ANIMAL BREEDING NOTES

CHAPTER 16M EQVE EQVA FXNA

MULTIBREED ANIMAL MODEL WITH EQUAL RESIDUAL VARIANCES, EQUAL ADDITIVE GENETIC VARIANCES, AND NO RANDOM NONADDITIVE GENETIC EFFECTS

Multibreed Animal Model with Equal Residual Variances, Equal Additive Genetic Variances, and no random nonadditive genetic effects (MAM_EQVE_EQVA_FXNA)

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. Only fixed nonadditive genetic effects are accounted for in the model. Random nonadditive genetic effects are considered to be part of the residual.

4) Multibreed additive genetic variances and covariances among records are the same for all purebred and crossbred animals;

5) Multibreed environmental variances and covariances among records are the same for all purebred and crossbred animals; and

6) 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_EQVA_FXNA** is:

$$y \;=\; Xb + Z_a Q_a\, g_a + Z_n Q_n\, g_n + Z_a\, a_a + \varepsilon$$

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

$$\mathrm{var}\begin{bmatrix} a_a \\ \varepsilon \end{bmatrix} = \begin{bmatrix} G_a & 0 \\ 0 & R_\varepsilon \end{bmatrix}$$

$$\Rightarrow \quad \mathrm{var}(y) \;=\; Z_a G_a Z_a{}' + R_\varepsilon,$$

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 × 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**),

ε = vector of unknown random residual effects; residual effects for the

    MAM_EQVE_EQVA_FXNA model contain all nonadditive and environmental

    effects, i.e., $\varepsilon = Z_n\, u_n + e = I_n\, u_n + e$, where Z_n is assumed to be equal to I_n,

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 random nonadditive genetic effects in vector

a_n (a_n is assumed to be part of the residual by the **MAM_EQVE_EQVA_FXNA**),

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 = $A*\sigma_a^2$, where A = matrix of additive relationships and σ_a^2 = additive genetic variance common to all animals (purebred and crossbred) in the multibreed population,

R_ε = $I*\sigma_\varepsilon^2$, where σ_ε^2 = residual variance common to all animals in the multibreed population

$= I*(\sigma_n^2 + \sigma_e^2)$, where σ_n^2 = common nonadditive genetic variance, and σ_e^2 = common environmental variance.

The general mixed model equations (MME) for the multibreed animal model are:

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

However, $G_a = A*\sigma_a^2$, $R = I*\sigma_\varepsilon^2$, and there are no random nonadditive genetic effects in

MAM_EQVE_EQVA_FXNA. Thus, after deleting the equations for random nonadditive genetic effects, and multiplying both sides by σ_e^2, the resulting **MME_EQVE_EQVA_FXNA** are:

$$\begin{bmatrix} X'X & X'Z_aQ_a & X'Z_nQ_n & X'Z_a \\ Q_a'Z_a'X & Q_a'Z_a'Z_aQ_a & Q_a'Z_a'Z_nQ_n & Q_a'Z_a'Z_a \\ Q_n'Z_n'X & Q_n'Z_n'Z_aQ_a & Q_n'Z_n'Z_nQ_n & Q_n'Z_n'Z_a \\ Z_a'X & Z_a'Z_aQ_a & Z_a'Z_nQ_n & Z_a'Z_a+G_a^{-1}*\sigma_\varepsilon^2 \end{bmatrix} \begin{bmatrix} b \\ g_a \\ g_n \\ a_a \end{bmatrix} = \begin{bmatrix} X'y \\ Q_a'Z_a'y \\ Q_n'Z_n'y \\ Z_a'y \end{bmatrix}$$

where

$$G_a^{-1} * \sigma_\varepsilon^2 = \left(A^{-1} * \sigma_a^{-2}\right) * \sigma_\varepsilon^2 = A^{-1} * \frac{\sigma_\varepsilon^2}{\sigma_a^2}$$

