

Discrete Models *

CURM Background Material, Fall 2014

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1 Introduction – Discrete Population Models

Consider the population of one species in a specified region, e.g., the number of people in the world, the number of pine trees in a forest, or the number of bacteria in an experiment. We will ignore any difference in the individuals that make up the group (i.e., gender, age, etc.).

In many situations involving a *large number* of members of a species, it is reasonable to approximate the population size $N(t)$ as a continuous function of time, perhaps by fitting a smooth curve through the data, since most populations are measured periodically (e.g., the census in the U.S.).

In modeling the population growth of a species, we must consider what factors affect that population. For example, the population of sharks in the Adriatic Sea will depend on the number of fish available for the sharks to consume (if there are none, the sharks could become extinct). In addition, the presence of a harmful bacteria will negatively impact the shark population. There are other factors that may also be significant, e.g., water temperature and salinity.

For simplicity, we first study a simple species, one that is not affected by any others. Such a species might be part of a lab experiment.

2 A Simple Discrete One-Species Model

Here, we will discuss one of the simplest models of population growth of a species. Suppose measurements have been taken over an interval of time Δt . The rate of change of the population as measured over the time interval Δt is

$$\frac{\Delta N}{\Delta t} = \frac{N(t + \Delta t) - N(t)}{\Delta t}.$$

This number indicates the absolute rate of increase of the population. The **growth rate per unit time** of the population, $R(t)$, as measured over the time interval Δt is

$$R(t) = \frac{N(t + \Delta t) - N(t)}{\Delta t N(t)}.$$

*Much of the material in this handout is taken directly from *Mathematical Models* by Richard Haberman

If the growth rate and initial population were known, then the population at later times could be calculated as

$$N(t + \Delta t) = N(t) + \Delta t R(t) N(t).$$

Assuming that the population of the species only changes due to births and deaths (i.e., ignoring the possibility of migration into and out of the area), we see that

$$N(t + \Delta t) = N(t) + (\# \text{ of births}) - (\# \text{ of deaths}).$$

We may define the reproductive birth rate b and the death rate d as

$$b = \frac{\# \text{ of births}}{\Delta t N(t)} \text{ and } d = \frac{\# \text{ of deaths}}{\Delta t N(t)}.$$

Then, the population at a time $t + \Delta t$ is

$$N(t + \Delta t) = N(t) + \Delta t(b - d)N(t),$$

so the growth rate $R = b - d$.

Since we are considering the total population in a region, the birth and death rates are averages, averaged over the entire population (i.e., not considering age as a factor). The model we are now developing may be modified to account for an age distribution.

As a first step in our model, we assume that the number of births and number of deaths are proportional to the total population, so the growth rate is constant, and we have

$$N(t + \Delta t) - N(t) = R\Delta t N(t),$$

or

$$N(t + \Delta t) = (1 + \Delta t R)N(t).$$

Given an initial population size $N(t_0) = N_0$, we may determine the population at future times:

$$\begin{aligned} N(t_0 + \Delta t) &= (1 + R\Delta t)N_0 \\ N(t_0 + 2\Delta t) &= (1 + R\Delta t)N(t_0 + \Delta t) = (1 + R\Delta t)^2 N_0 \\ &\vdots \\ N(t_0 + n\Delta t) &= (1 + R\Delta t)^n N_0. \end{aligned}$$

Since $n = \frac{t - t_0}{\Delta t}$, we can also write

$$N(t) = N(t_0 + \Delta t) = (1 + R\Delta t)^{\frac{t-t_0}{\Delta t}}.$$

3 Other Discrete Models

There are other occasions in which a discrete model might be appropriate. An example follows.

Example: Drug Dosage (Maple worksheet drugdosage.mw)

A doctor prescribes a patient take a pill containing 250 mg of a certain drug every 4 hours. Assume the drug is immediately ingested into the bloodstream once taken. Also, assume that every 4 hours, the patient's body eliminates 30% of the drug in his/her bloodstream. Suppose the patient had 0 mg of the drug in his bloodstream prior to taking the first pill. How much of the drug will be in his bloodstream after 72 hours?

