Evolutionary Mechanisms – The Mating Game and Computer Simulations
Developed by Drs. Patricia Peroni, Mark Stanback, and Chris Paradise

INTRODUCTION

Evolution can be defined as a change in the genetic composition of a population of organisms that occurs over time. More precisely, evolution is a change that occurs over time in the proportions of organisms in a population that differ genetically in one or more characteristics. Just as the life of an individual organism is dynamic, so is that of a species. In the study of biological evolution we can ask what factors are capable of causing change within a population.

Due to time constraints (thousands of generations may be required for one species to evolve into another), it is often difficult to perform evolution experiments on populations in a laboratory course. Our approach instead of conducting experiments with real creatures and real genes, is to first investigate these questions using a hypothetical population. We will conduct simulations to determine the factors that can facilitate or inhibit genetic change at one locus within this population. Our hypothetical population will be very simple, and we'll focus on how different factors affect the genotype and allele frequencies at one locus.

The simulation approach we will use represents a type of theoretical investigation. Why should we use this approach before we conduct experiments with real organisms? Theoretical inquiry serves as a guide for empirical research (i.e., research that involves taking measurements on real organisms). Real systems are complex, and experimental research with these systems is often time consuming and expensive. Theoretical research allows us to ask "what if" questions using very simple systems that we refer to as models. In a general sense, a model should be thought of as formalized working hypothesis. That is, in the context of a computer simulation model, the program itself is written to test a prediction about the mechanisms responsible for a given event (in this case, parameters affecting populations). If the hypothesis is correct, then the program will accurately simulate an event.

The results of such investigations can suggest questions that can be further tested with experiments and the types of results we might expect to obtain from such studies. If the predictions of theoretical investigations and empirical studies are at odds with each other, then we must refine our theoretical models to account for factors omitted from our initial inquires. The operation of testing a model, and changing it as required, is part of the scientific process. All active areas of research involve this type of interplay between theoretical and empirical research, and our understanding of how the world operates depends upon both types of investigations.

GAME PLAN

1. As a class we will simulate a very simple population of interbreeding organisms, and we will then investigate how changes in characteristics of the population and its environment affect the direction and rate of evolution at one particular locus.

Before we conduct each simulation, record your prediction for the simulation's outcome and the rationale you used to make that prediction.

CLASS SIMULATIONS

Our goal is to simulate a very simple population and look at one very simple genetic characteristic. In order to accomplish this goal, we will assume that:

1. Each individual in the population reaches reproductive maturity, mates, produces two offspring, and then dies.

2. Individuals in the population are hermaphrodites (i.e., can function as both mothers and fathers) but cannot self-fertilize.

3. The genetic trait under consideration is controlled by two alleles, A and a, at one locus. The A allele is dominant with respect to the a allele. Individuals in the population are homozygous for all other loci.

4. No individuals enter or leave our population (i.e., no immigration or emigration).

General Instructions

1. Each new simulation will begin with a population with an initial frequency (*p* and *q*) of 0.5 for alleles A and a, and genotype frequencies of 0.25 for the *aa* and AA genotypes and 0.50 for the *Aa* genotype.

2. Each of you will receive two index cards that represent your genotype at the locus of interest (e.g., if you receive two *a* cards, your genotype is *aa*). Record this genotype on your data sheet.

3. You will then proceed to mate. Unless instructed otherwise, you should be entirely promiscuous (remember, this is very safe sex - on paper only). Choose anyone else in the class (male or female - remember for our simulation purposes you are all hermaphrodites) and approach them confidently – introduce yourself. They will not refuse to mate. Once you find a mate, flip a coin to determine which allele you will contribute to your first offspring - your mate will do the same (if you are homozygous you obviously can skip this step). Record the genotype of your offspring on a piece of scrap paper. Now, repeat the process to produce a second offspring and record it's genotype. By having each couple produce two and only two offspring per generation, we keep the population size constant.

4. Once you and your mate have produced two offspring, wait for me to signal the end of that generation. At the end of the generation, you and your mate will "die", and each of you will assume the genotype of one of your two offspring (e.g., if you produce an AA and an *Aa* offspring, one of you assumes the AA genotype and the other assumes the *Aa* genotype). Record your new genotype on your data sheet.

5. When I signal the beginning of a new mating session, you will pick another mate and produce two new offspring using the alleles from your new genotype. Never mate with the same

person twice in a row, unless directed to do so.

6. We will complete 5 generations of mating for each simulation.

IMPORTANT NOTES

- **Mate with only one individual** each generation.
- Do not move on to a new generation of mating **until I instruct** you to do so.
- If you are heterozygous, you **sample with replacement** when you decide which allele to give to each offspring. This means that if you designate the A allele as heads and the other allele as tails, you could end up donating an A allele to both offspring.
- Remember to **record your new genotype** in the appropriate place on your data sheet.

SIMULATIONS

Null Model

If no evolutionary mechanisms influence the locus under consideration, then allele frequencies should remain constant over time and genotype frequencies should eventually match Hardy Weinberg predictions. We will calculate the allele and genotype frequencies of our populations at the beginning of each simulation. If the allele and genotype frequencies we calculate at the end of each generation deviate significantly form the initial conditions, then we know that some evolutionary mechanism affected the population during the simulation.

Simulation #1: Small population sizes

In this simulation we will examine the effects of population fragmentation and small population size on evolution. I will randomly split the class into 3 populations of four individuals each. Remember to clearly mark your data sheet with the name of your population. The individuals in each population will then proceed to mate following the instructions provided above. Record your data in Table 2. NOTE: Mate only with individuals in your population.

Simulation #2: Non-random mating

Begin this simulation with the genotype you were assigned at the beginning of simulation #1. In this case, we will again form one large population and examine the effects of non-random mating on evolution at our locus. We will again assume that the AA and *Aa* genotypes have the same phenotype (i.e., A dominant to a). When you pick a mate, keep trying to find one whose phenotype matches yours. Mate only with someone of a different phenotype as a last resort. Otherwise, proceed as you did for simulation #1. Record your genotype for each generation (and the class frequencies) in Table 3. How does this case compare to the first simulation? What happens to *p* and *q*? Has evolution occurred?

Table 1. Record your data from simulation 1 here to determine if your class is in Hardy-Weinberg Equilibrium.

Generation	Your Genotype	Class Data				
		A/A	*A/a*	*a/a*	*p*	*q*
Start-P					0.5*	0.5*
F_1						
F_2						
F_3						
F_4						
F_5						

Table 2. Record your data from simulation 2 here to examine genetic drift in small populations.

Generation	Your Genotype	Class Data				
		A/A	*A/a*	*a/a*	*p*	*q*
Start-P						
F_1						
F_2						
F_3						
F_4						
F_5						

Simulation #3: Selection Against Homozygous Recessives

Here we'll violate one of the assumptions of our model to see how allele frequencies change. Assume there is a genetic disease in our population in which offspring that are homozygous recessive (*a/a* genotype) do not survive. Individuals who have the *a/a* genotype are physically debilitated and die at a young age. Individuals of the other two genotypes, *A/A* and *A/a* (the homozygous dominant and heterozygous genotypes, respectively) survive equally well. Begin this simulation with the genotype you were assigned at the beginning of simulation #1. We'll assume that any homozygous recessives (*a/a*) will survive to mate in this parental generation (however, if you're *a/a* to start, you can't mate with another *a/a* in generation 1). Mate just like you have been. However, every time you and your partner produce a homozygous recessive child, it dies. Since we want to keep the same population size, continue to mate until you produce two viable offspring. Record your genotype for each generation (and the class frequencies) in Table 4. How does this case compare to the first simulation? What happens to *p* and *q*? Has evolution occurred? Are there recessive alleles left in the population?