Thus, an equivalent form of the **MME_EQVE_EQVA_FXNA** is:

$$\begin{bmatrix} X'X & X'Z_aQ_a & X'Z_nQ_n & X'Z_a \\ Q_a'Z_a'X & Q_a'Z_a'Z_aQ_a & Q_a'Z_a'Z_nQ_n & Q_a'Z_a'Z_a \\ Q_n'Z_n'X & Q_n'Z_n'Z_aQ_a & Q_n'Z_n'Z_nQ_n & Q_n'Z_n'Z_a \\ Z_a'X & Z_a'Z_aQ_a & Z_a'Z_nQ_n & Z_a'Z_a + A^{-1} * \frac{\sigma_\varepsilon^2}{\sigma_a^2} \end{bmatrix} \begin{bmatrix} b \\ g_a \\ g_n \\ a_a \end{bmatrix} = \begin{bmatrix} X'y \\ Q_a'Z_a'y \\ Q_n'Z_n'y \\ Z_a'y \end{bmatrix}$$

Example 1 for the MAM_EQVE_EQVA_FXNA 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 = $\sigma_{aAA}^2 = 36$ kg^2

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

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

Simplifying assumption: additive genetic variances are the same for all animals (purebred and crossbred).

Common additive genetic variance = $\sigma_a{}^2$ = 36 kg^2

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

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

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

Simplifying assumption: all nonadditive genetic effects are assumed to be part of the residual. The variance of nonadditive genetic effects is the same for all animals in the multibreed population.

Common nonadditive genetic variance = $\sigma_n{}^2$ = 16 kg^2

3) **Environmental variances:**

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

Residual Variance:

Common residual variance = $\sigma_\varepsilon{}^2$ = $\sigma_n{}^2$ + $\sigma_e{}^2$ = 16 kg^2 + 49 kg^2 = 65 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 + residual

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

Var (Wean wt) = var (animal additive genetic) + var (residual)

cov(Wean wt$_{ik}$, Wean wt$_{i'k'}$) = cov (animal additive genetic$_i$, animal additive genetic$_{i'}$)

+ cov (residual$_{ik}$, residual$_{i'k'}$)

The vectors and matrices of the **MAM_EQVE_EQVA_FXNA** model are:

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

$$
+
\begin{bmatrix}
\text{residual}_{anim1} \\ \text{residual}_{anim2} \\ \text{residual}_{anim3} \\ \text{residual}_{anim4} \\ \text{residual}_{anim5} \\ \text{residual}_{anim6}
\end{bmatrix}
$$

Multibreed Additive Genetic Variances

Multibreed additive genetic variances are the same for all purebred and crossbred animals. The common additive genetic variance (σ_a^2) for all animals in the **MAM_EQVE_EQVA_FXNA** example is assumed to be equal to 36 kg^2. Thus, the multibreed additive genetic variances for the 6 animals in the example are:

		Animal	
	Number	**Breed Group**	**Multibreed Additive Genetic Variance**
Parents	1	A	36
	2	B	36
	3	½ A ½ B	36
Non-parents	4	½ A ½ B	36
	5	½ A ½ B	36
	6	¾ A ¼ B	36

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:

$$G_a^{-1} = (I - \tfrac{1}{2} P') \, D_a^{-1} \, (I - \tfrac{1}{2} P)$$

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:

$$d_{aii}^{-1} = \left[\left(1 - \tfrac{1}{4}\delta_s\left(1+F_s\right) - \tfrac{1}{4}\delta_d\left(1+F_d\right)\right) * \sigma_a^2 \right]^{-1}$$

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_s and F_d are equal to zero. Thus, the expression for d_{aii}^{-1} simplifies to:

$$d_{aii}^{-1} = \left[\left(1 - \tfrac{1}{4}\delta_s - \tfrac{1}{4}\delta_d\right) * \sigma_a^2\right]^{-1}$$

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

	Animal		
	Number	**Breed Group**	$(d_{aii})^{-1}$
Parents	1	A	$[(1)*(36)]^{-1} = (36)^{-1}$
	2	B	$[(1)*(36)]^{-1} = (36)^{-1}$
	3	½ A ½ B	$[(1-¼)(36)]^{-1} = (27)^{-1}$
Non-parents	4	½ A ½ B	$[(1-¼)(36)]^{-1} = (27)^{-1}$
	5	½ A ½ B	$[(1-¼-¼)(36)]^{-1} = (18)^{-1}$
	6	¾ A ¼ B	$[(1-¼-¼)(36)]^{-1} = (18)^{-1}$

