

ANIMAL BREEDING NOTES

CHAPTER 21

MULTIPLE TRAIT MODELS

In multiple trait analysis animals are evaluated for several traits simultaneously, using information on all characters from the animals themselves and(or) their relatives.

Advantages:

- (i) Higher accuracy of prediction than in single trait analysis. The error variance of prediction will decrease depending on the amount and type (e.g., relatives, own performance) of information available. The largest benefits will probably be for animals with small amounts of information on each trait.
- (ii) Accounts for biases due to sequential selection, e.g., selection of animals at weaning results in a nonrandom sample of animals present as yearlings. A single trait analysis of yearling weights will be biased, whereas a multiple trait analysis will eliminate much of this bias because it includes the information used to select these calves, e.g., weaning weights.

Disadvantages:

- (i) Longer computing times for m-trait analysis than for m single trait analyses. Computer times m-trait multiple trait analyses will be higher than the time for m single traits analysis, because there will be more nonzero elements in the MME, thus less efficient computing strategies than those for single trait analysis (e.g., disk storage versus direct memory computations) may need to be used.
- (ii) Larger number of variances and covariances assumed to be known in an n-trait multiple traits analysis than in n single trait analysis, e.g.,

Number of traits (m)	m single trait analyses		m-trait multiple trait analysis	
	Add. Gen. Cov.	Res. Cov.	Add. Gen Cov.	Res. Cov.
2	2	2	3	3
3	3	3	6	6
4	4	4	10	10
5	5	5	15	15
6	6	6	21	21

These additive genetic and residual covariances must be estimated, which may take a substantially longer computer time. Also, estimates of covariance components are more difficult to compute accurately than estimates of variance components. A poor set of covariance estimates may offset any increase in accuracy of a multiple trait analysis, and it may yield predictions of additive genetic animal values that are more unreliable than those from single trait analyses.

General Multiple Trait Model (GMTM)

The **GMTM** is explained here using two traits. Extension to more than two traits is straightforward.

Let the equations for the records of traits 1 and 2 be:

$$y_1 = X_1b_1 + Z_1u_1 + e_1$$

and

$$y_2 = X_2b_2 + Z_2u_2 + e_2$$

Then, the **GMTM** for these two traits is:

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

$$E \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix}$$

$$\text{var} \begin{bmatrix} u_1 \\ u_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} & 0 & 0 \\ G_{21} & G_{22} & 0 & 0 \\ 0 & 0 & R_{11} & R_{12} \\ 0 & 0 & R_{21} & R_{22} \end{bmatrix}$$

where

y_i = vector of record for trait i , $i = 1, 2$,

b_i = vector of fixed effects for trait i , $i = 1, 2$,

u_i = vector of random additive genetic effects for trait i , $i = 1, 2$,

e_i = vector of residuals for trait i , $i = 1, 2$,

X_i = incidence matrix relating records for trait i to elements of b_i , $i = 1, 2$,

Z_i = incidence matrix relating records for trait i to elements of u_i , $i = 1, 2$,

G_{ij} = $A * g_{ij}$, additive genetic covariance matrix between traits i and j , $i, j = 1, 2$,

R_{ij} = $I * r_{ij}$, residual covariance matrix between traits i and j , $i, j = 1, 2$.

Let the inverse of the two trait additive covariance matrix G , where $G = \begin{bmatrix} G_{11} & G_{12} \\ G_{21} & G_{22} \end{bmatrix}$ be:

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

and define the inverse of the two trait residual covariance matrix R , where $R = \begin{bmatrix} R_{11} & R_{12} \\ R_{21} & R_{22} \end{bmatrix}$ be:

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

Then, the MME for the **GMTM for 2 traits** are:

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

Numerical example for GMTM with 2 traits

Suppose that birth weights (BW) and weaning weights (WW) were taken only for calves in the example used for single trait direct genetic effects models (Chapters 16 and 17). The resulting dataset will be analyzed using a multiple trait animal model (**MTAM**) and a multiple trait sire-maternal grandsire model (**MTSMM**).

1) Multiple trait animal model (**MTAM**): The 2-trait mixed model for BW and WW contains sex of calf as fixed effects and animal and residual as random effects. The **MTAM** with BW and WW records ordered by trait and animals within traits is:

$$\begin{bmatrix} 38 \\ 36 \\ 34 \\ 39 \\ 40 \\ \vdots \\ 289 \\ 285 \\ 265 \\ 290 \\ 288 \end{bmatrix} = \begin{bmatrix} 1 & 0 & | & 0 & 0 \\ 1 & 0 & | & 0 & 0 \\ 0 & 1 & | & 0 & 0 \\ 1 & 0 & | & 0 & 0 \\ 0 & 1 & | & 0 & 0 \\ \vdots & \vdots & | & \vdots & \vdots \\ 0 & 0 & | & 1 & 0 \\ 0 & 0 & | & 1 & 0 \\ 0 & 0 & | & 0 & 1 \\ 0 & 0 & | & 1 & 0 \\ 0 & 0 & | & 0 & 1 \end{bmatrix} \begin{bmatrix} b_{11} \\ b_{12} \\ \vdots \\ b_{21} \\ b_{22} \end{bmatrix} + \begin{bmatrix} 0 & \dots & 0 & 1 & 0 & 0 & 0 & 0 & | & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \dots & 0 & 0 & 1 & 0 & 0 & 0 & | & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \dots & 0 & 0 & 0 & 1 & 0 & 0 & | & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \dots & 0 & 0 & 0 & 0 & 1 & 0 & | & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \dots & 0 & 0 & 0 & 0 & 0 & 1 & | & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & | & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 & | & 0 & \dots & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 & | & 0 & \dots & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 & | & 0 & \dots & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 & | & 0 & \dots & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & \dots & 0 & 0 & 0 & 0 & 0 & 0 & | & 0 & \dots & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} u_{11} \\ \vdots \\ u_{1,10} \\ u_{1,11} \\ u_{1,12} \\ u_{1,13} \\ u_{1,14} \\ u_{1,15} \\ \vdots \\ u_{21} \\ \vdots \\ u_{2,10} \\ u_{2,11} \\ u_{2,12} \\ u_{2,13} \\ u_{2,14} \\ u_{2,15} \end{bmatrix} + \begin{bmatrix} e_{1,11} \\ e_{1,12} \\ e_{1,13} \\ e_{1,14} \\ e_{1,15} \\ \vdots \\ e_{2,11} \\ e_{2,12} \\ e_{2,13} \\ e_{2,14} \\ e_{2,15} \end{bmatrix}$$

