Quantitative characters - solutions to exercises

1. a) $Cov(HS) = \frac{1}{4}\sigma^2_{10} \quad + \quad 0\sigma^2_{01} \quad + \quad \frac{1}{16}\sigma^2_{20} \quad + \quad 0\sigma^2_{11} \quad + \quad 0\sigma^2_{02}$

b) $Cov(FS) = \frac{1}{2}\sigma^2_{10} \quad + \quad \frac{1}{4}\sigma^2_{01} \quad + \quad \frac{1}{4}\sigma^2_{20} \quad + \quad \frac{1}{8}\sigma^2_{11} \quad + \quad \frac{1}{16}\sigma^2_{02}$

c) $\sigma^2_D \quad = \quad \sigma^2_{01} \quad \approx \quad 4\left[Cov\ (FS) - 2\ Cov\ (HS)\right]$

Bias due to epistatic effects

2. a) $a_{XY} \quad = \quad (\frac{1}{2})^{2+2}(1+F_A) + (\frac{1}{2})^{2+2}(1+F_B) \quad = \quad \frac{1}{16}+\frac{1}{16} \quad = \quad \frac{1}{8}$

$d_{XY} \quad = \quad \frac{1}{4}(a_{ED} \times a_{CF} + a_{EF} \times a_{CD}) \quad = \quad \frac{1}{4}\left(0 \times 0 + 0 \times \frac{1}{2}\right) \quad = \quad 0$

b) $Cov(X,Y) \quad = \quad \sum_{i=0}^{n} \sum_{j=0}^{n} (\frac{1}{8})^i \quad (0)^j \quad \sigma^2_{ij}$

$1 \leq i+j \leq n$

When maximum three loci are considered: *Cov(X,Y)* =

$$= \quad (\frac{1}{8})^1(0)^0\sigma^2_{10} \quad + \quad (\frac{1}{8})^0(0)^1\sigma^2_{01} \quad + \quad (\frac{1}{8})^2(0)^0\sigma^2_{20} \quad + \quad (\frac{1}{8})^1(0)^1\sigma^2_{11} \quad +$$

$$+ \quad (\frac{1}{8})^0(0)^2\sigma^2_{02} \quad + \quad (\frac{1}{8})^3(0)^0\sigma^2_{30} \quad + \quad (\frac{1}{8})^2(0)^1\sigma^2_{21} \quad + \quad (\frac{1}{8})^1(0)^2\sigma^2_{12} \quad +$$

$$+ \quad (\frac{1}{8})^0(0)^3\sigma^2_{03} \quad + \quad . \quad . \quad . \quad .$$

$$= \quad \frac{1}{8}\sigma^2_{10} \quad + \quad 0 \quad + \quad \frac{1}{64}\sigma^2_{20} \quad + \quad 0 \quad + \quad 0 \quad + \quad \frac{1}{512}\sigma^2_{30} \quad + \quad 0 \quad + \quad 0 \quad + \quad 0 \quad . \quad . \quad .$$

The genetic covariance between cousins is composed only of additive variance and epistatic variance between additive gene effects

3. $a_{XY} = (\frac{1}{2})^{2+2}(1+F_A) + (\frac{1}{2})^{2+2}(1+F_B) + (\frac{1}{2})^{2+2}(1+F_C) + (\frac{1}{2})^{2+2}(1+F_D)$

$$= \frac{1}{16} + \frac{1}{16} + \frac{1}{16} + \frac{1}{16} = \frac{4}{16} + = \frac{1}{4}$$

$$d_{XY} = \frac{1}{4}(a_{FE} \times a_{GH} + a_{FH} \times a_{GE}) = \frac{1}{4}(\frac{1}{2} \times \frac{1}{2} + 0 \times 0) = \frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$$

$$\text{Cov (X,Y)} = (\frac{1}{4})^1(\frac{1}{16})^0\sigma^2_{10} + (\frac{1}{4})^0(\frac{1}{16})^1\sigma^2_{01} + (\frac{1}{4})^2(\frac{1}{16})^0\sigma^2_{20} + (\frac{1}{4})^1(\frac{1}{16})^1\sigma^2_{11} + (\frac{1}{4})^0(\frac{1}{16})^2\sigma^2_{02}$$

$$= \frac{1}{4}\sigma^2_{10} + \frac{1}{16}\sigma^2_{01} + \frac{1}{16}\sigma^2_{20} + \frac{1}{64}\sigma^2_{11} + \frac{1}{256}\sigma^2_{02}$$

