ANIMAL BREEDING NOTES

CHAPTER 18

REPEATABILITY MODELS

Simple Repeatability Model (SRM)

Objectives:

(i) To predict the **BV of individuals**, i.e., $\hat{u}$, based on their own records and (or) their relatives' records.

(ii) To predict the **environmental effect common to all records of an animal**, i.e., $\hat{p}_i$, the "**permanent environmental effect**" of animal i.

(iii) To predict the "**real producing ability**" of an animal, defined as the **sum of the predicted BV and permanent environmental effects for an animal**, i.e., $\hat{v}_i = \hat{u}_i + \hat{p}_i$.

Assumptions:

(i) Animals are from one population only.

(ii) Animals may have one or more records. If they have two or more records, covariances among them will be due, in part to genetic factors, and in part to permanent environmental factors. Because the various records of an animal are assumed to be measurements of the same trait, no matter how far apart in time they are, the genetic correlation between any two records is assumed to be 1.

(iii) There is no selection in the population or, if there is selection, its effects can be accounted for using the regular MME.

Remarks:

(i) The **SRM** assumes the same correlation among records of an individual. This correlation, usually called **repeatability** (r), is:

$$r = \frac{\sigma^2_A + \sigma^2_{E_p}}{\sigma^2_A + \sigma^2_{E_p} + \sigma^2_{E_t}}$$

where

σ^2_A = additive genetic variance,

$\sigma^2_{E_p}$ = permanent environment variance, and

$\sigma^2_{E_t}$ = temporary environment variance.

The assumption of equal correlations between any two records of an individual is unrealistic. Thus, more general covariance structures among an animal's records have been considered (e.g., covariances based on autoregressive processes, Quaas et al., 1984).

(ii) The assumption that the various records of an animal for a trait, taken over a period of time, are measurements of the same biological character may be incorrect, e.g., milk yield from several lactations of a cow. In such cases, a multiple trait analysis, where each record represents a separate character, may be more appropriate.

The SRM is an extension of the AM (or the EAM) in that an additional source of covariance among records of an individual is assumed. Thus, the **SRM for animals with multiple records** is:

$$y_{ijk} = \mu + \sum_i b_i + u_j + p_j + e_{ijk}$$

$$E[y_{ijk}] = \mu + \sum_i b_i$$

$$\text{var}\begin{bmatrix} u_j \\ p_j \\ e_{ijk} \end{bmatrix} = \begin{bmatrix} a_{jj}\sigma_A^2 & 0 & 0 \\ 0 & \sigma_{E_p}^2 & 0 \\ 0 & 0 & \sigma_e^2 \end{bmatrix}$$

$$\text{var}\begin{bmatrix} u_j \\ p_j \\ e_{ijk} \end{bmatrix} = \begin{bmatrix} a_{jj}\alpha_1 & 0 & 0 \\ 0 & \alpha_2 & 0 \\ 0 & 0 & 1 \end{bmatrix}\sigma_e^2$$

where

b_i = i^{th} fixed effect,

u_j = BV of the j^{th} animal,

p_j = permanent environmental effect common to all the records of the j^{th} individual,

e_{ijk} = residual effects (temporary environmental effects),

a_{jj} = additive relationship of the j^{th} animal with itself,

$\alpha_1 = \dfrac{\sigma_A^2}{\sigma_e^2}$ = ratio of the additive genetic variance to the residual variance,

$\alpha_2 = \dfrac{\sigma_{E_p}^2}{\sigma_e^2}$ = ratio of the permanent environment variance to the residual variance.

Remarks:

(i) The parameter α_1 from the **SRM** is **not** the same as the parameter α from the **AM**. In terms of the **SRM**, the parameter α from the **AM** is:

$$\alpha = \frac{\sigma_A^2}{\sigma_{E_p}^2 + \sigma_e^2} = \frac{\left(\frac{\sigma_A^2}{\sigma_P^2}\right)}{1-\left(\frac{\sigma_A^2}{\sigma_P^2}\right)} = \frac{h^2}{1-h^2}$$

where

$$\sigma_P^2 = \sigma_A^2 + \sigma_{E_p}^2 + \sigma_e^2 ,$$

whereas α_1 is:

$$\alpha_1 = \frac{\sigma_A^2}{\sigma_e^2} = \frac{\left(\frac{\sigma_A^2}{\sigma_P^2}\right)}{1-\left(\frac{\sigma_A^2+\sigma_{E_p}^2}{\sigma_P^2}\right)} = \frac{h^2}{(1-r)}$$

