Reasons for multiple trait genetic evaluation

- Increased accuracy
  - Information from correlated traits (> index)

- To avoid selection bias
  - Sequential selection
  - Contemporary selection

Multiple Trait mixed model

Definition of model and equations

example

advantages

- Effect on selection bias
- Effect on accuracy of EBV (depending on parameters!)

Single trait model

$$\mathbf{y = Xb + Z\,u + e}$$

$$\mathbf{var(u) = G = A}\,\sigma^2$$

$$\mathbf{var(e) = R = I}\,\sigma^2$$

Multiple Trait Model

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

$$\text{var}(u) = G = \begin{pmatrix} G_{11} & G_{12} \\ G_{21} & G_{22} \end{pmatrix}$$

$$\text{var}(e) = R = \begin{pmatrix} R_{11} & R_{12} \\ R_{21} & R_{22} \end{pmatrix}$$

$$R_{ij} = I\sigma_{e_{ij}}$$

only if all animals all traits;

Remember the general definition of the model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

$\text{var}(u) = G$

$\text{var}(e) = R$

$\text{var}(y) = ZGZ' + R$

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

simple version

$\text{var}(u) = A \quad \sigma_a^2$

$\text{var}(e) = I \quad \sigma_e^2$

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + \lambda A^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

Mixed model equations

$$\begin{bmatrix} X_{1'}r^{11}X_1 & X_{1'}r^{12}X_2 & X_{1'}r^{11}Z_1 & X_{1'}r^{12}Z_2 \\ X_{2'}r^{21}X_1 & X_{2'}r^{22}X_2 & X_{2'}r^{21}Z_1 & X_{2'}r^{22}Z_2 \\ Z_{1'}r^{11}X_1 & Z_{1'}r^{12}X_2 & Z_{1'}r^{11}Z_1 + g^{11}A^{-1} & Z_{1'}r^{12}Z_2 + g^{12}A^{-1} \\ Z_{2'}r^{21}X_1 & Z_{2'}r^{22}X_2 & Z_{2'}r^{21}Z_1 + g^{21}A^{-1} & Z_{2'}r^{22}Z_2 + g^{22}A^{-1} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ u_1 \\ u_2 \end{bmatrix} = \begin{bmatrix} X_{1'}(r^{11}y_1 + r^{12}y_2) \\ X_{2'}(r^{21}y_1 + r^{22}y_2) \\ Z_{1'}(r^{11}y_1 + r^{12}y_2) \\ Z_{2'}(r^{21}y_1 + r^{22}y_2) \end{bmatrix}$$

Just remember that MT Blup models expand to large sets of equations.

Example of multiple trait model

Individual	Herd	Weaning Weight	Yearling Weight
1	**1**	**160**	**-**
2	**1**	**180**	**320**
3	**1**	**210**	**330**
4	**2**	**190**	**-**
5	**2**	**228**	**360**
6	**2**	**210**	**350**

$$Z_2 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

$\sigma_{p1 = 20}$ $h^2_1 = .42$

$r_g = .769$; $r_e = 0.60$

$\sigma_{p2 = 40}$ $h^2_2 = .39$

	Single Trait		Multiple Trait	
b1	**183**	**325**	**183**	**309**
b2	**209**	**355**	**209**	**342**
u1	**-9.86**	**0**	**-9.86**	**-14.58**
u2	**-1.41**	**-1.95**	**-1.00**	**2.87**
u3	**11.27**	**1.95**	**10.86**	**11.72**
u4	**-8.17**	**0**	**-8.17**	**-12.08**
u5	**7.89**	**1.95**	**7.70**	**9.35**
u6	**0.28**	**-1.95**	**0.47**	**2.73**

WW YW **WW YW**

Average EBV is zero within herds

Average of selected animals >0

	Single Trait		Multiple Trait	
b1	**183**	**325**	**183**	**309**
b2	**209**	**355**	**209**	**342**
u1	**-9.86**	**0**	**-9.86**	**-14.58**
u2	**-1.41**	**-1.95**	**-1.00**	**2.87**
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u4	**-8.17**	**0**	**-8.17**	**-12.08**
u5	**7.89**	**1.95**	**7.70**	**9.35**
u6	**0.28**	**-1.95**	**0.47**	**2.73**

WW YW **WW YW**

→ Animals without records get an EBV for trait 2.

	Single Trait		Multiple Trait	
b1	**183**	**325**	**183**	**309**
b2	**209**	**355**	**209**	**342**
u1	**-9.86**	**0**	**-9.86**	**-14.58**
u2	**-1.41**	**-1.95**	**-1.00**	**2.87**
u3	**11.27**	**1.95**	**10.86**	**11.72**
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u5	**7.89**	**1.95**	**7.70**	**9.35**
u6	**0.28**	**-1.95**	**0.47**	**2.73**

Difference larger in MT model

WW YW **WW YW**

	Single Trait		Multiple Trait	
b1	**183**	**325**	**183**	**309**
b2	**209**	**355**	**209**	**342**
u1	**-9.86**	**0**	**-9.86**	**-14.58**
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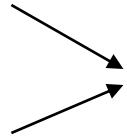
u6	**0.28**	**-1.95**	**0.47**	**2.73**



Herd effect on YW overestimated with ST

WW YW **WW YW**

Notes to the solutions

- **Average EBV is zero within herd**
- **Animal 1 has no observation for trait 2, EBV_2 based on trait 1.**
- **The single trait EBV's and (and fixed effect solutions) deviate from the multiple trait solutions.**
  - **ST EBV's for animals 1 and 4 are zero for YW**
  - **Difference in EBV for YW between animal 2 and 3 (5 and 6) is larger in the multiple trait case**

- **Difference between herd effect for WW and YW is larger in ST**

  This difference is overestimated / biased by selection
- **MT EBV's of unculled animals have EBV"s >0**
- **MT evaluation is able to <u>correct for sequential selection</u>**

Advantages of Multiple Trait BLUP evaluation

- **increase in accuracy of EBV's**
- **correct for selection on correlated trait.**
  - **(not only sequential!)**

- **The benefit depends on**

  - the information available on each animal

  - parameter structure

Increased accuracy from using info from correlated traits

(derive with selection index theory)

depends on

- **heritability of the trait considered**
- **correlations**
- **difference between re and rg!**

Relative accuracy of

MT selection vs ST selection:

Accuracy of Trait 1 (with h_1^2)

using information from

Trait 1 and correlated

Trait 2 (with h_2^2)

Message:

Information from other traits will boost accuracy more if ST EBV has a low accuracy (i.e. low h2 and little info on relatives)

Selection on phenotype only

		h^2_1		
	h^2_2	0.1	0.3	0.5
$r_g=r_e=0.5$	0.1	1.00	1.02	1.03
	0.3	1.09	1.00	1.01
	0.5	1.25	1.02	1.00
$r_g=-r_e=0.5$	0.1	1.40	1.18	1.10
	0.3	1.59	1.23	1.11
	0.5	1.70	1.25	1.12

Using relatives information for each trait

	h^2_2	0.1	0.3	0.5
$r_g=r_e=0.5$	0.1	1.00	1.01	1.02
	0.3	1.03	1.00	1.00
	0.5	1.08	1.01	1.00
$r_g=-r_e=0.5$	0.1	1.18	1.08	1.05
	0.3	1.22	1.10	1.06
	0.5	1.25	1.11	1.07