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Genetic evaluation methods for populations with dominance and inbreeding

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Summary. The effect of inbreeding on mean and genetic covariance matrix for a quantitative trait in a population with additive and dominance effects is shown. This genetic covariance matrix is a function of five relationship matrices and five genetic parameters describing the population. Elements of the relationship matrices are functions of Gillois' (1964) identity coefficients for the four genes at a locus in two individuals. The equivalence of the path coefficient method (Jacquard 1966) and the tabular method (Smith and Mäki-Tanila 1990) to compute the covariance matrix of additive and dominance effects in a population with inbreeding is shown. The tabular method is modified to compute relationship matrices rather than the covariance matrix, which is trait dependent. Finally, approximate and exact Best Linear Unbiased Predictions (BLUP) of additive and dominance effects are compared using simulated data with inbreeding but no directional selection. The trait simulated was affected by 64 unlinked biallelic loci with equal effect and complete dominance. Simulated average inbreeding levels ranged from zero in generation one to 0.35 in generation five. The approximate method only accounted for the effect of inbreeding on mean and additive genetic covariance matrix, whereas the exact accounted for all of the changes in mean and genetic covariance matrix due to inbreeding. Approximate BLUP, which is computable for large populations where exact BLUP is not feasible, yielded unbiased predictions of additive and dominance effects in each generation with only slightly reduced accuracies relative to exact BLUP.

Key words: Best linear unbiased prediction – Dominance – Inbreeding

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Introduction

Genetic variation may be composed of additive and non-additive variance. Non-additive genetic variation included dominance variance, resulting from interaction between genes at the same locus, and epistasis, resulting from interaction between genes at different loci. Genetic covariance between individuals in a random mating, non-inbred population for quantitative traits in a well-defined linear function of the genetic variance components (Cockerham 1954) assuming small contributions from many unlinked loci.

Inbreeding may reduce the mean phenotypic value of a population, a phenomenon referred to as inbreeding depression (Falconer 1989). Inbreeding also complicates the genetic covariance structure of a population. Genetic covariance between inbred relatives in a population with additive and dominance gene action but without epistasis can be modelled as a linear function of additive and dominance variance in an infinite random mating base population and additional genetic parameters. Extra parameters are: dominance variance and covariance between additive and dominance effects in a completely inbred population with allelic frequencies identical to those in the base population (Gillois 1964; Harris 1964; Jacquard 1974) and, in certain settings, the sum over loci of squared effects of complete inbreeding depression (Gillois 1964; Harris 1964; Jacquard 1974; Cockerham and Weir 1984). Genetic covariance between inbred relatives is the sum of the genetic parameters each multiplied by a different coefficient of relationship. Coefficients of relationship are functions of probabilities that any of the four genes at the same or two different loci in two individuals are identical by descent. Two basic methods are used to compute additive relationships, a path coefficient method (Wright 1921) and a tabular method (Emik and

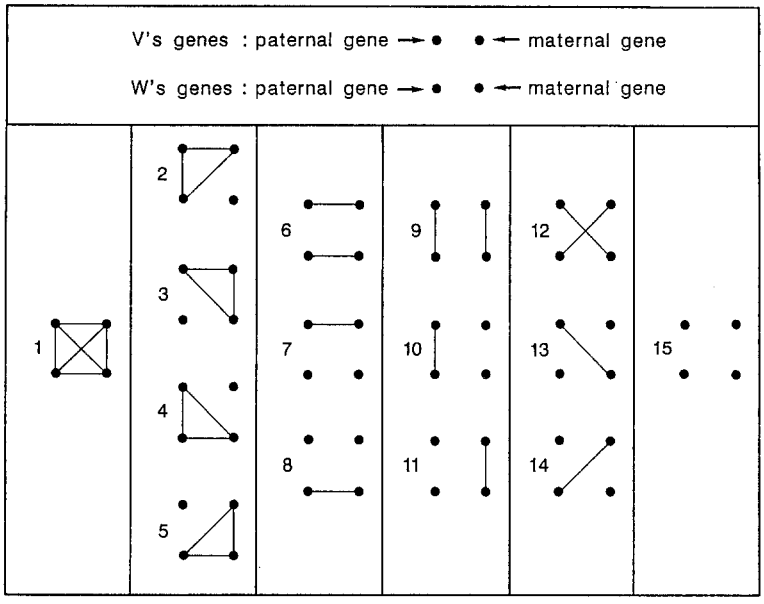

Fig. 1. Fiften possible identity modes between the paternal and the maternal gene of individual V and the paternal and the maternal gene of individual W at a particular locus. Genes identical by descent are connected by a *line* (reproduced from Jacquard 1974, p 105)

Terrill 1949). More generally, the genetic covariance matrix of a population with additive and dominance variation but without epistasis can be computed from path coefficients (Jacquard 1966) or from a tabular method (Smith and Mäki-Tanila 1990).

In this paper, genotypic variance as a special case of genotypic covariance in a population with additive and dominance gene action and inbreeding is rederived first, with additive and dominance effects defined in an infinite, random mating base population. Different settings lead to slightly different formulae for genotypic variance, which are reviewed and related.

Subsequently, formulae for genetic covariance are used to model phenotypic performance of a population for a quantitative trait via a mixed model including effect of inbreed depression and a covariance matrix among individual additive and dominance effects. The equivalence of the path coefficient (Jacquard 1966) and tabular method (Smith and Mäki-Tanila 1990) to compute the covariance matrix is shown and used to derive a modified tabular method. The latter computes relationship matrices, which must be formed only once for a given population. The covariance matrix among additive and dominance effects depends on the values of the genetic parameters, and hence would have to be recomputed for each trait in a given population by the method of Smith and Mäki-Tanila (1990).

Finally, approximate and exact Best Linear Unbiased Prediction (BLUP) of additive and dominance effects are compared using data simulated with the individual locus model of De Boer and Van Arendonk (1992). Approximate BLUP only accounts for effects of inbreeding on mean and additive genetic covariance, while exact BLUP accounts for all changes in mean and genetic covariance matrix with inbreeding. Approximate BLUP can be implemented for livestock populations of a moderate to large size, where exact BLUP is not feasible.

Theory

Genetic variance

Genotypic covariances among individuals in which additive and dominance variation and inbreeding were taken into account have been derived by several authors. If the situations considered are limited to those where a trait was affected by several to many loci and additive and dominance effects were defined in an infinite, random mating base population, four different settings can be found. The assumptions appear to be (i) many finite subpopulations derived in an identical fashion from an infinite base population (Gillois 1964; Chevalet and Gillois 1977); (ii) a large population derived from an infinite random mating base by some system of inbreeding with no selection, unlinked loci, and all individuals having identical inbreeding coefficients (Harris 1964); (iii) as setting (ii) but with variation among individuals in inbreeding coefficients (Cockerham and Weir 1984); and (iv) one particular finite population (Chevalet 1971). In setting (i), genotypic variance represents total genetic variance across lines (Falconer 1989; Chevalet and Gillois 1977). For (ii) or (iii), genotypic variance may represent total genetic variance among unrelated individuals with common or average inbreeding level F.

Common to all four settings is the derivation of genotypic covariance based on identity coefficients. Identity coefficients refer to the possible identity modes pertaining

to the four genes at the same locus in two individuals (Fig. 1) or at two different loci (Cockerham and Weir 1984). An identity coefficient represents the probability of a particular identity mode. The four settings differ in the definition of identity coefficients and in the types of identity modes that need to be considered.

Following Chevalet (1971), let S_k^l represent an indicator variable for identity mode k (k = 1, ..., 15) pertaining to the four genes at locus l in two individuals and let δ_k represent the probability of this identity mode. Then, δ_k equals the frequency of identity mode k in the limit, or

$$\delta_k = \lim_{n\to\infty} \left\{ \frac{1}{n} [S_k^l(u_1) + S_k^l(u_2) + \ldots + S_k^l(u_n)] \right\} \quad (1)$$

where $S_k^l(u_i)$ equals 1 if identity mode k is realized at locus l and 0 otherwise, and u_i represents a pair of individuals (covariance) or one individual (variance). In setting (i), u_i is a (pair of) individual(s) in subpopulation i. In settings (ii) and (iii), u_i may represent n independent pairs or n unrelated individuals in a large population. In setting (iv), δ_k is defined differently as

$$\delta_k = \lim_{n\to\infty} \left\{ \frac{1}{n} [S_k^1(u) + S_k^2(u) + \ldots + S_k^n(u)] \right\} \quad (2)$$

where u represents a pair of individuals in one particular finite population and δ_k is the limit taken over n independent loci. Setting (iv) requires the assumption of a large number of loci and a small ratio of largest to smallest contribution relative to number of loci (Chevalet 1971). The other settings are general with respect to number of loci and size of their contributions.

