

CoreModels

Peppered Moth

A CORE LEARNING GOALS ACTIVITY FOR SCIENCE AND MATHEMATICS

Summary

Students will use a STELLA model based on the Hardy-Weinberg principle to examine the effects of natural selection on the appearance of the peppered moth.

This activity was found at the web site for the course, Introduction to Global Change, at the University of Michigan. See http://www.sprl.umich.edu/GCL/globalchange1/fall2000/labs/peppered_moth/pepperedmoth.html

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Natural Selection: The Case of the Peppered Moth

Objective

The purpose of this lab exercise is to model the effects of natural selection on the appearance and genetic make-up of a natural population (the peppered moth). We will use a STELLA model for this population that incorporates the basic principles of population genetics.

Before we begin, we will need to define some important genetics terminology:

- Alternative forms of a gene are called alleles.
- The genetic constitution of an individual is called its genotype.
- The physical expression of a genotype is called the phenotype.
- If two alleles are identical, an individual is said to be homozygous for that gene; if two alleles are different, the individual is said to be heterozygous.
- A dominant allele has such a strong phenotypic effect in heterozygous individuals that it conceals the presence of the weaker (recessive) allele.

Introduction

The case of the peppered moth (*Biston betularia*) is a classic example of evolution through directional selection (selection favoring extreme phenotypes). Prior to the industrial revolution in England (pre-1740), the peppered moth was found almost entirely in its light form (light body colored with black spots). The moths would spend daylight hours on trees covered by a light colored lichen, their light colors giving them almost perfect camouflage against predatory birds. There were a few dark individuals in the population, but their occurrence was very rare.

Scientists have determined that body color in the peppered moth is controlled by a single gene. The allele (version of the gene) for dark body color is dominant, which means that a moth possessing at least one such allele will have a dark body. (Each individual will have two copies of the gene—one from each of its parents.) To have a light body, the moth has to have both alleles for light body color. Dark moths were at a distinct disadvantage, however, due to their increased vulnerability to bird predation. Thus the frequency of the dark allele was very low (about .001%), maintained primarily by spontaneous mutations from light to dark alleles.

By 1819, the proportion of dark moths in the population had increased significantly. Researchers found that the light-colored lichens covering the trees were being killed by sulfur dioxide emissions from the new coal burning mills and factories built during the industrial revolution. Without the light background of the trees, the light moths were more visible to vision-oriented predators (birds). They were losing their selective advantage to the dark moths, which, against the trees' dark bark background, were less visible to birds. In 1848, the dark moths comprised 1% of the population and by 1959 they represented approximately 90% of the population.

In this exercise, we will construct a model simulating the effects of differential predation pressures on a hypothetical peppered moth population. To do this, we will need to incorporate the genetics of moth body color into a population dynamics model. We are assuming that body color is the only trait that confers any significant selective advantages on peppered moths.

Hardy-Weinberg

Researchers G.H. Hardy and W. Weinberg developed an expression to describe the equilibrium of genotype frequencies that are obtained under random mating of sexual, diploid organisms under several important conditions, which include large population size, no mutation, no migration, and no natural selection. The Hardy-Weinberg principle states that, with random mating for a gene with two alleles A and a at respective frequencies p and q, the genotype frequencies of AA, Aa and aa are:

$$AA: p^2$$

$$Aa: 2pq$$

$$aa: q^2$$

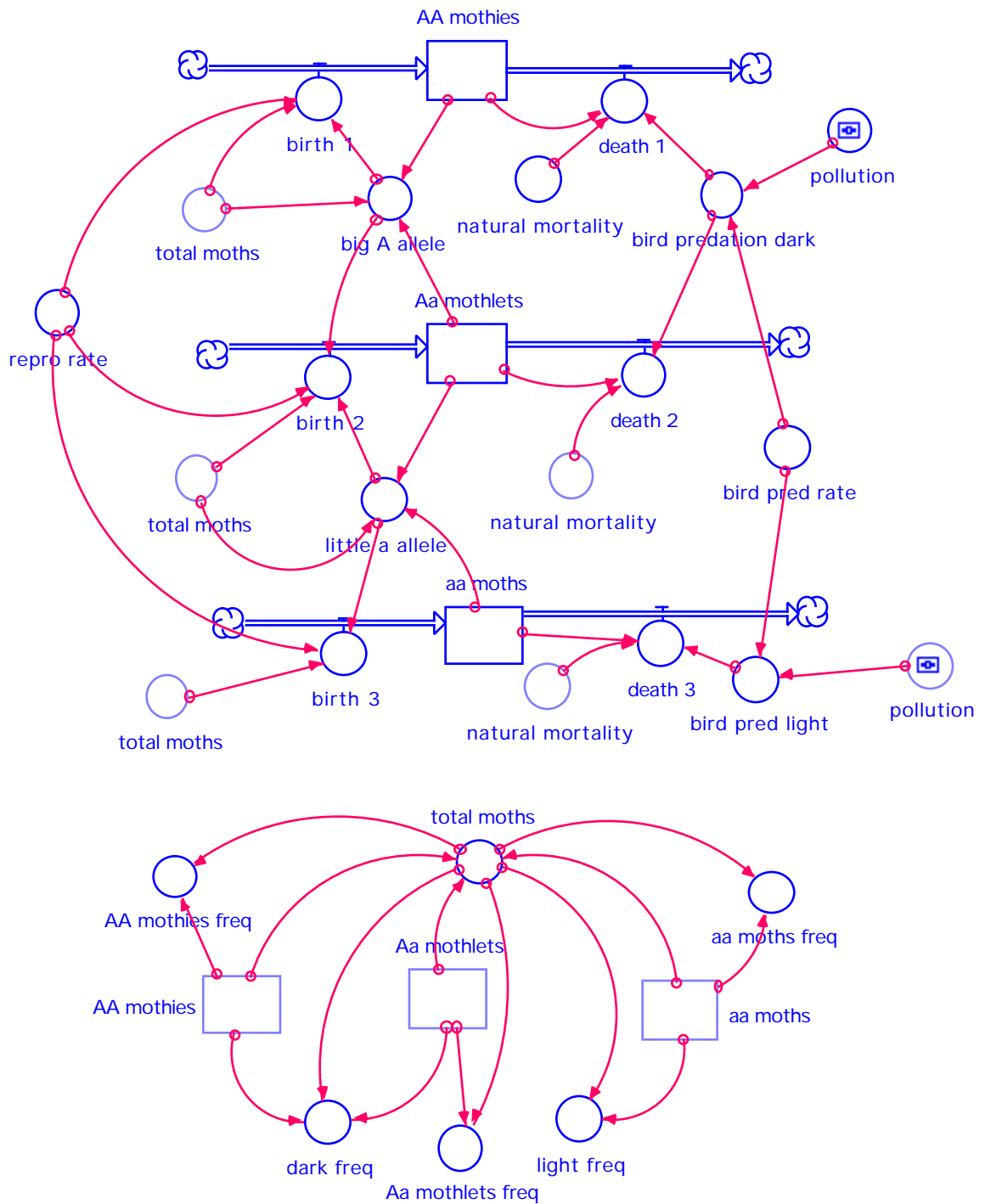
The genotype frequencies in a population must sum to one, so $p^2 + 2pq + q^2 = 1$. One of the most important implications of the Hardy-Weinberg principle is that, with random mating, and in the absence of selective pressures, the allele frequencies remain the same generation after generation, constituting the Hardy-Weinberg equilibrium for two alleles. As allele frequencies change due to natural selection, however, the Hardy-Weinberg equation can be used to calculate expected genotype (and allele) frequencies for the next generation. (See Hartl 1988 for a thorough treatment of the Hardy-Weinberg principle.)

Sources:

Futuyma, Douglas J. 1979. *Evolutionary Biology*. Sinauer Associates, Sunderland, Massachusetts.

Hartl, Daniel L. 1988. *A Primer of Population Genetics*, second edition. Sinauer Associates, Sunderland, Massachusetts.

The Peppered Moth Model



Stocks, Flows, and Converters

Stocks - the three genotypes:

AA moths: homozygous dominant moths that are dark in color.

Aa mothlets: heterozygous moths that are also dark in color

aa moths: homozygous recessive moths that are light in color

Note: STELLA will not let you repeat variable names. Because STELLA is not case sensitive, it doesn't distinguish between the names "aa moths" and "Aa moths," so we have to vary them (i.e. "moths" vs. "mothlets.")

Flows - births and deaths - and associated converters

Births:

birth1 = (repro rate * total moths) * (big A allele²)

birth2 = (repro rate * total moths) * (2*big A allele*little a allele)

birth3 = (repro rate * total moths) * (little a allele²)

In these flows, the birth rate is calculated by multiplying the reproduction rate of the total population with the frequency of occurrence specific to that genotype.

repro rate = .055

Remember that these frequencies are derived from the Hardy-Weinberg (H-W) equation (p^2 for AA, $2pq$ for Aa and q^2 for aa.) For clarity, we have used "little a allele" instead of p , and "big A allele" instead of q .

The allele frequencies are also derived from the H-W equation, and calculated as:

big A allele = $(2*AA \text{ moths} + Aa \text{ mothlets}) / (2*\text{total moths})$

little a allele = $(2*aa \text{ moths} + Aa \text{ mothlets}) / (2*\text{total moths})$

The term for total moths is calculated by using the GHOST to make copies of the 3 stocks and adding them together:

total moths = AA moths + Aa mothlets + aa moths

Deaths:

Now let's look at the death flows for our stocks:

death1 = AA moths * (natural mortality + bird predation dark)

death2 = Aa mothlets * (natural mortality + bird predation dark)

death3 = aa moths * (natural mortality + bird predation light)

The death flows incorporate a natural mortality rate

natural mortality = .045

as well as death resulting from predation by birds.

Notice that the bird predation rates are different for dark and light moths.

bird predation light = bird pred rate * pollution

bird predation dark = bird pred rate * (1 - pollution)

bird pred rate = .04

pollution = 0.0 (for now)

Bird pred rate and pollution are both proportions between 0 and 1. Notice that with high rates of pollution, bird predation light is higher, while bird predation dark is highest when pollution is low. Converters to calculate frequencies of phenotypes and genotypes:

dark freq = (AA mothies + Aa mothlets) / total moths

light freq = aa moths / total moths

AA mothies freq = AA mothies/total moths

Aa mothlets freq = Aa mothlets/total moths

aa moths freq = aa moths/total moths

Initial values for genotype stocks:

AA mothies = 250

Aa mothlets = 500

aa moths = 250

The model is set to run for 200 years.