# Unknown-parent groups and incomplete pedigrees in single-step genomic evaluation

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# Introduction

- ssGBLUP - single-step genomic BLUP
  - Replaces $A^{-1}$ with $H^{-1}$ matrix
  - Any model
  - Efficient implementation (BLUPF90 package)
- Many applications at UGA or using UGA software
- In comparisons usually most accurate
  - No approximations with DYD or DP
  - Parental index included automatically
  - Simpler

# Problems

- Biases and convergence problems in some data sets using unknown parent groups (UPG)
- Convergence problems with complicated data sets – better with weight on $A_{22}^{-1}$

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - 0.7A_{22}^{-1} \end{bmatrix}$$

# Unknown parent groups (Westell et al., 1987)

$$\mathbf{y} = .. + \mathbf{ZQg} + \mathbf{Za} + \mathbf{e}$$

g – unknown parent group effect
a –animal effect
Q –matrix relating animals to UPG
Z – matrix relating records to animals

$$\begin{bmatrix} \mathbf{Z'Z+A^{-1}} & \mathbf{Z'ZQ} \\ \mathbf{-Q'Z'Z} & \mathbf{Z'Q'QZ} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{a}} \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{Z'y} \\ \mathbf{(ZQ)'y} \end{bmatrix}$$

BLUP with unknown parent groups after QP transformation (Quaas, 1988)

$$\mathbf{y} = .. + \mathbf{Zu} + \mathbf{e}, \qquad \mathbf{u} = \mathbf{Qg} + \mathbf{a}$$

$$\begin{bmatrix} Z'Z+A^{-1} & -A^{-1}Q \\ -Q'A^{-1} & Q'A^{-1}Q \end{bmatrix} \begin{bmatrix} \hat{u} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} Z'y \\ 0 \end{bmatrix}$$

$$\begin{bmatrix} A^{-1} & -A^{-1}Q \\ -Q'A^{-1} & Q'A^{-1}Q \end{bmatrix}$$

easy to create from pedigree

# Unknown parent groups in single-step GBLUP

$$\begin{bmatrix} \mathbf{Z}'\mathbf{Z}+\mathbf{H}^{-1} & -\mathbf{H}^{-1}\mathbf{Q} \\ -\mathbf{Q}'\mathbf{H}^{-1} & \mathbf{Q}'\mathbf{H}^{-1}\mathbf{Q} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{u}} \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{Z}'\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$

$$\begin{bmatrix} \mathbf{Z}'\mathbf{Z}+\mathbf{H}^{-1} & -\left(\mathbf{A}^{-1}+\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1}-\mathbf{A}_{22}^{-1} \end{bmatrix}\right)\mathbf{Q} \\ -\mathbf{Q}'\left(\mathbf{A}^{-1}+\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1}-\mathbf{A}_{22}^{-1} \end{bmatrix}\right) & \mathbf{Q}'\left(\mathbf{A}^{-1}+\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1}-\mathbf{A}_{22}^{-1} \end{bmatrix}\right)\mathbf{Q} \end{bmatrix} \rightarrow$$

