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# Alternative single-step type genomic prediction equations

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**N. Gengler <sup>\*1</sup>, G. Nieuwhof <sup>2,3</sup>, K. Konstantinov <sup>2,3</sup>, M. Goddard <sup>3,4</sup>**

<sup>1</sup> ULg - Gembloux Agro-Bio Tech, B-5030 Gembloux, Belgium

<sup>2</sup> ADHIS, Bundoora, Australia

<sup>3</sup> DPI, Victoria, Bundoora, Australia

<sup>4</sup> University of Melbourne, Melbourne, Australia



# Partitioning Genetic (Co)variances

## ⇒ General Model for Genomic Prediction

- **Two sources of genetic (co)variances**
  1. **Explained by genomic differences** between animals
    - Currently SNP based
    - But can also be known QTLs, major gene effects or copy-number variant (CNV) based effects
  2. **Explained by pedigree** ⇒ polygenic “residual”
- **Logical choice**
  - **Random mixed inheritance model**
  - Jointly modelling and estimating:
    - SNP (or similar) effects and
    - residual polygenic effects

# General Model

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u}^* + \mathbf{e} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{Z}\mathbf{Q}\mathbf{g} + \mathbf{e}$$

- Expectation and variances

$$\mathbf{E} \begin{pmatrix} \mathbf{g} \\ \mathbf{u} \\ \mathbf{u}^* \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{pmatrix} \quad \text{and} \quad \text{Var} \begin{pmatrix} \mathbf{g} \\ \mathbf{u} \\ \mathbf{u}^* \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{D} & \mathbf{0} & \mathbf{D}\mathbf{Q}' & \mathbf{0} \\ \mathbf{0} & \mathbf{G} & \mathbf{G} & \mathbf{0} \\ \mathbf{Q}\mathbf{D} & \mathbf{G} & \mathbf{G}^* & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{R} \end{pmatrix}$$

$$\text{with } \mathbf{G}^* = \mathbf{G} + \mathbf{Q}\mathbf{D}\mathbf{Q}' = \mathbf{G} + \mathbf{F}$$

- Remarks:

- $\mathbf{G}$ ,  $\mathbf{Q}$  and  $\mathbf{D}$  can have whatever structure needed
- $\mathbf{G}$  always function of  $\mathbf{A}$  (pedigree based relationship) and polygenic (co)variances  $\mathbf{G}_0$  (e.g.,  $\mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0$ )
- $\mathbf{u}^*$ ,  $\mathbf{G}^*$  where “\*” indicates linked to polygenic **AND** SNP effects
- $\mathbf{F}$  strictly genomic (co)variance structure

# Traditional MME for

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u}^* + \mathbf{e} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{Z}\mathbf{Q}\mathbf{g} + \mathbf{e}$$

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix} \quad (1)$$



$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z}\mathbf{Q} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}\mathbf{Q} \\ \mathbf{Q}'\mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Q}'\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{Q}'\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}\mathbf{Q} + \mathbf{D}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Q}'\mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix} \quad (2)$$

# Traditional MME for

$$y = X\beta + Zu^* + e = X\beta + Zu + ZQg + e$$

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix} \quad (1)$$



$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}ZQ \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & Z'R^{-1}ZQ \\ Q'Z'R^{-1}X & Q'Z'R^{-1}Z & Q'Z'R^{-1}ZQ + D^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ Q'Z'R^{-1}y \end{bmatrix} \quad (2)$$

**Simpler MME?**

# Traditional MME for

$$y = X\beta + Zu^* + e = X\beta + Zu + ZQg + e$$

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix} \quad (1)$$



$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}ZQ \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & Z'R^{-1}ZQ \\ Q'Z'R^{-1}X & Q'Z'R^{-1}Z & Q'Z'R^{-1}ZQ + D^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ Q'Z'R^{-1}y \end{bmatrix} \quad (2)$$

**Simpler MME?  $\Rightarrow$  Similarity to Genetic Groups!**

# Alternative MME based on Quaas-Pollack Transformation

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & 0 \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & -G^{-1}Q \\ 0 & -Q'G^{-1} & Q'G^{-1}Q + D^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ 0 \end{bmatrix} \quad (3)$$

