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# DYNAMICAL COMPLEXITY OF A SPATIAL PREDATOR-PREY SYSTEM

BO-LI XIE[1,*], ZHI-JUN WANG[2], YA-KUI XUE[1]

[1]Department of Mathematics, North University of China, Taiyuan, Shan'xi, 030051, China

[2]School of Mechatronic Engineering, North University of China, Taiyuan, Shan'xi, 030051, China



**Abstract.** In this paper, we analyze the dynamical complexity of a spatial predator-prey system. We get the critical line of Hopf and Turing bifurcation in a spatial domain. Based on the mathematical analysis, we obtain the condition of the emergence of spatial patterns through diffusion instability, i.e., Turing pattern. The obtain results show that this system has rich dynamics, these patterns shows that it is useful the reaction-diffusion model to reveal the spatial dynamics in the real model.

**Keywords**: predator-prey; pattern formation; diffusion; spatial predator-prey system.

**2010 AMS Subject Classification:** 92D25.

## 1. Introduction

Ecological systems are characterized by the interaction between different species and their natural environment. One of the important types of interaction, which effects population dynamics of all species is predation. Thus predator-prey models have been in the focus of ecological science since the early days of this discipline [1]. In the past, investigations have revealed that spatial inhomogeneities like the inhomogeneous distribution of nutrients as well as interactions on spatial scales, which are essentially based on the assumption that the motion of individuals

* Corresponding author

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of given population is random and isotropic, i.e., without any preferred direction, can have an important impact on the dynamics of ecological populations [2, 3, 4, 5]

There has been a large group of papers on stationary spatial pattern in predator-prey system. These arise via diffusion driven instability and rely on significant differences between predator and prey diffusion coefficients [6, 7, 8]. In addition to that, the effect of equal diffusion coefficients of spatial models had also been well investigated [9, 10, 11, 12, 13, 14, 15, 16, 17, 18]. However, to the best of our knowledge, there is little work on the dynamical behavior of both migration and diffusion in the predator-prey model. As a result,in the present paper, we are aim to study the dynamical complexity of a spatial predator-prey system. More specifically, the present paper is main to investigate the spatial patterns.

The paper is organized as follows. In Section 2, we obtain a spatial predator-prey model, and interpret the biological meaning of these parameters of the model. In Section 3, we analyze the spatial model. With respect to these parameters, we derive the mathematical expression for the Hopf bifurcation and Turing bifurcation critical line. Based on these conditions performing a series of simulations. In Section 4, by performing a series of simulations, we illustrate the emergence of Turing patterns. Finally, some conclusions are given.

## 2. Analysis for the model

Since the traditional predator-prey model with Michaelis-Menten-type functional response received great attention among theoretical and mathematical biologists [19, 20], we will focus our attention here on the following model:

$$\begin{aligned} \frac{dU}{d\tau} &= RU(1-\frac{U}{K}) - \frac{AUV}{V+AHU}, \\ \frac{dV}{d\tau} &= \frac{AUV}{V+AHU} - DV. \end{aligned} \tag{1}$$

where $U$ and $V$ stand for prey and predator density, respectively. All parameters are positive constants, and $R$ stands for maximal growth rate of the prey, $K$ for carrying capacity, $A$ for capture rate, $H$ for handling time, $B$ for conversion efficiency, and $D$ for predator death rate.

Following Wang [21], with the next scaling

$$u = \frac{AHU}{BK}, \quad v = \frac{AHU}{B^2K}, \quad r = \frac{RH}{B},$$

$$d = \frac{HD}{B}, \quad s = \frac{AH}{B}, \quad t = \frac{B\tau}{H},$$

we arrive at the following equations containing dimensionless quantities:

$$\begin{aligned} \frac{du}{dt} &= ru(1-\frac{u}{s}) - \frac{suv}{v+su}, \\ \frac{dv}{dt} &= \frac{suv}{v+su} - dv. \end{aligned} \tag{2}$$

When combined with spatial factor, diffusion and migration terms, the original spatially extended model is written as the following system

$$\begin{aligned} \frac{\partial u}{\partial t} &= ru(1-\frac{u}{s}) - \frac{suv}{v+su} + D_1\nabla^2 u, \\ \frac{\partial v}{\partial t} &= \frac{suv}{v+su} - dv + D_2\nabla^2 v. \end{aligned} \tag{3}$$

where $\nabla^2 = \frac{\partial^2}{\partial x^2}$ or $\nabla^2 = \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2}$ is the usual Laplacian operator in the one or two-dimensional space. The diffusion coefficients are denoted by by $D_1$ and $D_2$, respectively. Here, $\nabla = \frac{\partial}{\partial x}$ or $\nabla = \frac{\partial}{\partial y}$ and $c_1$ and $c_2$ are the migration coefficients.

