

Generating data in models including direct and maternal dominance effects

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Abstract. Algorithms are presented to simulate multiple generations of animal data by a model including direct additive genetic, maternal additive genetic, direct dominance, maternal dominance and permanent environmental effects. Dominance effects were computed as parental subclasses. Testing involved five single trait models that included direct contemporary group and direct additive effects, and different combinations of maternal, permanent environmental, and dominance effects. Simulated populations included 5 generations of animals and 20 contemporary groups per generation. The base population contained 200 sires and 600 dams. Variance components were estimated by Average-Information Restricted Maximum Likelihood (AIREML). No significant bias was observed. The simulation algorithms can be used in research involving dominance models, such as evaluation of mating systems exploiting special combining abilities of prospective parents.

Key words: algorithms, dominance effects, maternal effects, simulation.

Introduction

A standard model used for beef cattle evaluation includes additive genetic, maternal genetic and permanent environmental effects. Due to advances in computing power, dominance effects also can be included in the model; however, the impact of accounting for these effects in the evaluation is not well known. This impact may be partly studied by simulation. Generation of data with dominance effects for each offspring is not straightforward since the effects come from particular mating of sires and dams. Generation of data with simple direct additive effects was described previously (SORENSEN, KENNEDY 1984, Van Der WERF, de BOER, 1990). This paper presents an algorithm to generate data with dominance and maternal dominance effects for simulation studies.

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Simulation model

The following single trait models are of interest in beef cattle:

$$\text{Model I: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{e}$$

$$\text{Model II: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{W}\mathbf{p} + \mathbf{e}$$

$$\text{Model III: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{M}_1\mathbf{m} + \mathbf{e}$$

$$\text{Model IV: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{d} + \mathbf{e}$$

$$\text{Model V: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{M}_1\mathbf{m} + \mathbf{W}\mathbf{p} + \mathbf{e}$$

$$\text{Model VI: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{M}_1\mathbf{m} + \mathbf{Z}_2\mathbf{d} + \mathbf{W}\mathbf{p} + \mathbf{e}$$

$$\text{Model VII: } \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_1\mathbf{a} + \mathbf{M}_1\mathbf{m} + \mathbf{Z}_2\mathbf{d} + \mathbf{M}_2\mathbf{q} + \mathbf{W}\mathbf{p} + \mathbf{e}$$

where \mathbf{y} = vector of observations, β = vector of fixed effects, \mathbf{a} = random vector of additive effects, \mathbf{m} = random vector of maternal effects, \mathbf{d} = random vector of dominance effects, \mathbf{q} = random vector of maternal dominance effects, \mathbf{p} = random vector of maternal permanent environmental effects, \mathbf{e} = random vector of residual effects, and \mathbf{X} , \mathbf{Z}_1 , \mathbf{Z}_2 , \mathbf{M}_1 , \mathbf{M}_2 , and \mathbf{W} are known incidence matrices relating records to their respective fixed and random effects.

The variance structure for the last model is:

$$\text{Var} \begin{pmatrix} \mathbf{a} \\ \mathbf{m} \\ \mathbf{d} \\ \mathbf{q} \\ \mathbf{p} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{A}\sigma_a^2 & \mathbf{A}\sigma_{am} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{A}\sigma_{am} & \mathbf{A}\sigma_m^2 & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{D}\sigma_d^2 & \mathbf{D}\sigma_{dq} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{D}\sigma_{dq} & \mathbf{D}\sigma_q^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_p^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_e^2 \end{pmatrix}$$

where $\sigma_a^2, \sigma_m^2, \sigma_d^2, \sigma_q^2, \sigma_p^2, \sigma_e^2$ = direct additive, maternal additive, direct dominance, maternal dominance, maternal permanent environmental, and residual variances, σ_{am} = covariance between direct and maternal additive effects, σ_{dq} = covariance between direct and maternal dominance effects, \mathbf{A} = numerator relationship matrix for additive genetic effect, \mathbf{D} = numerator relationship matrix for dominance genetic effect. For other models, the (co) variance structure is a subset of the last model.