LHS

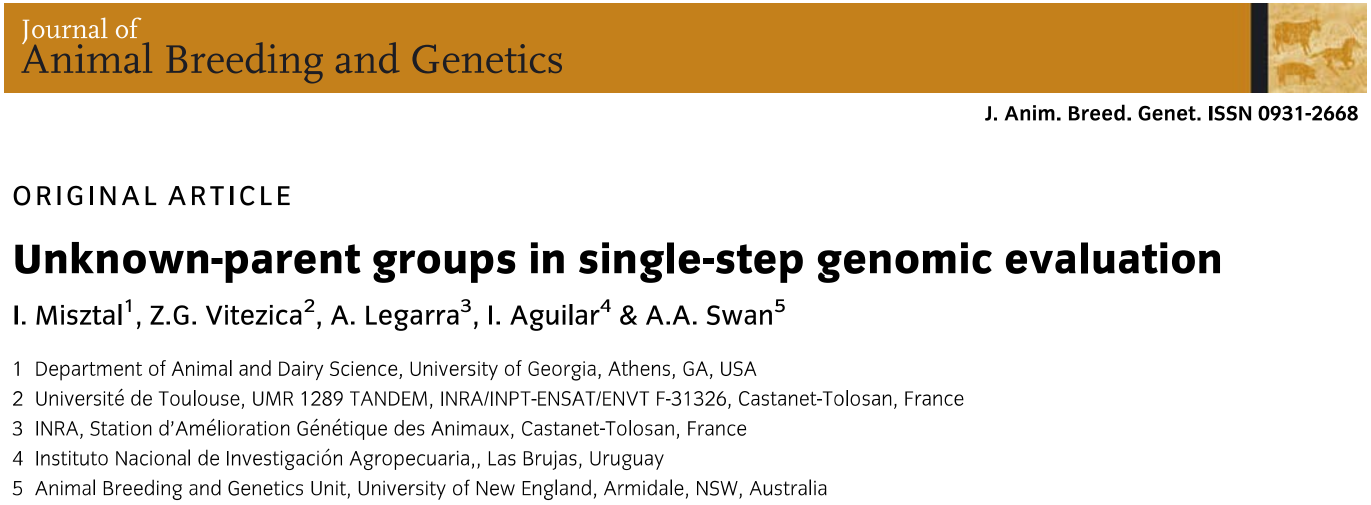
$$\begin{bmatrix} \mathbf{Z}'\mathbf{Z}+\mathbf{H}^{-1} & -\mathbf{A}^{-1}\mathbf{Q} \\ -\mathbf{Q}'\mathbf{A}^{-1} & \mathbf{Q}'\mathbf{A}^{-1}\mathbf{Q} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{u}} \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{Z}'\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$

Approximation

# Why unknown parent groups

- Different line
- Different breed (Harris and Johnson, 2012)

- Unrecorded parents across generations



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**Unknown-parent groups in single-step genomic evaluation**

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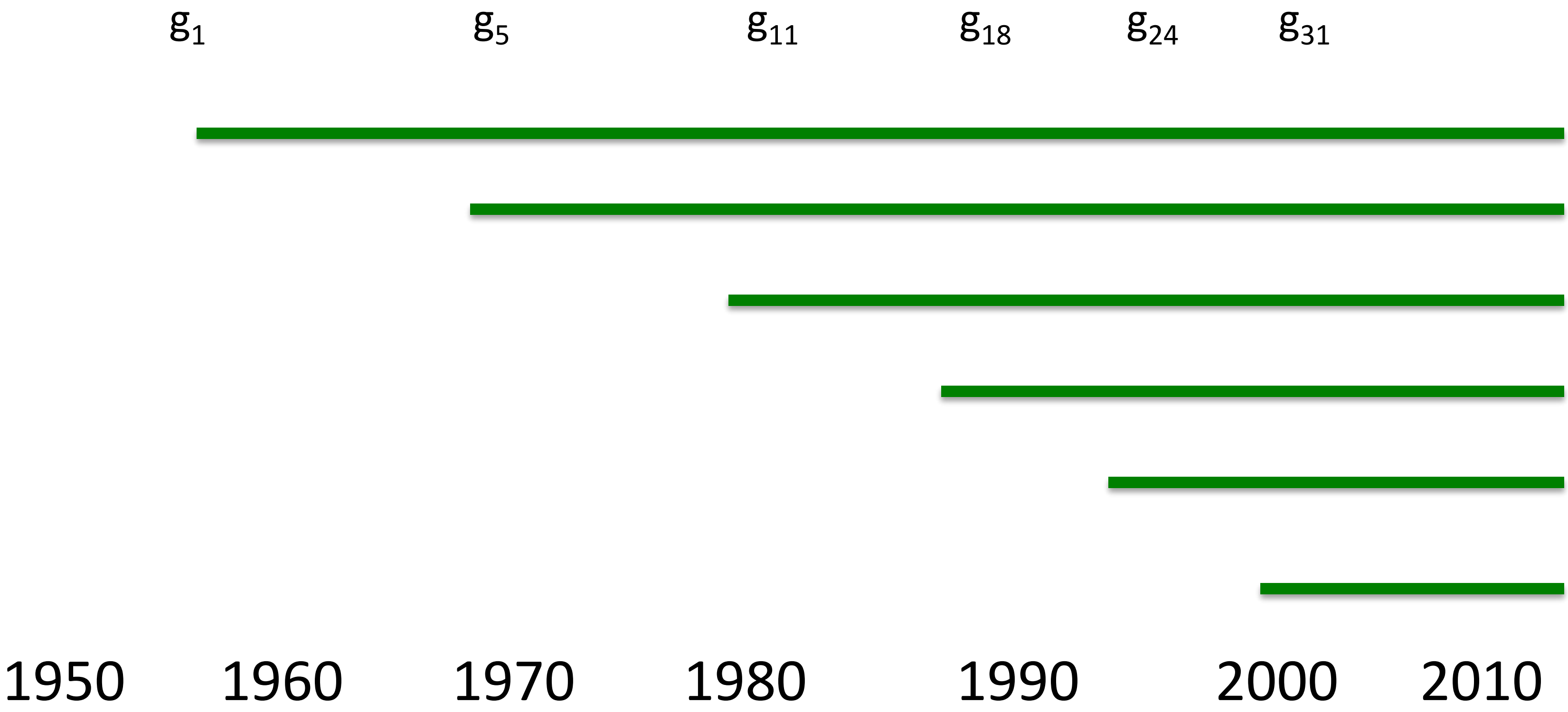
# Pedigree depth for young animals