$$\text{var} \begin{bmatrix} u_1 \\ u_2 \\ \vdots \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A g_{11} & A g_{12} & | & 0 & 0 \\ A g_{21} & A g_{22} & | & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & | & I_{r_{11}} & I_{r_{12}} \\ 0 & 0 & | & I_{r_{21}} & I_{r_{22}} \end{bmatrix}$$

The matrix of additive genetic variances and covariances for BW and WW in the **MTAM** is equal to:

$$G_o = \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix} = \begin{bmatrix} \sigma_{A_{11}} & \sigma_{A_{12}} \\ \sigma_{A_{21}} & \sigma_{A_{22}} \end{bmatrix} = \begin{bmatrix} 2 & 3 \\ 3 & 22 \end{bmatrix}$$

The matrix of additive genetic covariances among all animals in the **MTAM** is $G = A * G_o$, where $*$ = direct product. The **inverse of matrix G** computed as $G^{-1} = A^{-1} * G_o^{-1}$, where A^{-1} is computed using Henderson's rules and G_o^{-1} by direct inversion, is shown in the **SAS IML output** for the **MTAM** model.

The matrix of environmental variances and covariances for BW and WW in the **MTAM** is:

$$R_o = \begin{bmatrix} r_{11} & r_{12} \\ r_{21} & r_{22} \end{bmatrix} = \begin{bmatrix} \sigma_{E_{11}} & \sigma_{E_{12}} \\ \sigma_{E_{21}} & \sigma_{E_{22}} \end{bmatrix} = \begin{bmatrix} 8 & 8 \\ 8 & 88 \end{bmatrix}$$

The matrix of residual variances and covariances among nonparents with records in the **MTAM** is equal to:

$$R = I * R_o = \begin{bmatrix} R_{11} & R_{12} \\ R_{21} & R_{22} \end{bmatrix}$$

where $*$ = direct product.

The **inverse of R**, i.e., $R^{-1} = I_n * R_o^{-1}$, where I_n is an identity matrix, R_o^{-1} is computed by direct inversion and $*$ = direct product. Matrix R^{-1} for the **MTAM** is equal to:

R^{-1}									
0.1375	0	0	0	0	-0.0125	0	0	0	0
0	0.1375	0	0	0	0	-0.0125	0	0	0
0	0	0.1375	0	0	0	0	-0.0125	0	0
0	0	0	0.1375	0	0	0	0	-0.0125	0
0	0	0	0	0.1375	0	0	0	0	-0.0125
-0.0125	0	0	0	0	0.0125	0	0	0	0
0	-0.0125	0	0	0	0	0.0125	0	0	0
0	0	-0.0125	0	0	0	0	0.0125	0	0
0	0	0	-0.0125	0	0	0	0	0.0125	0
0	0	0	0	-0.0125	0	0	0	0	0.0125

The MME for the **MTAM** are:

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

The **left hand side** (34×34) and the **right hand side** (34×1) of the MME are shown in the SAS IML output for **MTAM**. Notice that the elements of the right hand side for animals without records (pedigree animals 1 to 10) are equal to zero.

The **MTAM** solutions for sex effects and their standard errors are:

Effect	b_{iBW}^0	$SE(b_{iBW}^0)$	b_{iWW}^0	$SE(b_{iWW}^0)$
Male	37.63	1.95	287.87	6.47

Female	37.00	2.32	276.51	7.70
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The **MTAM** predicted breeding values and standard errors of prediction for all animals are:

Effect	\hat{u}_{iBW}	SEP(\hat{u}_{iBW})	\hat{u}_{iWW}	SEP(\hat{u}_{iWW})
Animal 1	-0.03	1.41	-0.07	4.68
Animal 2	-0.08	1.40	-0.22	4.63
Animal 3	-0.11	1.55	-0.30	5.15
Animal 4	-0.45	1.38	-1.48	4.59
Animal 5	0.53	1.36	1.71	4.52
Animal 6	-0.13	1.62	-0.35	5.37
Animal 7	-0.21	1.70	-0.57	5.65
Animal 8	-0.40	1.51	-1.34	5.00
Animal 9	0.19	1.50	0.52	4.99
Animal 10	0.51	1.59	1.68	5.27
Animal 11	-0.08	1.66	-0.21	5.50
Animal 12	-0.45	1.48	-1.25	4.92
Animal 13	-0.72	1.57	-2.52	5.21
Animal 14	0.46	1.55	1.25	5.15
Animal 15	0.79	1.60	2.71	5.30

