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A note on using 'forward prediction' to assess precision and bias of genomic predictions

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Motivation

- Investigation focuses on the property of reliabilities as measures of precision of estimates
 - ◆ How much will a future, more reliable estimate deviate from the current one?
 - ◆ How will selection affect the conditions in a validation sample?

Methods

- calculations based on model-derived reliabilities and related multivariate-normal distributions of TBV and BLUPs

Methods

- calculations based on related multivariate BLUPs

$$\begin{bmatrix} TBV \\ PA \\ GEBV \\ EBV \end{bmatrix} \sim N\{\boldsymbol{\mu}, \mathbf{V}\}$$

$$\begin{bmatrix} TBV \\ PA \\ GEBV \\ EBV \end{bmatrix} \sim N\left\{ \begin{bmatrix} 100 \\ 100 \\ 100 \\ 100 \end{bmatrix}, \begin{bmatrix} R_{TBV}^2 & R_{PA}^2 & R_{GEBV}^2 & R_{EBV}^2 \\ R_{PA}^2 & R_{PA}^2 & R_{PA}^2 & R_{PA}^2 \\ R_{GEBV}^2 & R_{PA}^2 & R_{GEBV}^2 & R_{M1M2}^2 \\ R_{EBV}^2 & R_{PA}^2 & R_{M1M2}^2 & R_{EBV}^2 \end{bmatrix} * 144 \right\}$$

$$R_{M1M2}^2 = R_{PA}^2 + (R_{GEBV}^2 - R_{PA}^2)(R_{EBV}^2 - R_{PA}^2)/(1 - R_{PA}^2)$$

Methods

- calculations based on model-derived reliabilities and related multivariate-normal distributions of TBV and BLUPs
- effects of selection:
 - ◆ explicit calculations in one step selection scenarios via conditional means and (co-)variances

Methods

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$$E(A|B) = \boldsymbol{\mu}_A + \mathbf{V}_{AB}\mathbf{V}_B^{-1}(B - \boldsymbol{\mu}_B)$$

$$\text{Var}(A|B) = \begin{bmatrix} \mathbf{V}_A - \mathbf{V}_{AB}\mathbf{V}_B^{-1}\mathbf{V}_{BA} & \mathbf{V}_{AB}\mathbf{V}_B^{-1}\mathbf{V}_{B_s} \\ \mathbf{V}_{B_s}\mathbf{V}_B^{-1}\mathbf{V}_{BA} & \mathbf{V}_{B_s} \end{bmatrix}$$

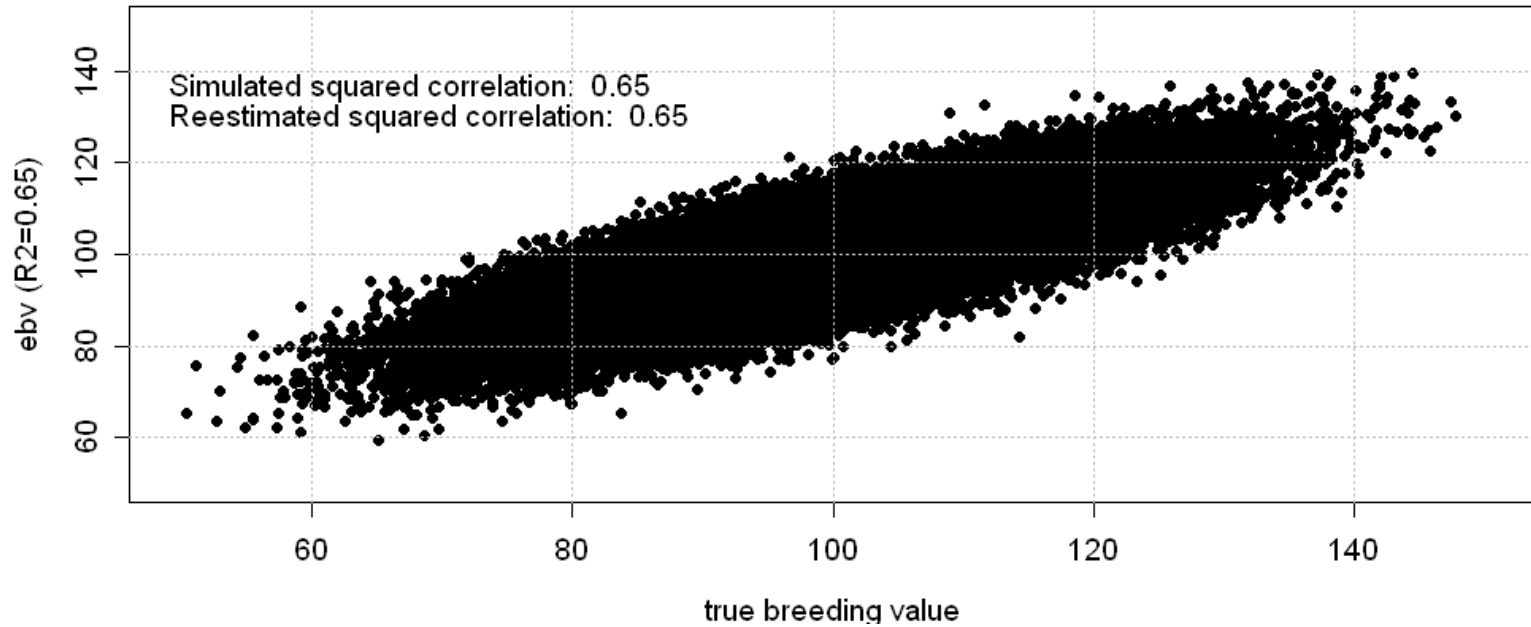
Henderson, 1975

Methods

- calculations based on model-derived reliabilities and related multivariate-normal distributions of TBV and BLUPs
- effects of selection:
 - ◆ explicit calculations in one step selection scenarios via conditional means and (co-)variances
 - ◆ via simulation in multistep scenarios