4. a) Parent-Offspring Cov(PO) $= \frac{1}{2}\sigma^2_{10} + \frac{1}{4}\sigma^2_{20}$

c)

	σ^2_{10}	σ^2_{01}	σ^2_{20}	σ^2_{11}	σ^2_{02}
2 x Cov(OP)	1		$\frac{1}{2}$		
2 x Cov(FS)	1	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{1}{4}$	$\frac{1}{8}$
4 x Cov(HS)	1		$\frac{1}{4}$		

* Cov(OP) and Cov(HS) only give bias due to epistatic (add. x add.) gene effects. This bias is smaller for Cov(HS) compared to Cov(OP).
* Cov(FS) gives biased estimates of σ^2_A due to influence of dominance effects and also all types of epistatic effects.

  The estimates of σ^2_{10} calculated from the genetic covariance between half sibs contains the least bias as regards non-additive components.

5. a) $Y_{ij} = \mu + s_i + e_{ij}$ $E(S_i) = 0$ $E(S_i^2) = \sigma_S^2$

$E(e_{ij}) = 0$ $E(e_{ij}^2) = \sigma_e^2$

Source of var.	**d.f.**	**SS[1]**	**MS**	**E(MS)**
Between sires	4	C-B	4299	$\sigma_e^2 + 8\,\sigma_S^2$
Within sires	35	A-C	2334	σ_e^2
Total	39	A-B		

b)

[1] $A = \sum_i \sum_j Y_{ij}^2 = 18773473$

$B = (\sum_{ij} Y_{ij})^2 / N = (27331)^2 / 40 = 18674589$

$C = \sum_i (\sum_j Y_{ij})^2 / n_i = \frac{(5720)^2}{8} = + \ldots\ldots + \frac{(5466)^2}{8} = 18691786$

c) $\sigma_e^2 = 2334$ $\sigma_s^2 = \frac{4299 - 2334}{8} = 246$

$\sigma_A^2 = 4\,\sigma_s^2 = 4 \times 246 = 984$

$\sigma_P^2 = \sigma_s^2 + \sigma_e^2 = 2334 + 246 = 2580$

d) The genetic covariance (HS) has the following composition:

$\frac{1}{4}\sigma_{10}^2 + \frac{1}{16}\sigma_{20}^2 + \frac{1}{64}\sigma_{30}^2 + \ldots.$

- Interaction between non-allelic genes, i.e. σ_{20}^2, σ_{30}^2 give some bias as an overstimation of σ_A^2.

- Interaction between non-allelic genes (dominance), i.e. σ_{01}^2, is not included in Cov(HS) and thus do not affect the estimate of σ_A^2.

e) $h^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{984}{2580} = 0.38$

6.

Source of var.	**d.f.**	**SS**[1]	**MS**	**E(MS)**
Between sires	39	5000	128.20	$\sigma_e^2 + 88\sigma_s^2$
Within sires	3480	46800	13.45	σ_e^2
Total	3519	51800		

a) $$n = \frac{3520}{40} = 88$$

$$\sigma_e^2 = 13.45; \qquad \sigma_s^2 = \frac{128.20 - 13.45}{88} = 1.30$$

$$\sigma_A^2 = \frac{1}{a_{HS}} \times \sigma_s^2 = \frac{1}{0.28} \times 1.30 = 4.64$$

$$\sigma_P^2 = \sigma_s^2 + \sigma_e^2 = 1.30 + 13.34 = 14.75$$

b) Yes. The trait is sex limited and the covariance sire-offspring can not be used. The covariance dam-offspring is not so good since the environmental covariance dam-daughter is usually $\neq 0$.

c) $$\hat{h}^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{4.64}{14.75} = 0.31$$

