

Theoretical Accuracies

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Understanding Accuracy

- Prediction Accuracy
 - Validation
 - $\rho = COR(U, \hat{U})$
 - $\Delta G = i \rho \sigma_u / L$
 - Population
 - Very popular with genomics

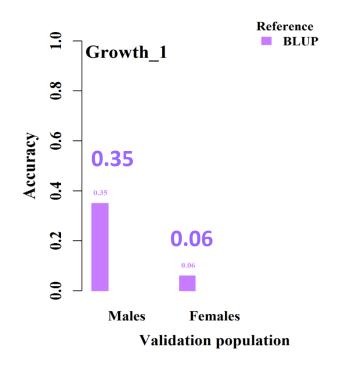
- Theoretical Accuracy
 - Precision of EBV
 - How much EBV changes
 - PEV = Diag(C^{ZZ+})

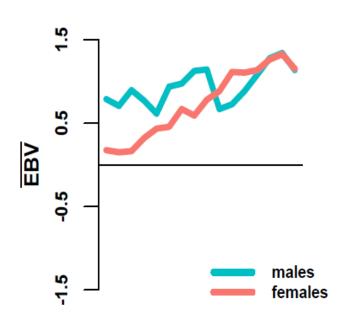
•
$$Acc = \sqrt{(1 - \frac{PEV}{\sigma_u^2})}$$

Individual

Understanding Accuracy

- Under selection
 - Theoretical accuracy ≠ Prediction accuracy
 - Theoretical is NOT affected by selection
 - Prediction is affected and varies if different i





- EBV are published with accuracy
 - "how much we can trust EBV"
 - amount of info used to calculate EBV

Diag(C^{ZZ+}) = PEV
$$\begin{bmatrix} x'x & x'z \\ z'x & Z'z+A^{-1}\lambda \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} x'y \\ z'y \end{bmatrix}$$
Records Pedigree

- Relies on the inverse of $Z'Z + A^{-1}\lambda$
- What if we have large datasets?
- Can we invert $z'z + A^{-1}\lambda$?

$$\operatorname{Diag(CZZ^{+)}_{ii}} = \frac{1}{(\lambda + d_i^r + d_i^p)}$$
 Ac

Accuracy_i =
$$\sqrt{1 - Diag(CZZ^+)_{ii}}$$

- d_i^r and d_i^p are approximated (Misztal and Wiggans, 1988)
- Implemented in accf90

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If (small data) then
use blupf90 to get PEV
else
use approximation
```

What if we have genomic data?

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If (small data) then
  use blupf90 to get PEV
else
  use approximation
```

Which approximation?

Approx. accuracy from ssGBLUP - Misztal et al. (2013)

$$\begin{bmatrix} x'x & x'z \\ z'x & z'z+H^{-1}\lambda \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} x'y \\ z'y \end{bmatrix}$$

$$\begin{cases}
\mathbf{Z}'\mathbf{Z} + \lambda \mathbf{A}^{-1} + \lambda \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix} \end{cases}$$
How to approximate the diagram of the property of the property

How to approximate d_i^g ?

$$Diag(CZZ^{+)}_{ii} = \frac{1}{(\lambda + d_i^r + d_i^p + d_i^g)}$$

• Misztal et al. (2013) – Method 1

$$\mathbf{Diag(CZZ^+)_{ii}} \quad \approx \left\{ \left[\mathbf{D}_i^r + \mathbf{D}_i^p + \left(\mathbf{I} + \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \right) \mathbf{\alpha} \right]^{-1} \right\}_{ii}$$

Problem: G^{-1} and A_{22}^{-1}

• Misztal et al. (2013) - Method 2

$$\mathsf{Diag}(\mathsf{CZZ}^+)_{ii} \approx \left\{ \mathbf{D} + \left[\mathbf{I} + \mathrm{diag} \left(\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \right) \right] \alpha \right\}^{-1}$$

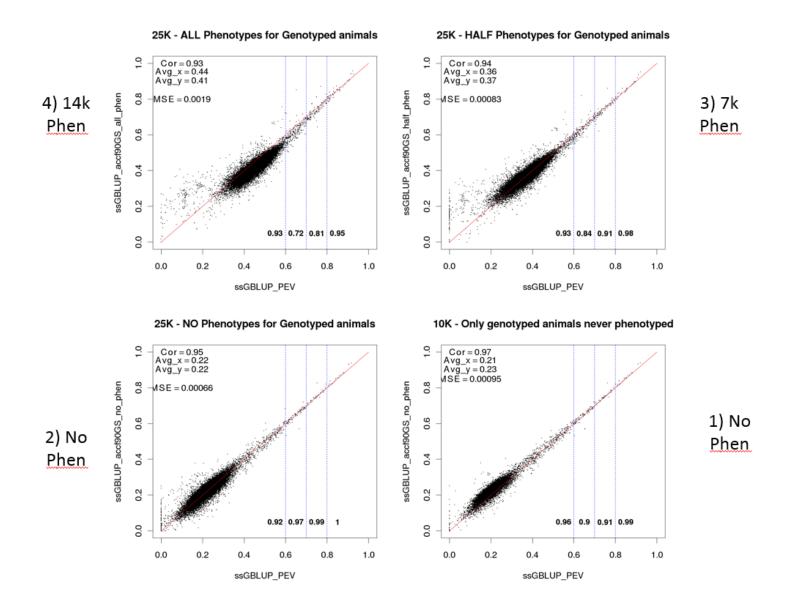
Implemented in accf90GS

Problem: A_{22}^{-1} in APY

Lourenco et al.; Tsuruta et al. (2016)

$$d_i^g = var_ratio *[\overline{Rel} + (1 - g_{ii}) + zeta * \overline{Rel - Rel_{PA}}]$$

- Implemented in accf90GS
- Used for commercial evaluations in the US
- Problem: COR(true,approx.) < 0.90 depending on the data
- Problem: genomic contribution relies on genotyping strategy



- Approximating accuracies of GEBV is still an unsolved issue
- True for all software
- Several approximations and tricks proposed and applied
- Approximation in accf90GS works, but...
- Need more accurate algorithm

Ideas

- Liu et al. (2017)
 - Based on SNP BLUP

$$\mathbf{C}^{-1} = \begin{bmatrix} \mathbf{C}^{\mu\mu} & \mathbf{C}^{\mu g} \\ \mathbf{C}^{g\mu} & \mathbf{C}^{gg} \end{bmatrix}$$

Reliability of DGV

$$\Re_{i}^{SNP} = 1 - \mathbf{z}_{i} \mathbf{C}^{gg} \mathbf{z}_{i}' \boldsymbol{\sigma}_{u}^{-2}$$

- ABGG_UGA (2018-2019)
 - Based on G_{APY}^{-1} and YAMS
 - Solving this issue = high impact research