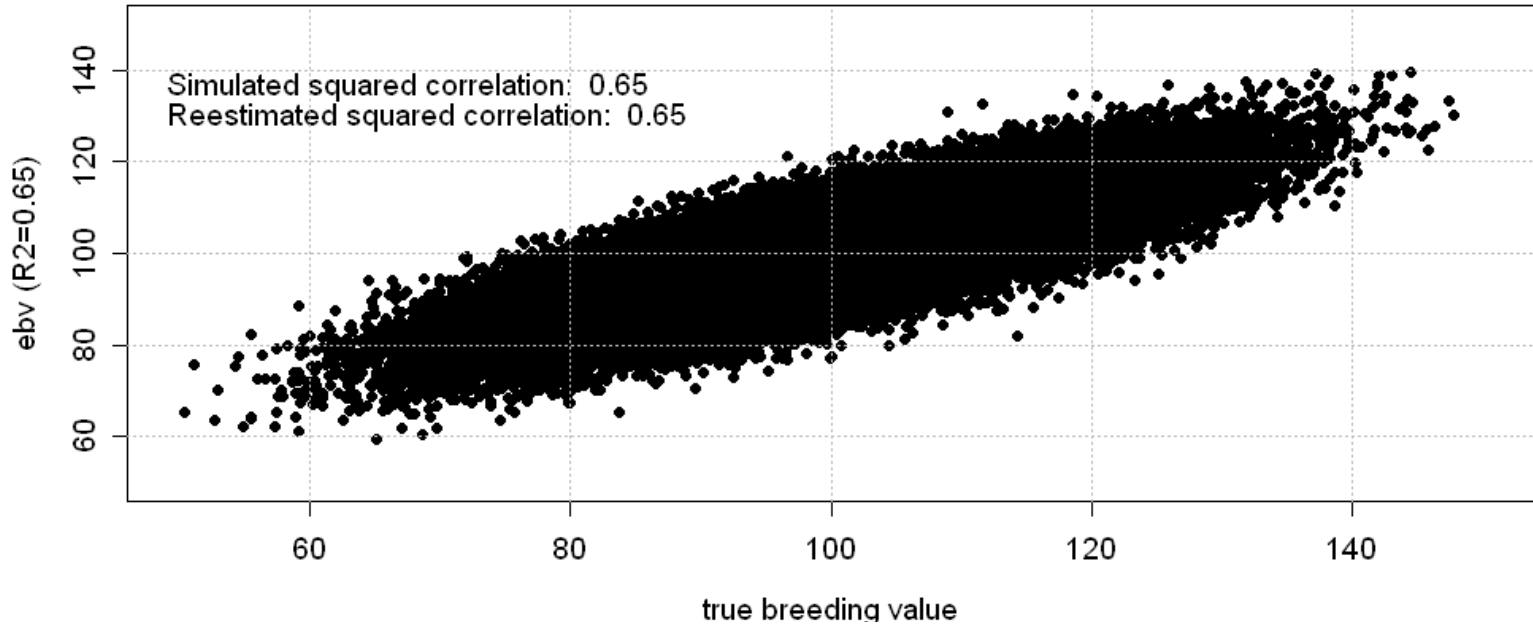
Illustration

Correlation between true and estimated BV

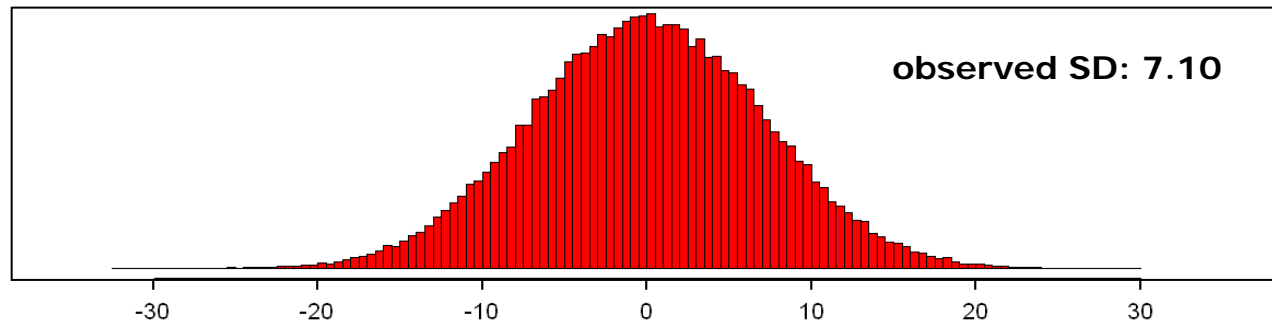


Illustration

Correlation between true and estimated BV

