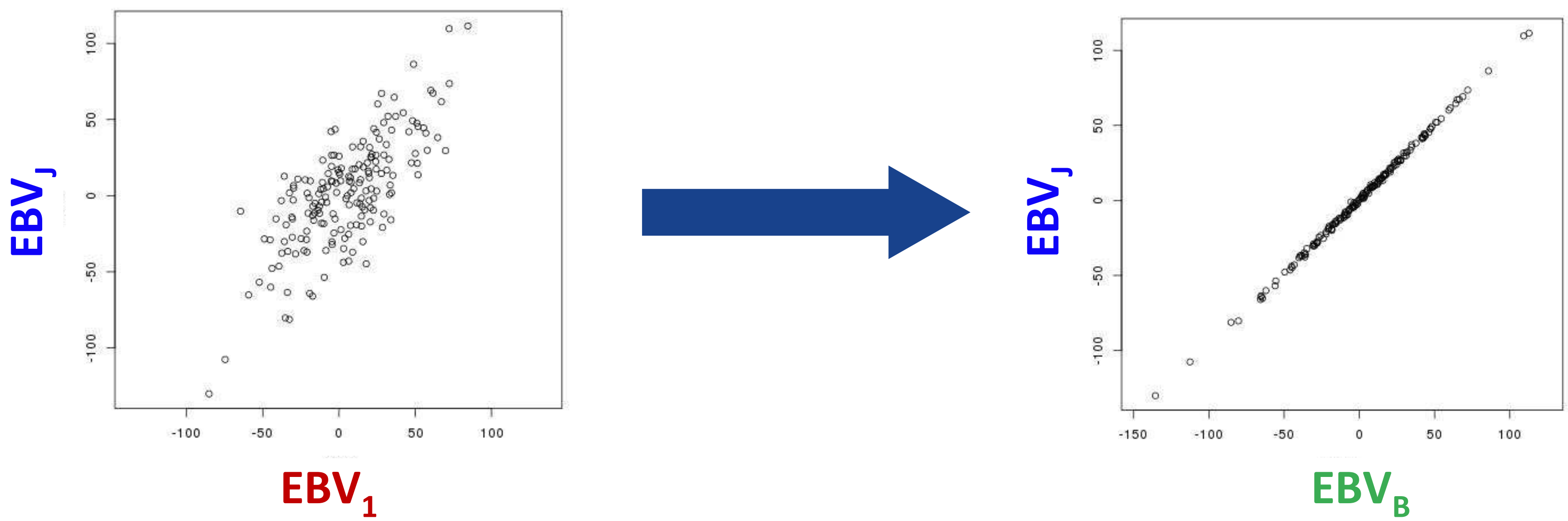
| | 0.10 | 0.25 | 0.50 | 0.75 | 0.90 |
| Trait 1 | **0.987** (0.004) | **0.927** (0.020) | **0.777** (0.053) | | |
| Bayesian | **>0.999** (0.000) | **>0.999** (0.000) | **0.999** (0.000) | | |



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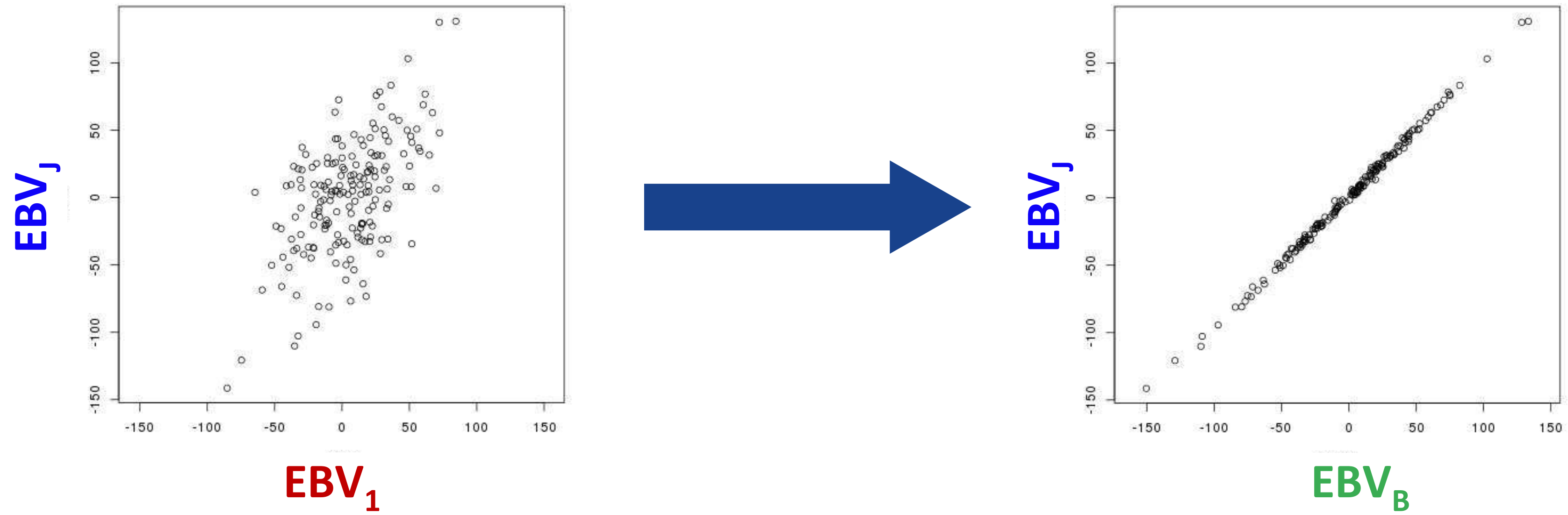
| Bayesian | **>0.999** (0.000) | **>0.999** (0.000) | **0.999** (0.000) | **0.999** (0.000) | |



