

Question. Contrast the definitions of Malthusian fitness and Darwinian fitness. Compare their solutions under a simple selection pressure.

Answer. Suppose that in a haploid, one locus, two allele model, we have the alleles A and a occurring proportions q_A and $q_a = 1 - q_A$, respectively.

In the Malthusian model, fitness of allele A is described the value F_A , the expected number of offspring per individual with allele A . Therefore, the total number of individuals with allele A can be modeled as

$$\dot{N}_A = F_A N_A$$

and the proportion of individuals with allele A , q_A , evolves according to the continuous time described by

$$\frac{dq_A}{dt} = \sigma q_A (1 - q_A)$$

where σ denotes the difference in the fitnesses of individuals with the A allele versus a allele, i.e. $\sigma = F_A - F_a$.

This implies that $q_A(t)$ evolves according to equation

$$q_A(t) = \frac{q_A(0)e^{\sigma t}}{1 - q_A(0) + q_A(0)e^{\sigma t}}$$

In contrast, the Darwinian model uses discrete time and with the mean fitness of the population being denoted by

$$\bar{w} = q_A w_A + q_a w_a$$

The mean frequency of A in the next generation is

$$q_A = \frac{w_A q_A}{\bar{w}}$$

If we consider the evolution of $q_A(t)$ under Malthusian fitness over a single unit of time, we have

$$q_A(t+1) = \frac{q_A(t)e^{\sigma}}{1 - q_A(t) + q_A(t)e^{\sigma}}$$

which is equivalent to the mean frequency given by Darwinian fitness assuming that $w_A = e^{\sigma}$ and $w_a = e^0 = 1$.

Note that in the lectures, Darwinian fitness is described using diploid genomes. This was adjusted for consistency with the Malthusian definition.