

**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  $\sigma$  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.