2) Multiple trait sire maternal grandsire model (**MTSMM**): The 2-trait mixed model for BW and WW contains sex of calf as fixed effects, and sires and maternal grandsires and residual as random

effects. The **MTSMM** with BW and WW records ordered by trait and animals within traits is:

$$\begin{bmatrix} 38 \\ 36 \\ 34 \\ 39 \\ 40 \\ \vdots \\ 289 \\ 285 \\ 265 \\ 290 \\ 288 \end{bmatrix} = \begin{bmatrix} 1 & 0 & | & \\ 1 & 0 & | & \\ 0 & 1 & | & 0 \\ 1 & 0 & | & \\ 0 & 1 & | & \\ \vdots & \vdots & | & \vdots \\ & & | & 1 & 0 \\ & & | & 1 & 0 \\ & 0 & | & 0 & 1 \\ & & | & 1 & 0 \\ & & | & 0 & 1 \end{bmatrix} \begin{bmatrix} b_{11} \\ b_{12} \\ \vdots \\ b_{21} \\ b_{22} \end{bmatrix} + \begin{bmatrix} 0 & 1.5 & 0 & 0 & | & \\ 0 & 0.5 & 1 & 0 & | & \\ 0 & 0 & 1.5 & 0 & | & \\ 0 & 0 & 0 & 1.5 & | & 0 \\ 0 & 0 & 0 & 1.5 & | & \\ \vdots & \vdots & \vdots & \vdots & | & \vdots \\ & & & & | & 0 & 1.5 & 0 & 0 \\ & & & & | & 0 & 0.5 & 1 & 0 \\ & 0 & & & | & 0 & 0 & 1.5 & 0 \\ & & & & | & 0 & 0 & 0 & 1.5 \\ & & & & | & 0 & 0 & 0 & 1.5 \end{bmatrix} \begin{bmatrix} u_{11} \\ u_{13} \\ u_{14} \\ u_{15} \\ \vdots \\ u_{21} \\ u_{23} \\ u_{24} \\ u_{25} \end{bmatrix} + \begin{bmatrix} 1/4 u_{mgd_1} + 1/2 \phi_{d_1} + \phi_{n_1} + e_{n_1} \\ 1/4 u_{mgd_2} + 1/2 \phi_{d_2} + \phi_{n_2} + e_{n_2} \end{bmatrix}$$

$$\text{var} \begin{bmatrix} u_1 \\ u_2 \\ \vdots \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A g_{11} & A g_{12} & | & 0 & 0 \\ A g_{21} & A g_{22} & | & 0 & 0 \\ \vdots & \vdots & | & \vdots & \vdots \\ 0 & 0 & | & (D_n \sigma_{A11} + I_n \sigma_{E11}) & (D_n \sigma_{A12} + I_n \sigma_{E12}) \\ 0 & 0 & | & (D_n \sigma_{A21} + I_n \sigma_{E21}) & (D_n \sigma_{A22} + I_n \sigma_{E22}) \end{bmatrix}$$

The matrix of additive genetic variances and covariances for BW and WW in the **MTSMM** is equal to:

$$G_o = \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix} = (0.25) \begin{bmatrix} \sigma_{A11} & \sigma_{A12} \\ \sigma_{A21} & \sigma_{A22} \end{bmatrix} = \begin{bmatrix} 0.5 & 0.75 \\ 0.75 & 5.5 \end{bmatrix}$$

The matrix of additive genetic covariances among sires and maternal grandsires in the **MTSMM** is $\mathbf{G} = \mathbf{A} * \mathbf{G}_o$, where $*$ = direct product. The inverse of matrix \mathbf{G} , i.e., \mathbf{G}^{-1} , computed as $\mathbf{A}^{-1} * \mathbf{G}_o^{-1}$, where \mathbf{A}^{-1} is obtained using Henderson's rules and \mathbf{G}_o^{-1} by direct inversion, is equal to:

$$G^{-1} = \begin{bmatrix} 0.5 & 0.375 & 0.25 & 0.25 & | & 0.75 & 0.5625 & 0.375 & 0.375 \\ & 0.625 & 0.1875 & 0.1875 & | & 0.5625 & 0.9375 & 0.28125 & 0.28125 \\ & & 0.5 & 0.125 & | & 0.375 & 0.28125 & 0.75 & 0.1875 \\ & & & 0.5 & | & 0.375 & 0.28125 & 0.1875 & 0.75 \\ --- & --- & --- & --- & | & --- & --- & --- & --- \\ & & & & | & 5.5 & 4.125 & 2.75 & 2.75 \\ & & & & | & & 6.875 & 2.0625 & 2.0625 \\ & & & & | & & & 5.5 & 1.375 \\ & & & & | & & & & 5.5 \end{bmatrix}^{-1}$$

Symmetric

The matrix of environmental variances and covariances for the **MTSMM** is:

$$R_o = \begin{bmatrix} r_{11} & r_{12} \\ r_{21} & r_{22} \end{bmatrix} = \begin{bmatrix} \sigma_{E11} & \sigma_{E12} \\ \sigma_{E21} & \sigma_{E22} \end{bmatrix} = \begin{bmatrix} 8 & 8 \\ 8 & 88 \end{bmatrix}$$

The matrix of residual variances and covariances among nonparents with records in the **MTSMM** is equal to:

$$R = D_n * G_0 + I * R_o = \begin{bmatrix} R_{11} & R_{12} \\ R_{21} & R_{22} \end{bmatrix}$$

where $*$ = direct product, and $D_n = (I - \frac{1}{2} P_{\text{sire}} - \frac{1}{4} P_{\text{mgs}})$ is the matrix of coefficients of residual genetic variances and covariances for nonparents in the **MTSMM**. Matrix D_n (from Chapter 17, page 19) is equal to:

$$D_n = \begin{bmatrix} 0.609375 & & & & \\ & 0.671875 & & & \\ & & 0.6875 & & \\ & & & 0.6875 & \\ & & & & 0.6875 \end{bmatrix}$$

Thus, the matrix of residual variances and covariances among nonparents with records in the

MTSMM is equal to:

$$R = D_n * \begin{bmatrix} 2 & 3 \\ 3 & 22 \end{bmatrix} + I_n * \begin{bmatrix} 8 & 8 \\ 8 & 88 \end{bmatrix}$$

$$R = \begin{bmatrix} D_n * (2) + I_n(8) & D_n * (3) + I_n(8) \\ D_n * (3) + I_n(8) & D_n * (22) + I_n(88) \end{bmatrix}$$

and the inverse of R is:

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

Matrix R^{-1} for the **MTSMM** is:

R^{-1}									
0.1209742	0	0	0	0	-0.011725	0	0	0	0
0	0.1195062	0	0	0	0	-0.011645	0	0	0
0	0	0.1191449	0	0	0	0	-0.011626	0	0
0	0	0	0.1191449	0	0	0	0	-0.011626	0
0	0	0	0	0.1191449	0	0	0	0	-0.011626
-0.011725	0	0	0	0	0.0109977	0	0	0	0
0	-0.011645	0	0	0	0	0.0108642	0	0	0
0	0	-0.011626	0	0	0	0	0.0108314	0	0
0	0	0	-0.011626	0	0	0	0	0.0108314	0
0	0	0	0	-0.011626	0	0	0	0	0.0108314

The MME for the **MTSMM** are:

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

The left hand side of the MME for **MTSMM** is:

0.359625	0	-0.035	0	0	0.241214	0.119506	0.178717	0	-0.02341	-0.01165	-0.01744
0	0.23829	0	-0.02325	0	0	0.178717	0.178717	0	0	-0.01744	-0.01744
-0.035	0	0.032693	0	0	-0.02341	-0.01165	-0.01744	0	0.021929	0.010864	0.016247
0	-0.02325	0	0.021663	0	0	-0.01744	-0.01744	0	0	0.016247	0.016247
0	0	0	0	6.247619	-2.74286	-1.67619	-1.67619	-0.85195	0.374026	0.228571	0.228571
0.241214	0	-0.02341	0	-2.74286	3.959211	0.059753	0	0.374026	-0.52799	-0.00582	0
0.119506	0.178717	-0.01165	-0.01744	-1.67619	0.059753	3.739963	0	0.228571	-0.00582	-0.49495	0
0.178717	0.178717	-0.01744	-0.01744	-1.67619	0	0	3.888533	0.228571	0	0	-0.50946
0	0	0	0	-0.85195	0.374026	0.228571	0.228571	0.567965	-0.24935	-0.15238	-0.15238
-0.02341	0	0.021929	0	0.374026	-0.52799	-0.00582	0	-0.24935	0.359928	0.005432	0
-0.01165	-0.01744	0.010864	0.016247	0.228571	-0.00582	-0.49495	0	-0.15238	0.005432	0.339997	0
-0.01744	-0.01744	0.016247	0.016247	0.228571	0	0	-0.50946	-0.15238	0	0	0.353503

The right hand side of the MME for **MTSMM** is:

3.4670989
2.3877353
8.0975408
5.1294392
0
2.304549

2.4384748
4.0392275
0
5.4377116
6.3896163
8.013142

The **MTSMM** solutions for sex effects and their standard errors are:

Effect	b_{iBW}^0	$SE(b_{iBW}^0)$	b_{iWW}^0	$SE(b_{iWW}^0)$
Male	37.63	1.95	287.87	6.47
Female	37.00	2.32	276.51	7.70

The **MTSMM** predictions of transmitting abilities (i.e., $\frac{1}{2}$ BV) for sires and maternal grandsires and their standard errors of prediction are:

Effect	\hat{u}_{iBW}	$SEP(\hat{u}_{iBW})$	\hat{u}_{iWW}	$SEP(\hat{u}_{iWW})$
Sire 1	-0.00	0.71	0.01	2.34
Sire 3	-0.00	0.78	0.02	2.57
Sire 4	-0.24	0.69	-0.77	2.29
Sire 5	0.24	0.69	0.76	2.27

Special cases of multiple trait analysis

The structure of the data vector, the pedigree of the animals being evaluated and the model used for each trait allow, in some cases, to develop more efficient and less expensive algorithms to compute

the solutions of multiple trait analyses.

[1] **Animals have measurements on all traits, parents are either non-inbred or have the same level of inbreeding, the incidence matrices of the fixed effects are equal for all traits and the incidence matrices for the random effects are equal for all traits.**

Under these conditions, the **GMTM** becomes:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X & 0 \\ 0 & X \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z & 0 \\ 0 & Z \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

$$E \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X & 0 \\ 0 & X \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix}$$

$$\text{var} \begin{bmatrix} u_1 \\ u_2 \\ \vdots \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A g_{11} & A g_{11} & | & 0 & 0 \\ A g_{21} & A g_{22} & | & 0 & 0 \\ \hline 0 & 0 & | & I_n r_{11} & I_n r_{12} \\ 0 & 0 & | & I_n r_{21} & I_n r_{22} \end{bmatrix}$$

Let the above model be multiple trait model 1 (MTM1). The **MTM1** can also be written, using the direct product notation, as follows:

$$y = (I_2 * X)b + (I_2 * Z)u + e$$

$$E[y] = (I_2 * X)b$$

$$\text{var} \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} A * G_o & 0 \\ 0 & I * R_o \end{bmatrix}$$

where

$$y = \begin{bmatrix} y_1 \\ y_2 \end{bmatrix}, \quad b = \begin{bmatrix} b_1 \\ b_2 \end{bmatrix}, \quad u = \begin{bmatrix} u_1 \\ u_2 \end{bmatrix}, \quad e = \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

$$G_o = \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix}, \text{ and } R_o = \begin{bmatrix} r_{11} & r_{12} \\ r_{21} & r_{22} \end{bmatrix}.$$

The MME for the **MTM1** are:

$$\begin{bmatrix} R_o^{-1} * X'X & R_o^{-1} * X'Z \\ R_o^{-1} * Z'X & R_o^{-1} * Z'Z + G_o^{-1} * A^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} (R_o^{-1} * X')y \\ (R_o^{-1} * Z')y \end{bmatrix}$$

More explicitly the MME for the **MTM1** are:

$$\begin{bmatrix} r^{11}X'X & r^{12}X'X & r^{11}X'Z & r^{12}X'Z \\ & r^{22}X'X & r^{21}X'Z & r^{22}X'Z \\ & & r^{11}Z'Z + A^{-1}g^{11} & r^{12}Z'Z + A^{-1}g^{12} \\ \text{Symmetric} & & & r^{22}Z'Z + A^{-1}g^{22} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ u_1 \\ u_2 \end{bmatrix} = \begin{bmatrix} r^{11}X'y_1 + r^{12}X'y_2 \\ r^{21}X'y_1 + r^{22}X'y_2 \\ r^{11}Z'y_1 + r^{12}Z'y_2 \\ r^{21}Z'y_1 + r^{22}Z'y_2 \end{bmatrix}$$

If $r^{12} = 0$ and $g^{12} = 0$ the set of MME for the **MTM1** becomes two independent single trait analyses.