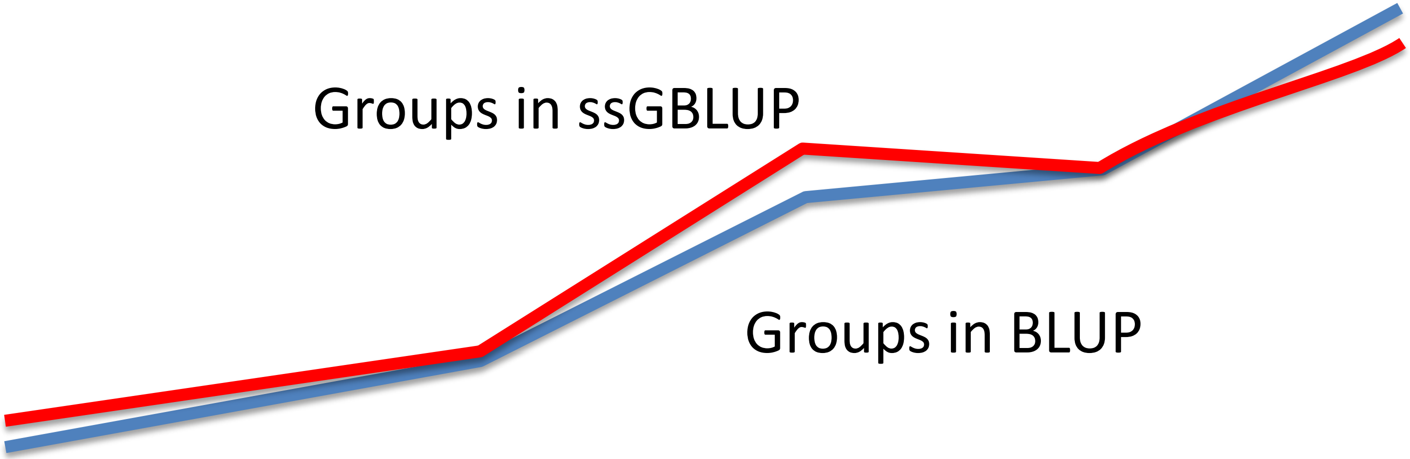


# Choices – add equations

$$\begin{bmatrix} 0 & -\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1}-\mathbf{A}_{22}^{-1} \end{bmatrix}\mathbf{Q} \\ -\mathbf{Q}'\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1}-\mathbf{A}_{22}^{-1} \end{bmatrix} & \mathbf{Q}'\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1}-\mathbf{A}_{22}^{-1} \end{bmatrix}\mathbf{Q} \end{bmatrix}$$

