Math 5233: Measures of genetic diversity and Tajima's D-test

Due 4/29. Group members (1 to 3):

- (0) Consider the following five sequences of bases at six segregating sites (S = 6 in a genetic sample.)
- (1) Calculate the genetic diversity parameter $\pi = (\sum_{i < j} k_{ij}) / {n \choose 2}$ for this sample.

 $(n = 5 \text{ is the number of samples}, k_{ij} \text{ is the number of differences between sequence } i$ and sequence j.)

(2) Calculate the site-frequency spectra η_i , where η_i is the number of sites with *i* copies of one base and n - i copies of another base. (For this example $i \in \{1, 2\}$.)

(3) Find a formula for the parameter π in terms of the η_i rather than the k_{ij} . (Hint: think about the contribution to π from each column, rather than from two rows.) Doublecheck your formula by using it to calculate π for the above example.

(4) (Optional) Tajima's *D*-test is a widely used statistical test for the null hypothesis that sites evolve neutrally in a constant-size population. Under the null hypothesis, the expected value of the two quantities π and S/a_1 should be equal, where

$$a_1 = \sum_{i=1}^{n-1} \frac{1}{i}.$$

If the null hypothesis were true, we would expect that the coefficient of variation of $d = \pi - S/a_1$ would be small, usually between 0 and 1. Tajima's *D*-test studies a signed version of the coefficient of variation, denoted *D*:

$$D = \frac{d}{Var(d)} = \frac{\pi - \frac{S}{a_1}}{e_1 S + e_2 S(S - 1)}$$

where $a_2 = \sum_{i=1}^{n-1} \frac{1}{i^2}$ and
 $e_1 = \frac{c_1}{a_1} \quad e_2 = \frac{c_2}{a_1^2 + a_2}$

in which

$$c_1 = b_1 - \frac{1}{a_1}$$
 $c_2 = b_2 - \frac{n+2}{a_1n} + \frac{a_2}{a_1^2}$

which in turn need

$$b_1 = \frac{n+1}{2(n-1)}$$
 $b_2 = \frac{2(n^2+n+3)}{9n(n-1)}$

If D is not between -2 and 2, it constitutes strong evidence that the null hypothesis is false.

In order to boast to any population geneticists that you ever meet that you have calculated D by hand, calculate D for the example on the previous page.