ANIMAL BREEDING NOTES

CHAPTER 15

SIRE-MATERNAL GRANDSIRE APPROXIMATION TO THE MATRIX OF ADDITIVE RELATIONSHIPS AND ITS INVERSE

Definition of the sire-maternal grandsire model

Models used to analyze animal breeding data are often simpler versions of a complete model. These models rest on simplifying assumptions made with respect to the data, whose objectives could be, for instance, to reduce computations or generate a better behaved set of mixed model equations. One possibility is to assume that:

(i) parents have no records of their own, and

(ii) dams are related only through their sires.

These simplifying assumptions reduce an animal model to a sire-maternal grandsire model. Because dams are ignored in A, a set of rules that account for sire (s) and maternal grandsire (mgs) contributions must be used to compute the matrix of additive relationships (A) and its inverse (A^{-1}).

A model for the breeding value of an animal is:

$$u_i = \frac{1}{2} u_{s_i} + \frac{1}{2} u_{d_i} + \frac{1}{2} \varepsilon_{s_i} + \frac{1}{2} \varepsilon_{d_i} \qquad [1]$$

$$E[u_i] = 0$$

$$\begin{aligned} \mathrm{var}(u_i) &= a_{ii}\, \sigma_A^2 \\ &= \left(1 + \frac{1}{2} a_{s_i d_i}\right) \sigma_A^2 \\ &= \left(1 + F_i\right) \sigma_A^2 \end{aligned}$$

where

s_i = sire of animal i,

d_i = dam of animal i.

Assuming that the sire and the dam of animal i have no records and that dams are unrelated except through their sires, model [1] can be written as:

$$u_i = \frac{1}{2}u_{s_i} + \frac{1}{2}\left[\frac{1}{2}u_{mgs_i} + \frac{1}{2}u_{mgd_i} + \frac{1}{2}\varepsilon_{mgs_i} + \frac{1}{2}\varepsilon_{mgd_i}\right] + \frac{1}{2}\varepsilon_{s_i} + \frac{1}{2}\varepsilon_{d_i} \qquad [2]$$

$$u_i = \frac{1}{2}u_{s_i} + \frac{1}{4}u_{mgs_i} + \phi_i$$

$$E[u_i] = 0$$

$$\mathrm{var}(u_i) = \left(1 + \frac{1}{4}a_{s_i\,mgs_i}\right)\sigma_A^2$$

$$= \left(1 + F_i\right)\sigma_A^2$$

where

mgs_i = maternal grandsire of animal i,

mgd_i = maternal granddam of animal i,

$$\varphi_i = \frac{1}{4}u_{mgd_i} + \frac{1}{4}\varepsilon_{mgs_i} + \frac{1}{4}\varepsilon_{mgd_i} + \frac{1}{2}\varepsilon_{s_i} + \frac{1}{2}\varepsilon_{d_i}$$

Remarks:

$$F_i = \frac{1}{2}a_{s_i\,d_i},$$

$$= \frac{1}{2}\left[\frac{1}{2}a_{s_i\,mgs_i} + \frac{1}{2}a_{s_i\,mgd_i}\right],$$

$= \frac{1}{4}a_{s_i mgs_i}$, because, by assumption, $a_{s_i\,mgd_i} = 0$.

Derivation of the rules to compute the additive relationship matrix among sires and maternal grandsires directly

In matrix notation model [2] is:

$$u = \frac{1}{2} P_s \; u + \frac{1}{4} P_m \; u + \phi$$

$$\Rightarrow \qquad u = \left(I - \frac{1}{2} P_s - \frac{1}{4} P_m \right)^{-1} \phi$$

$$E[u] = 0$$

$$var(u) = \left(I - \frac{1}{2} P_s - \frac{1}{4} P_m \right)^{-1} var\left(\phi\right) \left(I - \frac{1}{2} P_s' - \frac{1}{4} P_m' \right)^{-1}$$

$$= \left(I - \frac{1}{2} P_s - \frac{1}{4} P_m \right)^{-1} D \left(I - \frac{1}{2} P_s' - \frac{1}{4} P_m' \right)^{-1} \sigma_A^2$$

where

D = diag$\{d_{ii}\}$, d_{ii} = coefficient of var(φ_i),

u = vector of breeding values of males ordered so that sires and mgs' precede sons and maternal grandsons (mgsons),

P_s = lower triangular matrix relating sires to sons. A row of P contains at most one non-zero element, i.e., a 1, in the column corresponding to the sire of a male, if it is known.

