Genome evolution 09 – Ex 1   Due: April 28

Work independently, or in pairs. You can use any available resource (books, papers, the web), but please cite what you use.

1. In a model of selection you assume two alleles A and a and fitness f(AA) = 1, f(Aa) = 1+s, f(aa) = 1, s>0. What would be the equilibrium allele frequency (the allele frequency after sufficiently many generations)? Assume an infinite population.

2. For an Ashkenazi population, the incidence of death at birth due to Tye-Sachs was measured to be 1 out of 6000, compared to other groups where it was 1 in 500,000 births. What incidence of Tay-Sachs is expected when mating two random individuals of the two populations? What would be the incidence when mating offsprings of this first inter-breeding generation?

3. To achieve some novel function for a protein, we need two mutations. Assume that the first mutation has no fitness effect and the second mutation has relative fitness 1+s. We argued that the **substitution** rate for a mutation with fitness 1+s is approximately 4Nsµ. Discuss qualitatively how the substitution rate can be approximated in our case. You can assume mutations are very slow (so the population is homogenous).

4. We are using the Wright-Fischer model and defining the effective population size as the idealized size generating the sample variance observed in the real population. To remind you, sampling variance (sqrt(np(1-p))) is what drives the drift of allele frequencies in the population, and it is dependent on the population size n. A population is driven near extinction due to changes in the environment, decreasing in size from 2^16 to 1024 in 6 generations and than back to 2^16 in exponential growth (doubling each generation). Compute the effective population size using simulation (* optionally, you can try to prove the general formula of the harmonic mean we showed in class)

5. In the previous example, we now assume an allele A have selection coefficient s<0, and that s is very small. Would the intensity of purifying selection (probability of removal of the deleterious allele) be stronger, weaker, or unchanged due to the bottleneck scenario described in Q4. Support your conclusions using analytic computation or simulation.

Good luck!