- Please note **three advantages**:

1. Inverted **G** here based on inverted **A**, no genomic relationships!

⇒ **Major advantage, usual method to set-up  $A^{-1}$**

2. Explicit equations for estimation of SNP effects (**g**)

⇒ **Major advantage of multi-step genomic prediction (MS-GP)**

3. Direct estimation of  $\hat{u}^*$

⇒ **Major advantage of single-step genomic prediction (SS-GP)**

# General MME based on Quaas-Pollack Transformation

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{0} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} & -\mathbf{G}^{-1}\mathbf{Q} \\ \mathbf{0} & -\mathbf{Q}'\mathbf{G}^{-1} & \mathbf{Q}'\mathbf{G}^{-1}\mathbf{Q} + \mathbf{D}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$



# Identification Of Two Blocks in Transformed MME – 1<sup>st</sup> Block

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & 0 \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & -G^{-1}Q \\ 0 & -Q'G^{-1} & Q'G^{-1}Q + D^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ 0 \end{bmatrix}$$



$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y + G^{-1}Q\hat{g} \end{bmatrix}$$

# Identification Of Two Blocks in Transformed MME – 2<sup>nd</sup> Block

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & 0 \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & -G^{-1}Q \\ 0 & -Q'G^{-1} & Q'G^{-1}Q + D^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}^* \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ 0 \end{bmatrix}$$



$$\left[ Q'G^{-1}Q + D^{-1} \right] \hat{g} = Q'G^{-1}\hat{u}^*$$

# Practical Considerations

- In practice **not all animals genotyped**
  - Non-genotyped animals = “1”
  - Genotyped animals = “2”
- Definition of **direct SNP contribution to GEBV (dGV)**
  - For genotyped animals:

$$\hat{\mathbf{d}}_2 = \mathbf{Q}_2 \hat{\mathbf{g}}$$

- For non-genotyped animals predicted from dGV of genotyped animals using selection index theory:

$$\hat{\mathbf{d}}_1 = \mathbf{G}_{12} \mathbf{G}_{22}^{-1} \hat{\mathbf{d}}_2 = \mathbf{G}_{12} \mathbf{G}_{22}^{-1} \mathbf{Q}_2 \hat{\mathbf{g}}$$

$$\mathbf{Q}_1 = \mathbf{G}_{12} \mathbf{G}_{22}^{-1} \mathbf{Q}_2$$

# Not All Animals Are Genotyped (System II: “SNP” System)

$$\left[ \mathbf{Q}' \mathbf{G}^{-1} \mathbf{Q} + \mathbf{D}^{-1} \right] \hat{\mathbf{g}} = \mathbf{Q}' \mathbf{G}^{-1} \hat{\mathbf{u}}^*$$

$$\mathbf{G}^{-1} = \begin{bmatrix} \mathbf{G}^{11} & \mathbf{G}^{12} \\ \mathbf{G}^{21} & \mathbf{G}^{22} \end{bmatrix}$$



$$\mathbf{Q} = \begin{bmatrix} \mathbf{G}_{12} & \mathbf{G}_{22}^{-1} \\ \mathbf{I} & \end{bmatrix} \mathbf{Q}_2 = \begin{bmatrix} -(\mathbf{G}^{11})^{-1} \mathbf{G}^{12} \\ \mathbf{I} \end{bmatrix} \mathbf{Q}_2$$

$$\left[ \mathbf{Q}_2' \mathbf{G}_{22}^{-1} \mathbf{Q}_2 + \mathbf{D}^{-1} \right] \hat{\mathbf{g}} = \mathbf{Q}_2' \mathbf{G}_{22}^{-1} \hat{\mathbf{u}}_2^*$$

NB: 1 = non-genotyped, 2 = genotyped animals

# Not All Animals Are Genotyped (System I: “BLUP” System)

- First assume only genotyped animals have records

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}_{22}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}_2^* \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} + \mathbf{G}_{22}^{-1}\mathbf{Q}_2\hat{\mathbf{g}} \end{bmatrix}$$

- Recovering genetic (co)variance not explained by strictly polygenic effect by assuming proportionality between polygenic and total (co)variance:

$$\mathbf{G} = \varphi\mathbf{T} \text{ then } \mathbf{G}^{-1} = \frac{1}{\varphi}\mathbf{T}^{-1}$$

