Math 142-2, Optional Homework 1

Solutions

April 7, 2014

Preliminary

All mammals are capable of sexual reproduction. We will consider a simple view of this, where each organism receives one set of genes from its mother and another set from its father. In this way, each organism contains two possibly slightly different copies of each gene. When this organism later reproduces, it passes on copies of each gene at random to its offspring. We will be concerned with one particular gene, which comes in two versions (*alleles*), R and r. Since each individual contains two copies, its *genotype* may be RR, Rr, or rr (Rr is the same as rR). We will assume that it does not matter which copy was received from each parent; the two copies will be treated the same way. We wish to model the change in frequency of the r and R genes through a population of this particular species in the presence of resource limitations. To do this, we make a number of assumptions.

- No mutations are occurring to this gene
- $A(t)$ is the number of individuals with genotype RR
- $B(t)$ is the number of individuals with genotype Rr
- $C(t)$ is the number of individuals with genotype rr
- The death rates are a for RR, b for Rr, and c for rr.
- Other than their differing death rates, the three types of individuals are indistinguishable

In addition to these assumptions, there are some reasonable properties we would expect such a model to exhibit.

- In the case that the gene is irrelevant ($a = b = c$), the total population $T(t) = A(t) + B(t) + C(t)$ should obey a logistic equation.
- If only one allele is initially present ($A(0) = B(0) = 0$ or $B(0) = C(0) = 0$), the total population should also obey a logistic equation, and the allele that is initially absent should remain absent forever.
- The model should be symmetric with respect to the identity of r and R.

Problem 1

Propose a model to describe the evolution of the populations $A(t)$, $B(t)$, and $C(t)$ over time. You will need to introduce additional parameters (eg, some characterization of the birth rate) What additional assumptions have you made? Justify your model.

Your solution goes here

Problem 2

Implement your model in Matlab/Octave, C++, or any other programming language you like. Use this implementation to explore the following by running simulations with a variety of initial conditions and parameters. In each case, determine what affect the parameters have on the long term behavior of the population. Does the fraction of r allele vs R allele, $\frac{2A(t)+B(t)}{2C(t)+B(t)}$, change over time? Does it approach some fixed value (such as 0 (R does off), 1 (equality), or ∞ (r dies off))?

(a) $a = b = c$.

Your solution goes here

(b) $a = c$ but $b < a$. (heterozygote advantage).

Your solution goes here

(c) $a = c$ but $b > a$. (heterozygote disadvantage).

Your solution goes here

(d) $a = b$ but $c < a$. (rr offers some advantage).

Your solution goes here

(e) $a = b$ but $c > a$. (rr offers some disadvantage).

Your solution goes here

(f) $a = b$ but $c = 1$. (rr is absolutely fatal; such individuals die immediately after birth and never reproduce).

Your solution goes here

(g) $c > a > b$. This can occur with recessive traits, where the recessive trait rr is harmful, but yet the trait offers heterozygote advantage. How do the results differ qualitatively from

those of case (e)?

Your solution goes here

Problem 3

Sickle-cell and Cystic fibrosis are two fairly common genetic diseases. Both are recessive and, without significant medical intervention, both are effectively fatal. Sickle-cell is known to confer heterozygote advantage (such individuals fare better when infected with malaria). Cystic fibrosis has no known heterozygote advantage. Yet even though no such advantage has been found, it is nevertheless hypothesized that such an advantage must exist. Why?

Your solution goes here