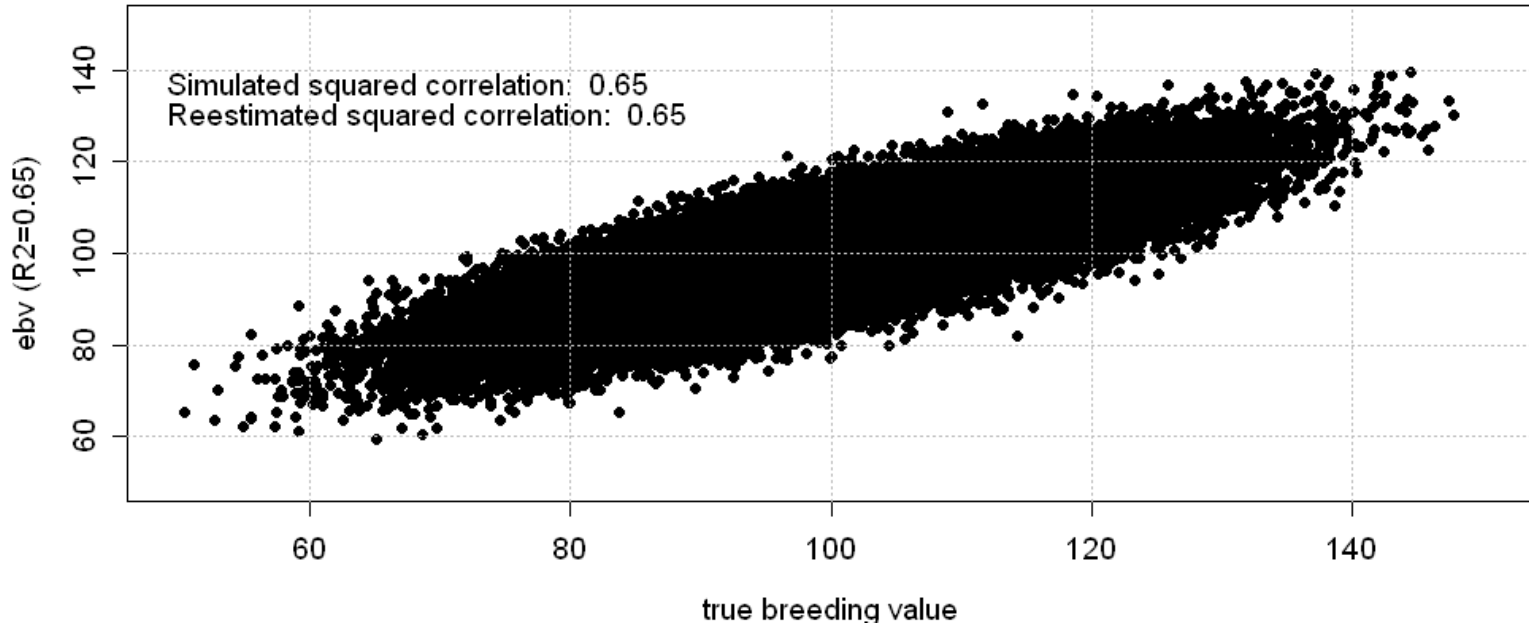


Prediction error distribution

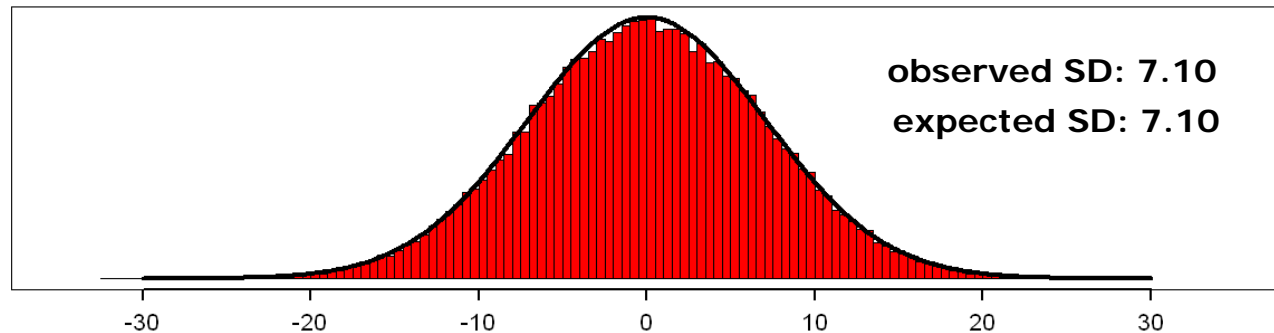


Illustration

Correlation between true and estimated BV

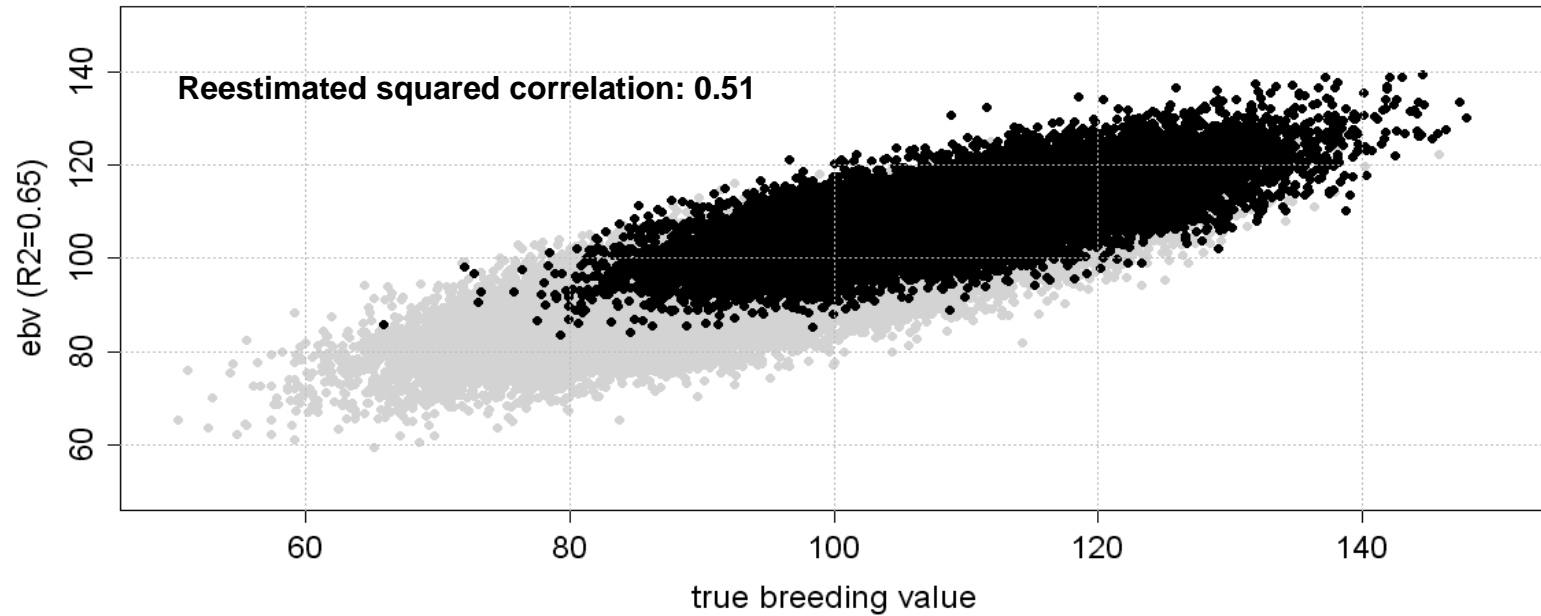


Prediction error distribution