(ii) The parameter α_2 is:

$$\alpha_2 = \frac{\sigma_{E_p}^2}{\sigma_e^2} = \frac{\left(\frac{\sigma_P^2-\sigma_A^2-\sigma_e^2}{\sigma_P^2}\right)}{1-\left(\frac{\sigma_A^2+\sigma_{E_p}^2}{\sigma_P^2}\right)} = \frac{(1-h^2)-(1-r)}{(1-r)} = \frac{(r-h^2)}{(1-r)}$$

In matrix notation the SRM is:

$$y = Xb + [0 \quad Z]\begin{bmatrix} u_0 \\ u_1 \end{bmatrix} + Zp + e$$

$$E[y] = Xb$$

$$\mathrm{var}\begin{bmatrix} u_0 \\ u_1 \\ p \\ e \end{bmatrix} = \begin{bmatrix} A_{00}\alpha_1 & A_{01}\alpha_1 & 0 & 0 \\ A_{10}\alpha_1 & A_{11}\alpha_1 & 0 & 0 \\ 0 & 0 & I\alpha_2 & 0 \\ 0 & 0 & 0 & I \end{bmatrix}\sigma_e^2$$

where

u_0 = vector of BV's of animals without records needed to construct A^{-1} directly using a list of animals and their parents, where

$$A^{-1} = \begin{bmatrix} A^{00} & A^{01} \\ A^{10} & A^{11} \end{bmatrix}$$

u_1 = vector of BV's of animals with records,

p = vector of permanent environmental effects for animals with repeated observations,

e = vector of temporary environmental (residual) effects,

Z = incidence matrix relating records to animals, and

vectors y and b, and matrix X are as defined for the **AM**.

The **MME for the SRM** are:

$$\begin{bmatrix} X'X & 0 & X'Z & X'Z \\ 0 & A^{00}\alpha_1^{-1} & A^{01}\alpha_1^{-1} & 0 \\ Z'X & A^{10}\alpha_1^{-1} & Z'Z + A^{11}\alpha_1^{-1} & Z'Z \\ Z'X & 0 & Z'Z & Z'Z + I\alpha_2^{-1} \end{bmatrix} \begin{bmatrix} b \\ u_0 \\ u_1 \\ p \end{bmatrix} = \begin{bmatrix} X'y \\ 0 \\ Z'y \\ Z'y \end{bmatrix}$$

If the objective of the analysis were to predict the BV of animals, then the BLUP of p, $\hat{p}$, would be of little interest. If so, **because submatrix** $Z'Z + I\alpha_2^{-1}$ is **diagonal**, **the equations for p could be absorbed into those for b, u_0 and u_1**. The **resulting set of MME** is:

$$\begin{bmatrix} X'R^{-1}X & 0 & X'R^{-1}Z \\ 0 & A^{00}\alpha_1^{-1} & A^{01}\alpha_1^{-1} \\ Z'R^{-1}X & A^{10}\alpha_1^{-1} & Z'R^{-1}Z + A^{11}\alpha_1^{-1} \end{bmatrix} \begin{bmatrix} b \\ u_0 \\ u_1 \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ 0 \\ Z'R^{-1}y \end{bmatrix}$$

where

$$\begin{aligned} R^{-1} &= I - Z\,(Z'Z + I\alpha_2^{-1})^{-1}\,Z' \\ &= (Z\,(I\,\alpha_2)\,Z' + I)^{-1} \\ &= (ZZ'\alpha_2 + I)^{-1} \end{aligned}$$

Thus, the MME for the **SRM** with the p equation absorbed correspond to the **equivalent SRM (ESRM)**

$$y = Xb + [0 \;\; Z]\begin{bmatrix} u_0 \\ u_1 \end{bmatrix} + (Zp + e)$$

$$y = Xb + [0 \;\; Z]\begin{bmatrix} u_0 \\ u_1 \end{bmatrix} + e_1$$

$$E[y] = Xb$$

$$\text{var}\begin{bmatrix} u_0 \\ u_1 \\ --- \\ e_1 \end{bmatrix} = \text{var}\begin{bmatrix} u_0 \\ u_1 \\ ------ \\ Zp+e \end{bmatrix}$$

$$= \left[\begin{array}{cc|c} A_{00}\alpha_1 & A_{01}\alpha_1 & 0 \\ A_{10}\alpha_1 & A_{11}\alpha_1 & 0 \\ \hline 0 & 0 & ZZ'\alpha_2 + I \end{array}\right]\sigma_e^2$$

