

EXPERIMENT PARAMETER CONTROLS

These set up the problem with 'Lab Report' fields, and overall configuration of the experiment.

LAB REPORT FIELDS

The following text boxes provide space to think about the problem being studied and notes useful in preparing lab reports.

Title

This is used as label for graphs and exported files.

It's a good idea to label all experiments with abbreviated problem and important parameters. E.g.:

- “*Drift pop 250-500*” would indicate a study of genetic drift in populations of 250-500 individuals.
- “*Sel 4 Rec .716 .413 pop 2-10k*” would label results of an experiment selecting for a recessive allele averaging 70% survival and 6 offspring versus a dominant averaging 40% survival and 3 offspring.

Well trained scientists carefully write down an explicit question, think carefully about the design of their experiment, and make specific predictions about what they expect happen before doing an experiment.

Question

What is the fundamental question that is being asked? E.g.,

- “Do dominant alleles evolve faster than recessives?”, or more specifically,
- “Will a dominant allele increase in frequency faster than recessive alleles with the same phenotype?”

Experimental Design

Be specific about how you were designing your experiments. E.g.,

- “Compare two experiments: EXP. 1. Allele A dominant: AA & AB high fitness, BB lower fitness; initial A freq. = 0.01. EXP. 2: Allele A recessive: AA high fitness, AB & BB lower fitness; initial A freq. = 0.01.”

Predictions

It is important to be specific, e.g.,

- “A will reach freq. of 0.5 sooner in Exp. 1 than in Exp.2” or
- “A will reach a freq. of 1.0 sooner in Exp. 1 than in exp. 2.” or
- “B will become extinct sooner in Exp. 1 than in exp. 2.”

Results

Describe specific landmarks in the course of the experiment as if you were reading to someone over the phone. E.g.:

- “The A allele reached a freq. 0.5 in generation 20” or
- “The B allele became extinct in generation 83.”

Notes

These can be a reminder of mistakes you made, surprising results, additional questions suggested by the experiment, etc. E.g.,

- “I was surprised that ... because...”
- “Will incompletely dominant alleles behave more like dominants or like recessives?”

EVOLUTION SETUP FIELDS

These set up the basic simulation parameters.

Number of Alleles

Select either the 2 or 3 radio buttons; 2 is the default.

Most students will want to stay with 2. However, in the real world most genes have many more than 3 alleles. Students who wish to explore more complex evolutionary scenarios can try 3 alleles, e.g., to model evolution of the ABO blood groups.

Three alleles is slightly more realistic, but can require significantly longer run times and more inputs — 2 alleles produce 3 genotypes and 9 mating combinations, 3 produce 6 genotypes and 36 mating combinations.

Seed

A number will be automatically generated in this field. You may leave it alone or change it to another number of your choice.

The role of the 'seed' can be confusing. EVOLVE takes the seed Number and performs a series of mathematical operations to produce a series of "random" numbers that are used to, for example, randomly pick pairs of parents from the adult population, and let the survival rate vary slightly from the average values you enter. If you input 0.6 (60%) as the survival rate of a genotype, the rates used in 5 consecutive generations might be 61.8%, 66.3%, 53.9%, 57.5%, and 60.3%, for an average of 59.96%. If you use another seed, the 5 survival rates would be different, but would still average out to about 60%. This simulates processes such as variation in food supply or number of predators.

If you use the same seed in different experiments you can be sure that any variations in output are caused by changes in other variables. If you use different seeds with no change in other parameters, you can assess the influence of chance. In essence, this amounts to running the same experiment again with a slightly different ecology. Moreover, if you want to ask your instructor about a particular run, using the same seed and inputs will produce the same exact results.

Active Evolutionary Forces

These checkboxes determine which of the evolutionary forces are active. Unchecking boxes turns off those evolutionary forces, gray out the panels' controls and prevents you from entering values, thus reducing the number of inputs you must enter. Details on each force are discussed in separate sections below.

Genetic Drift

You cannot uncheck this box because every population has a finite size and thus subject to at least some genetic drift. Each generation is a random or biased *sample* of the previous generation's gene pool, so the smaller the population size, the greater the effect of this 'sampling error'.

Natural Selection

Checking this box will allow you to vary survival and reproduction rates of each genotype to see how differences in fitness affect evolution. Depending on the values that are entered, you may set any pattern of inheritance to model selection for or against alleles that are dominant, recessive, incompletely dominant, etc. Leaving it unchecked means that all genotypes have a default equal fitness.

Mutation

If this box is unchecked there will be no mutation. Checking this box allows you to set mutation rates from each allele to the other(s).

Migration

If unchecked, each subpopulation is isolated from the others and they all evolve independently. Checking this box allows you to set the amount of migration between subpopulations of one large metapopulation.

Sexual Selection

Checking this allows you to explore the effect of non–random (preferential or biased) mating. You will enter values to determine whether genotypes tend to mate more or less often with some genotypes than they would at random — which is what happens if the box is unchecked.