Step 1: Identify the Problem

Determine the relationship between the amount of drug in the bloodstream and time.

Step 2: Identify Relevant Facts about the Problem

- The drug is administered every 4 hours.
- The patient had no drug in his system prior to taking the initial pill.

Step 3: Choose the Type of Modeling Method

We will use a deterministic discrete model.

Step 4: Make Simplifying Assumptions

The model assumes the following.

- The patient is of normal size and health.
- There are no other drugs being taken that will affect the prescribed drug.
- There are no internal or external factors that will affect the drug absorption rate.
- The patient always takes the prescribed dosage at the correct time.

The relevant variables are as follows.

- $a(n)$ - amount of drug in the bloodstream after period n , where $n = 0, 1, 2, \dots$ 4-hour period (mg)
- n - number of 4-hour time periods

Step 5: Construct the Model

So, we have

- $a(n + 1)$ = amount of drug in the bloodstream in the future (mg)
- $a(n)$ = amount of drug currently in the bloodstream (mg)

Define change as follows

$$\text{Change} = \text{dose} - \text{loss in the system}$$

$$\text{Change} = 250 - 0.3a(n)$$

So,

$$\text{Future} = \text{Present} - \text{Change}$$

$$a(n+1) = a(n) - 0.30a(n) + 250$$

$$\implies a(n+1) = 0.70a(n) + 250$$

Step 6: Solve and Interpret the Model

We can solve this difference equation analytically to obtain

$$a(n) = \frac{2500}{3} - \frac{2500}{3}(0.7)^n.$$

Alternately, in Maple we can do: $\text{rsolve}(a(n+1) = 0.7a(n)+250, a(0) = 0)$.

We want to find the value after 72 hours, so

$$n = \frac{72}{4} = 18, \text{ and } a(18) \approx 831.98 \text{ mg.}$$

We can plot the results, as well (see the Maple worksheet), and find the limit as $n \rightarrow \infty$:

$$\lim_{n \rightarrow \infty} a(n) = \frac{2500}{3} \approx 833.33 \text{ mg.}$$

If this is a safe and effective dosage level, then the dosage schedule is acceptable.

4 Equilibrium Values and Long-term Behavior

Definition The number a_e is called an **equilibrium value** or **fixed point** for a discrete model $a(k) = f(a(k))$ if $a(k) = a_e$ for all values of k when the initial value is set to a_e ; i.e., $a(k) = a_e$ is a constant solution to the recurrence relation for the dynamical system. (So, a_e is an equilibrium value for $a(n+1) = f(a(n), a(n-1), \dots, n)$ if and only if $a_e = f(a_e, a_e, \dots, a_e)$.)

Notes

1. Not all such discrete models have equilibrium values.
2. Many such discrete models have equilibrium values the system may never achieve.

Example: Drug Dosage Revisited

Recall: The model was governed by the difference equation $a(n+1) = 0.7a(n) + 250$. To determine the equilibrium value(s), let $a(n) = a(n+1) = a_e$. Then,

$$\begin{aligned} a_e &= 0.7a_e + 250 \\ \implies a_e &= \frac{250}{0.3} = \frac{2500}{3} \end{aligned}$$

4.1 Graphically Analyzing Equilibrium Values

Analyze models of the form $a(n+1) = ra(n) + b$, where r and b are constants. (Maple worksheet: graphicalequilib.mw).

Example: $a(n+1) = ra(n) + 50$

Equilibrium value: $a_e = \frac{50}{1-r}$. Therefore, there are three cases.

Case 1: $r > 1$ In this case, $a_e < 0$. Assuming a physical system, this can never be attained. Example: $r = 2$. See the Maple worksheet.

Case 2: $0 < r < 1$ In this case, $a_e > 0$. Example: $r = 0.25$. See the Maple worksheet.

Case 3: $r < 0$ In this case, $a_e > 0$. Example: $r = -1.01$. See the Maple worksheet.

Suppose $b = 0$. Then, the difference equation is $a(n+1) = ra(n)$, and the only equilibrium value is $a_e = 0$.

4.2 Stability and Long-term Behavior

Given a discrete dynamical system, if the values of $a(n)$ converge to a_e for an initial condition close to a_e , then a_e is called a **stable equilibrium value**, or an **attracting fixed point** (i.e., if $\lim_{n \rightarrow \infty} a(n) = a_e$).

Example: (Maple worksheet stability_drug.mw)

We revise our drug dosage problem to have the dosage of medicine be 240 mg (for ease of analysis). In the worksheet, we try two different initial conditions, and analyze the solution. The result is an apparent convergence to the equilibrium value of 800. To verify, solve the difference equation and take the limit as $n \rightarrow \infty$.

5 A Discrete One-Species Model with an Age Distribution

When modeling a species with age distribution, it is necessary to take into account the different birth and death rates for the different age groups. As an example, we consider a model using discrete population changes as measured every year (so, $\Delta t = 1$). Note that for

some species, this time interval is actually too long. So, let

$$\begin{aligned}
 N_0(t) &= \text{number of individuals less than one year old,} \\
 N_1(t) &= \text{number of individuals one year old,} \\
 N_2(t) &= \text{number of individuals two years old,} \\
 &\vdots \\
 N_m(t) &= \text{number of individuals } m \text{ years old, where } m \text{ terminates at } M, \\
 &\quad \text{the oldest age at which there is a significant population.}
 \end{aligned}$$

If we let b_n and d_n represent the birth and death rate, respectively, of the population n years old, then the difference equations describing the population are

$$\begin{aligned}
 N_0(t + \Delta t) &= b_0 N_0(t) + b_1 N_1(t) + \cdots + b_M N_M(t), \\
 N_1(t + \Delta t) &= (1 - d_0) N_0(t), \\
 N_2(t + \Delta t) &= (1 - d_1) N_1(t), \\
 &\vdots \\
 N_m(t + \Delta t) &= (1 - d_{m-1}) N_{m-1}(t), \\
 &\vdots \\
 N_M(t + \Delta t) &= (1 - d_{M-1}) N_{M-1}(t).
 \end{aligned}$$

If M is large, then we would necessarily solve the problem computationally. We can write the above equation in in vector-matrix form as follows. First, define

$$\mathbf{N}(t) = \begin{bmatrix} N_0(t) \\ N_1(t) \\ \vdots \\ N_M(t) \end{bmatrix}.$$

Then, the system of difference equations describing the population may be written as

$$\mathbf{N}(t + \Delta t) = A\mathbf{N}(t),$$

where A is the $M \times M$ matrix defined by

$$A = \begin{bmatrix} b_0 & b_1 & b_2 & \cdots & 0 & b_M \\ 1 - d_0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 1 - d_1 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 1 - d_2 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & 1 - d_{M-1} & 0 \end{bmatrix}.$$

A simplified model with age distribution is more frequently desired. In this case, the population will be separated into larger groups. As a very simplified example, consider the human population divided into three age groups: group 1 – ages 0 to 14; group 2 – ages 15 - 39; and group 3 – ages 40 and older. The number of individuals in group 1 consists of the number born and surviving one year plus the number who survived from group 1 but did not advance into group 2 (i.e., those 13 years of age and younger). Since there are 15 years in group 1 (0 to 14), an individual who was 14 at time t will be 15 at time $t + \Delta t$, where $\Delta t = 1$, and will

have left group 1 and joined group 2. So, $\frac{14}{15}$ of the individuals in group 1 at time t will still be in group 1 at time $t + \Delta t$. And a similar analysis goes for group 2. Note that once an individual has entered group 3, s/he stays there until dying. If we know the average birth and death rates for each group, this simplified model might look like

$$\begin{aligned} N_1(t + \Delta t) &= b_1 N_1(t) + b_2 N_2(t) + b_3 N_3(t) + \frac{14}{15}(1 - d_1)N_1(t), \\ N_2(t + \Delta t) &= \frac{1}{15}(1 - d_1)N_1(t) + \frac{24}{25}(1 - d_2)N_2(t), \\ N_3(t + \Delta t) &= \frac{1}{25}(1 - d_2)N_2(t) + (1 - d_3)N_3(t). \end{aligned}$$

Note that b_1 and b_3 are much less than b_2 , so the model may be further simplified by approximating b_1 and b_3 by 0.

Both of the above models are linear discrete systems.

These kinds of models may be used to compare the growths of two similar populations which differ only in their age distribution. We can also calculate how much faster a population consisting mostly of individuals of child-bearing age will double in size.

6 Nonlinear Discrete Models

A nonlinear discrete model cannot be written in the form

$$a(n + 1) = b_0 a(n) + b_1 a(n - 1) + \dots + b_n,$$

where b_i may be functions of n .

7 Modeling with Discrete Nonlinear Systems

Example: Discrete SIR Model of Epidemics

Consider a disease that is spreading throughout the United States, such as the new flu. The Centers for Disease Control and Prevention is interested in knowing and experimenting with a model for this new disease before it actually become a real epidemic. Let us consider the population being divided into three categories: susceptible, infected, and removed.

Step 1: Identify the Problem

Determine the spread of the new flu.

Step 2: Identify Relevant Facts about the Problem

- The average length of the disease is two weeks, over which time the person is infectious and can spread the disease.
- Once someone gets the flu, they cannot get it again this year.

Step 3: Choose the Type of Modeling Method

We will use a deterministic model, the discrete SIR model.

Step 4: Make Simplifying Assumptions

This model assumes the following.

- The population can be considered as divided into three categories: susceptible, infected, and removed.
- No one enters or leaves the community, and there is no contact outside the community.
- Each person is susceptible (able to catch this new flu), infected (currently has the illness and can spread it), or removed (already had the flu and will not get it again, which includes having died from it).
- Initially every person in the community is either susceptible or infected.
- Once someone gets the illness, they cannot get it again (e.g., chicken pox).
- Our time period for the model will be one week.
- The average length of the disease is three weeks, over which time the person is deemed infected and can spread the disease.
- The spread of disease is proportional to both the number of susceptible individuals and the number of infected individuals.
- Initially, assume that the transmission coefficient is constant (actually, it is probabilistic).

The relevant variables are as follows.

$S(n)$ = the number of people susceptible after time period n .

$I(n)$ = the number of people infected after time period n .

$R(n)$ = the number of people removed after time period n .

n = the number of one-week periods.

a = the rate at which the disease is spread (the transmission coefficient) (per week).

Step 5: Construct the Model

Since we have assumed that a person is sick for three weeks, one third of the infected people will be removed each week. Therefore,

$$R(n + 1) = R(n) + \frac{1}{3}I(n).$$

The value $\frac{1}{3}$ is the removal rate per week, and represents the proportion of infected persons removed from the infected population each week. The population of infected people, $I(n)$,

will have terms that both increase and decrease its amount over time (from susceptible individuals becoming infected and from infected individuals becoming removed). So,

$$I(n + 1) = I(n) + aS(n)I(n) - \frac{1}{3}I(n).$$

Finally, the susceptible population decreases as a result of individuals becoming infected. Therefore,

$$S(n + 1) = S(n) - aS(n)I(n).$$

Step 6: Solve and Interpret the Model

See the Maple worksheet *discrsir.mw* on the References for Undergraduate Research in Epidemiology web page.