

SOLUTIONS TO EXERCISES FOR CHAPTER 11

Exercise 11.1.

It would appear that my derivation of equation (11.27) is correct. With the assumption that all loci contributed equally, maybe Wright assumed that the difference, $\mu_1 - \mu_0$, was that for a single locus and was the same for all loci, i.e., $\mu_1 - \mu_0 = \mu_{1k} - \mu_{0k}$, for $k = 1, \dots, n$. Then the difference summed over all loci would be $n(\mu_1 - \mu_0)$ and the expression for the genotypic variance would be

$$\begin{aligned} \sigma_{G(F)}^2 &= (1-F)\sigma_{G(0)}^2 + F\sigma_{G(1)}^2 + F(1-F) \left[\frac{[n(\mu_1 - \mu_0)]^2}{n} \right] \\ &= (1-F)\sigma_{G(0)}^2 + F\sigma_{G(1)}^2 + F(1-F)n(\mu_1 - \mu_0)^2 \end{aligned}$$

But even with these redefinitions of μ_1 and μ_0 , Wright would have omitted an n in the $F(1-F)(\mu_1 - \mu_0)^2$ term.

Exercise 11.2.

The parameters are (see p. 11.8):

$\sigma_A^2 = 2 \sum_{i=1}^m p_i \alpha_i^2$ equals twice the variance of the average effects of the m alleles in the original reference population,

$\sigma_D^2 = \sum_{i=1}^m \sum_{j=1}^m p_i p_j \delta_{ij}^2$ equals the variance of the dominance effects in the original reference population,

$D_1 = \text{cov}(\alpha_i, \delta_{ii})$ equals the covariance between the additive effects of the m alleles and the corresponding dominance deviations of the homozygotes,

$$= \sum_{i=1}^m p_i \alpha_i \delta_{ii}$$

$D_2 = \sigma_{\delta_{ii}}^2 = \sum_{i=1}^m p_i \delta_{ii}^2 - (\sum p_i \delta_{ii})^2$ equals the variance of the dominance deviations of the homozygotes,

$h = \sum_{i=1}^m p_i \delta_{ii} = \mu_1 - \mu_0$ equals total inbreeding effect.

Exercise 11.3.

The sum of the effects associated with the homozygous genotypes weighted by their allelic frequencies is equal to the total inbreeding depression [see equation (11.3)].

Exercise 11.4.

Identity by descent has been used in the following places:

- 1) used to measure the degree of relationship between relatives involving two-gene, three-gene, and four-gene states of identity for autosomal loci (Sections 4.1 to 4.11A, pp. 4.1 to 4.131),
- 2) used to measure the degree of relationship between relatives involving two-gene states of identity for X-linked loci (Section 4.12, pp. 4.131 to 4.140),
- 3) used to define descent measures for two loci (Section 4.11A, pp. 4.115 to 4.131),

- 4) genotypic composition of a partial inbred population in equilibrium [Chapter 5, equation (5.9)],
- 5) derivation of general expression for the covariance between relatives [Chapter 9, equation (9.63) for a single locus, equation (9.143) for two loci with epistasis, equation (9.144) for any number of loci],
- 6) derivation of the population mean of any arbitrarily inbred population [Chapter 11, equations (11.1) and (11.2)],
- 7) derivation of genotypic variance for any arbitrarily inbred population [Chapter 11, equations (11.4) and (11.15)].

Exercise 11.5.

The linear regression coefficient is calculated as follows (see Steel, R.G.D., J. H. Torrie, and D. A. Dickey, 1997, Principles and Procedures of Statistics: A Biometrical Approach. Third edition, McGraw-Hill, NY, p. 256):

$$b = \frac{\sum XY - \frac{(\sum X)(\sum Y)}{n}}{\sum X^2 - \frac{(\sum X)^2}{n}}$$

$$= \frac{4,069,958 - \frac{(8248)(9145)}{19}}{3,730,463 - \frac{(8249)^2}{19}} = \frac{90,584.05}{149,094.53} = 0.608$$

The regression coefficient is less than one because the measurements of seed weight of the parents in 1901 are influenced by the environment, including genotype \times environmental effects. The presence of an environmental effect in the offspring has no influence on the expectation of the regression coefficient—only that in the parents has an effect. The number of offspring individuals observed per line is unknown, but it is unimportant in that it has no influence on the expected value of b . The environmental effect in the offspring does influence the variability of the estimate of the regression coefficient or the standard error of the regression coefficient.

Exercise 11.6.

a. The main criticism of Figure 22.14a in Russell's book is that for $b = h^2 = 1.0$ there should be no scatter of points about the regression line. All points should lie on the regression line. The genetic variance consists entirely of additive genetic variance, and there is no environmental variance. The only source of variation is the additive genetic variance. The wording which discusses Figure 22.14a should be changed to: When the true slope of the parent-offspring regression is 1, as in Figure 22.14a, the true mean offspring phenotype is exactly equal to the mean of the phenotype of the two parents, and genes with additive effects determine all the phenotypic differences.

b. The main criticism of the statement is that it implies that all of the effects, additive genes, genes with dominance, genes with epistasis, and environmental factors are required to account for the intermediate heritability value. Actually only additive genes with environment factors may account for the intermediate heritability value. I would change the last "and" to "and/or".

c. I think that Russell infers "Mean parent wing length" to be the "Mean wing length of two parents" in his whole discussion, but the latter would be clearer. The proper interpretation of the diagrams depends entirely upon the X axis being the mean of the two parents rather than the mean of the two wing lengths of a single parent.