Analysis Methods for Infectious Disease Using Mathematical Models

Kawata, Yukichik and Kyo, Koki

Obihiro University of Agriculture and Veterinary Medicine, Obihiro University of Agriculture and Veterinary Medicine

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by

Yukichika Kawata

and R codes by

Koki Kyo

Department of Animal and Food Hygiene
Obihiro University of Agriculture and Veterinary Medicine
Inada-cho, Obihiro, Hokkaido 080-8555, Japan

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1. Introduction

For both human beings and animals, infectious disease has always been one of the most important factors influencing fatality. Currently, infectious diseases affect many economic aspects of livestock husbandry, and the prevention of epidemic infections is a serious issue, especially due to recent globalization. When dealing with infectious diseases, it is important to estimate specific disease-related factors; infectious disease models can be used for such purposes. This material provides simple explanations for infectious disease modelling. In the following material, several models of infectious disease are provided; these models are often referred to as SIR models. To facilitate understanding of this material, demonstrations using MS Excel and sometimes the R codes are provided as supplementary materials.

The SIR-type epidemiological model dates back to publications by Kermack – McKendrick (1927); however, no solid research followed these studies for decades. Indeed, after a long period without additional studies on SIR-type models, the Kermack – McKendrick (1927) model was finally appreciated, and full-fledged studies were started in the 1970s. Most recent works are more directly traced back to Anderson and May (1979), May and Anderson (1979), and Anderson (1991).

Some introductory texts and papers, which include similar materials, are provided on the website of the Swiss Federal Institute of Technology, Zurich (ETH Zürich, 2009, 2010), as well as in papers published by Keeling and Rohani (2008) and Tassier (2013).

2. Basic Things to Know

2.1. Infectious status

Infectious diseases are caused when certain types of parasites invade into a host. Some of these types of parasites are shown in Table 1. In the text that follows, we will mainly discuss diseases incurred from microparasites. In SIR models, individuals in a population are divided into susceptible (S), exposed/latent (E), infectious (I), and recovered/removed (R) individuals, and the models are referred to on the basis of the infections statuses of included individuals (Figure 1).

Here,

S: Susceptible individuals are those who can be infected but have not been infected.

E: Exposed individuals are those who have been exposed to the disease and infected, but are not infectious (namely, those whose disease is in the latent stage).

I: Infectious individuals are those who are infectious.

R: Removed individuals are those who recovered from the disease and have immunity. In some models, removed individuals will be reverted to the S stage once they have lost immunity. Additionally, Rs may be removed individuals from the population because of disease-related death.

Table 1. Infectious agents

Type of agent	**Characteristics [Examples]**
Microparasites	
Virus	Small, simple, obligatory parasites of larger cells [Ex.: influenza]
Bacteria	Large and more complex than viruses; many are able to grow independently, but some require a cellular host [Ex.: *Salmonella typhi* (typhoid fever)]
Protozoa	Large single-celled organisms, more complex than bacteria, many are able to grow independently, but some require a cellular host [Ex.: *Plasmodium falciparum* (malaria)]
Macroparasites	
Helminths (worms)	Large (1 mm to 10 m) multicellular organisms [Ex.: *Schistosoma mansoni* (schistosomiasis)]
Arthropods	Insects, lice, ticks, and their relatives [Ex.: *Ixodes* spp. (ticks)]

Source: Vynnycky and White (2010), Table 1.1.

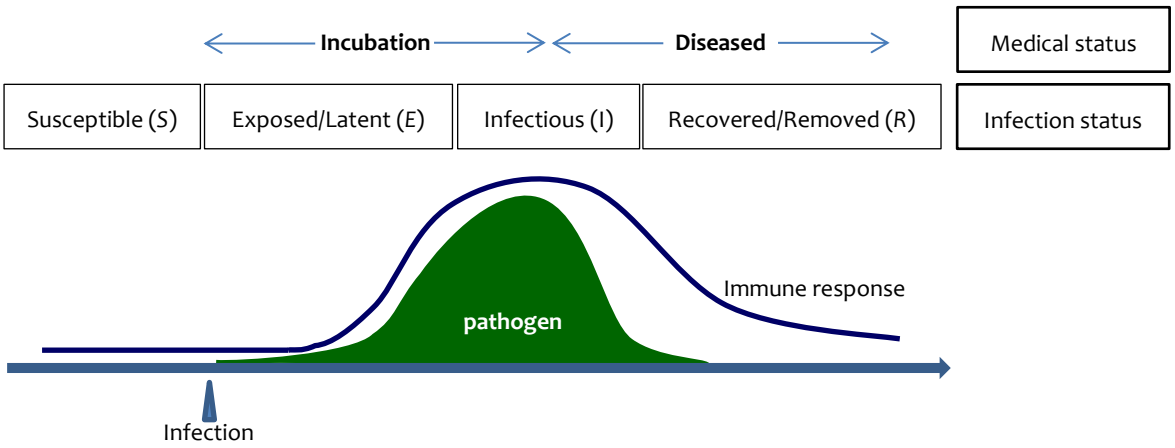

Figure 1. Infection status

Source: Keeling and Rohani (2008) Figure 1.2

2.2. Variables and parameters

Because exposed and recovered individuals E and R have already been infected and have acquired immunity, only susceptible individuals S can be infected when contacting infectious individuals I. Let us suppose *p* represents the probability that S will be infected when contacting I and that *c* represents the number of opportunities an individual in S has to come in contact with individuals I within a certain period. Then, the infection rate is *pc*. It can be easily inferred that the expected number of individuals who transition from S to I in a certain period will be $pc\,SI$.

S, E, I, and R are referred to as variables, whose values change over time, while *c* and *p* are referred to as parameters, whose values are constant over time. A parameter is always a coefficient of some variable. If it is not related to the variable, it is simply called a 'constant'. With empirical data and/or previous studies, we often set initial values of variables and values for parameters and constants.

2.3. Discrete time and difference equation

Two different time spans are used in modelling. In particular, discrete time is used when we use the difference equation. As explained above, values of variables change over time. Let us define time explicitly. For example, the population size of some animal at the beginning of any two sequential times t and $t+1$ can be

given as N_t tons and N_{t+1} tons, respectively. Specifically, let us suppose that two sequential times implies two sequential years. Population sizes will change during these sequential years because of the following reasons:

(1) increases in the number of individuals by immigration from outside of a population and/or decreases in the number of individuals by emigration from inside of the population
(2) increases in the number of individuals by births inside of the population and/or decreases in the number of individuals by deaths inside of the population

Here (1) can be regarded as a situation where immigration and emigration occur between several populations within the metapopulation. However, for the sake of simplicity, a single population is sometimes assumed, and immigrants and emigrants are ignored. Then, the population size changes based on births and deaths. That is,

$$N_{t+1} = N_t + B_t - D_t \tag{1}$$

Here,
B_t: number of births in this population in year t
D_t: number of deaths in this population in year t

Under some assumptions and after a few complicated calculations, we have the famous logistic equation as follows (see Appendix I):

$$N_{t+1} - N_t = \bar{r}\left[1 - \frac{N_t}{K}\right]N_t \tag{2}$$

Here,
K: carrying capacity (tons)
$\bar{r}$: growth rate (per year)

The amount of population increase or decrease during a certain period of time (e.g., one year) is 'flow', while the population size at a certain time (e.g., at the beginning of the year) is 'stock'. Differences in stocks are considered flow. In our case, both N_t and N_{t+1} are stock, and the difference in these stocks (namely, $N_{t+1} - N_t$) is flow. It can be easily inferred that the unit of measure of N_t and N_{t+1} is, for

example, tons; however, that of $N_{t+1} - N_t$ should be, for example, tons/year.

Let us check the consistency of units on both the left hand side (l.h.s.) and right hand side (r.h.s) of eq. (2). As stated above, the unit of the l.h.s. is 'tons/year' and that of the r.h.s. is as follows:

$$\Delta_r/\text{year}\left[1 - \frac{\Delta_N tons}{\Delta_K tons}\right]\Delta_N tons \qquad (3)$$

Because $\frac{tons}{tons}$ is cancelled out and will be unit free, the above representative can be reduced to 'tons/year', which is consistent with the units of the l.h.s. of eq. (2).

[Example 1] Consistency of units

Suppose r = 0.2/year, K = 100 tons. If the stock size of year t is 50 tons,

$$\underbrace{55\text{ tons} - 50\text{ tons}}_{} = 0.2/\text{year} \times \left[1 - \frac{50\text{tons}}{100\text{tons}}\right] 50\text{ tons} \qquad (E1)$$

Because the l.h.s. is the difference between the stocks,
this is flow, and we need to add '/year'

2.4. Continuous time and differential equation

If we analyse species that reproduce during some specific season and for which changes in generations occur simultaneously, it is appropriate to use discrete time (Teramoto, 1997). However, if the reproductive season is not common, it is more appropriate to use a differential equation to describe the dynamics of such species (Teramoto, 1997).

Because the reproductive season of microparasites usually varies, we often use a differential equation. A continuous version of the logistic equation can be obtained as follows:

$$\frac{dN}{dt} = r\left[1 - \frac{N}{K}\right]N \tag{4}$$

Here, r is the instantaneous growth rate. If necessary, we substitute N_{t+1} and N_t with $N(t)$ and $N(t+1)$ to distinguish between the discrete and continuous versions of population sizes.

The interpretation of the growth rate $\bar{r}$ and the instantaneous growth rate r is completely different because of the difference in the time span. However, when conducting numerical simulations, r and $\frac{dN}{dt}$ are often interpreted as $\bar{r}$ and $N_{t+1} - N_t$, respectively, and we often use parameter values and differences in population sizes between two sequential times for calculation. We will see some examples later.

Finally, you may think that N_t and N_{t+1} should be non-negative integral numbers. In a real numerical simulation, calculated figures will not necessarily be an integral number because they may be interpreted as the average of several individuals or the average of several trials.

2.5. Other model categories

First, we have to distinguish between deterministic and stochastic models. If there is no randomness among parameters, results of numerical simulations for the same initial values will always be the same. On the other hand, if randomness exists at least in one parameter, results of numerical simulations will be different every time (sometimes the same result may be obtained). In the following text, we use only deterministic models.

Second, we need to distinguish the closed model. In subsection 2.3, we assume that neither immigration nor emigration occur. When considering a very short period, it can be realistic to ignore both birth and death. In other words, if the dynamics of infectious disease are far faster than that of the population, the closed model is applicable. If all of these four factors (i.e., immigration, emigration, birth, and death) are omitted, such a model is referred to as the closed model. We will examine the closed model in section 3.

However, it is more realistic to consider birth and death, especially when the time span of disease is long. In such cases, the steady model is used. However, this model has a unique restriction: the number of births should always coincide with the number of deaths. In other words, the parameter value of birth rate is the same as that of death rate. As we will see later, total population size will be constant over time. We will examine the steady model in section 4.

Both closed and steady models are appropriate under specific conditions and easy to use because of simplifying assumptions; however, in some cases, these assumptions are less valid, and more realistic models can be used. In section 5, we examine the SEI model in the context of rabies among the red fox, where total population size is no longer constant overtime.

3. Closed Models

3.1. SIR model (1)

The following is a revised version of the classical Kermack and McKendrick (1927) model. Susceptible individuals S decrease by αSI in proportion to the rate α $(= pc)$, defined as the rate at which susceptible individuals meet infectious individuals and become infected (in short, α is the infection rate).

$$\frac{dS}{dt} = -\alpha SI \tag{5}$$

Infectious individuals I increase by αSI and decrease by βI in proportion to the rate β, which is the rate of immunity-acquired individuals.

$$\frac{dI}{dt} = \alpha SI - \beta I \tag{6}$$

The number of recovered individuals with lifelong immunity will increase by βI. Therefore,

$$\frac{dR}{dt} = \beta I \tag{7}$$

Eqs. (5), (6), and (7) comprise a modified Kermack and McKendrick-type SIR model.

If $\frac{dI}{dt} = 0$, the number of I is constant over time. By substituting this condition into eq. (6) and after some simple calculations, we have the following:

$$I(\alpha S - \beta) = 0 \tag{8}$$

Because we are interested in the situation where infectious individuals exist, $\alpha S - \beta$ should be zero (otherwise, I will be zero to obtain equality with eq. (8)). Then, if the following condition holds, the number of I is constant over time.

$$\frac{\alpha S}{\beta} = 1 \tag{9}$$

Let us denote $\frac{\alpha S(t)}{\beta} = \hat{R}_t$.[1] It is straightforward to obtain following conditions.

If $\hat{R}_t$ > 1, the infectious disease will prevail (epidemic may occur)
if $\hat{R}_t$ < 1, the infectious disease will die out (epidemic will not occur)

$\hat{R}_t = 1$ is the epidemic threshold (in some other contexts, this is also referred to as the endemic threshold). $\hat{R}_t$ is referred to as the reproduction number. Let us define the initial stage as the time when infectious disease does not invade the population, and let us denote the initial stage as t = 0. Then, $S(0) = N$, $I(0) = 0$, and $R(0) = 0$, and the following holds: $\frac{\alpha S(0)}{\beta} = \frac{\alpha N}{\beta} = \hat{R}_0$. Here, N is the total population size, and $\hat{R}_0$ is referred to as the basic reproduction number. For further understanding, a numerical example would be helpful. However, it might be appropriate to provide an additional explanation before checking a numerical example.

[1] Usually R is used. However, in this text, to distinguish it from the recovered individuals, we will use $\hat{R}_t$.

If summing up eqs. (5) to (7), all terms will cancel out, and we have the following:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{10}$$

Therefore, total number of population N is constant over time. That is,

$$N(0) = N(t) = S(t) + I(t) + R(t) \text{ for } {}^{\forall}t \tag{11}$$

There are two interpretations for R in the SIR model. First, as explained above, R represents recovered individuals. Measles, mumps, and chicken pox would be typical examples. Once an individual has measles (or others), he/she rarely suffer from the same infection after transitioning to become a recovered individual R. Recovered individuals Rs are not infectious. If the population size is conserved (as shown by eq. (11)), the number of R increases while those of S and I decrease. Therefore, after a long period, I will be reduced to zero, and only S and R remain in the population.

The second interpretation of R is 'removed'. In other words, some individuals die instead of recovering. The Black Death (the Bubonic Plague) is a typical example. In this case, interpretation of eq. (11) is a bit complicated. We have to sum up all the dead in addition to S and I. That is,

$$N(0) = N(t) = S(t) + I(t) + \mathrm{R}(t) + \sum_{i=1}^{t-1} D(i) \text{ for } {}^{\forall}t \tag{12}$$

Here, $\mathrm{D}(i)$ is the number of deaths at each time between $t = 1$ and $t - 1$.

Now, we are ready to examine some numerical examples.

[**Example 2**] **Numerical example of the SIR model (1)**

Let α = 0.02, β = 0.5 and fill in A4 and B4 with '0.02' and '0.5', respectively. Fill in between the first, third, and sixth lines as well as row A (A6 and below) on the basis of Figure 2. Use the initial values of $S(0)$, $I(0)$, and $R(0)$ as 50, 0, and 0, respectively and fill in B7, C7, and D7 with '50', '0', and '0', respectively. Then fill in

B8, C8, and D8 as follows.

'=B7-$A$4*B7*C7',
'=C7+$A$4*B7*C7-$B$4*C7',
'=D7+$B$4*C7'.

Copy these cells until line 57. Now, most of Figure 2 is reproduced in your MS Excel spreadsheet. The dynamics of S, I, and R are demonstrated by Figure 3. Because there is no infectious disease in a population, S is constant at 50.

Suppose one infected individual has entered the population (although we suppose there is no immigration or emigration, ignore this restriction here). Then, you will have completely different results, which are shown in Figures 4 and 5.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5						
5								
6	t	S	I	R		Rt	S	
7	0	50	0	0		2	25	
8	1	50	0	0		2		
9	2	50	0	0		2		
10	3	50	0	0		2		
11	4	50	0	0		2		
12	5	50	0	0		2		
13	6	50	0	0		2		
14	7	50	0	0		2		
15	8	50	0	0		2		
16	9	50	0	0		2		
17	10	50	0	0		2		
18	11	50	0	0		2		
19	12	50	0	0		2		
20	13	50	0	0		2		

Figure 2. SIR model (1) ($S(0)$ = 50, $I(0)$ = 0, and $R(0)$ = 0)

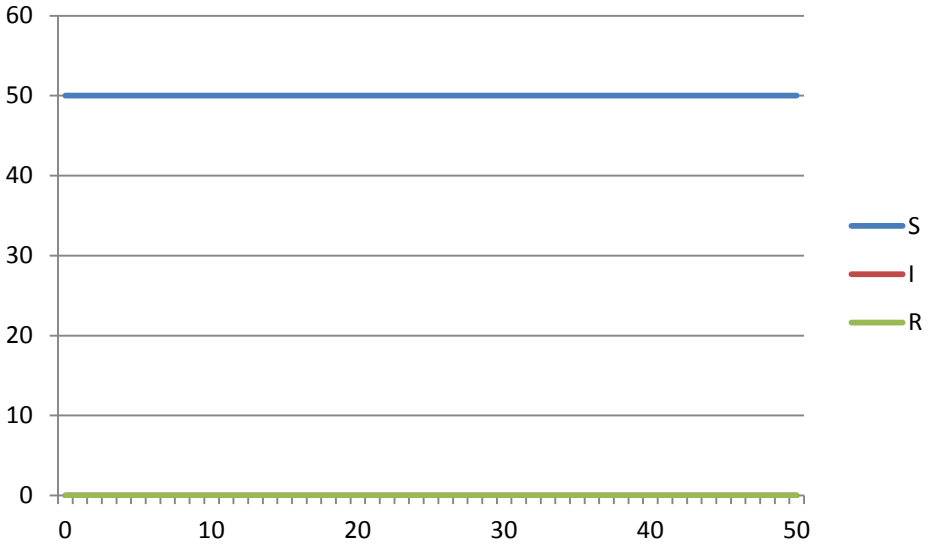

Figure 3. Dynamics of S, I, and R ($S(0)$ = 50, $I(0)$ = 0, and $R(0)$ = 0)
Note: Vertical and horizontal axes are population size and time, respectively

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5						
5								
6	t	S	I	R		Rt	S	
7	0	50	1	0		2	25	
8	1	49	1.5	0.5		1.96		
9	2	47.53	2.22	1.25		1.9012		
10	3	45.41967	3.220332	2.36		1.816787		
11	4	42.49434	4.535494	3.970166		1.699774		
12	5	38.63968	6.122404	6.237913		1.545587		
13	6	33.90833	7.792557	9.299115		1.356333		
14	7	28.62368	9.18093	13.19539		1.144947		
15	8	23.36784	9.846304	17.78586		0.934714		
16	9	18.7661	9.524889	22.70901		0.750644		
17	10	15.1912	8.337345	27.47145		0.607648		
18	11	12.65811	6.701758	31.64013		0.506325		
19	12	10.96148	5.047511	34.99101		0.438459		
20	13	9.854918	3.63032	37.51476		0.394197		

Figure 4. SIR model (1) ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

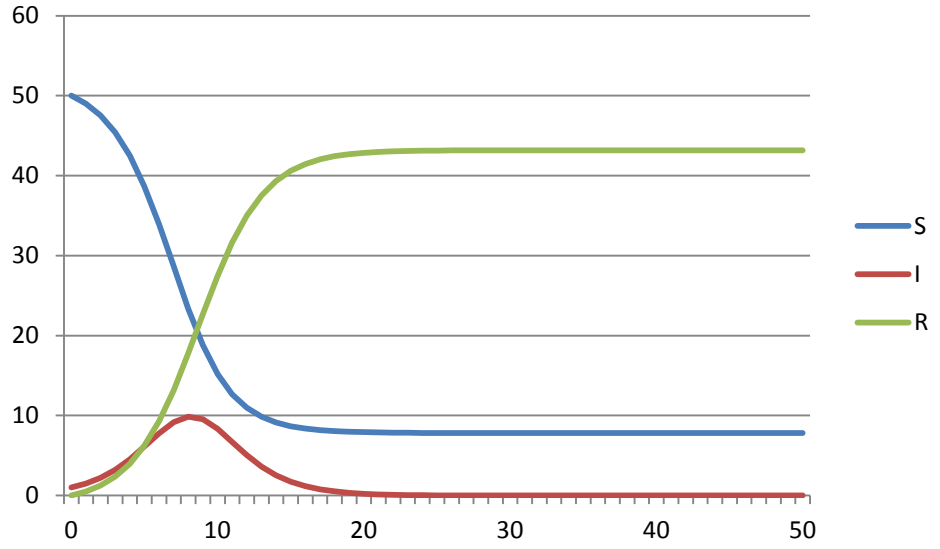

Figure 5. Dynamics of S, I, and R ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)
Note: Vertical and horizontal axes are population size and time, respectively

The R code for the latter case is provided in Appendix II.

[Example 3] Endemic threshold and herd immunity

Next, let us check the endemic threshold. Because when t = 0, $S(0)$ = 50, it follows that

$$\hat{R}_0 = \frac{\alpha S(t)}{\beta} = \frac{0.02 \times 50}{0.5} = 2 > 1 \qquad \text{(E2)}$$

Because $\hat{R}_0 > 1$, this infectious disease will take hold. Note that the value of $\hat{R}_0$ is shown in F7 of Figures 2 and 4, where you should fill in F7 with '$A$4*B7/$B$4'. Copy F7 until line 57, and $\hat{R}_t$s are shown.

Next, let us calculate the value of $S(t)$, which brings $\hat{R}_t = 1$. The value is $S(t) = 0.5/0.02 = 25$ individuals, as shown in G7 of Figures 2 and 4 (you should fill in G7 with '=B4/A4'). This suggests that as time passes, the disease will take hold in the earlier phase, but $S(t)$ decreases. When the number of $S(t)$ is less than 25 individuals, the disease prevalence begins to decrease. We can check this result in Figures 4 and 5, where t = 8 and $S(t)$ = 23.37 individuals, which is less than 25 individuals. Then, as is shown in Figure 5, $I(t)$ starts to decrease. Finally, the

population sizes almost stabilize at 7.8, 0, and 43 for S, I, and R, respectively when t is around 27.

This result suggests another important thing. At first, there were 50 susceptible individuals, 7.8 of which were not infected. This phenomenon is referred to as herd immunity. In our case, once the size of the susceptible individual population is less than 25 individuals, the disease prevalence begins to decrease, where the sizes of infectious $I(t)$ and recovered $R(t)$ individual populations have nothing to do with the herd immunity. It follows that when we vaccinate susceptible individuals, we can calculate the least number of susceptible individuals who will be required to be vaccinated. By doing so, we can minimize the risk of side effects of vaccines and minimize the cost of vaccination.

3.2. SIRS model

The SIRS model can be shown as follows.

$$\frac{dS}{dt} = -\alpha SI + \gamma R \tag{13}$$

$$\frac{dI}{dt} = \alpha SI - \beta I \tag{14}$$

$$\frac{dR}{dt} = \beta I - \gamma R \tag{15}$$

Here,

γ : immunity decay rate

The same procedure (solving $\frac{dI}{dt} = 0$) provides the reproduction number as before:

$$\hat{R}_t = \frac{\alpha S(t)}{\beta} \tag{16}$$

The value of $S(t)$, which brings $\hat{R}_t = 1$ is as follows.

$$\mathrm{S}(t) = \frac{\beta}{\alpha} \tag{17}$$

If summing up eqs. (13) to (15), the following equation holds.

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{18}$$

Therefore, total number of individuals in population N is constant over time.

The SIRS model is a simple extension of the SIR model when R represents the recovered population. The common cold is a typical example.

[**Example 4**] **Numerical example of the SIRS model**

Provide some modifications on the basis of Figure 6: Let γ = 0.05, and fill in C4 with '0.05'. Then fill in B8 and D8 as follows.

'=B7-$A$4*B7*C7+$C$4*D7',
'=D7+$B$4*C7-$C$4*D7'.

Copy these cells until line 57. Now, Figure 6 is reproduced in your MS Excel spreadsheet. The dynamics of S, I, and R are demonstrated by Figure 7.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5	0.05					
5								
6	t	S	I	R		Rt	S	
7	0	50	1	0		2	25	
8	1	49	1.5	0.5		1.96		
9	2	47.555	2.22	1.225		1.9022		
10	3	45.50481	3.221442	2.27375		1.820192		
11	4	42.68667	4.542543	3.770784		1.707467		
12	5	38.99709	6.149392	5.853516		1.559884		
13	6	34.4936	7.870865	8.635536		1.379744		
14	7	29.49549	9.365321	12.13919		1.179819		
15	8	24.57775	10.20735	16.21489		0.98311		
16	9	20.37102	10.12115	20.50783		0.814841		
17	10	17.27285	9.184142	24.54301		0.690914		
18	11	15.32727	7.764796	27.90793		0.613091		
19	12	14.34241	6.262661	30.39493		0.573696		
20	13	14.06572	4.927763	32.00652		0.562629		

Figure 6. SIRS model ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

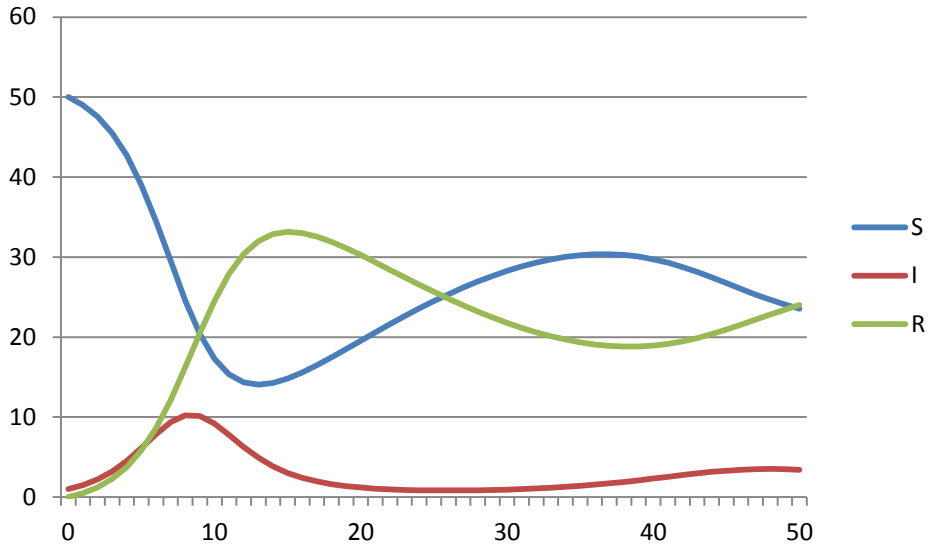

Figure 7. Dynamics of *S*, *I*, and *R* ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)
Note: Vertical and horizontal axes are population size and time, respectively

The R code for this case is provided in Appendix II.

