

## ANIMAL BREEDING NOTES

### CHAPTER 16M EQVE

#### MULTIBREED ANIMAL MODEL WITH EQUAL RESIDUAL VARIANCES

##### Multibreed Animal Model with Equal Residual Variances (MAM\_EQVE)

**Objective:** to predict additive genetic effects (**AMBV**), nonadditive genetic effects (**NMBV**), and total genetic effects (**TMBV**) of animals based on their own records and records of their relatives in a multibreed population.

##### Assumptions

- 1) Animals belong to a multibreed population, i.e., a population composed of purebred and crossbred animals that interbreed;
- 2) Animals may have 1 or more records;
- 3) Nonadditive genetic effects are explained in terms of intrabreed and interbreed interaction effects at 1 or more loci that are modeled as independent regression effects;
- 4) Multibreed additive genetic variances and covariances among records are linear combinations of intrabreed and interbreed additive genetic variances and covariances;
- 5) Multibreed nonadditive genetic variances and covariances among records are linear combinations of intrabreed and interbreed nonadditive genetic variances and covariances;
- 6) **Multibreed environmental variances and covariances among records are the same for all purebred and crossbred animals; and**
- 7) There is either no selection in the population, or:
  - a. if selection occurred based on records, selection was within fixed effects, and
  - b. if selection occurred based on **AMBV**, the relationship matrix was complete.

The **MAM\_EQVE** is:

$$y = Xb + Z_a Q_a g_a + Z_n Q_n g_n + Z_a a_a + Z_n a_n + e$$

$$E[y] = Xb + Z_a Q_a g_a + Z_n Q_n g_n$$

$$\text{var} \begin{bmatrix} a_a \\ a_n \\ e \end{bmatrix} = \begin{bmatrix} G_a & 0 & 0 \\ 0 & G_n & 0 \\ 0 & 0 & R \end{bmatrix}$$

$$\Rightarrow \text{var}(y) = Z_a G_a Z_a' + Z_n G_n Z_n' + R,$$

where

$y$  = vector of animal records,

$b$  = vector of unknown fixed effects (e.g., contemporary groups, sex of calf, age of dam),

$g_a$  = vector of unknown additive group genetic effects (e.g., breed, breed  $\times$  year of birth),

$g_n$  = vector of unknown nonadditive group genetic effects (e.g., heterosis at 1 locus, heterosis at 2 loci),

$a_a$  = vector of unknown random additive genetic effects (**AMBV**),

$a_n$  = vector of unknown random nonadditive genetic effects (**NMBV**),

$e$  = vector of unknown random residual effects,

$X$  = known incidence matrix relating records to fixed effects in vector  $b$ ,

$Z_a$  = known incidence matrix relating records to elements of vector  $a_a$ ,

$Z_n$  = known incidence matrix relating records to elements of vector  $a_n$ ,

$Q_a$  = known incidence matrix relating random additive genetic effects to additive genetic groups in vector  $g_a$ ,

$Q_n$  = known incidence matrix relating random nonadditive genetic effects to nonadditive genetic groups in vector  $g_n$ ,

$G_a$  =  $\{g_{ij}\}$ , where  $g_{ij}$  = additive genetic covariance between animals  $i$  and  $j$ ,

$G_n$  =  $\text{diag}\{A_m * \sigma_{nm}^2, m = 1, \dots, N_m\}$ , where  $A_m$  is the matrix of probabilities that pairs of animals received the same alleles at  $m$  loci, and  $\sigma_{nm}^2$  is the variance of interaction effects among alleles at  $m$  loci. If  $m = 1$ , then  $G_n = A * \sigma_{n1}^2$ , where  $A$  = matrix of additive relationships and  $\sigma_{n1}^2$  = variance of intralocus interaction effects (intra-breed and inter-breed). Further, if only inter-breed intralocus effects are included in the model, then  $\sigma_{n1}^2$  = variance of intralocus inter-breed interaction effects = variance of random heterosis effects,

$R$  =  $\text{diag}\{\sigma_{ei}^2\}$ , where  $\sigma_{ei}^2$  = residual variance for animal  $i$ . However, animals of all breed compositions are assumed to be similarly affected by environmental effects, and residual nonadditive genetic effects are assumed to be equal across breed compositions, thus  $R = I * \sigma_e^2$ , where  $\sigma_e^2$  = residual variance common to all animals in a multi-breed population.

The general mixed model equations (MME) for the multi-breed animal model are:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z_aQ_a & X'R^{-1}Z_nQ_n & X'R^{-1}Z_a & X'R^{-1}Z_n \\ Q_a'Z_a'R^{-1}X & Q_a'Z_a'R^{-1}Z_aQ_a & Q_a'Z_a'R^{-1}Z_nQ_n & Q_a'Z_a'R^{-1}Z_a & Q_a'Z_a'R^{-1}Z_n \\ Q_n'Z_n'R^{-1}X & Q_n'Z_n'R^{-1}Z_aQ_a & Q_n'Z_n'R^{-1}Z_nQ_n & Q_n'Z_n'R^{-1}Z_a & Q_n'Z_n'R^{-1}Z_n \\ Z_a'R^{-1}X & Z_a'R^{-1}Z_aQ_a & Z_a'R^{-1}Z_nQ_n & Z_a'R^{-1}Z_a + G_a^{-1} & Z_a'R^{-1}Z_n \\ Z_n'R^{-1}X & Z_n'R^{-1}Z_aQ_a & Z_n'R^{-1}Z_nQ_n & Z_n'R^{-1}Z_a & Z_n'R^{-1}Z_n + G_n^{-1} \end{bmatrix} \begin{bmatrix} b \\ g_a \\ g_n \\ u_a \\ u_n \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Q_a'Z_a'R^{-1}y \\ Q_n'Z_n'R^{-1}y \\ Z_a'R^{-1}y \\ Z_n'R^{-1}y \end{bmatrix}$$

