Evaluation of animals in practice

- Need proper data (centralized)
  - recording system (management groups)
  - correct animal identification
  - other issues?

- Need proper model
  - Account for bias and selection
  - Account for other effects (maternal, permanent environment, multiple trait, different breeds)

A data collection system

- Rules for recording
- Rules for invalid data
- Avoid selective recording
- Rules for defining management groups
- Impetus for doing the right thing
  - What are mechanisms for regulating the system?

How to expand the simple mixed model

- Simple mixed model

  y = contempgrp + animal + residual

- More general
  - y = fixed effects + random effects + residual

fixed effects	random effects	residual
• cg	• animal	homo/
• age	• maternal	heterogeneous
• …..	• permanent env.	

y = Xb + Zu + e

A sire model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zs} + \boldsymbol{\varepsilon}$$

$$\text{var(u)} = \text{A}\,\sigma_s^2$$

$$\text{var(e)} = \text{I}\,\sigma_\varepsilon^2$$

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

$$\lambda = \sigma_\varepsilon^2 / \sigma_s^2$$

originally used (pre-1985)

fewer equations for amount of data

ignores dam-side

Some formal definitions of the model

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

var(u) = G

var(e) = R

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

var(u) = A σ_a^2

var(e) = I σ_e^2

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

Animal Model in ASREML

IN ASREML:

```
Analysis of some kind
  anim !P     The variable 'anim' is related to a
   pedigree file
  dage 10 !A
  rt 6
  wwt
  grp 322 !A
example.ped
example.dat
wwt ~ mu rt dage !r anim  !f grp      #model definition
```

Repeatability model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Zp} + \boldsymbol{\varepsilon}$$

$$G = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_c^2 \end{pmatrix} \qquad \mathrm{var}\begin{pmatrix} u \\ p \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_c^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{pmatrix} = \begin{pmatrix} \mathrm{G} & 0 \\ 0 & \mathrm{R} \end{pmatrix}$$

$$\begin{pmatrix} X'X & X'Z & X'Z \\ Z'X & Z'Z + \alpha A^{-1} & Z'Z \\ Z'X & Z'Z & Z'Z + \gamma I \end{pmatrix} \begin{pmatrix} b \\ u \\ p \end{pmatrix} = \begin{pmatrix} X'y \\ Z'y \\ Z'y \end{pmatrix}$$

Repeatability Model in ASREML

```
Analysis of some kind
  anim !P          The variable 'anim' is related to a pedigree file
  dage 10 !A
  rt 6
  wwt
  grp 322 !A
example.ped
example.dat
wwt ~ mu rt dage !r anim  ide(anim) !f grp      #model definition
0 0 1                                           #R struc: # sites, dim Ro, #G struct
anim 2                                          #G structure: model term, dimensions
2 0 DIAG .3 .2                                  #order Go, 0, model  starting_values
anim                                            #inner dimension of G structure
```

Maternal effects model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_1u} + \mathbf{Z_2m} + \boldsymbol{\varepsilon}$$

Direct animal effect

Maternal effect

$$G = \begin{pmatrix} A\sigma_a^2 & A\sigma_{am} \\ A\sigma_{am} & A\sigma_{mc}^2 \end{pmatrix}$$

Covariance

$$\mathrm{var}\begin{pmatrix} u \\ m \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & A\sigma_{am} & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{pmatrix}$$

$$\begin{pmatrix} X'X & X'Z_1 & X'Z_2 \\ Z_1'X & Z_1'Z_1 + \alpha_{11}A^{-1} & Z_1'Z_2 + \alpha_{12}A^{-1} \\ Z_2'X & Z_2'Z_1 + \alpha_{21}A^{-1} & Z_2'Z_2 + \alpha_{22}A^{-1} \end{pmatrix} \begin{pmatrix} b \\ u \\ m \end{pmatrix} = \begin{pmatrix} X'y \\ Z_1'y \\ Z_2'y \end{pmatrix}$$

Maternal Effects Model in ASREML

```
 Analysis of some kind
  anim !P          The variable ‘anim’ is related to a pedigree fil
  dam !P           The variable ‘dam’ is related to a pedigree file
  dage 10 !A
  rt 6
  wwt
  grp 322 !A
example.ped
example.dat
wwt ~ mu rt dage !r anim  dam !f grp          #model definition
0 0 1                              #R struc: # sites, dim Ro, #G struct
anim 2                              #G structure: model term, dimensions
2 0 US .2 0 .15                     #order Go, 0, model  starting_values
anim
```

$$G = \begin{pmatrix} A\sigma_a^2 & \mathrm{cov} / 0 \\ \mathrm{cov} / 0 & A\sigma_{mc}^2 \end{pmatrix}$$