For genotypic variance, u represents an individual, and identity modes other than 1, 9 and 12 cannot be realized (Fig. 1). Hence, only S_1^l, S_9^l and S_{12}^l are random variables, which are redefined as $F^l(u) = S_1^l(u)$ and $1 - F^l(u) = S_9^l(u) + S_{12}^l(u)$. If alleles at locus l in individual u are identical by descent (i.b.d.), $F^l(u)$ equals 1, unless $F^l(u)$ is zero.

The common starting point in all four settings is to define the genotypic value at locus l in an infinite, random mating base (b) population at the sum of breeding value and dominance deviation, or

$$G_b^l = BV_b^l + D_b^l. \quad (3)$$

The expectation of G_b^l with respect to the distribution of alleles for a given individual u is

$$E^{p_l|u}(G_b^l) = F^l(u)\, E_{ibd}^{p_l}(G_b^l) + [1 - F^l(u)]\, E_{not\,ibd}^{p_l}(G_b^l) \quad (4)$$

where E_{ibd}^p denotes the expectation conditional on the alleles being i.b.d. and p_l is the allelic frequency at locus l. Knowing that in the absence of inbreeding ($E_{not\,ibd}^p$) the expectation of dominance effects is zero, whereas the expectation of additive effects is zero with (E_{ibd}^p) and without inbreeding ($E_{not\,ibd}^p$) (Jacquard 1966), Eq. 4, reduces, e.g. for a biallelic locus, to

$$E^{p_l|u}(G_b^l) = F^l(u)\,[p_l D_{11}^l + q_l D_{22}^l] = F^l(u)\, \Delta_i^l \quad (5)$$

where D_{ij}^l is the dominance deviation of genotype ij at locus l in the base, $q_l = 1 - p_l$, and $\Delta_i^l = 2 p_l q_l d_l$ is the complete inbreeding depression at locus l. Variance of G_b^l with respect to the distribution of alleles for a given individual u is

$$Var^{p_l|u}(G_b^l) = E^{p_l|u}[(G_b^l)^2] - [E^{p_l|u}(G_b^l)]^2. \quad (6)$$

Using

$$E^{p_l|u}[(G_b^l)^2] = F^l(u)\, E_{ibd}^{p_l}[(G_b^l)^2] + [1 - F^l(u)]\, E_{not\,ibd}^{p_l}[(G_b^l)^2]$$

with, for a biallelic locus,

$$E_{ibd}^{p_l}[(G_b^l)^2] = p_l (BV_{11}^l + D_{11}^l)^2 + q_l (BV_{22}^l + D_{22}^l)^2$$

and

$$E_{not\,ibd}^{p_l}[(G_b^l)^2] = p_l^2 (BV_{11}^l + D_{11}^l)^2 + 2 p_l q_l (BV_{12}^l + D_{12}^l)^2 + q_l^2 (BV_{22}^l + D_{22}^l)^2$$

in Eq. 6 yields

$$Var^{p_l|u}(G_b^l) = [1 + F^l(u)]\, \sigma_{ar(l)}^2 + [1 - F^l(u)]\, \sigma_{dr(l)}^2 + F^l(u)\, \sigma_{di(l)}^2 + 2 F^l(u)\, \sigma_{adi(l)} \quad (7)$$

where, omitting subscript l,

$$\sigma_{ar}^2 = p^2 BV_{11}^2 + 2 p q BV_{12}^2 + q^2 BV_{22}^2 = 2 p q [a + d(q - p)]^2 = 2 p q \alpha^2 \quad (8)$$

$$\sigma_{dr}^2 = p^2 D_{11}^2 + 2 p q D_{12}^2 + q^2 D_{22}^2 = (2 p q d)^2 \quad (9)$$

$$\sigma_{di}^2 = p^2 D_{11}^2 + q^2 D_{22}^2 - (p D_{11} + q D_{22})^2 = 4 p q (p^3 + q^3) d^2 - (2 p q d)^2 \quad (10)$$

$$\sigma_{adi} = p\, BV_{11}\, D_{11} + q\, BV_{22}\, D_{22} = 4 p q (p - q)\, \alpha d \quad (11)$$

where $\alpha = a + d(q - p)$, and a and d are genotypic values of the favourable homozygote and the heterozygote, respectively (Falconer 1989). Variances σ_{ar}^2 and σ_{dr}^2 are additive and dominance variances at locus l in the base, and σ_{di}^2 and σ_{adi} are dominance variance and covariance between additive and dominance effects among homozygotes or in a completely inbred population with the same allelic frequency as the base. Values of inbreeding depression, Δ_i, and of the (co)variances defined in Eqs. 8–11 are given in Fig. 2 for varying allelic frequency. Figure 2 shows that the relative importance of the (co)variance components changes strongly with allelic frequency.

In settings (i), (ii) and (iii), expectations are taken jointly with respect to the distribution of allelic frequencies and u, with u representing independent subpopulations or unrelated individuals. Using

$$E^{p_l,u}(.) = E^u[E^{p_l|u}(.)]$$

the joint expectation of G_b^l for biallelic locus is

$$E^{p_l,u}(G_b^l) = E^u[F^l(u)]\,(p_l D_{11}^l + q_l D_{22}^l) = F\,\Delta_i^l \qquad (12)$$

where $F = \delta_1$ is the inbreeding coefficient. Similarly, the variance of G_b^l is

$$\begin{aligned}
\mathrm{Var}^{p_l,u}(G_b^l) &= E^u[F^l(u)]\,E_{ibd}^{p_l}[(G_b^l)^2] \\
&\quad + E^u[1-F^l(u)]\,E_{not\,ibd}^{p_l}[(G_b^l)^2] - F^2(\Delta_i^l)^2 \\
&= F\,E_{ibd}^{p_l}[(G_b^l)^2] \\
&\quad + (1-F)\,E_{not\,ibd}^{p_l}[(G_b^l)^2] - F^2(\Delta_i^l)^2 \\
&= (1+F)\,\sigma^2_{ar(l)} + (1-F)\,\sigma^2_{dr(l)} + F\,\sigma^2_{di(l)} \\
&\quad + F(1-F)(\Delta_i^l)^2 + 2F\,\sigma_{adi(l)}. \qquad (13)
\end{aligned}$$

If several biallelic loci contribute to the genotypic value for a trait, $G_b = \Sigma_l G_b^l$ is the total genotypic value with mean

$$E^{p_l,u}(G_b) = F\sum_{l=1}^{L}\Delta_i^l = F\,\Delta_I \qquad (14)$$

where L is number of loci, and variance

$$\begin{aligned}
\mathrm{Var}^{p_l,u}(G_b) &= E^{p_l,u}\left[\left(\sum_{l=1}^{L} G_b^l\right)^2\right] - F^2(\Delta_I)^2 \\
&= \sum_{l=1}^{L} E^{p_l,u}[(G_b^l)^2] \\
&\quad + \sum_{l\neq}^{L}\sum_{l'}^{L} E^{p_l,u}(G_b^l G_b^{l'}) - F^2(\Delta_I)^2 \\
&= (1+F)\sum_{l=1}^{L}\sigma^2_{ar(l)} + (1-F)\sum_{l=1}^{L}\sigma^2_{dr(l)} \\
&\quad + 2F\sum_{l=1}^{L}\sigma_{adi(l)} \\
&\quad + F\left[\sum_{l=1}^{L}\{p_l(D_{11}^l)^2 + q_l(D_{22}^l)^2\}\right] \\
&\quad + \sum_{l\neq}^{L}\sum_{l'}^{L} E^{p_l,u}(G_b^l G_b^{l'}) - F^2(\Delta_I)^2 \\
&= (1+F)\,\sigma^2_{AR} + (1-F)\,\sigma^2_{DR} + 2F\,\sigma_{ADI} + F\,\sigma^2_{DI} \\
&\quad + F\Delta_I^2 - F^2(\Delta_I)^2 + \sum_{l\neq}^{L}\sum_{l'}^{L} E^{p_l,u}(G_b^l G_b^{l'}) \qquad (15)
\end{aligned}$$

where

$$\Delta_I^2 = \sum_{l=1}^{L}(\Delta_i^l)^2 \quad \text{and} \quad (\Delta_I)^2 = \left(\sum_{l=1}^{L}\Delta_i^l\right)^2 \qquad (16)$$

and

$$\begin{aligned}
\sum_{l\neq}^{L}\sum_{l'}^{L} E^{p_l,u}(G_b^l G_b^{l'}) &= \sum_{l\neq}^{L}\sum_{l'}^{L} E^u[F^l(u)\,F^{l'}(u)]\,E^{p_l p_{l'}}(G_b^l G_b^{l'}) \\
&= \sum_{l\neq}^{L}\sum_{l'}^{L} E^u[F^l(u)\,F^{l'}(u)] \\
&\quad \cdot (p_l G_{11}^l + q_l G_{22}^l)\,(p_{l'} G_{11}^{l'} + q_{l'} G_{22}^{l'}) \\
&= F^- \sum_{l\neq}^{L}\sum_{l'}^{L}\Delta_i^l\Delta_i^{l'} = F^-[(\Delta_i)^2 - \Delta_i^2] \qquad (17)
\end{aligned}$$

