A Leslie Matrix Approach to an Age-Structured Epidemic

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June 28, 2012

Abstract

We consider a Leslie-type matrix approach to an SIR epidemic in discrete time. We give examples of the population of susceptibles, infectives and removals for different birthrates and two different infection rates. Finally, when the infection rate depends on the number of infectives, we derive conditions for a steady state.

1   Introduction

An interesting problem in epidemiology is the modelling of age-structured epidemics. Several such studies in continuous time have been carried out in recent years, among them [2, 3, 5, 7].

For example, the authors of [2] derive a set of partial differential equations for the time-dependent age-specific densities of susceptible, infective and removed individuals in an SIR epidemic. Among other results, the authors obtain conditions for the existence of steady states.

Their calculations are lengthy and result in a complicated system of equations, from which, it is not easy to get an intuitive insight. One is led to consider if a simpler model based on a discrete time Leslie-type matrix [4], might serve equally well as a model. Models of this type have already been used by Zhou, Ma and Brauer [8] for the transmission of SARS in China, and by Powell, Slapnicar and van der Werf [6] for the spread of plant pathogens.

The purpose of this paper is not to develop new mathematical methods, but rather to indicate that discrete time age-structured epidemic models can characterise SIR epidemics very adequately. We propose to examine this alternative, and find conditions under which steady-state solutions exist.

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2 The simplest Leslie-type matrix

Suppose that at time $t = 0, 1, 2, \cdots$ we have a population consisting of $N + 1$ groups of size $s(0, t), s(1, t), \cdots, s(N, t)$ of susceptibles $s(a, t)$ of ages $0 \leq a \leq N$ (from a to $a + 1 - 0$), with death occurring when $a = N + 1$. There are $i(t)$ infectives who spread the disease, while birth rates $f(a) \geq 0$ apply to each of these age groups, with some of the $f(a) = 0$. If we assume that there is a probability $0 < q < 1$ of non-infection, independent of the number of infectives, an infection rate $p = 1 - q$ and a removal rate $r > 0$ of infectives in an SIR type epidemic process, then we can write

$$\boldsymbol{y}(t + 1) = A\boldsymbol{y}(t), \tag{1}$$

where $\boldsymbol{y}(t + 1) \in \mathbb{R}^{N+2}$, $y(t)_a = s(a, t)$ for $0 \leq a \leq N$ and $y(t)_{N+1} = i(t)$ and

$$A = \begin{bmatrix} f(0) & f(1) & f(2) & \cdots & f(N-2) & f(N-1) & f(N) & 0 \\ q & 0 & 0 & \cdots & 0 & 0 & 0 & 0 \\ 0 & q & 0 & \cdots & 0 & 0 & 0 & 0 \\ 0 & 0 & q & \cdots & 0 & 0 & 0 & 0 \\ \vdots & \vdots & & \ddots & & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & q & 0 & 0 & 0 \\ 0 & 0 & 0 & \cdots & 0 & q & 0 & 0 \\ p & p & p & \cdots & p & p & p & 1-r \end{bmatrix}. \tag{2}$$

We see that the total number of births in $(t, t + 1)$ is the sum $\sum_{a=0}^{N} f(a)s(a, t)$ while the number of infectives remaining after removal is

$$i(t + 1) = (1 - r)i(t) + p\sum_{a=0}^{N} s(a, t). \tag{3}$$

We now present some numerical examples of such populations.

Example 2.1 *Let us suppose that we have a population of insects of ages $a = 0, 1$ and 2, where only the group aged 1 can give birth at the rate of $f(1) = 0.85$. We may start at $t = 0$ with $s(0,0) = 412$, $s(1,0) = 492$, $s(2,0) = 465$ with death occurring when $a = 3$. At $t = 0$, $i(0) = 1$ so we begin with one infective in the population, with the probability 0.9 of non-infection and a removal rate $r = 0.5$.*

Thus, for the matrix

$$A = \begin{bmatrix} 0 & 0.85 & 0 & 0 \\ 0.9 & 0 & 0 & 0 \\ 0 & 0.9 & 0 & 0 \\ 0.1 & 0.1 & 0.1 & 0.5 \end{bmatrix}, \tag{4}$$

we find as $t = 0, 1, 2, 3, 4, 5$ the population evolves as shown in Table 1 with the total population size decreasing from 1370 to 896. The calculations were done in

