

# Effect of blending and tuning relationship matrices in single-step genomic BLUP

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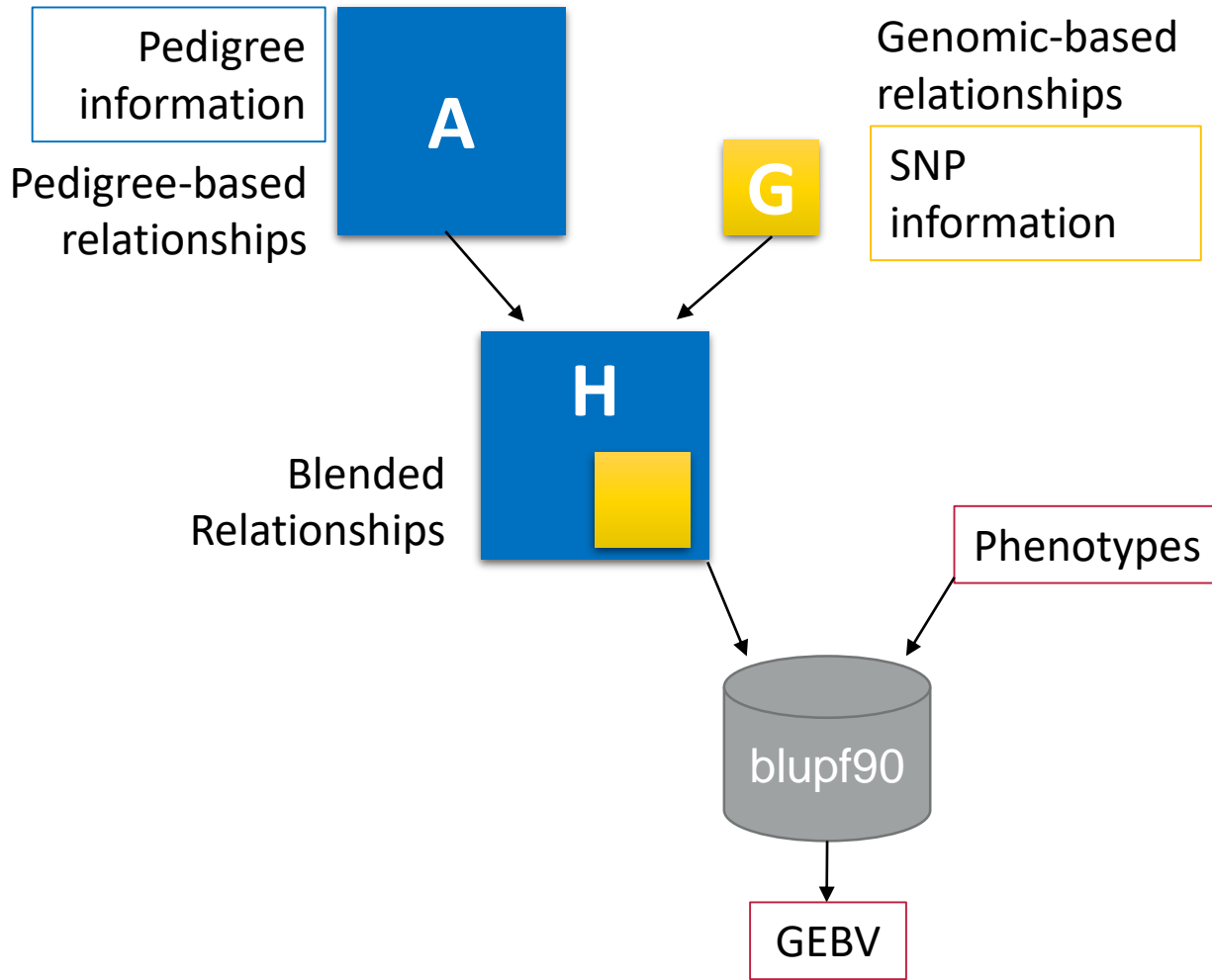
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# Introduction: ssGBLUP



Matrix Notation:

$$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \mathbf{H}^{-1}\lambda \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\boldsymbol{\mu}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{bmatrix}$$