P_m = lower triangular matrix relating mgs' to mgsons. A row of P contains a 1 in the column of the mgs of a male if the mgs is identified or a 0 otherwise, and zeroes elsewhere.

φ = vector of independent random variables, where

$$\varphi_i = \frac{1}{4} u_{mgd_i} + \frac{1}{4} \varepsilon_{mgs_i} + \frac{1}{4} \varepsilon_{mgd_i} + \frac{1}{2} \varepsilon_{s_i} + \frac{1}{2} \varepsilon_{d_i}$$

if s_i and mgs_i are known

$$\varphi_i \quad = \quad \frac{1}{2}u_{d_i} + \frac{1}{2}\varepsilon_{s_i} + \varepsilon_{d_i}$$

if s_i is known only

$$\varphi_i \quad = \quad \frac{1}{2}u_{s_i} + \frac{1}{4}u_{mgd_i} + \frac{1}{4}\varepsilon_{mgs_i} + \frac{1}{4}\varepsilon_{mgd_i} + \frac{1}{2}\varepsilon_{s_i} + \frac{1}{2}\varepsilon_{d_i}$$

if mgs_i is known only

$$\varphi_i \quad = \quad u_i \quad \text{if neither } s_i \text{ nor } mgs_i \text{ are known}$$

Thus, the var(φ_i) = $d_{ii}\,\sigma_A^2$ are:

(i) if s_i and mgs_i are identified,

$$\begin{aligned}
\mathrm{var}(\varphi_i) \quad &= \quad \mathrm{var}\left(u_i\right) - \mathrm{var}\left(\frac{1}{2}u_{s_i} + \frac{1}{4}u_{mgs_i}\right) \\
&= \left[\left(1 + \frac{1}{4}a_{s_i\,mgs_i}\right) - \left(\frac{1}{4}a_{s_i\,s_i} + \frac{1}{16}a_{mgs_i\,mgs_i} + \frac{1}{4}a_{s_i\,mgs_i}\right)\right]\sigma_A^2 \\
&= \left[1 - \frac{1}{4}a_{s_i\,s_i} - \frac{1}{16}a_{mgs_i\,mgs_i}\right]\sigma_A^2 \\
&= \left[1 - \frac{1}{4}\left(1 + F_{s_i}\right) - \frac{1}{16}\left(1 + F_{mgs_i}\right)\right]\sigma_A^2 \\
&= \left[\frac{11}{16} - \frac{1}{4}F_{s_i} - \frac{1}{16}F_{mgs_i}\right]\sigma_A^2
\end{aligned}$$

where

$$F_{s_i} \quad = \quad \frac{1}{4}a_{ss_i\,mgss_i}$$

$$F_{mgs_i} \quad = \quad \frac{1}{4}a_{smgs_i\,mgsmgs_i}$$

and subscripts,

ss_i	=	sire of s_i
$mgss_i$	=	mgs of s_i
$smgs_i$	=	sire of mgs_i
$mgsmgs_i$	=	mgs of mgs_i

(ii) if s_i is identified only,

$$\begin{aligned} \mathrm{var}(\varphi_i) &= \mathrm{var}\left(u_i\right) - \mathrm{var}\left(\frac{1}{2}u_{s_i}\right) \\ &= \left[1 - \frac{1}{4}a_{s_i s_i}\right]\sigma_A^2 \\ &= \left[1 - \frac{1}{4}\left(1 + F_{s_i}\right)\right]\sigma_A^2 \\ &= \left[\frac{3}{4} - \frac{1}{4}F_{s_i}\right]\sigma_A^2 \end{aligned}$$