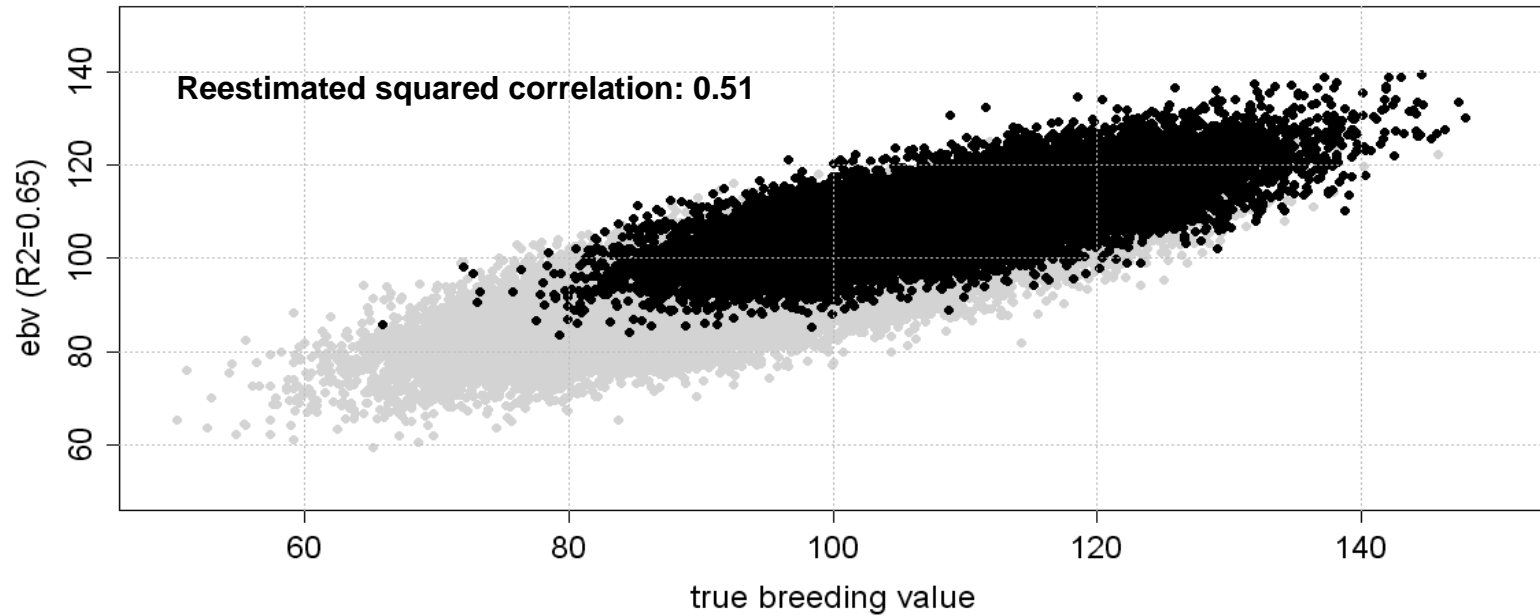
Illustration

Selection applied to correlated PA ($R^2=0.38$), $p = 0.25$

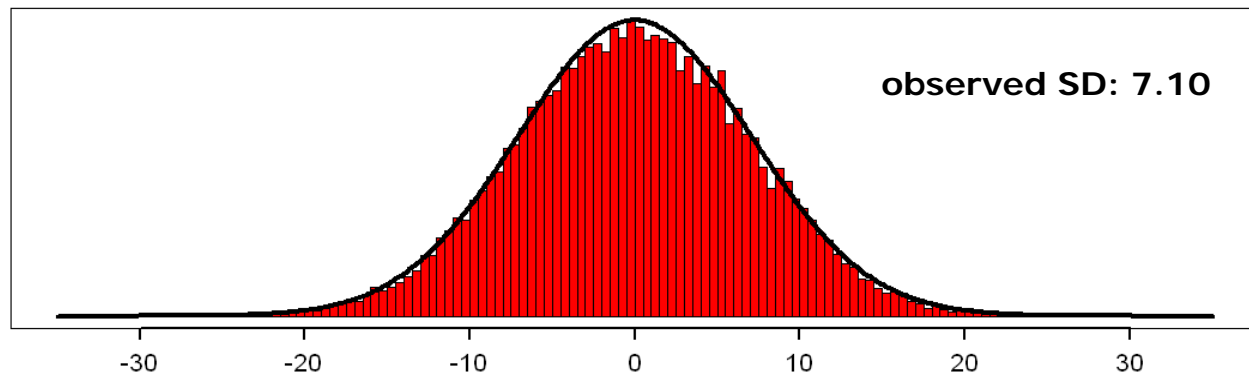


Illustration

Selection applied to correlated PA ($R^2=0.38$), $p = 0.25$

