Errata for the first edition of *Population Genetics*

Last updated: January 04, 2024

Chapter 2

p. 21, line 14 from bottom in right column – should read "it still does not"

p. 24, line 8 in right column – should read "expected number of events"

p. 25, equation 2.8 – should read $\chi^2 = \frac{(-21.6)^2}{186.61} + \frac{(43.2)^2}{518.80} + \frac{(-21.6)^2}{360.58} = 7.39$

p. 27, line 2 from bottom in left column – should read "fa = $\sqrt{fa^2} = \sqrt{0.5}$"

p. 27, Table 2.7, line for O blood group under hypothesis 1 – observed - expected should read -32.02 and (observed – expected)^2/expected should read 5.70.

p. 28, line 12 in the left column – should read $\chi^2 = 40.32$.

p. 32, caption for Figure 2.11 – cathode and anode should be interchanged.

p. 33, Figure 2.12 – see corrected version of figure below.

p. 35, caption for Figure 2.13 – recursion equations should read $f_{t+1} = ½(1+F_t)$ for selfing and $f_{t+1} = ½(1+F_t)(s)$ for mixed mating.

p. 36, equation 2.19 – f_A should read F_A.

p. 37, line 17 from bottom in right column – delete "be."

p. 43, last two lines – ρ^2 ranges between 0 and +1 while ρ is a correlation and has a range of -1 to +1.

p. 51, answer for Problem box 2.1- The expected genotype frequency for the D5S818 locus is 2(0.3538)(0.1462) = 0.1035. The resulting ten locus genotype expected frequency is 1.210 x 10^{-12} and an odds ratio of one in 826,551,506,311.

Chapter 3

p. 56, Figure 3.3 and its caption – should read 2N = 4 and 2N = 20.

p. 60, Figure 3.5 caption – should read 2N = 4 and 2N = 20.

p. 61, Figure 3.7 caption – should read 2N = 20.

p. 62 - equation 3.13 should read $P_{i\to j} = \binom{2N}{j} p^j q^{2N-j}$.

p. 64, line 2 in Figure 3.10 caption – should read 2N = 4.

p. 65, last line in right column – should read "it is possible."

p. 69, equation 3.22 should read $x^2_{i(t=1)} = x^2_{i(t=0)} + 2x_{i(t=0)}\delta + \delta^2$

p. 69, equation 3.23 should read $\sigma^2(x_{i(t=1)}) = \frac{1}{N}\sum_{i=1}^{N} x^2_{i(t=0)} + 2x_{i(t=0)}\delta + \delta^2$

p. 90, line 10 in right column – should read "20 generations" rather than 30 generations.

p. 97, line 1 in right column – should be reference to Figure 3.23.

p. 97, line 28 in right column – should read equation 3.79 rather than equation 3.63.

p. 98, equation 3.86 - should read $P_{NC} \approx e^{-\frac{t}{2N_e}} = e^{(-\frac{1}{2N_{e(t=1)}})+(-\frac{1}{2N_{e(t=2)}})+(-\frac{1}{2N_{e(t=3)}})}$

p. 101, line five in Chapter 3 review – should read "chance."

p. 104, the solution for Problem Box 3.4 should read

$H_{t=1}$	$H_{t=4}$	$\ln(H_{t=4}/H_{t=1})$	N_e^i
0.50	0.4505	-0.1044	14.4
0.50	0.4594	-0.0847	17.7
0.50	0.3474	-0.3641	4.1
0.50	0.4376	-0.1332	11.3
0.50	0.3773	-0.2816	5.3
0.50	0.4999	-0.0001	10415.9
0.50	0.4566	-0.0908	16.5
0.50	0.4857	-0.0291	51.5
0.50	0.3577	-0.3348	4.5
0.50	0.4551	-0.0942	15.9

The average of N_e^i is 1055.7 with all replicates and 15.7 without the sixth replicate. The expressions should be $ln(\frac{H_{t=4}}{H_{t=1}})$ and $N_e^i = \frac{1}{2}\frac{3}{ln(\frac{H_{t=4}}{H_{t=1}})}$.

Chapter 4

p. 107, line 29 – should read "individuals."

p. 119, line 7 in right column - $\hat{H}$ should read $\overline{H}$.

p. 120, caption for Figure 4.6 – H_I in line 4 should read H_I; there is an extra left parenthesis in the equation in line 9 so the equation should read H_S = ½[2(0.65)(0.35) + 2(0.35)(0.65)] = 0.455

p. 121, Table 4.6 – should read $F_{IS} = \frac{H_S - H_I}{H_S}$ without a bar over H_I.

p. 127, bottom of left column – equation 4.30 should read $Freq(AA)_S = p_2 +$ var(p) and equation 4.31 should read $Freq(aa)_S = q_2 +$ var(q) where S refers to subpopulations. The sentence above the equations should read "...expected frequencies of homozygote genotypes in subpopulations are..."

p. 127, line 8 in top of right column – should read "...expected genotype frequencies in the subpopulations..."

p. 129, equation 4.36 should read $\text{var}(q) = \frac{(0.4 - 0.2)^2 + (0.0 - 0.2)^2}{2} = 0.08$. The incorrect version as printed is a sampling variance while the correct version above is a parametric variance as explained in the appendix. See correct version in Table 4.7.

p. 137, lines 1-7 – should read "We can also see this by noting that $2m(1\text{-}m)$ genotypes heterozygous and m^2 genotypes homozygous for alleles entering the subpopulation by gene flow are expected each generation. Together, these two classes of genotypes bearing alleles that entered the population by gene flow reduce the autozygosity by a factor of $1 - 2m(1\text{-}m) - m^2 = 1 - 2m + 2m^2 - m^2 = (1- m)^2$."

p. 138, equation 4.59 should read $F_{eq} = \frac{\frac{1}{2N_e}(1-m)^2}{1-(1-\frac{1}{2N_e})(1-m)^2}$

p. 145, line 14 in right column – should read Figure 4.17 rather than Figure 4.18.