If the BLUP of p, $\hat{p}$, is needed, it can be obtained by **backsolving for $\hat{p}$ in the SRM**, i.e.

$$\hat{p} = (Z'Z + I\,\alpha_2^{-1})^{-1}[y - Z'X\,b^\circ - Z'Z\,\hat{u}_1]$$

which can be solved one animal at a time. For the j^{th} animal the equation for $\hat{p}$ is:

$$\hat{p}_j = (n_{\bullet j} + \alpha_2^{-1})^{-1}[y_{\bullet j \bullet} - \sum_i n_{ij} b_i^\circ - n_{\bullet j}\,\hat{u}_j]$$

$$= \frac{\sigma^2_{E_p}}{n_{\bullet j}\,\sigma^2_{E_p} + \sigma^2_e}[y_{\bullet j \bullet} - \sum_i n_{ij}\,b_i^\circ - n_{\bullet j}\,\hat{u}_j]$$

$$= \frac{r - h^2}{(n_{\bullet j} - 1)\,r - n_{\bullet j}\,h^2 - 1}[y_{\bullet j \bullet} - \sum_i n_{ij}\,b_i^\circ - n_{\bullet j}\,\hat{u}_j]$$

where the b_i° and the $\hat{u}_j$ come from the solution vector of the **ESRM**. Also, notice that, by

subtracting the equations for p from those for u in the MME for the SRM, we get:

$$A^{21} \alpha_1^{-1} u_0 + A^{22} \alpha_1^{-1} u_1 - I \alpha_2^{-1} p = 0$$

$$\Rightarrow \quad \hat{p} = \frac{\alpha_2}{\alpha_1} A^{21} \hat{u}_0 + \frac{\alpha_2}{\alpha_1} A^{22} \hat{u}_1$$

$$= \frac{\alpha_2}{\alpha_1} \begin{bmatrix} A^{10} & A^{11} \end{bmatrix} \begin{bmatrix} \hat{u}_0 \\ \hat{u}_1 \end{bmatrix}$$

$$= \frac{\sigma^2_{E_p}}{\sigma^2_A} \begin{bmatrix} A^{10} & A^{11} \end{bmatrix} \begin{bmatrix} \hat{u}_0 \\ \hat{u}_1 \end{bmatrix}$$

$$= \frac{r - h^2}{h^2} \begin{bmatrix} A^{10} & A^{11} \end{bmatrix} \begin{bmatrix} \hat{u}_0 \\ \hat{u}_1 \end{bmatrix}$$

The above formulae **can also be used to backsolve** for $\hat{p}$.

The **covariance matrix among the residual effects of the ESRM is block diagonal**, i.e.,

$$R = (ZZ'\alpha_2 + I)\, \sigma_e^2$$

$$= \text{block diag } \{R_{jj}\, \sigma_e^2\}$$

where

$$R_{jj}\, \sigma_e^2 = (1\ 1'\alpha_2 + I)_j\, \sigma_e^2$$

$$= \left(J_{n_{\bullet j}} \alpha_2 + I_{n_{\bullet j}} \right) \sigma_e^2$$

The **inverse of R** is:

$$R^{-1} = \text{block diag } \{R_{jj}^{-1}\, \sigma_e^{-2}\}$$

where

$$R_{jj}^{-1}\, \sigma_e^{-2} = \left[J_{n_{\bullet j}} \alpha_2 + I_{n_{\bullet j}} \right]^{-1} \sigma_e^{-2}$$

$$= \left\lfloor J_{n_{\bullet j}} \left(-\frac{\alpha_2}{n_{\bullet j}\,\alpha_2 + 1} \right) + I_{n_{\bullet j}} \right\rfloor \sigma_e^{-2},$$

where $n_{\bullet j}$ = number of records of animal j,

$$= \left\lfloor J_{n_{\bullet j}} \left(-\frac{1}{n_{\bullet j} + \alpha_2^{-1}} \right) + I_{n_{\bullet j}} \right\rfloor \sigma_e^{-2}$$

