Introduction to mathematical modeling

Ousmane Seydi

Polytechnic School of Thies (Senegal).

African Mathematical School : Insight from Mathematical Modeling into Problems in Conservation, Ecology, and Epidemiology

Outline

Introduction

- Epidemiological and ecological problems as well as other scientific disciplines have increased the need to connect mathematics to real-life situations through mathematical modeling.
- Mathematical modeling is positioned nowadays as a valuable decision-making tool, to which recourse is more and more frequent.
- It is very important because it allows to describe the evolution of a real life situation (epidemic, ecological problems, disease ...) in a population, a human body, a material ... and to test several control measures that can be envisaged.

Introduction

Mathematical models are usually composed with dependent variables (the number of individuals, density of the population, concentration ...) and independent variables (time, size, age ...). There are several types of mathematical models. Some of them are listed below :

- **Discrete time models** : the dependent variables may be continuous or discrete and the independent variable is always discrete. The model can be either deterministic or stochastic.
  - **Deterministic** : If we know the dependent variable at time t_0 then we can obtain the dependent variable for all time $t \geq t_0$ with absolute certainty by solving the corresponding model.
  - **Stochastic** : If we know the independent variable at time t_0 the model provide only the probability of an outcome for $t \geq t_0$.
- **Continuous time models** : the dependent and the independents variables are continuous. The model can also be either deterministic or stochastic

Intuitive compartmental modeling

Let us consider a population of individuals categorized in a compartment **C**. Denote by $C(t)$ the number of individuals in **C** at time t. Here t is the independent variable and C is the dependent variable. After a duration of Δt we have

$$C(t+\Delta t) = C(t) + \textbf{ Enter in C } - \textbf{ Leave C}.$$

One of the main aspect on modeling is to describe the evolution in time of the law

$$\textbf{Enter in C } - \textbf{ Leave C}.$$

- **Enter in C** account several facts for example birth in class **C**, immigration, individuals coming from other classes ...
- **Leave C** may includes for example death in **C**, emigration, individuals moving from **C** to other compartments, harvesting ...

Leaving **C** after average time spent in **C**

We assume that the probability of an individual to be still in **C** after a duration Δt if he was in **C** at time t depends only on Δt. This probability will be denoted by $p(\Delta t)$.

Discrete time : Let t be a given discrete time expressed in the unit T. More precisely we have

$$t = nT, \ n \in \mathbb{N}_0.$$

After one unit of time the evolution in **C** is described as follow

$$C(t+T) = C(t) + \textbf{ Enter in C } - \textbf{ Leave C}.$$

We define the rate at which an individual leaves **C** by

$$\eta := \frac{1-p(T)}{T}.$$

Leaving **C** after average time spent in **C**

Since the probability does not have a unit, it is now easy to see that the unit of the rate will be T^{-1} $(s^{-1},\ min^{-1},\ day^{-1},\ year^{-1}\ \ldots)$. If we assume that

$$\textbf{Enter in C} = 0$$

for any time and individuals leaving **C** are only those that were in **C** at time t then we will have

$$C(t+T) = C(t) - (1 - p(T))C(t) = C(t) - \eta T C(t).$$

The discrete time model is usually expressed by setting $C_n := C(nT)$ for all $n \in \mathbb{N}_0$ so that

$$C_{n+1} = (1 - \eta T)C_n,\ \forall n \in \mathbb{N}_0. \tag{1}$$

Leaving **C** after average time spent in **C**

The factor $1-\eta T$ will depends on the choice of the unit of times. For example if we know that the rate at which an individual leaves **C** is $1/10$ per day then we must make conversion to the unit T before incorporating it in the discrete time model. For example

$$\begin{cases} 1-\eta T = 1-\frac{1}{10} & \text{if} \quad T = 1 \text{ day} \\ 1-\eta T = 1-\frac{7}{10} & \text{if} \quad T = 1 \text{ week} \end{cases}$$

If $T=\frac{1}{k}$ day for some $k \in \mathbb{N}$ then

$$1-\eta T = 1-\frac{1}{10k}.$$

Leaving **C** after average time spent in **C**

Observe that we have

$$C_n = (1-\eta T)^n C_0,\ \forall n \in \mathbb{N}_0.$$

Then the probability of an individual to be still in **C** after nT times is

$$\frac{C_n}{C_0} = (1-\eta T)^n = p(T)^n$$

Consequently the probability of an individual to leave **C** at time nT is

$$p(T)^{n-1}(1-p(T))$$

and the average time spent in **C** by an individual is

$$\sum_{n=0}^{+\infty} nTp(T)^{n-1}(1-p(T)) = \frac{T}{1-p(T)} = \frac{1}{\eta}.$$

Leaving **C** after average time spent in **C**

Continuous time : Let t be a given continuous time expressed in the unit T that is to say that

$$t = \omega T, \ \omega \in \mathbb{R}_+.$$

We assume that

$$\textbf{Enter in C} = 0$$

for any time and individuals leaving **C** are only those that were in **C** at time t. Therefore it follows that $C(t)$ is decreasing in time and the quantity

$$c(t) := \frac{C(t)}{C(0)} \in (0,1], \ \forall t \geq 0$$

represents the probability that an individual is still in **C** after t units of times.

Leaving **C** after average time spent in **C**

Hence the probability of an individual to stay in **C** after a period Δt if he was in **C** at time t is

$$p(\Delta t) = \frac{c(t+\Delta t)}{c(t)}.$$

We define the rate at which an individual leaves **C** by

$$\eta := \lim_{\Delta t \to 0} \frac{1 - p(\Delta t)}{\Delta t} = \lim_{\Delta t \to 0} \frac{c(t) - c(t+\Delta t)}{c(t)\Delta t}$$

providing that

$$c'(t) = -\eta c(t), \ t > 0, \ c(0) = 1$$

and

$$C'(t) = -\eta C(t), \ t > 0. \tag{2}$$

Leaving **C** after average time spent in **C**

Since the probability does not have a unit and the unit of Δt is T, it follows that the unit of the rate will be T^{-1} (with T the same unit as the one chosen for the time). Solving the above differential equation gives

$$c(t) = e^{-\eta t}, \ \forall t \geq 0.$$

Hence using the foregoing expression of $c(t)$ we obtain

$$p(\Delta t) = \frac{c(t+\Delta t)}{c(t)} = e^{-\eta \Delta t}, \ \forall \Delta t \geq 0 \Longrightarrow p(t) = e^{-\eta t}, \ \forall t \geq 0,$$

Thus the average time spent in **C** by an individual is

$$\int_0^{+\infty} t(1-p(t))' dt = \frac{1}{\eta}.$$

Leaving due to interaction

By interaction we mean contact between an individual in **C** and an individual in another compartment. Let **D** be a compartment interacting with **C** and denote by $D(t)$ the number of individuals in **D** at time t.
Assume that **D** and **C** are parts of the same population. Denote by $N(t)$ the total number of individual of the considered population. If we divide our population into two compartments **C** and **D** then we will have

$$N(t) = C(t) + D(t).$$

If we have more compartments then

$$N(t) = C(t) + D(t) + \textbf{Individuals in the other compartments}.$$

Let

- c denotes the average number of contacts of one individual per T (unit of time)
- p be the probability that a contact leads to leave **C**

Leaving due to interaction

Discrete time : Let t be a given discrete time expressed in the unit T. After a period T the number of contacts made by 1 individual in **D** is

$$1 \times cT$$

and since the fraction of individuals of **C** in the population is $\dfrac{C(t)}{N(t)}$, the number of contacts made by 1 individual in **D** with individuals in **C** is

$$1 \times cT \times \frac{C(t)}{N(t)}.$$

Observe that the unit of c is T^{-1}.

Leaving due to interaction

The number of contacts between individuals in **C** and **D** is

$$D(t) \times cT \times \frac{C(t)}{N(t)}$$

and the number of individuals leaving **C** is

$$p \times D(t) \times cT \times \frac{C(t)}{N(t)}.$$

Finally if we assume that no one enters in **C** and individuals leaving **C** only those that were in **C** at time t we obtain

$$C(t+T) = C(t) - \frac{pcTD(t)}{N(t)}C(t)$$

and by setting $C_n := C(nT),\ D_n := D(nT)$ and $N_n := N(nT)$ we obtain the following discrete time description

$$C_{n+1} = C_n - \frac{pcTD_n}{N_n}C_n,\ \ n \in \mathbb{N}_0.$$

Leaving due to interaction

Continuous time : Let t be a given continuous time expressed in the unit T. Then by using similar arguments as in the discrete time case one obtains after a duration Δt

$$C(t+\Delta t) = C(t) - \frac{pc\Delta t D(t)}{N(t)} C(t), \ \forall t \geq 0, \ \Delta t > 0.$$

Hence

$$\lim_{\Delta t \to 0} \frac{C(t+\Delta t) - C(t)}{\Delta t} = -\frac{pcD(t)}{N(t)} C(t), \ \forall t > 0$$

that is

$$C'(t) = -\frac{pcD(t)}{N(t)} C(t), \ \forall t > 0.$$

Leaving due to interaction

Note that one may assume that the number of contacts depends on $N(t)$ so that we will have

$$\begin{cases} C'(t) = -pc_0 D(t)C(t), \; t > 0 \\ C_{n+1} = C_n - pc_0 T D_n C_n, \; n \in \mathbb{N}_0 \end{cases} \quad (3)$$

if $c(N) = c_0 N$. The are several other forms of $c(N)$. However we will not have enough time to develop it.

Leaving due to interaction

Note that we should model **Leave C** by another way if for example we have two different populations interacting (predator and prey, two chemical products ...). In fact this situation we will not always be able to use the total population. Therefore we may assume that the number of contacts made by 1 individual in **D** per T (unit of time) is proportional to the number of individuals in **C** that is after T

$$1 \times \rho T \times C(t),$$

with $\rho > 0$ is the number of contacts made by 1 individual in **D**. If p denote the probability that a contact implies **Leave C** then the number of individuals leaving **C** after T will be

$$p\rho T D(t) C(t).$$

We will arrive at the same formulas in (3). Note that the unit of ρ will be **Unit of D(t)**$^{-1}.T^{-1}$.

Enter in **C**

Individuals that enter in **C** may be due to several fact.

- Individuals coming from **C** them selves : birth, cell division ...
- Individuals coming from other compartments : usually those leaving their own compartment, recruitment, immigration ...

If we assume that no one leave **C** then in the discrete time case one has

$$C(t+T) = C(t) + \textbf{Enter in C}.$$

Enter in **C**

If we assume that the number of individuals that enter in **C** per unit of time is proportional to $C(t)$ then we have

$$C(t+T) = C(t) + rC(t) \times T$$

and by setting $C_n := C(nT)$ we obtain

$$C_{n+1} = (1 + rT)C_n. \textbf{ (Exponential growth)}$$

Here $r > 0$ is referred as a growth rate. Its unit will be T^{-1}. The term $rTC(t)$ can represents for example the number of new born in **C** and in this case r will be referred as the birth rate. The equivalent description of the exponential growth in continuous time is

$$C'(t) = rC(t), \;\; t > 0.$$

Enter in **C**

Note that using exponential growth to describe the number of individuals that enter in **C** suggests that the number of individuals that can contains **C** is unlimited.
It is very often that the number of individuals that can contains **C** is limited due to resources limitations, limited available places ...
Denote the maximum number of individuals that can contain **C** by K. The parameter K is known as **the carrying capacity**. If we assume that after T (a unit of time) the number of individuals that can enter in **C** is proportional to the fraction of available "space" and no one leave C then we have

$$C(t+T) = C(t) + rT\frac{K - C(t)}{K}C(t). \textbf{ (Logistic growth)}$$

Enter in **C**

By setting $C_n := C(nT)$ the discrete version is

$$C_{n+1} = C_n + rT\frac{K - C_n}{K}C_n, \;\; n \in \mathbb{N}_0.$$

Here the growth rate is $r\dfrac{K - C(t)}{K}$ and r is the maximal growth rate. The continuous time analogy is

$$C'(t) = r\frac{K - C(t)}{K}C(t), \;\; t > 0.$$

Enter in **C**

Some time one can describe **Enter in C** by a constants recruitment which account for example immigration, birth ... Mathematically it is stated as follow :

$$C(t+T) = C(t) + \Lambda T$$

if we assume that no one leaves **C**. It is now clear that the unit of the constant recruitment Λ is **Unit of C(t)**.T^{-1}. The continuous time analogy is

$$C'(t) = \Lambda, \ \ t > 0.$$

We may have very general growth for **C**. Some general classes are

$$C'(t) = r(C(t))C(t), \ C'(t) = r(D(t))C(t), \ C'(t) = r(N(t))C(t)$$

The growth may depend on another compartment for example resources.

An epidemic model example

Consider an epidemic in a **closed population of humans** which is divided into three compartments. The compartments of susceptible **S**, infectious **I** and recovered **R**. We assume that the epidemic occur in a short time period such as 1 month and there is no mortality due to the disease. Therefore the birth and the natural mortality can be neglected.

We assume that the average infectious period is given by $\frac{1}{\eta}$.

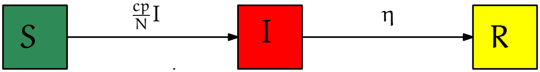
Set

$$N(t) = S(t) + I(t) + R(t), \ \forall t \geq 0$$

the total population at time t.

Kermack-McKendrick (1927, 1932, 1933)

We assume that a susceptible individual becomes infectious through a contact with an infectious individual. Denote by c the average number of contacts of one individual in the population per T (a chosen unit of time). Let p denote the probability that a contact provide an infection. The assumptions can be illustrated by the following diagram flux



Kermack-McKendrick (1927, 1932, 1933)

Then the models describing the dynamics are : in discrete time

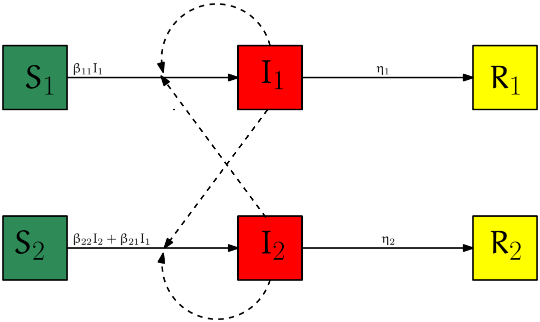
$$\begin{cases} S_{n+1} = S_n - \dfrac{pcT}{N_n} I_n S_n, \ \ n \in \mathbb{N}_0 \\ I_{n+1} = I_n + \dfrac{pcT}{N_n} I_n S_n - \eta T I_n, \ \ n \in \mathbb{N}_0 \\ R_{n+1} = R_n + \eta T I_n, \ \ n \in \mathbb{N}_0 \end{cases}$$

and in continuous time

$$\begin{cases} S'(t) = -\dfrac{pc}{N(t)} I(t) S(t), \ \ t > 0 \\ I'(t) = \dfrac{pc}{N(t)} I(t) S(t) - \eta I(t), \ \ t > 0 \\ R'(t) = \eta I(t), \ \ t > 0 \end{cases}$$

A two groups SIR model

We now consider two groups of a given population interacting each other. We assume that a disease spread in the two groups. We assume that if there is no interaction then the disease dynamic can be described by an SIR model in each group. Finally we assume the number of contact per individual is proportional with the total population. The diagram summarizing the interactions is



A two groups SIR model

Without interactions the model in group 1 is

$$\begin{cases} S_1'(t) = -p_{11}cI_1(t)S_1(t), \ t > 0 \\ I_1'(t) = p_{11}cI_1(t)S_1(t) - \eta_1 I(t), \ t > 0 \\ R_1'(t) = \eta_1 I_1(t), \ t > 0 \end{cases}$$

and the model in group 2 is

$$\begin{cases} S_2'(t) = -p_{22}cI_2(t)S_2(t), \ t > 0 \\ I_2'(t) = p_{22}cI_1(t)S_2(t) - \eta_2 I(t), \ t > 0 \\ R_2'(t) = \eta_2 I_2(t), \ t > 0 \end{cases}$$

Set $\beta_{ij} = cp_{ij}$ with p_{ij} the probability that a contact between an infectious of group j and a susceptible of group i leads to a contamination.

A two groups SIR model

The full model describing the dynamic is

$$
\begin{cases}
S_1'(t) = -\beta_{11} I_1(t) S_1(t) - \beta_{12} I_2(t) S_1(t), \;\; t > 0 \\
I_1'(t) = \beta_{11} I_1(t) S_1(t) + \beta_{12} I_2(t) S_1(t) - \eta_1 I(t), \;\; t > 0 \\
R_1'(t) = \eta_1 I_1(t), \;\; t > 0 \\
S_2'(t) = -\beta_{22} I_2(t) S_2(t) - \beta_{21} I_1(t) S_2(t), \;\; t > 0 \\
I_2'(t) = \beta_{22} I_2(t) S_2(t) + \beta_{21} I_1(t) S_2(t) - \eta_2 I(t), \;\; t > 0 \\
R_2'(t) = \eta_2 I_2(t), \;\; t > 0
\end{cases}
$$

A predator-prey example

Consider two different populations with one acting as a predator and the other represents the preys. Denote by **X** the compartment of the **preys** and by **Y** the compartment of the **predators**. We assume that in the absence of predator, the preys growth exponentially at a rate $r > 0$. In the absence of preys, the population of predators cannot growth and the number of predators will decrease at a rate μ. In the presence of both populations, the preys are consumed by the predators through interactions.

A predator-prey example

Let T be a general unit of time. We assume that the interactions work as follow :

- After T a predator will interact with $cTx(t)$ preys
- Once a predator interact with a prey the probability that the prey is consumed by the predator is p
- The growth rate of the prey is proportional with the number of consumed preys. More precisely the growth rate is $\alpha pcx(t)$.

A predator-prey example

The mathematical description of the foregoing dynamics in discrete time is

$$\begin{cases} x_{n+1} = x_n + rTx_n - pcTx_ny_n, \ n \in \mathbb{N}_0 \\ y_{n+1} = y_n + \alpha pcTx_ny_n - \mu Ty_n, \ \ n \in \mathbb{N}_0 \end{cases}$$

and in continuous time is

$$\begin{cases} x'(t) = rx(t) - pcx(t)y(t), \ t > 0 \\ y'(t) = \alpha pcx(t)y(t) - \mu y(t), \ t > 0. \end{cases}$$

The foregoing model is the very first models for predator prey interaction derived by Volterra (1926) and Lotka (1925). The parameter α is the conversion efficiency of preys.

A predator-prey example

Note that one may assume that in the absence of predator, the preys have logistic growth with carrying capacity K. Then we have

$$\begin{cases} x_{n+1} = x_n + rT\dfrac{K - x_n}{K}\, x_n - pcTx_ny_n, & n \in \mathbb{N}_0 \\ y_{n+1} = y_n + \alpha pcTx_ny_n - \mu Ty_n, & n \in \mathbb{N}_0 \end{cases}$$

and in continuous time is

$$\begin{cases} x'(t) = r\dfrac{K - x(t)}{K}x(t) - pcx(t)y(t), & t > 0 \\ y'(t) = \alpha pcx(t)y(t) - \mu y(t), & t > 0. \end{cases}$$

Of course the are many other models. The model can also be derived by following the approach of Holling (1959).

Age structured population models

We have discussed the rate at which an individual leaves a compartment. Note that in preceding slides our assumptions led to a constant rate. However it is very often that the rate depends on time, chronological age, age of infection, size ...

An example of chronological age model

We will give in this section a simple chronological age structured population model. Let **C** be a given compartment. **The model will be derived informally**. Let T and $A = \kappa T$ be respectively the unit of time and age with κ a positive constant. Thus a variation Δt in time is equivalent to a variation $\Delta a = \kappa \Delta t$ in age. Denote by $u(t, a)$ the population density of **C** at time t in the age range $[a, a + \Delta a]$. More precisely we assume that $u(t, a)\delta a$ is the number of individuals with age in $[a, a + \delta a]$ if $0 < \delta a < \Delta a$.

An example of chronological age model

Note that $c(t,a)$ is given in **unit of C(t).** A^{-1}. Thus for $0 < a$ the number of individuals with age in $[0,a]$ is

$$\sum_{k=1}^{n} c(t,a_k)\Delta a_k$$

with n large enough such that

$$0 < \frac{a}{n} < \Delta a,\ \ a_k = k\frac{a}{n},\ \ \Delta a_k = a_k - a_{k-1} = \frac{a}{n}.$$

An example of chronological age model

Hence if Δa goes to 0 then the number of individuals with age in $[0, \bar{a}]$ is given by

$$\int_0^{\bar{a}} c(t,a)da.$$

Assume that no individual enter in **C** with age $a > 0$. Let $a > 0$ and $t > 0$ be given. After an increment of Δt in time we have

$$c(t+\Delta t, a+\Delta a)\Delta a = c(t,a)\Delta a - \textbf{Leave C}.$$

Let $\eta(a)$ be the rate at which an individual leave **C** with age in the range $[a, a+\Delta a]$. Then we have

$$c(t+\Delta t, a+\Delta a)\Delta a = c(t,a)\Delta a - \eta(a)\Delta t \times c(t,a)\Delta a$$

so that

$$\frac{c(t+\Delta t, a+\kappa\Delta t) - c(t,a)}{\Delta t} = -\eta(a)c(t,a).$$

An example of chronological age model

Therefore

$$\lim_{\Delta t \to 0} \frac{c(t+\Delta t, a+\kappa \Delta t) - c(t,a)}{\Delta t} = -\eta(a) c(t,a), \; t>0, \; a>0,$$

and if u is sufficiently smooth we obtain

$$\partial_t c(t,a) + \kappa \partial_a c(t,a) = -\eta(a) c(t,a), \; t>0, \; a>0.$$

An example of chronological age model

Let $\beta(a)$ be the rate at which new offspring come from individuals with age in $[a, a+\Delta a]$. Then after an increment Δt

$$\beta(a)\Delta t \times c(t,a)\Delta a$$

is the number of new offspring coming from individuals with age in $[a, a+\Delta a]$.

An example of chronological age model

Let $n \in \mathbb{N}$ be large enough such that

$$0 < \frac{a_\dagger}{n} < \Delta a,$$

and set

$$a_k = k\frac{a_\dagger}{n}, \; k = 0, \ldots, n, \; \Delta a_k = \frac{a_\dagger}{n}.$$

Then the total number of offspring coming from all individuals in **C** is given by

$$\Delta t \sum_{k=0}^{n} \beta(a_k) \times c(t, a_k)\Delta a_k,$$

which is also equal to

$$c(t + \Delta t, 0)\Delta a.$$

An example of chronological age model

By letting $\Delta a \to 0^+$ (implying that $\Delta t \to 0^+$ and $n \to +\infty$) the equality

$$c(t+\Delta t, 0)\kappa = \sum_{k=0}^{n} \beta(a_k) \times c(t, a_k)\Delta a_k$$

implies that

$$\kappa c(t, 0) = \int_0^{a_\dagger} \beta(a)c(t, a)da.$$

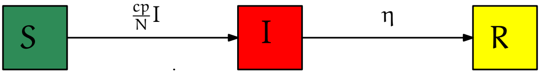
System

$$\begin{cases} \partial_t c(t,a) + \kappa\partial_a c(t,a) = -\eta(a)c(t,a), \ t>0, \ a>0. \\ \kappa c(t,0) = \displaystyle\int_0^{a_\dagger} \beta(a)c(t,a)da. \end{cases}$$

supplemented with an initial distribution was first derived by McKendrick (1926) and later on by Von Foerster (1959).

An example of infection age model

Consider an epidemic in a **closed population of humans** which is divided into three compartments. The compartments of susceptible **S**, infected **I** and recovered **R**. We assume that the epidemic occur in a short time period such as 1 month and there is no mortality due to the disease. Therefore the birth and the natural mortality can be neglected.
Let $i(t, a)$ denote the density of infected individuals at time t in the age of infection range $[a, a + \Delta a]$. Here age of infection means the time since an individual has be infected. Therefore an increment of Δt in time corresponds to an increment $\Delta a = \Delta t$ in age. Let $\eta(a)$ be the recovered rate of an individual with age of infection a. The diagram summarizing the above dynamic is



An example of infection age model

Therefore the corresponding model is

$$\begin{cases} S'(t) = -\dfrac{pc}{N(t)} S(t) \displaystyle\int_0^{a_\dagger} i(t,a)da, \ \ t > 0 \\ \partial_t i(t,a) + \partial_a i(t,a) = -\eta(a) i(t,a), \ \ t > 0 \\ R'(t) = \displaystyle\int_0^{a_\dagger} \eta(a) i(t,a)da, \ \ t > 0 \\ i(t,0) = \dfrac{pc}{N(t)} S(t) \displaystyle\int_0^{a_\dagger} i(t,a)da. \end{cases}$$

Delayed model

Since the beginning of this course we have always assumed that **Leave C** and **Enter in C** only depend on $C(t)$. However they may depend on the past generations in **C**.

Discrete time : Let $\tau = qT$ with T a general unit of time. Assume that no one enters in **C**. If we assume in addition that the individuals that leave **C** are only those that where in **C**, qT ago we will have

$$\begin{aligned} C(t+T) &= C(t) - (1-p(T))p(T)^q C(t-\tau) \\ &= C(t) - \eta T(1-\eta T)^q C(t-\tau). \end{aligned}$$

where $\dfrac{1}{\eta}$ is the average time spent in **C** by an individual. By setting $C_n := C(nT)$ we obtain the following discrete time model

$$C_{n+1} = C_n - \eta T(1-\eta T)^q C_{n-q}, \; n \in \mathbb{N}_0.$$

Delayed model

Note that to solve the discrete time model we must give as initial condition $C_k = \varphi_k$ for $k = -q, \ldots, 0$. The sequence $\varphi_.$ is some time called the history sequence.
The corresponding analogy in continuous time is

$$C'(t) = -\eta e^{-\eta\tau} C(t-\tau), \ t > 0.$$

The initial condition must be stated as

$$C(\theta) = \varphi(\theta), \ \theta \in [-\tau, 0]$$

with φ the history function.

Delayed model

We now want to model **Leave C** whenever there is an interaction with delay. Assume that we have another compartment **D** that interact with **C**. Assume that the average time spent by an individual in **D** is $\dfrac{1}{\eta_D}$. Assume that **C** and **D** are parts of the same population. Finally assume that the individuals of **D** that provoke leaving **C** are those who were in D, τ times ago.

Discrete time : If we set $\tau = qT$ then using the assumptions as in the case $q = 0$ we obtain

$$C(t+T) = C(t) - (1-\eta_D T)^q \frac{pcTD(t-\tau)}{N(t)} C(t)$$

Delayed model

and by setting $C_n := C(nT)$, $D_n := D(nT)$ and $N_n := N(nT)$ we obtain the following discrete time description

$$C_{n+1} = C_n - (1-\eta_D T)^q \frac{pcTD_{n-q}}{N_n} C_n,\ \ n \in \mathbb{N}_0.$$

Continuous time : It is easy to see that we have

$$C'(t) = -e^{-\eta_D \tau} \frac{pcD(t-\tau)}{N(t)} C(t),\ \ t > 0$$

A delayed SIR model

We make the same assumption as our first SIR model example excepted that the infectious individuals are only those that were infected τ time ago. Then the corresponding delayed epidemic models are

$$\begin{cases} S_{n+1} = S_n - (1-\eta T)^q \dfrac{pcT}{N_n} I_{n-q} S_n, \ n \in \mathbb{N}_0 \\ I_{n+1} = (1-\eta T)^q \dfrac{pcT}{N_n} I_{n-q} S_n - \eta T I_n, \ n \in \mathbb{N}_0 \\ R_{n+1} = R_n + \eta T I_n, \ n \in \mathbb{N}_0 \end{cases}$$

and

$$\begin{cases} S'(t) = -e^{-\eta\tau} \dfrac{pc}{N(t)} I(t-\tau) S(t), \ t > 0 \\ I'(t) = e^{-\eta\tau} \dfrac{pc}{N(t)} I(t-\tau) S(t) - \eta I(t), \ t > 0 \\ R'(t) = \eta I(t), \ t > 0 \end{cases}$$

References

- H.W. Hethcote, The mathematics of infectious diseases, SIAM Review **42 (4)** (2000) 599-653.
- P. Magal, O. Seydi and G. Webb, Final size of a multi-group SIR epidemic model: Irreducible and non-irreducible modes of transmission, Mathematical Biosciences (to appear)
- P. Magal, O. Seydi and G. Webb, Final size of an epidemic for a two group SIR model, SIAM Journal on Applied Mathematics, 76 (2016), 2042-2059.
- M. Martcheva, *An introduction to mathematical epidemiology*, New York: Springer, 2015
- G. De Vries, et al. A, et al. *A course in mathematical biology: quantitative modeling with mathematical and computational methods*, Siam, 2006.
- J. A. Metz, and O. Diekmann, *The dynamics of physiologically structured populations*. Vol. 68. Springer, 2014.