Thus, the task is to transform the data such that the records of an animal for different traits are uncorrelated. This can be achieved by using a **canonical transformation**.

Let

$$\mathcal{L} = \begin{bmatrix} L^{-1} * I_n & 0 \\ 0 & L^{-1} * I_n \end{bmatrix}$$

where

n = number of animals with records

L = $t \times t$ matrix, where t is the number of traits.

The matrix L is chosen such that:

(i) $L'R^{-1}L = I$

(ii) $L'G^{-1}L = D$ a diagonal matrix

How to find L ?

Quaas's (1986) approach:

(i) Decompose R_o using any transformation, e.g., Cholesky decomposition, so that:

$$\mathbf{R}_o = \mathbf{T}\mathbf{T}'$$

(ii) Compute $\mathbf{B} = \mathbf{T}'\mathbf{G}_o^{-1}\mathbf{T}$. Then, decompose B as follows:

$$\mathbf{B} = \mathbf{U}\mathbf{D}\mathbf{U}'$$

where

\mathbf{D} = diagonal matrix, whose elements are the eigenvalues of B

\mathbf{U} = orthogonal matrix whose columns are the orthonormal eigenvectors of B ,

i.e.,

$$\mathbf{U}\mathbf{U}' = \mathbf{U}'\mathbf{U} = \mathbf{I}$$

(iii) Compute $\mathbf{L} = \mathbf{T}\mathbf{U}$.

Proof that $\mathbf{L} = \mathbf{T}\mathbf{U}$:

$$\begin{aligned} \text{(i) } \mathbf{L}'\mathbf{R}^{-1}\mathbf{L} &= \mathbf{U}'\mathbf{T}'\mathbf{T}^{-1}\mathbf{T}^{-1}\mathbf{T}\mathbf{U} \\ &= \mathbf{I} \end{aligned}$$

$$\begin{aligned} \text{(ii) } \mathbf{L}'\mathbf{G}_o^{-1}\mathbf{L} &= \mathbf{U}'\mathbf{T}'\mathbf{G}_o^{-1}\mathbf{T}\mathbf{U} \\ &= \mathbf{U}'\mathbf{T}'\mathbf{T}^{-1}\mathbf{B}\mathbf{T}^{-1}\mathbf{T}\mathbf{U} \\ &= \mathbf{U}'\mathbf{B}\mathbf{U} \\ &= \mathbf{U}'\mathbf{U}\mathbf{D}\mathbf{U}'\mathbf{U} \\ &= \mathbf{D} \end{aligned}$$

Using $\mathcal{L} = \begin{bmatrix} \mathbf{L}^{-1} * \mathbf{I}_n & 0 \\ 0 & \mathbf{L}^{-1} * \mathbf{I}_n \end{bmatrix}$ on the **MTM1**, where $\mathbf{L} = \mathbf{T}\mathbf{U}$, yields **MTM2**.

$$(L^{-1} * I_n)y = (L^{-1} * I_n)(I_t * X)b + (L^{-1} * I_n)(I_t * Z)u + (L^{-1} * I_n)e$$

$$(L^{-1} * I_n)y = (L^{-1} I_t * I_n X)b + (L^{-1} I_t * I_n Z)u + (L^{-1} * I_n)e$$

$$(L^{-1} * I_n)y = (L^{-1} * X)b + (L^{-1} * Z)u + (L^{-1} * I_n)e$$

$$(L^{-1} * I_n)y = (I_t * X)(L^{-1} * I_f)b + (I_t * Z)(L^{-1} * I_r)u + (L^{-1} * I_n)e$$

or

$$y^* = (I_t * X)b^* + (I_t * Z)u^* + e^*$$

where

$$n = \text{number of animals with records,}$$

$$t = \text{number of traits,}$$

$$f = \text{number of fixed effects per trait,}$$

$$r = \text{number of random effects per trait,}$$

$$b^* = (L^{-1} * I_f)b$$

$$u^* = (L^{-1} * I_r)u$$

$$e^* = (L^{-1} * I_n)e$$

$$y^* = (L^{-1} * I_n)y$$

$$E[y^*] = (L^{-1} * I_n)Xb$$

$$= (L^{-1} * X)b$$

$$\text{var}(u^*) = (L^{-1} * I_r)(G_o * A)(L^{-T} * I_r)$$

$$= L^{-1}G_oL^{-T} * A$$

But,

$$B = T'G^{-1}T$$

$$= UDU'$$

$$\Rightarrow G_0^{-1} = T^{-T}UDU'T^{-1}$$

$$\Rightarrow G_0^{-1} = L^{-T}DL^{-1}$$

$$\Rightarrow G_0 = LD^{-1}L'$$

Thus,

$$\begin{aligned}\text{var}(u^*) &= L^{-1}LD^{-1}L'L^{-T}A \\ &= D^{-1}A\end{aligned}$$

and

$$\begin{aligned}\text{var}(e^*) &= (L^{-1}I_n)(R_0I_n)(L^{-1}I_n) \\ &= L^{-1}R_0L^{-T}I_n \\ &= U'T^{-1}TT'T^{-T}U \\ &= I_tI_n\end{aligned}$$

