

## **Instructions**

For this lab activity, you will examine how evolutionary forces affect allele frequencies and fitness in populations using a browser-based software called **evolfoRces**, written by Dr. Spielman.

Once you have launched evolfoRces, you will see three header tabs at the top of the website:

- Single Population
- Migration
- About and Help

We will use the "Single Population" tab for Parts 1-4 of this lab, and the "Migration" tab for Part 5 of this lab. In evolfoRces, you can evolve a population which has a single gene controlled by two alleles, **A** and **a** ("big A" and "little a"). Please refer to the "About and Help" tab for a description of what each tab does.

For each simulation, you will need to keep track of the *fate of alleles* in each population. For any population, one of the following will occur:

1. Allele A will fix in the population
2. Allele A will be lost from the population
3. Allele frequencies will reach a stable equilibrium over time
4. Allele frequencies will not reach a stable equilibrium over time

If either 1, 2, 3 occurred, the fixation/loss/stabilization will be achieved at a certain generation. In addition, the final results table will report the *population fitness* and the *population heterozygosity* reached after the simulation. **For ALL simulations, record your results in the appropriate table.**

For Parts 1, 2, and 5, you will see columns "Prediction?" and "Result?" in the results tables. These columns represent your prediction and observed result for the fate of allele "A". You should write one of the following in "Prediction?" and "Result?": **fix, loss, stabilization, or no stabilization**. The column "Result Generation" refers to the exact generation where either fixation, loss, or stabilization occurred. If no stabilization occurred, you should write "N/A" in this column.

For Parts 3 and 4, you will not see these columns, but instead you will simply record your results for how many and when each allele fixed in the simulation replicates. Again, if fixation did not occur for either allele, you will record "N/A" in the "Range generations..." columns. Note: range in this case means "low value - high value". For example, the way to record range of numbers 12, 15, 37, 100 is 12-100.

For all recorded table numbers, use no more than 3 decimal points.

### Part 1: Investigating Natural Selection

Use evolvoRces to examine how different modes and strengths of natural selection affect populations over time. For all simulations in Part 1, use the following shared settings:

- 250 generations
- Mutation rates set to 0
- Genetic drift turned OFF

1. First, simulate a population under *directional selection*, where natural selection favors allele "A" and disfavors allele "a". Set the starting allele A frequency to 0.5, and set the fitnesses to  $AA = 1.0$  ;  $Aa = 0.9$  ;  $aa = 0.8$ . Make your prediction and record your simulation results in the table.

*Think: Were the results consistent with your observation? What do your results imply about the effect directional selection has on genetic variation?*

2. Simulate a population under *stronger directional selection*, where natural selection favors allele "A" and disfavors allele "a" to a much stronger degree. Set the starting allele A frequency to 0.5, and set the fitnesses to  $AA = 1.0$  ;  $Aa = 0.6$  ;  $aa = 0.2$ . Make your prediction and record your simulation results in the table.

*Think: how did your strong directional selection results differ from question #1? What do your results imply about the effect of selection strength?*

3. Simulate a population under *directional selection*, but use a different starting allele A frequency of 0.2. This means, at the start of the simulation, 20% of alleles are "A" and 80% are "a". Set fitnesses to  $AA = 1.0$  ;  $Aa = 0.9$  ;  $aa = 0.8$ . Make your prediction and record your simulation results in the table.

*Think: how did your strong directional selection results differ from question #1? What do your results imply about the effect of starting allele frequency?*

4. Simulate a population under *balancing selection*, where natural selection favors heterozygotes and disfavors homozygotes. Set the starting allele A frequency to 0.5, and set the fitnesses to  $AA = 0.7$ ;  $Aa = 1.0$ ;  $aa = 0.7$ . Make your prediction and record your simulation results in the table.

*Think: Were the results consistent with your observation? What do your results imply about the effect balancing selection has on genetic variation?*

5. Simulate a population under *balancing selection*, but use a different starting allele A frequency of 0.2. Set fitnesses to the following values  $AA = 0.7$ ;  $Aa = 1.0$ ;  $aa = 0.7$ .

Make your prediction and record your simulation results in the table.