Table 1: Change in the population size for Example 2.1

t	0	1	2	3	4	5
$s(0,t)$	412	418	315	320	241	245
$s(1,t)$	492	371	376	284	288	217
$s(2,t)$	465	443	334	339	255	259
$i(t)$	1	137	192	198	193	175

double precision, but the $s(a,t)$ and $i(t)$ presented in the table are rounded off to the nearest integer. The continual decrease in the population in the long-term is shown in figures 1 and 2.
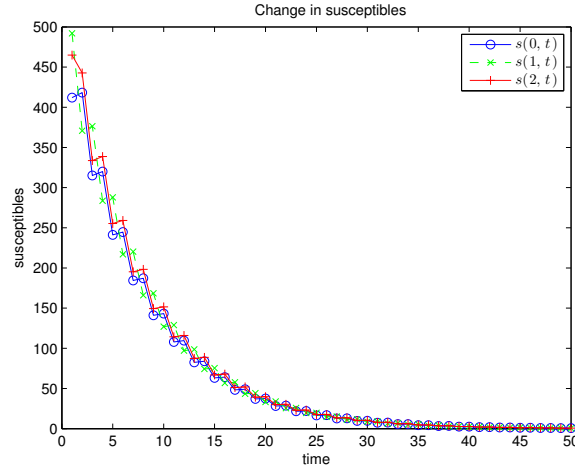

Figure 1: Change in the number of susceptibles in each age-group over time for Example 2.1.

One may well ask if such models can lead to the gradual extinction of the infectives $i(t)$. From our simple insect model, we can see that $i(t+1) < i(t)$ if

$$p\left(s(0,t) + s(1,t) + s(2,t)\right) + (1-r)i(t) < i(t),$$

or

$$\frac{p}{r}S(t) < i(t),$$

where $S(t) = \sum_{a=0}^{N} s(a,t)$ and $p/r = 1/5$ in the example given.

For Example 2.1, with a birth rate of 0.85, the size of the population rapidly decreases, as does also the number $i(t)$ of infectives. For $t = 15$ the population is $\boldsymbol{y}(t) = \begin{bmatrix} 65 & 58 & 69 & 48.19 \end{bmatrix}^T$ or $S(t)/5 = 192/5 = 38.4$ so that a further decline of the infectives is expected. In fact, the decline in both susceptibles and infectives is steady, by $t = 30$, $S(30) = 28$, $i(30) = 7.41$.
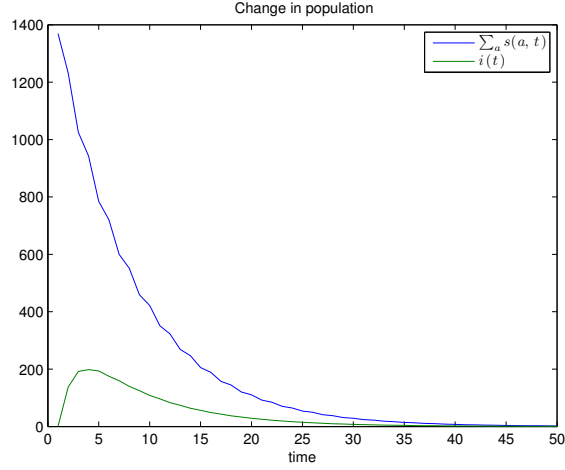
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Figure 2: Change in the population size over time for Example 2.1.

Table 2: Change in the population size for Example 2.2

t	0	1	2	3	4	5
$s(0,t)$	412	566	426	586	441	606
$s(1,t)$	492	371	509	384	527	397
$s(2,t)$	465	443	334	458	345	474
$i(t)$	1	137	207	230	258	260

Example 2.2 *In the next example we increase $f(1)$ to 1.15. All other parameters are the same as Example 2.1.*

In which case

$$A = \begin{bmatrix} 0 & 1.15 & 0 & 0 \\ 0.9 & 0 & 0 & 0 \\ 0 & 0.9 & 0 & 0 \\ 0.1 & 0.1 & 0.1 & 0.5. \end{bmatrix}. \qquad (5)$$

The change in each age-group for $t = 0, 1, 2, 3, 4, 5$ is given in Table 2. The apparent growth evident in the table is confirmed over the long-term in Figure 3.