The model $(0.3)$ needs to be analyzed with the inatial populations

$$u(0) > 0, \quad v(0) > 0.$$

We also assume that no external input is imposed from outside. Hence, the boundary conditions are taken as

$$\left.\frac{\partial u}{\partial n}\right|_{(x,y)} = \left.\frac{\partial u}{\partial n}\right|_{(x,y)} = 0, \tag{4}$$

where $(x,y) \in \partial\Omega$ and $\Omega$ is the spatial domain.

We firstly find the steady state as follows:

(i) $E_0 = (u,0)$, which is corresponding to extinction of the predator;

(ii) interior equilibrium point $E^*(u^*, v^*)$, which is corresponding to coexistence of prey and predator and

$$u^* = \frac{s[r+(d-1)s]}{r},$$
$$v^* = \frac{s(1-d)u^*}{d}.$$

The condition to ensure the coexistence of steady state is feasible for $1-\frac{r}{s} < d < 1$. From the biological point of view, we are interested to study the stability behavior of the interior equilibrium point $E^*$. The jacobian corresponding to this equilibrium point is that

$$\mathbf{J} = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix}$$

We obtain that the eigenvalue is the root of the following equation:

$$\lambda^2 + \alpha(k^2)\lambda + \beta(k^2) = 0, \tag{5}$$

where

$$\begin{aligned} \alpha(k^2) &= (D_1+D_2)k^2 - (a_{11}+a_{22}), \\ \beta(k^2) &= a_{11}a_{22} - a_{12}a_{21} - (a_{11}D_2 - a_{22}D_1)k + D_1D_2k^4. \end{aligned} \tag{6}$$

Therefore, the solution of $(0.5)$ for $k > 0$ reduces to

$$\lambda(k^2) = \frac{-\alpha(k^2) \pm \sqrt{(\alpha(k^2)^2) - 4\beta(k^2)}}{2}. \tag{7}$$

In the following, we will give the expressions of the two bifurcation critical line.

The onset of Hopf instability corresponds to the case, when a pair of imaginary eigenvalues cross the real axis from the negative to the positive side. And this situation occurs only when the diffusion vanishes.Mathematically speaking, the Hopf bifurcation occurs when

$$Im(\lambda k) \neq 0, \quad Re(\lambda k) = 0 \quad \text{at} \quad k = 0. \tag{8}$$

Then we can get the critical value of the transition, Hopf bifurcation parameter-$s$, equal to

$$s_H = \frac{-r-d+d^2}{-1+d^2}. \tag{9}$$

Mathematically speaking, the Turing bifurcation occurs when

$$Im(\lambda k) = 0, \quad Re(\lambda k) \neq 0 \quad \text{at} \quad k = k_T \neq 0. \tag{10}$$

and the wave number

$$k_T^2 = \sqrt{\frac{a_{11}a_{22} - a_{12}a_{21}}{D_1 D_2}}. \tag{11}$$

We can obtain the critical value of bifurcation parameter $s$ equals

$$s_T = \frac{d(d^2-1)D_1 - r(d+1)D_2 + 2d(-dD_1 + D_1 + \sqrt{P})}{(d-1)(d+1)^2 D_2}, \tag{12}$$

where

$$P = 2d^2D_1^2 - dD_1^2 - d^3D_1^2 - rd^2D_1D_2 + rD_1D_2.$$

Now, let us discuss the bifurcations represented by these formulas in the parameter space spanned by the parameters $s$ and $d$ which can be seen from Figure 1.

