

Multiple Interacting Species

MATH 469, Texas A&M University

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Predator-Prey Interactions

Recall that for predator-prey interactions, we set

y_{1_t} = Number of prey at time t

y_{2_t} = Number of predators at time t ,

and by augmenting the discrete Lotka-Volterra model, we arrived at the system,

$$y_{1_{t+1}} - y_{1_t} = ay_{1_t} \left(1 - \frac{y_{1_t}}{K}\right) - by_{1_t}y_{2_t}$$
$$y_{2_{t+1}} - y_{2_t} = -ry_{2_t} + \frac{cy_{1_t}y_{2_t}}{M + y_{1_t}}.$$

Similarly as with the discrete logistic model, this system has the deficiency that the values of y_{1_t} and y_{2_t} can become negative.

Predator-Prey Interactions

To see this, let's write the prey equation as

$$y_{1_{t+1}} = y_{1_t} \left(1 + a - \frac{a}{K} y_{1_t} - b y_{2_t} \right).$$

Clearly, if

$$1 + a < \frac{a}{K} y_{1_t} + b y_{2_t},$$

then we will have $y_{1_{t+1}} < 0$. In principle, the predator equation can have the same problem, but only if $r > 1$.

Predator-Prey Interactions

An alternative model, based on Ricker's approach, is as follows:

$$y_{1_{t+1}} = y_{1_t} e^{a(1 - \frac{y_{1_t}}{K}) - by_{2_t}}$$
$$y_{2_{t+1}} = (1 - r)y_{2_t} + \frac{cy_{1_t}y_{2_t}}{M + y_{1_t}}.$$

Here, in the absence of predators, the prey population grows precisely according to Ricker's model, and as with the discrete Lotka-Volterra model, the prey population is reduced by interactions with the predator population. The predator equation is the same as before, just written in a different form.

Keep in mind that there are several other models for which the populations remain positive (e.g., Beverton-Holt).

Predator-Prey Interactions

We can extend such models to interactions among three or more species. For example, suppose we have a three-species system with:

y_{1_t} = Amount of vegetation at time t

y_{2_t} = Number of herbivores at time t

y_{3_t} = Number of carnivores at time t .

An initial model could be

$$y_{1_{t+1}} - y_{1_t} = ay_{1_t} - by_{1_t}y_{2_t}$$

$$y_{2_{t+1}} - y_{2_t} = -ry_{2_t} + cy_{1_t}y_{2_t} - fy_{2_t}y_{3_t}$$

$$y_{3_{t+1}} - y_{3_t} = -gy_{3_t} + hy_{2_t}y_{3_t}.$$

We can then modify the individual terms as appropriate, depending on what we know about the species.

Competition Interactions

A second type of interaction between species involves competition for environment. E.g., we might think of a population of rabbits (y_{1_t}) and a population of deer (y_{2_t}). A natural model, based on the discrete logistic model, is as follows:

$$y_{1_{t+1}} - y_{1_t} = r_1 y_{1_t} \left(1 - \frac{y_{1_t} + s_1 y_{2_t}}{K_1} \right)$$
$$y_{2_{t+1}} - y_{2_t} = r_2 y_{2_t} \left(1 - \frac{s_2 y_{1_t} + y_{2_t}}{K_2} \right).$$

Notice that the different species might not entirely share resources, so we allow the carrying capacities to differ. Here, s_1 records the amount of resources (available to species 1) that an individual in the second population uses, and similarly for s_2 .

Competition Interactions

The Ricker's version for this system would be:

$$y_{1,t+1} = y_{1,t} e^{r_1 \left(1 - \frac{y_{1,t} + s_{12}y_{2,t}}{K_1}\right)}$$
$$y_{2,t+1} = y_{2,t} e^{r_2 \left(1 - \frac{s_{21}y_{1,t} + y_{2,t}}{K_2}\right)}.$$

In order to model competition among three or more species, we simply extend the same idea. For three populations, the resulting system would be

$$y_{1,t+1} - y_{1,t} = r_1 y_{1,t} \left(1 - \frac{y_{1,t} + s_{12}y_{2,t} + s_{13}y_{3,t}}{K_1}\right)$$
$$y_{2,t+1} - y_{2,t} = r_2 y_{2,t} \left(1 - \frac{s_{21}y_{1,t} + y_{2,t} + s_{23}y_{3,t}}{K_2}\right)$$
$$y_{3,t+1} - y_{3,t} = r_3 y_{3,t} \left(1 - \frac{s_{31}y_{1,t} + s_{32}y_{2,t} + y_{3,t}}{K_3}\right),$$

and similarly for the Ricker's version.

