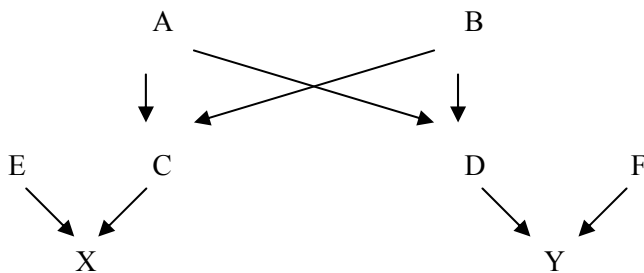


Quantitative characters - exercises

1.
 - a) Calculate the genetic covariance between half sibs, expressed in the σ_{ij}^2 notation (Cockerham's notation), when up to 2 loci are considered.
 - b) Calculate the genetic covariance between full sibs, expressed in the σ_{ij}^2 notation, when up to 2 loci are considered.
 - c) Show how the covariances between full-sibs and half-sibs, respectively can be combined to get an estimation of the particular part of variation in a trait that is caused by dominance effects ($\sigma_D^2 = \sigma_{01}^2$)

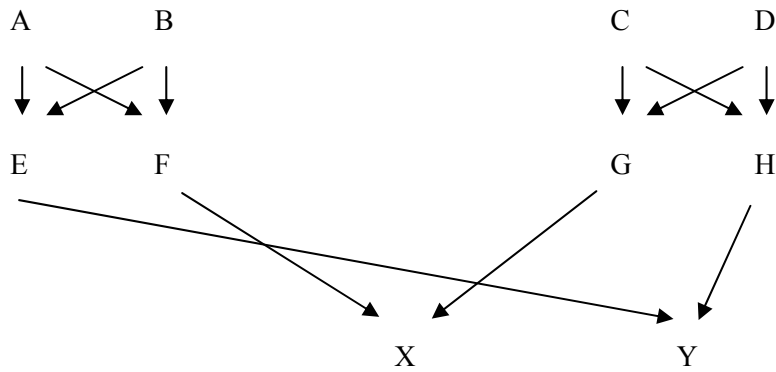
2. Two individuals X and Y are cousins and thus have the following pedigree:



- a) What is the respective additive and dominance relationship between X and Y?
- b) What is the composition of the genetic covariance for this type of relatives?

Note that: $(X)^0 = (0)^0 = 1$
 $(0)^1 = (0)^2 = 0$

3.



What is the genetic covariance (expressed in σ^2 -units) between the individuals X and Y when 2 loci are considered?

4.

- a) Calculate the composition of the genetic covariance between parent – offspring.
- b) Put the results from 4.a), 1.a) and 1.b) together in the upper part of the following table:

Covariance	σ_{10}^2	σ_{01}^2	σ_{20}^2	σ_{11}^2	σ_{02}^2
b.					
Parent – offspring					
Half-sibs					
Full-sibs					
c.					
Parent – offspring					
Half-sibs					
Full-sibs					

- c) Multiply the respective covariances above by a figure each so that you get an estimate of the total additive genetic variance σ_A^2 . Fill in the results in the lower part of the table above.

Compare the covariances regarding bias that appears as non-additive components in the estimation.

5. The following table gives the weight at 8 weeks for chicken. The chicken were progenies from five different, randomly selected cocks. Only half-sibs were found within each progeny group.

Sires					
	A	B	C	D	E
Offspring	687	618	618	600	717
	691	680	687	657	658
	793	592	763	669	674
	675	683	747	606	611
	700	631	678	718	678
	753	691	737	693	788
	704	694	731	669	650
	717	732	603	648	690
Y_i	5720	5321	5564	5260	5466

$$\sum_i \sum_j Y_{ij} = 27331$$

$$\sum_i \sum_j Y_{ij}^2 = 18773473$$

$$N = 40$$

- Set up a statistical model which describes the data set.
- Set up the ANOVA-table and calculate MS (mean squares) and E(MS) (expected mean squares).
- Solve for the statistical variance components and “translate” these into biological components, i.e. the additive genetic and phenotypic variances for the weight at 8 weeks.
- In what way will the estimation of the additive genetic variance be affected if the trait above is affected by
 - interaction between non-allelic genes
 - interaction between allelic genes
- Calculate the heritability for the weight at 8 weeks.