However,  $R = I * \sigma_e^2$  for the **MAM\_EQVE**. Thus, after multiplication of both sides by  $\sigma_e^2$ , the resulting **MME\_MAM\_EQVE** are:

$$\begin{bmatrix} X'X & X'Z_a Q_a & X'Z_n Q_n & X'Z_a & X'Z_n \\ Q_a'Z_a'X & Q_a'Z_a'Z_a Q_a & Q_a'Z_a'Z_n Q_n & Q_a'Z_a'Z_a & Q_a'Z_a'Z_n \\ Q_n'Z_n'X & Q_n'Z_n'Z_a Q_a & Q_n'Z_n'Z_n Q_n & Q_n'Z_n'Z_a & Q_n'Z_n'Z_n \\ Z_a'X & Z_a'Z_a Q_a & Z_a'Z_n Q_n & Z_a'Z_a + G_a^{-1} * \sigma_e^2 & Z_a'Z_n \\ Z_n'X & Z_n'Z_a Q_a & Z_n'Z_n Q_n & Z_n'Z_a & Z_n'Z_n + G_n^{-1} * \sigma_e^2 \end{bmatrix} \begin{bmatrix} b \\ g_a \\ g_n \\ a_a \\ a_n \end{bmatrix} = \begin{bmatrix} X'y \\ Q_a'Z_a'y \\ Q_n'Z_n'y \\ Z_a'y \\ Z_n'y \end{bmatrix}$$

**Example 1 for the MAM\_EQVE for a Non-inbred Multibreed Population**

Animal	Breed Composn	Sex	Weaning weight (kg)	Sire	Breed Composn	Dam	Breed Composn
1	A	M	289	0	A	0	A
2	B	F	245	0	B	0	B
3	½ A ½ B	F	256	0	A	2	B
4	½ A ½ B	F	261	1	A	0	B
5	½ A ½ B	M	292	1	A	2	B
6	¾ A ¼ B	M	286	1	A	3	½ A ½ B

**Assumptions for the Example**

**1) Additive genetic variances:**

Intrabreed additive genetic variance for breed A =  $\sigma_{aAA}^2 = 36 \text{ kg}^2$

Intrabreed additive genetic variance for breed B =  $\sigma_{aBB}^2 = 9 \text{ kg}^2$

Interbreed additive genetic variance for combination of breeds AB =  $\sigma_{aAB}^2 = 4 \text{ kg}^2$

**2) Nonadditive genetic variances due to sire × breed group of dam interaction effects = nonadditive genetic variances due to dam × breed group of sire interaction effects.**

Variation from nonadditive effects due to sire × dam intra and interbreed interaction effects are assumed to be part of the residual variance.

**Nonadditive genetic variances:**

Intrabreed nonadditive genetic variance for breed A =  $\sigma_{nAA}^2 = 4 \text{ kg}^2$

Intrabreed nonadditive genetic variance for breed B =  $\sigma_{nBB}^2 = 9 \text{ kg}^2$

Interbreed nonadditive genetic variance for combination of breeds AB =  $\sigma_{nAB}^2 = 16 \text{ kg}^2$

**Simplifying assumption:** only intralocus interbreed sire × breed group of dam and dam × breed group of sire interaction effects (i.e., **sire and dam random heterosis effects**) are important. Intralocus intrabreed AA and BB nonadditive effects and interactions among alleles at 2 or more loci due to sire × breed group of dam and dam × breed group of sire interactions are assumed to be contained in the residual. *Thus, only intralocus interbreed interactions will be fitted in the model for the example.* Consequently, only  $\sigma_{nAB}^2 = 16 \text{ kg}^2$  will be needed.

**3) Environmental variances:**

Common environmental variance =  $\sigma_e^2 = 49 \text{ kg}^2$

**4) Environmental covariances among records of different animals are zero.**

**Multibreed Animal Model**

Wean wt = overall mean + breed regression + heterosis regression + sex  
 + animal additive genetic + animal nonadditive genetic regression  
 + residual

E [Wean wt] = overall mean + breed regression + heterosis regression + sex

$$\text{Var}(\text{Wean wt}) = \text{var}(\text{animal additive genetic}) + \text{var}(\text{animal nonadditive genetic regression}) \\ + \text{var}(\text{residual})$$

$$\text{cov}(\text{Wean wt}_{ik}, \text{Wean wt}_{i'k'}) = \text{cov}(\text{animal additive genetic}_i, \text{animal additive genetic}_{i'}) \\ + \text{cov}(\text{animal nonadditive genetic}_i, \text{animal nonadditive genetic}_{i'}) + \text{cov}(\text{residual}_{ik}, \text{residual}_{i'k'})$$