Mutualistic Interactions

In some cases, two species can interact in such a way that they both benefit. For example, plants can have this sort of interaction with certain insects that disperse the plant's seeds, and there are plant-bird interactions that work the same way. The starting point for interactions like this is

$$y_{1_{t+1}} - y_{1_t} = r_1 y_{1_t} \left(1 - \frac{y_{1_t}}{K_1}\right) + b_1 y_{1_t} y_{2_t}$$
$$y_{2_{t+1}} - y_{2_t} = r_2 y_{2_t} \left(1 - \frac{y_{2_t}}{K_2}\right) + b_2 y_{1_t} y_{2_t}.$$

Alternatively, we could use the Ricker's form, and it's clear how to include additional species.

Epidemic Models

The starting point for epidemic models is the SIR model, which is based on the following three populations:

y_{1_t} = # of susceptible individuals in the population at time t

y_{2_t} = # of infected/infective individuals in the population at time t

y_{3_t} = # of recovered/removed individuals in the population at time t .

The SIR model is

$$y_{1_{t+1}} - y_{1_t} = -ay_{1_t}y_{2_t}$$

$$y_{2_{t+1}} - y_{2_t} = ay_{1_t}y_{2_t} - by_{2_t}$$

$$y_{3_{t+1}} - y_{3_t} = by_{2_t}.$$

Notice that the first two equations form a closed system (i.e., y_{3_t} doesn't appear in either of them).

Epidemic Models

If we let N_t denote the total number of individuals at time t ,

$$N_t = y_{1_t} + y_{2_t} + y_{3_t},$$

then we see from the equations that $N_{t+1} = N_t$ (just add the equations together). This means that $N_t = N_0$ for all t , where N_0 is the initial number of individuals. Using this, we can solve the first two equations for y_{1_t} and y_{2_t} and then compute y_{3_t} from

$$y_{3_t} = N_0 - y_{1_t} - y_{2_t}.$$

In order to interpret the parameter b , let's recall our relationship from earlier in the semester between death rate d and life expectancy L : $L = \frac{1}{d}$. By the same reasoning, we can interpret $\frac{1}{b}$ as the duration of the infection for an individual.

Epidemic Models

Notice that the quantity $ay_{1_t}y_{2_t}$ is the number of newly infected individuals in generation $t + 1$. This means that the quantity ay_{1_t} can be viewed as the average number of people infected by each infected/infective individual in generation t .

We set

$$\begin{aligned} R_t &:= ay_{1_t} \frac{1}{b} \\ &= \# \text{ of infections caused by one infected/infective individual} \\ &\quad * \text{ expected time of the infection} \\ &= \# \text{ of infections caused by one infected/infective individual} \\ &\quad \text{during the course of the infection.} \end{aligned}$$

The quantity $R_0 = \frac{a}{b}y_{1_0}$ is called the *basic reproduction number*.

Epidemic Models

Notice that if we write the infected/infective equation as

$$y_{2_{t+1}} - y_{2_t} = y_{2_t}(ay_{1_t} - b),$$

we see that if $ay_{1_0} - b > 0$ then the initial infection will increase, while if $ay_{1_0} - b < 0$ the initial infection will decrease. In terms of R_0 , this asserts:

$$R_0 > 1 \implies \text{epidemic}$$

$$R_0 < 1 \implies \text{no epidemic.}$$

Epidemic Models

The standard SIR model assumes the recovered class is immune to infection. Suppose that after a period of immunity, recovered individuals become susceptible again. The model in that case would be

$$y_{1_{t+1}} - y_{1_t} = -ay_{1_t}y_{2_t} + cy_{3_t}$$

$$y_{2_{t+1}} - y_{2_t} = ay_{1_t}y_{2_t} - by_{2_t}$$

$$y_{3_{t+1}} - y_{3_t} = by_{2_t} - cy_{3_t}.$$

How should we interpret c in this case?

Epidemic Models

It's also common to introduce a fourth population of individuals that are infected but not yet infective (typically introduced as y_{2_t}). In this case, the populations are:

y_{1_t} = # of susceptible individuals in the population at time t

y_{2_t} = # of infected/non-infectious individuals in the population at time t

y_{3_t} = # of infective individuals in the population at time t

y_{4_t} = # of recovered/removed individuals in the population at time t .

model would be

$$y_{1_{t+1}} - y_{1_t} = -ay_{1_t}y_{3_t} + fy_{4_t}$$

$$y_{2_{t+1}} - y_{2_t} = ay_{1_t}y_{3_t} - by_{2_t}$$

$$y_{3_{t+1}} - y_{3_t} = by_{2_t} - cy_{3_t}$$

$$y_{4_{t+1}} - y_{4_t} = cy_{3_t} - fy_{4_t}.$$