Complicated

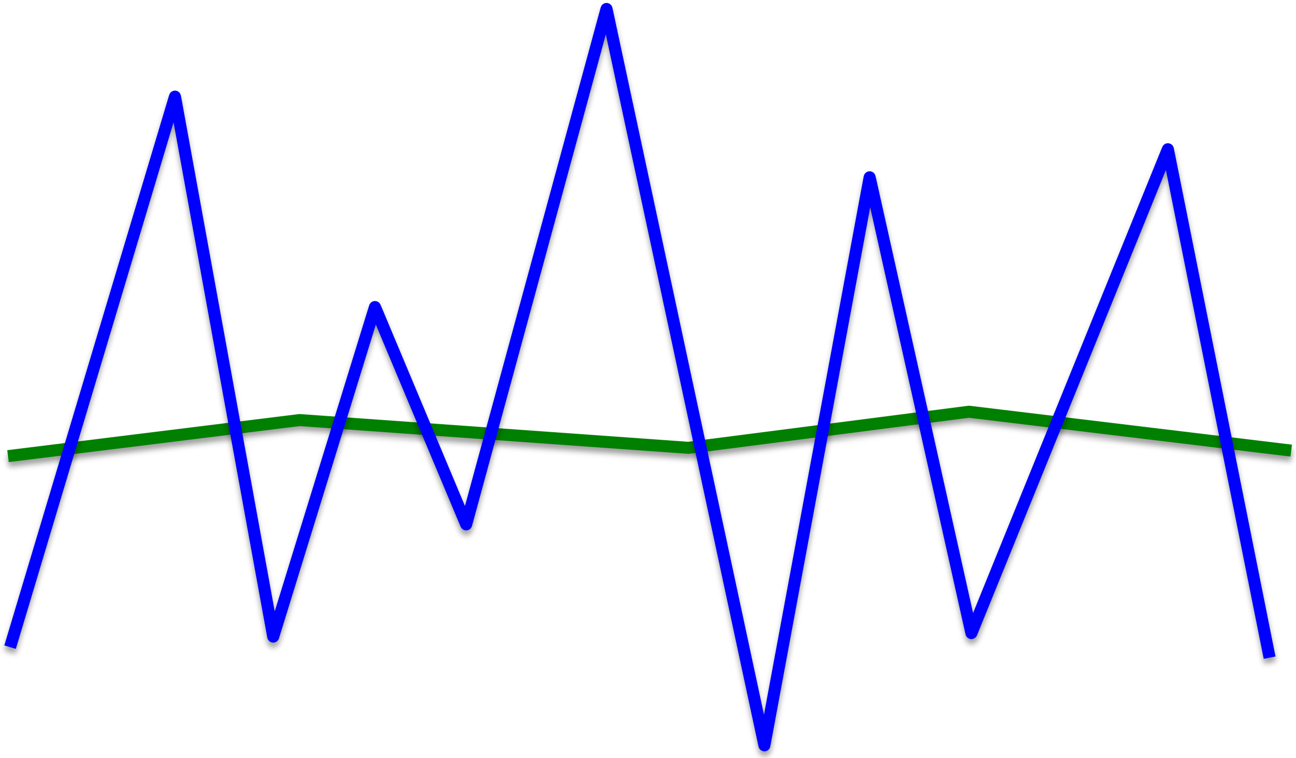
# Choices – do nothing



Groups in ssGBLUP

Groups in BLUP

# Choices – remove UPG from model

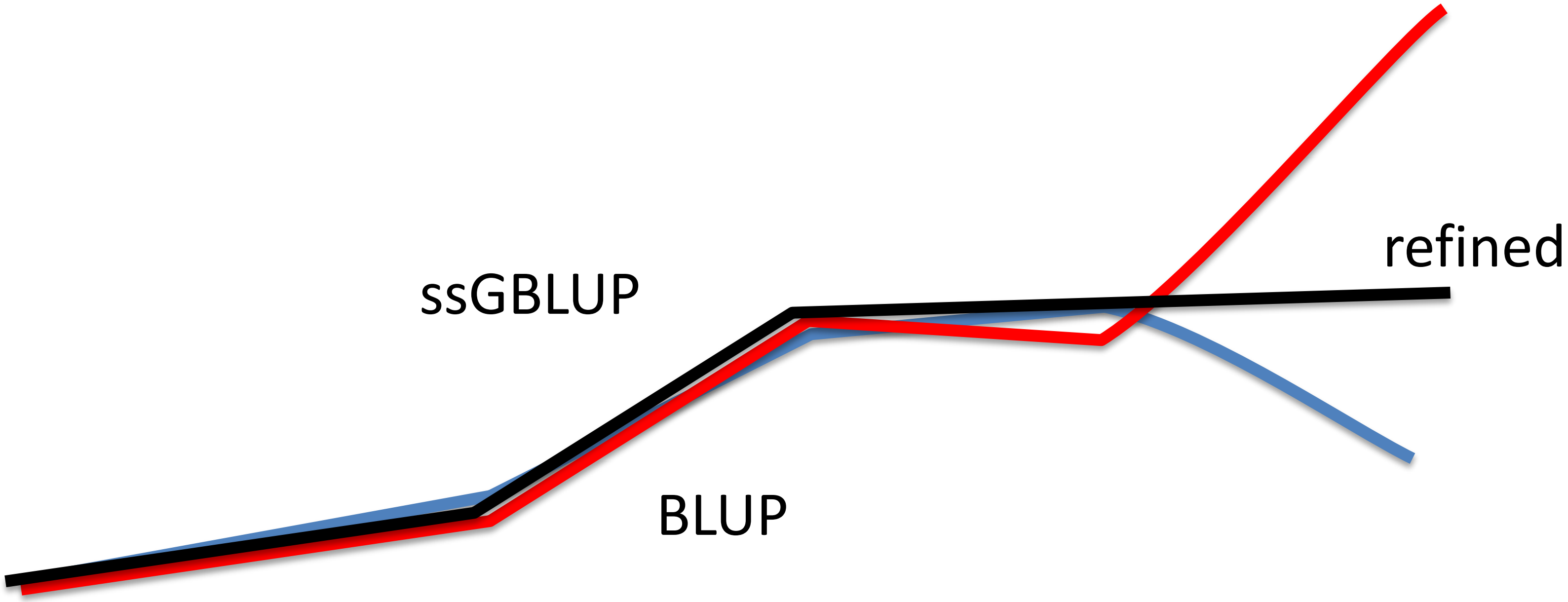


Trend

UPG in BLUP or ssGBLUP

No trend and large fluctuations in UPG