The vectors and matrices of the **MAM\_EQVE** model are:

$$\begin{bmatrix} 289 \\ 245 \\ 256 \\ 261 \\ 292 \\ 286 \end{bmatrix} = \begin{bmatrix} 1 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 1 & 1/2 & 1/2 & 1 & 0 & 1 \\ 1 & 1/2 & 1/2 & 1 & 0 & 1 \\ 1 & 1/2 & 1/2 & 1 & 1 & 0 \\ 1 & 3/4 & 1/4 & 1/2 & 1 & 0 \end{bmatrix} \begin{bmatrix} \text{mean} \\ \text{breed}_A \\ \text{breed}_B \\ \text{heterosis}_{AB} \\ \text{sex}_M \\ \text{sex}_F \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \text{animal 1}_{add} \\ \text{animal 2}_{add} \\ \text{animal 3}_{add} \\ \text{animal 4}_{add} \\ \text{animal 5}_{add} \\ \text{animal 6}_{add} \end{bmatrix}$$

$$+ \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 \\ 1/2 & 0 & 1/2 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \text{animal1}_{nadd} \\ \text{animal2}_{nadd} \\ \text{animal3}_{nadd} \\ \text{animal4}_{nadd} \\ \text{animal5}_{nadd} \\ \text{animal6}_{nadd} \end{bmatrix} + \begin{bmatrix} \text{residual}_{anim1} \\ \text{residual}_{anim2} \\ \text{residual}_{anim3} \\ \text{residual}_{anim4} \\ \text{residual}_{anim5} \\ \text{residual}_{anim6} \end{bmatrix}$$

### Multibreed Additive Genetic Variances

Multibreed additive genetic variances are computed by conditioning them on breed of origin of alleles using the expression:

$$\sigma_{at}^2 = E[\text{var}(t | b) + \text{var}(E[t | b])] \\ \sigma_{at}^2 = \sum_{b=1}^{n_b} p_b^i (\sigma_{at}^2)_b + \sum_{b=1}^{n_b-1} \sum_{b'>b}^{n_b} (p_b^s p_{b'}^s + p_b^d p_{b'}^d) (\sigma_{at}^2)_{bb'}$$

where a = additive genetic, t = trait, superscripts i = individual, s = sire, and d = dam, subscripts

b and b' represent two breeds, and

- $n_b$  = number of breeds,
- $p_b^x$  = expected fraction of breed b in animal x, x = i, s, d,
- $(\sigma_{at}^2)_b$  = additive intrabreed genetic variance for trait t for breed b,
- $(\sigma_{at}^2)_{bb'}$  = additive interbreed genetic variance for trait t for pair of breeds b and b'.

The multibreed additive genetic variances for the 6 animals in the example are:

	Animal		
	Number	Breed Group	Multibreed Additive Genetic Variance
<b>Parents</b>	1	A	36
	2	B	9
	3	½ A ½ B	½ (36) + ½ (9) = 22.5
<b>Non-parents</b>	4	½ A ½ B	½ (36) + ½ (9) = 22.5
	5	½ A ½ B	½ (36) + ½ (9) = 22.5
	6	¾ A ¼ B	¾ (36) + ¼ (9) + [(1)(0) + (½)(½)](4) = 30.25

### Inverse of the Multibreed Additive Genetic Covariance Matrix

The equation for the inverse of the covariance matrix of multibreed additive genetic effects,  $G_a^{-1}$ , is:

$$G_a^{-1} = (I - 1/2 P') D_a^{-1} (I - 1/2 P)$$

where

$I$  = identity matrix,

$P$  = matrix that relates animals to their sires and dams; each row of  $P$  contains up to 2 nonzero elements: a 1 for the sire and a 1 for the dam of an animal,

$D_a$  = diagonal matrix of residual additive genetic variances.

The diagonal elements of the  $D_a^{-1}$  matrix are computed using the expression:

$$d_{a_{ii}}^{-1} = \left[ (\sigma_{at})_i^2 - 1/4 \delta_s \left( (\sigma_{at})_s^2 + \sum_{c=1}^{n_{cs}} F_{cs} (\sigma_{at})_{cs}^2 \right) - 1/4 \delta_d \left( (\sigma_{at})_d^2 + \sum_{c=1}^{n_{cd}} F_{cd} (\sigma_{at})_{cd}^2 \right) \right]^{-1}$$

where  $F_{cs}$  and  $F_{cd}$  are the coefficients of inbreeding of common ancestors of the sire and the dam of animal  $i$ , and  $\delta_s = 1$  if the sire is known, else  $\delta_s = 0$ , and  $\delta_d = 1$  if the dam is known, else  $\delta_d = 0$ .

In **non-inbred** multibreed populations the  $F_{cs}$  and  $F_{cd}$  are equal to zero. Thus, the expression for  $d_{a_{ii}}^{-1}$  simplifies to:

$$d_{a_{ii}}^{-1} = \left[ (\sigma_{at})_i^2 - 1/4 \delta_s (\sigma_{at})_s^2 - 1/4 \delta_d (\sigma_{at})_d^2 \right]^{-1}$$

The  $d_{a_{ii}}^{-1}$  for the six animals in the example, computed using the formula for a non-inbred multibreed population, are:



	Animal		
	Number	Breed Group	$d_{a_{ii}}^{-1}$
<b>Parents</b>	1	A	$(36)^{-1}$
	2	B	$(9)^{-1}$
	3	½ A ½ B	$[22.5 - \frac{1}{4} (9)]^{-1} = (20.25)^{-1}$
<b>Non-parents</b>	4	½ A ½ B	$[22.5 - \frac{1}{4} (36)]^{-1} = (13.5)^{-1}$
	5	½ A ½ B	$[22.5 - \frac{1}{4} (36) - \frac{1}{4} (9)]^{-1} = (11.25)^{-1}$
	6	¾ A ¼ B	$[30.25 - \frac{1}{4} (36) - \frac{1}{4} (22.5)]^{-1} = (15.625)^{-1}$