Note that if at any time $t > 0$, $i(t) > S(t)p/r$ then $i(t+1) < i(t)$. From Equation (3),

$$i(t+1) - i(t) = pS(t) - ri(t) = pS(t) - r\left(\frac{S(t)p}{r} + \epsilon\right), \quad \epsilon > 0,$$

so that for this t, $i(t+1) - i(t) = -r\epsilon < 0$. In Section 3, we state in detail the conditions under which both $S(t)$ and $i(t)$ decrease as t increases.
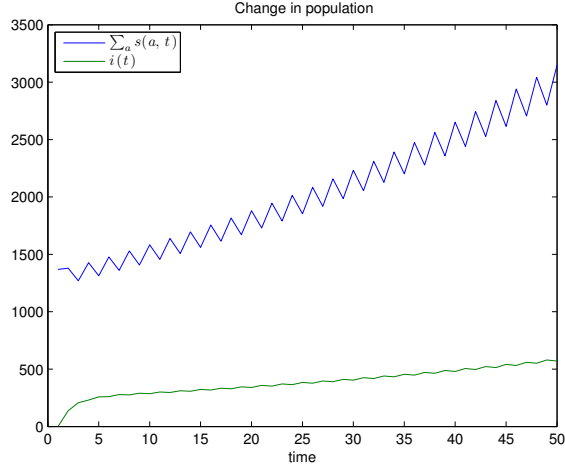
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Figure 3: Change in the population size over time for Example 2.2.

3 Some consequences of the matrix structure

Consider the Leslie-type matrix given in (2). We can write the matrix in block form as

$$A = \begin{bmatrix} L & \mathbf{0} \\ \boldsymbol{x}^T & 1 - r \end{bmatrix},$$

where L is the standard Leslie matrix

$$L = \begin{bmatrix} f(0) & f(1) & f(2) & \cdots & f(N-2) & f(N-1) & f(N) \\ q & 0 & 0 & \cdots & 0 & 0 & 0 \\ 0 & q & 0 & \cdots & 0 & 0 & 0 \\ 0 & 0 & q & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & & \ddots & & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & q & 0 & 0 \\ 0 & 0 & 0 & \cdots & 0 & q & 0 \end{bmatrix}, \quad (6)$$

and $\boldsymbol{x}$ is a vector with $x_a = p$ $(0 \leq a \leq N)$. Consequently, by cofactor expansion,

$$|A - \lambda I_2| = (1 - r - \lambda)\,|L - \lambda I_1|,$$

and hence the eigenvalues of A are $1 - r$ together with the eigenvalues of L. The matrices $I_2 \in \mathbb{R}^{(N+2)\times(N+2)}$ and $I_1 \in \mathbb{R}^{(N+1)\times(N+1)}$ are identity matrices. The standard Leslie matrix is well known and techniques for calculating its eigenvalues appear in elementary linear algebra text books such as [1].

Consider the eigenvalue $\lambda_{N+1} = 1 - r$. Let $\boldsymbol{u}_{N+1}$ be a vector such that the $(N+2)$th entry is one, and all remaining entries are zero. Then

$$(A - \lambda_{N+1}I_2)\boldsymbol{u}_{N+1} = \begin{bmatrix} L - \lambda_{N+1}I_1 & \mathbf{0} \\ \boldsymbol{x}^T & 0 \end{bmatrix} \boldsymbol{u}_{N+1} = 0.$$

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So, $\boldsymbol{u}_{N+1}$ is an eigenvector.

We now focus on λ_a, ($0 \le a \le N$), where λ_a is an eigenvalue of L with corresponding eigenvector $\boldsymbol{v}_a$. Let $\boldsymbol{u}_a = \begin{bmatrix} \boldsymbol{v}_a^T & \alpha \end{bmatrix}^T$ for some scalar term α. Then

$$
(A - \lambda_a I_2) \begin{bmatrix} \boldsymbol{v}_a \\ \alpha \end{bmatrix} = \begin{bmatrix} L - \lambda_a I_1 & \boldsymbol{0} \\ \boldsymbol{x}^T & 0 \end{bmatrix} \begin{bmatrix} \boldsymbol{v}_a \\ \alpha \end{bmatrix}
$$
$$
= \begin{bmatrix} (L - \lambda_a I)\boldsymbol{v}_a \\ \boldsymbol{x}^T \boldsymbol{v}_a + \alpha(1 - r - \lambda_a) \end{bmatrix}
$$
$$
= \begin{bmatrix} \boldsymbol{0} \\ \boldsymbol{x}^T \boldsymbol{v}_a + \alpha(1 - r - \lambda_a) \end{bmatrix}.
$$

Therefore, if $\alpha = -\boldsymbol{x}^T \boldsymbol{v}_a / (1 - r - \lambda_a)$, $\boldsymbol{u}_a$ is an eigenvector.

