



# AlleleA1

## Software for Evolutionary Analysis

<http://www.prenhall.com/freeman>

AlleleA1 2.0 © 2003 by Jon C. Herron

AlleleA1 is free. You may give it to anyone you like, so long as you distribute it as a stand-alone application and include this manual along with it. You may not sell it. You may not include it in a collection with other software, regardless of whether you are selling the collection or giving it away.

I make no warranties or guarantees about the quality of AlleleA1, or the accuracy of the simulations it runs. Use it in good health, but at your own risk.

If you have comments or suggestions, please send them to me at [herronjc@attbi.com](mailto:herronjc@attbi.com).

## Introduction

AlleleA1 simulates evolution at a single locus in an ideal population of imaginary organisms. The locus of interest has 2 alleles:  $A_1$  and  $A_2$ . The user enters values for parameters controlling selection, mutation, migration, genetic drift, and inbreeding. As the simulation runs, the software plots a graph showing the frequency of allele  $A_1$  over time.

The equations AlleleA1 uses are presented in Chapters 5 and 6 of *Evolutionary Analysis*, 2e.

# Using AlleleA1

## Setting the Parameters

Set the parameters by entering values in the boxes in the AlleleA1 window. For example, to set the initial frequency of allele  $A_1$  to 0.01, double click in the box labeled Starting frequency of allele  $A_1$ , then type 0.01.

## Running the Simulation

Run the simulation by going to the Simulation menu and selecting Run, by pressing command-R, or by clicking on the Run button.

## Setting the Number of Generations

By default, the simulation will run for 500 generations. You can select a different number of generations by using the popup menu at the lower right corner of the graph. Click on the small black triangle, and hold the button down. Then move the cursor to the number of generations you want.

## Setting the Graph Line Mode

By default, the graph will clear itself at the start of each run. To overlay the graph for a new run onto the graph for the previous run, click on the Multiple radio button under Graph lines at the bottom right of the AlleleA1 window.

## Setting the Graph Line Color

To change the color of the graph line for your next run, click on the color you want in the palette at the lower right of the AlleleA1 window. The currently selected color is shown in the larger rectangle to the left of the palette. If you select Auto, the software will automatically cycle through all eight colors.

## Clearing the Graph

To clear the graph, but leave the parameters unchanged, go to the Simulation menu and select Clear, or press command-K, or click on the Clear button.

## Restoring All Settings To Their Default Values

To clear the graph and restore all settings to their default values, go to the Simulation menu and select Reset, or press command-D, or click on the Reset button.

# The Parameters

## Starting frequency of allele $A_1$

As its name suggests, this parameter controls the frequency of allele  $A_1$  at the start of the simulation. The frequency of allele  $A_2$  is determined automatically by subtraction. The starting frequency of allele  $A_1$  should not be less than zero or greater than one.

## Fitness of genotypes $A_1A_1$ , $A_1A_2$ , and $A_2A_2$

These parameters determine the relative fitnesses of the three genotypes (that is, the relative probability that an individual of each genotype will survive to reproduce). The fitnesses should be positive, but otherwise all that matters is their values relative to each other.

## Mutation rates

These parameters determine the rate at which copies of allele  $A_1$  turn into allele  $A_2$  and vice versa. The mutation rates should not be less than zero or greater than one.

## Fraction of migrants

This parameter controls the fraction of individuals in each generation that are migrants newly arrived from another population. The fraction of migrants should not be less than zero or greater than one.

## Frequency of allele $A_1$ in the source population

This parameter controls the frequency of allele  $A_1$  among the newly arrived migrants. It should not be less than zero or greater than one.

## Population size

By default, the population size is infinite, and the population evolves according to a deterministic equation. Entering a positive integer for the population size makes the population finite. Each generation, the allele frequencies are determined by sampling from the previous generation's gene pool.

## Coefficient of inbreeding

This parameter, also known as  $F$ , determines the probability that an individual's two alleles are identical by descent from a common ancestor. A value of 0 represents outbreeding; a value of 1 represents selfing.  $F$  should not be less than zero or greater than one.

## Advanced Features

### Graphing frequencies other than that of allele $A_1$

On the allele frequency graph in the AlleleA1 window, a popup menu under the Y-axis label will let you select other frequencies to plot.

### Saving the data from a simulation

At the upper right of the AlleleA1 window there is a small disclosure triangle. Clicking on the triangle will reveal a table on the upper right. As you run a simulation, AlleleA1 fills this table with data. At the end of the run, you can select rows in the table, copy the data, and paste them into a spreadsheet or text file.

### Graphing mean fitness and $\Delta Fr(A_1)$ for your model

At the upper right of the AlleleA1 window there is a small disclosure triangle. Clicking on the triangle will reveal additional graphs on the lower right. These show the mean fitness for your population and the change from one generation to the next in the frequency of allele  $A_1$ , both as functions of the frequency of allele  $A_1$ .