Biol4250 – Mutation / Selection equilibrium lab exercise   2021.10.21 smc

Mutation: Use the GSM / mutation worksheet to investigate the following scenarios.

1) Calculate $\hat{q}$ from the exact equation to **g = 2,000** generations:
   under what conditions to the exact and approximate solutions diverge?

2) Calculate H_{exp} for $\hat{q}$ in the table above (*Hint*: use **p = 1** as appropriate).
   What level of variation can mutation maintain in a population?
   What is the ratio of **f(AB) / f(BB)** at **g = 2,000** generations?
   What does this tell you about the effect on **population variation**
        of selection under recurrent mutation?

3) **Neutral Mutation Theory** suggests many mutations have **s << 0.01.**
   Calculate $\hat{q}$, where **s** varies over the same range as μ.

4) Suppose **myopia** is due to a recessive allele **B** at a single locus,
   with mutation rate $\mu = 10^{-5}$ from **A →B**.
   Suppose that myopia historically resulted in a selection coefficient **s = 0.3**,
        and that vision correction has now reduced selection by **90%**.
   a) What is the *former* vs the new $\hat{q}$ of the **B** allele?
   b) What is the *former* vs new equilibrium frequency of **persons with myopia** ?

Migration: Use the GSM / migration worksheet to investigate the following scenarios.

1) Explore the **migration as m** simulation for different values of **t** or **s**, and **m**. What levels
    of island population variation (measured as **f(AB)** and (or) **f(BB)**) can be maintained for
    mildly, moderately, or severely deleterious alleles over a range of migration rates **m =
    0.001, 0.01, & 0.1.** Compare this with the approximation solution for **m** vs **s**.

2) Lake Erie Water Snakes (*Nerodia sipedon insularum*) are distributed on interconnected islands in Lake
    Erie. Migration rates m between islands and the Ohio & Ontario mainlands are roughly proportional to
    distance. Genotype and allele frequencies may be estimated from observed frequencies of Banded
    (**BB**), Un-banded (**AA**), and Intermediate (**AB**) patterns, corresponding to pattern classes in Ehrlich &
    Raven (1958) of **A**, **B+C**, and **D** respectively.
    1) Estimate phenotype proportions to the closest 10% from Ehrlich & Raven. Taking these as genotype
        frequencies, calculate f(B) for Kelly's Is, Bass Is, and Pelee Is.
    2) *Hypothesize* patterns of interconnectedness and migration rates in the **four-island model** of the
        Migration worksheet. [It may be convenient to disregard the source population **qs** and use only **q1
        q2 q3** & **q4.**
            a.   What patterns are produced?
            b.   Which most closely approximates the observed patterns?