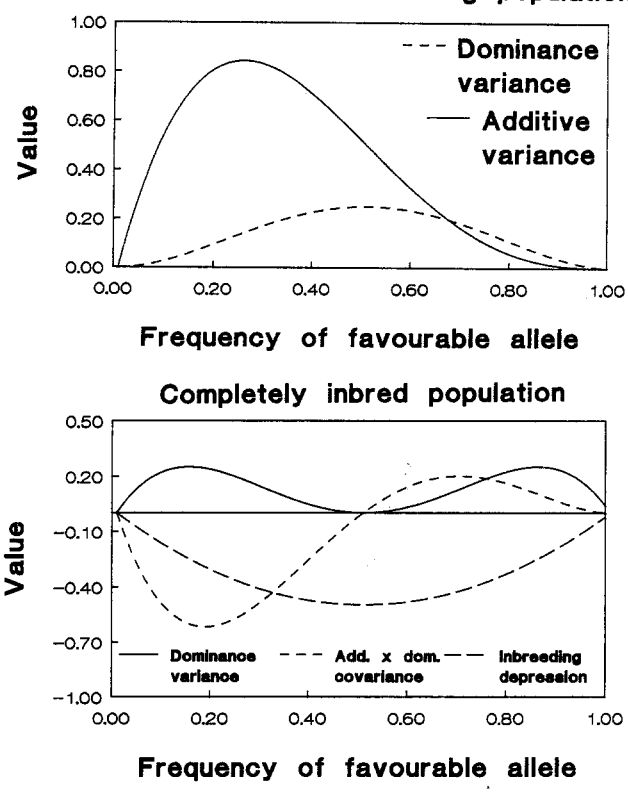

Fig. 2. Magnitude of the components of genetic variance at a biallelic locus with complete dominance (a = d = 1) as a function of allelic frequency

with

$$F^- = E^u[F^l(u)\,F^{l'}(u)]. \qquad (18)$$

Hence, using Eq. 17 in Eq. 15

$$\begin{aligned}
\mathrm{Var}^{p_l,u}(G_b) &= (1+F)\,\sigma^2_{AR} + (1-F)\,\sigma^2_{DR} + F\,\sigma^2_{DI} + 2F\,\sigma_{ADI} \\
&\quad + F(1-F)\,\Delta_I^2 + (F^- - F^2)\,[(\Delta_I)^2 - \Delta_I^2]. \qquad (19)
\end{aligned}$$

From Eq. 18, $F^- - F^2$ is the covariance among $F^l(u)$ and $F^{l'}(u)$. Let $F^l(u)$ be composed of its expected value and a residual or $F^l(u) = F + R^l(u)$. Hence, $F^- - F^2 = \mathrm{Cov}(F^l(u), F^{l'}(u))$ may be partitioned as $\sigma_F^2 + \mathrm{Cov}(R^l(u), R^{l'}(u))$. For unlinked loci the last term is equal to zero, and $F^- - F^2 = \sigma_F^2$, with σ_F^2 representing variation among individuals in inbreeding coefficient. If σ_F^2 is zero and loci are unlinked, $F^- = F^2$; hence the last term in the right-hand side of Eq. 19 is zero.

Equation 19 is general and holds for any number of alleles per locus (Cockerham and Weir 1984). Equation 19 is obtained in setting (iii), while for settings (i) and (ii) $\sigma_F^2 = 0$, and hence genotypic variance equals Eq. 19 but without its last term. For setting (iv), the genotypic mean is

$$E(G_b) = \sum_{l=1}^{L} E^{p_l|u}[F^l(u)]\,E_{ibd}^{p_l}(G_b^l) \simeq F\,\Delta_I$$

Table 1. Equivalence between the parameterizations of genetic covariance used in this paper and those in Harris (1964, p 1329), Jacquard (1974, p 135) and Cockerham and Weir (1984, p 160)

	Present paper	Harris (1964)[a]	Jacquard (1974)	Cockerham and Weir (1984)
Covariances	σ^2_{AR}	σ^2_{AR}	V_A	σ^2_A
	σ^2_{DR}	σ^2_{DR}	V_D	σ^2_D
	σ^2_{DI}	σ^2_{DI}	$V_H - D^2_H$	D^*_2
	σ_{ADI}	σ_{ADI}	$2\,\mathrm{Cov}_H(A, D)$	$2D_1$
	Δ^2_I	D^2_I	D^2_H	H^*
	$(\Delta_I)^2 - \Delta^2_I$	—	—	$H^2 - H^*$
Relationship coefficients	a_{vw}	$2r_{vw}$	$2\Phi_{vw}$	$2\theta_{vw}$
	dr_{vw}	u_{vw}	Δ_I	$2(\Delta_{v+w} - \delta_{\bar{v}\bar{w}})$
	di_{vw}	t_{vw}	Φ_4	$\delta_{\bar{v}\bar{w}}$
	$c_{vw} + c_{wv}$	$s_{vw} + s_{wv}$	$\Phi_3 + \Phi_4$	$2(\gamma_{\bar{v}w} + \gamma_{v\bar{w}})$
	u_{vw}	$t_{vw} + v_{vw} - F_v F_w$	$\Delta_2 - F_v F_w + \Phi_4$	$\Delta_{v+w} - F_v F_w$
	t_{vw}	—	—	$\Delta_{vw} - F_v F_w$

[a] Formula (26) on page 1329 from Harris (1964) is based on a one-locus model

with a proof of this approximation given by Chevalet (1971). Similarly, genotypic variance is approximated as

$$\mathrm{Var}(G_b) = \sum_{l=1}^{L} \mathrm{Var}^{p_l \mid u}(G^l_b)$$
$$\simeq (1+F)\,\sigma^2_{AR} + (1-F)\,\sigma^2_{DR} + F\,\sigma^2_{DI} + 2F\,\sigma_{ADI},$$

which is Eq. 19 with the last two terms omitted.

Genetic covariance between relatives

Equation 19 represents the special case of the genetic covariance of an individual with itself. A general formula for the genetic covariance between individuals V and W with arbitrary inbreeding coefficients is (Cockerham and Weir 1984)

$$\sigma_{G_v G_w} = a_{vw}\,\sigma^2_{AR} + dr_{vw}\,\sigma^2_{DR} + di_{vw}\,\sigma^2_{DI} + c_{wv}\,\sigma_{ADI} + u_{vw}\,\Delta^2_I + t_{vw}[(\Delta_I)^2 - \Delta^2_I] \quad (20)$$

where

- a_{vw} is the additive genetic relationship between individuals V and W;
- dr_{vw} is the relationship between individuals V and W due to dominance variance in the base population;
- di_{vw} is the relationship between individuals V and W due to dominance variance in the completely inbred population;
- c_{vw} is the relationship between the additive effect of individual V and the dominance effect of individual W;
- c_{wv} is the relationship between the additive effect of individual W and the dominance effect of individual V;
- u_{vw} is the relationship between individuals V and W due to the sum of squared inbreeding depressions; and
- t_{vw} is the relationship between individual V and W due to component $(\Delta_I)^2 - \Delta^2_I$.

Genotypic covariance derived in settings (i) and (ii) (Gillois 1964; Harris 1964; Jacquard 1974) does not include the last term of Eq. 20. Table 1 shows the equivalence of Eq. 20 and the equations given by Harris (1964, p 1329), Jacquard (1974, p 135) and Cockerham and Weir (1984, p 160). Genotypic covariance in setting (iv) is equal to Eq. 20 with the last two terms omitted (Chevalet 1971; Chevalet and Gillois 1977).