To be more specific, let us look at the examples in which the Leslie matrix is of the form
$$
L = \begin{bmatrix} f(0) & f(1) & 0 \\ q & 0 & 0 \\ 0 & q & 0 \end{bmatrix}.
$$

The eigenvalues of L are
$$
\lambda_1 = \frac{f(0) - \sqrt{f^2(0) + 4f(1)q}}{2}, \quad \lambda_2 = \frac{f(0) + \sqrt{f^2(0) + 4f(1)q}}{2} \text{ and } \lambda_3 = 0
$$

with corresponding eigenvectors
$$
\boldsymbol{v}_1 = \begin{bmatrix} f(1)/(\lambda_1 - f(0)) \\ 1 \\ q/\lambda_1 \end{bmatrix}, \boldsymbol{v}_2 = \begin{bmatrix} f(1)/(\lambda_2 - f(0)) \\ 1 \\ q/\lambda_2 \end{bmatrix} \text{ and } \boldsymbol{v}_3 = \begin{bmatrix} 0 \\ 0 \\ 1 \end{bmatrix}.
$$

So, the eigenvalues of
$$
A = \begin{bmatrix} f(0) & f(1) & 0 & 0 \\ q & 0 & 0 & 0 \\ 0 & q & 0 & 0 \\ p & p & p & 1 - r \end{bmatrix}
$$

are λ_1, λ_2 and λ_3, as listed above, with $\lambda_4 = 1 - r$ and corresponding eigenvectors
$$
\boldsymbol{u}_1 = \begin{bmatrix} \frac{f(1)}{\lambda_1 - f(0)} \\ 1 \\ \frac{q}{\lambda_1} \\ \alpha_1 \end{bmatrix}, \boldsymbol{u}_2 = \begin{bmatrix} \frac{f(1)}{\lambda_2 - f(0)} \\ 1 \\ \frac{q}{\lambda_2} \\ \alpha_2 \end{bmatrix}, \boldsymbol{u}_3 = \begin{bmatrix} 0 \\ 0 \\ 1 \\ \alpha_3 \end{bmatrix} \text{ and } \boldsymbol{u}_4 = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 1 \end{bmatrix},
$$

where
$$
\alpha_1 = \frac{-p\left[q(\lambda_1 - f(0)) + \lambda_1(\lambda_1 - f(0)) + f(1)\lambda_1\right]}{\lambda_1(\lambda_1 - f(0))(1 - r - \lambda_1)},
$$
$$
\alpha_2 = \frac{-p\left[q(\lambda_2 - f(0)) + \lambda_2(\lambda_2 - f(0)) + f(1)\lambda_2\right]}{\lambda_2(\lambda_2 - f(0))(1 - r - \lambda_2)},
$$
$$
\alpha_3 = \frac{-p}{1 - r}.
$$

Once we obtain the eigenvalues and eigenvectors we can determine the long-term behaviour of the system.

Consider examples 2.1 and 2.2 from Section 2. In this case $f(0) = 0$, so the eigenvalues are $\lambda_1 = -\sqrt{fq}$, $\lambda_2 = \sqrt{fq}$, $\lambda_3 = 0$ and $\lambda_4 = 1 - r$, where $f(1) = f$. Given that the eigenvectors $\boldsymbol{u}_1$, $\boldsymbol{u}_2$, $\boldsymbol{u}_3$ and $\boldsymbol{u}_4$ form a basis, our initial population distribution can be written as

$$\boldsymbol{y}(0) = c_1\boldsymbol{u}_1 + c_2\boldsymbol{u}_2 + c_3\boldsymbol{u}_3 + c_4\boldsymbol{u}_4,$$

for some scalar terms c_1, c_2, c_3 and c_4. Consequently,

$$\begin{aligned} \boldsymbol{y}(t) &= c_1\lambda_1^t\boldsymbol{u}_1 + c_2\lambda_2^t\boldsymbol{u}_2 + c_3\lambda_3^t\boldsymbol{u}_4 + c_4\lambda_4^t\boldsymbol{u}_4 \\ &= c_1(-\sqrt{fq})^t\boldsymbol{u}_1 + c_2(\sqrt{fq})^t\boldsymbol{u}_2 + c_4(1-r)^t\boldsymbol{u}_4. \end{aligned}$$

As $(1 - r) < 1$, the last term will always approach zero. If $\sqrt{fq} < 1$, or $fq < 1$, the overall population will decrease with time, while if $\sqrt{fq} > 1$ it will increase with time. If $\sqrt{fq} = 1$, the population will achieve a steady-state solution that oscillates between $c_1\boldsymbol{u}_1 + c_2\boldsymbol{u}_2$ and $-c_1\boldsymbol{u}_1 + c_2\boldsymbol{u}_2$. With Example 2.1, where A is defined in (4), $fq = 0.9 \times 0.85 = 0.765 < 1$ and we see that the population decreases with time. However, with Example 2.2, , where A is defined in (5), $fq = 0.9 \times 1.15 = 1.035 > 1$ and the population increases with time.