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

↑

# Introduction: $H^{-1}$ construction

**Problem 1:** singularity of  $G$

**Solution:** blending (VanRaden, 2008)

- procedure in which a weighted sum of  $G$  and a positive-definite matrix is used

$$G^* = (1 - \beta)G + \beta A_{22} \quad \text{where } 0 < \beta < 1$$

**Problem 2:** differences in the genetic base between  $G$  and  $A_{22}$

**Solution:** tuning by scaling  $G$  to  $A_{22}$

- multiplying and adding constants obtained from  $A_{22}$  to  $G$ 
  - **Chen et al. (2011):** adjusts mean diagonals and off-diagonals of  $G$  to be similar to  $A_{22}$
  - **Vitezica et al. (2011):** adjusts based on the fixation index



# Introduction: opportunity

- In BLUPF90 software, blending is currently done before tuning
  - Why?
    - Solution for singularity of  $\mathbf{G}$  appeared before solution for the difference in genetic base between  $\mathbf{G}$  and  $\mathbf{A}_{22}$
- Current order of blending  $\mathbf{G}$  before tuning may add bias to GEBV as blended  $\mathbf{G}$  contains a portion of  $\mathbf{A}_{22}$



# Objectives

- Main objectives:
  - Investigate impact of order of blending and tuning
  - Assess this impact on predictivity, bias, and inflation of GEBV from ssGBLUP
- Secondary objectives:
  - Assess the changes of indirect predictions (IP)

# Materials & methods: data

## American Angus Association

3-trait model: **BW, WW, PWG**

**Pedigree:** 8.2 m animals

**Phenotypes:**

BW: 6.2 m records

WW: 6.9 m records

PWG: 3.4 m records

**Genotypes:** 51,478 animals (50k SNP)

**Validation:** 19,056 animals

## Holstein Association USA

Single-trait model: Udder depth (**UD**)

**Pedigree:** 8.3 m animals

**Phenotypes:**

UD: 9.2 m records

**Genotypes:** 105,116 animals (60k SNP)

**Validation:** 1,711 bulls



# Materials & methods: $H^{-1}$ construction

## BlendFirst\_TunedGc

Blend First

Tune G based on **Chen et al. (2011)**

## TuneFirst\_TunedGc

Tune First

Tune G based on **Chen et al. (2011)**

## BlendFirst\_TunedGv

Blend First

Tune G based on **Vitezica et al. (2011)**

## TuneFirst\_TunedGv

Tune First

Tune G based on **Vitezica et al. (2011)**



# Materials & methods: validation method

- Linear regression method (LR; Legarra and Reverter, 2018) using complete (c) and reduced (r) datasets

- Accuracy: 
$$\rho_{c,r} = \sqrt{\frac{\text{cov}(\hat{\mathbf{u}}_c, \hat{\mathbf{u}}_r)}{(1 - \bar{F})\sigma_u^2}}$$

- Bias as deviation from 0: 
$$\mu_{cr} = \overline{\hat{\mathbf{u}}_r} - \overline{\hat{\mathbf{u}}_c}$$