# Choices – redefine groups



See Tsuruta et al., 2013

# Choices – use explicit UPG

$$\mathbf{y} = .. + \mathbf{ZQg} + \mathbf{Za} + \mathbf{e}$$

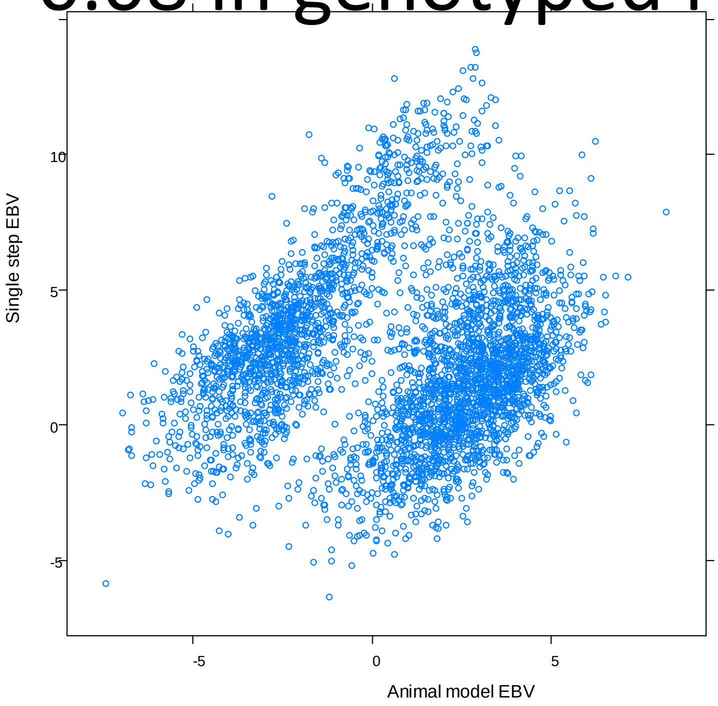
Q difficult to create if many groups
Adds many fixed effects

