Article

A generalized model for overlap infection of pathogens

GuangHua Liu[1], **YanHong Qi**[2], **WenJun Zhang**[3]

[1]Guangdong AIB Polytech College, Guangzhou 510507, China

[2]Sun Yat-sen University Libraries, Sun Yat-sen University, Guangzhou 510275, China

[3]School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, China

E-mail: zhwj@mail.sysu.edu.cn, wjzhang@iaees.org

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Abstract

From the same source or multiple sources, the pathogen may trigger multiple infection processes, and each infection process will cause different theoretical incidence. However, some of the previously infected individuals may be re-infected in the ongoing infection process, that is, the previous and ongoing infections overlap. The higher the previous incidence, the greater the subsequent infections overlap. In the total incidence calculation, the overlap should be removed. In this study, an infection overlap model, based on the probability principles, was proposed as the following

$$A(t_i)=B(t_1),\ \ i=1$$
$$A(t_i)= B(t_i)(1-\sum_{j=1}^{i-1}A(t_j)),\ \ i=2,3,\ldots$$

where $A(t_i)$ is the newly occurred infection incidence in i-th infection, t_i is the time for occurrence of i-th infection, and $B(t_i)$ is the theoretical incidence calculated. The total incidence dynamics is thus

$$S(t_i)=\sum_{j=1}^{i}A(t_j),\ \ i=1,2,3,\ \ldots$$

The model can be used as a fundamental model frame for the epidemic with repeated re-infections by pathogens.

Keywords pathogens; re-infection; overlap; model; incidence.

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1 Introduction

Epidemiolocal models are useful tools to explain and predict disease epidemic (Anderson and May, 1981; Fuxa and Tanada, 1987; Zhang, 1993; Zhang et al., 1997; Zhang et al., 2011; Zhang, 2012, 2016, 2018; Shams

and Khansari, 2019; Zhang et al., 2020). From the same source or multiple sources, the pathogen may trigger multiple infection processes, and each infection process will cause different theoretical incidence. However, some of the previously infected individuals may be re-infected in the ongoing infection process, that is, the previous and ongoing infections overlap. The higher the previous incidence, the greater the subsequent infections overlap. In the total incidence calculation, the overlap should be removed (Zhang, 1993). In present study, we aims to propose an infection overlap model, in order to provide a fundamental model frame for the epidemic with repeated re-infections by pathogens.

2 Model

It is assumed that for each infection process, each individual has the same probability of being infected and diseased, and the first infection process occurs at time t_1. The theoretical incidence $B(t_1)$ of the first infection process is equal to the newly occurred infection incidence $A(t_1)$, i.e.,

$$B(t_1)=A(t_1)$$

The second infection process occurs at time t_2, and the corresponding theoretical infection incidence is $B(t_2)$. According to the principle of probability independence and multiplication theorem of probability, the overlapped infection incidence between the two infection processes is

$$B(t_1)B(t_2)$$

Thus, the newly occurred incidence for the second infection process is

$$A(t_2)= B(t_2)-B(t_1)B(t_2)$$

Similarly, the third infection process occurs at time t_3, and the corresponding theoretical infection incidence is $B(t_3)$. Know the total incidence of the first and the second infection processes, $A(t_1)+A(t_2)$, the overlapped infection incidence of the third infection process is

$$B(t_3)(A(t_1)+A(t_2))$$

And the newly occurred incidence is thus

$$A(t_3)=B(t_3)-B(t_3)(A(t_1)+A(t_2))=B(t_3)(1-\sum_{j=1}^{2}A(t_j))$$

In such a way, we have the following infection overlap model

$$A(t_i)=B(t_1), \quad i=1$$
$$A(t_i)=B(t_i)(1-\sum_{j=1}^{i-1}A(t_j)), \quad i=2,3,\ldots$$

where $A(t_i)$ is the newly occurred infection incidence in i-th infection, t_i is the time for occurrence of i-th infection, and $B(t_i)$ is the theoretical incidence calculated. The total incidence dynamics is thus

$$S(t_i)=\sum_{j=1}^{i}A(t_j), \quad i=1,2,3, \ldots$$

or

$$S(t_1)=A(t_1), \quad i=1$$
$$S(t_i)= S(t_{i-1})+A(t_i), \quad i=2,3, \ldots$$

The Matlab codes for the model are as follows

```
B=[0.3 0.25 0.2 0.17 0.13 0.08 0.03];
n=size(B,2);
A=zeros(1,n);
S=zeros(1,n);
A(1)=B(1);
for i=2:n
for j=1:i-1
A(i)=A(i)+A(j);
end
A(i)=B(i)*(1-A(i));
end
S(1)=A(1);
for j=2:n
S(j)=S(j-1)+A(j);
end
fprintf('Newly occurred infection incidence (A(t)):\n')
A
fprintf('Total incidence (S(t)):\n')
S
plot(1:n,S*100,'-o');
xlabel('Time (t) ');
ylabel('Total incidence (S(t); %)');
```

3 Model Application

As an example, we use four datasets to fit the model (Table 1). The calculated newly occurred infection incidence ($A(t)$) and total incidence dynamics ($S(t)$) are shown in Table 1 and Fig. 1.