Thus,

$$\text{var}\begin{bmatrix} u^* \\ e^* \end{bmatrix} = \begin{bmatrix} D^{-1}A & 0 \\ 0 & I_tI_n \end{bmatrix}$$

The transformed model for the i^{th} trait is:

$$y = Xb + Zu + e$$

$$E[y] = XB$$

$$\text{var}\begin{bmatrix} u_i \\ e_i \end{bmatrix} = \begin{bmatrix} d_i^{-1}A & 0 \\ 0 & I_n \end{bmatrix}$$

The MME of the transformed records for the i^{th} trait are:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + d_iA^{-1} \end{bmatrix} \begin{bmatrix} b_i^* \\ u_i^* \end{bmatrix} = \begin{bmatrix} X'y_i^* \\ Z'y_i^* \end{bmatrix}$$

The untransformed solutions can be obtained as follows:

$$(i) \quad \hat{\mathbf{b}}^* = (\mathbf{L}^{-1} * \mathbf{I}_f) \hat{\mathbf{b}}$$

$$\Rightarrow \quad \hat{\mathbf{b}} = (\mathbf{L} * \mathbf{I}_f) \hat{\mathbf{b}}^*$$

$$\Rightarrow \quad \hat{b}_i = \sum_{j=1}^t \ell_{ij} \hat{b}_j^*$$

$$(ii) \quad \hat{\mathbf{u}}^* = (\mathbf{L}^{-1} * \mathbf{I}_r) \hat{\mathbf{u}}$$

$$\Rightarrow \quad \hat{\mathbf{u}} = (\mathbf{L} * \mathbf{I}_r) \hat{\mathbf{u}}^*$$

$$\Rightarrow \quad \hat{u}_i = \sum_{j=1}^t \ell_{ij} \hat{u}_j^*$$

Cholesky Decomposition

If a matrix \mathbf{A} is symmetric positive definite, then there exists a lower triangular matrix \mathbf{T} with positive diagonal entries such that $\mathbf{A} = \mathbf{T}\mathbf{T}'$ (Golub and Van Loan, 1984).

Computing algorithm (row version)

For $i = 1, \dots, n$ compute:

$$t_{ii} = \left(a_{ii} - \sum_{k=1}^{i-1} t_{ik}^2 \right)^{1/2}$$

For $\ell = i + 1, \dots, n$ compute:

$$t_{\ell j} = \left(a_{\ell j} - \sum_{k=1}^{i-1} t_{\ell k} t_{jk} \right) * t_{\ell \ell}^{-1}$$

Example:

Consider the matrix R_o for the case of a model with four traits.

Let R_o be:

$$R_o = \begin{bmatrix} 64 & 32 & 6 & 8 \\ 32 & 51 & 14 & 28 \\ 16 & 14 & 30 & 41 \\ 8 & 28 & 41 & 147 \end{bmatrix}$$

Then,

$$t_{11} = (64)^{1/2} = 8$$

$$t_{21} = 32/8 = 4$$

$$t_{31} = 16/8 = 2$$

$$t_{41} = 8/8 = 1$$

$$t_{22} = (52 - 4^2)^{1/2} = 6$$

$$t_{32} = (14 - 4*2)/6 = 1$$

$$t_{42} = (28 - 4*1)/6 = 4$$

$$t_{33} = (30 - 2^2 - 1^2)^{1/2} = 5$$

$$t_{43} = (41 - 2*1 - 1*4)/5 = 7$$

$$t_{44} = (147 - 1^2 - 4^2 - 7^2)^{1/2} = 9$$

Thus,

$$T = \begin{bmatrix} 8 & 0 & 0 & 0 \\ 4 & 6 & 0 & 0 \\ 2 & 1 & 5 & 0 \\ 1 & 4 & 7 & 9 \end{bmatrix}$$

[II] Animals have missing records following some pattern, parents are either non-inbred or

have the same level of inbreeding and the incidence matrices for the fixed and for the random effects are the same for all traits.

(a) **Missing records in traits that are recorded sequentially, e.g., birth weight (BW), weaning weight (WW), yearling weight (YW).** If calves are selected after BW as well as after WW, the following patterns for residual covariance matrices will exist:

$$R_{01} = \begin{bmatrix} r_{11} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, R_{02} = \begin{bmatrix} r_{11} & r_{12} & 0 \\ r_{21} & r_{22} & 0 \\ 0 & 0 & 0 \end{bmatrix}, \text{ and } R_{03} = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix}.$$

Is there an **transformation of the data vector that uncorrelates the residual effects**? The task here is to find a matrix T such that:

$$(i) \quad T'R_oT = I$$

$$\Rightarrow R_o = (T')^{-1}T^{-1}$$

$$\Rightarrow R_o^{-1} = TT'$$

$$(ii) \quad T_i'R_{oi}T = \text{diag}\{\delta_i 1\} \text{ for } 1 \leq i \leq t$$

$$\Rightarrow R_{oi} = (T_i')^{-1}T$$

$$\Rightarrow R_{oi}^{-1} = T_iT_i'$$

where

$$R_o = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix}$$

$T_i =$ matrix T with the rows and columns for the traits not measured on an animal replaced by zeroes.

$$\delta_i = \text{Kronecker delta} \begin{cases} = 1 & \text{if a trait was measured on an animal} \\ = 0 & \text{otherwise} \end{cases}$$

R_{oi} = matrix R_o with zeroes substituted for the elements of the rows and columns corresponding to traits not measured on an animal.

