THEORETICAL BASIS TO EXTEND SINGLE-STEP GENOMIC PREDICTION OF DOMINANCE IN A PIG POPULATION
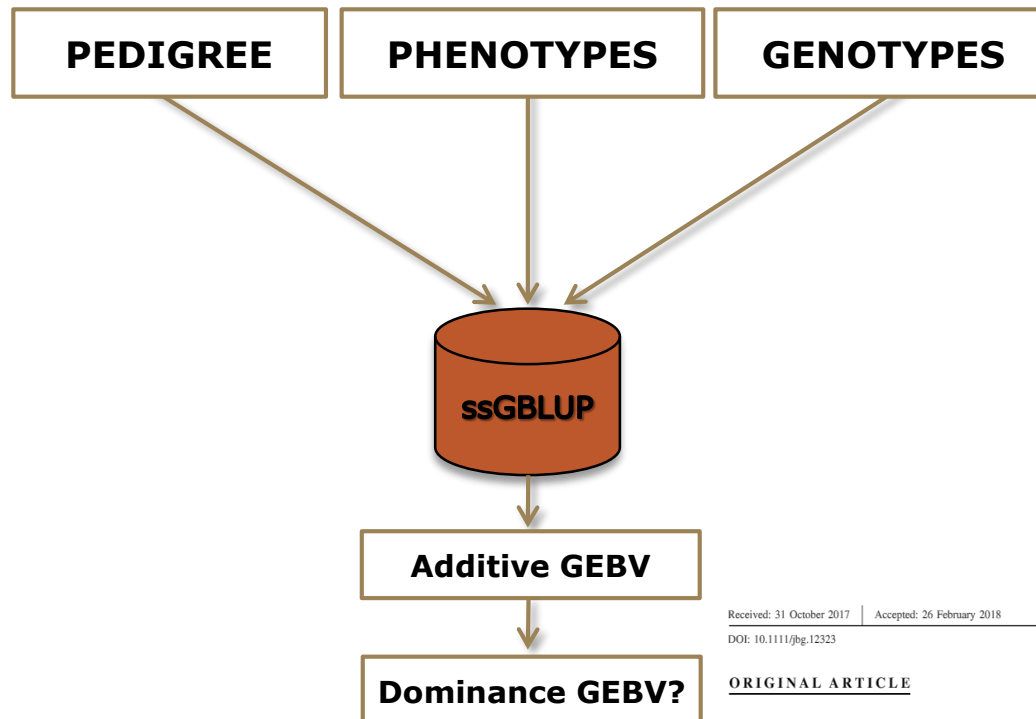
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SINGLE-STEP OVERVIEW

PEDIGREE   PHENOTYPES   GENOTYPES

ssGBLUP

Additive GEBV

Dominance GEBV?

Considering dominance in reduced single-step genomic evaluations

J. Ertl | C. Edel | E.C.G. Pimentel | R. Emmerling | K.-U. Götz

OBJECTIVE

- Theoretical basis illustration – extension and validation

- Strategy to account for inbreeding

Christensen and Lund (2010)

Vitezica et al. (2013)

THEORETICAL BASIS - EXTENSION

$$g = Hu$$

g = individual dominance deviations

H = matrix of heterozygosity coefficients

u = vector of dominance values

if AA, $-2q^2$

if AB, $2pq$

if BB, $-2p^2$

Vitezica et al. (2013)

THEORETICAL BASIS - EXTENSION

$$G = HH^{\mathsf{T}} / \sum_{i=1}^{m} (2p_i q_i)^2$$

$$H = \begin{bmatrix} H^g \\ H^{ng} \end{bmatrix}$$

Christensen and Lund (2010)
Vitezica et al (2013)

THEORETICAL BASIS - EXTENSION

- ✓ Unknown heterozygosity coefficients

- ✓ Additive effects analogy (Gengler et al., 2008; Fernando et al., 2014)

$$\hat{\mathbf{g}}^{g} = \mathbf{H}^{g}\hat{\mathbf{u}} \text{ (and } \hat{\mathbf{g}}^{ng} = \mathbf{H}^{ng}\hat{\mathbf{u}})$$

$$\hat{\mathbf{g}}^{ng} = \mathbf{D}_{ng,g}\mathbf{D}_{g}^{-1}\hat{\mathbf{g}}^{g}$$

$$\hat{\mathbf{g}}^{ng} = \mathbf{D}_{ng,g}\mathbf{D}_{g}^{-1}\mathbf{H}^{g}\hat{\mathbf{u}}$$

$$E[\mathbf{H}^{ng}|\mathbf{H}^{g}] = \mathbf{D}_{ng,g}\mathbf{D}_{g}^{-1}\mathbf{H}^{g}$$

Christensen and Lund (2010)