The additive genetic relationships between individuals V and W, a_{vw}, equals twice the probability that a gene taken at random from V is i.b.d. to a gene taken at random from W. This occurs one-quarter of the time for identity modes 10, 11, 13 and 14 in Fig. 1, one-half of the time for identity modes 2, 3, 4, 5, 9 and 12, and always for identity mode 1, or

$$a_{vw} = 2[\delta_1 + \tfrac{1}{2}(\delta_2 + \delta_3 + \delta_4 + \delta_5 + \delta_9 + \delta_{12}) + \tfrac{1}{4}(\delta_{10} + \delta_{11} + \delta_{13} + \delta_{14})]. \quad (21)$$

Dominance relationship dr_{vw} equals the probability that each gene in V is i.b.d. to a different gene in W and genes in the same individual are not i.b.d., an event represented by identity modes 9 and 12, or

$$dr_{vw} = \delta_9 + \delta_{12}. \quad (22)$$

Dominance relationship di_{vw} is the probability that all four genes in V and W are i.b.d., or

$$di_{vw} = \delta_1. \quad (23)$$

Relationship c_{vw} equals the probability that a gene taken at random from V is i.b.d. to both genes in W, involving identity modes 1, 4 and 5, or

$$c_{vw} = \delta_1 + \tfrac{1}{2}(\delta_4 + \delta_5). \quad (24)$$

Similarly,

$$c_{wv} = \delta_1 + \tfrac{1}{2}(\delta_2 + \delta_3). \quad (25)$$

From results in Jacquard (1974, p 135) and Table 1,

$$u_{vw} = (\delta_1 + \delta_6 - F_v F_w) \tag{26}$$

where F_v and F_w are the inbreeding coefficients of individuals V and W, respectively, which can also be expressed in terms of the identity coefficients (Jacquard 1974, p 109) or

$$F_v = \delta_1 + \delta_2 + \delta_3 + \delta_6 + \delta_7 \quad \text{and}$$

$$F_w = \delta_1 + \delta_4 + \delta_5 + \delta_6 + \delta_8.$$

Relationship coefficient t_{vw} was defined by Cockerham and Weir (1984) (see Table 1) and depends on identity coefficients involving genes at two different loci.

Equation 20 reduces to Eq. 19 when considering covariance of an individual with itself. In this case the only non-zero identity coefficients are $\delta_1 = F_v$ and $(\delta_9 + \delta_{12}) = 1 - F_v$.

Genetic covariance matrix for a quantitative trait

A linear model for phenotypic measurements of individuals for a quantitative trait with additive and dominance variance includes additive and dominance genetic values, with dominance values partitioned into the effect of inbreeding depression plus dominance effects, and systematic environmental effects, or

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{Z}(\mathbf{f}\Delta_I + \mathbf{d}) + \mathbf{e} \tag{27}$$

where $\boldsymbol{\beta}$ is a vector of fixed environmental effects, $\mathbf{a}$ is a vector of random additive effects, $\mathbf{d}$ is a vector of random dominance effects, $\mathbf{X}$ and $\mathbf{Z}$ are known incidence matrices, $\mathbf{f}$ is a known vector of inbreeding coefficients F, Δ_I is the fixed effect of the complete inbreeding depression and $\mathbf{e}$ is a vector of random residuals.

Mean and covariance matrix of $\mathbf{y}$ are $E(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{f}\Delta_I$ and $\mathrm{Var}(\mathbf{y}) = [\mathbf{Z}, \mathbf{Z}]\,\mathbf{G}\,[\mathbf{Z}, \mathbf{Z}]' + \mathbf{I}\sigma_e^2$ with error variance σ_e^2, respectively, and $\mathbf{G}$ is the covariance matrix of $[\mathbf{a}', \mathbf{d}']'$, or

$$\mathrm{Var}\begin{bmatrix}\mathbf{a}\\ \mathbf{d}\end{bmatrix} = \mathbf{G} = \begin{bmatrix}\mathbf{A}\,\sigma_{AR}^2 & \mathbf{C}\,\sigma_{ADI}\\ \mathbf{C}'\,\sigma_{ADI} & (\mathbf{D}_R\,\sigma_{DR}^2 + \mathbf{D}_I\,\sigma_{DI}^2 + \mathbf{U}\Delta_I^2)\end{bmatrix} \tag{28}$$

where $\mathbf{A}$ is a matrix of additive genetic relationships (a_{vw}), $\mathbf{C}$ is a matrix of relationships between additive and dominance effects (c_{vw} and c_{wv}), $\mathbf{D}_R$ is a matrix of relationship due to the dominance variance in the base population (dr_{vw}), $\mathbf{D}_I$ is a matrix of relationships due to dominance variance in the completely inbred population (di_{vw}), and $\mathbf{U}$ is a matrix of relationships due to the sum of squared inbreeding depressions (u_{vw}).

Covariance matrix (28) does not include the last term in the right-hand side of Eqs. 19 or 20 because variance among individuals in their inbreeding coefficients, and hence in inbreeding depression, is eliminated by partitioning dominance effects into $\mathbf{f}\Delta_I$ and $\mathbf{d}$ in Eq. 27. Treating $\mathbf{f}$ as a random variable rather than a known constant, $\mathrm{Var}(\mathbf{f}\Delta_I) = \sigma_F^2(\Delta_I)^2$. If number of loci, L, tends to infinity and Δ_i is constant across loci, $(\Delta_I)^2 = L^2\Delta_i^2$ and $(\Delta_I)^2 - \Delta_I^2 = L(L-1)\Delta_i^2 \simeq L^2\Delta_i^2$. Hence, $(\Delta_I)^2 \simeq (\Delta_I)^2 - \Delta_I^2$. The term $\mathbf{U}\Delta_I^2$ should be dropped if Eq. 28 represents the covariance matrix of genetic effects of individuals in a finite population.

Matrix $\mathbf{G}$ can be computed with a path coefficient method (Jacquard 1966) and a tabular method (Smith and Mäki-Tanila 1990). Both methods will be described briefly and their equivalence will be shown.

Path coefficient method

The path coefficient method of Jacquard (1966) determines the genetic covariance between two individuals V and W computing probabilities of all of the identity modes in Fig. 1. The following steps are required: (1) find all common ancestors of V and W; (2) determine all possible paths of origin of their four genes at a locus; (3) determine the probability of each path; (4) for each path, determine the various identity modes and their probabilities; (5) sum the probabilities by identity mode across paths.

The path coefficient method is useful for single and simple pedigrees, but is not suitable for computing the genetic covariance matrix of a large population.

Tabular method

The tabular method of Smith (1984) and Smith and Mäki-Tanila (1990) determines the exact genetic covariance structure in a population using an extended genomic table following Harris (1964) and Gillois (1964), or for settings (i) and (ii). The extended genomic table, denoted by $\mathbf{E}$, contains the first moments or expected values of additive effects of gametes and dominance effects of gamete pairs in its first row and column, except for the first element equal to one, and second moments of all effects in its remaining rows and columns. Elements of $\mathbf{E}$ are computed using recursive rules of Smith and Mäki-Tanila (1990, pp 21–72). An initial list of gametes and gamete pairs includes all gametes and gamete pairs represented in individuals of a population. Smith and Mäki-Tanila (1990) give an algorithm to form the list of gametes and gamete pairs, which adds ancestral gamete pairs and produces an ordering required to compute $\mathbf{E}$ recursively.

After absorption of the first row and column, $\mathbf{E}$ represents a matrix of covariances, which may be partitioned into a submatrix of covariances among additive effects of gametes, a submatrix of covariances among additive effects of gametes and dominance effects of gamete pairs, its transpose, and a submatrix of covariances among dominance effects of gamete pairs.

Equivalence between path coefficient and tabular methods

Equivalence between the path coefficient (Jacquard 1966) and tabular method (Smith 1984; Smith and Mäki-

Tanila 1990) will be shown for each submatrix of **E** separately.

Covariance between additive effects

The additive genetic relationship between individual V with paternal and maternal gametes i and j and individual W with paternal and maternal gametes k and m is computed from **E** as (Smith 1984):

$$a_{vw} = [E(a_i, a_k) + E(a_i, a_m) + E(a_j, a_k) + E(a_j, a_m)]/\sigma^2_{AR} \quad (29)$$

where $E(a_i, a_k)$ is the element in **E** corresponding to row a_i and column a_k, which is the second moment or covariance between additive effects of gamete $i(a_i)$ and $k(a_k)$. Second moments equal covariances because the expected value of a gamete's additive effect is zero. The additive genetic covariance between gametes i and k is equal to the probability that a gene in gamete i is i.b.d. to another gene at the same locus in gamete k, denoted by $P(i \equiv k)$, times the additive variance among gametes or $\frac{1}{2}\sigma^2_{AR}$ (Smith and Allaire 1985), Hence,

$$a_{vw} = \tfrac{1}{2}[P(i \equiv k) + P(i \equiv m) + P(j \equiv k) + P(j \equiv m)]. \quad (30)$$

Each probability in Eq. 30 may be computed by adding all of the probabilities of identity modes (Fig. 1) containing the particular identity, e.g. for $i \equiv k$

$$\begin{aligned} P(i \equiv k) = {} & P(i \equiv j \equiv k \equiv m) + P(i \equiv j \equiv k \not\equiv m) \\ & + P(i \equiv k \equiv m \not\equiv j) + P(i \equiv k \not\equiv j \equiv m) \\ & + P(i \equiv k \not\equiv j \not\equiv m) = \delta_1 + \delta_2 + \delta_4 + \delta_9 + \delta_{10}. \end{aligned} \quad (31)$$

The use of Eq. 31 and similar identities in Eq. 30 yields the additive relationships in terms of identity coefficients given in Eq. 21.