3.3. SIS model

The SIS model can be shown as follows:

$$\frac{dS}{dt} = -\alpha SI + \beta I \tag{19}$$

$$\frac{dI}{dt} = \alpha SI - \beta I \tag{20}$$

We have the following:

$$\hat{R}_t = \frac{\alpha S(t)}{\beta} \tag{21}$$

$$\mathrm{S}(t) = \frac{\beta}{\alpha} \tag{22}$$

and

$$\frac{dS}{dt} + \frac{dI}{dt} = 0 \tag{23}$$

The SIS model is also simple extension of the SIR model where R is removed. The common cold is a typical example. The SIS model fits to describe endemic diseases. Note that endemic diseases prolong disease status in some areas, while epidemic diseases occur within a relatively short period of time.

[**Example 5**] **Numerical example of the SIS model (1)**

Provide some modifications on the basis of Figure 8: Remove unnecessary cells. Then fill in B8 and C8 as follows.

'=B7-$A$4*B7*C7+$B$4*C7'
'=C7+$A$4*B7*C7-$B$4*C7'

Copy these cells until line 57. Figure 8 is reproduced in your MS Excel spreadsheet. The dynamics of S, I, and R are demonstrated by Figure 9.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5						
5								
6	t	S	I			Rt	S	
7	0	50	1			2	25	
8	1	49.5	1.5			1.98		
9	2	48.765	2.235			1.9506		
10	3	47.7027	3.297296			1.908108		
11	4	46.20555	4.794446			1.848222		
12	5	44.17218	6.827824			1.766887		
13	6	41.55409	9.445908			1.662164		
14	7	38.42672	12.57328			1.537069		
15	8	35.05036	15.94964			1.402015		
16	9	31.84437	19.15563			1.273775		
17	10	29.22221	21.77779			1.168888		
18	11	27.3832	23.6168			1.095328		
19	12	26.25753	24.74247			1.050301		
20	13	25.63524	25.36476			1.02541		

Figure 8. SIS model ($S(0)$ = 50, and $I(0)$ = 1)

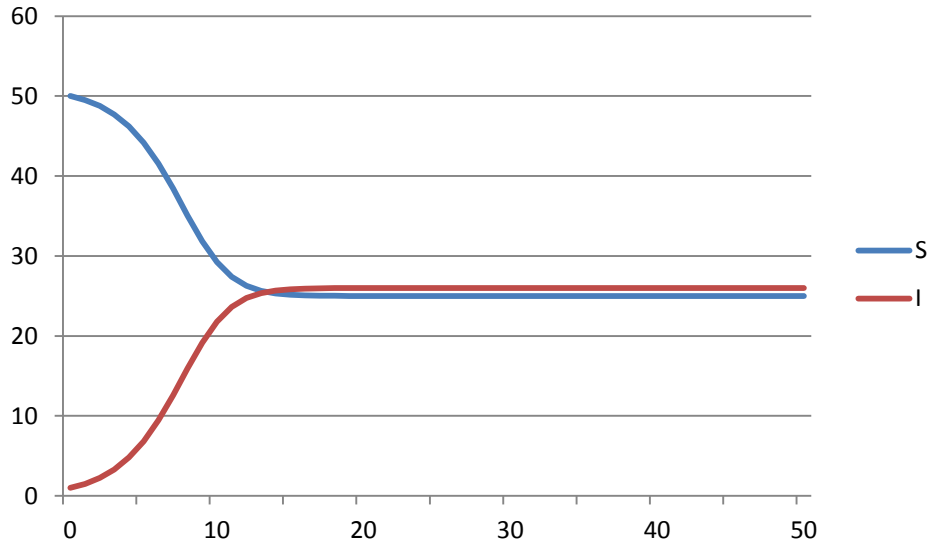

Figure 9. Dynamics of S and I ($S(0)$ = 50, and $I(0)$ = 1)

Note: Vertical and horizontal axes are population size and time, respectively

There are two cases for the SIS model. In Figure 9, both susceptible and infected

individuals coexist, and their numbers are constant after t = 30, where S = 25 and I = 26. This coexistence is referred to as persistence. In the other case, the number of infected individuals is reduced to zero, and only susceptible individuals are left; the endemic disease is eradicated. You may find such examples by changing initial value of parameters and/or variables.

[**Example 6**] **Numerical example of the SIS model (2)**

In Example 5, the initial value of $S(0)$ = 50. Here, let us suppose $S(0)$ = 10. Then, we have results shown in Figures 10 and 11. Infected individuals are completely eradicated after t = 37.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5						
5								
6	t	S	I			Rt	S	
7	0	10	1			0.4	25	
8	1	10.3	0.7			0.412		
9	2	10.5058	0.4942			0.420232		
10	3	10.64906	0.350939			0.425962		
11	4	10.74979	0.250213			0.429991		
12	5	10.8211	0.178901			0.432844		
13	6	10.87183	0.128169			0.434873		
14	7	10.90805	0.091953			0.436322		
15	8	10.93396	0.066037			0.437359		
16	9	10.95254	0.047459			0.438102		
17	10	10.96587	0.034126			0.438635		
18	11	10.97545	0.024547			0.439018		
19	12	10.98234	0.017662			0.439294		
20	13	10.98729	0.01271			0.439492		

Figure 10. SIS model ($S(0)$ = 10, and $I(0)$ = 1)

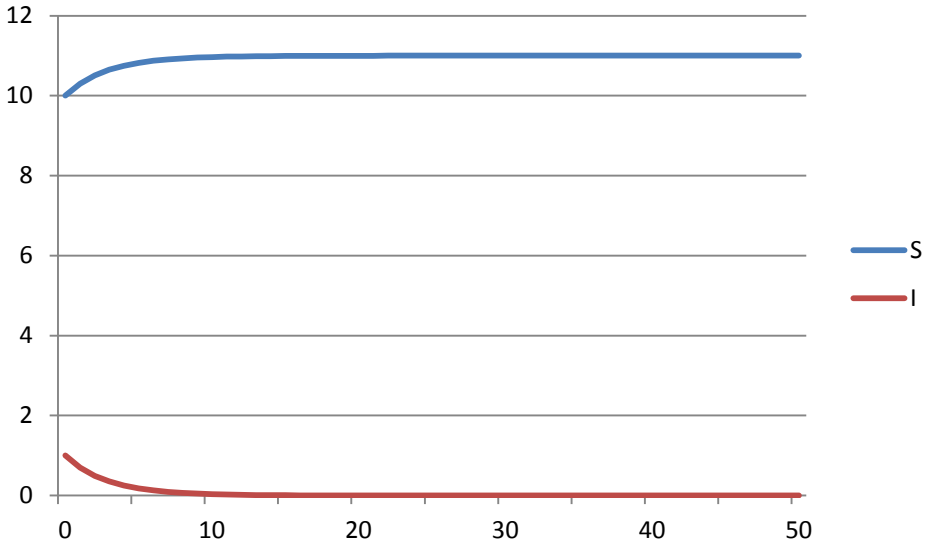

Figure 11. Dynamics of S and I ($S(0)$ = 10, and $I(0)$ = 1)

Note: Vertical and horizontal axes are population size and time, respectively

Specifically, if the parameter value of β = 0, the model is called the SI model, which may describe, for example, the natural history of HIV (Vynnycky and White, 2010).[2]

4. Steady Model

4.1. SIR model (2)

The steady version of the SIR model can be shown as follows:

$$\frac{dS}{dt} = mN - mS - \alpha SI \tag{24}$$

$$\frac{dI}{dt} = \alpha SI - (m + \delta + \beta)I \tag{25}$$

$$\frac{dR}{dt} = \beta I - mR \tag{26}$$

Here,

δ: the disease death rate

[2] Tassier (2013) pointed out that the SIR type model is the most appropriate for HIV, but when considering the longevity of infection period, the SI model is sometimes applied.

We introduce both birth and death from hereon. We further suppose that 'mortality rate' = 'birth rate', both of which are denoted as m. Because of this condition, the total population size is constant (and, therefore, the model is called the steady model).

We have the following:

$$\hat{R}_t = \frac{\alpha S(t)}{m+\delta+\beta} \tag{27}$$

and

$$\mathrm{S}(t) = \frac{m+\delta+\beta}{\alpha} \tag{28}$$

Additionally, the total number of individuals in population N is constant over time.

