



# A recipe for multiple trait deregression

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# Why this paper

- Original idea: Deregression into existing BLUP software
  - Easy to use
    - Get all benefits from existing software
  - Easy to program
- Deregression convergence
  - Convergence can be accelerated?
  - Many methods to choose



# Base deregression equation system

Unknowns

$$\begin{bmatrix}
 \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1} & \mathbf{0} & \mathbf{0} \\
 \mathbf{R}^{-1}\mathbf{X} & \mathbf{R}^{-1} + \mathbf{A}^{bb} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ba} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{bg} \otimes \mathbf{G}_0^{-1} \\
 \mathbf{0} & \mathbf{A}^{ab} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{aa} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ag} \otimes \mathbf{G}_0^{-1} \\
 \mathbf{0} & \mathbf{A}^{gb} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ga} \otimes \mathbf{G}_0^{-1} & (\mathbf{A}^{gg} + \mathbf{I}) \otimes \mathbf{G}_0^{-1}
 \end{bmatrix}
 \begin{bmatrix}
 \hat{\boldsymbol{\mu}} \\
 \hat{\mathbf{t}}_b \\
 \hat{\mathbf{t}}_a \\
 \hat{\mathbf{g}}
 \end{bmatrix}
 =
 \begin{bmatrix}
 \mathbf{r}_\mu \\
 \mathbf{r}_b \\
 \mathbf{0} \\
 \mathbf{0}
 \end{bmatrix}$$

$b$ : Bulls with known EBVs ( $\mathbf{a}_b$ )

$a$ : Ancestors to bulls with known EBVs

$$\hat{\mathbf{t}}_b = \mathbf{a}_b - \mathbf{X}\hat{\boldsymbol{\mu}}$$

$g$ : Random genetic groups

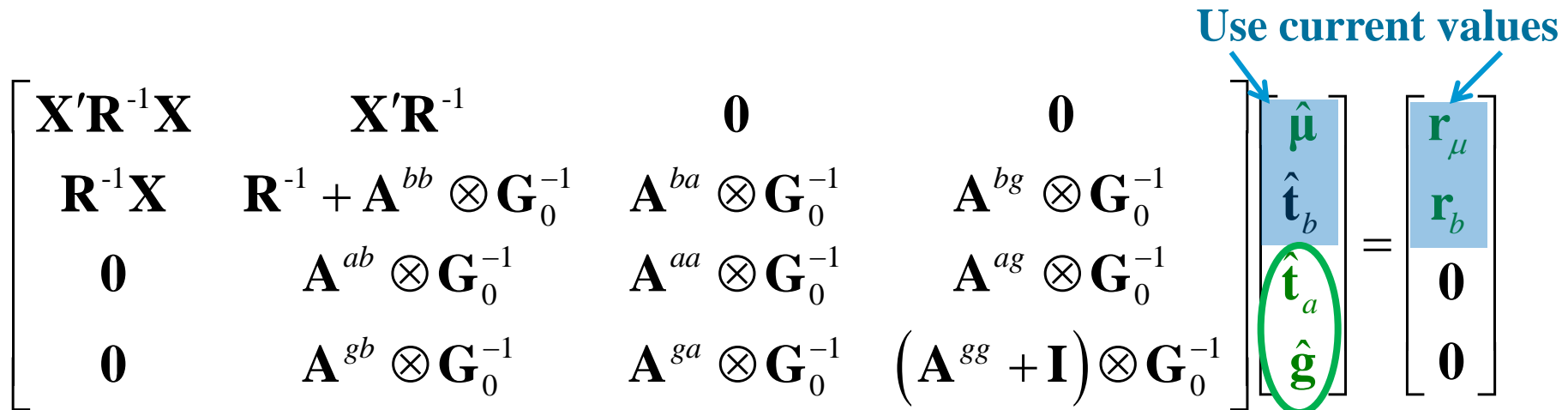
Relationship:  $\mathbf{r}_b = \mathbf{R}^{-1}\mathbf{y}$        $\mathbf{r}_\mu = \mathbf{X}'\mathbf{r}_b$