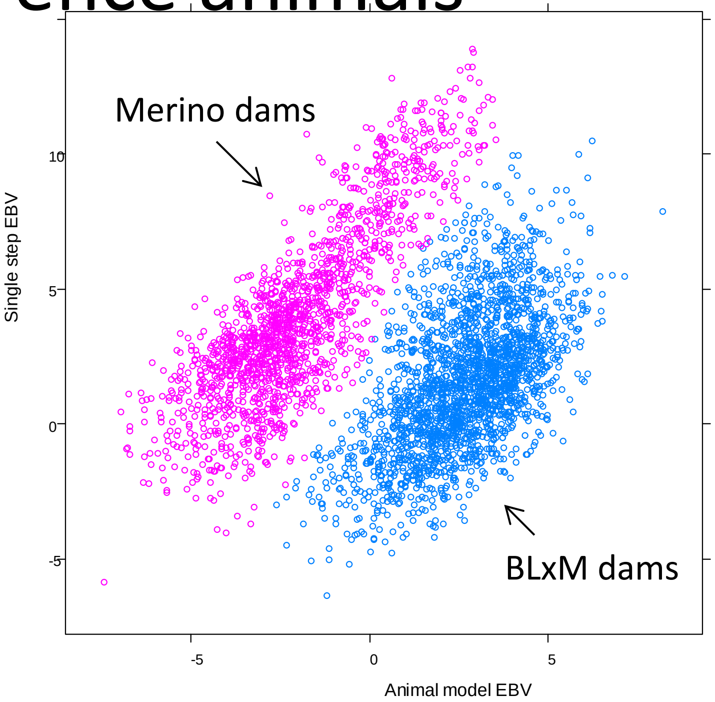
Choice in multiple-trait models if information very unequal per trait