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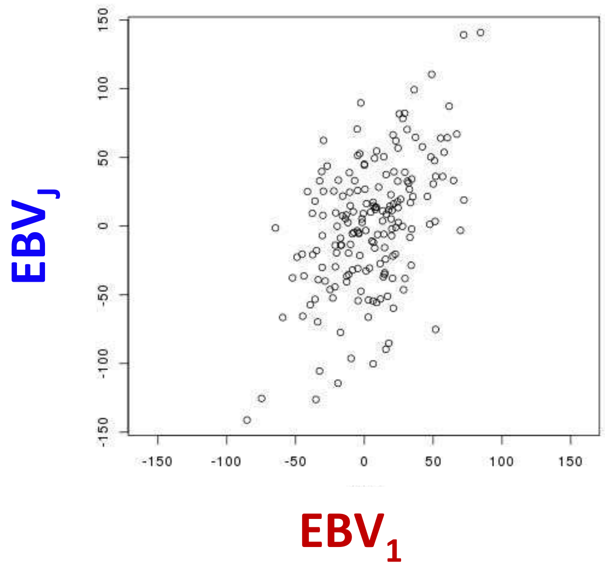
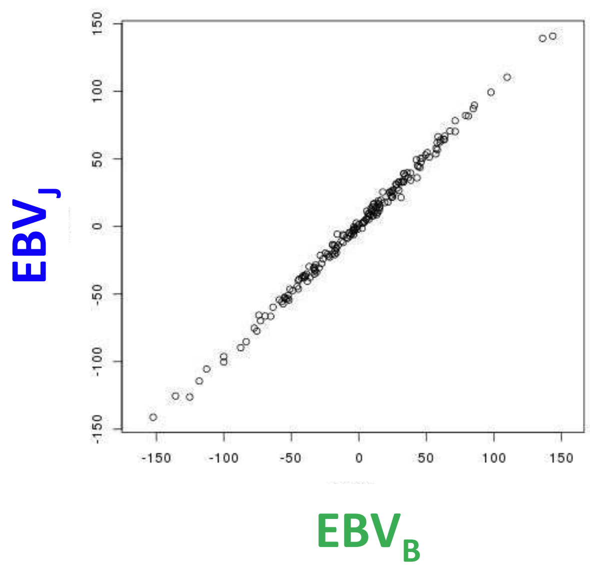
|---|---|---|---|---|---|
| | 0.10 | 0.25 | 0.50 | 0.75 | 0.90 |
| Trait 1 | **0.987** (0.004) | **0.927** (0.020) | **0.777** (0.053) | **0.634** (0.079) | **0.563** (0.091) |
| Bayesian | **>0.999** (0.000) | **>0.999** (0.000) | **0.999** (0.000) | **0.999** (0.000) | **0.998** (0.000) |



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| 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 ± 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
  - 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

# Acknowledgments

✓CECI for computational resources

✓Animal and Dairy Science Department, University of Georgia Athens, USA

✓Animal Science Department, University of Ljubljana, Slovenia

✓Financial supports

- ❑ National Fund for Scientific Research
- ❑ Wallonie Brussels International
- ❑ University of Liege