Deregressed EBVs

# Block solving strategy: Step 1

$$\begin{bmatrix}
 \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1} & \mathbf{0} & \mathbf{0} \\
 \mathbf{R}^{-1}\mathbf{X} & \mathbf{R}^{-1} + \mathbf{A}^{bb} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ba} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{bg} \otimes \mathbf{G}_0^{-1} \\
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 \end{bmatrix}
 =
 \begin{bmatrix}
 \mathbf{r}_\mu \\
 \mathbf{r}_b \\
 \mathbf{0} \\
 \mathbf{0}
 \end{bmatrix}$$

Use current values



*b*: Bulls with known EBVs ( $\mathbf{a}_b$ )

*a*: Ancestors to bulls with known EBVs

*g*: Random genetic groups

Solve for ancestors to bulls with known EBV and genetic groups

Needs solving a linear system of equations

# Block solving strategy: Step 2

$$\begin{bmatrix}
 \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1} & \mathbf{0} & \mathbf{0} \\
 \mathbf{R}^{-1}\mathbf{X} & \mathbf{R}^{-1} + \mathbf{A}^{bb} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ba} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{bg} \otimes \mathbf{G}_0^{-1} \\
 \mathbf{0} & \mathbf{A}^{ab} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{aa} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ag} \otimes \mathbf{G}_0^{-1} \\
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 =
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 \mathbf{r}_\mu \\
 \mathbf{r}_b \\
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 \end{bmatrix}$$

$b$ : Bulls with known EBVs ( $\mathbf{a}_b$ )

$a$ : Ancestors to bulls with known EBVs

$g$ : Random genetic groups

Calculate right-hand side

Needs coefficient matrix times vector product

# Block solving strategy: Step 3

$$\begin{bmatrix}
 \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1} & \mathbf{0} & \mathbf{0} \\
 \mathbf{R}^{-1}\mathbf{X} & \mathbf{R}^{-1} + \mathbf{A}^{bb} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{ba} \otimes \mathbf{G}_0^{-1} & \mathbf{A}^{bg} \otimes \mathbf{G}_0^{-1} \\
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$b$ : Bulls with known EBVs ( $\mathbf{a}_b$ )

$a$ : Ancestors to bulls with known EBVs

$g$ : Random genetic groups

Calculate general mean:  $\hat{\boldsymbol{\mu}}^{[k+1]} = \hat{\boldsymbol{\mu}}^{[k]} - \Delta^{[k]}$   $k$ = iteration number

$$\Delta^{[k]} = (\mathbf{X}'\mathbf{R}^{-1}\mathbf{X})^{-1} (\mathbf{r}_\mu^{[k+1]} - \mathbf{X}'\mathbf{r}_b^{[k+1]})$$

# Block solving steps

## 1. Solve $\mathbf{t}_a$ and $\mathbf{g}$

Needs solving a linear system of equations

- Use existing BLUP solver: PCG iteration

## 2. Calculate new right-hand side

- Matrix times vector product
  - Available: operation needed by PCG iteration

## 3. Update general mean

Iterate steps 1 to 3 until convergence



# Accelerate solving of general mean

- Update in step 3:

$$\hat{\boldsymbol{\mu}}^{[k+1]} = \hat{\boldsymbol{\mu}}^{[k]} - \boldsymbol{\Delta}^{[k]}$$

$$\boldsymbol{\Delta}^{[k]} = (\mathbf{X}'\mathbf{R}^{-1}\mathbf{X})^{-1} (\mathbf{r}_{\mu}^{[k+1]} - \mathbf{X}'\mathbf{r}_b^{[k+1]})$$

- Root finding method in update of general mean
  - Use  $\boldsymbol{\Delta}^{[k]}$  as value for function at current general mean  $\hat{\boldsymbol{\mu}}^{[k]}$
- Methods considered:
  - None
  - Bisection
  - Secant
  - Broyden