[**Example 7**] **Numerical example of the SIR model (2)**

Provide some modifications on the basis of Figure 12. Finally, you may reproduce Figures 12 and 13.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5		0.1	0.0001			
5								
6	t	S	I	R		Rt	S	
7	0	50	1	0		1.666389	30.005	
8	1	49.0001	1.3999	0.5		1.633064		
9	2	47.62839	1.931725	1.1999		1.587348		
10	3	45.7886	2.612595	2.165642		1.526032		
11	4	43.39654	3.437319	3.471724		1.44631		
12	5	40.41387	4.357938	5.190036		1.346905		
13	6	36.8924	5.265163	7.368486		1.229542		
14	7	33.00878	5.990429	10.00033		1.100109		
15	8	29.05564	6.350307	12.99454		0.96836		
16	9	25.36733	6.229733	16.1684		0.845437		
17	10	22.20894	5.651904	19.28165		0.740175		
18	11	19.70098	4.770652	22.10567		0.65659		
19	12	17.82393	3.787514	24.48879		0.594032		
20	13	16.47659	2.864794	26.38009		0.549128		

Figure 12. SIR model (2) ($S(0) = 50$, $I(0) = 1$, and $R(0) = 0$)

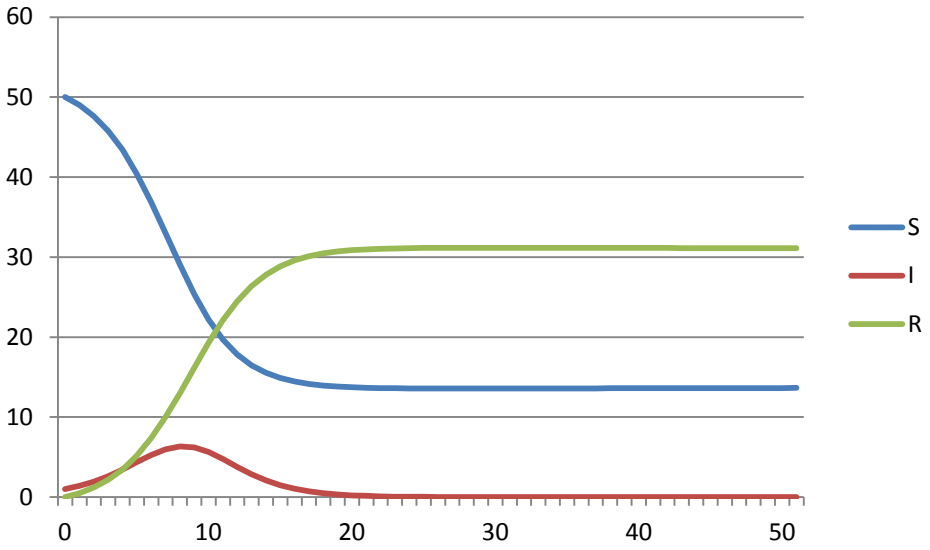

Figure 13. Dynamics of S, I, and R ($S(0) = 50$, $I(0) = 1$, and $R(0) = 0$)

Note: Vertical and horizontal axes are population size and time, respectively

[Example 8] Total population size

In the above text, I stated that the total number of individuals in population N is constant over time. Here, let's confirm this statement using an MS Excel spreadsheet (you may check the same for other models). Fill in G8, H8, and H9 as follows:

'=SUM(B8:D8)+H8'
'=C7*$D$4'
'=H8+C8*$D$4'

Copy G8 and H9 until line 57. Then, we have Figure 14, and we can confirm that population size is conserved at 51 for all periods.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5		0.1	0.0001			
5								
6	t	S	I	R		Rt	S	
7	0	50	1	0		1.666389	30.005	
8	1	49.0001	1.3999	0.5		1.633064	51	0.1
9	2	47.62839	1.931725	1.1999		1.587348	51	0.23999
10	3	45.7886	2.612595	2.165642		1.526032	51	0.433162
11	4	43.39654	3.437319	3.471724		1.44631	51	0.694422
12	5	40.41387	4.357938	5.190036		1.346905	51	1.038154
13	6	36.8924	5.265163	7.368486		1.229542	51	1.473948
14	7	33.00878	5.990429	10.00033		1.100109	51	2.000464
15	8	29.05564	6.350307	12.99454		0.96836	51	2.599507
16	9	25.36733	6.229733	16.1684		0.845437	51	3.234537
17	10	22.20894	5.651904	19.28165		0.740175	51	3.857511
18	11	19.70098	4.770652	22.10567		0.65659	51	4.422701
19	12	17.82393	3.787514	24.48879		0.594032	51	4.899766
20	13	16.47659	2.864794	26.38009		0.549128	51	5.278518

Figure 14. Total population size

4.2. SIR model with hunting

We assume that we cannot distinguish susceptible, exposed, and infectious individuals when hunting and that all three types of individuals are hunted by the same probability. Let h denote the per capita hunting rate; then, the SIR model

with hunting can be shown as follows:

$$\frac{dS}{dt} = mN - mS - \alpha SI - hS \tag{29}$$

$$\frac{dI}{dt} = \alpha SI - (m + \delta + \beta)I - hI \tag{30}$$

$$\frac{dR}{dt} = \beta I - mR - hR \tag{1}$$

Here,

h: hunting rate

We have the following:

$$\hat{R}_t = \frac{\alpha S(t)}{m+\delta+\beta+h} \tag{32}$$

and

$$\mathrm{S}(t) = \frac{m+\delta+\beta+h}{\alpha} \tag{33}$$

Additionally, the total number of individuals in population N is constant over time.

[**Example 9**] **Numerical example of the SIR model with hunting**

After similar procedures above, we have Figures 15 and 16.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5		0.1	0.0001	0.1		
5								
6	t	S	I	R		Rt	S	
7	0	50	1	0		1.428367	35.005	
8	1	44.0001	1.2999	0.5		1.256966		
9	2	38.45636	1.533755	1.0999		1.098596		
10	3	33.43133	1.639625	1.756677		0.955044		
11	4	28.99224	1.588021	2.400647		0.828231		
12	5	25.17261	1.397053	2.954352		0.719115		
13	6	21.95243	1.122326	3.357148		0.627123		
14	7	19.26488	0.829341	3.58226		0.550347		
15	8	17.01929	0.568263	3.638347		0.486196		
16	9	15.12436	0.36385	3.558279		0.432063		
17	10	13.50225	0.219179	3.384021		0.385724		
18	11	12.0932	0.12492	3.15487		0.345471		
19	12	10.85399	0.067677	2.901527		0.31007		
20	13	9.7542	0.034988	2.644923		0.278652		

Figure 15. SIR model with hunting ($S(0) = 50$, $I(0) = 1$, and $R(0) = 0$)

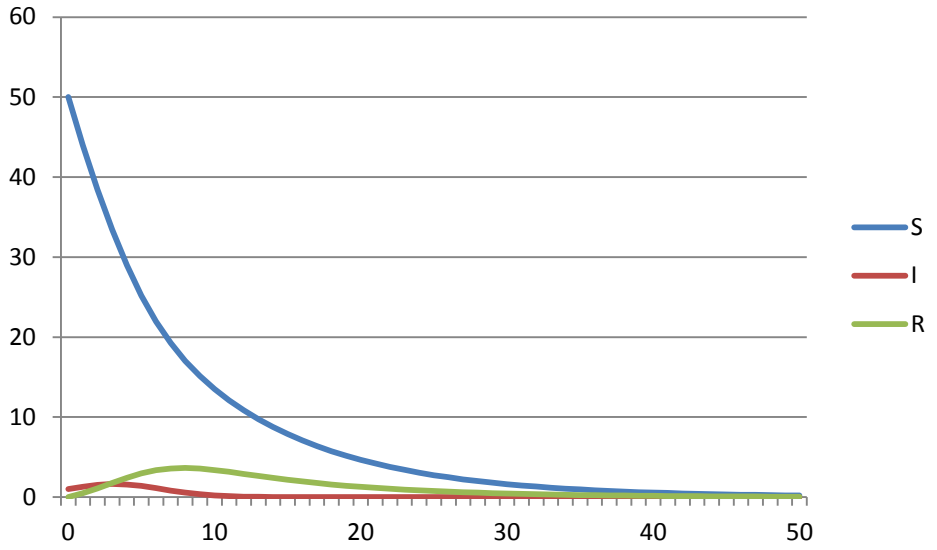

Figure 16. Dynamics of S, I, and R ($S(0) = 50$, $I(0) = 1$, and $R(0) = 0$)

Note: Vertical and horizontal axes are population size and time, respectively

The model in this subsection is less satisfactory because we introduce hunting while the birth and death rates are assumed to be the same. On the basis of eq. (33), we

may set the value of h so that $\hat{R}_t$ is less than 1 (so that the infectious disease will be eradicated). However, higher values of h yield smaller population sizes, as Figure 16 demonstrates (even if the value of h is low, the population size will decrease in the long run). In section 5, we will examine a more realistic model.

4.3. SIR model with vaccination

The SIR model with vaccination can be shown as follows:

$$\frac{dS}{dt} = mN - mS - \alpha SI - vS \tag{34}$$

$$\frac{dI}{dt} = \alpha SI - (m + \delta + \beta)I \tag{35}$$

$$\frac{dR}{dt} = \beta I - mR + vS \tag{36}$$

Here,

v: vaccination rate

We have the following:

$$R_t = \frac{\alpha S(t)}{m+\delta+\beta} \tag{37}$$

and

$$\mathrm{S}(t) = \frac{m+\delta+\beta}{\alpha} \tag{38}$$

Additionally, the total number of individuals in population N is constant over time.