*Think: how did your results differ from question #4? What do your results imply about the effect of starting allele frequency for balancing selection?*

6. Simulate a population under *balancing selection*, but use a different starting allele A frequency of 0.8. Set fitnesses to the following values  $AA = 0.7$ ;  $Aa = 1.0$ ;  $aa = 0.7$ .

Make your prediction and record your simulation results in the table.

*Think: Were the results consistent with your observation? How did your selection results differ from questions #4/5? What do your combined results imply about the effect of starting allele frequency in balancing selection?*

7. Simulate a population under *disruptive selection*, where natural selection favors homozygotes and disfavors heterozygotes. Set the starting allele A frequency to 0.5, and set the fitnesses to  $AA = 1.0$ ;  $Aa = 0.7$ ;  $aa = 1.0$ . Make your prediction and record your simulation results in the table. Make your prediction and record your simulation results in the table.

*Think: Were the results consistent with your observation? What do your results imply about the effect disruptive selection has on genetic variation?*

8. Simulate another population under *disruptive selection*, but use a different starting allele A frequency of 0.2. Set fitnesses to  $AA = 1.0$ ;  $Aa = 0.7$ ;  $aa = 1.0$ .

*Think: Were the results consistent with your observation? How did your results differ from question #7? What do your results imply about the effect of starting allele frequency in disruptive selection?*

9. Simulate another population under *disruptive selection*, but use a different starting allele A frequency of 0.8. Set fitnesses to  $AA = 1.0$ ;  $Aa = 0.7$ ;  $aa = 1.0$ .

*Think: Were the results consistent with your observation? How did your selection results differ from questions #7/8? What do your combined results imply about the effect of starting allele frequency in disruptive selection?*

## Part 2: Investigating Mutation

Use *evolveRces* to examine how mutation affects populations over time. We will specify directional selection for all simulations in Part 2. Therefore, results from these simulations represent how *mutation and selection jointly* affect populations.

For all simulations in Part 2, use the following shared settings:

- Starting allele A frequency of 0.5
- Fitness: AA = 1.0; Aa = 0.9; aa = 0.8
- 250 generations
- Genetic drift turned OFF

1. Simulate a population with the mutation rate from  $a \rightarrow A = 0.1$ , and no mutation from  $A \rightarrow a$ . This means, at every generation, 10% of "a" alleles will mutate to "A", the *more* fit allele. Make your prediction and record your simulation results in the table.

*Think: Were your results consistent with your predictions? What is the effect of only having mutation towards the more fit allele? Compare your results to Part 1, question 1 (the same settings but without mutation) when considering the role of mutation.*

2. Simulate a population with the opposite mutation rates: mutation from  $a \rightarrow A = 0$ , and  $A \rightarrow a = 0.1$ . This means, at every generation, 10% of "A" alleles will mutate to "a", the *less* fit allele. Make your prediction and record your simulation results in the table.

*Think: Were your results consistent with your predictions? What is the effect of only having mutation towards the less fit allele?*

3. Simulate a population with both forward and reverse mutation rates equal to 0.1: mutation from  $a \rightarrow A = 0.1$ , and  $A \rightarrow a = 0.1$ . This means, at every generation, 10% of "A" alleles will mutate to "a", the *less* fit allele, *and vice versa!* Make your prediction and record your simulation results in the table.

*Think: Were your results consistent with your predictions? Do the forward/backward mutation rates cancel each other out, or not? What is the effect of have all types of mutation on genetic variation?*

### Part 3: Investigating Population Size

Use *evolvoRces* to examine how the size of the population ( $N$ , the number of individuals) affects populations over time. We will specify *no selection* for these simulations, but we will turn ON genetic drift. Previously, turning genetic drift OFF meant that population sizes were "infinite," and therefore all results could be directly predicted from simulation settings. As we will learn, we cannot always easily predict what will happen to populations that have a finite size (note, this is all real-life populations).

For all simulations in Part 3, use the following shared settings:

- Starting allele A frequency of 0.5
- Fitness: AA = 1.0; Aa = 1.0; aa = 1.0
- 250 generations
- Genetic drift turned ON
  - 10 replicate populations

You will perform five simulations, each of which will produce 10 replicate populations under the given settings. Each simulation will differ in the specified **Population Size,  $N$**  (do NOT use commas when entering these numbers!!):

- 10
- 100
- 1000
- 10000
- 100000

When recording your results, you will have to determine how many of each allele A/a fixed across the 10 replicates, the mean number of generations to allele fixation, and the *range* in final heterozygosity (i.e., low-high).