Chapter 5

p. 177, bottom of left column – should read "From the opposite perspective, noting that $2\mu(1-\mu)$ genotypes heterozygous and μ^2 genotypes homozygous for a new mutation are expected each generation. Together, these two classes of genotypes with mutations reduce the autozygosity by a factor of $1 - 2\mu(1-\mu) - \mu^2 = (1-\mu)^2$."

Chapter 6

p. 190, equation 6.11 – the rightmost genotype should read aa : q^2N_t.

p. 191, equation 6.12 – the rightmost genotype should read aa : $\ell_{aa}q^2N_t$.

p. 192, Table 6.3 – the average fitness should read $p_t^2w_{AA} + 2p_tq_tw_{Aa} + q_t^2w_{aa}$.

p. 204, between equations 6.50 and 6.51 – should read "…substituting in the expression for $\overline{w}'$ from equation 6.49 gives…"

Chapter 7

p. 209, Figure 7.1 – the apex labels for "Frequency of Aa" and "Frequency of aa" should be switched.

p. 212-213, equation 7.6 – should have a minus sign inside the rightmost term of the numerator so that $x_{1(t+1)} = \dfrac{x_1(w_{11}x_1 + w_{12}x_2 + w_{13}x_3 + w_{14}x_4) - r(w_{14}x_1x_4 - w_{23}x_2x_3)}{\overline{w}}$. This change of sign then changes the text on p. 213 to "Applying this assumption to equation 7.6, we can $w_{14} = w_{23}$ and then the $r(w_{14}x_1x_4 - w_{23}x_2x_3)$ term becomes $rw_{14}(x_1x_4 - x_2x_3)$ to give $x_{1(t+1)} = \dfrac{x_1(w_{11}x_1 + w_{12}x_2 + w_{13}x_3 + w_{14}x_4) - rw_{14}(x_1x_4 - x_2x_3)}{\overline{w}}$." as well as "We can then substitute D for $x_1x_4 - x_2x_3$ in equation 7.7…"

p. 221, equation 7.31 should read $N_{t+1} = \overline{\lambda}N_t$.

p. 221, caption for Figure 7.6 – $K_{AA} = 8000$ should read $K_{aa} = 8000$.

Chapter 8

p. 250, equation 8.31 – sum should be taken over all i,j to read

$$\hat{\pi} = \frac{k}{k-1}\sum_{i=1}^{k}\sum_{j=1}^{k}p_ip_jd_{ij}$$

p. 261, equation 8.50 – should have a minus sign in the numerator to read

$$\chi^2 = \frac{(n_{ijj} - n_{iji})^2}{n_{ijj} + n_{iji}}$$

p. 268, Table 8.6 – the number of nonsynonymous and synonymous changes at fixed and polymorphic sites have been switched in case (c). The table should read 7 nonsynonymous and 17 synonymous changes at with a ratio of 0.412 fixed sites and 2 nonsynonymous and 42 synonymous changes with a ratio of 0.048 at polymorphic sites.

p. 280 – only the text and paper references should be indented rather than all of the text.

Chapter 9

p. 284, Figure 9.1 – The coefficient of variation (CV) values should read 4.87, 17.86, 20.68 and 11.23 (starting at top left and working clockwise).

p. 304 – 11 lines down in the first full paragraph on the right column, the sentence "The diagonal elements in a *G* matrix are simply the narrow-sense heritabilities for each trait." Should read "The diagonal elements in a *G* matrix are simply the additive genetic variances for each trait."

p. 305 – The definition box should read "***G* matrix** The genetic additive variance/covariance matrix that expresses the additive genetic variance of each trait (the diagonal elements) as well as the genetic covariance between all pairs of traits (the off-diagonal elements)."

p. 318 – in Table 9.5 the row under "Marker-class contribution of F2 population mean value" for the M_1M_2 marker genotype should read $\overline{G}^{pop}_{M_1M_2}$.

Chapter 10

p. 351, Figure 10.6 – In the general case (a), the figure should read "bilineal" rather than "bilinear" and "unilineal" rather than "unilinear."

Chapter 11

p. 361, middle of right column – should refer to equation 11.5 rather than equation 11.6.

p. 362, equation 11.16 should read "If each locus is completely independent then the mean fitness for the entire genome is $\overline{w} = [1- (0.3)(0.1)]^{3000} = (0.97)^{3000} = 2.04 \times 10^{-40}$ and the segregational load is $L = 1 - 2.04 \times 10^{-40}$ which is nearly its maximum value."

Corrected version of Figure 2.12