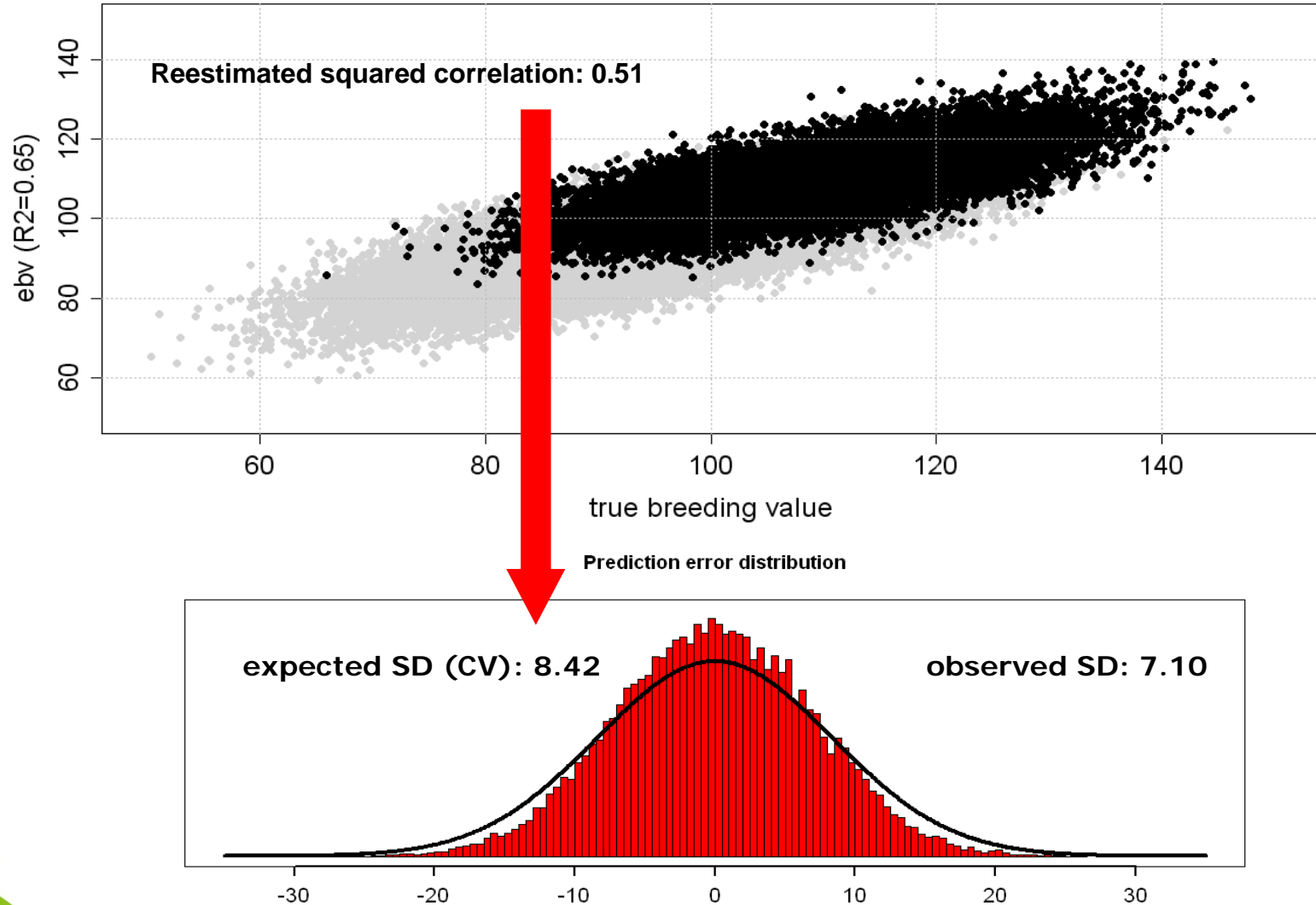


Prediction error distribution



Illustration

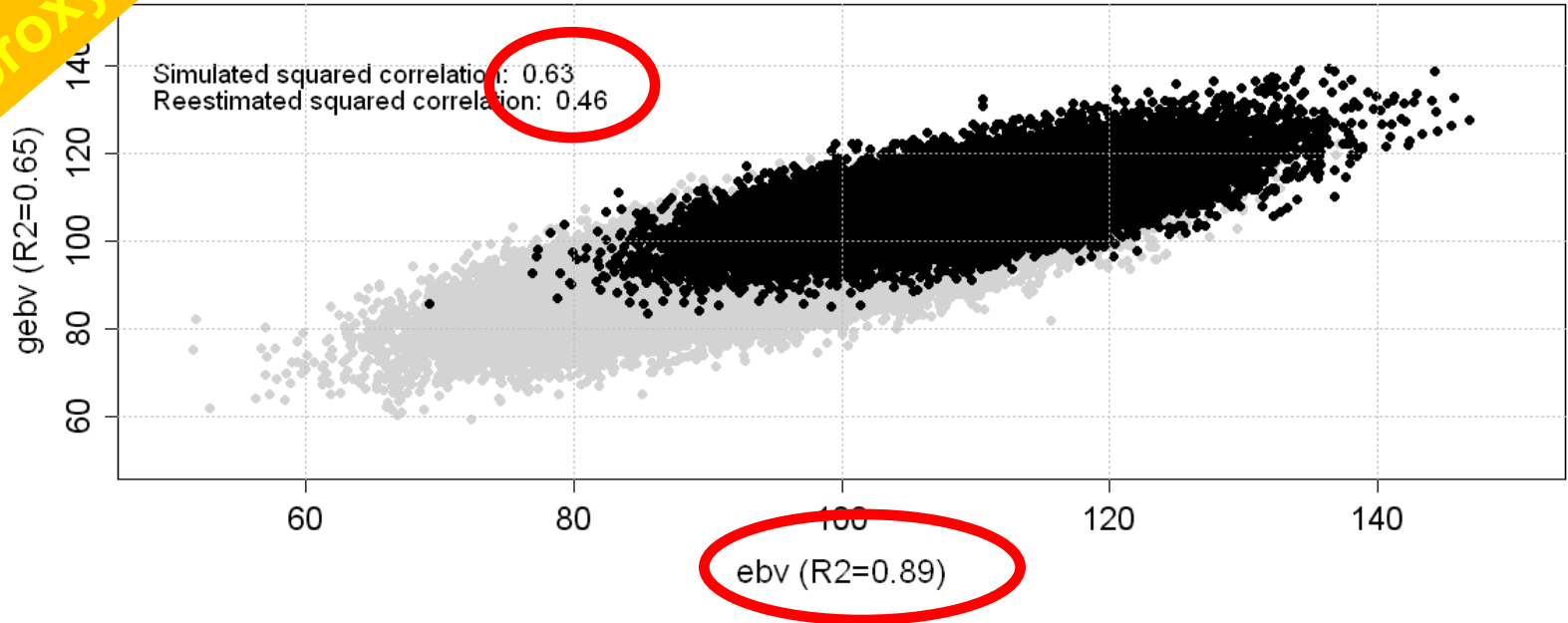
Selection applied to correlated PA ($R^2=0.38$), $p = 0.25$



