Genome evolution – Ex 4

Solve 4 questions for 120 points. 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 are 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?

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. What is the minimal and maximal possible F fixation index? Give examples.

4. 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  $4Ns\mu$ . Discuss qualitatively how the substitution rate can be approximated in our case. You can assume mutations are very slow (so the population is homogenous).

5. A population is driven near extinction due to changes in the environment, decreasing in size from 1 million to 1000 in 10 generations and than back to 1 million in exponential growth (doubling each generation).

a. what is the effective population size?

b. qualitatively, what would be the effect of the bottleneck on heterozygosity? Selection? Linkage?

Good luck!