LAB08: EVOLUTION — SELECTION OF OTHER INHERITANCE PATTERNS

INTRODUCTION

Now that you have had several weeks with natural selection, we will move on to the other evolutionary forces, and give you a chance to design more of your own experiments. The goals of this lab are to:

- Learn about genetic drift:
  - Improve your understanding of randomness and evolution by genetic drift, and see how random change can still be 'predicted':
  - Learn how random changes in allele frequencies in small populations can result in evolutionary change;
  - See how chance can cause independent, identical populations to evolve differently from one another.
- Learn about migration/gene flow, and how it interacts with selection and drift.
- Learn about mutation.
- Practice designing experiments.
- Explore the interaction of the various evolutionary forces, e.g.: selection with drift and gene flow; mutation with population size.
- Continue learning to present data and speak to groups.

THE *POPG* COMPUTER PROGRAM

PopG is another population genetic simulation. It is conceptually like EVOLVE, but it

- Uses *a* instead of *B* for the 2nd allele;
- Is simpler in that:
  - You enter only relative fitnesses, not survival & reproductive rates, 3 instead of 6 numbers;
  - It graphs only P[A];
  - It has a constant population size, no max & post–crash.
- Is more complex because it adds
  - Mutation
  - Gene flow ("Migration");
  - Multiple populations;
  - Variable number of generations.

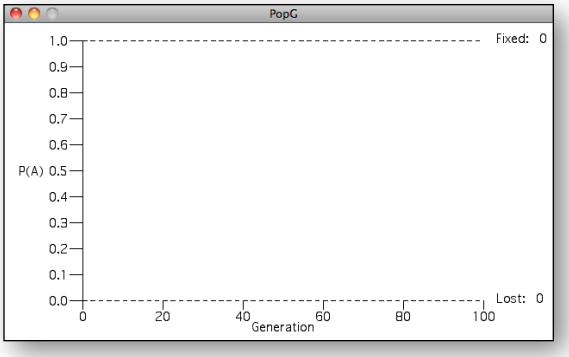


Figure 1. PopG's initial display.

1. Download the appropriate version of *PopG* for your computer and double click on the PopG icon to unpack it & save the app to your network drive. When it opens you should see the display in Fig. 1. The vertical–axis is P[A]; the horizontal–axis is the number of generations that the simulation has run.

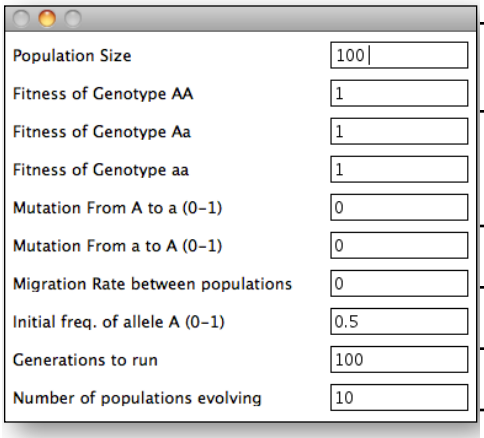
   In the upper right, note the "*Fixed: 0*" and in the lower right corner you will see the term "*Lost: 0*". Fixation means that there is only the *A* allele left in the population. If the frequency of allele *A* goes to 100%, then the frequency of allele *a* goes to 0%, we say that allele *A* has fixed and *a* is lost. Without mutation or gene flow, there will be no more *a* alleles in the population and the frequency of allele *A* won't change. Likewise, when P[*A*] = 0 there are no more *A* alleles in the population and so *A* is said to be lost and the population has 'fixed' for *a*.

2. From the menu, select Run > New Run. This will bring up the input dialog box shown in Table 1, which shows the input dialog with explanations of parameters that you can set to run different evolutionary experiments.

   Check the settings to see that yours are set to the values shown in Table 2.

Click "OK" and the computer will run 10 different experimental populations of 100 organisms for 100 generations each, and will generate a graph that looks roughly like the Fig. 2 below. Each line on the graph represents P[A] for a different population over the 100 generations. Arrows point to populations where the A allele was lost (one in about generation 73) or fixed (two in about generations 82 and 95)

Table 1. Summary of PopG's Input Parameters. *The default parameters set up an experiment with genetic drift and no selection, mutation or gene flow.*

INPUT DIALOG	PARAMETER	(RANGE) NOTES
	**Population size:** (Genetic Drift)	(1–10,000) Number in each population; unlike EVOLVE, this will remain constant.
	Fitness of Genotypes (*AA, Aa, aa*) *(Selection)*	(0.0–1.0) Relative fitness of each genotype. Different values can simulate all of our patterns of inheritance and selection.
	Mutation from A to a & *a* to *A* *(Mutation, of course)*	(0.0–1.0) Frequency *A* mutates to *a* and *a* to *A* (the back mutation). E.g., 0.000001 (1e-06) would be one mutation in 1 million egg or sperm.
	Migration rate (Gene Flow)	(0–0.9 = 0-90%) Proportion of ea. Population moving to another population.
	Initial frequency of A (experiment control)	(0.0–1.0) Frequency of A allele in 1st generation.
	Generations to run (experiment control)	(1–10,000) Unlike EVOLVE, this can vary.. Large values slow program.
	Number of populations (replicated simulations)	(1–200). Large values slow program.