(iii) if mgs_i is identified only,

$$\begin{aligned} \mathrm{var}(\varphi_i) &= \mathrm{var}\left(u_i\right) - \mathrm{var}\left(\frac{1}{4}u_{mgs_i}\right) \\ &= \left[1 - \frac{1}{16}a_{mgs_i\, mgs_i}\right]\sigma_A^2 \\ &= \left[1 - \frac{1}{16}\left(1 + F_{mgs_i}\right)\right]\sigma_A^2 \\ &= \left[\frac{15}{16} - \frac{1}{16}F_{mgs_i}\right]\sigma_A^2 \end{aligned}$$

(iv) if neither s_i nor mgs_i are identified,

$$\mathrm{var}(\varphi_i) = \mathrm{var}\left(u_i\right)$$

$$= [1]\,\sigma_A^2$$

$$= \sigma_A^2$$

Because

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

$$\text{var}(u) = \left(I - \frac{1}{2}P_s - \frac{1}{4}P_m\right)^{-1} D \left(I - \frac{1}{2}P_s{'} - \frac{1}{4}P_m{'}\right)^{-1} \sigma_A^2$$

$$\Rightarrow \quad A = \left(I - \frac{1}{2}P_s - \frac{1}{4}P_m\right)^{-1} D \left(I - \frac{1}{2}P_s{'} - \frac{1}{4}P_m{'}\right)^{-1} \quad \text{if only males are included in A}$$

$$\Rightarrow \quad A^{-1} = \left(I - \frac{1}{2}P_s{'} - \frac{1}{4}P_m{'}\right) D^{-1} \left(I - \frac{1}{2}P_s - \frac{1}{4}P_m\right)$$

$A^{-1} = D^{-1}$	diagonals
$-\frac{1}{2}D^{-1}P_s$	sons-sires
$-\frac{1}{2}P_s{'}D^{-1}$	sires-sons
$-\frac{1}{4}D^{-1}P_m$	mgsons-mgs'
$-\frac{1}{4}P_m{'}D^{-1}$	mgs'-mgsons
$+\frac{1}{4}P_s{'}D^{-1}P_s$	sires-sires
$+\frac{1}{8}P_s{'}D^{-1}P_m$	sires-mgs'
$+\frac{1}{8}P_m{'}D^{-1}P_s$	mgs'-sires

$$+\frac{1}{16}P_m'D^{-1}P_m \qquad \text{mgs'-mgs'}$$

where the right hand column indicates where the elements of the matrices on the left column are located in the A^{-1} matrix, e.g., sires-sires means that the matrix $\frac{1}{4}P_s'D^{-1}P_s$ contributes with nonzero elements to the sire-sire elements of A^{-1}. Based on the contributions of the component matrices, i.e., $D^{-1},\ldots,\frac{1}{16}P_m'D^{-1}P_m$, to A^{-1}, the **rules to compute A^{-1}, using a list of males where sires and mgs′ precede sons and mgsons**, are (Henderson, 1976):

(1) if s_i and mgs_i are known, add:

d_{ii}^{-1} to $i \times i$

$-\frac{1}{2}d_{ii}^{-1}$ to $i \times s_i$, $s_i \times i$

$-\frac{1}{4}d_{ii}^{-1}$ to $i \times mgs_i$, $mgs_i \times i$

$\frac{1}{4}d_{ii}^{-1}$ to $s_i \times s_i$

$\frac{1}{8}d_{ii}^{-1}$ to $s_i \times mgs_i$, $mgs_i \times s_i$

$\frac{1}{16}d_{ii}^{-1}$ to $mgs_i \times mgs_i$

where

$$d_{ii}^{-1} = \left[1 - \frac{1}{4}a_{s_i s_i} - \frac{1}{16}a_{mgs_i\, mgs_i}\right]^{-1}$$