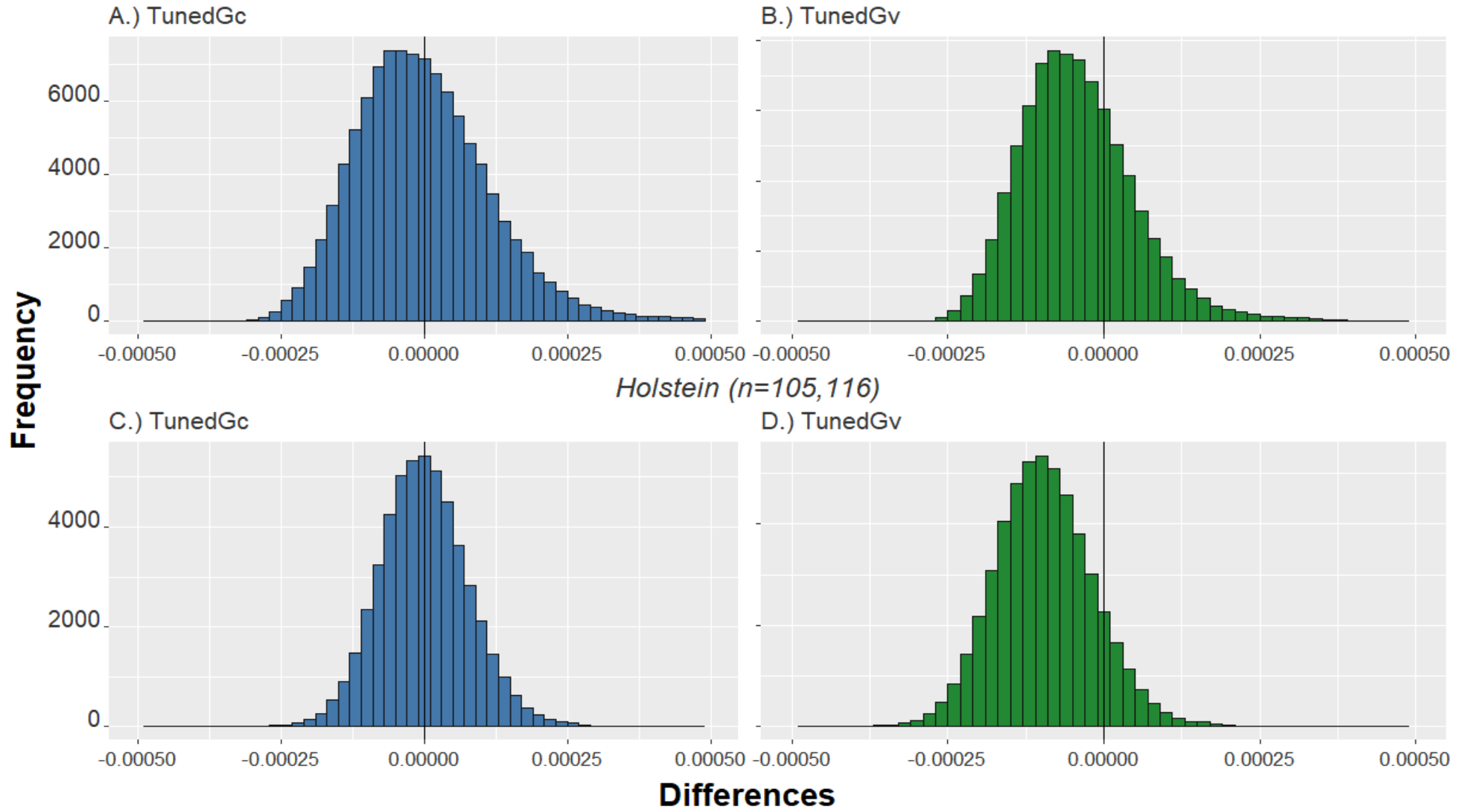
- Dispersion as deviation of regression coefficient ( $b_1$ ) from 1: 
$$\hat{\mathbf{u}}_c = b_0 + b_1 \hat{\mathbf{u}}_r$$



# Results

## Differences in Diagonal Elements of G matrices

Angus (n=51,478)



# Results: LR validation statistics

- Accuracy, bias, and dispersion were similar for all scenarios within a trait
- Max. change between BF and TF
  - Accuracy: 0.0003
  - Bias: 0.0068
  - Dispersion: 0.0003