The R_{jj}^{-1} will be used to build the MME for the ESRM. The **contributions of a record of an animal with n.j records to the MME of the ESRM** are:

(i) $1 - \dfrac{1}{n_{\bullet j} + \alpha_2^{-1}}$ to the diagonals of fixed effects and to the offdiagonals between two fixed effects affecting the animals' records,

(ii) $-\dfrac{1}{n_{\bullet j} + \alpha_2^{-1}}$ to the offdiagonals between fixed effects affecting different records of an animal,

(iii) $1 - \dfrac{n_{\bullet j}}{n_{\bullet j} + \alpha_2^{-1}}$ to the offdiagonals between the fixed effects affecting the records of an animal and u_1,

(iv) $n_{\bullet j} - \dfrac{(n_{\bullet j})^2}{n_{\bullet j} + \alpha_2^{-1}}$ to the diagonal of u_1 corresponding to animal j,

(v) $y_{ijk} - \dfrac{y_{\bullet j \bullet}}{n_{\bullet j} + \alpha_2^{-1}}$ to the element of the RHS corresponding to the i^{th} fixed effect affecting the k^{th} record of animal j,

(iv) $y_{ijk} - \dfrac{n_{\_j}\ y_{\bullet j \bullet}}{n_{\bullet j} + \alpha_2^{-1}} = \dfrac{y_{\bullet j \bullet}\, n_{\bullet j \bullet} + y_{\bullet j \bullet}\, \alpha_2^{-1} - y_{\bullet j \bullet}\, n_{\bullet j}}{n_{\bullet j} + \alpha_2^{-1}}$

$$= \frac{\alpha_2^{-1}\, y_{\bullet j \bullet}}{n_{\bullet j} + \alpha_2^{-1}}$$ to the element of the RHS corresponding to animal j.

After all the contributions of the records of all animals with records have been added to the MME the contribution of $A^{-1}\ \alpha_1^{-1}$ are added to it. These contributions are the a^{jj}, computed using the rules of Henderson, times α_1^{-1}, i.e., $a^{jj}\ \alpha_1^{-1}$.

Autoregressive Repeatability Model (ARM)

The covariance matrix of the residual effects of the **SRM** is:

$$R = \text{block diag}\ \{R_{jj}\ \sigma_e^2\}$$

where

$$R_{jj}\ \sigma_e^2 = (1\ 1'\ \alpha_2 + I)_j\ \sigma_e^2$$

$$= \begin{bmatrix} (1+\alpha_2) & \alpha_2 & \alpha_2 & \cdots & \alpha_2 \\ \alpha_2 & (1+\alpha_2) & \alpha_2 & \cdots & \alpha_2 \\ \alpha_2 & \alpha_2 & (1+\alpha_2) & \cdots & \alpha_2 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ \alpha_2 & \alpha_2 & \alpha_2 & \cdots & (1+\alpha_2) \end{bmatrix} \sigma_e^2$$

This structure of R assumes that the records of an animal are equally correlated regardless of the difference in time when they were measured. A more realistic approach would be to assume that covariances among records of an individual vary depending of the time elapsed between measurements. The problem of this model is the computation of all the different covariances that may be needed. Thus, a less general model, which assumes a more realistic covariance structure among these residuals, may be a better computational alternative. Quaas et al. (1984) presented two structures for R based on autoregressive processes:

(i) R = block diag $\{R_{jj}\,\sigma_\varepsilon^2\}$, where

$$R_{jj}\,\sigma_\varepsilon^2 = \begin{bmatrix} 1 & \rho & \rho^2 & \rho^3 & \cdots & \rho^{n\bullet j} \\ \rho & 1 & \rho & \rho & \cdots & \rho^{n\bullet j-1} \\ \rho^2 & \rho & 1 & \rho & \cdots & \rho^{n\bullet j-2} \\ \rho^3 & \rho^2 & \rho & 1 & \cdots & \rho^{n\bullet j-3} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \rho^{n\bullet j} & \rho^{n\bullet j-1} & \rho^{n\bullet j-2} & \rho^{n\bullet j-3} & \vdots & 1 \end{bmatrix} \sigma_\varepsilon^2$$

The number of parameters needed is the same as for the **SRM**, i.e., 2.