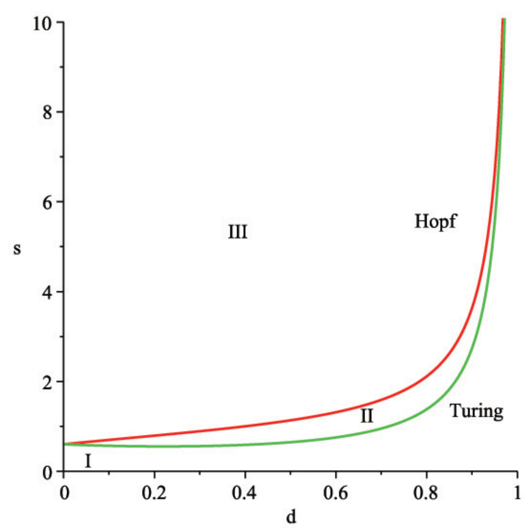


FIGURE 1. (Color online) Bifurcation diagram for the system (2.3). We set the parameter values are $r = 0.6, D_1 = 0.1, D_2 = 1.6$.

The lower part of the displayed parameter space (where is marked by I) corresponds to systems with homogeneous equilibria, which is unconditionally stable. If this region is left via a bifurcation (Hopf or Turing), the qualitative behavior of such equilibria changes. Domain II is pure Turing instabilities, which can be destabilized by a homogeneous perturbation. In domain III, both Hopf and Turing instabilities can be found.

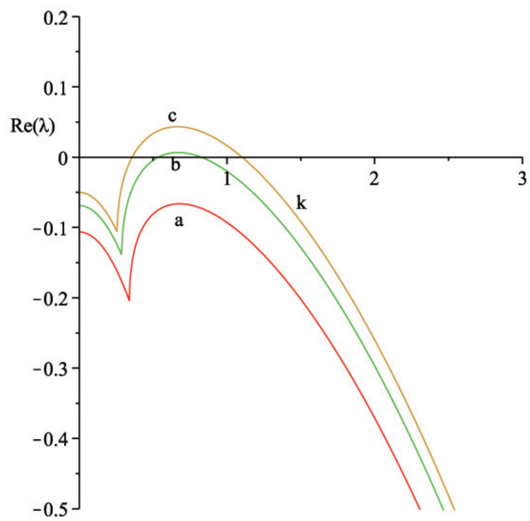


FIGURE 2. (Color online) Bifurcation diagram for the system (2.3). We set the parameter values are $r = 0.6, d = 0.5, D_1 = 0.1, D_2 = 1.6$. And the value of s are that $(a) : s = 0.85; (b) : s = 0.95; (c) : s = 1.0$.

In order to see the effects of the cross-diffusion, we plot the dispersion relation corresponding to several values of one parameter while keeping the others fixed in Figure 2. Here, we set $r = 0.6, d = 0.5, D_1 = 0.1, D_2 = 1.6$. It can be seen from Figure 2 that when $s$ is increased, Turing modes $Re(\lambda > 0)$ can be available.

## 3. Pattern Structures

In practice, the continuous problem defined by the reaction-diffusion system in two-dimensional space is solved in a discrete domain with $M \times N$ latticesites. The spacing between the lattice points is defined by the lattice constant $\triangle h$. For $\triangle h \longrightarrow 0$ the differences approach the derivatives. The time evolution is also discrete, i.e., the time goes in step of $\triangle t$. In the present paper, we set $\triangle h = 1$, $\triangle t = 0.05$, and $M = N = 200$. Note that when $\triangle h$, $\triangle t$ are further decreased, the dynamics does not change any more.

Figure 3 shows the evolution of the spatial patterns of infected population with small random perturbation of the stationary solution $u^*$ and $v^*$. And the values of the parameters are that $r = 0.6, d = 0.5, D_1 = 0.1, D_2 = 1.6$, and $s = 0.95$. After irregular transient pattern, we can see that the regular spotted patterns with the same radius prevail over the whole domain finally, and the dynamics of the system does not undergo any further changes.

Figure 4, the values of the parameters are that $r = 0.6, d = 0.5, D_1 = 0.1, D_2 = 1.6$, and $s = 1.0$. We can see that the regular stripe patterns prevail over the whole domain at last, and the dynamics of the system does not undergo any further changes.