THEORETICAL BASIS – EXTENSION

$$G^* = \begin{bmatrix} G & GD_g^{-1}D_{g,ng} \\ D_{ng,g}D_g^{-1}G & D_{ng,g}D_g^{-1}GD_g^{-1}D_{g,ng} + D_{ng} - D_{ng,g}D_g^{-1}D_{g,ng} \end{bmatrix}$$
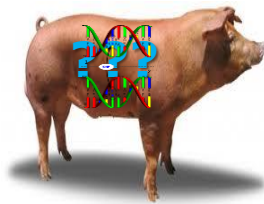
ORIGINAL ARTICLE

WILEY *Journal of Animal Breeding and Genetics*

Considering dominance in reduced single-step genomic evaluations
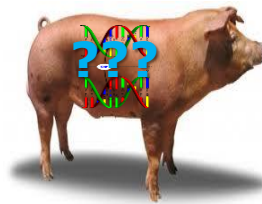
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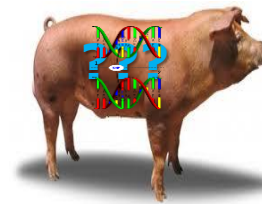
Christensen and Lund (2010)

NUMERICAL EXAMPLE

full sibs

$$\mathbf{D} = \begin{bmatrix} 1.0000000 & 0.2500000 & 0.2500000 \\ 0.2500000 & 1.000000 & 0.2500000 \\ 0.2500000 & 0.2500000 & 1.0000000 \end{bmatrix} \quad \mathbf{G} = \begin{bmatrix} 1.1380922 & 0.2561112 & 0.2970772 \\ 0.2561112 & 1.1335810 & 0.2763618 \\ 0.2970772 & 0.2763618 & 1.1304518 \end{bmatrix}$$

$$\mathbf{G}^* = \begin{bmatrix} \mathbf{G} & \mathbf{G}\mathbf{D}_g^{-1}\mathbf{D}_{g,ng} \\ \mathbf{D}_{ng,g}\mathbf{D}_g^{-1}\mathbf{G} & \mathbf{D}_{ng,g}\mathbf{D}_g^{-1}\mathbf{G}\mathbf{D}_g^{-1}\mathbf{D}_{g,ng} + \mathbf{D}_{ng} - \mathbf{D}_{ng,g}\mathbf{D}_g^{-1}\mathbf{D}_{g,ng} \end{bmatrix} = \begin{bmatrix} 1.1380922 & 0.2561112 & 0.2666194 \\ 0.2561112 & 1.1335810 & 0.2524342 \\ 0.2666194 & 0.2524342 & 1.0024342 \end{bmatrix}$$
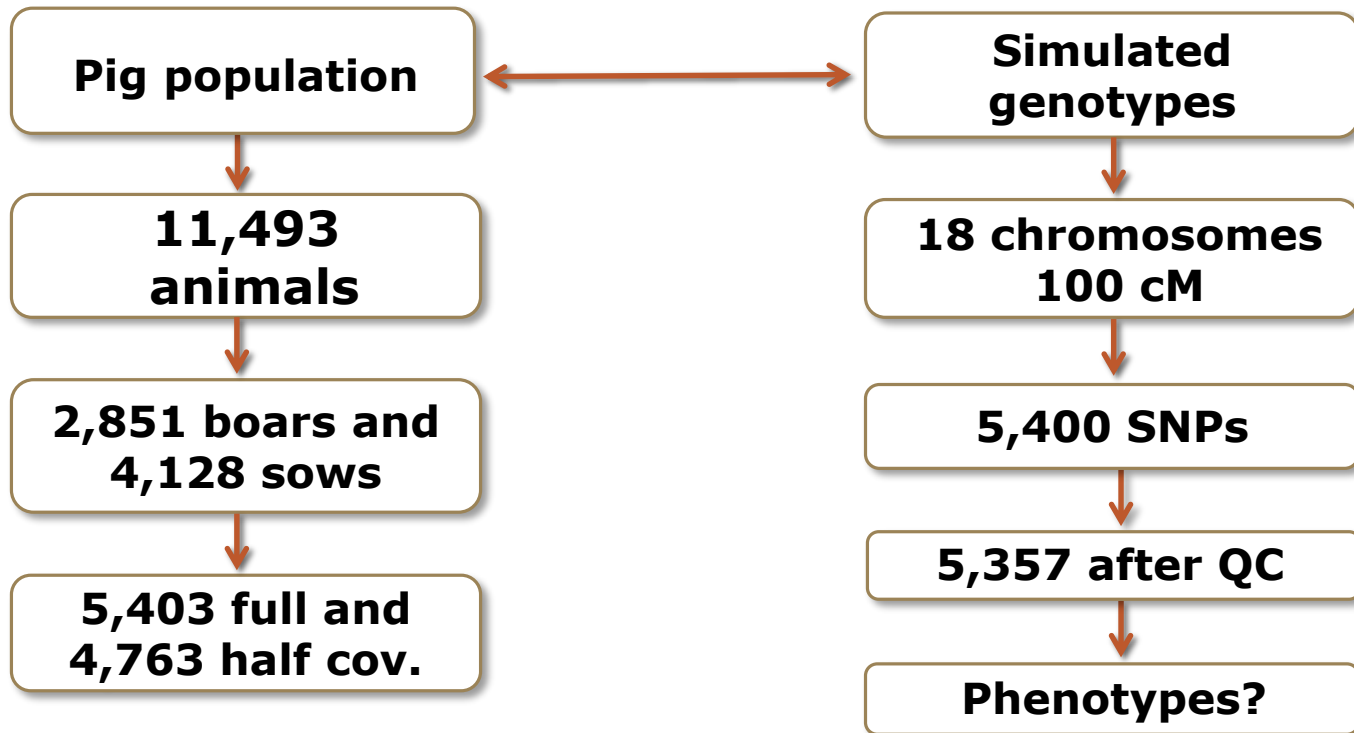
INBREEDING?