Furthermore, the probabilities of gene identities in Eq. 30 can be computed recursively using the following rules. Let $i \geq k$, if i is a descendant of k. Base gametes do not have any known parental gametes. If i and k are base gametes,

$$P(i \equiv k) = 1 \quad \text{if } i = k, \quad \text{else } P(i \equiv k) = 0. \quad (32)$$

If i is not a base gamete, and x and y are the parental gametes of i, then for $i \neq k$

$$\begin{aligned} P(i \equiv k) &= P(x \equiv k) \cdot P(i = x) + P(y \equiv k) \cdot P(i = y) \\ &= \tfrac{1}{2}[P(x \equiv k) + P(y \equiv k)] \end{aligned} \quad (33)$$

where, e.g. $P(i = x)$ is the probability that gene in gamete i is a copy of gene at the same locus in parental gamete x. For $i = k$,

$$P(i \equiv k) = P(i \equiv i) = \tfrac{1}{2}[P(x \equiv x) + P(y \equiv y)] = 1. \quad (34)$$

Equations 32–34 are analogous to recurrencies for covariances or second moments among additive effects of gametes presented by Smith and Mäki-Tanila (1990, p 71).

Covariance between additive and dominance effects

The relationships coefficient between the additive effect of individual V with gametes i and j, and the dominance effect of individual W with gametes k and m, c_{vw}, is computed from **E** as:

$$c_{vw} = [E(a_i, d_{km}) + E(a_j, d_{km})]/\sigma_{ADI} \quad (35)$$

where $E(a_i, d_{km})$ is the second moment of covariance between the additive effect of gamete $i(a_i)$ and the dominance effect of gamete pair km (d_{km}). Similar to the covariance among additive effects of gametes, $Cov(a_i, d_{km})$ equals the probability that a gene at a particular locus in gamete i is i.b.d. to both genes at the same locus in gamete pair km, denoted by $P(i \equiv k \equiv m)$, times $\frac{1}{2}\sigma_{ADI}$. Then, the relationship coefficient between the additive effect of individual V and the dominance effect of individual W can be written as:

$$c_{vw} = \tfrac{1}{2}[P(i \equiv k \equiv m) + P(j \equiv k \equiv m)]. \quad (36)$$

Both probabilities in Eq. 36 can be written in terms of identity coefficients (Fig. 1), e.g.

$$\begin{aligned} P(i \equiv k \equiv m) = {} & P(i \equiv j \equiv k \equiv m) \\ & + P(i \equiv k \equiv m \not\equiv j) = \delta_1 + \delta_4 \end{aligned} \quad (37)$$

yielding the additive-dominance relationship coefficient in Eq. 24.

The probabilities of gene identities in Eq. 36 can again be computed recursively. Let $i \geq k \geq m$. If i is a base gamete, implying that k and m are also base gametes, then

$$P(i \equiv k \equiv m) = 1 \quad \text{if } i = k = m, \quad \text{else } P(i \equiv k \equiv m) = 0. \quad (38)$$

If i has known parental gametes x and y, then for $i \neq k \neq m$

$$\begin{aligned} P(i \equiv k \equiv m) = {} & P(x \equiv k \equiv m) \cdot P(i = x) + P(y \equiv k \equiv m) \\ & \cdot P(i = y) = \tfrac{1}{2}[P(x \equiv k \equiv m) + P(y \equiv k \equiv m] \end{aligned}$$

and for $i = k$, (39)

$$P(i \equiv k \equiv m) = P(i \equiv m) = \tfrac{1}{2}[P(x \equiv m) + P(y \equiv m)]. \quad (40)$$

Recurrence (39) was given in Harris (1964, p 1322), and recurrencies (38–40) are given by Smith and Mäki-Tanila (1990, p 71) for second moments rather than identity probabilities.

Covariance between dominance effects

The covariance between dominance effects of individuals $V(d_{ij})$ and $W(d_{km})$ is the element of **E** pertaining to gamete pairs ij and km, which is by definition

$$Cov(d_{ij}, d_{km}) = \sum_{l=1}^{L} [E(d^l_{ij}\, d^l_{km}) - E(d^l_{ij})\, E(d^l_{km})] \quad (41)$$

where d^l_{ij} is the dominance effect of gamete pair ij at locus l with $d_{ij} = \Sigma\, d^l_{ij}$, L is number of loci, $E(d^l_{ij})$ is the first

moment or expected value of d_{ij}^l, and $E(d_{ij}^l\, d_{km}^l)$ is the second moment among the dominance effects of gamete pairs ij and km at locus l.

The first moment of d_{ij}^l is equal to the probability that the genes in gamete par ij at locus l are i.b.d. times the inbreeding depression at locus l, or $E(d_{ij}^l) = P(i \equiv j)\, \Delta_I^l$. Then the part of Eq. 41 pertaining to first moments becomes

$$\sum_{l=1}^{L} E(d_{ij}^l)\, E(d_{km}^l) = P(i \equiv j)\, P(k \equiv m) \sum_{l=1}^{L} (\Delta_I^l)^2$$

$$= P(i \equiv j)\, P(k \equiv m)\, \Delta_I^2. \qquad (42)$$

Probabilities in Eq. 42 can be obtained from identity coefficients, e.g.

$$P(i \equiv j) = P(i \equiv j \equiv k \equiv m) + P(i \equiv j \equiv k \not\equiv m) + P(i \equiv j \equiv m \not\equiv k) + P(i \equiv j \not\equiv k \equiv m) + P(i \equiv j \not\equiv k \not\equiv m) = \delta_1 + \delta_2 + \delta_3 + \delta_6 + \delta_7 = F_v. \qquad (43)$$

Similarly, $P(k \equiv m) = F_w$; hence Eq. 42 can be rewritten as

$$\sum_{l=1}^{L} E(d_{ij}^l)\, E(d_{km}^l) = F_v\, F_w\, \Delta_I^2. \qquad (44)$$

Each second moment in Eq. 41 is a weighted sum of the dominance variance in the noninbred base population, the dominance variance in the completely inbred population and the sum of squared inbreeding depressions, or

$$E(d_{ij}^l\, d_{km}^l) = [P(i \equiv k \not\equiv j \equiv m) + P(i \equiv m \not\equiv j \equiv k)]\, \sigma^2_{dr(l)} + P(i \equiv j \equiv k \equiv m)\, \{\sigma^2_{di(l)} + (\Delta_I^l)^2\} + P(i \equiv j \not\equiv k \equiv m)\, (\Delta_I^l)^2 \qquad (45)$$

where $\sigma^2_{dr(l)}$, $\sigma^2_{di(l)} + (\Delta_I^l)^2$, and $(\Delta_I^l)^2$ are second moments conditional on the four identity cases above. Second moments for all other identity cases (Fig. 1) are zero due to relationships (Harris 1964)

$$\sum_{i=1}^{s} p_i\, d_{ij} = \sum_{j=1}^{s} p_j\, d_{ij} = 0$$

where s is the number of alleles per locus. Summation over loci yields

$$\sum_{l=1}^{L} E(d_{ij}^l\, d_{km}^l) = [P(i \equiv k \not\equiv j \equiv m) + P(i \equiv m \not\equiv j \equiv k)]\, \sigma^2_{DR} + P(i \equiv j \equiv k \equiv m)\, \sigma^2_{DI} + [P(i \equiv j \equiv k \equiv m) + P(i \equiv j \not\equiv k \equiv m)]\, \Delta_I^2. \qquad (46)$$

Expressing the probabilities in Eq. 46 as identity coefficients (Fig. 1) and combining Eq. 46 with Eq. 44 in Eq. 41 yields

$$\mathrm{Cov}(d_{ij}, d_{km}) = (\delta_9 + \delta_{12})\, \sigma^2_{DR} + \delta_1\, \sigma^2_{DI} + (\delta_1 + \delta_6 - F_v\, F_w)\, \Delta_I^2 \qquad (47)$$

with coefficients equal to those in Eqs. 22, 23 and 26.

The probabilities in Eq. 46 were referred to as "four-way coefficients" and "two-pair coefficients de parenté" by Harris (1964), and recursive rules for their computation were given.