7. a) $$Y_{ijk} = \mu + s_i + d_{ij} + v_K + e_{ijk}$$

$$E(s_i) = 0 \qquad E(s_i^2) = \sigma_S^2$$

$$E(d_{ij}) = 0 \qquad E(d_y^2) = \sigma_d^2$$

$$E(e_{ijk}) = 0 \qquad E(e_{ijk}^2) = \sigma_e^2$$

b)

Source of var.	**d.f.**	**SS**	**MS**	**EMS**
Between sires	137	184.9	1.35	$\sigma_e^2 + 2\sigma_d^2 + 6\sigma_s^2$
Between sows	276	223.5	0.81	$\sigma_e^2 + 2\sigma_d^2$
Within weights	1	9.4	9.40	$\sigma_e^2 + K\,\kappa^2$
Residual	413	251.9	0.61	σ_e^2
Total	827	669.7		

c) $\sigma_e^2 = 0.61$ $\qquad$ $\sigma_s^2 = \dfrac{1.35 - 0.81}{6} = 0.09$

$$\sigma_d^2 = \frac{0.81 - 0.61}{2} = 0.10$$

d) $\sigma_A^2 = 4\sigma_S^2 = 4 \times 0.09 = 0.36$

σ_s^2 does not give any bias due to dominance or maternal effects and smaller bias due to epistatic effects compared to σ_d^2.

e) $\sigma_P^2 = \sigma_s^2 + \sigma_d^2 + \sigma_e^2 = 0.09 + 0.10 + 0.61 = 0.80$

f) $h^2 = \dfrac{\sigma_A^2}{\sigma_P^2} = \dfrac{0.36}{0.80} = 0.45$

g) $\hat{r}_g = \dfrac{\sigma_{s\tilde{s}}}{\sqrt{\sigma_s^2 \times \sigma_{\tilde{s}}^2}} = \dfrac{0.06}{\sqrt{0.09 \times 0.40}} = 0.32$

$$\hat{r}_p = \frac{\sigma_{s\tilde{s}} + \sigma_{d\tilde{d}} + \sigma_{e\tilde{e}}}{\sqrt{(\sigma_s^2 + \sigma_d^2 + \sigma_e^2)(\sigma_{\tilde{s}}^2 + \sigma_{\tilde{d}}^2 + \sigma_{\tilde{e}}^2)}} = \frac{0.65}{\sqrt{0.8 \times 2.1}} = 0.50$$

8. a) Weight gain: $\sigma_e^2 = 0.0110; \quad \sigma_s^2 = \frac{0.0187 - 0.0110}{17} = 0.00045$

Height at withers: $\sigma_e^2 = 1258.5; \quad \sigma_s^2 = \frac{3097.2 - 1258.5}{17} = 108.159$

Covariance comp.: $\sigma_{e\tilde{e}} = 1.1746; \quad \sigma_{s\tilde{s}} = \frac{3.1978 - 1.1746}{17} = 0.119$

b) $\sigma_A^2 = 4\sigma_s^2 = 4 \times 0.00045 = 0.0018$

$\sigma_{\tilde{A}}^2 = 4\sigma_{\tilde{s}}^2 = 4 \times 108.159 = 432.636$

$\sigma_{A\tilde{A}} = 4\sigma_{s\tilde{s}} = 4 \times 0.119 = 0.476$

c) $\sigma_{E\tilde{E}} = \sigma_{e\tilde{e}} - 3\sigma_{s\tilde{s}} = 1.1746 - 3 \times 0.119 = 0.8176$

$\sigma_{P\tilde{P}} = \sigma_{s\tilde{s}} + \sigma_{e\tilde{e}} = 0.119 + 1.1746 = 1.2936$

d) $0.476 + 0.8176 = 1.2936 \quad \because \quad \sigma_{P\tilde{P}} = \sigma_{A\tilde{A}} + \sigma_{E\tilde{E}}$

e) $\hat{r}_g = \frac{\sigma^2_{A\tilde{A}}}{\sqrt{\sigma_A^2 \times \sigma_{\tilde{A}}^2}} = \frac{0.476}{\sqrt{0.0018 \times 432.636}} = 0.54$

$\hat{r}$ can also be calculated directly from the statistical components according to:

$\hat{r}_g = \frac{\sigma_{s\tilde{s}}}{\sqrt{\sigma_s^2 \times \sigma_{\tilde{s}}^2}} = \frac{0.119}{\sqrt{0.00045 \times 108.159}} = 0.54$

Conclusions: When we select for weight gain we will also get a correlated increase in height at withers or vice versa. The correlation is high enough for an indirect selection.

f)

$$\hat{r}_p = \frac{\sigma_{P\tilde{P}}}{\sqrt{\sigma_P^2 \times \sigma_{\tilde{p}}^2}} = \frac{\sigma_{s\tilde{s}} + \sigma_{e\tilde{e}}}{\sqrt{(\sigma_s^2 + \sigma_e^2)(\sigma_{\tilde{s}}^2 + \sigma_{\tilde{e}}^2)}} = \frac{0.119 + 1.1746}{\sqrt{(0.00045 + 0.0110)(108.159 + 1258.5)}} = 0.33$$

g) $$\hat{r}_e = \frac{\sigma_{e\tilde{e}}}{\sqrt{\sigma_e^2 \times \sigma_{\tilde{e}}}}$$

$$\sigma_{e\tilde{e}} = 0.8176$$

$$\sigma_E^2 = \sigma_e^2 - 3\sigma_s^2 = 0.0110 - 3 \times 0.00045 = 0.00965$$

$$\sigma_{\tilde{E}}^2 = \sigma_{\tilde{e}}^2 - 3\sigma_{\tilde{s}}^2 = 1258.5 - 3 \times 108.159 = 934.023$$

$$\hat{r}_e = \frac{0.8176}{\sqrt{0.00965 \times 934.023}} = 0.27$$

9. a)

$$\sigma_{P_1'P_2'} = \underbrace{\sigma_{G_1'G_2'}}_{\substack{\text{Genetic}\\ \text{covariance}\\ \text{between}\\ \text{halfsibs}}} + \underbrace{\sigma_{G_1'E_2} + \sigma_{G_2'E_1}}_{\substack{\text{Covariance between}\\ \text{genotype and}\\ \text{environment of}\\ \text{halfsibs}}} + \underbrace{\sigma_{E_1E_2}}_{\substack{\text{Covariance}\\ \text{between}\\ \text{environments of}\\ \text{the halfsibs}}}$$

$$\sigma_{G_1'G_2'} = Cov(XY) = \underbrace{\frac{1}{4}\sigma^2_{10}}_{\substack{\text{Add.}\\ \text{genetic}\\ \text{variance}}} + \underbrace{\underbrace{\frac{1}{16}\sigma^2_{20}}_{\substack{\text{Add. x Add.}\\ \text{genetic}\\ \text{variance}}} + \underbrace{\frac{1}{64}\sigma^2_{30}}_{\substack{\text{Add. x Add. x Add.}\\ \text{genetic}\\ \text{variance}}} + }_{\text{Variance due to epistatic effects, } \sigma^2_I}$$

b) $\sigma_{G_1'E_2}$ $\sigma_{G_2'E_1}$ $\sigma_{E_1E_2}$ *and* σ^2_I

10. Quantitative traits are influenced both by a number of genes and by environment. They can be described by μ and σ^2 but gene frequencies and genotypes can not be estimated. The estimated biological variances covariances are used for:

- Calculation of genetic parameters ⇒ description of the traits.
- Breeding values: Calculations of selection index and BLUP assumes known values of

  σ^2_A, σ^2_P (or quotas), $\sigma_{A\tilde{A}}$ and $\sigma_{P\tilde{P}}$.
- Prediction of genetic gain and changes in correlated traits assumes known values of

  σ^2_A and $\sigma_{A\tilde{A}}$.

11. * σ_A^2 constitutes the major part of the genetic variance for most of the traits.

* σ_A^2 is that part of the genetic variance which is utilized in selection. Individuals submit genes and not genotypes to their offspring.

12. * The traits are measured at the same time and on the same type of animals.

* Also sex limited and carcass traits can be measured

* Effects of $\sigma_M^2 + \sigma_C^2$ are omitted for paternal halfsibs, but often occur for example between mothers and daughters.

* Large materials of sibs are available in field data

* Half sibs give less epistatic bias than parent-offspring