Notice that R_{jj} from the **SRM** can be written as:

$$R_{jj}\,\sigma_\varepsilon^2 = \begin{bmatrix} 1 & \rho & \rho & \cdots & \rho \\ \rho & 1 & \rho & \cdots & \rho \\ \rho & \rho & 1 & \vdots & \rho \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ \rho & \rho & \rho & \cdots & 1 \end{bmatrix} \sigma_\varepsilon^2$$

where

$$\sigma_\varepsilon^2 = \sigma_{E_p}^2 + \sigma_e^2$$

$$\rho = \frac{\sigma_{E_p}^2}{\sigma_{E_p}^2 + \sigma_e^2}$$

which could also be assumed to be the definitions of σ_ε^2 and ρ in the first autoregressive repeatability model (**ARM1**). The **ARM1** assumes equal correlation among records equally separated in time and this correlation **decreases progressively** as records are farther apart.

The inverse of R for the **ARM1** is:

$$R^{-1} \quad = \quad \text{block diag } \{R_{jj}^{-1}\,\sigma_{\varepsilon}^{-2}\},$$

where

$$R_{jj}^{-1} \quad = \quad \begin{bmatrix} a & b & & & & & & \\ b & c & b & & & & 0 & \\ & b & c & b & & & & \\ & & b & c & & & & \\ & & & & \ddots & & & \\ & & & & & c & b & \\ & 0 & & & & b & c & b \\ & & & & & & b & a \end{bmatrix},$$

where

$$a = \frac{1}{1-\rho^2},$$

$$b = \frac{-\rho}{1-\rho^2}, \text{ and}$$

$$c = \frac{(1+\rho^2)}{(1-\rho^2)}.$$

The MME for the **ARM1** are:

$$\begin{bmatrix} X'R^{-1}X & 0 & X'R^{-1}Z \\ 0 & A^{00}\alpha^{-1} & A^{01}\alpha^{-1} \\ Z'R^{-1}X & A^{10}\alpha^{-1} & Z'R^{-1}Z + A^{11}\alpha^{-1} \end{bmatrix} \begin{bmatrix} b \\ u_0 \\ u_1 \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ 0 \\ Z'R^{-1}y \end{bmatrix}$$

where

$$\alpha = \frac{\sigma_A^2}{\sigma_{E_p} + \sigma_e^2} = \frac{\left(\frac{\sigma_A^2}{\sigma_P^2}\right)}{1-\left(\frac{\sigma_A^2}{\sigma_P^2}\right)} = \frac{h^2}{1-h^2}$$

if

$$\sigma_\varepsilon^2 = \sigma_{E_p}^2 + \sigma_e^2, \text{ and } \rho = \frac{\sigma_{E_p}^2}{\sigma_{E_p}^2 + \sigma_e^2}.$$

(ii) R = block diag $\{R_{jj}\, \sigma_\varepsilon^2\}$,

where

$$R_{jj}\,\sigma_\varepsilon^2 = \begin{bmatrix} 1 & b\rho & b\rho^2 & b\rho^3 & \cdots & b\rho^{n\bullet j} \\ b\rho & 1 & b\rho & b\rho^2 & \cdots & b\rho^{n\bullet j-1} \\ b\rho^2 & b\rho & 1 & b\rho & \cdots & b\rho^{n\bullet j-2} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ b\rho^{n\bullet j} & b\rho^{n\bullet j-1} & b\rho^{n\bullet j-2} & b\rho^{n\bullet j-3} & \cdots & 1 \end{bmatrix} \sigma_\varepsilon^2.$$

This $R_{jj}\,\sigma_\varepsilon^2$ has **no** simple inverse. However, although the computation of the contributions of each records to the MME will require **inverting R_{jj} directly**, this may **not** be a big disadvantage, especially **if the number of records per animal is small**, e.g., less than 10.