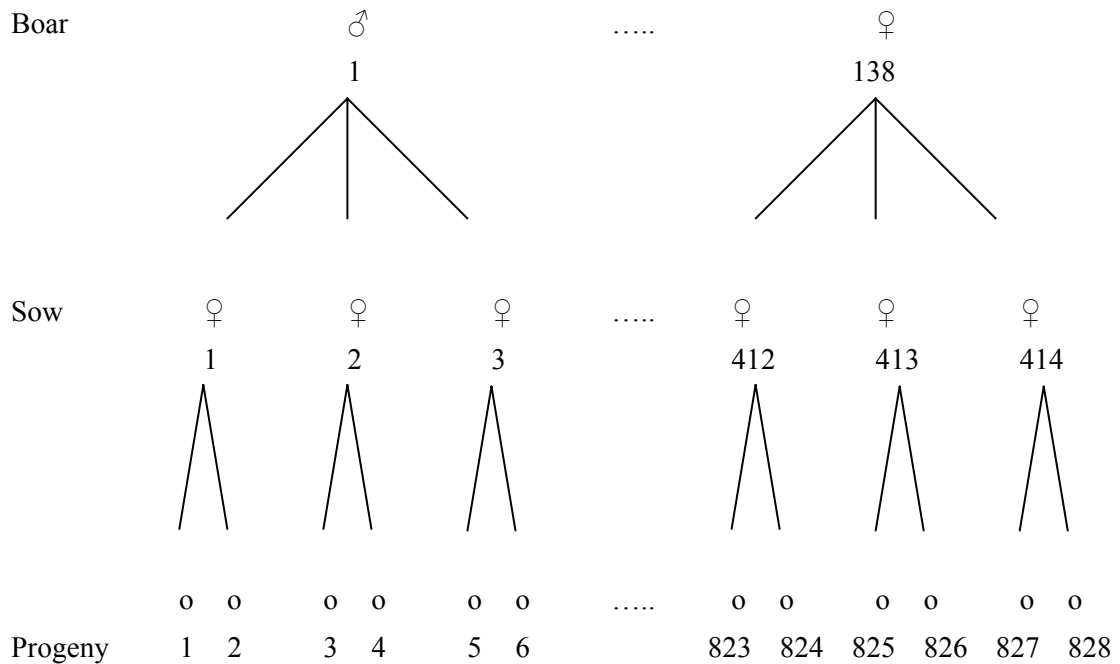
6. Within the cow recording system an investigation has been conducted where the daily milk yield has been recorded on 3520 cows. These cows were the progeny of 40 sires, which had all an equal number of progenies. The relationship (= additive relationship) was calculated to 0.28. The sires were not selected.

The following sums of squares were calculated in the analysis of variance:

Source of variation	d.f.	SS	MS	E(MS)
Between sires		5 000		
Within sires		46 800		
Total				

- a) Calculate the statistical parameters that are needed and then estimate the additive genetic variance and the phenotypic variance for daily milk yield.
- b) Is the covariance between half-sibs the most appropriate method for estimation of the additive genetic variance in daily milk yield? Explain why!
- c) Calculate the heritability for daily milk yield.

7. The tenderness of meat from 828 Landrace pigs was estimated. The pigs were progenies of 138 boars which were mated to 3 sows each. Two full-sibs from each litter were slaughtered at 90 and 100 kg live weight respectively, and the shear force was measured. The structure of the data set was thus:



The effects of boar and sow can be considered as random and weight as fixed. The following sums of squares were calculated:

Source of variation	d.f.	SS	MS	E(MS)
Between boars	137	184.9		
Between sows within boars	276	223.5		
Between weights	1	9.4		
Residual	413	251.9		
Total	827	669.7		

- Set up a complete statistical model for the analysis above.
- Calculate the mean squares (MS) and fill in the expected mean squares (EMS) in the table.
- Solve for the variance components.

- d) Estimate the additive genetic variance, σ_A^2 , from the statistical variance component which, according to you, gives the best unbiased estimate. State the reasons for your choice.
- e) Estimate the phenotypic variance σ_p^2 .
- f) How high is the heritability (h^2) for tenderness in this data set?
- g) The taste of the meat has also been estimated in the same material. The following variance and covariance components were calculated:

Taste: $\sigma_{\bar{s}}^2 = 0.40$; $\sigma_{\bar{d}}^2 = 0.50$; $\sigma_{\bar{e}}^2 = 1.20$

Tenderness – taste: $\sigma_{\bar{s}\bar{s}} = 0.06$; $\sigma_{\bar{d}\bar{d}} = 0.09$; $\sigma_{\bar{e}\bar{e}} = 0.50$

Calculate the genetic and the phenotypic correlation between the two traits tenderness and taste.

8. The daily weight gain and the height at withers have been recorded on 527 young bulls, which make equal groups of half-sibs from 31 sires. In the variance/covariance analysis the following mean squares and mean products have been calculated.

Source of variation	d.f.	Mean square (MS)		MCP
		Weight gain	Height at withers	Weight gain x Height at withers
Between sires	30	0.0187	3097.2	3.1978
Within sires	526	0.0110	1258.5	1.1746

- Calculate the statistical variance and covariance components.
- Estimate the additive genetic variance for the two traits respectively (σ_A^2 and σ_A^2) and the additive genetic covariance (σ_{AA}) between them.
- Estimate the environmental covariance (σ_{EE}) and the phenotypic covariance (σ_{PP}) between the two traits.
- What is the association between the three biological covariance components?
- Calculate the genetic correlation between daily weight gain and height at withers. What conclusions could be drawn from the result?
- Calculate the phenotypic correlation between the two traits.
- Calculate the environmental correlation.

9. a) Which biological variance- and covariance components contribute to the phenotypic covariance between half-sibs? Explain the meaning of the components.
- b) Which of these components are assumed to be zero or negligible when we estimate σ_A^2 ?
10. Why do we estimate biological variance/covariance components in animal breeding, and what are the estimates used for?
11. When we estimate genetic variances most attention is often paid to the additive genetic variance (σ_A^2). Why?
12. What are the advantages of using data on half-sibs instead of parent – offspring when we estimate (σ_A^2)?