LAB 6: EVOLUTION 1 - SELECTION

Note the pre–lab homework (pp. 11–13) that is due at the start of lab this week.

INTRODUCTION

GOALS

- To see how scientists use simulations, esp. computers, to model complex phenomena.
- To gain experience with experimental design.
- To improve your understanding of basic genetics
- To improve your understanding of evolution, especially:
  - The nature of evolutionary fitness;
  - How pattern of inheritance of phenotypes of different genotypes affect evolution;
  - How speed of evolution is affected by patterns of inheritance;
  - The role of selection, population size (genetic drift), and migration between populations (gene flow) in evolution.

EVOLUTION

For these labs, we define evolution as *changes in allele or genotype frequencies within a local population*. Evolution within populations is sometimes termed *microevolution;* evolution at a larger scale is sometimes termed *macroevolution* (e.g., the evolution of mammals and reptiles from a common ancestor). In these labs you will simulate evolution using beads and computer programs to illustrate the mechanical basis of fundamental evolutionary forces.

In our first simulation, beads will represent alleles in a population and you will perform a simulation experiment to see how natural selection affects allele frequencies in a gene pool. You will then use computer simulations that more rapidly perform the same procedures you performed by hand. This will speed up the process and allow you to do experiments that show the long–term effects in many populations. Computer simulations allow you to make and test predictions about evolution with just a few keystrokes.

BASIC CONCEPTS

Genetics is so intimately integrated with evolution that discussion of one often requires some mention of the other. Here are key terms from each disciple that you must learn for the next few labs. I suggest you memorize them.

Gene = a sequence of DNA units that affects one or more characteristics of an organism. E.g., one of the genes that Gregor Mendel studied affected the color of pea seeds. In today's simulations, we will `study a hypothetical gene for pigment color in a hypothetical spider population.

Allele = a genetic variant, one of a number of alternative forms of a gene that may or may not produce different phenotypes. E.g., Mendel's peas had two alleles of the seed–color gene, an allele that produced green seeds and another that produced yellow seeds. There are usually more than two alleles for a given gene and they are symbolized by more than a capital and lowercase letters like *A* and *a* so try to unlearn that mindset. For example, the ABO blood groups are produced by a gene that has three alleles symbolized *i*, I^A, and I^B.

In today's simulations, *"A"* will represent an allele that produces red pigment and *"B"* an allele that produces a yellow pigment. Most organisms we will consider in this course, and the hypothetical spiders in this lab, inherit two alleles for each gene, one inherited from their father and the other inherited from their mother.

Genotype = the genetic makeup of an organism; we will us the term to refer to the genetic makeup of an individual organism at one genetic location on a chromosome. Most organisms have two copies of each gene, one from each parent. Since our spider population has two alleles, there are three possible genotypes: *AA, AB* and *BB*.

Phenotype = an observable characteristic of an organism. Phenotypes may be anatomical, physiological, biochemical, behavioral, or the product of behavior (e.g., a beaver's dam). Phenotypes may be produced by genes, the environment, or an interaction of the two, but we will consider only phenotypes directly produced by genes.Phenotypes are typically the result of several different genes interacting with each other and their environment. However, our spiders will have two phenotypes, *red* and *yellow*, corresponding to the pigments produced by the two alleles, with no environmental effect.

Genotype denotes an organism's heredity and *phenotype is* what that heredity produces (perhaps influenced by environment).

Homozygote = An organism with a pair of identical alleles of one gene. If two alleles are symbolized with the letters *A* and *a*, a homozygote would be either *AA* or *aa*. The use of capital and lowercase letters implies that the capital letter symbolizes a dominant allele and the lowercase represents a recessive allele (see Patterns of Inheritance below). Dominant/recessive alleles are actually rather rare, so you will often see different symbols, e.g., the ABO blood group alleles are symbolized *i*, I^A, and I^B (the 'I' comes from the proteins they code, "Immunoglobulins") At the *ABO* gene, homozygotes might be *ii*, I^AI^A, or I^BI^B. Our spiders with *AA* or *BB* genotypes are homozygotes.

Heterozygote = An organism with two different alleles at one gene location. E.g., *AB* (our spiders), or I^Ai, I^AI^B, and I^Bi for the *ABO* gene.

Patterns of Inheritance: alleles may interact in a number of ways to produce phenotypes. The best way to tell them apart is to pay attention to the phenotype of the heterozygote. There are many different types of interactions between alleles and between different gene, but we will restrict ourselves to just four. Table 1 provides examples of each pattern.