Maternal Effects Model in ASREML

```
 Analysis of some kind
  anim !P       The variable 'anim' is related to a pedigree fil
  dam !P        The variable 'dam' is related to a pedigree file
  dage 10 !A
  rt 6
  wwt
  grp 322 !A
example.ped
example.dat
wwt ~ mu rt dage !r anim  dam !f grp          #model definition
0 0 1                                 #R struc: # sites, dim Ro, #G struct
anim 2                                 #G structure: model term, dimensions
2 0 DIAG .2  .15                          #order Go, 0, model  starting_values
anim
```

$$G = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & A\sigma_{mc}^2 \end{pmatrix}$$

Maternal Effects Model in ASREML

```
Analysis of some kind
 anim !P          The variable 'anim' is related to a pedigree fil
 dam !P           The variable 'dam' is related to a pedigree file
 dage 10 !A
 rt 6
 wwt
 grp 322 !A
example.ped
example.dat
wwt ~ mu rt dage !r anim  ide(dam) !f grp          #model definition
```

$$G = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & A\sigma_{mc}^2 \end{pmatrix}$$

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

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

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

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

Multiple Trait Model

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

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

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

only if all animals all traits; $R_{ij} = I\sigma_{e_{ij}}$

Remember the general definition of the model

$$y = Xb + Zu + e$$

var(u) = G

var(e) = R

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

var(u) = A σ_a^2

var(e) = I σ_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

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

Note: all traits measured on all animal here

Multiple Trait Model in ASREML

Analysis of some kind
 anim !P   The variable 'anim' is related to a pedigree fil
 dage 10 !A
 rt 6
 wwt
 ywt
example.ped
example.dat
wwt ywt ~ Trait Trait.rt Trait.dage !r Trait.anim   #model definition
1 2 1   #R struc: # sites, dim Ro, #G struct
0
2 0 US 4.9 0 5.7 !GP
Trait.anim 2   #G structure: model term, dimensions
2 0 US 2 0 3   #order Go, 0, model starting_values
anim

$$G = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & A\sigma_{mc}^2 \end{pmatrix}$$

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

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

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

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

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

SOLUTIONS

	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

SOLUTIONS

	Single Trait		Multiple Trait	
b1	183	325	183	309
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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. (arrows point to u1 and u4)

SOLUTIONS

	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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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

Difference larger in MT model

SOLUTIONS

	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

Herd effect on YW overestimated with ST

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)

Selection on phenotype only

	h^2_2	h^2_1 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

What is a Covariance Function?

A continuous function to give:

the variance and covariance of traits measured at different points on a trajectory

trajectory can be time, environment (continuous variable)

Random effect is a function of t

$$y_t = Xb + u_t + e_t$$

$\alpha_0 + \alpha_1 * t$ → u_t

1^{st} order

What is a Covariance Function?

$u_t = \alpha_0 + \alpha_1 * t$ Random effect is a function of t

$$u_t = \begin{pmatrix} 1 & t \end{pmatrix} \begin{pmatrix} \alpha_0 \\ \alpha_1 \end{pmatrix}$$

$$var(u_t) = var(\alpha_0) + 2\, t\, cov(\alpha_0 , \alpha_1 t) + t^2\, var(\alpha_1)$$

$$var(u_t) = \begin{pmatrix} 1 & t \end{pmatrix} \; var \begin{pmatrix} \alpha_0 \\ \alpha_1 \end{pmatrix} \begin{pmatrix} 1 \\ t \end{pmatrix}$$

1 measurement
order 2 (k=2)

$$= \Phi \quad K \quad \Phi'$$

K: order k by k

What is a Covariance Function?

2 measurements

$$\mathrm{Var}\begin{pmatrix} u_1 \\ u_2 \end{pmatrix} = \begin{pmatrix} 1 & t_1 \\ 1 & t_2 \end{pmatrix} \mathrm{var}\begin{pmatrix} \alpha_0 \\ \alpha_1 \end{pmatrix} \begin{pmatrix} 1 & 1 \\ t_1 & t_2 \end{pmatrix}$$

$$= \quad \Phi \quad K \quad \Phi' \quad = G$$

Order *t x k* *k x k* *k x t*

t = number of traits (ages) measured

k = order of the CF

Random Regression notation

$$y = Xb + \sum_{i=0}^{k-1} Z_i a_i + \sum_{i=0}^{k-1} Z_i p_i + \varepsilon$$

order equations by animal:

$$y = Xb + Z^* a + Z^* p + \varepsilon$$

Z^* block diagonal *size n by k*q*

blocks $Z_j = \mathbf{\Phi}_j$ *size n_i by k*

Note: in a 'normal animal model' Z_j = 1 or $\begin{pmatrix} 1 \\ 1 \end{pmatrix}$