The P matrix is:

$$
P = \begin{bmatrix}
0 & & & | & & & \\
0 & 0 & & | & & & \\
0 & 1 & 0 & | & & & \\
- & - & - & | & - & - & - \\
1 & 0 & 0 & | & 0 & & \\
1 & 1 & 0 & | & 0 & 0 & \\
1 & 0 & 1 & | & 0 & 0 & 0
\end{bmatrix}
$$

$$D_a^{-1} = \begin{bmatrix} (36)^{-1} & & & | & & & \\ & (36)^{-1} & & | & & & \\ & & (27)^{-1} & | & & & \\ - & - & - & | & - & - & - \\ & & & | & (27)^{-1} & & \\ & & & | & & (18)^{-1} & \\ & & & | & & & (18)^{-1} \end{bmatrix}$$

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

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

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

$$\qquad\qquad \downarrow \qquad\qquad\qquad \downarrow$$
$$\qquad\quad \text{parents} \qquad\quad \text{non-parents}$$

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

1) Add d_{aii}^{-1} to $i \times i$,

2) Add $-\tfrac{1}{2} d_{aii}^{-1}$ to $i \times s$ and $s \times i$ if the sire of animal i is identified,

3) Add $-\tfrac{1}{2} d_{aii}^{-1}$ to $i \times d$ and $d \times i$ if the dam of animal i is identified, and

4) Add $\frac{1}{4}\,d_{aii}^{-1}$ to s × s, s × d, d × s, and d × d if the sire and dam of animal i are identified.

Thus,

g_a^{11} $= (36)^{-1} + \frac{1}{4}\,(27)^{-1} + \frac{1}{4}\,(18)^{-1} + \frac{1}{4}\,(18)^{-1} = 0.065$

g_a^{12} $= \frac{1}{4}\,(18)^{-1} = 0.014$

g_a^{13} $= \frac{1}{4}\,(18)^{-1} = 0.014$

g_a^{14} $= -\frac{1}{2}\,(27)^{-1} = -0.019$

g_a^{15} $= -\frac{1}{2}\,(18)^{-1} = -0.028$

g_a^{16} $= -\frac{1}{2}\,(18)^{-1} = -0.028$

g_a^{22} $= (36)^{-1} + \frac{1}{4}\,(27)^{-1} + \frac{1}{4}\,(18)^{-1} = 0.051$

g_a^{23} $= -\frac{1}{2}\,(27)^{-1} = -0.019$

g_a^{25} $= -\frac{1}{2}\,(18)^{-1} = -0.028$

g_a^{33} $= (27)^{-1} + \frac{1}{4}\,(18)^{-1} = 0.051$

g_a^{36} $= -\frac{1}{2}\,(18)^{-1} = -0.028$

g_a^{44} $= (27)^{-1} = 0.037$

g_a^{55} $= (18)^{-1} = 0.056$

g_a^{66} $= (18)^{-1} = 0.056$

Thus, G_a^{-1} is equal to :

$$G_a^{-1} = \begin{bmatrix} 0.065 & 0.014 & 0.014 & -0.019 & -0.028 & -0.028 \\ 0.014 & 0.051 & -0.019 & 0 & -0.028 & 0 \\ 0.014 & -0.019 & 0.051 & 0 & 0 & -0.028 \\ -0.019 & 0 & 0 & 0.037 & 0 & 0 \\ -0.028 & -0.028 & 0 & 0 & 0.056 & 0 \\ -0.028 & 0 & -0.028 & 0 & 0 & 0.056 \end{bmatrix}$$

Multibreed Residual Variances

Multibreed residual variances are assumed to be the sum of nonadditive genetic and environmental variances. Multibreed nonadditive genetic variances are assumed to be the same for all purebred and crossbred animals. Similarly, multibreed environmental variances and covariances among records are the same for all purebred and crossbred animals. The common residual variance is assumed to be the sum of the common nonadditive genetic variance ($\sigma_n^2 = 16$ kg^2) and the common environmental variance ($\sigma_e^2 = 49$ kg^2), i.e., $\sigma_\varepsilon^2 = \sigma_n^2 + \sigma_e^2 = 16$ kg^2 + 49 kg^2 = 65 kg^2.

