Physica A xx (xxxx) xxx–xxx

Contents lists available at ScienceDirect

Physica A

journal homepage: www.elsevier.com/locate/physa

Dynamics of an epidemic model with spatial diffusion

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HIGHLIGHTS

- We obtained a spatial epidemic model with logistic growth.
- Using multiple-scale analysis, we present amplitude equations.
- There are different types of stationary patterns.
- Reaction diffusion epidemic systems have rich dynamics.

ARTICLE INFO

Article history:
Received 7 March 2014
Received in revised form 11 April 2014
Available online xxxx

Keywords:
Epidemic model
Spatial diffusion
Amplitudes equation
Pattern selection

ABSTRACT

Mathematical models are very useful in analyzing the spread and control of infectious diseases which can be used to predict the developing tendency of the infectious disease, determine the key factors and to seek the optimum strategies of disease control. As a result, we investigated the pattern dynamics of a spatial epidemic model with logistic growth. By using amplitude equation, we found that there were different types of stationary patterns including spotted, mixed, and stripe patterns, which mean that spatial motion of individuals can form high density of diseases. The obtained results can be extended in other related fields, such as vegetation patterns in ecosystems.

1. Introduction

With the development of human civilization, infectious diseases have been effectively controlled. However, in some areas, especially in developing countries these infectious cases often appear. We take SARS (Severe Acute Respiratory Syndrome) as an example. From November in 2002 to May in 2003, the firstly familial aggregation case occurred in China and then the SARS showed the tendency of a rapid spread. SARS cases were found in more than 30 countries and regions around the world which threaten globally human health [1]. In February 2013, a new type of avian influenza, H7N9, appeared in Mainland China which caused more than 100 people to be infected [2]. As a result, it is also necessary to investigate the mechanisms of disease spreading.

Mathematical models have been important methods in disease control which can be used to determine the spread and seek the best strategies to prevent and control its spread. The transmission or other interactions formation of many important epidemiological phenomenon are largely affected by space interaction [3,4] and thus many studies have proposed spatial epidemic models. In these studies, the reaction–diffusion equations have been used which belong to temporal and spatial forms. The reaction term is the process of individuals changes or the interaction among species in the absence of diffusion, and the diffusion term describes the spatial movement of individuals [5,6].

Pattern structures are non-uniform macro-structures having a regularity in space or time which widely exist in the real life. Viewed from the perspective of thermodynamics, it can be divided into two categories. The first category is presented under thermodynamic equilibrium conditions, such as the crystal structure in inorganic chemistry, and self-organized pattern

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http://dx.doi.org/10.1016/j.physa.2014.04.028
0378-4371/

Q3 formation in organic polymers. The second category is not in thermodynamic equilibrium conditions. For the first one, its mechanism is more systematic and well understood. Such pattern formation can be explained by the equilibrium thermodynamics and statistical physics [7,8].

In this article, we will use the standard multi-scale analysis to study pattern selection of a spatial epidemic model, where the parameter controlled method is used to study a small parameter ε and the Fredholm solvability condition. In the vicinity of the bifurcation point (such as the Turing and Hopf bifurcations) the critical amplitude A_j ($j = 1, 2, 3$) follows the general form, and its standard form can be derived by standard technically analysis and symmetry breaking theory [9–11]. Normal forms of the critical amplitude can be well applied to the study of pattern formation and the subtle changes of the pattern formation are derived through appropriately spatial symmetry terms [12].

2. A spatial epidemic model

To begin this section, we firstly give some assumptions, which are as follows.

(i) The population, in which a pathogenic agent is active, comprises two subgroups: the healthy individuals who are susceptible (S) to infection and the already infected individuals (I) who can transmit the disease to the healthy ones.
(ii) Infected populations do not migrate and the disease-related death rate from the infected is d.
(iii) All the parameters are constant which means they do not depend on the space and time.

Denote $S + I = N$ and the model is as follows:

$$\frac{dS}{dt} = rN\left(1 - \frac{N}{K}\right) - \beta\frac{SI}{N} - (\mu + m)S, \tag{1a}$$

$$\frac{dI}{dt} = \beta\frac{SI}{N} - (\mu + d)I, \tag{1b}$$

where r is the intrinsic growth rate, K is the carrying capacity, β denotes the contact transmission rate, μ is the natural mortality, d denotes the disease-induced mortality, m is the per-capita emigration rate of the susceptible. Here, $dN/dt =$ Q4 $rN(1 - N/K)$ means population N satisfies logistic growth. More details about this model can be found in Ref. [13].

Define the basic reproductive number R_0:

$$R_0 = \frac{\beta}{\mu + d}. \tag{2}$$

In the fields of mathematical biology, when $R_0 > 1$, the infectious disease will spread; when $R_0 < 1$, the infectious diseases will disappear. Therefore, R_0 is a quantity which determines whether an infectious disease will outbreak.

Define the basic demographic reproductive number R_d:

$$R_d = \frac{r}{\mu + m}. \tag{3}$$

$R_d \geq 1$ the population grows and $R_d \leq 1$ implies that the population does not survive.

Let $S \to \frac{S}{K}$, $I \to \frac{I}{K}$, $t \to \frac{t}{\mu+d}$ and we have:

$$\begin{aligned} \frac{\partial S}{\partial t} &= vR_d(S + I)(1 - (S + I)) - R_0\frac{SI}{S + I} - vS + d_1\nabla^2 S, \\ \frac{\partial I}{\partial t} &= R_0\frac{SI}{S + I} - I + d_2\nabla^2 I, \end{aligned} \tag{4}$$

where $v = \frac{\mu+m}{\mu+d}$.

Supposing that the susceptible and the infectious individuals move randomly in space, we use a simply spatial model Q5 describing the model (4). Let $dt \to (S + I)dt$ and the simplified reaction–diffusion equation is as follows:

$$\begin{aligned} \frac{\partial S}{\partial t} &= vR_d(S + I)^2[1 - (S + I)] - R_0 SI + d_1\nabla^2 S, \\ \frac{\partial I}{\partial t} &= R_0 SI - I(S + I) + d_2\nabla^2 I. \end{aligned} \tag{5}$$

In the two dimension space consisting of x and y, $\nabla^2 = \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2}$ denotes the Laplace operator in two-dimension space, d_1 and d_2 are the diffusion coefficients of S and I, respectively. In this paper, all the parameters are positive.

The initial condition of system (5) is

$$S(r, 0) = S_0(r) \geq 0, \qquad I(r, 0) = I_0(r) \geq 0, \qquad r = (x, y) \in \Omega = [0, L] \times [0, L].$$

The boundary condition is

$$\frac{\partial S}{\partial n} = \frac{\partial I}{\partial n} = 0,$$

where n is space vector, $(x, y) \in \partial\Omega$ and Ω is the space domain.