Choice if parents have few phenotypes

# Australian sheep

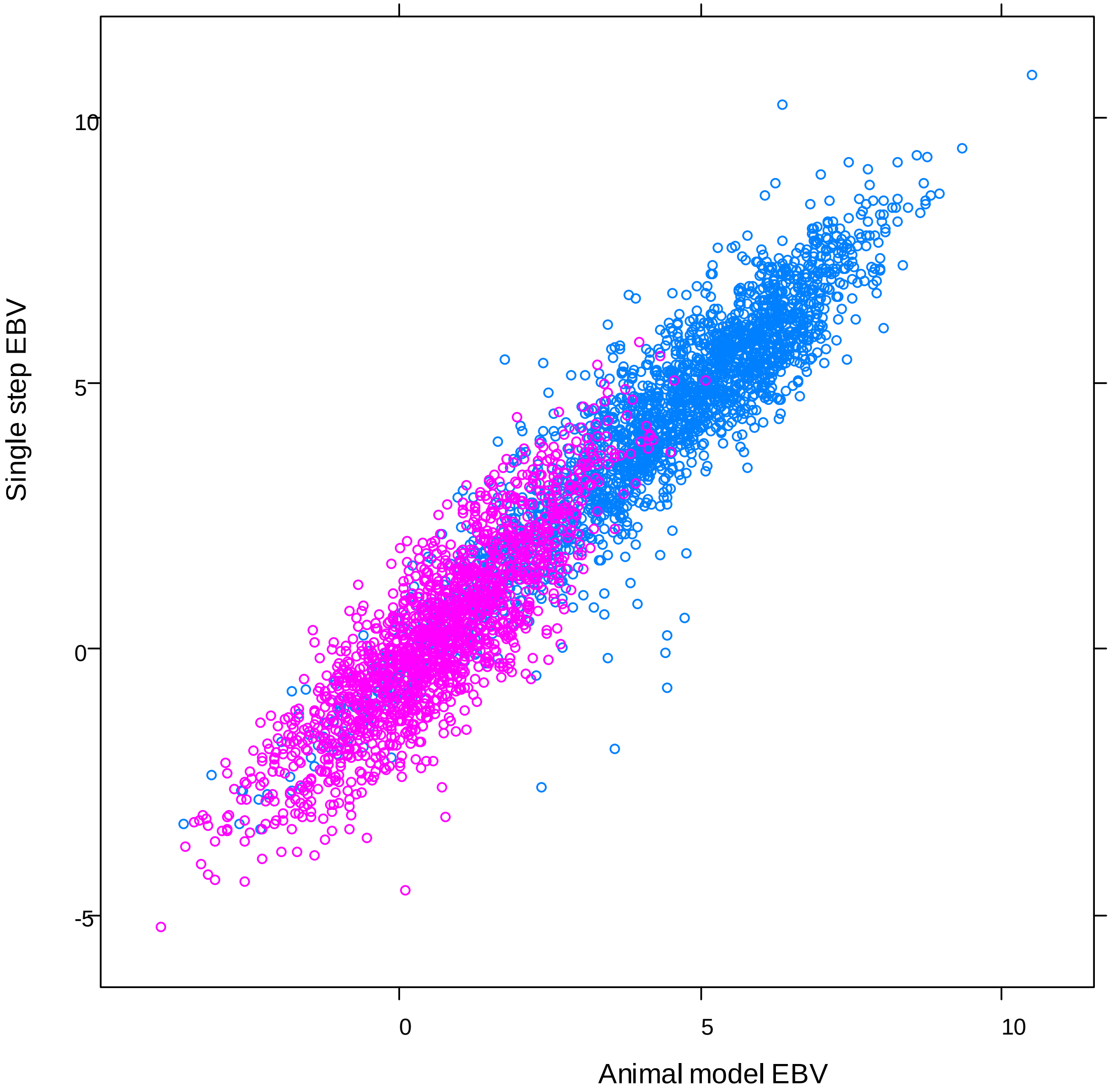
- Correlation between ssBLUP and BLUP EBVs = 0.08 in genotyped reference animals





Swan, 2012

# With explicit UPG model



# Choices – two animal effects

Polygenic effect with UPG

Genomic effect

$$\mathbf{y} = .. + \mathbf{Zu} + \mathbf{Za}_2 + \mathbf{e}$$

$$\mathbf{u}_1 \sim N(\mathbf{Qg}, \eta \mathbf{A} \sigma_a^2)$$

$$\mathbf{a}_2 \sim N(0, (1-\eta) \mathbf{H} \sigma_a^2)$$

Slows down convergence,
Some approximation

# Pedigree length and convergence

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

Big $A_{22}$ makes H less PD,
Reduces convergence rate

$$G^{-1} - A_{22}^{-1}$$

Good convergence and genotyped animals biased down

$$G^{-1} - \mathbf{A}_{22}^{-1}$$

Bad convergence and genotyped animals biased up

$$G^{-1} - \underset{\text{Long}}{A_{22,1}^{-1}} - \underset{\substack{\text{medium}\\ \text{pedigrees}}}{A_{22,2}^{-1}} - \underset{\text{short}}{A_{22,3}^{-1}}$$

