1(a) df= 10 + (13 - 1) - 2 = 20 since one zero is dropped in the second sample. With a 2-sided test .02 < p < .05 and we conclude that the two groups have different variances (reject “σ₁ = σ₂”).

(b) Using the t-test that does not require equal variance we get
\[ s^2_{y_1 - y_2} = \frac{8.06^2 + 2.05^2}{13} = 6.82 \text{ and } t = (90.20 - 86.65)/\sqrt{6.82} = 1.398. \]
Using df= 9 and a 2-sided test we get .10 < p < .20. We fail to reject “μ₁ = μ₂”: there is no significant difference between the average size of the two Lyrebird species.

2(a) the Mann-Whitney test p-value is 0.028 because the ranks do not change. The t-test p-value is smaller than 0.006 because only \( y_1 - y_2 \) changes (increases). Sample sizes (4) and variability (\( s_1 \) and \( s_2 \)) stay the same. So t increases and the p-value decreases.

(b) Data set 3 (top). Since the ranks are the same in data set 3 and in data set 1, the p-value from Mann-Whitney test is 0.028, which is < .05. With data set 4 the rank sums would be 23 and 13, and 13 is too small, by 86 p < 0.05 level (the table says we need 10 or less). Note: data set 3 returns \( \hat{p}_A = 220/220 = 1 \) and data set 4 also returns \( \hat{p}_A = 80/80 = 1 \) with a t-test because the variability in sample “b” is large. Data set 4 also returns \( p > .05 \) with a t-test because the difference in sample means is small.

(c) For data set 3, Mann-Whitney test would be most appropriate, because we are not sure the data are normally distributed (presence of an ‘outlier’ in sample “b”) and the sample size in each sample is small (4). For data set 4, a t-test would be most appropriate, because the normal distribution seems appropriate in each sample and the t-test is more powerful than Mann-Whitney test when both can be used.

3(a) Smaller with a one-sided test in the correct direction. The formula for \( n \) is \( \sigma^2 (z_{\alpha/2} + z_{\beta})^2 / (\mu_0 - \mu_a)^2 \) for a 2-sided test, while we replace \( z_{\alpha/2} = z_{0.05} = 1.65 \) by \( z_{0.3} = 1.88 \) for a one-sided test. \( z_{\alpha} \) being smaller, \( n \) is also smaller for a one-sided test.

(b) Using \( n = \sigma^2 (z_{\alpha/2} + z_{\beta})^2 / (\mu_0 - \mu_a)^2 \) we get \( 25 = 104 * (2.17 + 1.65)^2 / (0.5 - 0.2)^2 \) i.e. \( z_{\beta} = \sqrt{6.01} - 2.17 = 0.281 \) and with Table A \( \beta = .3897 \) so the power is 61%. One can get the same result by determining the rejection region: outside \( 0 \pm 2.17 * \sqrt{104/25} = \pm 4.426 \). Then the power is \( P\{Z < -9.426/2.04\} + P\{Z > -0.574/2.04\} = 0 + P\{Z > -0.281\} = 1 - 0.3897 = 0.61. \)

4(a) \( \hat{p}_A = 63/220 = .2864, \hat{p}_C = 59/80 = .7375 \) and \( \hat{p} = (63 + 59)/300 = .4067 \). We can approximate the binomial with a normal distribution because 220 * \( \hat{p} = 41.3 > 5 \) and 220 * \( \hat{q} = 178.7 > 5 \) and similarly 80 * \( \hat{p} = 37.4 > 5 \) and 80 * \( \hat{q} > 5 \). Then \( z = (.7375 - .2864)/\sqrt{.4067 * .5933 * (1/220 + 1/80)} = 7.034. \) Using the normal distribution we get \( p < 2 * 2.9 * 10^{-7} \) is way smaller than .0001 and way smaller than \( \alpha = .10 \).

We strongly reject \( p_A = p_C: \) there is strong evidence that the locus is linked to some genetic region affecting flowering time, the C allele being linked to early flowering. Assumptions include random sampling of and independence among plants.

(b) Observations are clearly paired: each leaf observation is paired to the root observation made on the same plant. Therefore, one would use a two-sided paired-sample t-test, provided that the distribution of difference (leaf expression -root expression) is not too far from a normal distribution. Note: there is no need to assume that \( \sigma_1 = \sigma_2 \) and no need to assume normality of gene expression. Only the normality of the expression difference is needed.

5(a) FALSE: we mostly use a t-distribution. The normal distribution is only used when the variance is known. TRUE
TRUE because z-quantiles are smaller than t-quantiles.
FALSE: the confidence interval is centered at the sample mean (\( \bar{y} \), which is random) while the not-rejection region is centered at the null hypothesis \( \mu_0 \) (not random - known before collecting the data)
TRUE
TRUE: they both have the same length, which is twice
\( z_{\alpha/2} * \sigma / \sqrt{n}. \)

Summary of grades: