INTRODUCTION

EVOLVE is a computer program that allows you to experiment with evolution and to get quick results in a fashion that is impossible to do in any other way. You may control the starting population, overall population size, natural selection, pattern of inheritance and migration in a hypothetical population. By experimenting with EVOLVE you will develop:

- a better understanding of evolutionary processes and their interactions,
- a firmer grasp of some important concepts of Mendelian genetics,
- some understanding of experimental design, and
- of the use of models, plus
- an appreciation for one of the many uses of computers in biology.

BASIC GENETIC AND EVOLUTIONARY CONCEPTS AS USED IN EVOLVE

- A ***Species*** can be conceived of as a metapopulation, a set of more–or–less isolated subpopulations that are capable of reproducing within & amongst themselves and which cannot reproduce with other species. EVOLVE simulates a metapopulation with one or more subpopulations.
  - Each population in a metapopulation has 1 ***Gene*** that affects 1 or more traits (e.g., pigments, proteins, etc.)
    - Genes may have 2 or 3 ***Alleles*** (usu. more in nature) symbolized by A, B, C. Alleles have
      - ***Mutation Rates*** (A–>B, B–>A, A–>C, C–>A, B–>C, C–>B)
      - ***Patterns of inheritance***, determined by interactions between alleles and include
        - ***Dominant–Recessive***: heterozygote has same phenotype as dominant homozygote, recessive phenotype is homozygous recessive. E.g., if AA = 5, AB = 5, BB = 10, A is dominant, B is recessive
        - ***Incomplete Dominance***: heterozygote is in between phenotypes of homozygotes. E.g., If AA = 5, AB = 8, BB = 10, alleles are incompletely dominant.
        - ***Codominance***: heterozygote displays phenotypes of both homozygotes. E.g., AA = Protein1, BB **=** Protein 2, AB = Proteins 1 & 2.
        - ***Overdominance / Heterosis / Heterozygote superiority***: heterozygote phenotype is more extreme than either homozygote. E.g., AA = 5, AB = 13, BB =8
        - ***Underdominance / Heterozygote inferiority:*** heterozygote phenotype is less extreme than either homozygote. E.g., AA = 5, AB = 3, BB = 10
        - For examples of different inheritance patterns, see Tables 1 & 2 below.

Table 1. Human ABO Blood groups: Dominance/Recessive & Codominant Inheritance

	GENOTYPE			
(EVOLVE) (Medical)	**AA, AC AA, Ao**	**BB, BC BB, Bo**	**AB AB**	**CC oo**
Blood Phenotype	Only A protein, Type A	Only B protein, Type B	Both A & B proteins, Type AB	Neither protein, Type O
Pattern of Inheritance	A dominant, o recessive	B dominant, o recessive	A & B codominant	o recessive to A & B

Table 2. Sickle cell anemia: Inheritance pattern varies depending on the level of analysis.

	PHENOTYPE				
Genotype	**Disease***	**Protein†**	**Resistance to Malaria††**	**Fitness in Malaria Environment††**	**Fitness in Non–Malaria Environment***
Homozyg. AA (Hb*A* Hb*A*)	Normal	Hb*A*	Low	Fair	High
Heterozyg. AB (Hb*A* Hb*S*)	Sickle Cell Trait	Hb*A*, Hb*S*	10x higher than AA	Highest	High
Homozyg. BB (Hb*S* Hb*S*)	Sickle Cell Disease	Hb*S*	Low	Essentially Zero	Low
Hb*S* Inheritance Pattern	**Incompletely dominant**	**Co-dominant**	**Heterotic**	**Heterotic**	**Recessive**

* The HbS allele makes a protein with one amino acid substitution that causes the protein to form long crystals in low–oxygen environments. Red blood cells tend to form sickle shapes that clog capillaries and cause many painful symptoms. HbA homozygotes are

'normal'. HbS homozygotes have 'sickle cell disease'; in the past, most died in childhood. Heterozygote show a tendency to 'sickle' when dehydrated, stressed, or in low–oxygen environments and are said to have 'sickle cell trait'. In essence, they have a mild disease.

† At the molecular level alleles are considered codominant because heterozygotes produce both normal and abnormal proteins. HbS homozygotes produce only the sickle protein & so have a high tendency for red blood cells to sickle.

†† In malarial environments, homozygous HbA individuals are very susceptible to the disease, while heterozygotes have partial immunity and get less severe cases if they do get the disease. The heterozygotes thus have the highest fitness, i.e., they show 'heterosis' (AKA, 'heterozygote superiority") and the alleles are said to be 'heterotic'.

* In modern environments with good healthcare & without malaria, heterozygotes can stay as healthy as HbA homozygotes, to the HbA allele is dominant to the recessive HbS allele.

  - A Population consists of ***Organisms.***
  - Ea. Organism has 2 copies of each gene
    - Thus, organisms may have one of 3 (or 6) ***Genotypes*** symbolized AA, AB & BB if there are 2 alleles; if there are 3 alleles, add AC, BC & CC.
    - Genotypes may be ***Homozygous*** (2 copies of same allele, i.e., AA, BB, CC) or ***heterozygous*** (2 different alleles, i.e., AB, AC, BC)
  - Organisms have ***Phenotypes***: observable traits (e.g., pigments, proteins, structures, behaviors, etc.) produced by their genotype. Phenotypes of interest in EVOLVE include:
    - ***Survival rate*** (genotype's avg. proportion of young surviving to adulthood)
    - ***Reproductive rate*** (genotype's avg. number of young / adult)
    - ***Absolute Fitness*** (genotype's Survival Rate * its Reproductive rate) Values > 1 result in increasing population size, values < 1 result in population decline; they may go to extinction.
    - ***Relative Fitness*** (genotype's Absolute Fitness / the maximum absolute fitness) Values 0–1
    - ***Migration rates*** (proportion of individuals with the genotype moving to another population)
    - ***Mating preferences*** (non–randomness, preference or bias in mating of one genotype with another) Values 0–1. E.g., with *outcrossing*, individuals of a genotype prefer to mate with individuals unlike themselves. In a 2–allele population, AA individuals might proportionally mate 50% with BB, 40% with AB and 10% with AA.
- ***Evolution*** is defined as a change in the genetic makeup of a population, i.e., a change in allele or genotype frequencies.

Hardy–Weinberg Equilibrium Concept

- A population can be modeled as a ***Gene Pool*** made up of all of the alleles in a population. Gene pools have
  - ***Allele Frequencies***, the proportion of all alleles in a population that are a specific allele; e.g., the frequency of A = the number of A alleles / the total number of alleles. Traditionally, p = freq. of A, q = freq. B, r = freq. C), by definition, $p + q = 1$ in a 2–allele population or $p + q + r = 1$ in a 3–allele population.
  - ***Genotype frequencies,*** the proportion of all genotypes that are a specific genotype; e.g., freq. of *AA* = number of *AA* / Total population size.
  - ***Mating*** consists of randomly sampling pairs of alleles without replacement from the gene pool to produce the young of the next generation.
- All things being equal, allele frequencies will not change and what is sometimes called the *Hardy–Weinberg Law* states that genotype frequencies will be $p^2 + 2pq + q^2$ in a 2–allele population or $p^2 + 2pq + 2pr + 2qr + q^2 + r^2$ in a 3–allele population This is the null case of no evolution; allele and genotype frequencies won't change and the population is in *Hardy–Weinberg equilibrium* (HW).
- However, in the real world all things are not equal. HW makes 7 assumptions:
  1) Genotype frequencies in the two sexes are equal.
  2) Generations are discrete, i.e., do not overlap.
  3) Population size is infinitely large.
  4) Mating is random.
  5) There are no differences in survival and/or reproduction, i.e., no natural selection.
  6) population is closed, i.e., no migration in or out of population.
  7) alleles do not change, i.e., no mutation
- All of these assumptions are violated in real–word populations. EVOLVE avoids the first two by modeling organisms that are hermaphroditic and die after reproducing; you can experiment with the other 5 evolutionary forces:

- ***Mutation***: H–W assumes alleles don't change, or that mutation rates from one allele to another are equal. Mutations do occur in the real world and generate the genetic variation essential for evolution to occur.
- ***Natural selection:*** H–W assumes there are no differences in allele/genotype survival or reproduction. This of course is often violated and allows populations to adapt to their environments.
- ***Gene Flow:*** H–W assumes the population is closed, i.e., there is no differential emigration/immigration of alleles/genotypes between populations.
- ***Genetic Drift:*** H–W assumes the population is infinitely large. Any real population is finite and subsequent generations are a more–or–less accurate samples of the alleles present in the previous generation's gene pool.
- ***Sexual Selection / Non–Random mating:*** H–W assumes there are no differences in probability of genotypes mating w/ ea. other.

Modeled Organisms

The organisms modeled by EVOLVE are assumed to

- Be ***Diploid***: have 2 copies of a gene that has two or three alleles.
- Have ***non–overlapping generations***: e.g., animals where adults mate, lay eggs or give birth and die before the young become adults, or annual plants that cross–pollinate, set seeds and die before the seeds germinate. This avoids assumption 1) above.
- **Hermaphroditic**: having male and female organs that normally mate/pollinate with another individual, but are capable of self–fertilizing if they cannot find a mate or are not pollinated. This avoids assumption 2) above.
- ***Life cycle:*** adults mate, produce zygotes (eggs/seed/young), die. A % of young may emigrate; migration is random between populations. Immigrants are added to resident young. Young undergo selection, those that survive are adults of next generation.

EVOLVE AS AN EVOLUTIONARY LABORATORY

Perhaps it is belaboring the obvious to say that experiments in evolutionary biology are difficult -- you can't evolve something in a semester! Nevertheless, this is an important point because it has made the approach of evolutionary biologists somewhat different from that of many other biologists. And learning about evolution is difficult because students can't "get their hands dirty" by doing experiments like those in, for example, physiology or biochemistry.

A common, naive view of science is that experiments are required to test hypotheses. In most scientific disciplines we note some aspect of the "real world," formulate hypotheses about major factors involved in that phenomenon and test those hypotheses with experiments. Experiments essentially are simple models of the real world that hold most factors constant, vary one or a few factors, and observe the results. In many areas of biology, experimental design has become a sophisticated and elaborate affair of choosing organisms, equipment, statistical methods, etc.

Evolutionary biologists can apply that approach only with difficulty. We can do classical types of experiments using small organisms with short life cycles. Occasionally we can find a situation in nature that approaches a true experiment, but it is hard to coax Ma Nature into providing us with good experimental models. However, observational tests of hypotheses are quite common in evolutionary biology, as in other historical sciences like geology and astronomy.

Despite (or perhaps because of) difficulties with experimentation, biologists continue to develop models of evolutionary processes, many mathematical rather than experimental or observational. In essence, we simulate some aspect of the real world in mathematical, abstract form, and then manipulate the simulation to investigate its consequences. If the model is a good one, the consequences will clarify the real world. The Hardy-Weinberg formula and the mathematical population genetics that evolved from it are excellent examples of such models. Many of these models can be programmed into computers, which brings us to EVOLVE.

EVOLVE allows you to setup experiments that can illustrate the effects of all of the evolutionary forces on allele and genotype frequencies — Genetic Drift (population size), Natural Selection (differences in reproductive success), Mutation (change of alleles), Migration (migration of alleles between subpopulations), and Sexual Selection (non–random or preferential mating). These may be studied individually or in combination. In addition, you may allow the population size to vary within specific ranges, which allows you to see how evolution affects a key ecological variable, the intrinsic rate of population increase.

Using EVOLVE

When you launch EVOLVE, you will see its *Input Screen* where you configure your experiments by selecting options and entering parameter values. When finished, click on the Submit {or Run} button. EVOLVE performs the experiment and displays a graph to visualize different aspects of the results. You may modify the data that are graphed and export graphs to PDF image files. Input parameter values and numeric results are also exported to CSV files where they may be analyzed with spreadsheet or statistical software.