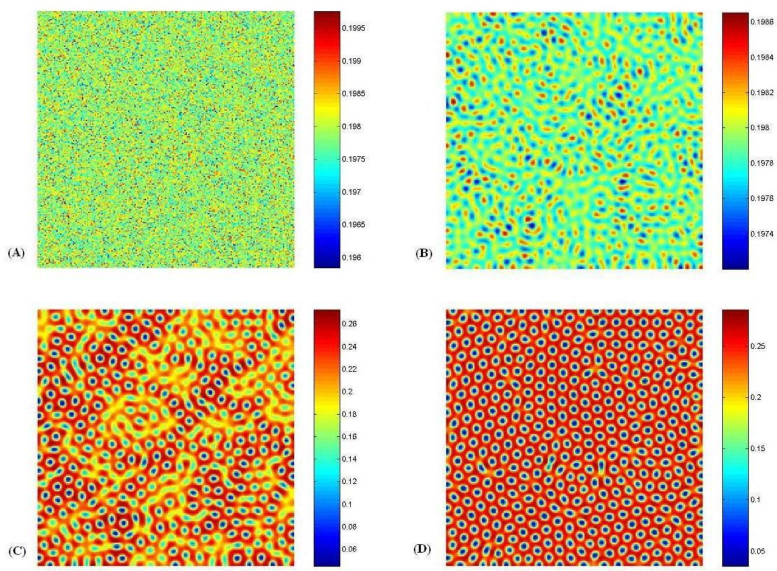


FIGURE 3. (Color online) Snapshots of the time evolution of the prey at different instants with $r = 0.6, d = 0.5, D_1 = 0.1, D_2 = 1.6$ and $s = 0.95$, which are in the Turing space. (**A**): 0 iteration; (**B**): 3000 iteration; (**C**): 20000 iteration; (**D**): 150000 iteration.

## 4. Discussions

Epidemic mathematical models have become important tools to study the transmission dynamics of infectious diseases in host populations. There have been lots of works on the stability of endemic equilibrium for some epidemic models. In this paper, by combining qualitative and bifurcation analysis we have studied the global behavior of an epidemic model with constant

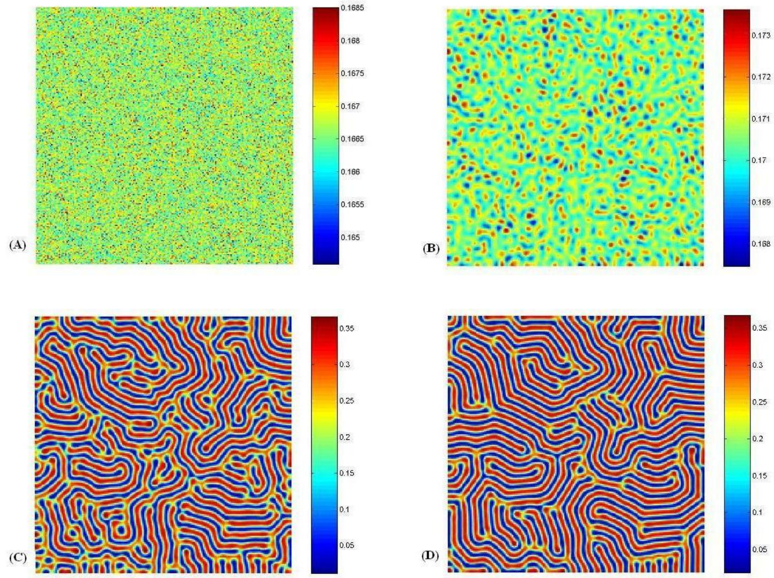


FIGURE 4. (Color online) Snapshots of the time evolution of the prey at different instants with $r = 0.6, d = 0.5, D_1 = 0.1, D_2 = 1.6$ and $s = 1.0$, which are in the Turing space. (**A**): 0 iteration; (**B**): 3000 iteration; (**C**): 20000 iteration; (**D**): 150000 iteration.

immigrant and nonlinear incident rate. From the analysis, we have found that there exist some values of the model such that the model can undergo a series of bifurcations, such as Hopf bifurcation and Turing bifurcation. Furthermore, our analysis and numerical simulations reveal that typical spatial dynamics involves the formation of isolated groups, i.e. spotted or striped groups.

Although more work is needed, in principle, it seems that diffusion is able to generate many different kinds of spatiotemporal patterns. For such reasons, we can predict that diffusion can be considered as an important mechanism for the appearance of complex spatiotemporal dynamics in ecology models.

**Conflict of Interests**

The authors declare that there is no conflict of interests.

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