$$R_o^{-1} = \text{inverse of } R_o$$

$$R_{oi}^- = \text{generalized inverse of } R_{oi}$$

$$T_i^- = \text{generalized inverse of } T_i$$

Consider a **triangular transformation** (Pollak, 1983, personal communication; Quaas et al., 1984), where T is a Cholesky decomposition of R_o^{-1} , i.e., T is a lower triangular matrix so that:

$$(i) R_o^{-1} = TT' \Rightarrow R_o = T^{-T}T^{-1} \Rightarrow T'R_oT = I$$

$$(ii) T_i'R_{oi}T_i = \text{diag} \{\delta_i 1\} \text{ for } 1 \leq i \leq t$$

For instance, for the BW, WW and YW case above,

$$T_{01} = \begin{bmatrix} t_{11} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, T_{02} = \begin{bmatrix} t_{11} & 0 & 0 \\ t_{21} & t_{22} & 0 \\ 0 & 0 & 0 \end{bmatrix}, \text{ and } T_{03} = \begin{bmatrix} t_{11} & 0 & 0 \\ t_{21} & t_{22} & 0 \\ t_{31} & t_{32} & t_{33} \end{bmatrix},$$

where

$$t_{ii} = \left(a_{ii} - \sum_{k=1}^{i-1} t_{ik}^2 \right)^{1/2}$$

$$t_{ij} = t_{jj}^{-1} \left(a_{ij} - \sum_{k=1}^{i-1} t_{jk} t_{ik} \right).$$

Remarks:

(1) The total number of combinations that exist among t traits is $(2^t - 1)$. However, the maximum number of combinations among t traits that the triangular transformation can handle is less than or equal to t , the maximum number of traits measured per animal.

(2) Define the inverse of T , i.e., T^{-1} as follows:

$$T^{-1} = \text{lower triangular } \{t^{ij}\}$$

where

$$t^{ii} = t_{ii}^{-1}$$

$$t^{ij} = -t_{ii}^{-1} \sum_{k=j}^{i-1} \prod_{\ell=j}^k t_{i\ell} t_{\ell\ell}^{-1}$$

Proof:

Consider the case of three traits and the following identity:

$$\begin{bmatrix} t_{11} & 0 & 0 \\ t_{21} & t_{22} & 0 \\ t_{31} & t_{32} & t_{33} \end{bmatrix} \begin{bmatrix} t^{11} & 0 & 0 \\ t^{21} & t^{22} & 0 \\ t^{31} & t^{32} & t^{33} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} = TT^{-1}$$

Thus, the formula for **diagonal terms of T^{-1}** is:

$$t^{ii} = t_{ii}^{-1}$$

For example, in the case of t^{11} we have that:

$$t_{11} t^{11} = 1$$

$$\Rightarrow t^{11} = t_{11}^{-1}$$

For offdiagonal terms of T^{-1} we have that:

$$(1) \quad t_{21} t^{11} + t_{22} t^{21} = 0$$

$$\Rightarrow t^{21} = -t_{22}^{-1} t_{21} t_{11}^{-1}$$

$$(2) \quad t_{31} t^{11} + t_{32} t^{21} + t_{33} t^{31} = 0$$

$$\Rightarrow \quad t_{31} = -t_{33}^{-1} (t_{31} t_{11}^{-1} + t_{32} t_{22}^{-1} t_{21} t_{11}^{-1})$$

$$(3) \quad t_{32} t^{22} + t_{33} t^{32} = 0$$

$$\Rightarrow \quad t^{32} = -t_{33}^{-1} t_{32} t_{22}^{-1}$$

By observing the pattern of formulae (1), (2) and (3), we obtain the formula for **offdiagonal terms of T^{-1}** , i.e.,

$$t^{ij} = -t_{ii}^{-1} \sum_{k=j}^{i-1} \prod_{\ell=j}^k t_{i\ell} t_{\ell\ell}^{-1}.$$

(4) The g-inverses of T_i for $i = 1, 2$ are:

$$T_1^- y = \begin{bmatrix} t_{11} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} y_1 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} t^{11} y_1 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} y_1^* \\ 0 \\ 0 \end{bmatrix}$$

where the t^{ij} are as defined in remark (2) above.

Thus, the triangular transformation to uncorrelate the residuals of the records of an animal having the i^{th} trait combination, will require to multiply the matrix T_i^- by the vector of recorded traits of this individual. In the weight traits case:

(i) if an animal has trait 1 (BW) recorded only,

$$T_1^{-1} y = \begin{bmatrix} t^{11} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} y_1 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} t^{11} y_1 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} y_1^* \\ 0 \\ 0 \end{bmatrix}$$

(ii) if an animal has traits 1 and 2 recorded,

$$T_2^{-1} y = \begin{bmatrix} t_{11} & 0 & 0 \\ t^{21} & t^{22} & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} t^{11} y_1 \\ t^{21} y_1 + t^{22} y_2 \\ 0 \end{bmatrix} = \begin{bmatrix} y_1^* \\ y_2^* \\ 0 \end{bmatrix}$$

(iii) if an animal has records on all three traits,

$$T_3^{-1} y = \begin{bmatrix} t^{11} & 0 & 0 \\ t^{21} & t^{22} & 0 \\ t^{31} & t^{32} & t^{33} \end{bmatrix} \begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} t^{11} y_1 \\ t^{21} y_1 + t^{22} y_2 \\ t^{31} y_1 + t^{32} y_2 + t^{33} y_3 \end{bmatrix} = \begin{bmatrix} y_1^* \\ y_2^* \\ y_3^* \end{bmatrix}$$

Thus, the **transformed model**:

(i) for animals with BW measured only is:

$$y = X_1 b + Z_1 u + e$$

$$E[y] = X_1 b, \quad b = t^{11} b_1$$

$$\begin{aligned} \text{var} \begin{bmatrix} u_1^* \\ e_1^* \end{bmatrix} &= \text{var} \begin{bmatrix} t^{11} u_1 \\ t^{11} e_1 \end{bmatrix} \\ &= \begin{bmatrix} t^{11} g_{11} t^{11*} A & 0 \\ 0 & t^{11} r_{11} t^{11*} I \end{bmatrix} \end{aligned}$$