The P matrix is:

$$P = \left[ \begin{array}{ccc|ccc} 0 & & & & & \\ 0 & 0 & & & & \\ 0 & 1 & 0 & & & \\ - & - & - & - & - & - \\ 1 & 0 & 0 & 0 & & \\ 1 & 1 & 0 & 0 & 0 & \\ 1 & 0 & 1 & 0 & 0 & 0 \end{array} \right]$$

$$D_a^{-1} = \left[ \begin{array}{ccc|ccc} (36)^{-1} & & & & & \\ & (9)^{-1} & & & & \\ & & (20.25)^{-1} & & & \\ - & - & - & - & - & - \\ & & & (13.5)^{-1} & & \\ & & & & (11.25)^{-1} & \\ & & & & & (15.625)^{-1} \end{array} \right]$$

The inverse of the multibreed additive genetic covariance matrix, in terms of parental and non-parental terms, is :

$$G_a^{-1} = D_a^{-1} - 1/2 D_a^{-1} P - 1/2 P' D_a^{-1} + 1/4 P' D_a^{-1} P$$

$$G_a^{-1} = \begin{array}{c} \left[ \begin{array}{ccc|ccc} g_a^{11} & g_a^{12} & g_a^{13} & g_a^{14} & g_a^{15} & g_a^{16} \\ g_a^{12} & g_a^{22} & g_a^{23} & 0 & g_a^{25} & 0 \\ g_a^{13} & g_a^{23} & g_a^{33} & 0 & 0 & g_a^{36} \\ - & - & - & - & - & - \\ g_a^{14} & 0 & 0 & g_a^{44} & 0 & 0 \\ g_a^{15} & g_a^{25} & 0 & 0 & g_a^{55} & 0 \\ g_a^{16} & 0 & g_a^{36} & 0 & 0 & g_a^{66} \end{array} \right] \begin{array}{l} \text{parents} \\ \\ \\ \\ \text{nonparents} \\ \\ \end{array} \\ \begin{array}{cc} \downarrow & \downarrow \\ \text{parents} & \text{non-parents} \end{array} \end{array}$$

The rules used to compute the elements of  $G_a^{-1}$  are :

- 1) Add  $d_{a_{ii}}^{-1}$  to  $i \times i$ ,
- 2) Add  $-1/2 d_{a_{ii}}^{-1}$  to  $i \times s$  and  $s \times i$  if the sire of animal  $i$  is identified,
- 3) Add  $-1/2 d_{a_{ii}}^{-1}$  to  $i \times d$  and  $d \times i$  if the dam of animal  $i$  is identified, and
- 4) Add  $1/4 d_{a_{ii}}^{-1}$  to  $s \times s$ ,  $s \times d$ ,  $d \times s$ , and  $d \times d$  if the sire and dam of animal  $i$  are identified.

Thus,

$$g_a^{11} = (36)^{-1} + 1/4 (13.5)^{-1} + 1/4 (11.25)^{-1} + 1/4 (15.625)^{-1} = 0.085$$

$$g_a^{12} = 1/4 (11.25)^{-1} = 0.022$$

$$g_a^{13} = 1/4 (15.625)^{-1} = 0.016$$

$$g_a^{14} = -1/2 (13.5)^{-1} = -0.037$$

$$g_a^{15} = -1/2 (11.25)^{-1} = -0.044$$

$$g_a^{16} = -1/2 (15.625)^{-1} = -0.032$$

$$g_a^{22} = (9)^{-1} + 1/4 (20.25)^{-1} + 1/4 (11.25)^{-1} = 0.146$$

$$g_a^{23} = -1/2 (20.25)^{-1} = -0.025$$

$$g_a^{25} = -\frac{1}{2} (11.25)^{-1} = -0.044$$

$$g_a^{33} = (20.25)^{-1} + \frac{1}{4} (15.625)^{-1} = 0.065$$

$$g_a^{36} = -\frac{1}{2} (15.625)^{-1} = -0.032$$

$$g_a^{44} = (13.5)^{-1} = 0.074$$

$$g_a^{55} = (11.25)^{-1} = 0.089$$

$$g_a^{66} = (15.625)^{-1} = 0.064$$

The  $G_a^{-1}$  is equal to :

$$G_a^{-1} = \begin{bmatrix} 0.085 & 0.022 & 0.016 & -0.037 & -0.044 & -0.032 \\ 0.022 & 0.146 & -0.025 & 0 & -0.044 & 0 \\ 0.015 & -0.025 & 0.065 & 0 & 0 & -0.032 \\ -0.037 & 0 & 0 & 0.074 & 0 & 0 \\ -0.044 & -0.044 & 0 & 0 & 0.089 & 0 \\ -0.031 & 0 & -0.031 & 0 & 0 & 0.064 \end{bmatrix}$$

### Multibreed Nonadditive Genetic Variances

Multibreed nonadditive genetic variances in a regression model that accounts for sire  $\times$  breed group of dam and dam  $\times$  breed group of sire interaction effects are equal to the intrabreed and interbreed interaction variances at 1 or more loci. **Nonadditive genetic regression effects are independent of each other.** For example, if 2 nonadditive genetic effects (e.g., intrabreed AA and interbreed AB) were fitted in a model, the matrix of multibreed nonadditive genetic variances would be block diagonal, i.e.,  $G_n = \text{diag}\{G_{nAA}, G_{nAB}\}$ . However, only a single random nonadditive genetic effect: intralocus interbreed interaction will be fitted here. Under this assumption,  $G_n = G_{nAB}$ , and the only nonadditive genetic variance needed for the example here is the variance of intralocus interbreed interaction effects,  $\sigma_{nAB}^2 = 16 \text{ kg}^2$ .