Illustration

Selection applied to correlated PA ($R^2=0.38$), $p = 0.25$

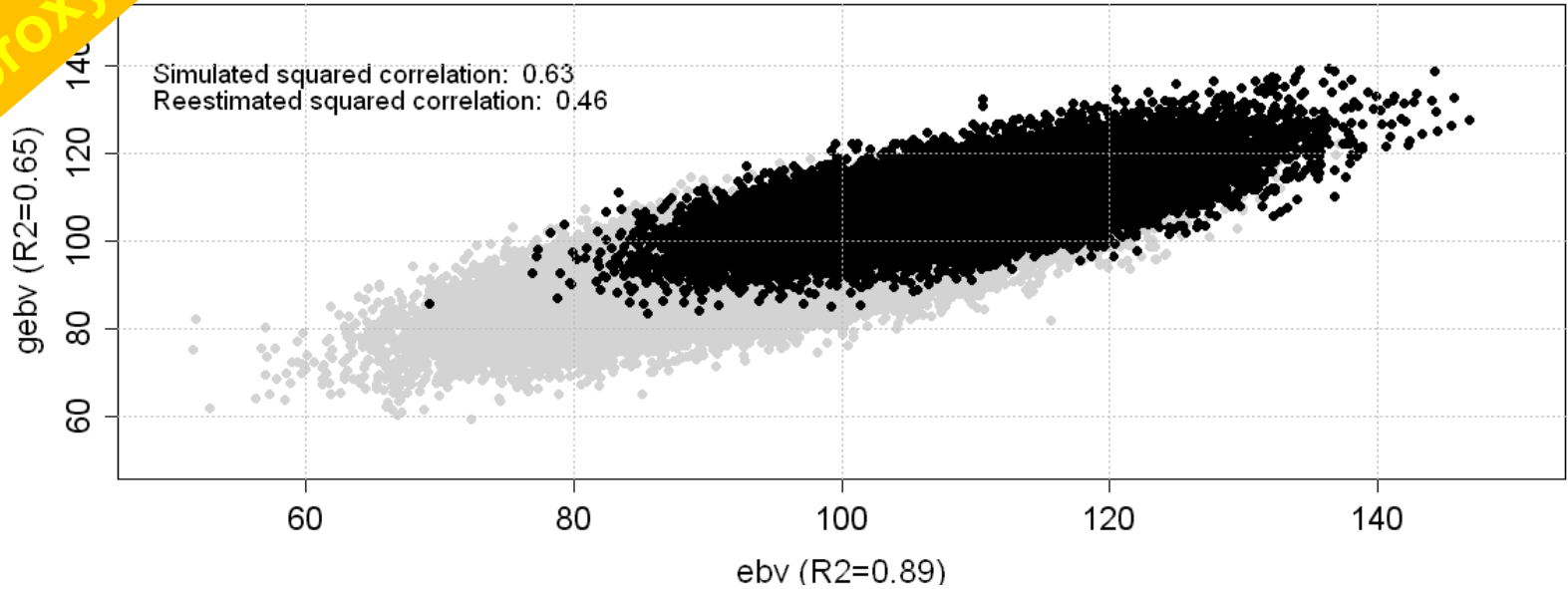
proxy



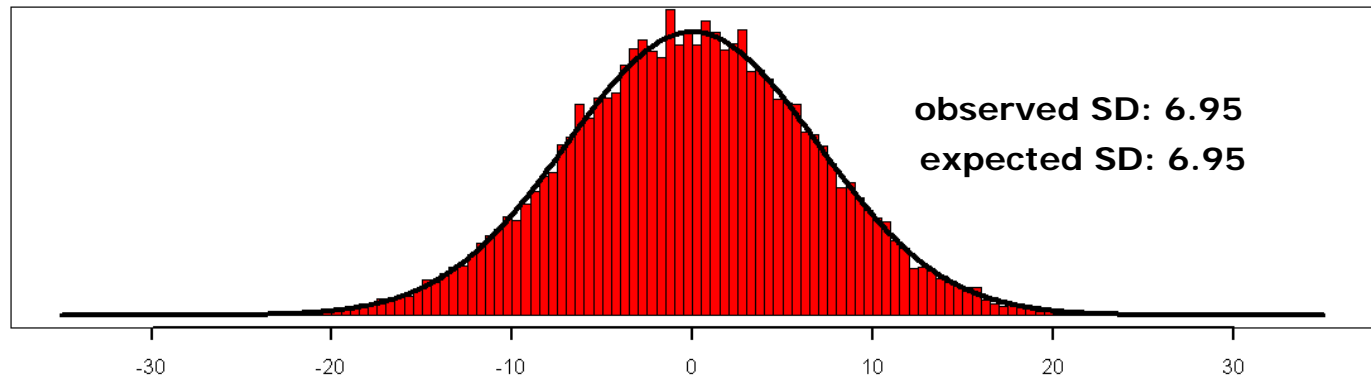
Illustration

proxy

Selection applied to correlated PA ($R^2=0.38$), $p = 0.25$



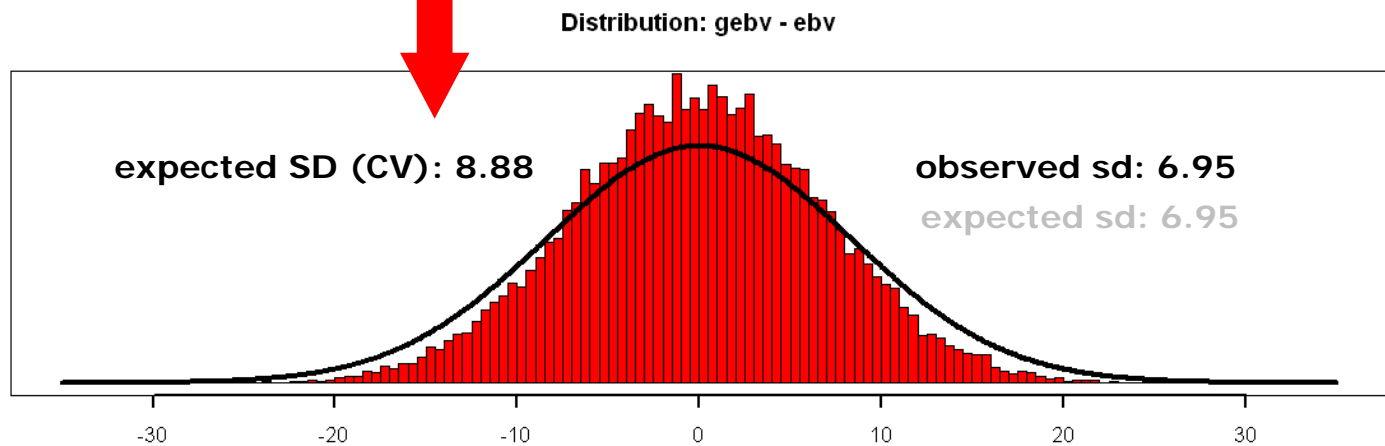
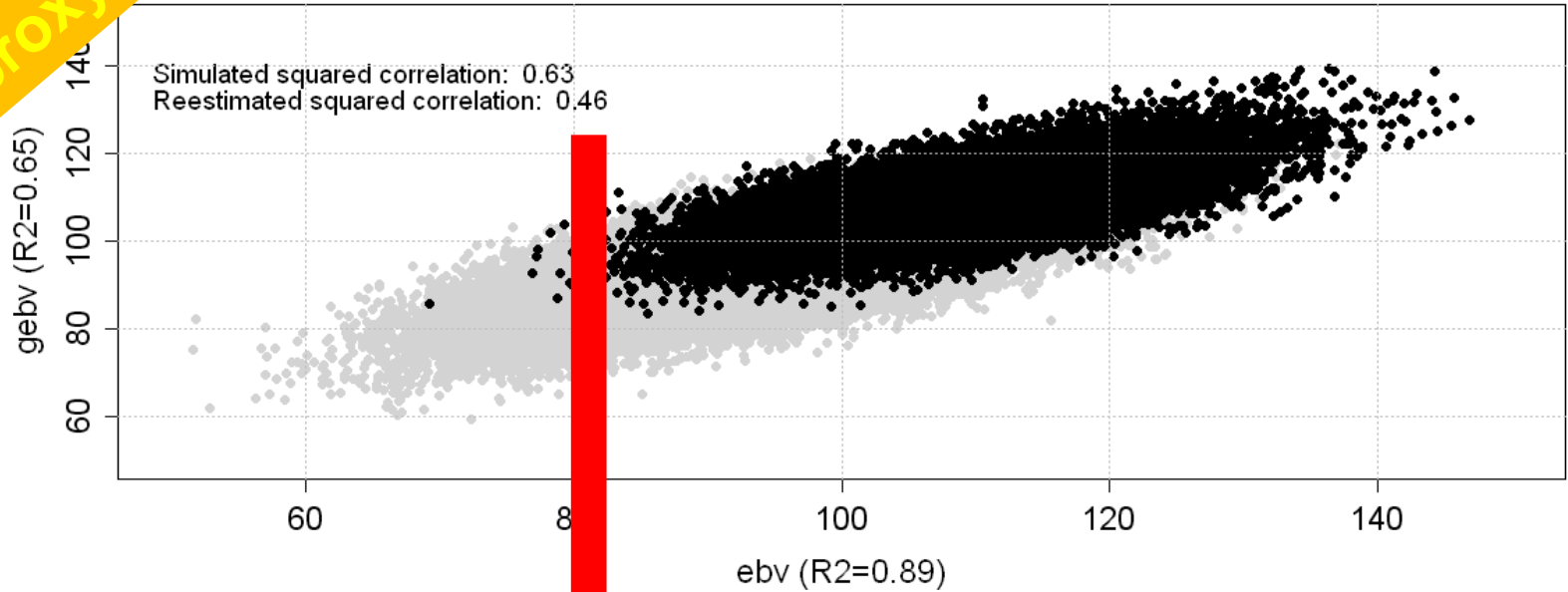
Distribution: gebv - ebv



Illustration

proxy

Selection applied to correlated PA ($R^2=0.38$), $p = 0.25$



Results

Table of expected values accounting for selection:

squared correlations and deviations

selection applied to	proportion selected (%)	$\rho^2_{\text{EBV_GEBV}}$	peSD proxy (GEBV-EBV) "observed"	peSD CV „expected“ from R^2 in CV
	100			
PA	25			
EBV	75			
PA/EBV	25/75			

Results

Table of expected values accounting for selection:

squared correlations and deviations

selection applied to	proportion selected (%)	$\rho^2_{\text{EBV_GEBV}}$	peSD proxy (GEBV-EBV) "observed"	peSD CV „expected“ from R^2 in CV
	100	0.63	6.95	6.95
PA	25	0.45	6.95	8.88
EBV	75	0.47	6.49	8.71
PA/EBV	25/75	0.33	6.24	9.86