[**Example 10**] **Numerical example of the SIR model with vaccination**

After similar procedures as above, we have Figures 17 and 18.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2								
3	α	β	γ	δ	m	h	v	σ
4	0.02	0.5		0.1	0.0001			
5								
6	t	S	I	R		Rt	S	
7	0	50	1	0		1.666389	30.005	
8	1	49.0001	1.3999	0.5		1.633064		
9	2	47.62839	1.931725	1.1999		1.587348		
10	3	45.7886	2.612595	2.165642		1.526032		
11	4	43.39654	3.437319	3.471724		1.44631		
12	5	40.41387	4.357938	5.190036		1.346905		
13	6	36.8924	5.265163	7.368486		1.229542		
14	7	33.00878	5.990429	10.00033		1.100109		
15	8	29.05564	6.350307	12.99454		0.96836		
16	9	25.36733	6.229733	16.1684		0.845437		
17	10	22.20894	5.651904	19.28165		0.740175		
18	11	19.70098	4.770652	22.10567		0.65659		
19	12	17.82393	3.787514	24.48879		0.594032		
20	13	16.47659	2.864794	26.38009		0.549128		

Figure 17. SIR model with vaccination ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

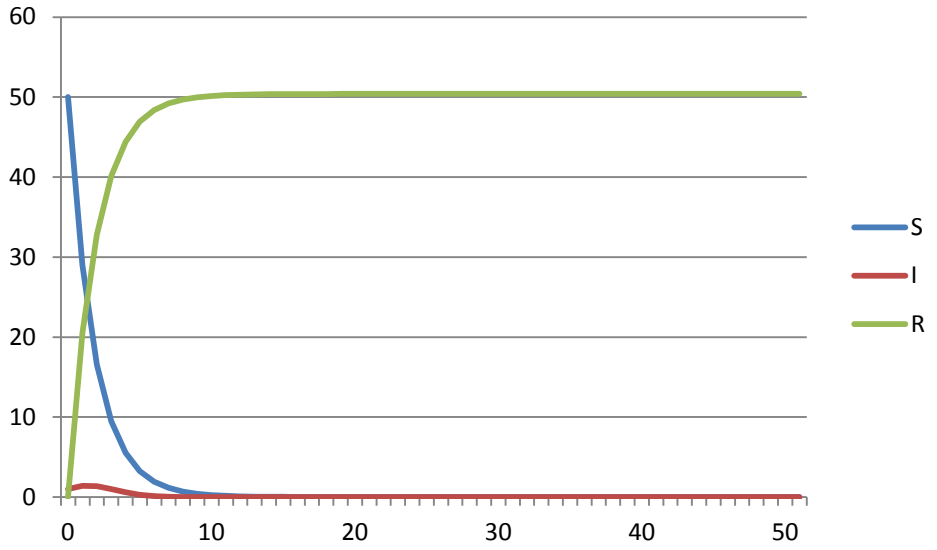

Figure 18. Dynamics of S, I, and R ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

Note: Vertical and horizontal axes are population size and time, respectively

5. Advanced model

5.1. SEI model for rabies

The SIR-type epidemiological model can be used to describe the transmission of rabies in the red fox. The model described below heavily depends on studies by Anderson et al. (1981) and Smith (1985).[3] Anderson et al. (1981) provide a model for a single population and ignore the spatial transmission of infectious diseases to other populations. However, by doing so, their model makes it possible to calculate the results analytically. After the publication of their paper, some articles examined the spatial transmission of infectious diseases; however, these papers could not provide solutions analytically and had to provide them numerically (Smith, 1985). It is necessary to take these aspects of the models into consideration when building models for real situations.

In the case of rabies, once rabies has developed, the infected animals will generally die without recovering, and therefore, R is removed from the model. In addition, acquisition of infectiousness does not occur soon after infection; there is a time lag, and those under this process are called exposed or latent individuals and are denoted as E. Therefore, the SEI model is usually used for rabies.

Here, let us examine the dynamics of susceptible S, exposed E, and infectious I individuals using mathematical equations. First, let us derive the equation for susceptible individuals. Suppose that only susceptible individuals are involved in procreation (Smith, 1985). Eq. (A5) in the Appendix I is modified as follows:

$$\frac{dS}{dt} = \left[b_1 - d_1 - r \times \frac{b_2+d_2}{r} \times N\right] S \tag{39}$$

Susceptible individuals will decrease by αSI, and eq. (39) can be rewritten as follows:

$$\frac{dS}{dt} = r\left[1 - \frac{N}{K}\right] S - \alpha SI \tag{40}$$

[3] Smith (1985) have also provided almost the same educational materials. When compared with Smith (1985), this material provides a more detailed derivation of mathematical expressions and more examples of numerical simulations, which make this material more introductory.

Next, let us derive the equation for exposed individuals. Eq. (A5) is modified as follows:

$$\frac{dE}{dt} = \left[-d_1 - r \times \frac{b_2+d_2}{r} N\right] E \tag{41}$$

Because it is assumed that exposed individuals are not involved in procreation, b_1 = 0. The population size of exposed individuals increases by αSI. On the other hand, let constant σ denote the rate that exposed individuals acquires infectiousness. Then, the number of exposed individuals will decrease by σE, and Eq. (41) can be rewritten as follows:

$$\frac{dE}{dt} = \alpha SI - \left[\sigma + d_1 + \frac{rN}{K}\right] E \tag{42}$$

Finally, let us derive the equation for infectious individuals. Eq. (A5) is modified as follows:

$$\frac{dI}{dt} = \left[-d_1 - r \times \frac{b_2+d_2}{r} \times N\right] I \tag{43}$$

The population size of infectious individuals increases by σE. On the other hand, here again, the number of infectious individuals will decrease by δI, and eq. (43) can be rewritten as follows.

$$\frac{dI}{dt} = \sigma E - \left[\delta + d_1 + \frac{rN}{K}\right] I \tag{44}$$

Eqs. (40), (41), and (42) comprise the SEI model for rabies, which is presented in Anderson et al. (1981).

[**Example 11**] **Numerical example of the SEI model**

After similar procedures above, we have Figures 19 and 20.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2	0.25	0.001	0.05	0.001	0.2	100		
3	α	β	γ	δ	m	h	v	σ
4	0.02			0.1				0.1
5								
6	t	S	E	I		N		
7	0	50	0	1		51		
8	1	53.9	1	0.748		55.648		
9	2	57.8748	1.545048	0.652551		60.0724		
10	3	61.74108	1.882986	0.630772		64.25484		
11	4	65.37608	2.137447	0.643395		68.15692		
12	5	68.69838	2.366719	0.672927		71.73802		
13	6	71.6569	2.596723	0.712111		74.96574		
14	7	74.22411	2.838437	0.758199		77.82074		
15	8	76.39104	3.096425	0.810305		80.29777		
16	9	78.16319	3.372691	0.868271		82.40415		
17	10	79.55655	3.668276	0.932201		84.15703		
18	11	80.59412	3.983866	1.002296		85.58028		
19	12	81.30283	4.319988	1.078784		86.7016		
20	13	81.71106	4.677055	1.161901		87.55001		

Figure 19. SEI model ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

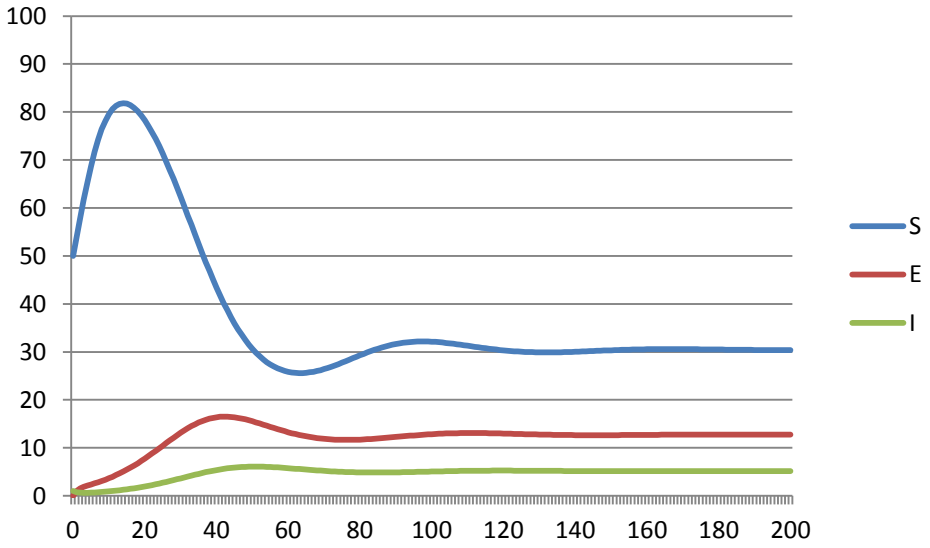

Figure 20. Dynamics of S, E, and I ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

Note: Vertical and horizontal axes are population size and time, respectively

5.2. SEI model with hunting

In this section, we suppose a situation where rabies has been prevalent in a red fox

population, and we examine hunting with guns (we may reach the same results if we consider traps and/or bait poison). Let h denote the per capita hunting rate, then eqs. (40), (41), and (42) are modified as follows:

$$\frac{dS}{dt} = r\left[1 - \frac{N}{K}\right]S - \alpha SI - hS \tag{45}$$

$$\frac{dE}{dt} = \alpha SI - \left[\sigma + d_1 + \frac{rN}{K}\right]E - hE \tag{46}$$

$$\frac{dI}{dt} = \sigma E - \left[\delta + d_1 + \frac{rN}{K}\right]I - hI \tag{47}$$