As t grows, we expect $\boldsymbol{y}(t)$ to approach

$$(\sqrt{fq})^t \left(c_1(-1)^t\boldsymbol{u}_1 + c_2\boldsymbol{u}_2 \right).$$

For the example given in (4), this means we expect $\boldsymbol{y}(t)$ to approach

$$(0.8746)^t \left(c_1(-1)^t \begin{bmatrix} -0.9718 \\ 1.0000 \\ -1.0290 \\ 0.0728 \end{bmatrix} + c_2 \begin{bmatrix} 0.9718 \\ 1.0000 \\ 1.0290 \\ 0.8010 \end{bmatrix} \right).$$

In this case there is no single dominant eigenvalue and the long-term $y(t)$ depends on the initial distribution $\boldsymbol{y}(0)$. However, we can still determine the qualitative behaviour of the different age-groups. For example, the $(-1)^t$ term indicates that $s(a, t)$ will oscillate. We would also expect $s(0, t)$, $s(1, t)$ and $s(2, t)$ to reach roughly similar percentages of the total population, as their corresponding entries in the eigenvector all have about the same absolute value (their absolute values are between 0.97 and 1.03). Finally, we can see that the infectives should represent a smaller percentage of the overall population. Using MATLAB to calculate the distribution of each group gives the results in Figure 4, where such qualitative behaviour is evident.

Example 3.1 *Instead of setting $f(0) = 0$, let us try $f(0) = 0.56$. All of the other parameters are the same as Example 2.1.*
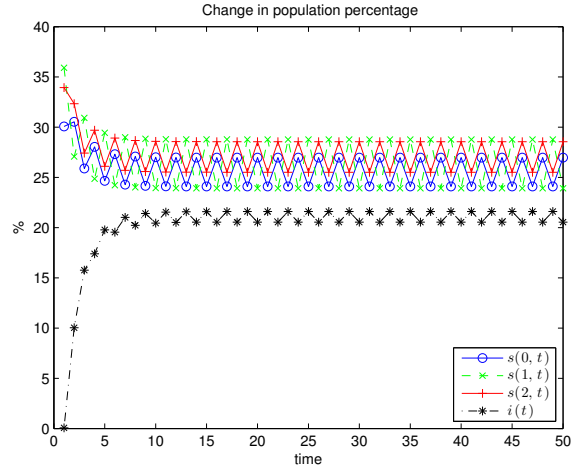
Figure 4: Change in the population ratio over time for Example 2.1 when A is given by (4).

So that,

$$A = \begin{bmatrix} 0.56 & 0.85 & 0 & 0 \\ 0.9 & 0 & 0 & 0 \\ 0 & 0.9 & 0 & 0 \\ 0.1 & 0.1 & 0.1 & 0.5 \end{bmatrix}. \tag{7}$$

Then, we have a single dominant eigenvalue

$$\lambda = \frac{f(0) + \sqrt{f^2(0) + 4f(1)q}}{2} = 1.1984,$$

with corresponding eigenvector

$$\boldsymbol{u} = \begin{bmatrix} 1.3315 \\ 1.0000 \\ 0.7510 \\ 0.4414 \end{bmatrix}.$$

Consequently, we expect the long-term solution to approach some multiple of $\boldsymbol{u}$. Figure 5 shows the distribution of each age-group when A is given by (7).
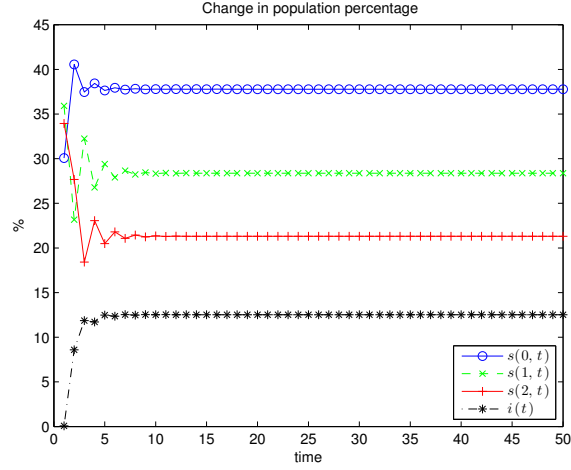
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Figure 5: Change in the population ratio over time for Example 3.1 when A is given by (7).