The MME for this second autoregressive **SRM** (**ARM2**) are:

$$\begin{bmatrix} X'R^{-1}X & 0 & X'R^{-1}Z \\ 0 & A^{00}\alpha^{-1} & A^{01}\alpha^{-1} \\ Z'R^{-1}X & A^{10}\alpha^{-1} & Z'R^{-1}Z + A^{11}\alpha^{-1} \end{bmatrix} \begin{bmatrix} b \\ u_0 \\ u_1 \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ 0 \\ Z'R^{-1}y \end{bmatrix}$$

where

$$\alpha = \frac{\sigma_A^2}{\sigma_\varepsilon^2} = \frac{h^2}{1-h^2}.$$

The **ARM2** becomes the **ARM1** when $b = 1$ and the **SRM** when $\rho = 1$.

The **ARM2** requires **3 parameters for R** (one more than the **ARM1** and the **SRM**): **b, ρ and σ_ε^2**.

Numerical example for SRM

Animal	Sex	Gestation Length (days)	Sire	Dam	Mgs
1	M				
2	F		1		
3	M		1	2	1
4	M		1		
5	F	282 284 285	3	2	1
6	F	280 278	4	5	3
7	F	275	3	6	1

$\sigma_A^2 = 2.5\ (\text{days})^2$; $\quad \sigma_{E_p}^2 = 1\ (\text{day})^2$; $\quad \sigma_e^2 = 5\ (\text{days})^2$

$$\alpha_1 = \frac{\sigma_A^2}{\sigma_e^2} = 0.5; \qquad \alpha_2 = \frac{\sigma_{E_p}^2}{\sigma_e^2} = 0.2$$

$$\alpha_1^{-1} = \frac{\sigma_e^2}{\sigma_A^2} = 2; \qquad \alpha_2^{-1} = \frac{\sigma_e^2}{\sigma_{E_p}^2} = 5$$

Consider the following **SRM**:

$$y_{ijk} = \mu + \text{sex}_i + \text{animal}_j + \text{permanent environment}_j + \text{residual}_{ijk}$$

$$E[y_{ijk}] = \mu + \text{sex}_i$$

$$\begin{aligned}\mathrm{var}(y_{ijk}) &= \mathrm{var}(\mathrm{animal}_j) + \mathrm{var}(\mathrm{permanent\ environment}_j) + \mathrm{var}(\mathrm{residual}_{ijk}) \\ &= a_{jj}\,\sigma_A^2 + \sigma_{E_p}^2 + \sigma_e^2 \\ \mathrm{cov}(y_{ijk}, y_{i'j'k'}) &= a_{jj'}\,\sigma_A^2 + \delta_{E_p}\,\sigma_{E_p}^2 + \delta_e\,\sigma_e^2\end{aligned}$$

where

$$\delta_{E_p} = \begin{cases} 1 & \text{if } j = j' \\ 0 & \text{otherwise} \end{cases}$$

$$\delta_e = \begin{cases} 1 & \text{if } ijk = i'j'k' \\ 0 & \text{otherwise} \end{cases}$$

In matrix notation the **SRM** is:

$$y = Xb + [0\ \ Z]\begin{bmatrix} u_0 \\ u_1 \end{bmatrix} + Zp + e$$

$$E[y] = Xb$$

$$\mathrm{var}\begin{bmatrix} u_0 \\ u_1 \\ ---- \\ p \\ e \end{bmatrix} = \left[\begin{array}{cc|cc} A_{00}\alpha_1 & A_{01}\alpha_1 & 0 & 0 \\ A_{10}\alpha_1 & A_{11}\alpha_1 & 0 & 0 \\ \hline 0 & 0 & I\alpha_2 & 0 \\ 0 & 0 & 0 & I \end{array}\right]\sigma_e^2$$

The **SRM** for the data of the example is:

[18-15]

$$\begin{bmatrix} 282 \\ 284 \\ 285 \\ 280 \\ 278 \\ 275 \end{bmatrix} = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} b + \begin{bmatrix} 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \\ u_6 \\ u_7 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} p_5 \\ p_6 \\ p_7 \end{bmatrix} + e$$

The matrix (I – ½P) is:

$$(I - \tfrac{1}{2}P) = \begin{bmatrix} 1 & & & & & & \\ -\tfrac{1}{2} & 1 & & & 0 & & \\ -\tfrac{1}{2} & -\tfrac{1}{2} & 1 & & & & \\ -\tfrac{1}{2} & 0 & 0 & 1 & & & \\ 0 & -\tfrac{1}{2} & -\tfrac{1}{2} & 0 & 1 & & \\ 0 & 0 & 0 & -\tfrac{1}{2} & -\tfrac{1}{2} & 1 & \\ 0 & 0 & -\tfrac{1}{2} & 0 & 0 & -\tfrac{1}{2} & 1 \end{bmatrix}$$