[**Example 12**] **Numerical example of the SEI model with hunting**

After similar procedures above, we have Figures 21 and 22.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2	0.25	0.001	0.05	0.001	0.2	100		
3	α	β	γ	δ	m	h	v	σ
4	0.02			0.1		0.1		0.1
5								
6	t	S	E	I		N		
7	0	50	0	1		51		
8	1	48.9	1	0.648		50.548		
9	2	48.21266	1.282648	0.52049		50.0158		
10	3	47.70925	1.335565	0.466567		49.51139		
11	4	47.31069	1.314613	0.437281		49.06258		
12	5	46.98562	1.270724	0.416514		48.67286		
13	6	46.71893	1.220747	0.398912		48.33859		
14	7	46.50144	1.170276	0.382693		48.05441		
15	8	46.32647	1.121149	0.367267		47.81488		
16	9	46.18864	1.07393	0.352444		47.61502		
17	10	46.08338	1.028755	0.338162		47.4503		
18	11	46.00671	0.98561	0.324406		47.31672		
19	12	45.95511	0.944433	0.311166		47.21071		
20	13	45.92548	0.905143	0.298437		47.12906		

Figure 21. SEI model with hunting ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)

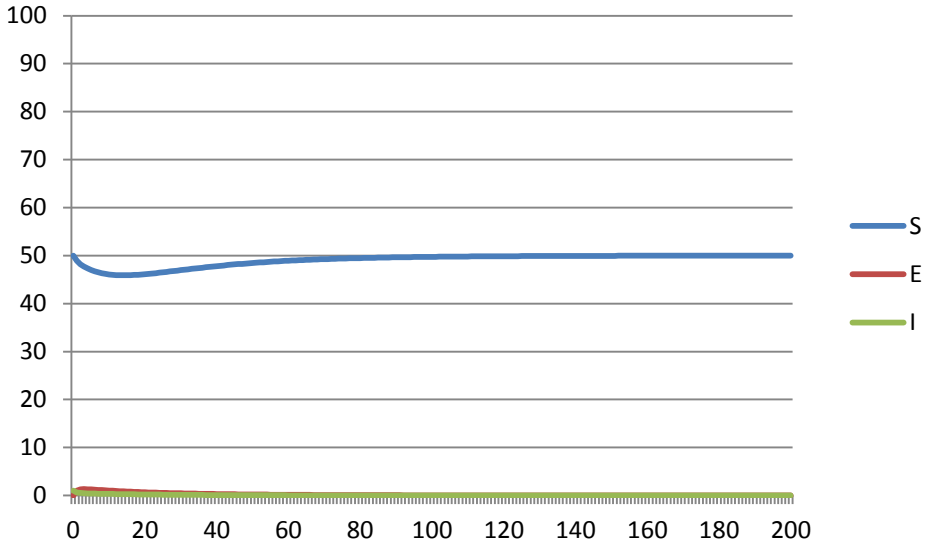

Figure 22. Dynamics of S, E, and I ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)
Note: Vertical and horizontal axes are population size and time, respectively

5.3. SEI model with vaccination

In this section, we suppose a situation where rabies has been prevalent in a red fox population, and we examine the effects of vaccination. Currently, in Europe, baits with vaccine have been dropped in habitats of red foxes from helicopters and planes. The following model can be used to examine the effects of this kind of vaccination.

For the sake of simplicity, suppose that vaccination is effective only for susceptible individuals and is not effective for exposed individuals. Let V denote vaccinated individuals. Further, suppose that vaccinated individuals are involved in procreation. Because individuals who are born from vaccinated individuals have not been vaccinated until they eat bait containing vaccine, the number of susceptible individuals increases by b_1V. Let constant v denote the rate of vaccinated individuals among susceptible individuals. Then, the number of susceptible individuals decreases by vS. Therefore, eq. (40) is modified as follows:

$$\frac{dS}{dt} = r\left[1 - \frac{N}{K}\right]S + b_1V - \alpha SI - vS \qquad (48)$$

Eq. (A5) is modified for vaccinated individuals as follows:

$$\frac{dV}{dt} = \left[-d_1 - r \times \frac{b_2+d_2}{r} \times N\right] V \tag{49}$$

The number of vaccinated individuals increases by vS. Therefore, eq. (49) is further modified as follows:

$$\frac{dV}{dt} = vS - \left[d_1 + \frac{rN}{K}\right] V \tag{50}$$

Eqs. (42) and (44), in addition to (48) and (50), comprise a modified SEI model for rabies under vaccination.

[**Example 13**] **Numerical example of the SEI model with vaccination**

After similar procedures as described above, we have Figures 23 and 24.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2	0.25	0.001	0.05	0.001	0.2	100		
3	α	β	γ	δ	m	h	v	σ
4	0.02			0.1			0.4	0.1
5								
6	t	S	E	I	V	N		
7	0	50	0	1	0	51		
8	1	33.9	1	0.748	20	55.648		
9	2	27.83992	1.245848	0.652551	30.33408	60.0724		
10	3	26.1473	1.272628	0.600852	36.30886	64.32964		
11	4	26.31675	1.232211	0.560682	40.28087	68.39051		
12	5	27.22888	1.173943	0.52311	43.28386	72.20979		
13	6	28.38681	1.113185	0.486491	45.76018	75.74667		
14	7	29.57288	1.053766	0.451135	47.89454	78.97232		
15	8	30.69423	0.996092	0.417587	49.76428	81.87219		
16	9	31.7141	0.939924	0.386181	51.40514	84.44534		
17	10	32.6214	0.885138	0.357024	52.83867	86.70223		
18	11	33.41716	0.831813	0.330075	54.08284	88.66188		
19	12	34.10818	0.780144	0.305215	55.15538	90.34892		
20	13	34.70391	0.730358	0.282295	56.07443	91.79099		

Figure 23. SEI model with vaccination ($S(0)$ = 10, $I(0)$ = 1, and $R(0)$ = 0)

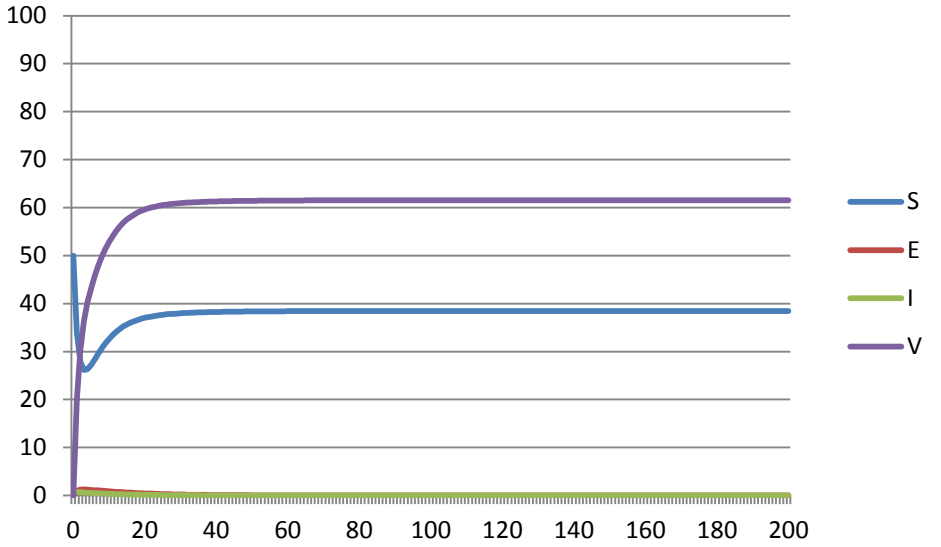

Figure 24. Dynamics of S, E, and I ($S(0)$ = 50, $I(0)$ = 1, and $R(0)$ = 0)
Note: Vertical and horizontal axes are population size and time, respectively

Appendix I

For a more concrete explanation, suppose there is a red fox population. As explained before, the size of the red fox population changes on the basis of birth and death. Namely,

$$\frac{dN}{dt} = B - D \tag{A1}$$

Here, B and D are the rate at which individuals born and die.

Further, suppose the population size of the red fox is relatively low compared to the carrying capacity of its habitat. Under such conditions, each red fox can easily obtain enough food, and litter sizes may be large. Conversely, suppose the population size of the red fox is relatively high. Under such conditions, red foxes in the same population may compete for food, and litter sizes may be small. Therefore, let b denote the average per capita birth rate, and suppose b decreases as a function of population size (as the population size N increases, the value of b decreases). Then, we have the following equation:

$$b = b_1 - b_2 N \tag{A2}$$

Under small population sizes, red foxes happen to be found by predators less frequently, and transmission of immunizing infections may be moderate or may not occur, which may result in a low average per capita death rate. On the other hand, if the population size is high, red foxes are more often found by predators, and immunizing infections may transmit more widely. Therefore, let d denote the average per capita death rate, and suppose d increases as a function of population size (as the population size N increases, the value of d increases). Then, we have the following equation.

$$d = d_1 + d_2 N \tag{A3}$$

Here, let us examine the case where $b = d$, that is, the average per capita birth rate and average per capita death rate are the same value. Population size under this condition is called the carrying capacity K. The carrying capacity is derived as follows from eqs. (A2) and (A3):

$$K = \frac{b_1 - d_1}{b_2 + d_2} = \frac{r}{b_2 + d_2} \tag{A4}$$

Here, $r = b_1 - d_1$.