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

		Animal	
	Number	**Breed Group**	**Multibreed Residual Variance**
Parents	1	A	65
	2	B	65
	3	½ A ½ B	65
Non-parents	4	½ A ½ B	65
	5	½ A ½ B	65
	6	¾ A ¼ B	65

The left hand side of the **MME_MAM_EQVE_EQVA_FXNA** 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
3.250	2.313	0.938	1.875	2.250	1.000	1.000	0.000	0.500	0.500	0.500	0.750
2.750	0.938	1.813	1.625	0.750	2.000	0.000	1.000	0.500	0.500	0.500	0.250
3.500	1.875	1.625	3.250	1.500	2.000	0.000	0.000	1.000	1.000	1.000	0.500
3.000	2.250	0.750	1.500	3.000	0.000	1.000	0.000	0.000	0.000	1.000	1.000
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	1.000	0.000	5.213	0.903	0.903	-1.204	-1.806	-1.806
1.000	0.000	1.000	0.000	0.000	1.000	0.903	4.310	-1.204	0.000	-1.806	0.000
1.000	0.500	0.500	1.000	0.000	1.000	0.903	-1.204	4.310	0.000	0.000	-1.806
1.000	0.500	0.500	1.000	0.000	1.000	-1.204	0.000	0.000	3.407	0.000	0.000
1.000	0.500	0.500	1.000	1.000	0.000	-1.806	-1.806	0.000	0.000	4.611	0.000
1.000	0.750	0.250	0.500	1.000	0.000	-1.806	0.000	-1.806	0.000	0.000	4.611

The vector of effects and the right hand side (RHS) of the **MME_MAM_EQVE_EQVA_FXNA**

for Example 1 are:

Effect	RHS
Mean	1629
$Breed_A$	908
$Breed_B$	721
$Heterosis_{AB}$	952
Sex_M	867
Sex_F	762
a_{a1}	289
a_{a2}	245
a_{a3}	256
a_{a4}	261
a_{a5}	292
a_{a6}	286

Remarks:

1) The rank of the left hand side matrix of the **MME_MAM_EQVE_EQVA_FXNA** is 10.

2) Differences between breed effects, heterosis, and differences between sex effects are estimable.

3) The set of **MME_MAM_EQVE_EQVA_FXNA** 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.,

   sol = ginvlhs * rhs

   b. Imposing restrictions on the solutions. The number of equations in Example 1 is 12 and the rank of the left hand side of the **MME_MAM_EQVE_EQVA_FXNA** is 10, 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_EQVA_FXNA * σ_ε**) are:

Effect	SOL	SESOL
Mean°	133.17	3.43
Breed$_A$°	71.58	9.12
Breed$_B$°	61.59	9.31
Heterosis$_{AB}$°	8.25	8.12
Sex$_M$°	82.53	5.61
Sex$_F$°	50.64	5.58
$\hat{a}_{a1}$	0.68	5.83
$\hat{a}_{a2}$	-0.39	5.86
$\hat{a}_{a3}$	-1.22	5.36
$\hat{a}_{a4}$	0.93	5.44
$\hat{a}_{a5}$	0.43	5.88
$\hat{a}_{a6}$	-0.84	5.71

Additive Multibreed Genetic Predictions

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

$$\text{AMBV}_i \quad = \quad \hat{u}_{ai} = \quad \text{Prob}_{\text{Aanim } i}*(\text{Breed}_A{}^\circ - \text{Breed}_B{}^\circ) + \hat{a}_{ai}$$

where

$\text{Prob}_{\text{Aanim } i}$ = 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:

$$\text{VEP}(\textbf{AMBV}) = \text{var}(\hat{u}_a - u_a) = K_a*(\text{ginvlhs})*K_a{'}*\sigma_\varepsilon{}^2$$

where

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

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

$\sigma_\varepsilon{}^2$ = common residual variance.

