**Note: read through the shiny Instructions in the Introduction folder if you haven’t already, or have forgotten how to make shiny run.**

**Directional Selection simulation.**

This simulator (“Selection.R”) simulates selection at a single locus with two alleles, ‘A’ and ‘a’, which can have different fitness effects. The fitness scheme for the genotypes is:

|  |  |  |
| --- | --- | --- |
| AA | Aa | aa |
| *wAA* = 1+*s* | *wAa* = 1 + *hs* | *waa* = 1 |

For *s* > 0, the A allele is beneficial compared to the a allele, and for s < 0, the A allele is deleterious compared to the a allele.

**Input:** The sliders on the left allow you to set up the simulation, including:

*p,* the initial frequency of the A allele.

*s,* the selection coefficient for the A allele in the fitness scheme shown above

*h*, the dominance coefficient that determines how much of the selected effect is expressed in the heterozygote.

And, finally, the number of generations to allow the simulation to run.

**Output:** The top plot on the right shows the frequency of the A allele over generations since the start of the simulation. The dotted line shows the initial allele frequency.

On the bottom, there’s

-a table showing the fitnesses and the frequencies at the start of the simulation for the different genotypes

-a barplot showing the fitnesses of the different genotypes, with a horizontal line at 1

Press escape to end the simulation when you are done.

**Questions to work through**

1. **Effect of the selection coefficient, beneficial allele edition.** Set up the simulator like this:

p = 0.01

s = 0.1

h = 0.5

number of generations = 150

(note that exact values don’t matter here-- the slider can sometimes be tricky to set to an exact value)

Look at the plot on the top left, which shows the frequency of the A allele over time, and the plot on the bottom left, which shows the fitness of the different genotypes.

Change s to larger and larger values, and note how the plots change.

1. Does selection act faster or slower as *s* increases?
2. Do the fitness differences between genotypes get more or less extreme as *s* increases?
3. Can you explain the answers to 1a and 1b to yourself so that they make sense?
4. **Effect of the selection coefficient, deleterious allele edition.** Set up the simulator like this:

p = 0.99

s = - 0.1 (note less than zero)

h = 0.5

number of generations = 150

(note that exact values don’t really matter here, and the slider can sometimes be tricky to set to an exact value)

Look at the plot on the top left, which shows the frequency of the A allele over time, and the plot on the bottom left, which shows the fitness of the different genotypes.

Change s to more and more *negative* values, and note how the plots change.

1. Does selection act faster or slower as s increases in magnitude (and decreases in value)?
2. Do the fitness differences between genotypes get more or less extreme as fitness increases?
3. Can you explain the answers to 2a and 2b?
4. Compare the results from questions 1 and 2; how do they relate to one another? You might want to look at the fitness scheme table for the same value of the selection coefficient when it is positive and when it is negative.
5. **Effect of the dominance coefficient.** Set up the simulator again as in question 1. Now, slide the dominance coefficient from 0 to 1-- remember, when h=0, the beneficial allele is recessive, and when h = 1, it is dominant (look at the values of ‘fitness’ in the table); you should see the plots on the right change.

The effect of dominance is a bit tricky to understand. To get it, you’ll have to pay attention to the frequencies of the genotypes, and the fitness differences between them.

For example, set p = 0.01. Because p is small, there are almost no AA genotypes in the population (p2 = 0.0001, or 00.01% of the population, hardly anything). So most individuals are either Aa or aa. For selection to work, there has to be a fitness difference between these two genotypes. The bigger this fitness difference, the better selection will work.

1. Compare the fitness difference between Aa and aa when h = 0.01 and h= 1. For which is it bigger?
2. When p is small, should the allele frequency of A change faster for h = 0.01 or h = 1?
3. Why?