Unlike EVOLVE, your graph will be different from this figure and each time you run it, even when the starting values are the same. Because the computer uses the same kind of random sampling of genotypes that you did in the manual bead simulation in Lab 5, every population will behave differently and every graph that is generated will be different from every other one. Notice in Fig. 2 that arrows point to three populations which fixed for one or the other allele. Thus, in this experimental run, it took about 95 generations for 3 populations to reach fixation.

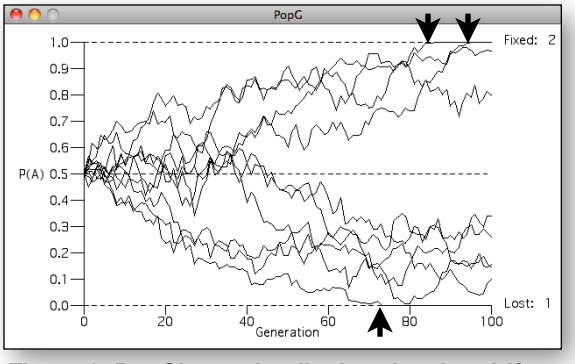


Figure 2. PopG's results display showing drift. *Input parameters were those in Table 1. Your results will differ.*

THE LAB

GET FAMILIAR WITH POPG, REVIEW SELECTION EXPERIMENTS, LEARN NOTEBOOK

3. Download the *Lab08_NtBk_Tmpl8.xlsx* file. It is a laboratory notebook file into which you will record your explorations of evolutionary questions, including output graphs from 'good' experiments — ones that show the patterns you think are typical for the question you're asking and that you would use to develop a talk or paper about your research. The first experiment is inserted for you as an example. *As soon as you open the file, remember to save it with your* lastname_initial *in place of "NtBk_*Tmpl8*".*

   When you start a new series of experiments to answer a question, create a new Tab with the question and add notes about
   - The question you're asking;
   - What your experimental design is;
   - One or more tables of input parameters;
   - What the results show — images of PopG's graphs;
   - Modifications to your experimental design;
   - Your answer to the question;
   - Other questions & thoughts.

When addressing a question first *play* with different input values & keep enter brief notes in your notebook file as you explore to help you refine your experimental design. You can have one input table & graph for a trial run with the value changed & a brief notes about the result. The exact notes will vary, but it's often a good idea to record sample values. Here is a sample from Question 2 below:

aa Fitness	*P[A] in generation*		
• *0.1*	*0.5 in gen. 2,*	*0.90 in gen. 12,*	*0.995 in gen. 100*
• *0.2*	*0.5 in gen. 4,*	*0.90 in gen. 14,*	*0.990 in gen. 100*

Notice that the single parameter that is changed is noted, along with some landmark values that can be compared. In this example, increasing the fitness of *aa* slows the rate of evolution.

Once you have settled on a good set of values, record landmark sets of inputs and graphs and answer the question. Ultimately, you should be able to summarize the patterns of P[A] change for each type of allele interaction and even be able to guess the pattern of inheritance just from the graph alone without knowing the input values.

You will not have a formal report for this lab, you will print & turn in your lab notebook.

4. To get a feeling for the program, set up experiments that duplicate the experiments you have done already. Use populations of 10,000, initial P[*A*]s of 0.01 (1%); keep other parameters the same as in Table 2.

Table 2. Input parameters for Exp't 1.

Population size:	10,000
Fitness of AA	0
Fitness of Aa	1
Fitness of aa	1
Mutation rate A –> a	0
Mutation rate a –> A	0
Migration rate:	0
Initial frequency of A:	0.99
Generations to run:	100
Number of populations:	10

5. **Q 1: What happens to a dominant allele when the recessive phenotype is lethal/sterile.** This is a rephrased version of our first spider scenario with beads and EVOLVE. The input values are shown in Table 2 and in the NB_Tmpl8 file as an example.

6. **Q 2: What happens to the evolution of an allele when the recessive allele's phenotype's fitness is greater than zero (is not sterile/lethal)?** Play with different values for the fitness of *AA* and settle on one that will result in the *A* allele going almost to extinction in 100–200 generations. You'll use those values in the next two experiments. In other words, Question 2 is the control for other experimental results to questions 3 & 4.

EXPLORE OTHER PATTERNS OF INHERITANCE

Once you have gotten a feel for how PopG compares with EVOLVE, answer the following questions. Be sure to duplicate the Templ8 tab before you modify it. You will need to try many experiments to get a feel for these evolutionary situations.

7. **Q 3: How does selection for an incompletely dominant allele compare with selection for dominant and recessive alleles?** Again, use the same homozygous fitnesses as exp't 2, but play with different heterozygote fitness values. Be sure to record several sets of input values and the resulting graphs. The results of Exp'ts 2 & 3 will be the controls for this experiment.
8. **Q 4: What happens when selection favors a heterotic phenotype** (one that shows heterosis)**.** For this one, you will need to do several exp'ts with different initial P[A] values and different combinations of homozygous fitness values.

WOULD YOU LIKE TO TRY SOMETHING ELSE?

If another question occurs to you (under–dominance anyone?), feel free to explore and report on it.