The multibreed nonadditive genetic variances for the 6 animals in the example is:

	Animal		
	Number	Breed Group	Multibreed Nonadditive Genetic Variance
<b>Parents</b>	1	A	16
	2	B	16
	3	½ A ½ B	16
<b>Non-parents</b>	4	½ A ½ B	16
	5	½ A ½ B	16
	6	¾ A ¼ B	16

### Inverse of the Multibreed Nonadditive Genetic Covariance Matrix

Covariances among sire × breed group of dam and dam × breed group of sire interaction effects are assumed to be caused by similarities among sires and(or) dams due to common ancestry. Thus, the equation for the inverse of the covariance matrix of multibreed nonadditive genetic effects due to intralocus interbreed sire × breed group of dam interaction and dam × breed group of sire interaction effects,  $G_n^{-1}$ , is:

$$G_n^{-1} = (I - \frac{1}{2} P') D_n^{-1} (I - \frac{1}{2} P)$$

where

I = identity matrix,

P = matrix that relates animals to their sires and dams; each row of P contains up to 2 nonzero elements: a 1 for the sire and a 1 for the dam of an animal,

$D_n$  = diagonal matrix of residual nonadditive genetic variances.

The diagonal elements of the  $D_n^{-1}$  matrix are computed using the expression:

$$d_{nii}^{-1} = \left[ \left( 1 - \frac{1}{4}\delta_s(1 + F_s) - \frac{1}{4}\delta_d(1 + F_d) \right) * \sigma_{nAB}^2 \right]^{-1}$$

where  $F_s$  and  $F_d$  are the coefficients of inbreeding of the sire and the dam of animal  $i$ , and  $\delta_s = 1$  if the sire is known, else  $\delta_s = 0$ , and  $\delta_d = 1$  if the dam is known, else  $\delta_d = 0$ .

In **non-inbred** multibreed populations the  $F_s$  and  $F_d$  are equal to zero. Thus, the expression for  $d_{nii}^{-1}$  simplifies to:

$$d_{nii}^{-1} = \left[ \left( 1 - \frac{1}{4}\delta_s - \frac{1}{4}\delta_d \right) * \sigma_{nAB}^2 \right]^{-1}$$

The diagonal elements of the  $D_n^{-1}$  matrix are:

	Animal		
	Number	Breed Group	$(d_{nii})^{-1}$
<b>Parents</b>	1	A	$[(1)*(16)]^{-1} = (16)^{-1}$
	2	B	$[(1)*(16)]^{-1} = (16)^{-1}$
	3	½ A ½ B	$[(1 - ¼)(16)]^{-1} = (12)^{-1}$
<b>Non-parents</b>	4	½ A ½ B	$[(1 - ¼)(16)]^{-1} = (12)^{-1}$
	5	½ A ¼ B	$[(1 - ¼ - ¼)(16)]^{-1} = (8)^{-1}$
	6	¾ A ¼ B	$[(1 - ¼ - ¼)(16)]^{-1} = (8)^{-1}$

The P matrix is:

$$P = \left[ \begin{array}{ccc|ccc} 0 & & & & & \\ 0 & 0 & & & & \\ 0 & 1 & 0 & & & \\ - & - & - & - & - & - \\ 1 & 0 & 0 & 0 & & \\ 1 & 1 & 0 & 0 & 0 & \\ 1 & 0 & 1 & 0 & 0 & 0 \end{array} \right]$$

$$D_n^{-1} = \begin{bmatrix} (16)^{-1} & & & | & & & \\ & (16)^{-1} & & | & & & \\ & & (12)^{-1} & | & & & \\ - & - & - & | & - & - & - \\ & & & | & (12)^{-1} & & \\ & & & | & & (8)^{-1} & \\ & & & | & & & (8)^{-1} \end{bmatrix}$$

The inverse of the multibreed nonadditive genetic covariance matrix is :

$$G_n^{-1} = D_n^{-1} - \frac{1}{2} D_n^{-1} P - \frac{1}{2} P' D_n^{-1} + \frac{1}{4} P' D_n^{-1} P$$

$$G_n^{-1} = \begin{bmatrix} g_n^{11} & g_n^{12} & g_n^{13} & | & g_n^{14} & g_n^{15} & g_n^{16} \\ g_n^{12} & g_n^{22} & g_n^{23} & | & 0 & g_n^{25} & 0 \\ g_n^{13} & g_n^{23} & g_n^{33} & | & 0 & 0 & g_n^{36} \\ - & - & - & | & - & - & - \\ g_n^{14} & 0 & 0 & | & g_n^{44} & 0 & 0 \\ g_n^{15} & g_n^{25} & 0 & | & 0 & g_n^{55} & 0 \\ g_n^{16} & 0 & g_n^{36} & | & 0 & 0 & g_n^{66} \end{bmatrix} \begin{matrix} \text{parents} \\ \\ \\ \\ \text{nonparents} \end{matrix}$$

parents                      non-parents

The rules used to compute the elements of matrix  $G_n^{-1}$  for intralocus interaction effects are :

- 1) Add  $d_{nii}^{-1}$  to  $i \times i$ ,
- 2) Add  $-\frac{1}{2} d_{nii}^{-1}$  to  $i \times s$  and  $s \times i$  if the sire of animal  $i$  is identified,
- 3) Add  $-\frac{1}{2} d_{nii}^{-1}$  to  $i \times d$  and  $d \times i$  if the dam of animal  $i$  is identified, and
- 4) Add  $\frac{1}{4} d_{nii}^{-1}$  to  $s \times s$ ,  $s \times d$ ,  $d \times s$ , and  $d \times d$  if the sire and dam of animal  $i$  are identified.