Note that $B = bN$ and $D = dN$. Substituting eqs. (A2) to (A4) into eq. (A1), we obtain the following:

$$\frac{dN}{dt} = \left[b_1 - d_1 - r \times \frac{b_2 + d_2}{r} \times N \right] N \tag{A5}$$

from which, we have the following:

$$\frac{dN}{dt} = r \left[1 - \frac{N}{K} \right] N \tag{A6}$$

Eq. (A6) is the same as eq. (4) in the body text and is called the logistic equation.

The logistic equation is often criticized because many factors such as cohorts and others are combined. However, in the real application of mathematical models, we often face the fact that enough cohort data are not available and/or it is difficult to selectively catch special cohorts (for more detail, see Munro and Scott, 1985). Simpler mathematical models make it possible to have analytical solutions. This is especially true when we incorporate socio-economic aspects into biological mathematical models; if we use complicated models, we will often find it impossible to have analytical solutions and to conduct qualitative analyses.

[**Example A1**] **Growth curve**

First, we calculate the values of the average per capita birth rate b, average per capita death rate d, growth rate r, and carrying capacity K, where death means natural deaths other than those caused by infectious disease. Suppose, b_1 = 0.25, b_2 = 0.001, d_1 = 0.05, and d_2 = 0.001. Let us calculate the values of b and d by changing the value of N. Fill in between the first and sixth lines (except E2 and F2) as well as row A on the basis of Figure A1. Then fill in cells E2 and F2 with '=A2-C2' and '=(A2-C2)/(B2+D2)', respectively. Fill in cells B7 and C7 with '=$A$2-$B$2*A7' and '=$C$2+$D$2*A7', respectively, and copy these cells until B19 and C19. Now, Figure A1 is reproduced in your MS Excel spreadsheet. You can easily check that K = 100 when $b = d$ = 0.15.

Next, let us draw a growth curve represented by eq. (A6). Fill in between the first and sixth lines, as well as row A on the basis of Figure A2. Then, fill in cell B7 with '=$E$2*(1-A7/$F$2)*A7', and copy this cell until B19. Now, Figure A2 is reproduced in your MS Excel spreadsheet. You can easily check that when population size is less than carrying capacity, population change between year t and $t+1$ is positive and vice versa. Finally, we draw the growth curve in Figure A3.

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2	0.25	0.001	0.05	0.001	0.2	100		
3	α	β	γ	δ	m	h	v	σ
4								
5								
6	N	b	d					
7	0	0.25	0.05					
8	10	0.24	0.06					
9	20	0.23	0.07					
10	30	0.22	0.08					
11	40	0.21	0.09					
12	50	0.2	0.1					
13	60	0.19	0.11					
14	70	0.18	0.12					
15	80	0.17	0.13					
16	90	0.16	0.14					
17	100	0.15	0.15					
18	110	0.14	0.16					
19	120	0.13	0.17					
20								

Figure A1. Calculation of the average per capita birth rate, death rate, growth rate, and carrying capacity

	A	B	C	D	E	F	G	H
1	b1	b2	d1	d2	r	K		
2	0.25	0.001	0.05	0.001	0.2	100		
3	α	β	γ	δ	m	h	v	σ
4								
5								
6	N	dN/dt						
7	0	0						
8	10	1.8						
9	20	3.2						
10	30	4.2						
11	40	4.8						
12	50	5						
13	60	4.8						
14	70	4.2						
15	80	3.2						
16	90	1.8						
17	100	0						
18	110	−2.2						
19	120	−4.8						
20								

Figure A2. Calculation of the growth curve

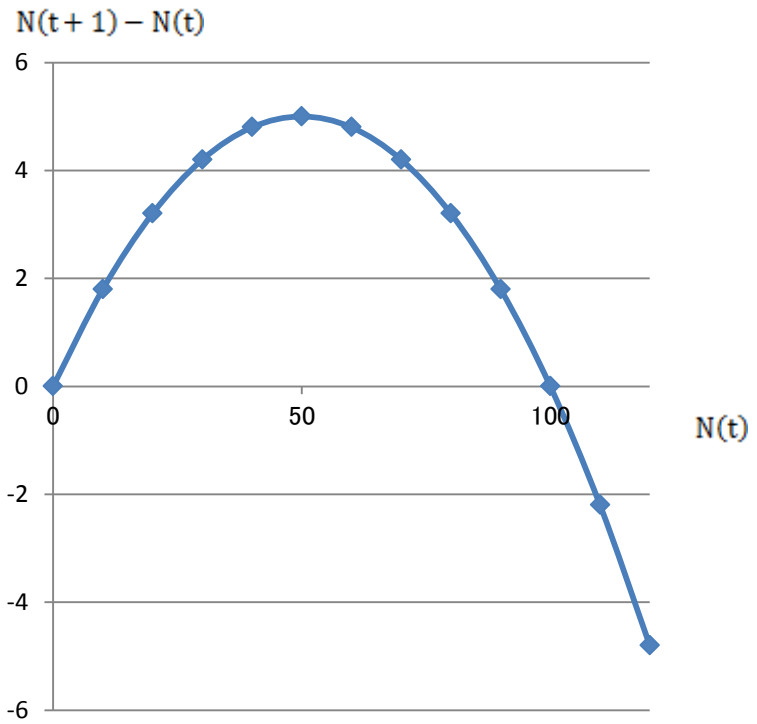

Figure A3. Growth curve

Appendix II

The R codes in Appendix II were originally written by Professor Koki Kyo from Obihiro University of Agriculture and Veterinary Medicine, with some modifications by the author of this material. Note that values of S, I, and R are restricted to be non-negative values.

You can copy the following R code and paste it on R. After pushing the 'Enter' key, a graph is automatically generated.

```
##### R code for SIR #####
# Parameter value setting
   a <- 0.02
   r <- 0.5

# Initial value setting
   So <- 50
```

```
  Io <- 1
  Ro <- 0

# Estimation period setting
  T <- 50

# Simulation
  S <- numeric(T); I <- numeric(T); R <- numeric(T)
  dS <- -a*So*Io
  dI <- a*So*Io - r*Io
  dR <- r*Io
  S[1] <- So + dS
  I[1] <- Io + dI
  R[1] <- Ro + dR
  for (i in 2:T)
    {
      dS <- -a*S[i-1]*I[i-1]
      dI <- a*S[i-1]*I[i-1] - r*I[i-1]
      if (dI > S[i-1])    {dI <- S[i-1]}
      dR <- r*I[i-1]
      if (dR > I[i-1])    {dR <- I[i-1]}
      S[i] <- S[i-1] + dS
      if(S[i] < 0) {S[i] <- 0}
      I[i] <- I[i-1] + dI
      if(I[i] < 0) {I[i] <- 0}
      R[i] <- R[i-1] + dR
      if(R[i] < 0) {R[i] <- 0}
    }

 # Graph depiction
  t <- c(1:T)
  plot(t, S, xlim=range(t), ylim=c(min(S,I,R), max(S,I,R)), type="l",
         xlab="year", ylab="", lwd=1)
  lines(t, I, lwd=2)
  lines(t, R, lwd=3)
```

```
# Calculation of R0
   R0 <- a*(S0+I0+R0)/r
   R0
```

```
##### R code for SIRS #####
# Parameter value setting
   a <- 0.02
   r <- 0.5
   v <- 0.05

# Initial value setting
   S0 <- 50
   I0 <- 1
   R0 <- 0

# Estimation period setting
   T <- 50

# Simulation
   S <- numeric(T); I <- numeric(T); R <- numeric(T)
   dS <- -a*S0*I0 + v*R0
   dI <- a*S0*I0 - r*I0
   dR <- r*I0-v*R0
   S[1] <- S0 + dS
   I[1] <- I0 + dI
   R[1] <- R0 + dR
   for (i in 2:T)
      {
        dS <- -a*S[i-1]*I[i-1] + v*R[i-1]
        dI <- a*S[i-1]*I[i-1] - r*I[i-1]
        if (dI > S[i-1])    {dI <- S[i-1]}
        dR <- r*I[i-1] - v*R[i-1]
        if (dR > I[i-1])    {dR <- I[i-1]}
        S[i] <- S[i-1] + dS
        if(S[i] < 0) {S[i] <- 0}
```

```
        I[i] <- I[i-1] + dI
        if(I[i] < 0) {I[i] <- 0}
        R[i] <- R[i-1] + dR
        if(R[i] < 0) {R[i] <- 0}
      }

# Graph depiction
   t <- c(1:T)
   plot(t, S, xlim=range(t), ylim=c(min(S,I,R), max(S,I,R)), type="l",
          xlab="year", ylab="", lwd=1)
   lines(t, I, lwd=2)
   lines(t, R, lwd=3)

# Calculation of R0
   R0 <- a*(S0+I0+R0)/r
   R0
```

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