Simulation strategies

The following steps are used in the simulation:

- 1) define all variance-covariance structures,
- 2) generate fixed effects,
- 3) generate random genetic effects for sires and dams of the base population; then store in separate arrays,

- 4) generate offspring for next generation by randomly mating sires and dams,
- 5) store genetic effects of offspring in an "animal array",
- 6) generate sex for each offspring, then add genetic effects to "sire array" if the offspring is male, and to "dam array" if the offspring is female,
- 7) generate random residual effect for each offspring,
- 8) generate offspring records by combining the generated effects under the desirable model,
- 9) in each generation, apply one of the following selection type: no selection, random selection, selection based on phenotype, selection based on BLUP,
- 10) write data and pedigree files.

Random number generators

Normal random variables were generated by the polar method (ROSS 1997) and based on uniform pseudo-random numbers that are generated by the shifting method and the multiplicative congruential method (MARSAGLIA et al. 1990).

Maternal effects generating strategies

Since maternal and additive effects are correlated, these effects cannot be generated independently but can be generated jointly as follows:

- Let

$$\mathbf{V} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}$$

where \mathbf{V} is a variance-covariance matrix of direct and maternal additive effects. Decompose \mathbf{V} by Cholesky factorization: $\mathbf{V} = \mathbf{LL}'$.

- Generate $H_{2 \times N}$ containing two independent normal variables:

$$\mathbf{H} = \begin{bmatrix} h_1 \\ h_2 \end{bmatrix} \sim N(\mathbf{0}, \mathbf{I}).$$

- Multiply \mathbf{L} by \mathbf{H} , then \mathbf{LH} becomes:

$$\begin{bmatrix} \mathbf{u} \\ \mathbf{m} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{V}).$$

Strategy for generation of dominance effects

Dominance effects can be generated from full-sib effects based on parental subclasses (HOESCHELE, VANRADEN 1991). Because dominance effects are not in-

herited through individuals, these can only be computed after knowing all matings in each generation. The dominance effect (d_i) can be expressed as:

$$d_i = f_{s,d} + \phi_{d_i} \quad (i)$$

where $f_{s,d}$ is full-sib effect produced by combination of genes from sire s and dam d , and ϕ_{d_i} is sampling error due to dominance effect. In addition, the maternal dominance effect can be expressed as:

$$q_i = g_{sd,dd} + \phi_{q_i} \quad (ii)$$

where $g_{sd,dd}$ is maternal full-sib effect produced by combination of genes from sire and dam of the dam, and ϕ_{q_i} is sampling error due to maternal dominance effect. Since dominance and maternal dominance effects are correlated, full-sib effects can be described as having the following distribution:

$$\begin{bmatrix} f_{s,d} \\ g_{sd,dd} \end{bmatrix} \sim N\left(\mathbf{0}, \frac{1}{4} \begin{bmatrix} \sigma_d^2 & \sigma_{dq} \\ \sigma_{dq} & \sigma_q^2 \end{bmatrix}\right) \sim N\left(\mathbf{0}, \begin{bmatrix} \sigma_f^2 & \sigma_{fg} \\ \sigma_{fg} & \sigma_g^2 \end{bmatrix}\right)$$

where σ_f^2 is direct full-sib variance, σ_g^2 is maternal full-sib variance, σ_{fg}^2 is covariance between direct full-sibs and maternal full-sibs, and

$$\begin{bmatrix} \phi_{d_i} \\ \phi_{q_i} \end{bmatrix} \sim N\left(\mathbf{0}, \frac{3}{4} \begin{bmatrix} \sigma_d^2 & \sigma_{dq} \\ \sigma_{dq} & \sigma_q^2 \end{bmatrix}\right)$$