MATRIX STANDARDIZATION

$G^{*}x$	D	G
$G^{*}1$	St_0	St_0
$G^{*}2$	St_1	St_1

St_0 = no standardization – Cockerham (1954) - **D** and Vitezica et al. (2013) - **G**

St_1 = diagonal standardization by replacing the diagonal elements by 1-F, being F the inbreeding coefficient – Ovaskainen et al. (2008)

THEORETICAL BASIS – VALIDATION

Pig population	↔	Simulated genotypes
↓		↓
11,493 animals		18 chromosomes 100 cM
↓		↓
2,851 boars and 4,128 sows		5,400 SNPs
↓		↓
5,403 full and 4,763 half cov.		5,357 after QC
		↓
		Phenotypes?

THEORETICAL BASIS – VALIDATION

✓ Additive effects assumed to be inexistent

✓ Equal dominance effects for all SNPs ➔ true dominance deviations

✓ True dominance deviations + random noise ➔ phenotypes
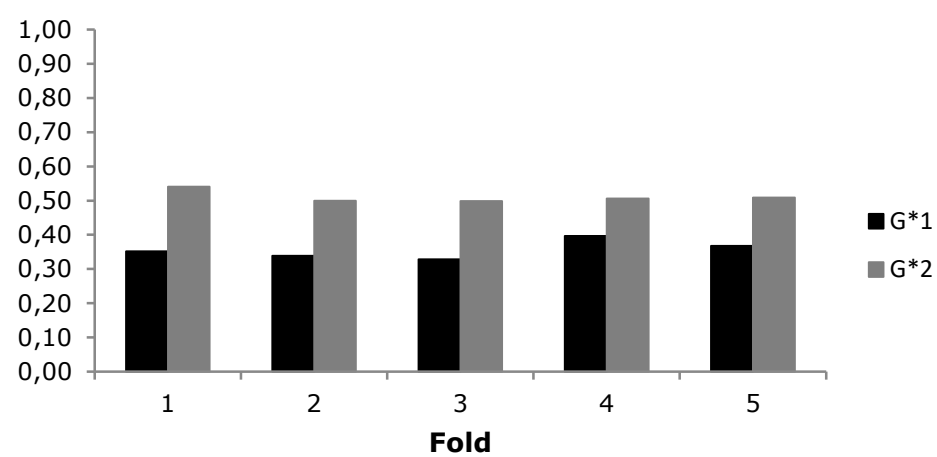
THEORETICAL BASIS – VALIDATION

- ✓ 5-fold cross validation ➔ random partitioning $(80\%_g / 20\%_{ng})$

- ✓ Accuracy ➔ correlation (true, predicted dominance deviations)
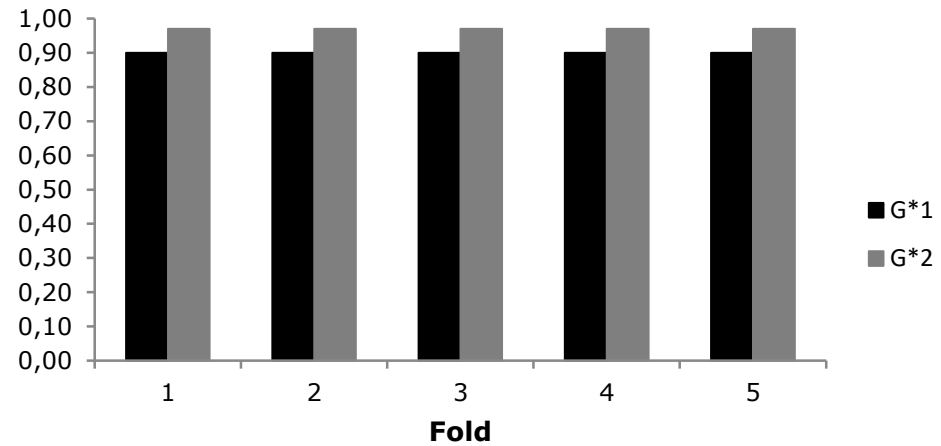
20% ng if inbred

- ✓ Bias ➔ regression true/predicted dominance deviations

RESULTS

Accuracy

Bias

TAKE HOME MESSAGES

✓ Dominance deviation for non-genotyped animals ➔ dominance ssGBLUP

✓ Better predictions by re-scaling **D** and **G** via **G*2**

ACKNOWLEDGMENTS

GENODOMICS project

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