Molecular Population Genetics (Two-locus Wahlund Effect)

Lab Assignment 4 (due 8 October, 2014) – email me this sheet along with script

Your Name:

In this assignment you will examine how linkage disequilibrium between two loci can be created by population subdivision. This can happen when samples from two populations that differ in allele frequencies at two loci are mistakenly treated as a single population. The disequilibrium (i.e. D ≠ 0) occurs even if the two populations are themselves in equilibrium (i.e. D for popn. 1 and D for popn. 2 = 0).

1. Write a script that assigns allele frequencies to two loci in two separate populations. Write the script so that the user can enter the allele frequencies.

2. Using those allele frequencies, randomly sample 40 two-locus haplotypes from each of the two populations.

Report the allele and haplotype frequencies in each of the two populations.

Report the coefficients of LD (D, D', and r2) in each of the two populations.

3. Mix all of the samples from the two populations together. Calculate the coefficients of LD on this population sample. Compare to the single population estimates.

4. Depict using a graph(s) how LD changes with varying differences in allele frequencies between the two populations, from the most extreme in which both loci are fixed for different alleles in the two populations to a situation in which allele frequencies are identical in the two populations.

5. Does changing the sample size (e.g. sampling 1000 instead of 40 two-locus haplotypes) have an effect?