For a particular mating, $f_{s,d}$ and $g_{s,d}$ can be expressed in terms of full-sib effects and maternal full-sib effects contributions from parental subclasses between: 1) sire and parents of dam, 2) dam and parents of sire, and 3) parents of sire and parents of dam. Following HOESCHELE and VANRADEN (1991):

$$f_{s,d} = 0.5(f_{s,ss} + f_{s,dd} + f_{ss,d} + f_{ds,d}) - 0.25(f_{ss,ss} + f_{ss,dd} + f_{ds,ss} + f_{ds,dd}) + e_i \quad (iii)$$

where ss , ds , sd , and dd are sire of sire, dam of sire, sire of dam, and dam of dam, respectively, and e_i is a sampling error due to full-sib effect. For the maternal full-sib effect:

$$g_{sd,dd} = 0.5(g_{sd,ssd} + g_{sd,ddd} + g_{ssd,dd} + g_{dsd,dd}) - 0.25(g_{ssd,ssd} + g_{ssd,ddd} + g_{dsd,ssd} + g_{dsd,ddd}) + r_i \quad (iv)$$

where ssd , dsd , sdd , and ddd are sire of sire of dam, dam of sire of dam, sire of dam of dam, and dam of dam of dam, respectively, and r_i is a sampling error due to maternal full-sib effects.

The equation (iii) and (vi) can be expressed as:

$$f_{s,d} = b'f_{par} + e_i \quad (v)$$

and

$$g_{ss,dd} = c'g_{par} + r_i \quad (vi)$$

where: $b' = [.5 .5 .5 .5 -.25 -.25 -.25 -.25]'$, $c' = [.5 .5 .5 .5 -.25 -.25 -.25 -.25]'$, f_{par} = parental full-sib subclasses as described in (iii), g_{par} = maternal full-sib subclasses as described in (iv).

To generate the full-sib effect, variances for a particular subclass and sampling error have to be defined. From equation [v], notice that variances for parental full-sib subclasses become:

$$\text{Var}\left(\begin{bmatrix} f_{s,d} \\ q_{sd,dd} \end{bmatrix}\right) = \text{Var}\left(\begin{bmatrix} b'_i f_{par} + e_i \\ c'_i g_{par} + r_i \end{bmatrix}\right) = \text{Var}\left(\begin{bmatrix} b'_i f_{par} \\ c'_i g_{par} \end{bmatrix}\right) + \text{Var}\left(\begin{bmatrix} e_i \\ r_i \end{bmatrix}\right)$$

Note that:

$$\text{Var}\left(\begin{bmatrix} b'_i f_{par} \\ c'_i g_{par} \end{bmatrix}\right) = \begin{bmatrix} b'_i F b_i \sigma_f^2 & b'_i F c_i \sigma_{fg} \\ c'_i F b_i \sigma_{fg} & c'_i Q c_i \sigma_g^2 \end{bmatrix}$$

Therefore:

$$\text{Var}(b'_i f_{par}) = b'_i \text{Var}(f_{par}) b_i = (b'_i F b_i) * \sigma_f^2 \tag{vii}$$

$$\text{Var}(c'_i g_{par}) = c'_i \text{Var}(g_{par}) c_i = (c'_i Q c_i) * \sigma_g^2$$

$$\text{Cov}(b'_i f_{par}, c'_i g_{par}) = b'_i \text{Cov}(f_{par}, g_{par}) c_i * \sigma_{fg} = (b'_i F c_i) * \sigma_{fg}$$

and,

$$\text{Var}\left(\begin{bmatrix} e_i \\ r_i \end{bmatrix}\right) = \begin{bmatrix} \sigma_f^2 & \sigma_{fg} \\ \sigma_{fg} & \sigma_g^2 \end{bmatrix} - \begin{bmatrix} b'_i F b_i \sigma_f^2 & b'_i F c_i \sigma_{fg} \\ c'_i F b_i \sigma_{fg} & c'_i Q c_i \sigma_g^2 \end{bmatrix} \tag{viii}$$

where F , and Q are relationship matrices among direct full-sib subclasses, maternal full-sib subclasses, and direct and maternal full-sib subclasses, respectively.

i) F for computing direct full-sib variance is:

	s, sd	s, dd	ss, d	ds, d	ss, sd	ss, dd	ds, sd	ds, dd
s, sd	1.0	0.0	0.25	0.25	0.5	0.0	0.5	0.0
s, dd	0.0	1.0	0.25	0.25	0.0	0.5	0.0	0.5
ss, d	0.25	0.25	1.0	0.0	0.5	0.5	0.0	0.0
ds, d	0.25	0.25	0.0	1.0	0.0	0.0	0.5	0.5
ss, sd	0.5	0.0	0.5	0.0	1.0	0.0	0.0	0.0
ss, dd	0.0	0.5	0.5	0.0	0.0	1.0	0.0	0.0
ds, sd	0.5	0.0	0.0	0.5	0.0	0.0	1.0	0.0
ds, dd	0.0	0.5	0.0	0.5	0.0	0.0	0.0	1.0