# Acceleration by root finding methods

- Secant: 
$$\boldsymbol{\mu}_i^{[k+1]} = \boldsymbol{\mu}_i^{[k]} - \frac{\boldsymbol{\mu}_i^{[k]} - \boldsymbol{\mu}_i^{[k-1]}}{\Delta_i^{[k]} - \Delta_i^{[k-1]}}$$
 for each trait  $i$

- Broyden: 
$$\boldsymbol{\mu}^{[k+1]} = \boldsymbol{\mu}^{[k]} - \mathbf{J}^{-1[k]} \Delta^{[k]}$$

$$\mathbf{J}^{-1[k]} = \mathbf{J}^{-1[k-1]} + \frac{\boldsymbol{\delta}^{[k]} - \mathbf{J}^{-1[k-1]} \Delta^{[k]}}{\boldsymbol{\delta}^{[k]'} \mathbf{J}^{-1[k-1]} \Delta^{[k]}} \boldsymbol{\delta}^{[k]'} \mathbf{J}^{-1[k-1]}$$

$$\boldsymbol{\delta}^{[k]} = \boldsymbol{\mu}^{[k]} - \boldsymbol{\mu}^{[k-1]}$$

- Extra computation due to acceleration is small

# Block solving steps with acceleration

## 1. Solve $\mathbf{t}_a$ and $\mathbf{g}$

Needs solving a linear system of equations

- Use existing BLUP solver: PCG iteration

## 2. Calculate new right-hand side

- Matrix times vector product
  - Available: operation needed by PCG iteration

## 3. Calculate function value at current general mean

$$\Delta^{[k]} = (\mathbf{X}'\mathbf{R}^{-1}\mathbf{X})^{-1} (\mathbf{r}_\mu^{[k+1]} - \mathbf{X}'\mathbf{r}_b^{[k+1]})$$