## Traits

**Angus:** BW, WW, PWG

**Holstein:** UD

## Scenarios

BlendFirst\_TunedGc

TuneFirst\_TunedGc

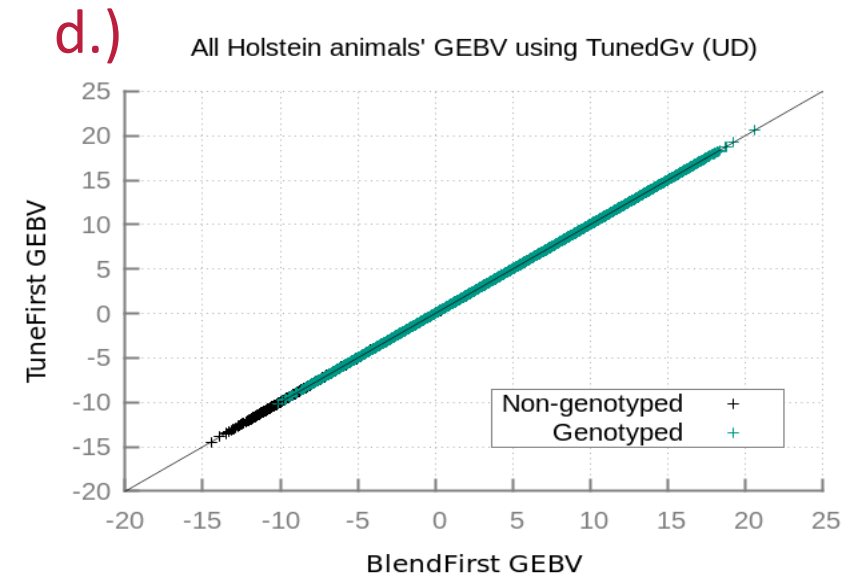
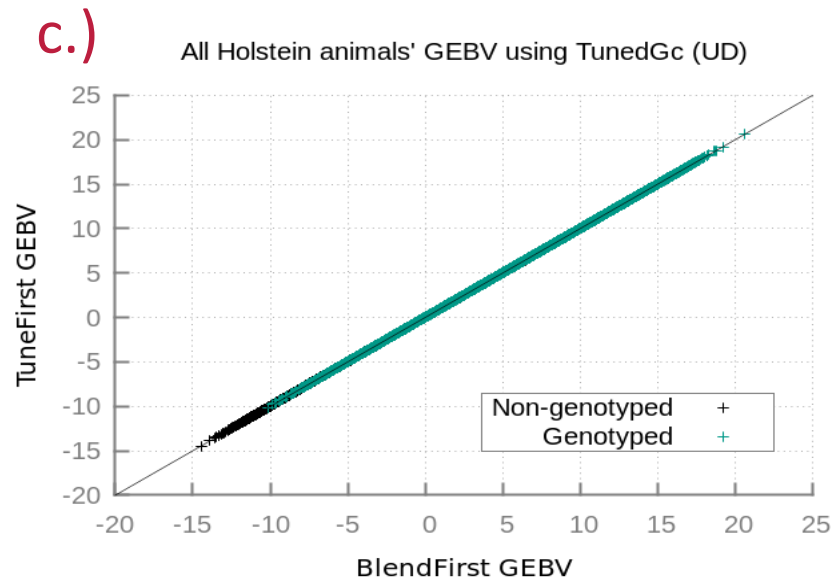
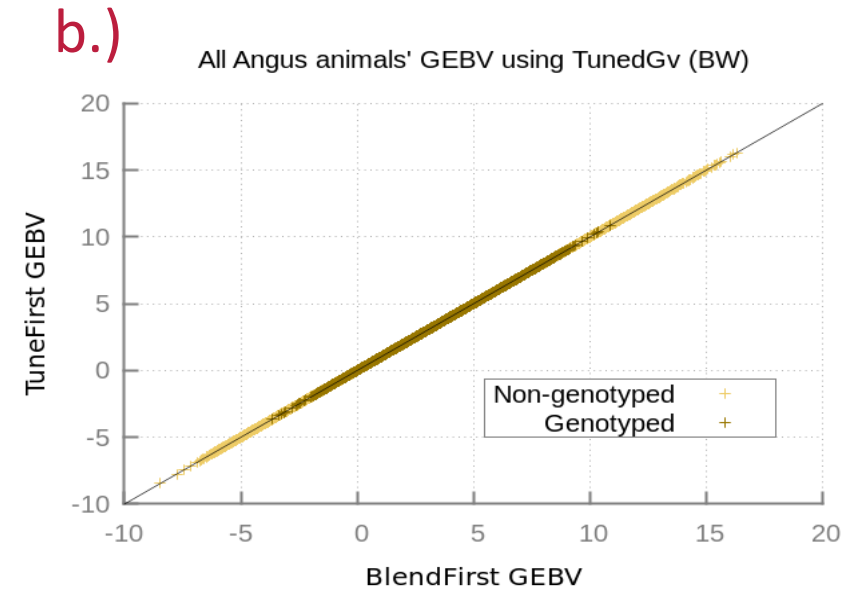
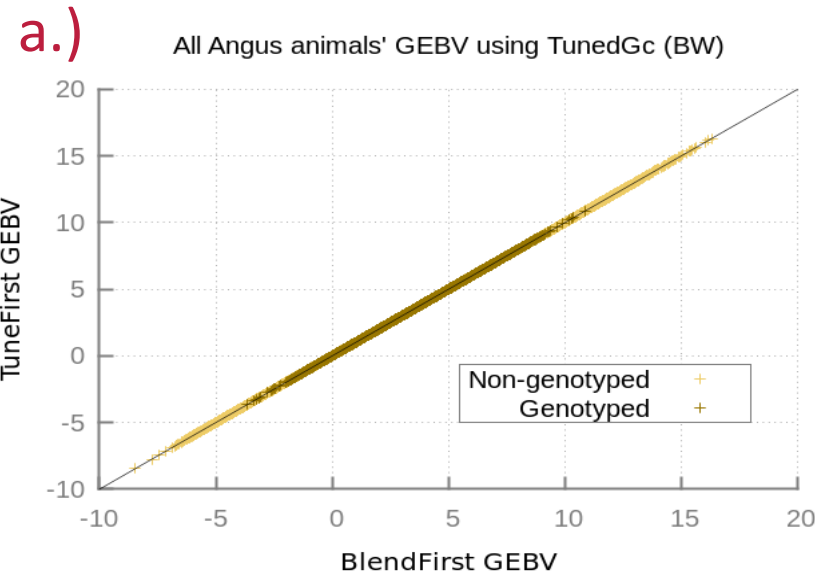
BlendFirst\_TunedGv