ii) Q for computing maternal full-sib variance is:

	sd,sdd	sd,ddd	ssd,dd	dsd,dd	ssd,sdd	ssd,ddd	dsd,sdd	dsd,ddd
sd,sdd	1.0	0.0	0.25	0.25	0.5	0.0	0.5	0.0
sd,ddd	0.0	1.0	0.25	0.25	0.0	0.5	0.0	0.5
ssd,dd	0.25	0.25	1.0	0.0	0.5	0.5	0.0	0.0
dsd,dd	0.25	0.25	0.0	1.0	0.0	0.0	0.5	0.5
ssd,sdd	0.5	0.0	0.5	0.0	1.0	0.0	0.0	0.0
ssd,ddd	0.0	0.5	0.5	0.0	0.0	1.0	0.0	0.0
dsd,sdd	0.5	0.0	0.0	0.5	0.0	0.0	1.0	0.0
dsd,ddd	0.0	0.5	0.0	0.5	0.0	0.0	0.0	1.0

Computing strategy

Generating dominance effects for each animal requires values of dominance effects for particular subclasses. The generation can be done as follows:

1. For each particular mating, generate correlated effects for all parental full-sib and maternal full-sib subclasses as follows:

– let

$$T = \frac{1}{4} \begin{bmatrix} \sigma_d^2 & \sigma_{dq} \\ \sigma_{dq} & \sigma_q^2 \end{bmatrix} = \begin{bmatrix} \sigma_f^2 & \sigma_{fg} \\ \sigma_{fg} & \sigma_g^2 \end{bmatrix}$$

decompose T by Cholesky factorization: $T = LL'$;

– generate $H_{2 \times 8}$ containing independent normal variables,

$$H = \begin{bmatrix} h_{1i} \\ h_{2i} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{I}), \quad \text{where } i = 1, \dots, 8;$$

– then LH becomes:

$$LH = \begin{bmatrix} Lh_1 \\ Lh_2 \end{bmatrix} = \begin{bmatrix} f_{s,sd} & f_{s,dd} & f_{ss,d} & f_{ds,d} & f_{ss,sd} & f_{ss,dd} & f_{ds,sd} & f_{ds,dd} \\ g_{sd,sdd} & g_{sd,ddd} & g_{ssd,dd} & g_{dsd,dd} & g_{ssd,sdd} & g_{ssd,ddd} & g_{dsd,sdd} & g_{dsd,ddd} \end{bmatrix}$$

2. Check for known direct parental full-sib subclasses and maternal full-sib subclasses computed previously: a) for known subclasses, replace $f_{i,j}$ and $q_{i,j}$ with known effects for subclass i and j ; b) for unknown subclasses, store $f_{i,j}$ and $q_{i,j}$ in arrays for particular subclass i and j .

3. Compute the sampling error variance due to direct and maternal full-sibs by: a) constructing coefficients b'_i for all direct parental subclasses, and c'_i for all maternal subclasses by setting zero to the related unknown subclass effects in step 2 above; b) compute direct and maternal full-sib variance for particular mating using equation (vii); c) compute sampling error variance due to direct and maternal full-sib using equation (viii).

4. Generate sampling errors due to direct and maternal full-sib for the mating using sampling error variance from the previous step as:

$$\begin{bmatrix} e_i \\ r_i \end{bmatrix} \sim N(\mathbf{0}, \text{Var} \begin{bmatrix} e_i \\ r_i \end{bmatrix}).$$

5. Complete the equation (iii) and (iv), using generated effects from step 2 and 4, then the full-sib effect becomes:

$$\begin{bmatrix} f_{s,d} \\ g_{sd,dd} \end{bmatrix} = \begin{bmatrix} f_{s,sd} & f_{s,dd} & f_{ss,d} & f_{ds,d} & f_{ss,sd} & f_{ss,dd} & f_{ds,sd} & f_{ds,dd} \\ g_{sd,sdd} & g_{sd,ddd} & g_{ssd,dd} & g_{dsd,dd} & g_{ssd,sdd} & g_{ssd,ddd} & g_{dsd,sdd} & g_{dsd,ddd} \end{bmatrix} + \begin{bmatrix} e_i \\ r_i \end{bmatrix}$$