Thus,

$$g_n^{11} = (16)^{-1} + \frac{1}{4} (12)^{-1} + \frac{1}{4} (8)^{-1} + \frac{1}{4} (8)^{-1} = 0.146$$

$$g_n^{12} = \frac{1}{4} (8)^{-1} = 0.031$$

$$g_n^{13} = \frac{1}{4} (8)^{-1} = 0.031$$

$$g_n^{14} = -\frac{1}{2} (12)^{-1} = -0.042$$

$$g_n^{15} = -\frac{1}{2} (8)^{-1} = -0.063$$

$$g_n^{16} = -\frac{1}{2} (8)^{-1} = -0.063$$

$$g_n^{22} = (16)^{-1} + \frac{1}{4} (12)^{-1} + \frac{1}{4} (8)^{-1} = 0.115$$

$$g_n^{23} = -\frac{1}{2} (12)^{-1} = -0.042$$

$$g_n^{25} = -\frac{1}{2} (8)^{-1} = -0.063$$

$$g_n^{33} = (12)^{-1} + \frac{1}{4} (8)^{-1} = 0.115$$

$$g_n^{36} = -\frac{1}{2} (8)^{-1} = -0.063$$

$$g_n^{44} = (12)^{-1} = 0.083$$

$$g_n^{55} = (8)^{-1} = 0.125$$

$$g_n^{66} = (8)^{-1} = 0.125$$

The  $G_n^{-1}$  is equal to :

$$G_n^{-1} = \begin{bmatrix} 0.146 & 0.031 & 0.031 & -0.042 & -0.063 & -0.063 \\ 0.031 & 0.115 & -0.042 & 0 & -0.063 & 0 \\ 0.031 & -0.042 & 0.115 & 0 & 0 & -0.063 \\ \hline -0.042 & -0.042 & 0 & 0.083 & 0 & 0 \\ -0.063 & -0.063 & 0 & 0 & 0.125 & 0 \\ -0.063 & 0 & -0.063 & 0 & 0 & 0.125 \end{bmatrix}$$

### Multibreed Environmental Variances

Multibreed environmental variances and covariances among records are the same for all purebred and crossbred animals. The environmental variance ( $\sigma_e^2$ ) for all animals in the example is assumed to be equal to 49 kg<sup>2</sup>.

The multibreed environmental variances for the 6 animals in the example are:

	Animal		
	Number	Breed Group	Multibreed Environmental Variance
<b>Parents</b>	1	A	49
	2	B	49
	3	½ A ½ B	49
<b>Non-parents</b>	4	½ A ½ B	49
	5	½ A ½ B	49
	6	¾ A ¼ B	49

The left hand side of the **MME\_MAM\_EQVE** for Example 1 is:



lhs																	
6.000	3.250	2.750	3.500	3.000	3.000	1.000	1.000	1.000	1.000	1.000	1.000	2.500	2.000	0.500	0.000	0.000	0.000
3.250	2.313	0.938	1.875	2.250	1.000	1.000	0.000	0.500	0.500	0.500	0.750	1.375	1.000	0.375	0.000	0.000	0.000
2.750	0.938	1.813	1.625	0.750	2.000	0.000	1.000	0.500	0.500	0.500	0.250	1.125	1.000	0.125	0.000	0.000	0.000
3.500	1.875	1.625	3.250	1.500	2.000	0.000	0.000	1.000	1.000	1.000	0.500	2.250	2.000	0.250	0.000	0.000	0.000
3.000	2.250	0.750	1.500	3.000	0.000	1.000	0.000	0.000	0.000	1.000	1.000	1.500	1.000	0.500	0.000	0.000	0.000
3.000	1.000	2.000	2.000	0.000	3.000	0.000	1.000	1.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.000
1.000	1.000	0.000	0.000	1.000	0.000	5.114	1.089	0.757	-1.815	-2.178	-1.514	0.000	0.000	0.000	0.000	0.000	0.000
1.000	0.000	1.000	0.000	0.000	1.000	1.089	8.138	-1.210	0.000	-2.178	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1.000	0.500	0.500	1.000	0.000	1.000	0.757	-1.210	4.177	0.000	0.000	-1.514	0.000	1.000	0.000	0.000	0.000	0.000
1.000	0.500	0.500	1.000	0.000	1.000	-1.815	0.000	0.000	4.630	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000
1.000	0.500	0.500	1.000	1.000	0.000	-2.178	-2.178	0.000	0.000	5.356	0.000	1.000	1.000	0.000	0.000	0.000	0.000
1.000	0.750	0.250	0.500	1.000	0.000	-1.514	0.000	-1.514	0.000	0.000	4.027	0.500	0.000	0.500	0.000	0.000	0.000
2.500	1.375	1.125	2.250	1.500	1.000	0.000	0.000	0.000	1.000	1.000	0.500	9.396	2.531	1.781	-2.042	-3.063	-3.063
2.000	1.000	1.000	2.000	1.000	1.000	0.000	0.000	1.000	0.000	1.000	0.000	2.531	7.615	-2.042	0.000	-3.063	0.000
0.500	0.375	0.125	0.250	0.500	0.000	0.000	0.000	0.000	0.000	0.000	0.500	1.781	-2.042	5.865	0.000	0.000	-3.063
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-2.042	0.000	0.000	4.083	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-3.063	-3.063	0.000	0.000	6.125	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-3.063	0.000	-3.063	0.000	0.000	6.125

The vector of effects and the right hand side (RHS) of the **MME\_MAM\_EQVE** for Example 1

are:

<b>Effect</b>	<b>RHS</b>
Mean	1629
Breed <sub>A</sub>	908
Breed <sub>B</sub>	721
Heterosis <sub>AB</sub>	952
Sex <sub>M</sub>	867
Sex <sub>F</sub>	762
a <sub>a1</sub>	289
a <sub>a2</sub>	245
a <sub>a3</sub>	256
a <sub>a4</sub>	261
a <sub>a5</sub>	292
a <sub>a6</sub>	286
a <sub>n1</sub>	696
a <sub>n2</sub>	548
a <sub>n3</sub>	143
a <sub>n4</sub>	0
a <sub>n5</sub>	0
a <sub>n6</sub>	0

**Remarks:**

- 1) The rank of the left hand side matrix of the **MME\_MAM\_EQVE** is 16.
- 2) Differences between breed effects, heterosis, and differences between sex effects are estimable.
- 3) The set of **MME\_MAM\_EQVE** can be solved directly by:
  - a. Obtaining the generalized inverse of the left hand side (ginvlhs) and multiplying it by the right hand side (rhs), i.e.,
$$\text{sol} = \text{ginvlhs} * \text{rhs}$$
  - b. Imposing restrictions on the solutions. The number of equations in Example 1 is 18 and the rank of the left hand side of the **MME\_MAM\_EQVE** is 16, thus 2 restrictions need to be imposed to obtain solutions. These 2 restrictions could be:
    - i. Set the solution of the mean to zero, and
    - ii. Set the solution for breed B to zero. This restriction is useful because the expectation of the solution for breed A estimates the difference between the effects of breed A and breed B. Thus, breed B can be used as the genetic base of comparison for additive multibreed genetic effects.
- 4) Fixed heterosis effects here are an estimate of the difference between the interbreed (AB and BA) interaction effects relative to the average of intrabreed interaction effects (AA and BB). Thus, fixed heterosis effects can be used as the genetic base of comparison for nonadditive multibreed genetic effects.

The vector of solutions (SOL; obtained without imposing restrictions on the solutions), and the standard error of solutions (SESOL; computed as the square root of the diagonals of the generalized inverse of the left hand side of the **MME\_MAM\_EQVE** \*  $\sigma_e$ ) are:

<b>Effect</b>	<b>SOL</b>	<b>SESOL</b>
Mean <sup>o</sup>	133.07	2.87
Breed <sub>A</sub> <sup>o</sup>	71.70	7.88
Breed <sub>B</sub> <sup>o</sup>	61.37	7.61
Heterosis <sub>AB</sub> <sup>o</sup>	8.25	8.15
Sex <sub>M</sub> <sup>o</sup>	82.40	4.91
Sex <sub>F</sub> <sup>o</sup>	50.68	4.95
$\hat{a}_{a1}$	0.84	5.79
$\hat{a}_{a2}$	-0.12	2.98
$\hat{a}_{a3}$	-1.00	4.34
$\hat{a}_{a4}$	0.77	4.42
$\hat{a}_{a5}$	0.59	4.62
$\hat{a}_{a6}$	-0.74	5.26
$\hat{a}_{n1}$	0.42	3.81
$\hat{a}_{n2}$	-0.25	3.78
$\hat{a}_{n3}$	-0.37	3.94
$\hat{a}_{n4}$	0.21	3.95
$\hat{a}_{n5}$	0.08	4.00
$\hat{a}_{n6}$	0.02	3.98

### Additive Multibreed Genetic Predictions

The **AMBV** computed as deviations from breed B (chosen as genetic base) are:

$$AMBV_i = \hat{u}_{ai} = \text{Prob}_{A_{anim\ i}} * (\text{Breed}_A^\circ - \text{Breed}_B^\circ) + \hat{a}_{ai}$$

where

$\text{Prob}_{A_{anim\ i}}$  = expected fraction of breed A in animal i,

$\text{Breed}_A^\circ$  = generalized least squares solution for breed A,

$\text{Breed}_B^\circ$  = generalized least squares solution for breed B, and

$\hat{a}_{ai}$  = BLUP solution for  $a_{ai}$ .

The matrix of variances and covariances of errors of prediction (VEP) for the vector of **AMBV** is:

$$\text{VEP}(\mathbf{AMBV}) = \text{var}(\hat{\mathbf{u}}_a - \mathbf{u}_a) = \mathbf{K}_a * (\text{ginvlhs}) * \mathbf{K}_a' * \sigma_e^2$$

where

$\mathbf{K}_a$  =  $n_{anim} \times n_{eq}$  matrix specifying the factors multiplying the components of the **AMBV**, where  $n_{anim}$  = number of animals, and  $n_{eq}$  = number of equations,  
and

$\text{ginvlhs}$  =  $n_{eq} \times n_{eq}$  generalized inverse matrix of the left hand side of the **MME\_MAM\_EQVE**,

$\sigma_e^2$  = common residual variance.

Matrix  $K_a$  for **MAM\_EQVE** Example 1 is:

Ka																	
0.00	1.00	-1.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.50	-0.50	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.50	-0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.50	-0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.75	-0.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00

The standard errors of prediction (SEP) of the **AMBV** are computed as the square roots of the diagonal elements of the **VEP(AMBV)** matrix.

