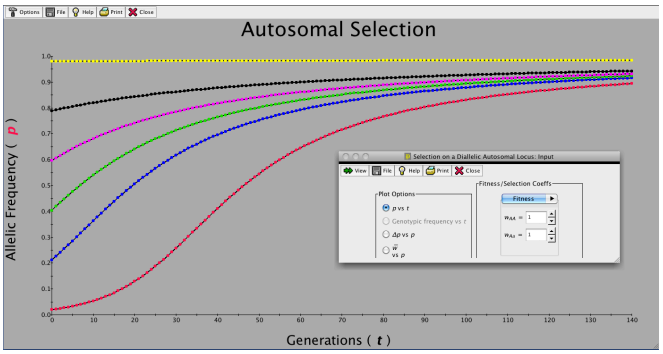
Name in Populas Model: Selection on a Dialleic autosomal locus

Mathematical Baisis for the model:

$$p_{t+1} = (p_t)\frac{p_t w_{AA} + q_t w_{Aa}}{p_t^2 w_{AA} + 2p_t q_t w_{Aa} + q_t^2 w_{aa}} \qquad (1)$$



p = frequency of the "A" allele in the population
q = 1-p = frequency of the "a" allele in the population
w_{AA} = the relative fitness of the AA phenotype
w_{Aa} = the relative fitness of the Aa phenotype
t= time
t+1 = time at one generation in the future from t

Here is a slightly more familiar form as it appears in most genetic texts:

Proportion of "A" allele remaining after selection.

Note: this = ½ $2p_tq_tw_{Aa}$

$$p_{t+1} = \frac{p_t^2 w_{AA} + p_t q_t w_{Aa}}{p_t^2 w_{AA} + 2p_t q_t w_{Aa} + q_t^2 w_{aa}} \qquad (2)$$

Frequency of the "A" allele in the next

Proportion of the total population remaining after selection ($\bar{w}$ or average fitness).

What does this model tell us?

Given that there are differences in fitnesses among genotypes allele frequencies will change until the population is at the highest (local) fitness. The rate of change is not constant and the amount of change from one generation to the next is dependent on the allele frequency. The amount of change between generations may be quantified by Δp:

$$\Delta p = p_{t+1} - p_t \qquad (3)$$

From formula #2 above and referring to the denominator as $\bar{w}$.

$$\Delta p = \frac{p_t^2 w_{AA} + p_t q_t w_{Aa}}{\bar{w}} - p_t = \frac{p_t^2 w_{AA} + p_t q_t w_{Aa} - p_t \bar{w}}{\bar{w}} \qquad (4)$$

$$\Delta p = \frac{pq[p(w_{AA} - w_{Aa}) + q(w_{Aa} - w_{aa})]}{\bar{w}} \qquad (5)$$

Amount of change is proportional to how much variation there is!

Also depends on how different the relative fitnesses (w) are from each other.

The direction of change depends on the differences in fitnesses and allele frequencies.