In conclusion, extracting elements from **E** to compute additive, additive-dominance, and dominance relationship coefficients is equivalent to computing these relationships from identity coefficients evaluated with the path coefficient method as defined in Eqs. 21–26. Recursive computation of **E**, however, requires use of the genetic parameters σ^2_{AR}, σ^2_{DR}, σ^2_{DI}, σ_{ADI} and Δ_I^2. This approach becomes inefficient if the same population is analysed for several traits with different genetic parameters values, or when parameter values are unknown and, if possible, estimated iteratively. Hence, a modified tabular method will be presented next.

Modified tabular method

Relationship coefficients can be computed from probabilities of gene identities by descent as shown in Eqs. 30, 36, 42, and 46. Hence, instead of computing a matrix with first and second moments (**E**), matrices with the required types of probabilities of gene identities may be computed recursively. A tabular method then consists of two main steps:

1) Form matrices including the following probabilities from a list of gametes and gamete pairs, respectively. Let ij and km represent gamete combinations of two individuals.

$$\mathbf{M}_1 = \{P(i \equiv k)\}; \quad \mathbf{M}_2 = \{P(i \equiv k \equiv m)\};$$

$$\mathbf{M}_3 = \{P(i \equiv k \not\equiv j \equiv m) + P(i \equiv m \not\equiv j \equiv k)\};$$

$$\mathbf{M}_4 = \{P(i \equiv j \equiv k \equiv m)\} \quad \text{and}$$

$$\mathbf{M}_5 = \{P(i \equiv j \equiv k \equiv m) + P(i \equiv j \not\equiv k \equiv m) - P(i \equiv j)\, P(k \equiv m)\}.$$

2) Compute relationship matrices in Eq. 28. Matrix **A** may be obtained from $\mathbf{M}_1$ but is computed more efficiently using the well-known tabular method described by Henderson (1976), **C** is obtained from $\mathbf{M}_2$ using Eq. 36, $\mathbf{D}_R = \mathbf{M}_3$, $\mathbf{D}_I = \mathbf{M}_4$, and $\mathbf{U} = \mathbf{M}_5$.

Step (1) consists of the following sub-steps:

1.1) Form ordered lists of gametes and gamete pairs, respectively. The list of gametes includes paternal and maternal gametes of all individuals. The list of gamete pairs includes those in all individuals, and ancestor pairs are added with the algorithm of Smith and Mäki-Tanila (1990, p 70).

1.2) Form $\mathbf{M}_1$ for all gametes i and k using Eqs. 32–34, or form **A** directly.

1.3) Form $\mathbf{M}_2$ for all gametes i and gamete pairs km. Identify rows of $\mathbf{M}_2$ by the ordered list of gametes and write the parental gametes on the left of each gamete. Identify the columns of $\mathbf{M}_2$ by the ordered

list of gamete pairs, and write the parental gamete pairs above each pair. Parental gamete pairs of gamete pair k m are x m and y m, if k ≥ m and x and y are parental gametes of k. Then, fill the matrix by proceeding from left to right within the row and from top to bottom within the column using the following rules.

a) If i ≥ k, and
- i is a base gamete, use Eq. 38
- i is not a base gamete, and
- i ≠ k and k ≠ m, use Eq. 39.
- i = k and k ≠ m, use Eq. 40.
- i = k = m, $M_2(i, km) = 1$.

b) If i < k, and
- k is a base gamete, $M_2(i, km) = 0$.
- k is not a base gamete, and
- k ≠ m, $M_2(i, km) = \frac{1}{2}[M_2(i, xm) + M_2(i, ym)]$.
- k = m, $M_2(i. km) = \frac{1}{2}[M_2(i, xx) + M_2(i, yy)]$.

1.4) To form $\mathbf{M}_3$, $\mathbf{M}_4$, and $\mathbf{M}_5$ identify rows and columns by the ordered list of gamete pairs. For gamete pairs ij and k m, let i ≥ j and k ≥ m. Computing only the lower half of the matrix implies that i ≥ k. Then $M_3(ij, km)$ may be computed with the following rules.

a) If i is a base gamete, $M_3(ij, km) = 1$ if i = k, j = m, i ≠ j and k ≠ m, and zero elsewhere.

b) If i is not a base gamete:
- i ≠ j, and
- i ≠ k, $M_3(ij, km) = \frac{1}{2}[M_3(xj, km) + M_3(yj, km)]$
- i = k, $M_3(ij, km) = \frac{1}{2}[M_3(xj, xm) + M_3(yj, ym)]$
- i = j, and
- i ≠ k, $M_3(ij, km) = \frac{1}{2}[M_3(xx, km) + M_3(yy, km)]$
- i = k, $M_3(ij, km) = \frac{1}{2}[M_3(xx, xx) + M_3(yy, yy)]$.

1.5) To form $\mathbf{M}_4$, apply the rules in (1.4), except replace a) with: if i is a base gamete, $M_4(ij, km) = 1$ if i = j = k = m, and zero elsewhere.

1.6) To form $\mathbf{M}_5$, include one extra row and column containing P(i ≡ j) for any gamete pair ij. The remaining rows and columns contain P(i ≡ j ≡ k ≡ m) + P(i ≡ j ≢ k ≡ m).

a) Start with the first column, using recurrences (32–34).

b) Compute remaining rows and columns of the lower triangular matrix with rules in (1.4), except replace a) with: if i is a base gamete, $M_5(ij, km) = 1$ if (i = j) and (k = m), and zero elsewhere.

c) Adjust each element in all rows and columns except the first by $M_5(ij, km) = M_5(ij, km) - M_5(1, km)\ M_5(ij, 1)$. Delete first row and column.

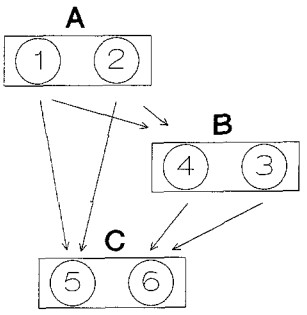

Fig. 3. Parent-offspring mating with animals represented by *blocks and letters*, parental gametes as *left-* and maternal gametes as *right-numbered circles within blocks*

Table 2. Probabilities of identity modes (IM) pertaining to the four genes of individuals B and C in Fig. 3 computed with the path coefficient method of Jacquard (1966)

Path	Probability path	Origin genes B		Origin genes C		IM[b]	Probability IM
		4	3	5	6		
1[a]	1/2	A	B	A	A		
		1	3	1	1	4	1/4
		1	3	2	1	13	1/4
		2	3	1	2	13	1/4
		2	3	2	2	4	1/4
2[a]	1/2	A	B	A	B		
		1	3	1	3	9	1/4
		1	3	2	3	11	1/4
		2	3	1	3	11	1/4
		2	3	2	3	9	1/4

[a] Origins of genes (4, 3, 5, 6) are A, B, A, A for path 1 and A, B, A, B for path 2, respectively
[b] Number of identity mode as presented in Fig. 1

Results

Numerical example for computation of covariance matrix

A parent-offspring mating, depicted in Fig. 3 with individuals identified by letters A, B and C, will be used to illustrate path coefficient and tabular methods for computing genetic covariance among individuals.

Path coefficient method

Computing the genetic covariance between individuals B and C requires evaluation of all 15 identity coefficients pertaining to the four genes in B and C at any locus. The four genes are defined as the paternal (4) and maternal (3) gene in B and the paternal (5) and maternal (6) gene in C. Identity coefficients are computed in five steps as follows. (1) The only common ancestor of B and C is A. (2) Genes 1, 2, and 3 in Fig. 3 are base genes. There are two paths

of origin of the four genes of interest (4, 3, 5, 6). In both paths, gene 3 is a base gene, and genes 4 and 5 derive from the base genes in A. The paths differ in the origin of gene 6 in C. In the first path, gene 6 is inherited from individual A through individual B, implying that 4 and 6 are copies of the same ancestral gene in A. In the second path, gene 6 is a copy of gene 3 in B. (3) The probability of each path of origin is ½. (4) The four genes of interest (4, 3, 5, 6) can be copies of the base genes 1, 2, and 3 in different ways, e.g. (4=1, 3=3, 5=1, 6=1). All possibilities are listed in Table 2 by path of origin. The case (4=1, 3=3, 5=1, 6=1) has probability $P(4=1) \times P(3=3) \times P(5=1) \times P(6=1 \mid 4=1) = ½ \times 1 \times ½ \times 1 = ¼$, and is represented by identity mode 4 of Fig. 2 (first line for path 1 in Table 2). Identity modes and their probabilities for all other cases are given in Table 2. (5) Multiplication of probability of path and probability of identity mode and summing by identity mode in Table 2 yields the only nonzero identity coefficients $\delta_4 = (½ \times ¼) + (½ \times ¼) = ¼$, $\delta_9 = ¼$, $\delta_{11} = ¼$, and $\delta_{13} = ¼$.