(2) if s_i is known only, add:

d_{ii}^{-1} to $i \times i$

$-\frac{1}{2} d_{ii}^{-1}$ to $i \times s_i, s_i \times i$

$\frac{1}{4} d_{ii}^{-1}$ to $s_i \times s_i$

where

$$d_{ii}^{-1} = \left[1 - \frac{1}{4} a_{s_i s_i}\right]^{-1}$$

(3) if mgs_i is known only, add:

d_{ii}^{-1} to $i \times i$

$-\frac{1}{4} d_{ii}^{-1}$ to $i \times mgs_i, mgs_i \times i$

$\frac{1}{16} d_{ii}^{-1}$ to $mgs_i \times mgs_i$

where

$$d_{ii}^{-1} = \left[1 - \frac{1}{16} a_{mgs_i\, mgs_i}\right]^{-1}$$

(4) if neither s_i nor mgs_i are known, add:

d_{ii}^{-1} to $i \times i$

where

$$d_{ii}^{-1} = 1$$

Non-inbred population

If there is no inbreeding the d_{ii} and d_{ii}^{-1} are:

Ancestor(s) identified	d_{ii}	d_{ii}^{-1}
s_i and mgs_i	$\frac{11}{16}$	$\frac{16}{11}$
s_i only	$\frac{3}{4}$	$\frac{4}{3}$
mgs_i only	$\frac{15}{16}$	$\frac{16}{15}$
none	1	1

So, the **rules to build A^{-1} simplify to those of Henderson (1975)**:

(1) if s_i and mgs_i are known, add:

$\frac{16}{11}$ to $i \times i$

$-\frac{8}{11}$ to $i \times s_i$, s_i x i

$-\frac{4}{11}$ to $i \times mgs_i$, $mgs_i \times i$

$\frac{4}{11}$ to $s_i \times s_i$

$\frac{2}{11}$ to $s_i \times mgs_i$, $mgs_i \times s_i$

$\frac{1}{11}$ to $mgs_i \times mgs_i$

(2) if s_i is known only, add:

$\frac{4}{3}$ to $i \times i$

$-\frac{2}{3}$ to $i \times s_i$, $s_i \times i$

$\frac{1}{3}$ to s_i x s_i

(3) if mgs_i is known only, add:

$\frac{16}{15}$ to $i \times i$

$-\frac{4}{15}$ to $i \times mgs_i$, $mgs_i \times i$

$\frac{1}{15}$ to $mgs_i \times mgs_i$

(4) if neither s_i nor mgs_i is known, add:

1 to $i \times i$.

Inbred population

If there is inbreeding in a population, then we need to know the diagonal elements of the A matrix to be able to compute the d_{ii}. Quaas' (1976) procedure to compute the diagonal of A, when males and females in the pedigree are accounted for, can be easily modified to the case when males are included in A only. Thus, to compute A^{-1}:

[1] Define:

u = vector of sums of squares of the elements of a row of L, where

$$L = \left(I - \frac{1}{2} P_s - \frac{1}{4} P_m \right)^{-1} D^{½}$$

v = vector containing the diagonal elements of L and also used to store the offdiagonal elements of L temporarily.

[2] Order and number males from 1 to n, sires and mgs preceding sons and mgsons. Set the number of the unknown sires and mgs' to zero.

[3] Process one male at a time, from male 1 to n. For the i^{th} male, compute:

(a) $v_i = c_{ii}$

$$= \left[1 - \frac{1}{4}u_{s_i} - \frac{1}{16}u_{mgs_i}\right]^{1/2} \qquad \text{if } s_i, mgs_i > 0$$

$$= \left[1 - \frac{1}{4}u_{s_i}\right]^{1/2} \qquad \text{if } s_i > 0,\ mgs_i = 0$$

$$= \left[1 - \frac{1}{16}u_{mgs_i}\right]^{1/2} \qquad \text{if } s_i = 0,\ mgs_i > 0$$