4   A more realistic Leslie-type matrix

If instead of a probability q of non-infection, we replace this by $q^{i(t)}$, for $i(t)$ independent infectives, then the Leslie-type matrix becomes

$$
A(t) = \begin{bmatrix}
f(0) & f(1) & f(2) & \cdots & f(N-2) & f(N-1) & f(N) & 0 \\
q^{i(t)} & 0 & 0 & \cdots & 0 & 0 & 0 & 0 \\
0 & q^{i(t)} & 0 & \cdots & 0 & 0 & 0 & 0 \\
0 & 0 & q^{i(t)} & \cdots & 0 & 0 & 0 & 0 \\
\vdots & \vdots & & \ddots & & \vdots & \vdots & \vdots \\
0 & 0 & 0 & \cdots & q^{i(t)} & 0 & 0 & 0 \\
0 & 0 & 0 & \cdots & 0 & q^{i(t)} & 0 & 0 \\
1-q^{i(t)} & 1-q^{i(t)} & 1-q^{i(t)} & \cdots & 1-q^{i(t)} & 1-q^{i(t)} & 1-q^{i(t)} & 1-r
\end{bmatrix}
\tag{8}
$$

and, once again, we can write the SIR process as $\boldsymbol{y}(t+1) = A(t)\boldsymbol{y}(t)$.

Example 4.1 *This starts with the same initial populations, $s(0,0) = 412$, $s(1,0) = 492$ and $s(2,0) = 465$ as for Example 2.1, but with the Leslie-type matrix*

$$
A = \begin{bmatrix}
0 & 0.85 & 0 & 0 \\
0.9^{i(t)} & 0 & 0 & 0 \\
0 & 0.9^{i(t)} & 0 & 0 \\
1-0.9^{i(t)} & 1-0.9^{i(t)} & 1-0.9^{i(t)} & 0.5
\end{bmatrix}.
$$

Example 4.2 *Similarly we apply the Leslie-type matrix* (8) *to Example 2.2 where $f(1) = 1.15$.*

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Example 4.3 *The final example applies the Leslie-type matrix* (8) *to Example 3.1 where* $f(1) = 0.56$ *and* $f(1) = 0.85$.
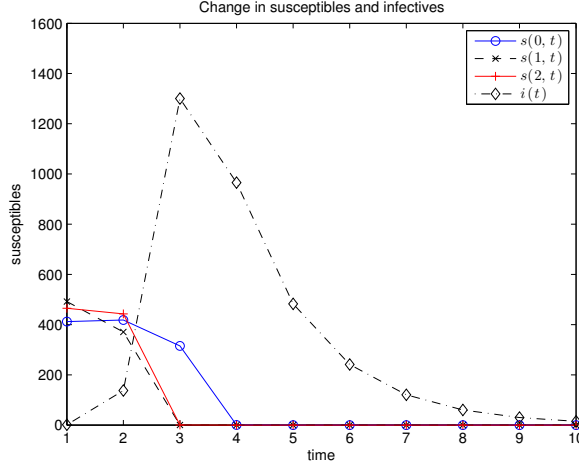

Figure 6: Change in the number of susceptibles and infectives in each age-group over time for Example 4.1.

The results for the SIR process $\boldsymbol{y}(t+1) = A(t)\boldsymbol{y}(t)$ using the examples 4.1, 4.2 and 4.3 are shown in figures 6, 7 and 8. We can see that the results are now markedly different from those shown in Sections 2 and 3. In these cases, as in the more realistic cases, most of the insects end up as infectives.

Is it possible to find examples where the steady-state solution does not have all susceptibles removed from the system? In other words, can we find $\boldsymbol{y}(t+1)$ such that $\boldsymbol{y}(t+1) - \boldsymbol{y}(t) = \boldsymbol{0}$, but $y(t+1)_a = s(a, t+1) \neq 0$ (for $0 \leq a \leq N$)?

Now, $\boldsymbol{y}(t+1) - \boldsymbol{y}(t) = \boldsymbol{0}$ if $\boldsymbol{y}(t)$ is in the null space of

$$(A(t) - I_2) = \begin{bmatrix} L(t) - I_1 & \boldsymbol{0} \\ \boldsymbol{x}(t)^T & -r \end{bmatrix}.$$

where $I_i \in \mathbb{R}^{(N+i) \times (N+i)}$, and

$$
L(t) = \begin{bmatrix}
f(0) & f(1) & f(2) & \cdots & f(N-2) & f(N-1) & f(N) \\
q^{i(t)} & 0 & 0 & \cdots & 0 & 0 & 0 \\
0 & q^{i(t)} & 0 & \cdots & 0 & 0 & 0 \\
0 & 0 & q^{i(t)} & \cdots & 0 & 0 & 0 \\
\vdots & \vdots & & \ddots & & \vdots & \vdots \\
0 & 0 & 0 & \cdots & q^{i(t)} & 0 & 0 \\
0 & 0 & 0 & \cdots & 0 & q^{i(t)} & 0
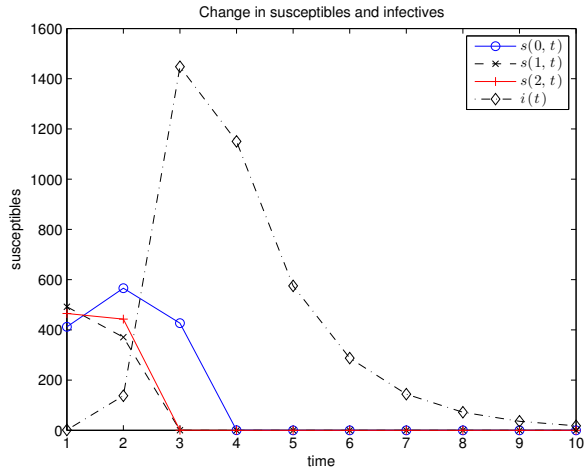\end{bmatrix}, \quad (9)
$$

Figure 7: Change in the number of susceptibles and infectives in each age-group over time for Example 4.2.
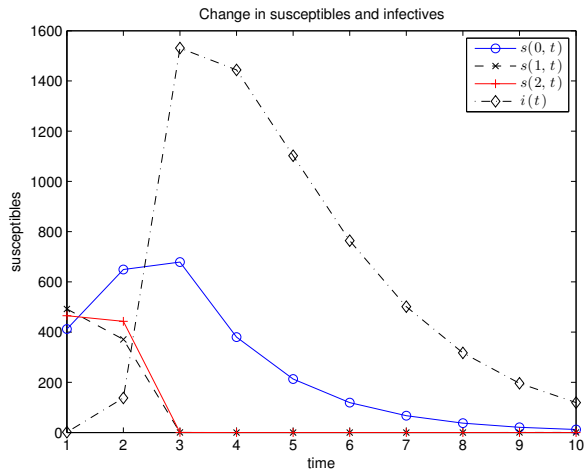

Figure 8: Change in the number of susceptibles and infectives in each age-group over time for Example 4.3.

with $\boldsymbol{x}(t)_a = 1 - q^{i(t)}$. Let us focus on $L(t) - I_1$. A vector $\boldsymbol{s} \in \mathbb{R}^{N+1}$ is in the null space of $L(t) - I_1$ if

$$
\begin{aligned}
\mathbf{0} &= (L - I_1)\boldsymbol{s} \\
&=
\begin{bmatrix}
f(0) - 1 & f(1) & f(2) & \cdots & f(N-2) & f(N-1) & f(N) \\
q^{i(t)} & -1 & 0 & \cdots & 0 & 0 & 0 \\
0 & q^{i(t)} & -1 & \cdots & 0 & 0 & 0 \\
0 & 0 & q^{i(t)} & \cdots & 0 & 0 & 0 \\
\vdots & \vdots & & \ddots & & \vdots & \vdots \\
0 & 0 & 0 & \cdots & q^{i(t)} & -1 & 0 \\
0 & 0 & 0 & \cdots & 0 & q^{i(t)} & -1
\end{bmatrix}
\begin{bmatrix}
s_0 \\ s_1 \\ s_2 \\ \vdots \\ s_{N-1} \\ s_N
\end{bmatrix} .
\end{aligned}
$$

Using back substitution, we get

$$
q^{i(t)} s_{N-1} - s_N = 0 \Rightarrow s_{N-1} = q^{-i(t)} s_N,
$$

$$
q^{i(t)} s_{N-2} - s_{N-1} = 0 \Rightarrow s_{N-2} = q^{-i(t)} s_{N-1} = q^{-2i(t)} s_N,
$$

and so forth, until finally

$$
q^{i(t)} s_0 - s_1 = 0 \Rightarrow s_0 = q^{-i(t)} s_1 = q^{-Ni(t)} s_N.
$$

But we still need to take the first row into account. From the first row,

$$
\begin{aligned}
0 &= (f(0) - 1)s_0 + f(1)s_1 + f(2)s_2 + \cdots + f(N)s_N \\
&= \left\{ (f(0) - 1)q^{-Ni(t)} + f(1)q^{-(N-1)i(t)} + \cdots + f(N) \right\} s_N.
\end{aligned}
$$

Recall that we are looking for the steady-state solutions, so we are assuming $i(t+1) = i(t) = i$ for all $t > T$, at some point T in time. Consequently, if the following constraint

$$
0 = (f(0) - 1)q^{-Ni} + f(1)q^{-(N-1)i} + \cdots + f(N) \tag{10}
$$

is satisfied, the non-trivial null space of $L(t) - I_1$ is spanned by,

$$
\boldsymbol{w} = \begin{bmatrix} q^{-Ni} & q^{-(N-1)i} & \cdots & q^{-i} & 1 \end{bmatrix}^T. \tag{11}
$$

If Constraint (10) is not satisfied, the null space of $L(t) - I_1$ only contains the zero vector.