- Predicting animals without genotypes  $\hat{\mathbf{u}}_1^* = \mathbf{T}_{12}\mathbf{T}_{22}^{-1}\hat{\mathbf{u}}_2^*$

# Further Modification “BLUP” System

- Introducing  $T_{22}^{-1}$

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + T_{22}^{-1} + G_{22}^{-1} - T_{22}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}_2^* \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y + G_{22}^{-1}Q_2\hat{g} \end{bmatrix}$$

- Predicting animals without genotypes inside MME  
(Henderson, 1976)
- Lifting restriction on records only for animals 2

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + \begin{bmatrix} T^{11} & T^{12} \\ T^{21} & T^{22} \end{bmatrix} + G_{22}^{-1} - T_{22}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}_1^* \\ \hat{u}_2^* \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y + \begin{bmatrix} 0 \\ G_{22}^{-1}Q_2\hat{g} \end{bmatrix} \end{bmatrix}$$

# Further Modification “BLUP” System

- Using again  $\mathbf{G}^{-1} = \frac{1}{\phi} \mathbf{T}^{-1}$ , following MME are derived

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + \left(\frac{1}{\phi} - 1\right)\mathbf{T}_{22}^{-1} \end{bmatrix} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}_1^* \\ \hat{u}_2^* \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} + \begin{bmatrix} 0 \\ \frac{1}{\phi} \mathbf{T}_{22}^{-1} \mathbf{Q}_2 \hat{\mathbf{g}} \end{bmatrix} \end{bmatrix}$$

- Please note similarity to **Bayesian procedures to integrate external information into genetic evaluations** (Vandenplas and Gengler, 2012)

# Reassembling Systems I and II

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{0} \end{bmatrix} + \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + \left(\frac{1}{\phi} - 1\right)\mathbf{T}_{22}^{-1} \end{bmatrix} \\ -\frac{1}{\phi} \begin{bmatrix} \mathbf{0} & \mathbf{Q}_2'\mathbf{T}_{22}^{-1} \end{bmatrix} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$





# Equivalence with Single-Step MME

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{0} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + \left(\frac{1}{\varphi} - 1\right)\mathbf{T}_{22}^{-1} \end{bmatrix} & -\frac{1}{\varphi} \begin{bmatrix} \mathbf{0} \\ \mathbf{T}_{22}^{-1} \end{bmatrix} \\ \mathbf{0} & -\frac{1}{\varphi} \begin{bmatrix} \mathbf{0} & \mathbf{T}_{22}^{-1} \end{bmatrix} & \frac{1}{\varphi} (\mathbf{T}_{22}^{-1} + \varphi\mathbf{F}^{-1}) \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \\ \hat{\mathbf{d}}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \end{bmatrix} \quad (3)$$



$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + (\varphi\mathbf{T}_{22} + \mathbf{F})^{-1} - \mathbf{T}_{22}^{-1} \end{bmatrix} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix} \quad (4)$$

## Equivalence derived from:

1. Absorb equations for  $\mathbf{d}$  into those for  $\mathbf{u}^*$
2. Apply rules inverse of sum of matrices:

$$(\varphi\mathbf{T}_{22} + \mathbf{F})^{-1} = \frac{1}{\varphi} \mathbf{T}_{22}^{-1} - \frac{1}{\varphi} \mathbf{T}_{22}^{-1} (\mathbf{T}_{22}^{-1} + \varphi\mathbf{F}^{-1})^{-1} \mathbf{T}_{22}^{-1}$$





# Polygenic and Genomic (Co)Variances

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{0} \end{bmatrix} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + \left(\frac{1}{\phi} - 1\right)\mathbf{T}_{22}^{-1} \\ -\frac{1}{\phi}[\mathbf{0} & \mathbf{T}_{22}^{-1}] \end{bmatrix} \begin{bmatrix} \mathbf{0} \\ -\frac{1}{\phi} \begin{bmatrix} \mathbf{0} \\ \mathbf{T}_{22}^{-1} \end{bmatrix} \\ \frac{1}{\phi}(\mathbf{T}_{22}^{-1} + \phi\mathbf{F}^{-1}) \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \\ \hat{\mathbf{d}}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$