6. Store the generated direct and maternal full-sib effects in the array for a particular s and d ,

7. Generate sampling errors due to direct and maternal dominance effect:
- let

$$\mathbf{T} = \frac{3}{4} \begin{bmatrix} \sigma_d^2 & \sigma_{dq} \\ \sigma_{dq} & \sigma_q^2 \end{bmatrix},$$

and decompose \mathbf{T} by Cholesky factorization: $\mathbf{T} = \mathbf{LL}'$

- generate $H_{2 \times 1}$ containing two independent normal variables,

$$\mathbf{H} = \begin{bmatrix} h_1 \\ h_2 \end{bmatrix} \sim N(\mathbf{0}, \mathbf{I}),$$

- later multiply \mathbf{L} by \mathbf{H} , then \mathbf{LH} becomes:

$$\begin{bmatrix} \phi_d \\ \phi_q \end{bmatrix} \sim N(\mathbf{0}, \mathbf{T}).$$

8. Complete equation i and ii , so that finally:

$$\begin{bmatrix} d_i \\ q_i \end{bmatrix} = \begin{bmatrix} f_{s,d} \\ g_{sd,dd} \end{bmatrix} + \begin{bmatrix} \phi_{d_i} \\ \phi_{q_i} \end{bmatrix}.$$

Algorithms

1. Generate effects of contemporary groups (Cg), Sex , and generation (Gen) for offspring:

$$Cg_{1,\dots,n_{cg}} \sim N(\mathbf{0}, \sigma_{cg}^2)$$

$$Sex_{1,2} \sim N(\mathbf{0}, \sigma_{sex}^2)$$

$$Gen_{1,\dots,n_g} \sim N(\mathbf{0}, \sigma_{gen}^2)$$

where n_{cg} is the number of contemporary groups, n_g is the number of generations.

2. Generate correlated additive and maternal effects for sires and dams for base population by algorithms described in the random number generator section:

$$\begin{bmatrix} u_s \\ m_s \end{bmatrix} \sim N(\mathbf{0}, \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}), \quad \begin{bmatrix} u_d \\ m_d \end{bmatrix} \sim N(\mathbf{0}, \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix})$$

where u_s and m_s are additive and maternal effects for sire, u_d and m_d are additive and maternal effects for dam, s is the number of sires and d is the number of dams in the base population; store the effects in separate arrays.

3. Generate maternal permanent environment effects for dams

$$PE_d \sim N(\mathbf{0}, \sigma_{pe}^2).$$

4. Randomly select sire and dam for each generation under the following assumptions: a) sire and dam must be born (generated) before offspring; b) unlimited mating for each sire; c) each dam can be used only once in each generation and cannot have twins; d) all females have full conception rates, e) offspring sex will be randomly generated based on 50% chance.

5. Generate additive and maternal effects for each offspring:

$$u_i = \frac{u_s + u_d}{2} + \phi_{A_i}$$

$$m_i = \frac{m_s + m_d}{2} + \phi_{M_i}$$

where u_i and m_i are additive and maternal effects for offspring, and ϕ_{A_i} and ϕ_{M_i} are Mendelian samplings deviated from average additive and maternal effects generated as:

$$\begin{bmatrix} \phi_{A_i} \\ \phi_{M_i} \end{bmatrix} \sim N(\mathbf{0}, \frac{1}{2} \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}).$$

To account for Mendelian samplings with parental inbreeding, generate:

$$\begin{bmatrix} \phi_{A_i} \\ \phi_{M_i} \end{bmatrix} \sim N(\mathbf{0}, \frac{1}{2} (1 - \frac{1}{2} F_s - \frac{1}{2} F_d) \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix})$$

where F_s and F_d are inbreeding coefficients for sire and dam of offspring i .