Table 1 Four sets of theoretical incidences ($B(t)$), calculated newly occurred infection incidence ($A(t)$) and total incidence dynamics ($S(t)$).

t		1	2	3	4	5	6	7
$B(t)$	I	0.3	0.25	0.2	0.15	0.1	0.05	0.01
	II	0.1	0.1	0.1	0.1	0.1	0.1	0.1
	III	0.2	0.3	0.4	0.5	0.6	0.7	0.8
	VI	0.25	0.35	0.1	0.3	0.28	0.05	0.08
	I	0.300	0.175	0.105	0.063	0.036	0.016	0.003

A(*t*)	II	0.100	0.090	0.081	0.073	0.066	0.059	0.053
	III	0.200	0.240	0.224	0.168	0.101	0.047	0.016
	VI	0.250	0.263	0.049	0.132	0.086	0.011	0.017
	I	0.300	0.475	0.580	0.643	0.679	0.695	0.698
S(*t*)	II	0.100	0.190	0.271	0.344	0.410	0.469	0.522
	III	0.200	0.440	0.664	0.832	0.933	0.980	0.996
	VI	0.250	0.513	0.561	0.693	0.779	0.790	0.807

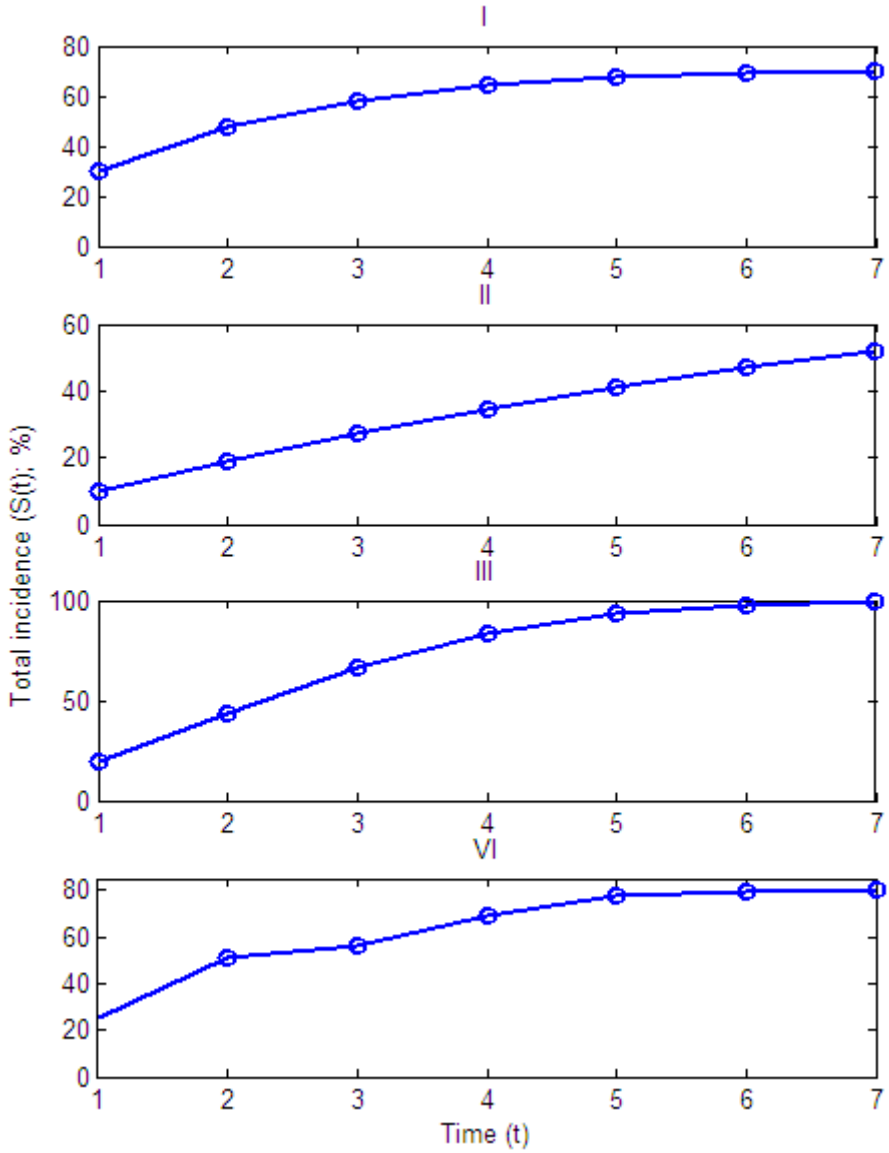

Fig. 1 The calculated total incidence dynamics (*S*(*t*)) based on Table 1.

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