

INVESTIGATING MICROEVOLUTION WITH COMPUTER MODELING: SELECTION

Using the "Web PopGen"

You can use the Web PopGen program from your home computer from the website: http://www.radford.edu/~rsheehy/Gen_flash/popgen/ or click on the Web PopGen link on the BIOL 231 home page.

GENERAL EXPERIMENTAL METHOD

In these investigations we will violate the Hardy-Weinberg assumptions one at a time in order to predict how populations should evolve in response to different evolutionary forces. Different forces may produce different patterns of evolution, which biologists can then use to determine what forces are working on natural populations.

In these investigations, we will always work with one gene that has only two possible alleles in the population. We always have to start with simplest cases!

Getting acquainted.

Click first on the ? button. Read the introductory material about the program. Read about the Display features. Skim through other portions to see what you can get help with when you need it. When you have questions, consult the help information before asking the professor .

I Effect of selection on a rare recessive trait.

Question:

The first question we'll ask is "What pattern of evolution results when selection favors a rare recessive trait?"

Method:

Control variables:

1. One assumption of the Hardy-Weinberg is no migration in or out of populations. Click on the Migration box and make sure the migration rate is zero.
2. Another assumption is that mutations don't produce more of one allele than another. We'll control this by setting both $A_1 \rightarrow A_2$ and $A_2 \rightarrow A_1$ mutation rates to 0.
3. A third assumption, no inbreeding, is no problem because the program is currently written to have random mating at all times.
4. A fourth assumption of the Hardy-Weinberg is an infinite population size. That is, there is no sampling error. Click on the box beside "Finite Pop." It will change to "Infinite Pop." Also make sure the "Bottle Neck?" box is NOT checked.
5. Set the number of generations to 200.
6. All populations will start with the same allele frequencies. You'll see that we can run 5 different populations (5 replicates of our experimental conditions) simultaneously. We will designate A_2 as the recessive allele. Our question asks what happens to an advantageous rare allele, so let's say that A_2 has an initial frequency of 0.05 in the population. What does that mean?

What is the " A_1 " (dominant) allele frequency? _____. Enter the A_1 allele frequency for all 5 populations. Click OK to close the window.

We will compare selection favoring the recessive trait (experimental treatment) with no selection (the control). We will do that by choosing the fitnesses of different phenotypes.

Control treatment. Run the control treatments first. Let's say that individuals of both the dominant and recessive phenotype have an average survival rate of 36% and then produce an average of 10 offspring per individual. Review your Fitness and Selection Coefficient worksheet to determine what the fitnesses should be if there is no selection. Enter those fitnesses in the boxes. Click Go to run the simulation. Only one line is produced because all 5 populations are doing exactly the same thing. Copy these graphs to a Word document as described by the handy-dandy Help thingy. Crop the image so only one graph is showing. Choose the graph that is most appropriate to your question. Label this Figure 1 and give it a descriptive legend.

Experimental treatment. To make a good experiment, we change only one thing at a time. Let's say individuals with the recessive phenotype have an average survival rate of 40% and produce an average of 10 offspring per individual, while the dominant phenotype individuals have the same survival rate as in our control (see above). Calculate the fitnesses:

Enter the fitnesses and click Go. Notice the curve is still changing at 200 generations. One should ask "What's going to happen?" Click Continue to run another 200 generations and find out.

Note that you see you have more complete results, but not all on one graph. Click Reset and change the number of generations to produce graphs with complete curves (but no more generations than necessary). Save graphs to the same Word document. Label this Figure 2 and give it a descriptive legend. To make control and experimental results equivalent, rerun the control at the same number of generations and paste it over (replace) the first graph.

Analysis

Describe the results in the two different figures. Describe not only the result at the end of 200 generations, but also the pattern of evolution -- how the population changed over those 200 generations. To do that, quantify the direction (increase, decrease, no change) and rate of change (remember from algebra that rate is the slope of the line (rise/run); this is most frequently taken at the steepest portion of the line).

Conclusion

In a sentence or two, answer the question of the experiment. Place these concluding sentences under figures 1 and 2.

II How does the frequency of an allele affects evolution by selection?

Now we can follow up the results of the first experiment by seeing if our conclusion about the pattern of evolution is always the same. We might ask "Is the pattern of change the same at any initial frequency of an advantageous recessive allele, whether it's rare or not?"

Plan out an experiment to explore that question.

Hint: Remember that you have 5 populations. Each population can be set to a different initial allele frequency so that you can, in affect, run 5 different experiments at once. Build on what you already know by changing as little as possible from the previous experiment. Present your plan to your instructor.

Play with the frequencies you choose and the generation time until you get good graphs to display in a paper. Copy graphs to Word document.

Do your analysis. What is going on here? Quantify your impressions by measuring and comparing slopes. Present comparisons of slopes in a table. Run more experiments to confirm what you think is happening. Add those data to your table. Draw a conclusion about the question.

III How does the phenotypic expression of an allele affects evolution by selection?

We can ask if our conclusions in the previous experiments continue to hold if we modify other parameters of a population. For example, we can ask "Will an advantageous dominant allele evolve in the same way as an advantageous recessive allele?"

Use your results in Part II as the control set of data. Set up experimental parameters to get equivalent curves when the adaptive allele is a dominant allele. Don't change a bunch of things willy-nilly. Think it through and have a reason for changing anything. Check your plan with your instructor.

Run the program until you get equivalent graphs. Do any other experiments to check your results and conclusions. Copy good graphs to your Word document.

Do your analysis. Quantify comparisons of the patterns of evolution of an advantageous recessive trait with the patterns of evolution of an advantageous dominant trait. Summarize your findings.

Report

Follow the Guidelines for writing research papers (link on D2L) to write a paper on the effect of phenotypic expression on evolution of a trait.

I won't ask you to do library search, so for your Introduction give background leading to the question(s) of the present research. In this paper, part 1 will be considered previous research. Just summarize what you found in a sentence or two, then lead the reader to the questions investigated in parts 2 and 3.

The Methods will be who's program you used, how you set parameters for comparing recessive and dominant traits. Specify all the things that were the same, highlight the differences (a table may be useful here).

In the Results you will present and discuss your figures and any tables that resulted from your analysis from Parts II and III (do not include practice graphs of Part I).

The Discussion can just be a reminder to the reader of your question and your summary of what your answer is. Then discuss new questions that this research produced.