$$= 1 \qquad \text{if } s_i = mgs_i = 0$$

(b) $v_j = c_{ji}$ for $j = i + 1, \ldots, n$

$$= \frac{1}{2}v_{s_j} + \frac{1}{4}v_{mgs_j} \qquad \text{if } i \le s_j, mgs_j$$

$$= \frac{1}{2}v_{s_j} \qquad \text{if } mgs_j < i \le s_j$$

$$= \frac{1}{4}v_{mgs_j} \qquad \text{if } s_j < i \le mgs_j$$

$$= 0 \qquad \text{if } s_j, mgs_j < i$$

(c) $u_j = u_j + (v_j)^2$ for $j = i, \ldots, n$

(d) $d_{ii}^{-1} = (v_i)^{-2}$

(e) Add the contributions of the i^{th} animal to A^{-1} using the rules for the case of males included in A only given previously. Use a matrix or the vectors of the a linked-list subroutine to sum and store the non-zero elements of A^{-1}. Store the row number, column number and the non-zero element after the n^{th} animal is processed.

Remarks:

[1] If a computer program for the sire-mgs approximation to A^{-1} is written, check for sire = mgs (i.e., sire-daughter matings). **If $s_i = mgs_i$, add**:

(i) $\left(\frac{1}{4}+2\left(\frac{1}{8}\right)+\frac{1}{16}\right)d_{ii}^{-1} - \frac{9}{16}d_{ii}^{-1}$ to $s_i \times s_i$ (= $mgs_i \times mgs_i$) if s_i (= mgs_i) is **inbred**

(ii) $\left(\frac{4}{11}+2\left(\frac{2}{11}\right)+\frac{1}{11}\right) - \frac{9}{16}$ to $s_i \times s_i$ (= $mgs_i \times mgs_i$) if s_i (= mgs_i) is **not inbred**.

[2] The sire-mgs approximation to A:

[2.1] **Treats full-sibs as paternal half-sibs**, e.g.,

true pedigree

s_1 d_1

$\downarrow \searrow \swarrow \downarrow$

$\downarrow \swarrow \searrow \downarrow$

p_1 p_2

sire-mgs approximation

mgs_i

$\swarrow \searrow$

d_1 s_1 d_2

$\downarrow \swarrow \searrow \downarrow$

p_1 p_2

[2.2] **Treats maternal half-sibs as mgs-grandprogeny**, e.g.,

true pedigree

s_1 d_1 s_2

$\downarrow \swarrow \searrow \downarrow$

p_1 p_2

sire-mgs approximation

mgs_i

$\swarrow \searrow$

s_1 d_1 d_2 s_2

$\downarrow \swarrow \searrow \downarrow$

p_1 p_2

[2.3] **is equal to an A that includes males and females, if**:

(a) all maternal granddams are base dams, i.e., unrelated and non-inbred, and

(b) there are no maternal half-sibs, i.e., each dam has only one calf.

Example of A^{-1} for the sire-mgs approximation

Animal	Sire	Mgs
1		
2	1	
3		1
4	3	2
5	4	3
6	4	4

Here,

$$P_s = \begin{bmatrix} 0 & & & & & \\ 1 & 0 & & & & \\ 0 & 0 & 0 & & & \\ 0 & 0 & 1 & 0 & & \\ 0 & 0 & 0 & 1 & 0 & \\ 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix} \quad \text{and} \quad P_m = \begin{bmatrix} 0 & & & & & \\ 0 & 0 & & & & \\ 1 & 0 & 0 & & & \\ 0 & 1 & 0 & 0 & & \\ 0 & 0 & 1 & 0 & 0 & \\ 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix}$$

