

Population Genetics Problem Set 8

1. For zoo animals, a minimum captive population size of 50 individuals is sometimes recommended. For a population of this size, how much of the current generation's heterozygosity will be lost in the next generation due to drift?

Answer: $H_{t+1} = (1 - (1/(2N))) \times H_t = (1 - 1/(2 \times 50)) H_t = (1 - 0.01) H_t = 0.99 H_t$
 Since .99 of heterozygosity is retained each generation, **.01 or 1%** of any remaining heterozygosity is lost due to drift each generation.

2. What is the expected number of effective alleles under neutrality?

number of effective alleles = $\theta + 1$ (theta plus one), where $\theta = 4N_e u$
 N_e is the effective population size and u (mu) is the mutation rate. (Remember the number of effective alleles is not the same thing as the effective population size.)

3. How would inbreeding or dominance affect the mutation-selection balance for a deleterious allele?

Inbreeding would reduce the equilibrium frequency of deleterious recessive alleles since relatively more of them would be in a homozygote state, confer the deleterious phenotypes and thus be subject to purifying selection (purging).

Dominance would reduce the equilibrium frequency of deleterious alleles since both homozygote and (due to dominance) heterozygotes would confer the deleterious phenotypes and thus be subject to purifying selection.

4. What is the difference between orthologous and paralogous genes?

Orthologous genes are separated by a speciation event (eg, most single copy genes in humans will also be found as a single copy gene in the chimpanzee).
 Paralogous genes are separated by a duplication event (eg, the genes encoding myoglobin and hemoglobin descend from duplication of an ancestral gene).

5. Give the best definition for the following terms:

a. Monoecious: plants with male and female reproductive organs on the same individual

b. Infinite allele model: assumes that every new mutation does not match any previous mutation (and is thus a novel allele). Model is used to examine the balance between the creation of new alleles by mutation and the elimination of alleles by drift

c. Relative rate test: determines if different lineages are evolving at the same pace

d. Molecular clock: Loci for which there is a constant rate of substitution, equal to the mutation rate, and constant over time; and can thus be used to estimate divergence times between taxa.

- e. Gene flow: the transfer of alleles of genes from one population to another.
- f. Continent-island model of migration: **unidirectional** gene flow due to migration. Allele frequencies shift only on the “island” towards that of the migrants.
- g. General model of migration: A population is divided into k subpopulations, with gene flow possible in all directions for all subpopulations. Allele frequencies shift towards a common frequency.
- h. Wahlund effect: subpopulation structure leads to reduction in overall heterozygosity, even if the subpopulations themselves are in Hardy-Weinberg equilibrium.
- i. Admixture: the proportion of gene flow from an outside population.
- j. Metapopulation: subpopulations in discrete habitat patches, that turnover with extinction and recolonization from other patches. The newly colonized patches may display the results of founder effects.
- k. Cline: a directional change in allele frequencies across (geographic) space or between subpopulations (or between species), potentially due to selection or substructure. May be stable or transient.
- l. Coalescence: the point at which common ancestry for two alleles occurs

6. What are the similarities and differences between Kimura's Neutral Theory and Ohta's Nearly Neutral Model?

Both theories argue that genetic variation is primarily influenced by mutation generating largely neutral variation and genetic drift eliminating it. The “Nearly Neutral” model also recognizes that variants subject to selection are effectively neutral when the selection coefficient $s < 1/(2N)$. Thus in a large population fewer loci are effectively neutral than in a small one, and selection plays a larger role in large populations while drift plays a larger role in small populations.

7. What are the three F coefficients of Wright?

F_{ST} : “Fixation index,” genetic differentiation over subpopulations. Always positive. Measures the degree of genetic variation that is due to the differences between two (or more) subpopulations.

F_{IS} : Deviation from Hardy-Weinberg proportions within subpopulations. Positive if excess of homozygotes; negative if deficiency of homozygotes.

F_{IT} : Deviation from Hardy-Weinberg proportions in the total population. Positive if excess of homozygotes; negative if deficiency of homozygotes.

8. What are the similarities and differences between the stepping-stone model of gene flow, and isolation by distance?

The stepping-stone model assumes gene flow occurs spatially in one dimension between separated populations; by contrast, isolation by distance can occur across continuous habitat and in two dimensions. Both are similar in generating distance-dependent gene flow, in which subpopulations separated by greater geographic distance also tend to display greater genetic distance (due to limited gene flow).

9. Describe 5 tests of selection (or neutrality)

1. Ewens-Watterson test: compares homozygosity under HWE to that expected under Neutral Theory.
2. Tajima's D: calculates theta using nucleotide diversity and also using segregating sites; the two estimates should be similar under neutrality
3. Hudson-Kreitman-Aguade test: compares within- and between-species variation; they should be similar under neutrality
4. McDonald-Kreitman test: Compares the synonymous to non-synonymous ratio in differences fixed between species to the ratio in polymorphisms within species. Under neutrality, the ratios should be similar.
5. Non-synonymous vs. silent substitutions: within species, are used to identify purifying and Darwinian selection. Non-synonymous will be less common after purifying selection, but more common after Darwinian selection.