## 4. Update general mean by acceleration method

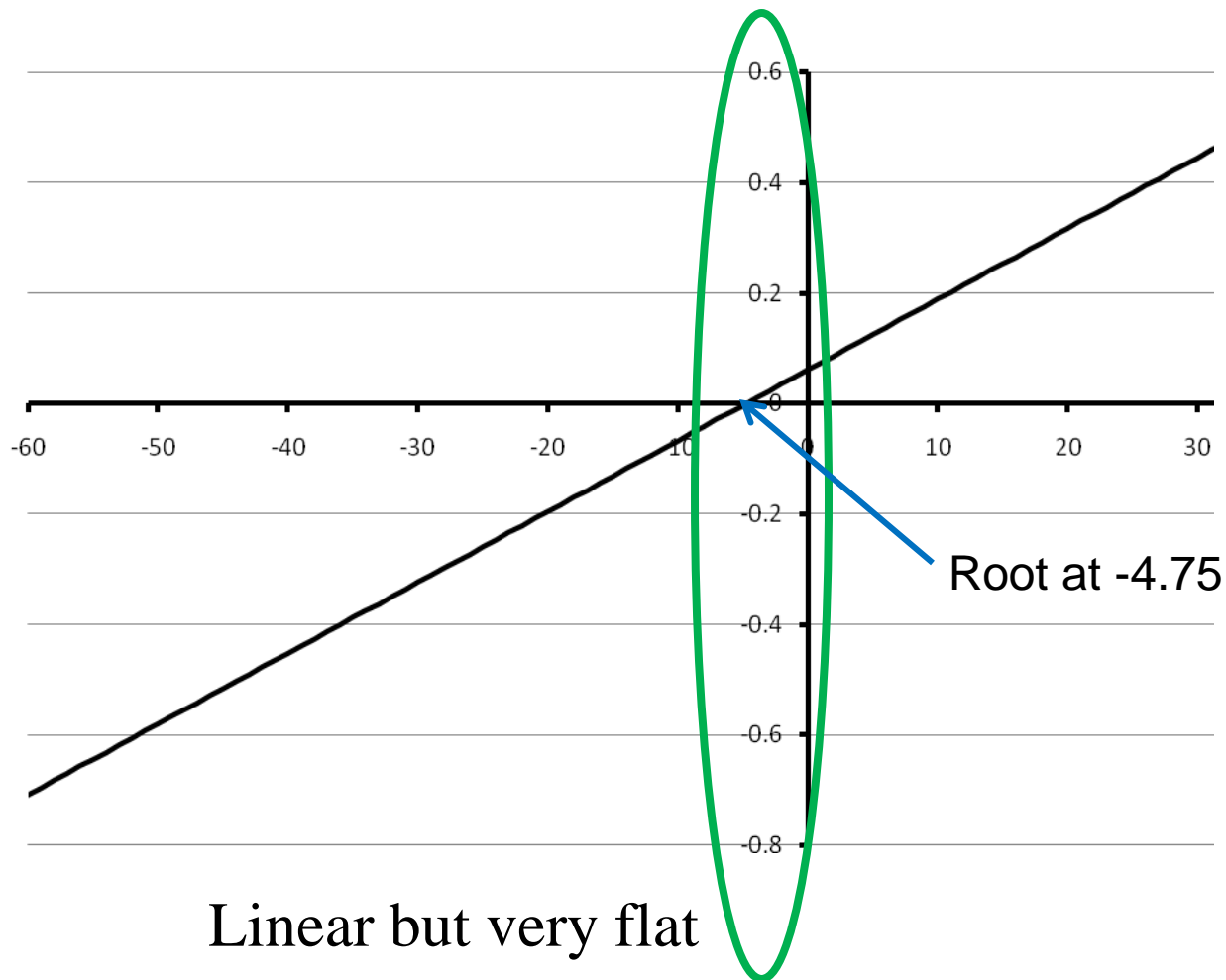
Iterate steps 1 to 4 until convergence

# Data

- Two data sets from a paper by Schaeffer (2001)
- Country A
  - EBVs for 1st, 2nd, 3rd 305-d lactation protein yield
  - 4 analyses: 1, 1+2, 1+2+3 multiple trait,  
1+2+3 as single trait
- Country B
  - EBVs for protein yield and somatic cell score (SCS)
  - 4 analyses: protein, SCS, protein+SCS multiple trait,  
protein+SCS single trait

# Results

# Function value with different values of general mean, 305-d protein yield in country B



# Iteration by different methods

## Country B, protein

Iteration	None	Bisection	Secant	Broyden
0	-8.333	-13.5	-8.333	-8.333
1	-8.287	10.75	-8.287	-8.287
2	-8.242	-1.375	4126.96	-4.748
3	-8.197	-7.438	-4.748	-4.748
4	-8.153	-4.406	-4.748	-
No. iterations	713	16	4	3

# Number of BLUP solver calls by analysis (total number of PCG iterations)

Country	Data	None	Bisection	Secant	Broyden
A	Lactation 1	138 (1656)	16 (191)	4 (48)	3 (36)
	MT <sub>1+2</sub>	154 (1849)	250 (3093)	8 (97)	6 (73)
	MT <sub>1+2+3</sub>	169 (2197)	269 (3497)	39 (506)	7 (91)
	All, ST <sup>1</sup>	138 (1794)	18 (233)	4 (51)	8 (104)
B	protein	713 (8556)	16 (192)	4 (49)	3 (36)
	SCS	149 (1506)	12 (128)	3 (47)	3 (34)
	MT <sub>protein + SCS</sub>	748 (8976)	444 (5329)	6 (73)	6 (72)
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Secant and Broyden methods are **very good**

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Secant is **good**, and Broyden methods is **very good**

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**Results follow the same pattern as number of solver calls**

# Practical experiences (real data)

- Acceleration has worked very well
- Convergence affected by definition of genetic groups
  - The more groups the faster convergence
- Changes in group definition has only small effect on deregressed proofs (correlation)
  - Variance is affected
- Random genetic groups essential

# Conclusions

- Deregression using existing BLUP software
  - Easy to implement
  - Gives all advantages of the existing software
    - User can start with deregression, and proceed to analyses with deregressed proofs easily:
      - same pedigree, same variance components etc.
- Acceleration methods work very well
  - No universally best among tested
  - Broyden's method was best when there were high genetic correlations between traits
  - Secant method was best when genetic correlations between traits were low