Computation of the d_{ii} using the sire-mgs version of Quaas' (1976) procedure

	Round (i)					
(j)	1	2	3	4	5	6
u_1	1.0	1.0	1.0	1.0	1.0	1.0
u_2	$(0.5)^2$	$u_{2(1)} + 0.75$	1.0	1.0	1.0	1.0
u_3	$(0.25)^2$	$u_{3(1)} + (v_{3(2)})^2$	$u_{3(2)} + 0.9375$	1.0	1.0	1.0
u_4	$(0.25)^2$	$u_{4(1)} + (v_{4(2)})^2$	$u_{4(2)} + (v_{4(3)})^2$	$u_{4(3)} + 0.6875$	1.03125	1.03125
u_5	$(0.1875)^2$	$u_{5(1)} + (v_{5(2)})^2$	$u_{5(2)} + (v_{5(3)})^2$	$u_{5(3)} + (v_{5(4)})^2$	$u_{5(4)} + 0.6796875$	1.1328125
u_6	$(0.1875)^2$	$u_{6(1)} + (v_{6(2)})^2$	$u_{6(2)} + (v_{6(3)})^2$	$u_{6(3)} + (v_{6(4)})^2$	$u_{6(4)} + (v_{6(5)})^2$	1.2578125
	1	2	3	4	5	6
v_1	$(1.0)^{½}$	1.0	1.0	1.0	1.0	1.0
v_2	0.5	$(0.75)^{½}$	$(0.75)^{½}$	$(0.75)^{½}$	$(0.75)^{½}$	$(0.75)^{½}$
v_3	0.25	0	$(0.9375)^{½}$	$(0.9375)^{½}$	$(0.9375)^{½}$	$(0.9375)^{½}$
v_4	0.25	$¼(0.75)^{½}$	$½(0.9375)^{½}$	$(0.6875)^{½}$	$(0.6875)^{½}$	$(0.6875)^{½}$
v_5	0.1875	$⅛(0.75)^{½}$	$½(0.9375)^{½}$	$½(0.6875)^{½}$	$(0.6796875)^{½}$	$(0.6796875)^{½}$
v_6	0.1875	$3/16(0.75)^{½}$	$⅜(0.9375)^{½}$	$¾(0.6875)^{½}$	0	$(0.677734375)^{½}$

Therefore, the matrix D^{-1} is:

$$D^{-1} = \begin{bmatrix} 1.0 & & & & & \\ & 0.75 & & & & \\ & & 0.9375 & & & \\ & & & 0.6875 & & \\ & & & & 0.6796875 & \\ & & & & & 0.677734375 \end{bmatrix}^{-1}$$

$$D^{-1} = \begin{bmatrix} 1.0 & & & & & \\ & 1.3333 & & & & \\ & & 1.0667 & & & \\ & & & 1.4545 & & \\ & & & & 1.4713 & \\ & & & & & 1.4755 \end{bmatrix}$$

The matrix A^{-1}, using the sire-mgs rules, is:

$$
A^{-1} = \left[\begin{array}{c|c|c|}
1+\frac{1}{4}(1.3333)+\frac{1}{16}(1.0667) & -\frac{1}{2}(1.3333) & -\frac{1}{4}(1.0667) \\
 & 1.3333+\frac{1}{16}(1.4545) & \frac{1}{8}(1.4545) \\
 & & 1.0667+\frac{1}{4}(1.4545)+\frac{1}{16}(0.4713) \\
\text{Symmetric} & & \\
 & & \\
 & &
\end{array}\right.
$$

$$
\left.\begin{array}{c|c|c}
0 & 0 & 0 \\
-\frac{1}{4}(1.4545) & 0 & 0 \\
-\frac{1}{2}(1.4545)+\frac{1}{8}(1.4713) & -\frac{1}{4}(1.4713) & 0 \\
1.4545+\frac{1}{4}(1.4713)+\frac{9}{16}(1.4755) & -\frac{1}{2}(1.4713) & -\frac{3}{4}(1.4755) \\
 & 1.4713 & 0 \\
 & & 1.4755
\end{array}\right]
$$

$$
A^{-1} = \begin{bmatrix}
1.4000 & -0.6667 & -0.2667 & 0 & 0 & 0 \\
 & 1.4242 & 0.1818 & -0.3636 & 0 & 0 \\
 & & 1.5223 & -0.5434 & -0.3678 & 0 \\
\text{Symmetric} & & & 2.6523 & -0.7356 & -1.1066 \\
 & & & & 1.4713 & 0 \\
 & & & & & 1.4755
\end{bmatrix}.
$$