*Think: Based on your results, do you find that alleles are more likely to fix in small or large populations? What is the observed relationship between population size and heterozygosity (and therefore genetic variation/diversity)?*

#### Part 4: Investigating Genetic Drift and Natural Selection

For this section, we will examine populations subject to *both genetic drift and natural selection* to view how the combination of these two forces affects populations. For all simulations in Part 4, use the following shared settings:

- Starting allele A frequency of 0.5
- 250 generations
- Genetic drift turned ON
  - 10 replicate populations

1. Simulate a population with *strong selection* and *strong drift*. Set fitnesses to the following values  $AA = 1.0$ ;  $Aa = 0.6$ ;  $aa = 0.2$ , and specify a population size of 100. Make your predictions and record your results in the table.

*Think: Were the results consistent with your observation? Do your results suggest that either drift or selection is the dominant force acting?*

2. Simulate a population with *weak selection* and *strong drift*. Set fitnesses to the following values  $AA = 1.0$ ;  $Aa = 0.9$ ;  $aa = 0.8$ , and specify a population size of 100. Make your predictions and record your results in the table.

*Think: Were the results consistent with your observation? Do your results suggest that either drift or selection is the dominant force acting?*

3. Simulate a population with *weak selection* acting with *extremely strong drift*. Set fitnesses to the following values  $AA = 1.0$ ;  $Aa = 0.9$ ;  $aa = 0.8$ , and specify a population size of 10. Make your predictions and record your results in the table.

*Think: Were the results consistent with your observation? Do your results suggest that either drift or selection is the dominant force acting?*

*Think: Based on your results for this section, is it TRUE or FALSE that evolution will always cause the most fit allele to fix in a population? In other words, is all evolution adaptation?*

### Part 5: Investigating Migration

For this section of the lab, we will use the "Migration" tab in *evolfor* to examine an *Island-Continent* model of migration. In this model, individuals migrate from a continent population to an island population. For the Migration tab, there is NO genetic drift. For all simulations in Part 5, use the following shared settings:

- **Continent** fixed allele A frequency = 0.8
    - This means 80% of alleles arriving to the island via gene flow will be "A".
  - Starting **island** allele A frequency = 0.5
  - 250 generations
1. Simulate an island-continent scenario with *no* natural selection to examine the effects of migration alone, using the following settings:
- Migration rate = 0.1.
    - This means 10% of islanders are new migrants each generation
  - Fitness AA = 1.0, Aa = 1.0, aa = 1.0

Make your predictions and record your results in the table.

*Think: Were the results consistent with your observation? What is the effect of migration on island allele frequencies? Do they become more or less similar compared to the continent?*

2. Simulate an island-continent scenario again with *no* natural selection to examine the effects of migration alone, using the same settings at #1, *except specify 0.3 for the migration rate*. Make your predictions and record your results in the table.
- Think: Were the results consistent with your observation? How does the migration rate itself island allele frequencies?*



3. Simulate an island-continent scenario *with natural selection* to examine the joint effects of migration and selection on the island population. In this case, the majority of migrant alleles are the most fit allele, "A". This means selection pressures are similar on the island and the continent. Use the following settings:

- Migration rate = 0.1
- Fitness AA = 1.0, Aa = 0.8, aa = 0.6

Make your predictions and record your results in the table.

*Think: Were the results consistent with your observation? How does migration affect how directional selection proceeds in an isolated population (i.e. one without migration)?*

4. Simulate an island-continent scenario with natural selection to examine the joint effects of migration and selection on the island population. In this case, the majority of migrant alleles are the *least* fit allele, "a". This means selection pressures are *different* between the island and the continent. Use the following settings (note the difference in fitness!):

- Migration rate = 0.1
- Fitness AA = 0.6, Aa = 0.8, aa = 1.0

Make your predictions and record your results in the table.

*Think: Were the results consistent with your observation? How does migration affect how directional selection proceeds in an isolated population (i.e. one without migration)?*