The **AMBV** and their **SEP** for the 6 animals in **MAM\_EQVE** Example 1 are:

Animal	Prob <sub>Aanim</sub>	Breed <sub>A</sub> <sup>o</sup> - Breed <sub>B</sub> <sup>o</sup>	$\hat{a}_{add}$	AMBV	SEP AMBV
1	1	10.33	0.84	11.17	14.61
2	0	10.33	-0.12	-0.12	2.98
3	0.5	10.33	-1.00	4.16	8.42
4	0.5	10.33	0.77	5.94	7.68
5	0.5	10.33	0.59	5.75	9.09
6	0.75	10.33	-0.74	7.01	11.67

### Nonadditive Multibreed Genetic Predictions

The **NMBV** computed assuming that males are mated to ½ A ½ B females, and vice versa, are:

$$\text{NMBV}_i = \hat{u}_{ni} = (\text{Prob}_{\text{Aanim } i} * \text{Prob}_{\text{Bmate}} + \text{Prob}_{\text{Banim } i} * \text{Prob}_{\text{Amate}})(\text{Heterosis}_{\text{AB}}^{\circ} + \hat{a}_{ni})$$

where

$\text{Prob}_{\text{Aanim } i}$  = expected fraction of breed A in animal i,

$\text{Prob}_{\text{Banim } i}$  = expected fraction of breed B in animal i,

$\text{Prob}_{\text{Amate}}$  = expected fraction of breed A in the mate of animal i,

$\text{Prob}_{\text{Bmate}}$  = expected fraction of breed B in the mate of animal i,

$\text{Heterosis}_{\text{AB}}^{\circ}$  = generalized least squares solution for the heterosis due to interaction between alleles of breeds A and B in 1 locus,

$\hat{a}_{ni}$  = BLUP solution for  $a_{ni}$ .

The matrix of variances and covariances of errors of prediction (VEP) for the vector of **NMBV** is:

$$\text{VEP}(\text{NMBV}) = \text{var}(\hat{u}_n - u_n) = \mathbf{K}_n * (\text{ginvlhs}) * \mathbf{K}_n' * \sigma_e^2$$

where

$\mathbf{K}_n$  =  $n_{\text{anim}} \times n_{\text{eq}}$  matrix specifying the factors multiplying the components of the **NMBV**, where  $n_{\text{anim}}$  = number of animals, and  $n_{\text{eq}}$  = number of equations, and

$\text{ginvlhs}$  =  $n_{\text{eq}} \times n_{\text{eq}}$  generalized inverse matrix of the left hand side of the **MME\_MAM\_EQVE**,

$\sigma_e^2$  = common residual variance.

Matrix  $K_n$  for **MAM\_EQVE** Example 1 is:

K <sub>n</sub>																	
0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00
0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00
0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00
0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50

The standard errors of prediction (SEP) of the **NMBV** are computed as the square roots of the diagonal elements of the **VEP(NMBV)** matrix.

The **NMBV** and their **SEP** for the 6 animals in **MAM\_EQVE** Example 1 are:

Animal	$\text{Prob}_{A_{\text{anim}}} * \text{Prob}_{B_{\text{mate}}}$ + $\text{Prob}_{B_{\text{anim}}} * \text{Prob}_{A_{\text{mate}}}$	Heterosis <sub>AB</sub> <sup>o</sup>	$\hat{a}_{\text{nadd}}$	NMBV	SEP NMBV
1	$1 * 0.5 + 0 * 0.5$	8.25	0.42	4.33	3.75
2	$0 * 0.5 + 1 * 0.5$	8.25	-0.25	4.00	3.79
3	$0.5 * 0.5 + 0.5 * 0.5$	8.25	-0.37	3.94	4.18
4	$0.5 * 0.5 + 0.5 * 0.5$	8.25	0.21	4.23	4.17
5	$0.5 * 0.5 + 0.5 * 0.5$	8.25	0.08	4.17	3.82
6	$0.75 * 0.5 + 0.25 * 0.5$	8.25	0.02	4.14	4.00



**Total Multibreed Genetic Predictions**

The **TMBV** are the sum of **AMBV** and **NMBV**, i.e.,

$$TMBV_i = AMBV_i + NMBV_i = \hat{u}_{ai} + \hat{u}_{ni}$$

The matrix of variances and covariances of errors of prediction (VEP) for the vector of **TMBV** is:

$$VEP(TMBV) = var(\hat{u}_t - u_t) = K_t * (ginvlhs) * K_t' * \sigma_e^2$$

where

$K_t$  =  $n_{anim} \times n_{eq}$  matrix specifying the factors multiplying the components of the **TMBV**, where  $n_{anim}$  = number of animals, and  $n_{eq}$  = number of equations, and

$ginvlhs$  =  $n_{eq} \times n_{eq}$  generalized inverse matrix of the left hand side of the **MME\_MAM\_EQVE**,

$\sigma_e^2$  = common residual variance.

Matrix  $K_t$  for **MAM\_EQVE** Example 1 is:

Kt																	
0.00	1.00	-1.00	0.50	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.50	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00	0.00
0.00	0.50	-0.50	0.50	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00
0.00	0.50	-0.50	0.50	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00
0.00	0.50	-0.50	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00
0.00	0.75	-0.75	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.50

The standard errors of prediction (SEP) of the **TMBV** are computed as the square roots of the diagonal elements of the VEP(**TMBV**) matrix.

The **TMBV** and their **SEP** for the 6 animals in **MAM\_EQVE** Example 1 are:

<b>Animal</b>	<b>AMBV</b>	<b>NMBV</b>	<b>TMBV</b>	<b>SEP TMBV</b>
1	11.17	4.33	15.50	14.58
2	-0.12	4.00	3.88	4.90
3	4.16	3.94	8.10	8.42
4	5.94	4.23	10.17	7.92
5	5.75	4.17	9.92	9.20
6	7.01	4.14	11.14	11.66

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