TuneFirst\_TunedGv

# Results

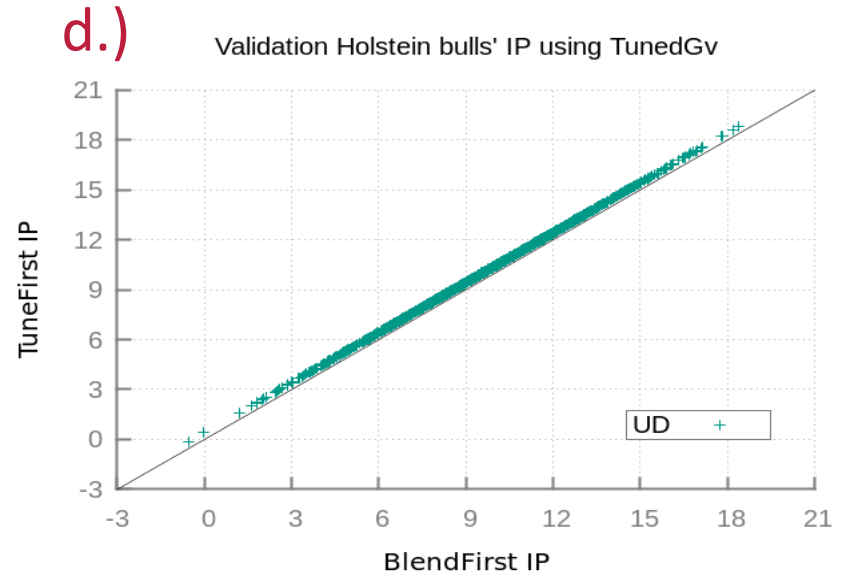
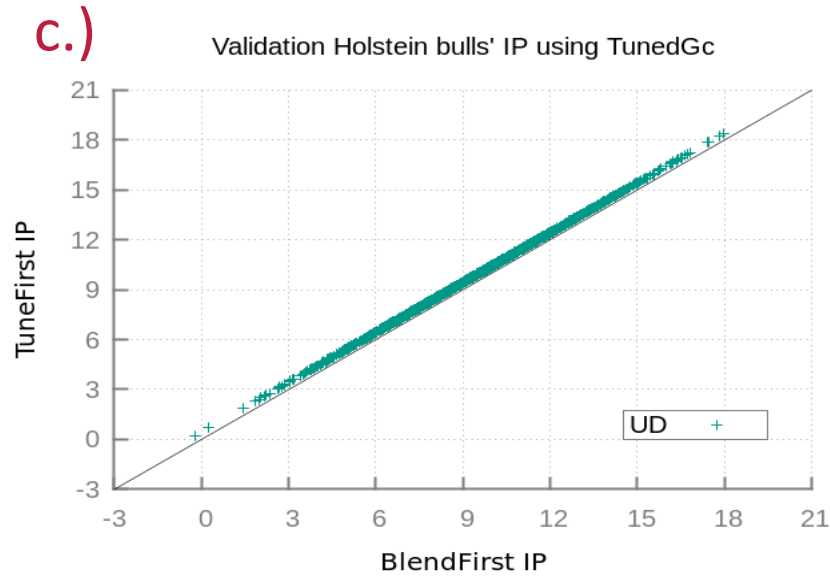
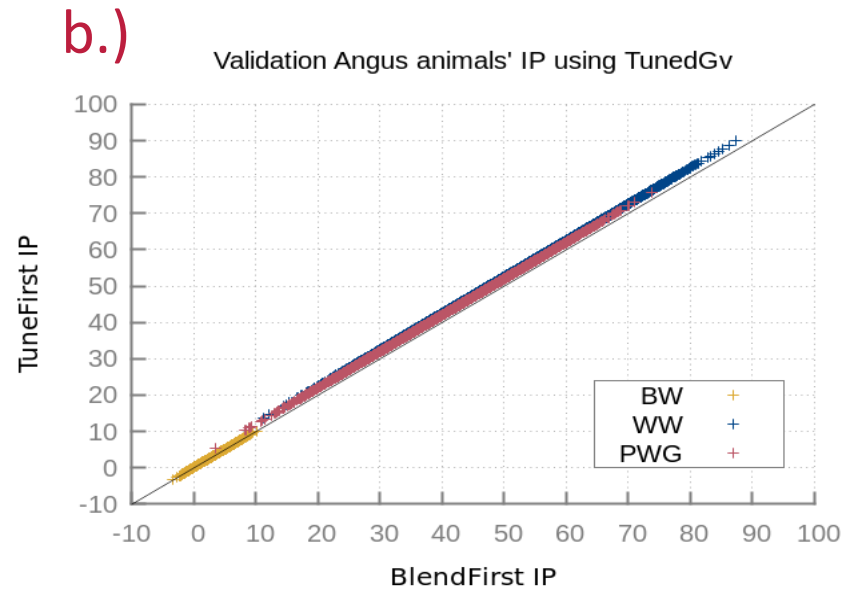
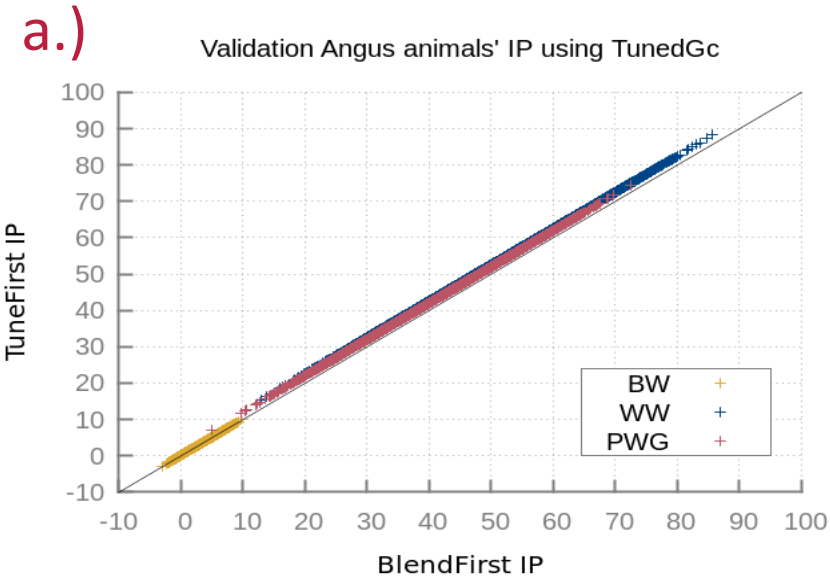
GEBV

All animals



# Results

Indirect prediction  
Validation animals



# Conclusions

- IP can be slightly more variable because they are a linear function of  $\mathbf{G}^{-1}$
- All scenarios are equally able to provide predictions that are accurate, unbiased, and neither over- nor under-dispersed
- Tuning before blending is theoretically more robust
  - This order of computations will be implemented in the BLUPF90 software suite for ssGBLUP models

# Acknowledgements

- Co-authors



André  
Garcia



Matias  
Bermann



Andrés  
Legarra



Ignacio  
Aguilar



Ignacy  
Misztal



Daniela  
Lourenco

- American Angus Association



- Holstein Association USA, Inc.



**Thank you.**