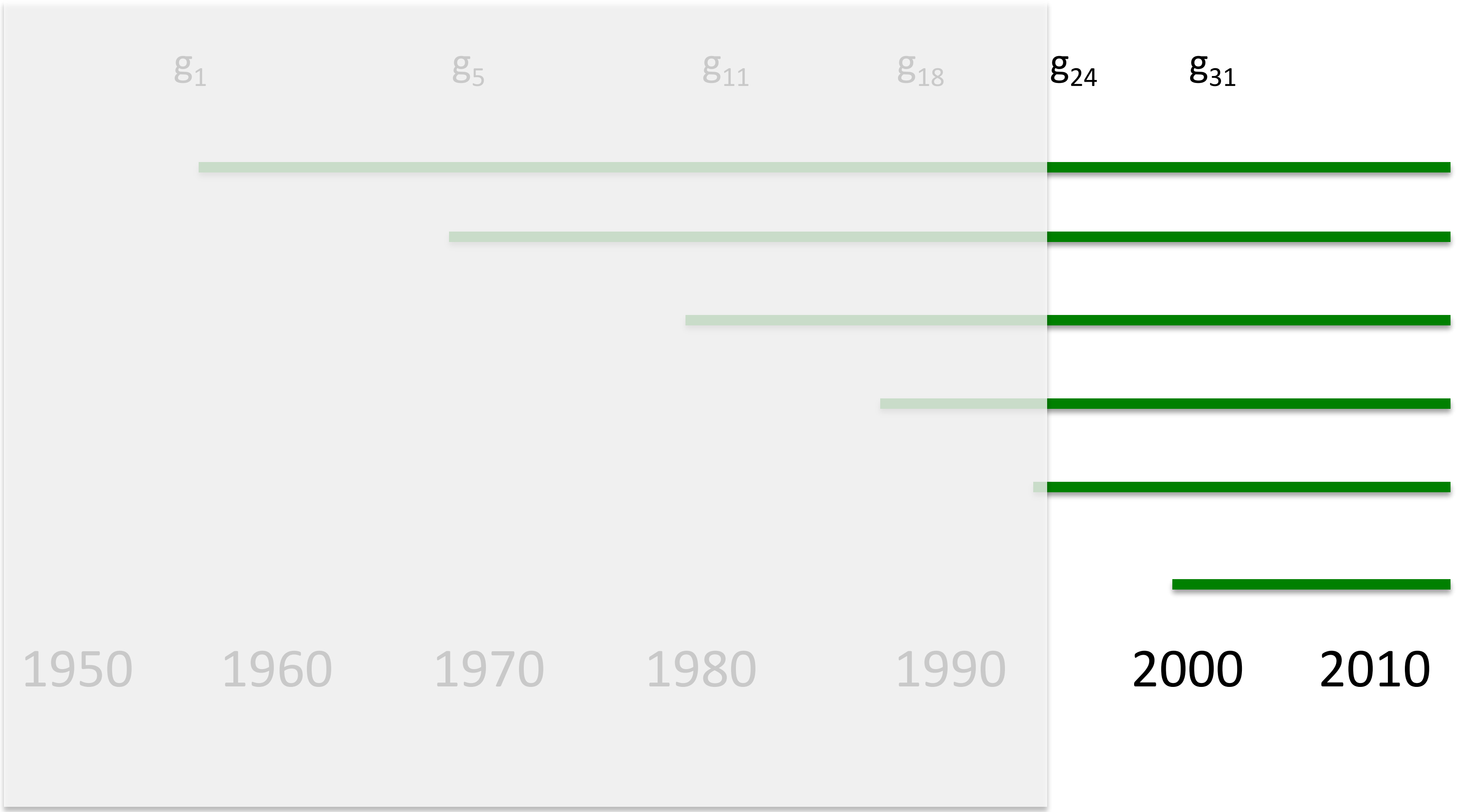
Bad convergence and genotyped animals biased down and up

# Why coefficient in $A_{22}^{-1}$ improves convergence rate?

$$\mathbf{G}^{-1} - 0.7\mathbf{A}_{22}^{-1} = \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}$$

$$\mathbf{G}^{-1} - 0.7(\mathbf{A}_{22,1}^{-1} - \mathbf{A}_{22,2}^{-1} - \mathbf{A}_{22,3}^{-1}) = \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} - \mathbf{A}_{22,2}^{-1} - \mathbf{A}_{22,3}^{-1}$$

# Cut pedigree and data?



# Is very old data useful?

- When some parents cut – convergence improved 10 times, same accuracy (Forni et al., 2012)
- Data cut from 8 to 2 generations → same accuracy and reduced inbreeding (Mehrabani-Yeganeh et al., 1999)
- Little information beyond 3 generations (Luan et al., 2012; Lino et al., 2013)

# Conclusions

- UPG can cause problems in BLUP and ssGBLUP
- Many solutions – choice data driven
- Data beyond 3-4 generations possibly not useful
- Validation procedures of genomic selection useful for model refinement

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