In our example problems we have $f(0) = f(2) = f(3) = 0$. So, for Constraint (10) to be satisfied, we must have $f(1) = q^{-i}$.

Suppose we have $\boldsymbol{s}$ that belongs to the null space of $L(t) - I_1$, then $\boldsymbol{s} = c\boldsymbol{w}$ for some scalar term c. Furthermore, $\boldsymbol{y} = \begin{bmatrix} \boldsymbol{s}^T & i \end{bmatrix}^T \in \mathbb{R}^{N+2}$ is in the null space

of $A(t) - I_2$ if $\boldsymbol{x}^T\boldsymbol{s} - ri = 0$. In other words,

$$
\begin{aligned}
i &= \frac{1}{r}\boldsymbol{x}^T\boldsymbol{s} \\
&= \frac{1}{r}\left(1 - q^i\right)\sum_{a=0}^{N} s_a \\
&= \frac{c}{r}\left(1 - q^i\right)\sum_{a=0}^{N} q^{-ai} \\
&= \frac{c}{r}\left(q^{-Ni} - q^i\right).
\end{aligned}
$$

Rearranging the terms in the above equations gives the following additional constraint on i

$$
0 = \frac{r}{c}i + q^i\left(1 - q^{-(N+1)i}\right). \tag{12}
$$

To find an example of a non-zero steady-state solution we set $q = 0.9$ and found an example of i that satisfied Constraint (12) with $r/c = 0.5$. That is, we set $i = 5.969091$. We then set $f(1) = q^{-i}$ and used Equation (11) to find $\boldsymbol{s}$, with $c = 1.5$. As shown in Figure 9, the solution does not change with time. This appears to be a stable equilibrium point. We tried changing i to $i = 2.4691$ (set $f(1) = q^{-i}$ and used Equation (11) to find $\boldsymbol{s}$), where the resulting system shown in Figure 10 is periodic.
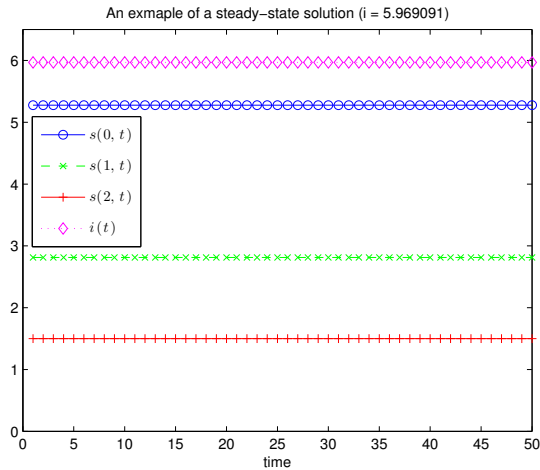

Figure 9: An example of a non-zero steady-state solution

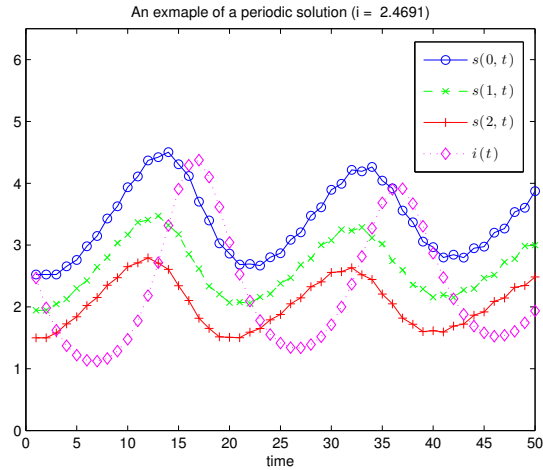An exmaple of a periodic solution (i = 2.4691)

Figure 10: An example of a periodic equilibrium solution

5   Conclusion

Our discrete time approach proves simpler than the continuous time analysis presented in [2]. It offers readily calculable results, such as those of Table 2 and the graphs in figures 2, 4, 5, and 6. From the view point of the practising epidemiologist, this simple applicability of the Leslie-type matrix approach is a distinct asset.

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