The diagonals of A, D and D^{-1} are:

i	a_{ii}	d_{ii}	d_{ii}^{-1}
1	1.0	1.0	1.0
2	1.0	0.75	1.3333
3	1.25	0.5	2.0
4	1.0	0.75	1.3333
5	1.375	0.4375	2.2857
6	1.15625	0.40625	2.4615
7	1.484375	0.4609375	2.1695

The matrix $A^{-1} = (I - ½P')D^{-1}(I - ½P)$ is:

$$A^{-1} = \begin{bmatrix} 2.1667 & -0.1667 & -1.0 & -0.6667 & 0 & 0 & 0 \\ & 2.4048 & -0.4286 & 0 & -1.1429 & 0 & 0 \\ & & 3.1138 & 0 & -1.1429 & 0.5424 & -1.848 \\ & & & 1.9487 & 0.6154 & -1.2308 & 0 \\ & & & & 2.9001 & -1.2308 & 0 \\ & & & & & 3.0039 & -1.0847 \\ & & & & & & 2.1695 \end{bmatrix}$$

The MME for the **SRM** are:

$$\left[\begin{array}{c|cccc|ccc|ccc} 6 & 0 & 0 & 0 & 0 & 3 & 2 & 1 & 3 & 2 & 1 \\ \hline & 4.333 & -0.333 & -2.0 & -1.333 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & 4.810 & -0.857 & 0 & -2.286 & 0 & 0 & 0 & 0 & 0 \\ & & & 6.228 & 0 & -2.286 & 1.085 & -2.170 & 0 & 0 & 0 \\ & & & & 3.897 & 1.231 & -2.462 & 0 & 0 & 0 & 0 \\ \hline & & & & & 8.802 & -2.462 & 0 & 3 & 0 & 0 \\ & & & & & & 8.008 & -2.170 & 0 & 2 & 0 \\ & & & & & & & 5.339 & 0 & 0 & 1 \\ \hline & & & & & & & & 8 & 0 & 0 \\ & & & & & & & & & 7 & 0 \\ & & & & & & & & & & 6 \end{array}\right] \left[\begin{array}{c} b \\ \hline u_1 \\ u_2 \\ u_3 \\ u_4 \\ \hline u_5 \\ u_6 \\ u_7 \\ \hline p_5 \\ p_6 \\ p_7 \end{array}\right] = \left[\begin{array}{c} 1684 \\ \hline 0 \\ 0 \\ 0 \\ 0 \\ \hline 851 \\ 558 \\ 275 \\ \hline 851 \\ 558 \\ 275 \end{array}\right]$$

The vector of solutions for the **SRM** is:

$$\begin{bmatrix} b^{\circ} \\ --- \\ \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \\ \hat{u}_4 \\ --- \\ \hat{u}_5 \\ \hat{u}_6 \\ \hat{u}_7 \\ --- \\ \hat{p}_5 \\ \hat{p}_6 \\ \hat{p}_7 \end{bmatrix} = \begin{bmatrix} 280.0926 \\ --------- \\ -0.0203 \\ 0.5604 \\ 0.2294 \\ -0.5503 \\ --------- \\ 1.0962 \\ -0.3121 \\ -0.8552 \\ --------- \\ 0.9292 \\ -0.2230 \\ -0.7062 \end{bmatrix}$$

The real producing abilities of animals 5, 6 and 7 are:

$$\begin{bmatrix} \hat{v}_5 \\ \hat{v}_6 \\ \hat{v}_7 \end{bmatrix} = \begin{bmatrix} 1.0962 + 0.9292 \\ -0.3121 - 0.2230 \\ -0.8552 - 0.7062 \end{bmatrix} = \begin{bmatrix} 2.0354 \\ -0.5351 \\ -1.5614 \end{bmatrix}.$$

References

Quaas, R. L., R. D. Anderson, and A. R. Gilmour. 1984. BLUP School Handbook. Use of mixed models for prediction and for estimations of (co)variance components. AGBU, Univ. of New England, N.S.W., 2351, Australia.