From the coefficients of identity, relationship coefficients are computed via Eqs. 21–26, or $a_{BC} = ¾$, $dr_{BC} = ¼$, $di_{BC} = 0$, $c_{BC} = ⅛$, $c_{CB} = 0$, and $u_{BC} = 0$. Consequently the genetic covariance between individuals B and C is:

$$\sigma_{G_B G_C} = \tfrac{3}{4}\sigma^2_{AR} + \tfrac{1}{4}\sigma^2_{DR} + \tfrac{1}{8}\sigma_{ADI}. \quad (48)$$

Table 3. Matrix $\mathbf{M}_1 = \{P(i \equiv k)\}$ in the modified tabular method for the list of gametes from the pedigree in Fig. 3. For gametes identifying rows, paternal and maternal gametes are given on the left

			1	2	3	4	5	6
		1	1					
		2	0	1				
		3	0	0	1			
1	2	4	1/2	1/2	0	1		
1	2	5	1/2	1/2	0	1/2	1	
4	3	6	1/4	1/4	1/2	1/2	1/4	1

Tabular method

To compute the genetic covariance matrix between individuals B and C from pedigree in Fig. 3 with the modified tabular method, lists of gametes and gamete pairs, respectively, must be created first. The list of gametes included the gametes indexed 1, 2, 3, 4, 5 and 6. The list of gamete pairs initially contains the pairs existing in individuals A, B and C, or 21, 43, 65. Subsequently, starting with the gamete pair of the youngest individual, 65, ancestral gamete pairs are added into the list: 54 and 53 for 65, 42 and 41 for 54, 32 and 31 for 53, 22 and 21 for 42, and 11 for 41, yielding the ordered list 11, 21, 22, 31, 32, 41, 42, 43, 53, 54, 65.

Matrices $\mathbf{M}_1$, $\mathbf{M}_2$, $\mathbf{M}_3$, $\mathbf{M}_4$ and $\mathbf{M}_5$ were computed from the two lists and rules (1.1)–(1.6) stated earlier, and are given in Tables 3–7.

The additive genetic relationship between individuals B (43) and individual C (65) is computed from $\mathbf{M}_1$ in Table 3 as:

$$a_{BC} = ½\,[M_1(3,5) + M_1(3,6) + M_1(4,5) + M_1(4,6)] = ¾.$$

The relationship coefficient between the additive effect of B and the dominance effect of C is computed from $\mathbf{M}_2$ in Table 4 as:

$$c_{CB} = ½\,[M_2(3,65) + M_2(4,65)] = ⅛.$$

The relationship between the dominance effect of B and the additive effect of C is computed from $\mathbf{M}_2$ in Table 4 as:

$$c_{BC} = ½\,[M_2(43,5) + M_2(43,6)] = 0.$$

The relationship between the dominance effects of individuals B and C due to σ^2_{DR} is element (43, 65) in $\mathbf{M}_3$ of Table 5, hence $dr_{BC} = ¼$. The relationships due to σ^2_{DI} and due to Δ^2_I are the corresponding elements in $\mathbf{M}_4$ of Table 6 and $\mathbf{M}_5$ of Table 7, respectively, hence $di_{BC} = u_{BC} = 0$. The total genetic covariance between B and C is therefore that given in Eq. 48. The matrix of genetic covariances between additive and dominance effects of all individuals in Fig. 3 is given in Table 8.

Table 4. Matrix $\mathbf{M}_2 = \{P(i \equiv k \equiv m)\}$ in the modified tabular method for the list of gametes and gamete pairs from the pedigree in Fig. 3. Parental gametes or gamete pairs are given on the left for gametes and on the top for gamete pairs, respectively

			11	21	22	31	32	11 21 / 41	21 22 / 42	31 32 / 43	31 32 / 53	41 42 / 54	53 54 / 65
		1	1	0	0	0	0	1/2	0	0	0	1/4	1/8
		2	0	0	1	0	0	0	1/2	0	0	1/4	1/8
		3	0	0	0	0	0	0	0	0	0	0	0
1	2	4	1/2	0	1/2	0	0	1/2	1/2	0	0	1/2	1/4
1	2	5	1/2	0	1/2	0	0	1/4	1/4	0	0	1/2	1/4
4	3	6	1/4	0	1/4	0	0	1/4	1/4	0	0	1/4	1/4

Table 5. Matrix $\mathbf{M}_3 = \{P(i \equiv k \neq j \equiv m) + P(i \equiv m \neq j \equiv k)\}$ in the modified tabular method for the list of gamete pairs from the pedigree in Fig. 3. For gamete pairs identifying rows, parental gamete pairs are given on the left

			11	21	22	31	32	41	42	43	53	54	65
		11	0										
		21	0	1									
		22	0	0	0								
		31	0	0	0	1							
		32	0	0	0	0	1						
11	21	41	0	1/2	0	0	0	1/2					
21	22	42	0	1/2	0	0	0	0	1/2				
31	32	43	0	0	0	1/2	1/2	0	0	1			
31	32	53	0	0	0	1/2	1/2	0	0	1/2	1		
41	42	54	0	1/2	0	0	0	1/4	1/4	0	0	1/2	
53	54	65	0	1/4	0	1/4	1/4	1/8	1/8	1/4	1/2	1/4	3/4

Table 6. Matrix $\mathbf{M}_4 = \{P(i \equiv j \equiv k \equiv m)\}$ in the modified tabular method for the list of gamete pairs from the pedigree in Fig. 3. For gamete pairs identifying rows, parental gamete pairs are given on the left

			11	21	22	31	32	41	42	43	53	54	65
		11	1										
		21	0	0									
		22	0	0	1								
		31	0	0	0	0							
		32	0	0	0	0	0						
11	21	41	1/2	0	0	0	0	1/2					
21	22	42	0	0	1/2	0	0	0	1/2				
31	32	43	0	0	0	0	0	0	0	0			
31	32	53	0	0	0	0	0	0	0	0	0		
41	42	54	1/4	0	1/4	0	0	1/4	1/4	0	0	1/2	
53	54	65	1/8	0	1/8	0	0	1/8	1/8	0	0	1/4	1/4

Table 7. Matrix $\mathbf{M}_5 = \{P(i \equiv j \equiv k \equiv m) + P(i \equiv j \neq k \equiv m) - P(i \equiv j)\,P(k \equiv m)\}$ in the modified tabular method for the list of gamete pairs from the pedigree in Fig. 3. For gamete pairs identifying rows, parental gamete pairs are given on the left

			11	21	22	31	32	41	42	43	53	54	65
		11	0										
		21	0	0									
		22	0	0	0								
		31	0	0	0	0							
		32	0	0	0	0	0						
11	21	41	0	0	0	0	0	1/4					
21	22	42	0	0	0	0	0	−1/4	1/4				
31	32	43	0	0	0	0	0	0	0	0			
31	32	53	0	0	0	0	0	0	0	0	0		
41	42	54	0	0	0	0	0	0	0	0	0	1/4	
53	54	65	0	0	0	0	0	0	0	0	0	1/8	3/16

Prediction of additive and dominance effects from simulated data

Data were simulated with an individual locus model described by De Boer and Van Arendonk (1992). The simulated trait was affected by 64 unlinked biallelic loci with complete dominance ($a = d = 1$) and no epistasis, and was measured on both males and females. A normaly distributed environmental deviation was added to each genotypic value based on a broad-sense heritability (H^2) of 0.2 or 0.5 in the base generation. Each simulated population included five generations. The initial generation con-

tained 20 males and 20 females whose genes were randomly chosen according to Hardy-Weinberg proportions and gametic phase equilibrium. Frequency of the favourable allele in the base generation was 0.2, 0.5 or 0.8 at all loci. In each generation, 5 randomly chosen males and all 20 females were mated, with each mating producing 1 male and 1 female offspring. Each of the 5 males was mated to its full sib and 3 related females, with the result that inbreeding levels increased from 0 to 0.35 in generation five. For each combination of heritability and allelic frequency, the simulated population was replicated 1000 times. In each replicate, average predicted minus simulated additive and dominance effects and correlation between predicted and simulated effects were computed within generation and averaged across replicates.