Recursive procedure to compute A for the sire-mgs approximation

The rules are based on approximating the additive relationship between two individuals by considering males only. Dams are assumed to be unrelated to sires and among themselves, **except** through their sires (the mgs' of calves). Thus,

(i) the additive relationship between two animals is approximately:

$$a_{ij} = \frac{1}{2}\left[a_{is_j} + a_{id_j}\right]$$

$$a_{ij} = \frac{1}{2}\left[a_{is_j} + \frac{1}{2}\left(a_{imgs_j} + a_{imgd_j}\right)\right]$$

$$\Rightarrow \quad a_{ij} \approx \frac{1}{2}a_{is_j} + \frac{1}{4}a_{imgs_j}$$

(ii) the coefficient of inbreeding of an animal is approximately:

$$F_i = \frac{1}{2}a_{s_i d_i}$$

$$F_i = \frac{1}{2}\left[\frac{1}{2}\left(a_{s_i\,mgs_i} + a_{s_i\,mgd_i}\right)\right]$$

$$\Rightarrow \quad F_i \approx \frac{1}{4}a_{s_i\,mgs_i}$$

Using the approximate formulae for a_{ij} and F_i, the following **recursive procedure to build a sire-mgs A** can be outlined:

[1] If s_j and mgs_j are known,

$$a_{ij} = \frac{1}{2}a_{is_j} + \frac{1}{4}a_{imgs_j}$$

$$a_{ii} = 1 + \frac{1}{4}a_{s_i\,mgs_i}$$

[2] If s_j is known only,

$$a_{ij} = \frac{1}{2} a_{is_j}$$

$$a_{ii} = 1$$

[3] If mgs_j is known only,

$$a_{ij} = \frac{1}{4} a_{imgs_j}$$

$$a_{ii} = 1$$

[4] If neither s_j nor mgs_j is known,

$$a_{ij} = 0$$

$$a_{ii} = 1$$

Example of a sire-mgs A matrix

The approximate additive genetic relationship matrix for the sire-mgs A^{-1} example is:

		1	1	3 2	4 3	4 4
	1	2	3	4	5	6
1	1.0	0.5	0.25	0.25	0.1875	0.1875
2	0.5	1.0	0.125	0.3125	0.1875	0.234375
3	0.25	0.125	1.0	0.53125	0.515625	0.3984375
4	0.25	0.3125	0.53125	1.03125	0.6488375	0.7734375
5	0.1875	0.1875	0.515625	0.6484375	1.1328125	0.486328125
6	0.1875	0.234375	0.3984375	0.7734375	0.486328125	1.2578125

Also, to check $A^{-1} = (I - \frac{1}{2}P_s' - \frac{1}{4}P_m')D^{-1}(I - \frac{1}{2}P_s - \frac{1}{4}P_m)$, matrix A could have been computed as:

$$A = (I - \tfrac{1}{2}P_s - \tfrac{1}{4}P_m)^{-1} D (I - \tfrac{1}{2}P_s' - \tfrac{1}{4}P_m')^{-1}$$

where

$$(I - \tfrac{1}{2}P_s - \tfrac{1}{4}P_m)^{-1} = \begin{bmatrix} 1 & & & & & \\ -\frac{1}{2} & 1 & & & & \\ -\frac{1}{4} & 0 & 1 & & & \\ 0 & -\frac{1}{4} & -\frac{1}{2} & 1 & & \\ 0 & 0 & -\frac{1}{4} & -\frac{1}{2} & 1 & \\ 0 & 0 & 0 & -\frac{3}{4} & 0 & 1 \end{bmatrix}$$

and

$$D = \begin{bmatrix} 1.0 & & & & & \\ & 0.75 & & & & \\ & & 0.9375 & & & \\ & & & 0.6875 & & \\ & & & & 0.6796875 & \\ & & & & & 0.677734375 \end{bmatrix}.$$

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