- **Dominance/Recessiveness:** If the heterozygote has a phenotype just like one of the homozygotes, that allele is dominant & the alternative is recessive. E.g., in Mendel's peas, when both the yellow allele, Y, and the green allele, y, are present, the heterozygotes, Yy, look exactly like YY homozygotes and the plants make yellow seeds. Yellow is dominant to the recessive green. In the ABO gene, the I^A and I^B alleles are dominant to the *i* allele.

  This pattern of inheritance is the one most taught in high school and the only one most students remember. However, it is actually the least common, and this is one of the things that must be unlearned in college. MOST phenotypic traits are affected by many genes, and the environment, including the environments of the parents.

  BEWARE: It is easy to misuse the word *dominant*. Do NOT use it in the sense of "becomes more common". Many students tend to say, "Allele *A* became dominant" when what is really happening is that *A* has become *more common*, or has a *higher frequency*. Do not make this mistake.

  Even if you consider just one gene, there are other patterns. Below are three more we will use in the future.

- **Incomplete dominance** *(also semidominant)*: Heterozygotes show a phenotype that is intermediate between the homozygotes. If *AA* produces a red phenotype and *BB* produces white, then the *AB* genotype might produce a pink phenotype.

- **Codominance:** Heterozygotes show both alleles' phenotypes; occurs when homozygotes produce different gene products. In our spiders, if *AA* is red, *BB* is yellow and they are codominant, the *AB* genotype might produce an orange phenotype.

  The ABO blood group gene exemplifies both dominant/recessive and codominant patterns. The I^A allele produces an A antigen (protein) on the surface of red blood cells; the I^B allele produces a B antigen; heterozygous I^AI^B genotypes produce both *A* and *B* phenotypes, so the A and B alleles are *codominant*. The *i* allele produces neither protein and is recessive to both: I^Ai genotypes have the *A* phenotype and I^Bi produces the *B* phenotype.

- **Heterosis** *(heterozygote superiority, also overdominance)*: The condition where the heterozygote is more extreme than either homozygote. We will go into this in more detail in next week's lab.

Gene Pool: The total of all alleles in a population. We will be looking at the frequency of two alleles of one gene. In the computer program that we will be using, the notation, P[*A*], represents the *proportion*, or the relative frequency, of the *A* allele. P[*B*] is the proportion of *B* alleles. As there are only two alleles in the population, the sum of the allele frequencies must equal one (P[*A*] + P[*B*] = 1.0). If you know the frequency of one of the alleles, subtracting it from 1.0 gives you the other's frequency. If P[*A*] = 0.6, then P[*B*] = 1.0 – 0.6 = 0.4.

Adaptation: noun: any trait of an organism (biochemical, anatomical, physiological, behavioral) that is influenced by genes and that improves the organism's chances of reproducing &/or surviving in a particular environment. Adaptation is an outcome or a *consequence* of the operation of natural selection; it is not a causal process in itself. The verb *adapt* indicates the process of evolving an adaptation.

Fitness: relative ability of a trait or allele to pass into the next generation, the result of both survival and reproduction. Natural selection is not "*survival of the fittest*", but the *greater reproductive success* of the fittest. Survival is essential, but not sufficient for evolutionary success; you must also produce offspring.

- **Absolute fitness** = the product of survival and reproduction. I.e., consider survival = 40% and reproduction of 5, then if you start with 100 young in one generation, on average 40 would survive to reproduce and produce 40 * 5 = 200 young. This is equivalent to what ecologists call the "*intrinsic rate of increase*", or *r*, of the population of 2.0. If a population's average absolute fitness is less than 1.0, then the population would decline to extinction
- ***Relative fitness*** is the sum of survival and reproduction divided by the maximum in the population. Values range from 0 (lethal or sterile) to 1.0 (the maximum possible, the most fit in the gene pool). A trait with low absolute fitness might have high relative fitness.

Examples of Genetic Definitions

Table 1 illustrates the basic patterns of inheritance. Note that *dominant* has no relationship to *bigger* or *better*, only that heterozygotes resemble one of the homozygotes. The other patterns also are defined by the relationship of the heterozyote's phenotype to the phenotype of the two homozygotes.

Table 1. Examples of patterns of inheritance.
A and *A′* represent two hypothetical alleles. Each row in the table shows examples of the hypothetical phenotypes that might be produced by each genotype given the pattern of inheritance on the left.