Results

Table of expected values accounting for selection:

means

selection applied to	proportion selected (%)	Ø TBV	Ø PA	Ø GEBV	Ø EBV
	100	100	100	100	100
PA	25	109	109	109	109
EBV	75	105	102 ↔	103 ↔	105
PA/EBV	25/75	113	110 ↔	111 ↔	113

Results

Table of expected values accounting for selection:

intercepts and slopes

selection applied to	proportion selected (%)	$b0_{TBV_GEBV}$	$b1_{TBV_GEBV}$	$b0_{EBV_GEBV}$	$b1_{EBV_GEBV}$
	100	0.00	1.00	7.37	0.93
PA	25	0.00	1.00	14.48	0.87
EBV	75	21.87	0.80	32.61	0.70
PA/EBV	25/75	28.30	0.76	46.15	0.60

General Conclusions

- ❑ squared correlations derived from CV can be heavily influenced by effects of selection on validation sample
 - ◆ selected animals (preselection on PA, selective genotyping, etc.)
 - ◆ data selection (best animals, most reliable animals, etc.)
- ❑ effects of selection might be hard to characterize both in scope and nature
- ❑ conclusions from CV-correlations about true precision and bias of estimates might be limited

General Conclusions

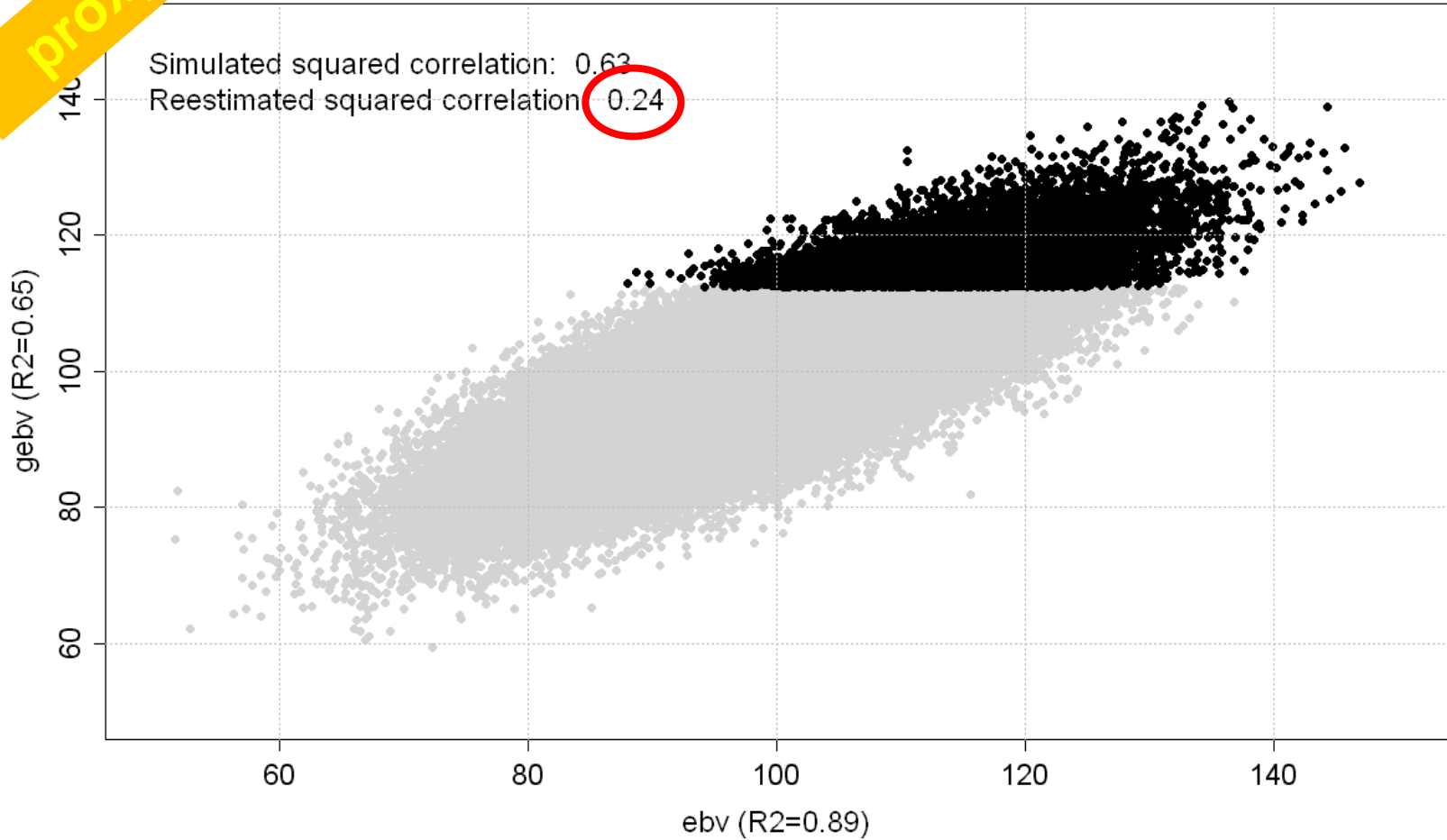
- distribution of differences (“peSD proxy”)
 - ◆ relatively robust: effects of selection are weak
 - ◆ could be a helpful extension to GEBV-test
- approach capable for calculation of “expected b_1 ” under selection
 - ◆ **using $b_1_{TBV_GEBV}$** : everything depends on deregression
 - ◆ **using $b_1_{EBV_GEBV}$** : tests simultaneously for coherence of estimates and assigned reliabilities

In the near future....

Perspectives

proxy

Selection applied to correlated GEBV ($R^2=0.65$) $p = 0.10$



Thank you for your attention