Name:

Genomics

**Evolutionary Forces in Populations Lab**

Adapted from Dr. Jonathan Brown, Grinnell College

**About the simulation program** – Red Lynx is a browser-based population genetics simulator

developed by Reed A. Cartwright, an evolutionary biologist at Arizona State University. It can be

accessed at <https://cartwrig.ht/apps/redlynx/>. Once the webpage has loaded, click “Start Red Lynx Simulator” to start the program.

Red Lynx allows you to investigate how the four evolutionary forces affect allele frequency over many generations. In this case, our allele of interest is called “A1”. Once the web page has been started, adjust the number of generations to 1000 (type it into the corresponding box to be exact), and run a number of simulations. If you select the “Help” hyperlink, descriptions for each variable will be displayed. You should see a variety of different outcomes in the frequency of A1. For the most part, the frequency will fluctuate through time, but A1 will still be present in the population – though in rare instances A1 will become either fixed (frequency = 100%) or completely lost (0%).

**Getting started:**

 Press “Clear Graph” and adjust the generations to 1000 by typing the number into the

adjacent box.

 Play with the existing settings until your simulated population reaches Hardy-Weinberg equilibrium, in which no further evolution is occurring.

1. What happens to the **allele frequency** in the population once Hardy-Weinberg equilibrium is achieved?

2. What adjustments had to be made to the population size? How did changing the population size affect allele frequency equilibrium?

3. Once the population is in Hardy-Weinberg equilibrium, how does the allele frequency change if the initial frequency is adjusted?

4. Is Hardy-Weinberg likely to exist in nature? **Why or why not?**

5. Refresh the page and restart Red Lynx to return to the original settings. Mutations are the only source of novel genetic material in biological organisms. The average mutation rate among humans is 2.5e-8 per base per generation (very low!). Type this number into the box for A2 -> A1 Mutation Rate.

 Be sure the population is set to 800 and the graph is clear.

 Set the number of generations to 10 (roughly 200 – 300 years for humans) and run 10

simulations.

What happened to the **allele frequency?**

6. Clear the graph, change the number of generations to 100, and run the simulation 10 times.

 Repeat the above instructions with 1000 generations (roughly 20,000 - 30,000 years).

What is happening as **time increases?**

7. What does this tell us about the effect of mutation alone on evolution?

8. Keeping the population size at 800 and the mutation rate at 2.5e-8, we will look at the effect of migration.

 Set the migration rate to 5% and the migrant allele frequency to 25%

 Change generations to 100, clear the graph, and run 5 simulations.

What happens to the allele frequency over time?

9. Is the overall variation within the population increasing or decreasing?

10. Clear the graph.

 Now we will investigate the effects of positive and negative selection. **Return the migration rate to 0%.**

 Set the selection strength to 0.006 and run 10 simulations.

What do you observe? Is the **overall variation** within the population increasing or decreasing?

11. Now set the selection strength to -0.006 and run 10 simulations. How do the results differ from those in the previous 10 simulations?

12. Which one of these two selection scenarios would be more common in nature? Hint: are mutations that have an effect on the phenotype usually beneficial or harmful? Why?