INHERITANCE PATTERN definition	**RELATIONSHIP OF GENOTYPES & PHENOTYPES**				
	AA		**AA′**		**A′A′**
Dominant/Recessive heterozygote = one Homozygote	**Tall** (10′)	=	**Tall** (10′) (A dom., A′ rec.)	≠	**Short** (5′)
	Short (5′)	=	**Short** (5′) (A dom., A′ rec.)	≠	**Tall** (10′)
	White	≠	**Red** (A′ dom., A rec)	=	**Red**
	Type A protein	=	**Type A blood** (A dom., A′ rec)	≠	**No protein**
	Type B protein	=	**Type B blood** (A dom., A′ rec)	≠	**No protein**
Incomplete (Semi)**Dominance** heterozygote intermediate to both Homozygote	**Tall**	>	**Medium** (A incomp. Dom. to A′)	>	**Short**
	Short (5′)	<	**Medium** (8′) (A incomp. Dom. to A′)	<	**Tall** (10′)
	Red	>	**Pink** (A incomp. Dom. to A′)	>	**White**
Codominance heterozygote has *both*	**Type A protein**	–>	**Both A & B proteins** (A & A′ Codom.)	<–	**Type B protein**
Heterosis Heterozygote more extreme than either Homozygote	**Shorter** (5′)	<	**Tall** (10′) (A & A′ Heterotic)	>	**Shorter** (8′)
	Taller (10′)	>	**Short** (5′) (A & A′ Heterotic)	<	**Taller** (9′)

EXAMPLES OF FITNESS

Table 2 will help you wrestle with these definitions; it gives hypothetical data on the survival & reproductive rates of four species with different genes and alleles and that live in different environments.

Here's an example of how to interpret Species 1 in Table 2:

- The dominant *A* genotypes (*AA* homozygotes & *AB* heterozygotes) average 20% survival and 6 offspring each.
  - If you consider 100 eggs as the start of a generation, then 20 would survive to reproductive age.
  - Those 20 adults would produce 120 offspring; the numbers in the 2nd generation would be 20 larger than the 1st.
  - These genotypes have an absolute fitness of 20 * 6 = 120.
- The recessive *BB* homozygous genotype averages 80% survival and 2 offspring.
  - If you consider 100 eggs as the start of a generation, then 80 would survive to reproductive age.
  - Those 80 adults would produce 160 offspring. The numbers in the 2nd generation would increase by 60.
  - The *BB* genotype has an absolute fitness of 80 * 2 = 160.
- Because all genotypes have absolute fitnesses greater than 100, the population of each would increase over time.
- Because the *BB*s have the highest absolute fitness, their relative fitness would be 160 / 160 = 1.00.
  - The relative fitness of the *AA* and *AB* genotypes would be 120 / 160 = 0.75; they are 25% less fit than the BB genotypes.

Table 2. Patterns of Inheritance and Fitness.
Each of the four species has different genes & alleles that affect survival and reproduction.
***Survival rates** are the average percent of young (e.g., fertilized eggs, seeds) of each genotype surviving to reproductive age.*
***Reproductive rates** are average number of young (fertilized eggs, seeds) per adult of each genotype. Adults are assumed to die after reproducing.*

Absolute fitness *measures whether numbers will increase or decrease. E.g., if 100 young are hatched in one generation and the survival rate is 40%, then on average 40 would live to reproduce. If the adults produce an average of 3 young each, the 40 adults would produce 40 x 3 = 120 young. If the whole population behaved this way, the r,* the intrinsic rate of natural increase *would be 1.2.*

Relative fitness*: Since we're interested in relative changes in the genotypes, we divide each absolute fitness by the highest absolute fitness value. In Species 1, the AA and AB genotypes are only 75% as successful as the BBs and we would expect the B allele to increase in frequency while the A would decrease.*

	Species 1			Species 2			Species 3			Species 4		
Genotypes	**AA**	**AB**	**BB**	**CC**	**CD**	**DD**	**EE**	**EF**	**FF**	**GG**	**GH**	**HH**
Survival Rate, *S*	20	20	80	40	20	20	20	80	80	80	50	20
Reproductive Rate, R	6	6	2	3	6	6	6	6	2	4	6	6
Absolute fitness, S*R	120	120	160	120	120	120	120	480	160	320	300	120
Relative fitness (Abs Fit)/Max(Abs. Fit)	120/160 = 0.75	120/160 = 0.75	160/160 = 1.00	120/120 = 1.00	120/120 = 1.00	120/120 = 1.00	120/480 = 0.25	480/480 = 1.00	160/480 = 0.33	320/320 = 1.00	300/320 = 0.94	120/320 = 0.38

These figures are in the *Pre–Lab 6 Homework* page at the back of this handout. It is due as you walk in the door for lab.

Experiment 1: Manual Simulation of Selection Against a Lethal Recessive Allele

A Scenario

Tay–Sach's (TS) disease is genetic and lethal. Infants seem to be normal for their first six months, but then a slow, relentless deterioration sets in. The child becomes blind and deaf; lacking nervous stimulation, muscles waste away and paralysis sets in; they become unable to swallow. Death usually occurs before the age of 4, even with state–of–the–art medical treatment. The disease is caused by a recessive allele and some populations have a surprisingly high frequency of the allele — up to 3.7%, with an incidence of 1 in 1,000 births. How can such a situation arise; why wouldn't selection eliminate the allele from the population?

To avoid human emotional intanglements, consider a hypothetical spider population that has a gene that affects color and no other trait, and that has two alleles, A and B. The spiders have been living on yellow flowers and are well camouflaged by the B allele that produces yellow pigment. The frequency of the B allele (abbreviated P[B]) is very high, with another allele, A, present at low frequency.

Recently, however, a plant with red flowers has invaded the ecosystem and is excluding the yellow–flower plant (competitive exclusion). The yellow spider phenotype is now very obvious to predators, so all yellow individuals are eaten by birds. An allele for red color, *A*, is also present at low frequency (P[A]) in the local spider gene pool because of gene flow from another population (young spiders were blown in). The red phenotype is very difficult to see on the red flowers.

How can you make quantitative predictions in a situation like this? It would be easy to guess that the yellow alleles would disappear from the population's gene pool, but how long would it take? Would the rate of change of allele frequencies be constant, or would they vary over time? These are the more detailed questions addressed by this lab.

In Experiment, 1 you will manually simulate a population of 50 spiders by walking through the basic processes of reproduction and survival over 5 generations. Selection will removed all yellow spiders and the survivors will make up the gene pool for the next generation. You will repeat this for four generations and graph the results. As you will see, this process is time–consuming and there are many ways to mess it up. Experiment 2 will show you why scientists more often use computers—you will run the same experiment as the first, but will model a population of thousands for 100 generations.

In Experiment 1, you will observe the action of selection in a population of 50 individuals (beginning with a gene pool of 10 red and 90 yellow alleles). In this scenario, red (*A*) is dominant and yellow (*B*) is recessive. Individuals (genotypes) that do not reproduce have a fitness of 0; those that reproduce successfully, have a fitness of 1. Use the information above to fill in the appropriate values for each genotype in Table 3 below.

Table 3. Genotypes, Phenotypes & Fitnesses of Simulated Population. *(fill in the values)*

Genotype	Phenotype (red/yellow)	Visible to predators? (yes/no)	Relative Fitness (0/1)
AA	Red	No	1
AB	Red	No	1
BB	Yellow	Yes	0

1. **Setup the gene pool with a P[A] of 10% & a P[B] of 90%.** From the trays of red and yellow beads, put a "population" of 50 spiders (10 red and 90 yellow alleles) in your 3rd ('gene pool') tray. Remember, each spider has 2 copies of the pigment gene so the 50 spiders make up the gene pool of 100 alleles for generation 1 (think of a generation as 1 year; all surviving spiders reproduce and die before the eggs hatch).

2. **Pre–Lab Question: What to you expect to happen to the frequency of red and yellow alleles over five generations?** (Make a quantitive, specific, numerical prediction—what will the allele frequencies at the start and at the start of the 5th generation? Copy your answer to the Pre–Lab homework. Have your instructor initial this copy, for you will use it in your lab report.
   The *A* allele will go from a frequency of _____ in generation 1 to a frequency of _____ in generation 5.

   The *B* allele will go from a frequency of _____ in generation 1 to a frequency of _____ in generation 5.

   (record ea. student's prediction on lab map, post on board) Instructor's initials:_____

PROCEDURE:

3. **Random Mating & Fertilization.** Combine alleles randomly.
   a. *Without looking*, one team member will pick two beads at a time and set each pair of beads on the table. Each pair represents an individual fertilized egg. The second team member will arrange each pair of beads in 3 separate columns, 1 for each genotype, until they have selected all the beads and have them laid out on the table. These 50 pairs of beads represent the spiders randomly produced from the gene pool in this generation.
   b. In lines 4a–c of Table 4, record how many *spiders* (not alleles!) you picked.
4. **Selection.** The homozygous recessive *BB* individuals (2 yellow beads) have the yellow phenotype and will be eaten by predators and lost from the population before they reproduce.
   a. Put the homozygous yellow pairs in the bin with other yellow beads.
   b. Record the surviving number of yellow & red *alleles* left on the table in lines 5a–5c of Table 5 and the total in line 6.
   c. Calculate the frequency of the red allele in the remaining individuals by dividing the number of reds (line 5b) by the total number (line 5c) and record it to 3 decimals in line 6. This is the allele frequency after one generation of selection, and will be the starting gene pool for the next generation.
5. **Reproduction.** The carrying capacity of this population is 50 spiders and all survivors are equally likely to reproduce because *AA* and *AB* have equal fitness. This means that after they reproduce, there will end up being 50 individuals in the population at the start of the next generation.
   a. Use the calculated allele frequency after one generation of selection to create the next generation of 50 individuals (with 100 alleles). Add or subtract red or yellow beads to the population to begin each new generation's gene pool of 50 individuals with allele frequencies equal to the adults of the previous generation (rounded to 2 decimal places).

Table 4 summarizes the above steps of mating, selection and reproduction; your data will go in Table 5.

Table 4. Example calculations *(your numbers will probably differ). Suppose in the first round of selection, 42 of the 50 individuals were homozygous recessive (2 yellow beads, line 4c), 6 were heterozygotes (line 4B), and 2 were homozygous red (line 4A). That would mean that you would remove 84 yellow alleles from the population. You would be left with 10 red + 6 yellow alleles = 16 alleles remaining. The new allele frequency for the population would be 10/16= 0.625 red (line 8) and 1 – 0.625 = 0.375 yellow after one generation of selection. You would then start the next round of selection with 50 individuals but there would need to be 63 red alleles and 37 yellow alleles to achieve that starting frequency. Remember, P[A] + P[B] = 1. The table below shows how this example would be appear in Table 4. {Red text in curly braces like this provides hints only & wouldn't appear in the data table.}*

		Generation	
		1	2
Gene Pool	1. Red freq. P[A]	0.10 *{10 red beads}*	0.63 *{63 red beads}*
	2. Yellow freq. P[B]	0.90 *{90 yellow beads}*	0.37 *{37 yellow beads}*
	3. Total # of spiders in pop.	50 *{100 alleles}*	50 *{100 alleles}*
Fertilized Eggs	4a. # of AA genotype = red spiders	2	
	4b. # of AB genotype = red spiders	6	
	4c. # of BB genotype = yellow spiders	42 *{84 alleles}*	
Adults - after selection	5a. # of B alleles left (line 4b)	6	
	5b. # of A alleles left (line 4b) + (2 * line 4a)	10	
	5c. Total # of alleles left (line 5a + line 5b)	16	
	6. P[A] after selection (line 5b / line 5c)	10/16 = 0.625 r= **0.63**	

Reproduction

6. **Enter formulas into the tan cells of the Excel template to automate calculations.** Download the *Lab06_D8a_Tmpl8.xlsx* file. The first worksheet tab provides a copy of Table 5 with check cells to help you verify your calculations. Enter formulas in the tan cells to do all calculations for you. Verify your formulas by entering the data from Table 4 into the spreadsheet, then erase the data in the Fertilized Eggs cells.
7. **Enter your data into Table 5 and the Excel template.** After completing the first generation and verifying your formulae, nter your bead data into the 1st generation column.
8. Repeat fertilization and selection process until you have completed Table 5, and entered your data into the template.
9. Report your numbers of yellow spiders (line 4C) to your instructor.
10. The Excel table will become Table 1 in your report.

Table 5. Data from Simulation of Selection against a Recessive Lethal Allele. *Selection in a population where the fitness of genotype BB = 0, fitness of AA, and AB = 1. You will enter your own data for generation 1 below and in the data template where you will enter formulas into the tan cells to do the calculations.*

	Generation				
	1	2	3	4	5
1. Red freq. P[A]	0.10	Round(l6, 2)			
2. Yellow freq. P[B]	0.90	=1 - l1			
3. Total # of spiders in pop.	50	50	50	50	50
4a. # of AA (red) spiders					
4b. # of AB (red) spiders					
4c. # of BB (yellow) spiders (Report to Instructor)					
5a. # of *B* alleles left (line 4b)	l4b				
5b. # of A alleles left (line 4b) + (2 * line 4a)	l4b + 2 * l4a				
5c. Total # of alleles left (line 5a + line 5b)	l5a + l5b				
6. P[A] after selection (line 5b / line 5c)	l5b / l5c				

11. In Excel, create a *scatter plot line graph* of the allele frequencies over time (plot the two allele frequencies on the V–axis and the generation number on the H–axis). This will become Fig. 1 in your report.

So now we know what happens over 5 generations, but the question remains — how long would it take for the lethal recessive allele to be eliminated?

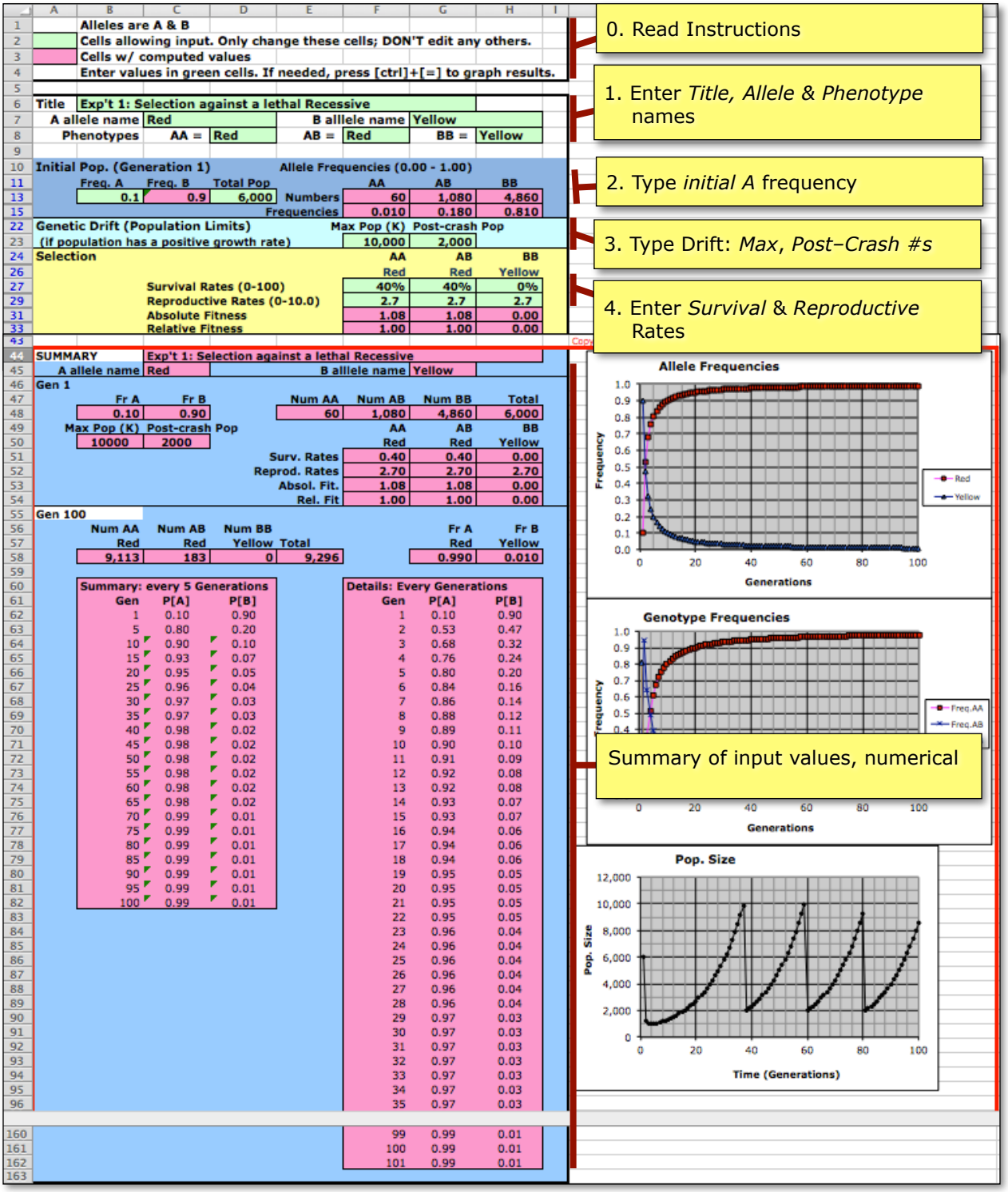

Figure 1. EVOLVE display. *Green cells are for you to enter experimental values. The dark blue area establishes the initial population; the pale blue area determines the range of population sizes; the yellow area determines the pattern of natural selection and calculates fitness coefficients. The graphs show the allele frequencies, genotype frequencies, and population size over the duration of the experiment. The red cells automatically calculate the frequency of B, and the Absolute and Relative fitnesses. The pink tables in the lower dark blue area summarize the allele frequencies every 5th generation (left), and in each of the 100 generations (right).*

EXPERIMENT 2: EVOLVE COMPUTER SIMULATION OF SELECTION AGAINST A RECESSIVE LETHAL ALLELE

Experiment 1 shows us what happens over 5 generations, but the method would be tedious, to say the least, to run for 100 generations. In situations like this scientists turn to computers. In Experiment 2 you will repeat experiment 1 using the computer simulation to examine the long–term fate of the recessive allele. A key question for any scientific simulation is whether the program accurately captures/imitates the real–world phenomena. In our case we will ask whether our Excel program duplicates the results of the manual simulation in Exp't 1. Do you have confidence in EVOLV's projection to 100 generations? This is a validation of our methodology for exploring evolution over the next few labs. Finally, of course, we want to answer the question of what happens to the two alleles' frequencies.

1. ***Based on the results of experiment 1*, what do you expect to happen to the frequency of the two alleles over 100 generations? (Make a quantitive, specific numerical predictions) Have your instructor initial it.**

   The *A* allele will go from a frequency of _____ in generation 1 to a frequency of _____ in generation 100.

   The *B* allele will go from a frequency of _____ in generation 1 to a frequency of _____ in generation 100.

   (record ea. student's prediction on lab map, post on board) Initials:_____

PROCEDURE USING EVOLVE

Now that you have experience simulating evolutionary processes with beads, let's let a computer do the tedious work so we can do more experiments over longer time periods. EVOLVE is an Excel program that simulates some evolutionary situations. It essentially automates the process you used in the first experiment.

1. Login to Engage and download *EVOLVE.xls* to the *desktop* of your computer (not a network drive) and open the file.
2. You should see something like Fig. 1. You determine the initial population size, the carrying capacity (Maximum population), and survival and reproductive rates, EVOLVE does the rest.
3. In the dark blue area, make sure the initial frequency of *A* (In.Fr A) is set to **0.1** (10%, the value in exp't 1), and the Initial population size (In. Total Pop) i**s 6,000.**
4. In the Genetic Drift section, set the maximum population size to **10,000** and the post–crash population to **2,000**. If the population grows (it might not), and exceeds the maximum, then it will 'crash' to the lower value. This simulates a J–type, exponential, population growth curve.
5. In the Selection area, set the survival rates of the genotypes to **40**%, **40**% and **0**%. This simulates our scenario from exp't 1 where the yellow, *BB*, genotype was lethal. For this experiment, the reproductive rate (number of offspring produced by each genotype) isn't important. The *B* allele only affects color, so set them all to **2.7**.
6. When you have set all the values, if the graphs don't update, press *Ctrl+=* to have Excel run the simulation.

If you want to see what happens over even longer time intervals, copy the *A* allele frequency and population size in generation 100 (0.990 and 9,296 in Fig. 1) up to the initial frequency and population size; you will see the results of another 100 generations.

Try other values for survival rate of the *AA* & *AB*. Can you explain what happens?
When you are finished exploring, continue with step 7.

7. Zoom the Excel window so you can see all of the graphs. Copy the entire window and paste it at the bottom of the report template file as Appendix A.
   a. PC users: Press *Shift+Printscreen Alt+PrtScr* or *fn+PrtScr* (varies with PC) to capture the screen to the clipboard. You will need to crop the resulting image after you *Paste > Special > Picture*
   b. Mac Users: Press *Commnd+Control+Shift+4* to get the crosshair cursor and drag it around the graphs and the input area. This captures just the area you want to show and puts it on the clipboard.

8. Download *Labxx_Rpt_Tmpl8.docx*; follow the instructions to write a report introducing, summarizing results and drawing conclusions about what happens to a recessive lethal allele over 100 generations. Note that you won't be using means and standard deviations in your report—there are none. Instead, you will describe the paths of the frequencies of the red and yellow alleles. Such a description must include 'landmark' frequency values showing where the frequencies started, where they ended, and important values in between. Do the results of Exp't 2 match those of Exp't 1?

LAB 6 PRE–LAB HOMEWORK

Use this copy of Table 2 to answer questions 1–8 below. #1 is done for you as an example. Note that these examples have nothing to do with our lab experiments.

Genotypes	Species 1			Species 2		
	AA	AB	BB	CC	CD	DD
Survival Rate, *S*	20	20	80	40	20	20
Reproductive Rate, R	6	6	2	3	6	6
Absolute fitness, S*R	120	120	160	120	120	120
Relative fitness (Abs Fit)/Max(Abs. Fit)	0.75	0.75	1.00	1.00	1.00	1.00

SPECIES 1

1. **Briefly explain why *A* is dominant and *B* is recessive for *survival rate*.** _____

   Genotype AB has the same 20% survival phenotype

2. **Briefly explain why *B* is recessive for *reproductive rate*.** _____

   2–young phenotype shows only in BB genotype

3. **Briefly explain why *A* is dominant for *fitness*.** _____

   AB has same 1.2 phenotype as AA genotype

4. **Briefly explain why *B* is evolutionarily *advantageous*.** _____

   BB genotype has higher relative fitness (1.00) than AA or AB (0.75) genotypes

SPECIES 2

5. **Briefly explain why *D* is dominant and *C* is recessive for *survival rate*.** _____

   CD genotype has same 20% phenotype as DD genotype; 40% phenotype shows only in CC genotype

6. **Briefly explain why *D* is dominant and *C* is recessive for *reproductive*.** _____

   CD genotype has same 6–young phenotype as DD genotype; 3–young phenotype shows only in CC genotype

7. **Briefly explain why both alleles have equal *fitness*.** _____

   40% survival & 3 young = 20%survival & 6 young

8. **Briefly explain why neither allele is evolutionarily *advantageous*.** _____

   all genotypes have the same fitness

Use this part of Table 2 to answer questions 9–16 below (9 & 10 done for you as an example).

Genotypes	Species 3			Species 4		
	EE	EF	FF	GG	GH	HH
Survival Rate, *S*	20	80	80	80	50	20
Reproductive Rate, R	6	6	2	4	6	6
Absolute fitness, S*R	120	480	160	320	300	120
Relative fitness (Abs Fit)/Max(Abs. Fit)	0.25	1.00	0.33	1.00	0.94	0.38

SPECIES 3

9. What is the pattern of inheritance for *survival* rate of each allele? (X all that apply)

__ *E* dominant, *F* recessive X *F* dominant, *E* recessive (xxx)

__ *E* & *F* codominant __ *E* & *F* incompletely dominant __ *E* & *F* show Heterosis __ None of these

10. What is the pattern of inheritance for *reproductive* rate of each allele? (X all that apply)

X *E* dominant, *F* recessive (xxx) __ *F* dominant, *E* recessive

__ *E* & *F* codominant __ *E* & *F* incompletely dominant __ *E* & *F* show Heterosis __ None of these

11. What is the pattern of inheritance for *fitness* of each allele? (X all that apply)

__ *E* dominant, *F* recessive __ *F* dominant, *E* recessive

__ *E* & *F* codominant __ *E* & *F* incompletely dominant __ *E* & *F* show Heterosis (xxx) __ None of these

12. Does one of the alleles have an evolutionary advantage over the other? (X all that apply)

__ Advantage *E* __ Disadvantage *E* (Slight) __ Advantage *F* (Slight) __ Disadvantage *F* __ Neither has advantage (xxx)

SPECIES 4

13. What is the pattern of inheritance for *survival* rate of each allele? (X all that apply)

__ *G* dominant, *H* recessive __ *H* dominant, *G* recessive

__ *G* & *H* codominant __ *G* & *H* incompletely dominant (xxx) __ *G* & *H* show Heterosis __ None of these

14. What is the pattern of inheritance for *reproductive* rate of each allele? (X all that apply)

__ *G* dominant, *H* recessive __ *H* dominant, *G* recessive (xxx)

__ A & B Codominant __ A & B incompletely dominant __ A & B show Heterosis __ None of these

15. What is the pattern of inheritance for *fitness* of each allele? (X all that apply)

__ *G* dominant, *H* recessive __ *H* dominant, *G* recessive

__ *G* & *H* codominant __ *G* & *H* incompletely dominant (xxx) __ *G* & *H* show Heterosis __ None of these

16. Does one of the alleles have an evolutionary advantage over the other? (X all that apply)

__ Advantage *G* (xxx) __ Disadvantage *G* __ Advantage *H* __ Disadvantage *H* (xxx) __ Neither has advantage

17. Fill in this copy of Table 3

Genotype	Phenotype (red/yellow)	Visible to predators? (yes/no)	Relative Fitness? (0/1)
AA	Red	No	1
AB	Red	No	1
BB	Yellow	Yes	0

18. In Experiment 1, what do you think will to happen to the frequency of red and the lethal yellow alleles over 5 generations? (Make a quantitive, specific, numerical prediction — what will happen to the alleles' frequencies?

The *A* allele will go from a frequency of _____ in generation 1 to a frequency of _____ in generation 5.

The *B* allele will go from a frequency of _____ in generation 1 to a frequency of _____ in generation 5.