Data from all five generations were used to predict additive and dominance effects with exact and approximate BLUP. Mixed model equations (MME) for exact BLUP were based on model (27) with $\mathbf{X}\,\boldsymbol{\beta}$ replaced by $\mathbf{1}\,\mu$, where μ was the mean in the base generation, and with genetic covariance matrix in (28). Approximate MME were also based on model (27), but the genetic covariance matrix was approximated by

$$\mathbf{G}^* = \begin{bmatrix} \mathbf{A}\,\sigma^2_{AR} & 0 \\ 0 & \mathbf{D}\,\sigma^2_{DR} \end{bmatrix}$$

where $\mathbf{D}$ is a dominance relationship matrix computed by ignoring inbreeding. For both approximate and exact MME, the total dominance effect of an individual V was predicted as $\hat{d}_v + \hat{\Delta}_I F_v$.

Average predictions of additive and dominance effects in each population and generation from both approximate and exact BLUP were empirically unbiased, which is expected and consistent with results from De Boer and Van Arendonk (1992). Mean predicted minus simulated additive effects in each generation ranged from -0.04 to 0.09, with corresponding standard errors of 0.06 and 0.12. Mean predicted minus simulated dominance effects in each generation ranged from -0.12 to 0.05, with corresponding standard errors of 0.12 and 0.04. Mean empirical accuracies of predicted additive and dominance effects in generations 1, 3 and 5 are given in Table 9 for varying H^2 and initial allelic frequency. The level of H^2 did not clearly affect differences in the accuracy of predicted additive effects between both methods. For initial allelic frequencies of 0.2 and 0.5, empirical accuracies of predicted additive effects were almost identical. For $p=0.8$, however, additive effects were predicted with a slightly higher accuracy with the exact than with the approximate method in generations with inbreeding. By comparison with Fig. 2, it appears that there is a noticeable difference in accuracy of predicted additive effects between the exact and the approximate method only if dominance variance is large relative to additive variance ($p=0.8$), whereas a large covariance between additive and dominance effects ($p=0.2$) has little impact. Differences in accuracy of predicted dominance effects were larger than for additive

Table 8. Genetic covariance matrix between additive (a) and dominance (d) effects of individuals A, B and C in Fig. 3

	a_A	a_B	a_C	d_A	d_B	d_C
a_A	σ^2_{AR}	$1/2\,\sigma^2_{AR}$	$3/4\,\sigma^2_{AR}$	0	0	$1/8\,\sigma_{ADI}$
a_B		σ^2_{AR}	$3/4\,\sigma^2_{AR}$	0	0	$1/8\,\sigma_{ADI}$
a_C			$5/4\,\sigma^2_{AR}$	0	0	$1/4\,\sigma_{ADI}$
d_A				σ^2_{DR}	0	$1/4\,\sigma^2_{DR}$
d_B					σ^2_{DR}	$1/4\,\sigma^2_{DR}$
d_C						$3/4\,\sigma^2_{DR} + 1/4\,\sigma^2_{DI} + 3/16\,\Delta^2_I$

Table 9. Mean empirical accuracies of predicted additive and dominance effects in generations 1, 3 and 5, averaged over 1000 replicates, for approximate and exact BLUP, for a broad-sense heritability of 0.20 and 0.50 and for varying initial allelic frequency p_i[a]

p_i	Generation	Broad heritability of 0.20				Broad heritability of 0.50			
		Approximate		Exact		Approximate		Exact	
		Additive	Dominance	Additive	Dominance	Additive	Dominance	Additive	Dominance
0.2	1	0.482	0.144	0.482	0.145	0.704	0.238	0.705	0.240
	3	0.528	0.450	0.529	0.463	0.704	0.494	0.705	0.509
	5	0.413	0.366	0.414	0.387	0.592	0.393	0.595	0.427
0.5	1	0.427	0.257	0.427	0.258	0.623	0.412	0.623	0.413
	3	0.511	0.575	0.511	0.578	0.667	0.637	0.668	0.641
	5	0.439	0.543	0.440	0.549	0.604	0.599	0.606	0.610
0.8	1	0.315	0.358	0.316	0.360	0.460	0.570	0.461	0.571
	3	0.464	0.624	0.472	0.634	0.593	0.758	0.601	0.765
	5	0.479	0.604	0.487	0.633	0.610	0.760	0.623	0.787

[a] Accuracy of prediction was computed as the correlation between predicted and simulated values; average inbreeding coefficients in generations 1, 3 and 5 were 0.00, 0.14, and 0.35, respectively

effects, but still quite small. The difference was largest for $p=0.2$ and $H^2=0.5$ in generation five. For $p=0.2$, dominance variance is small relative to the additive variance, σ^2_{DI} is much larger than σ^2_{DR}, and the covariance between additive and dominance effects is most important. For $p=0.5$, accuracies of predicted dominance effects were almost identical. For $p=0.8$, differences between both methods were larger for $H^2=0.2$ than for $H^2=0.5$.

Discussion

Inbreeding changes the mean and genetic covariance structure of a population. With inbreeding, genetic covariance remains a sum of products of relationship coefficients and (co)variance components. In addition to additive and dominance variance in an infinite, random mating base population, the extra parameters required are dominance variance and covariance between additive and dominance effects in the completely inbred population with allelic frequencies equal to those in the base population, and sum over loci of effects of inbreeding depression and squared effects of inbreeding depression (e.g. Harris 1964; Gillois 1964; Jacquard 1974; Cockerham and Weir 1984).

A mixed linear model for a phenotype of a quantitative trait with additive and dominance variation includes additive effect, expected value of dominance effect or effect of complete inbreeding depression times inbreeding coefficient, and dominance effect beyond inbreeding depression. Although there is an argument over the existence of a genetic model with an infinite number of loci in gametic phase equilibrium and directional dominance (Robertson and Hill 1983; Smith and Mäki-Tanila 1990), the two real and unresolved issues are whether the linear model can adequately describe data on a trait affected by a finite number of loci, in particular with selection, and whether all required genetic parameters can be estimated from real data. The present and previous simulations (Uimari and Kennedy 1990; De Boer and Van Arendonk 1992) showed that predictions of additive and dominance effects were empirically unbiased in unselected or selected populations with inbreeding, for a trait with a finite number of biallelic loci. Estimation of all of the required genetic parameters has been addressed by Chevalet and Gillois (1977).

Implementation of the mixed model with additive and dominance effects and the exact genetic covariance matrix in Eq. 28 for large populations is currently not feasible. Computation of $\mathbf{G}$ requires the calculation of five matrices with different probabilities of gene identities. The maximum order of these matrices is determined by the number of gametes and gamete pairs. The number of required gamete pairs will increase with the number of generations in the data and decrease due to inbreeding. For the simulated population with 200 individuals after generation five the number of gamete pairs was 1326. The size of these matrices for large populations and potential improvements in efficiency have not yet been investigated. More importantly, $\mathbf{G}^{-1}$ is required in MME and was computed by first creating $\mathbf{G}$ and subsequently inverting it, which is not feasible for large populations.

Smith and Mäki-Tanila (1990) presented a method for direct computation of $\mathbf{E}^{-1}$, the inverse of an extended genetic covariance matrix, which could be used in MME predicting additive effects of gametes and dominance effects of gamete pairs. This approach, however, could not be used for the simulated data because $\mathbf{E}$ is singular for biallelic loci, i.e. $\mathbf{E}^{-1}$ does not exist although $\mathbf{G}^{-1}$ exists. The singularity is caused by a linear relationship among additive effects of base gametes i and dominance effects of gamete pairs ii due to the identity $\sigma^2_{ar}\,\sigma^2_{di} = \frac{1}{2}\,\sigma^2_{adi}$ for two alleles.

Simulations of populations with inbreeding and additive and dominance variation have used individual loci models. Under the infinitesimal model, total genetic effects are normally distributed. A method for generating total additive and dominance effects taking full account of the covariance structure in Eq. 28 is not available. In the absence of inbreeding, recurrence equations exist which allow generating an offspring's additive effect as the average effect of sire and dam plus Mendelian sampling (e.g. Quaas 1988). An offspring's dominance effect is generated as a sire-dam combination effect plus Mendelian sampling, and a sire-dam combination effect is generated from the combination effects of sire with parents of the dam and of dam with parents of the sire (Hoeschele and Van Raden, 1991). These recurrences also permit computing $\mathbf{A}^{-1}$ (Henderson 1976; Quaas 1988) and $\mathbf{D}^{-1}$ (Hoeschele and Van Raden 1991) directly. However, they do not generate all of the genetic relationships among inbred animals and their close relatives, e.g. covariances among additive and dominance effects are ignored.

Approximate BLUP accounts only for the effect of inbreeding on mean and additive covariance, but is computationally feasible for large populations. Approximate predictions of additive and dominance effects had only slightly reduced accuracies relative to exact BLUP for traits affected by a finite number of loci and inbreeding.

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