

INITIAL POPULATION CONTROLS

This section sets up an experiment's duration and number of replications, as well as the starting population structure.

EXPERIMENT DURATION & REPLICATIONS

Number of Generations (integer, 10–)

Determines the number of generations EVOLVE will run before displaying the graph of results. Start with 100 generations and adjust as needed (don't enter commas). There is no upper limit to the number of generations, but large values (above about 10,000) may result in long run times if there are many populations or a complex scenario.

Number of Populations (integer, 1–)

Running with more than 1 population allows you to replicate an experiment to get a feel for the sort of variations that can occur due to random variations in the course of evolution. A value of 10 is a good start; you can increase it if needed. Large values can increase run times, especially if you want to simulate very large population sizes (> 10,000) &/or many generations (> 1,000).

To study gene flow (migration), you must run multiple subpopulations.

INITIAL POPULATION STRUCTURE

Population Size (integer, 10–)

This value, along with the *Initial Allele Frequencies* or *Genotype Frequencies* determines the makeup of the first generation. If there are multiple subpopulations they are identical in the first generation.

EVOLVE sets no limit on the value you enter, but avoid values above 10,000 (at least at first) as they can result in very slow experimental runs.

This section sets up the starting population for all of the subpopulations in the experimental run.

Enter Allele Frequencies (ON/off)

If you want to set up a Hardy-Weinberg equilibrium population, leave the **Enter Allele Frequencies** Radio button checked and enter a frequency for the A allele; the frequency of the B allele is calculated for you. If you are simulating three alleles, you must enter a frequency for both A & B and the C allele will be calculated.

Enter Genotype Numbers (OFF/on)

If you wish to start with a non-equilibrium population, click the **Enter Genotype Numbers** radio button and enter specific integers for each genotype. They will need to add up to the *Population Size*. E.g., if you wish to see what happens to a single mutant A allele in a population of 100, enter 0 in the AA box, 1 in AB and 99 in BB (make sure the initial *Population Size* was set to 100).