6. Generate maternal permanent environment effects for offspring. It will be used only if animal i is a dam in a later generation

$$PE_i \sim N(\mathbf{0}, \sigma_{pe}^2).$$

7. Generate effects of contemporary group, sex, and generations from step 1 for each offspring. Store u_i to u_s or u_d if offspring sex is male or female respectively, and store m_i to m_s or m_d if offspring is male and female respectively. Therefore offspring can be used as sire or dam for the next generation.

8. Generate dominance and maternal dominance effects by the method described in the previous section

$$\begin{bmatrix} d_i \\ q_i \end{bmatrix} \sim N(\mathbf{0}, \begin{bmatrix} \sigma_d^2 & \sigma_{dq} \\ \sigma_{dq} & \sigma_q^2 \end{bmatrix}).$$

9. Generate observation for offspring i by combining all effects plus overall mean and unexplained error.

$$Y_i = \mu + u_i + m_d + d_i + q_d + PE_d + Cg_i + Sex_i + By_i + Err_i,$$

where Y_i is record value, μ is overall mean, u_i is additive direct effect, m_d is additive maternal effect, d_i is parental dominance direct effect, q_d is parental dominance maternal effect, PE_d is permanent environmental maternal effect, Cg_i is contemporary group effect, Sex_i is sex effect, By_i is birth year effect, and Err_i is residual effect distributed as $N(0, \sigma_e^2)$. Store information about animals with record in array for subsequent selection.

10. Create a data file and a pedigree file to store information.

11. Store effects of male offspring in "sire array", and female in "dam array" for use in the next generation,

12. Repeat step 4 to 12 for the next generation.

Program testing

The algorithms were implemented in the program SIMF90 (DUANGJINDA et al., 2000) in FORTRAN 90. To verify the correctness of simulation, data were simulated under models mentioned earlier using the following conditions:

1. Records of animals were generated for 5 generations, with 20 contemporary groups per generation. The base population contained 200 sires and 600 dams, and the approximate number of animals in the pedigree was 10,000.

2. Estimates of variance components from each model were averaged from 30 replicates.

3. Contemporary groups, sex, and generations were treated as fixed effects by using the same seeds for the particular effects; therefore, the fixed effects would be the same for all replications.

4. Total variance for all random effects are 100 and variances for contemporary groups and sex were 10 and 20, respectively.

5. Variance components for particular models were estimated by the method of Average Information Restricted Maximum Likelihood (AIREML) (JENSEN et al. 1996) using the program AIREMLF90 (TSURUTA, MISZTAL 1999).

Table 1. Average estimates and empirical standard error of variance component estimates over 30 replicates by REML from various animal models simulated from non-selected populations

Model ^a	True	Estimate ^b	SE ^c
Model I			
σ_e^2	70	70.9	0.5
σ_a^2	30	29.4	0.7
Model II			
σ_e^2	60	60.8	0.5
σ_a^2	30	29.2	0.6
σ_p^2	10	10.4	0.5
Model III			
σ_e^2	60	60.5	0.7
σ_a^2	30	29.3	0.5
σ_m^2	15	15.4	0.7
σ_{am}	-5	-5.2	0.7
Model IV			
σ_e^2	65	65.8	1.1
σ_a^2	30	30.2	0.6
σ_f	5	5.4	1.0
Model V			
σ_e^2	50	50.5	0.5
σ_a^2	30	30.3	0.5
σ_m^2	15	14.4	0.6
σ_{am}	-5	-5.3	0.6
σ_p^2	10	10.7	0.4

^a σ_e^2 = error variance, σ_a^2 = direct additive genetic variance, σ_m^2 = maternal additive genetic variance, σ_p^2 = maternal permanent environmental variance, σ_f^2 = direct parental full-sib variance, σ_{am}^2 = direct and maternal genetic covariance.

^b non-significantly different from the true value ($p > 0.10$).

^c SE = standard error.

Results and conclusion

The average and standard deviation of the estimates from 30 samples of all population sizes for each model are shown in Table 1. The results showed that the estimates were not significantly biased from the true variance ($p > 0.10$) for all models. Standard errors in the model with dominance effect were slightly higher than in other models. This indicates that larger data sets are needed to obtain good estimates of dominance variance. The algorithms proposed in this paper can be used for simulation studies on dominance effects in animal breeding.

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