(ii) for animals with BW and WW measured is:

$$y = X_2 b + Z_2 u + e$$

$$E[y] = X_2 b, \quad b = t^{21} b_1 + t^{22} b_2$$

$$\text{var} \begin{bmatrix} u_2^* \\ e_2^* \end{bmatrix} = \text{var} \begin{bmatrix} t^{21} u_1 + t^{22} u_2 \\ t^{21} e_1 + t^{22} e_2 \end{bmatrix}$$

$$\begin{aligned}
&= \text{var} \begin{bmatrix} \begin{bmatrix} t^{21} & t^{22} \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} \\ \begin{bmatrix} t^{21} & t^{22} \end{bmatrix} \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \end{bmatrix} \\
&= \begin{bmatrix} (t^{21} g_{11} t^{21} + 2 t^{21} g_{12} t^{22} + t^{22} g_{22} t^{22}) * A & | & 0 \\ 0 & | & (t^{21} r_{11} t^{21} + 2 t^{21} r_{12} t^{22} + t^{22} r_{22} t^{22}) * I \end{bmatrix}
\end{aligned}$$

(iii) for animals with all three traits measured is:

$$\begin{aligned}
y &= X_3 b + Z_3 u + e \\
E[y] &= X_3 b, \quad b = t^{31} b_1 + t^{32} b_2 + t^{33} b_3 \\
\text{var} \begin{bmatrix} u_3^* \\ e_3^* \end{bmatrix} &= \text{var} \begin{bmatrix} t^{31} u_1 + t^{32} u_2 + t^{33} u_3 \\ t^{31} e_1 + t^{32} e_2 + t^{33} e_3 \end{bmatrix} \\
&= \begin{bmatrix} \sum_{i=1}^3 t^{3i} g_{ii} t^{3i} + \sum_{\substack{i,j=1 \\ i \neq j}}^3 t^{3i} g_{ij} t^{3j} & | & 0 \\ 0 & | & \sum_{i=1}^3 t^{3i} r_{ii} t^{3i} + \sum_{\substack{i,j=1 \\ i \neq j}}^3 t^{3i} r_{ij} t^{3j} \end{bmatrix}
\end{aligned}$$

Assuming that we are evaluating all animals for all traits (i.e., the Z_i matrices will contain columns of zeros for the traits animals have no records), the triangularly transformed **GMTM** (i.e., **MTM3**) is:

$$\begin{bmatrix} y_1^* \\ y_2^* \\ y_3^* \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1^* \\ b_2^* \\ b_3^* \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix} \begin{bmatrix} u_1^* \\ u_2^* \\ u_3^* \end{bmatrix} + \begin{bmatrix} e_1^* \\ e_2^* \\ e_3^* \end{bmatrix}$$

$$E \begin{bmatrix} y_1^* \\ y_2^* \\ y_3^* \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1^* \\ b_2^* \\ b_3^* \end{bmatrix}$$

The MME for the **MTM3** are:

$$\begin{bmatrix} X_1'X_1 & 0 & 0 & X_1'Z_1 & 0 & 0 \\ & X_2'X_2 & 0 & 0 & X_2'Z_2 & 0 \\ & & X_3'X_3 & 0 & 0 & X_3'Z_3 \\ & & & Z_1'Z_1 + \theta^{11}A^{-1} & \theta^{12}A^{-1} & \theta^{13}A^{-1} \\ \text{Symmetric} & & & & Z_2'Z_2 + \theta^{22}A^{-1} & \theta^{23}A^{-1} \\ & & & & & Z_3'Z_3 + \theta^{33}A^{-1} \end{bmatrix} \begin{bmatrix} b_1^* \\ b_2^* \\ b_3^* \\ \dots \\ u_1^* \\ u_2^* \\ u_3^* \end{bmatrix} = \begin{bmatrix} X_1'y_1^* \\ X_2'y_2^* \\ X_3'y_3^* \\ \dots \\ Z_1'y_1^* \\ Z_2'y_2^* \\ Z_3'y_3^* \end{bmatrix}$$

where

$$\begin{aligned} \{\theta_{ij}\} &= \begin{bmatrix} t^{11} & 0 & 0 \\ t^{21} & t^{22} & 0 \\ t^{31} & t^{32} & t^{33} \end{bmatrix} \begin{bmatrix} g_{11} & g_{12} & g_{13} \\ g_{21} & g_{22} & g_{23} \\ g_{31} & g_{32} & g_{33} \end{bmatrix} \begin{bmatrix} t^{11} & t^{21} & t^{31} \\ 0 & t^{22} & t^{32} \\ 0 & 0 & t^{33} \end{bmatrix} \\ &= T^{-1}G_0T^{-T} \end{aligned}$$

Thus, the inverse of $\{\theta_{ij}\}$ is:

$$\begin{aligned} \{\theta^{ij}\} &= (T^{-1}G_0T^{-T})^{-1} \\ &= T'G_0T \end{aligned}$$

Advantages of the **MTM3**

- (1) Blocks of zeroes on the LHS of the MME, wherein nonzero blocks existed in the GMTM.

(2) Absorption of the fixed effects becomes much faster, simpler and less expensive.

Disadvantages of the MTM3

Some of the requirements for the triangular transformation may not exist in some data sets. For instance, there can be **more combinations of traits than the total number of traits**, records from different traits may be **affected by one or more different fixed effects**.

Backtransforming the solutions

(1) Fixed effects

$$\{\hat{\mathbf{b}}_i\} = \left\{ \sum_{\ell=1}^i \mathbf{t}_{i\ell} \hat{\mathbf{b}}_{\ell}^* \right\}$$

(2) Random effects

$$\{\hat{\mathbf{u}}_i\} = \left\{ \sum_{\ell=1}^i \mathbf{t}_{i\ell} \hat{\mathbf{u}}_{\ell}^* \right\}$$

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