Matrix K_a for **MAM_EQVE_EQVA_FXNA** 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	1.00	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	0.50	-0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.00	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	0.75	-0.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00

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 Example 1 are:

Animal	$Prob_{Aanim}$	$Breed_A{}^\circ -$ $Breed_B{}^\circ$	$\hat{a}_{add}$	AMBV	SEP AMBV
1	1	9.99	0.68	10.68	17.69
2	0	9.99	-0.39	-0.39	5.86
3	0.5	9.99	-1.22	3.78	10.69
4	0.5	9.99	0.93	5.93	9.53
5	0.5	9.99	0.43	5.43	11.93
6	0.75	9.99	-0.84	6.66	14.28

Nonadditive Multibreed Genetic Predictions

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

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

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,
$\text{Heterosis}_{AB}^{\circ}$	=	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}, included in the residual of the

MAM_EQVE_EQVA_FXNA, and assumed to be zero for the computation of the NMBV.

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

$$\text{VEP}(\textbf{NMBV}) \quad = \quad \text{var}(\hat{u}_n - u_n) = \quad K_n*(\text{ginvlhs})*K_n{}'* \sigma_{\varepsilon}^2$$

where

K_n	=	$n_{\text{anim}} \times n_{\text{eq}}$ matrix specifying the factors multiplying the components of the **NMBV**, where n_{anim} = number of animals, and n_{eq} = number of equations, and
ginvlhs	=	$n_{\text{eq}} \times n_{\text{eq}}$ generalized inverse matrix of the left hand side of the **MME_MAM_EQVE_EQVA_FXNA**,
σ_{ε}^2	=	common residual variance.

Matrix K_n for **MAM_EQVE_EQVA_FXNA** Example 1 is:

Kn											
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	0.00	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	0.00	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	0.00	0.00	0.00

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_EQVA_FXNA** Example 1 are:

Animal	$Prob_{Aanim}*Prob_{Bmate}$ $+$ $Prob_{Banim}*Prob_{Amate}$	$Heterosis_{AB}°$	$\hat{a}_{nadd}$	NMBV	SEP NMBV
1	1*0.5 + 0*0.5	8.25	0	4.12	4.06
2	0*0.5 + 1*0.5	8.25	0	4.12	4.06
3	0.5*0.5 + 0.5*0.5	8.25	0	4.12	4.06
4	0.5*0.5 + 0.5*0.5	8.25	0	4.12	4.06
5	0.5*0.5 + 0.5*0.5	8.25	0	4.12	4.06
6	0.75*0.5 + 0.25*0.5	8.25	0	4.12	4.06

Total Multibreed Genetic Predictions

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

$$\text{TMBV}_i \quad = \quad \text{AMBV}_i + \text{NMBV}_i \quad = \quad \hat{u}_{ai} + \hat{u}_{ni}$$

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

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

where

$$K_t \quad = \quad n_{anim} \times n_{eq} \text{ matrix specifying the factors multiplying the components of the}$$

$$\text{TMBV, where } n_{anim} = \text{number of animals, and } n_{eq} = \text{number of equations, and}$$

$$\text{ginvlhs} \quad = \quad n_{eq} \times n_{eq} \text{ generalized inverse matrix of the left hand side of the}$$

MME_MAM_EQVE_EQVA_FXNA,

$$\sigma_\varepsilon^2 \quad = \quad \text{common residual variance.}$$

Matrix K_t for **MAM_EQVE_EQVA_FXNA** 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
0.00	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	-0.50	0.50	0.00	0.00	0.00	0.00	1.00	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	0.50	-0.50	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.00	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

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_EQVA_FXNA** Example 1 are:

Animal	AMBV	NMBV	TMBV	SEP TMBV
1	10.68	4.12	14.80	17.82
2	-0.39	4.12	3.73	7.44
3	3.78	4.12	7.91	10.87
4	5.93	4.12	10.06	9.73
5	5.43	4.12	9.55	12.09
6	6.66	4.12	10.78	14.43

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