

Errata for first printing of *Population Genetics*

Last updated: February 13, 2012

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 “ $f_a = \sqrt{fa} = \sqrt{0.5}$ ”
- 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. 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 1.210×10^{-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 $P_{i \rightarrow j} = \binom{2N}{j} p^j q^{2N-j}$.
- 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. 69, equation 3.24 should read $\sigma^2(x_{i(t=1)}) = \overline{x^2_{i(t=0)}} + \delta^2$ with x-squared bar rather than x-bar squared. Similarly, three lines down in the right hand column the expression should read $\overline{x^2_{i(t=0)}} = 0$.
- 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. 101, line five in Chapter 3 review – should read “chance.”

p. 104, Problem Box 3.4 answer – the heading of the third column should read $\ln\left(\frac{H_{t=4}}{H_{t=1}}\right)$

and the heading of the fourth column should read $\hat{N}_e^i = -\frac{1}{2} \frac{3}{\ln\left(\frac{H_{t=4}}{H_{t=1}}\right)}$. The estimates of N_e

in the fourth column should read (top to bottom) 14.39, 17.71, 4.12, 11.25, 5.32, 7499.25, 16.52, 51.33, 4.48, and 15.90 with a mean of 764.03 for all 10 estimates or a mean of 15.67 excluding the sixth replicate.

Chapter 4

p. 107, line 29 – should read “individuals.”

p. 119, line 7 in left column - \hat{H} should read \bar{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 $H_S = \frac{1}{2}[2(0.65)(0.35) + 2(0.35)(0.65)] = 0.455$

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 $Freq(AA)_S = \bar{p}^2 + \text{var}(p)$ and equation 4.31 should read $Freq(aa)_S = \bar{q}^2 + \text{var}(q)$ 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 $\text{var}(q) = \frac{(0.4 - 0.2)^2 + (0.0 - 0.2)^2}{2} = 0.04$. 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. 138, equation 4.59 should read $F_{eq} = \frac{\frac{1}{2N_e}(1-m)^2}{1 - \left(1 - \frac{1}{2N_e}\right)(1-m)^2}$

p. 139, lines 1-7 – should read “We can also see this by noting that $2m(1-m)$ 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 $1 - 2m(1-m) - m^2 = 1 - 2m + 2m^2 - m^2 = (1 - m)^2$.”

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 $aa : q^2 N_t$.
- p. 191, equation 6.12 – the rightmost genotype should read $aa : \ell_{aa} q^2 N_t$.
- p. 204, between equations 6.50 and 6.51 – should read “...substituting in the expression for \bar{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 $x_{1(t+1)} = \frac{x_1(w_{11}x_1 + w_{12}x_2 + w_{13}x_3 + w_{14}x_4) - r(w_{14}x_1x_4 - w_{23}x_2x_3)}{\bar{w}}$. This sign change then changes the text on p. 213 to “Applying this assumption to equation 7.6, we can set $w_{14} = w_{23}$ 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 $x_{1(t+1)} = \frac{x_1(w_{11}x_1 + w_{12}x_2 + w_{13}x_3 + w_{14}x_4) - rw_{14}(x_1x_4 - x_2x_3)}{\bar{w}}$.” 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 $N_{t+1} = \bar{\lambda} N_t$.
- p. 221, caption for Figure 7.6 – $K_{AA} = 8000$ should read $K_{aa} = 8000$.

Chapter 8

- 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. 318 – the row under “Marker-class contribution of F2 population mean value” should read $\bar{G}_{M_1M_2}^{pop}$.

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 $\bar{w} = [1 - (0.3)(0.1)]^{3000} = (0.97)^{3000} = 2.04 \times 10^{-40}$ ”

and the segregational load is

$$L = 1 - 2.04 \times 10^{-40}$$

which is nearly its maximum value.”

Corrected version of Figure 2.12