Definition of polygenic “residual” as part of total genetic (co)variance  $\mathbf{T}$

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \end{bmatrix} \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} \end{bmatrix} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + (\phi\mathbf{T}_{22} + \mathbf{F})^{-1} - \mathbf{T}_{22}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$



# Polygenic and Genomic (Co)Variances

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{0} \end{bmatrix} \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + \left(\frac{1}{\phi} - 1\right)\mathbf{T}_{22}^{-1} \\ -\frac{1}{\phi}[\mathbf{0} & \mathbf{T}_{22}^{-1}] \end{bmatrix} \begin{bmatrix} \mathbf{0} \\ -\frac{1}{\phi} \begin{bmatrix} \mathbf{0} \\ \mathbf{T}_{22}^{-1} \end{bmatrix} \\ \frac{1}{\phi}(\mathbf{T}_{22}^{-1} + \phi\mathbf{F}^{-1}) \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \\ \hat{\mathbf{d}}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$

Weight here defined as constant across all traits, however equations can be modified to allow different weights across traits

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} \\ \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \end{bmatrix} \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + (\phi\mathbf{T}_{22} + \mathbf{F})^{-1} - \mathbf{T}_{22}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$

# Most Useful MME $\Leftrightarrow$ No $F^{-1}$ Needed

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{0} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \begin{bmatrix} \mathbf{T}^{11} & \mathbf{T}^{12} \\ \mathbf{T}^{21} & \mathbf{T}^{22} + \left(\frac{1}{\phi} - 1\right)\mathbf{T}_{22}^{-1} \end{bmatrix} & -\frac{1}{\phi} \begin{bmatrix} \mathbf{0} \\ \mathbf{T}_{22}^{-1}\mathbf{Q}_2 \end{bmatrix} \\ \mathbf{0} & -\frac{1}{\phi} \begin{bmatrix} \mathbf{0} & \mathbf{Q}_2'\mathbf{T}_{22}^{-1} \end{bmatrix} & \frac{1}{\phi} (\mathbf{Q}_2'\mathbf{T}_{22}^{-1}\mathbf{Q}_2 + \phi\mathbf{D}^{-1}) \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}}^* \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \end{bmatrix}$$

- **Alternative Single Step Genomic Prediction (SS-GP)**
  - Allows combining advantages of SS-GP and MS-GP
- **Different implementations, other advantages**
  - Setting-up as one systems (cf. above)  $\Rightarrow$  direct solving
  - Setting-up two systems as seen before, some advantages:
    - Solving through parallel systems by updating RHS periodically
    - Alternative “SNP” Systems possible  $\Rightarrow$  alternative models, solvers
    - Excluding some  $\mathbf{u}^*$  (e.g., preferentially treated cows), adding other  $\mathbf{u}^*$  (e.g., external (G)EBV for external animals)



# Conclusions

- **Developed alternative genomic prediction equations have many advantages:**
  - Explicit weighting of genomic (SNP) and polygenic effects
  - Direct estimation of SNP effects
    - Better use of High-Density SNP panels
    - Other genetic effects (e.g. CNV) can be accommodated
  - Direct estimation of GEBV effects
  - Genomic relationship matrix never explicitly formed, stored or inverted
  - Implementation straight-forward
    - Based on use of existing software
    - System I and System II can run in parallel (updating of RHS)
- **But additional research required:**
  - Especially to test and validate proposed method for large data sets

# Final Remarks

- **General consensus**

- Single-step methods combine all sources of information into accurate rankings for animals with and without genotypes
- Especially adapted for novel traits (e.g., **milk fat composition**) and more complex models (e.g., **multitrait, random regression model**)
- With increasing number of genotyped animals equivalent models not requiring inverting genomic relationship matrix

- **Therefore currently different research efforts**

- To get these equivalent models

- **This development complementary approach because**

- Not based on (matrix of) relationship differences
- But on partitioning of genetic (co)variances
- However **still inverse of  $A_{22}$  needed**  $\Leftrightarrow$  **New methods** (Faux et al. 2012)

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[www.robustmilk.eu](http://www.robustmilk.eu)

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