Spatial Pattern of an Epidemic Model with Cross-diffusion *

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Pattern formation of a spatial epidemic model with both self- and cross-diffusion is investigated. From the Turing theory, it is well known that Turing pattern formation cannot occur for the equal self-diffusion coefficients. However, combined with cross-diffusion, the system will show emergence of isolated groups, i.e., stripe-like or spotted or coexistence of both, which we show by both mathematical analysis and numerical simulations. Our study shows that the interaction of self- and cross-diffusion can be considered as an important mechanism for the appearance of complex spatiotemporal dynamics in epidemic models.

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Applications of mathematical modelling to the spread of epidemics have a long history and were initiated by Daniel Bernoulli^[1] on the spread of smallpox in 1760.^[2] Most studies concentrate on the local temporal development of diseases and epidemics. Their geographical spread is less well understood, although important progress has been achieved in a number of case studies.^[3-5] The key problem, as well as difficulty, is how to include spatial effects and quantify the dispersal of individuals.^[2] This problem has been studied with some effort in various ecological systems, for instance, in plant dispersal by seeds.

In addition, many important epidemiological and ecological phenomena are strongly influenced by spatial heterogeneities because of the localized nature of transmission or other forms of interaction.^[6,7] Predicting the dynamics of these populations requires detailed estimates of spatial parameters and the mechanisms involved.^[8–11] Thus, spatial epidemic models are more suitable for describing the process of epidemiology.

However, in nature, the tendency of the susceptible would be to keep away from the infected for the reason that the susceptible individuals have ability to recognize the infected group and avoid them moving away from them, which has been generally overlooked despite their potential ecological reality and intrinsic theoretical interest. In general, the escape velocity of the susceptible may be taken as proportional to the dispersive velocity of the infected. This phenomenon is called the cross-diffusion. The value of the crossdiffusion coefficient may be positive, negative or zero. The term of positive cross-diffusion coefficient denotes the movement of the susceptible in the direction of lower concentration of the infected and negative crossdiffusion coefficient denotes that the susceptible tends to diffuse in the direction of higher concentration of the infected.

It is natural to ask how the cross-diffusion has influence on the distribution of the infected in both space and time. To well know this effect, we investigate the pattern formation of an epidemic model with both self- and cross-diffusion.

We focus our attention on the following model:

$$\frac{\partial S}{\partial t} = A - dS - \beta S^p I^q + D_1 \nabla^2 S + D \nabla^2 I,$$
(1a)

$$\frac{\partial I}{\partial t} = \beta S^p I^q - (d+\mu)I + D_2 \nabla^2 I, \qquad (1b)$$

where A is the recruitment rate of the population, d is the natural death rate of the population, β is the force of infection or the rate of transmission, and μ is the disease-related death rate from the infected. The nonlinear incidence rate $\beta S^{p}I^{q}$ is given by Liu *et al.*^[12,13] due to saturation or multiple exposures before infection. In this Letter, we set p = 1 and q = 2. Here, $\nabla^{2} = \frac{\partial^{2}}{\partial x^{2}} + \frac{\partial^{2}}{\partial y^{2}}$ is the usual Laplacian operator in two-dimensional space and D_{1} , D_{2} are, respectively, the susceptible and infected individuals diffusion coefficients. D is called the cross-diffusion coefficient. From the biological point of view, we assume all the parameters are positive throughout this study.

The model (1) needs to be analysed with the initial populations

$$S(0) > 0, \quad I(0) > 0.$$

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

$$\frac{\partial S}{\partial n}\Big|_{(x,y)} = \frac{\partial I}{\partial n}\Big|_{(x,y)} = 0, \qquad (2)$$

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

In this Letter, we set that D > 0, which means that the susceptible tends to diffuse in the direction

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of lower concentration of the infected. Such situations are common in nature in the process of the spread in the epidemic.

Simple calculations show that the system (1) has three equilibrium points:

(i) $E_1 = (A/d, 0)$, which corresponds to extinction of the epidemic.

(ii)
$$E_2 = \left(\frac{A\beta + \sqrt{A^2\beta^2 - 4d^3\beta - 8d^2\beta\mu - 4d\beta\mu^2}}{2d\beta}\right),$$
 which is

 $A\beta + \sqrt{A^2\beta^2 - 4d^3\beta - 8d^2\beta\mu - 4d\beta\mu^2}$, corresponding to the coexistence of the S and I.

(iii)
$$E^* = \left(\frac{A\beta - \sqrt{A^2\beta^2 - 4d^3\beta - 8d^2\beta\mu - 4d\beta\mu^2}}{2d\beta}, \frac{2d(d+\mu)}{A\beta - \sqrt{A^2\beta^2 - 4d^3\beta - 8d^2\beta\mu - 4d\beta\mu^2}}\right), \text{ which corresponds to the coexistence of the S and I.}$$

By direct calculations, we know that E_2 is unstable, which is a saddle. Thus, we are interested in studying the stability behaviour of the interior equilibrium point E^* . The Jacobian corresponding to this equilibrium point is that

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

Following the standard linear analysis of the reactiondiffusion equation,^[14] we consider a perturbation near the steady state,

$$S(\boldsymbol{r},t) = S^* + a(\boldsymbol{r},t), \qquad (3a)$$

$$I(\boldsymbol{r},t) = I^* + b(\boldsymbol{r},t), \qquad (3b)$$

and we assume that

$$a(\mathbf{r}, t) = \alpha \exp(\lambda t) \exp(i\mathbf{k} \cdot \mathbf{r}), \qquad (4a)$$

$$b(\boldsymbol{r},t) = \gamma \exp(\lambda t) \exp(i\boldsymbol{k} \cdot \boldsymbol{r}). \tag{4b}$$

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

$$\lambda^2 + \alpha_k \lambda + \gamma_k = 0, \tag{5}$$

where

$$\alpha_k = (D_1 + D_2)k^2 - (a_{11} + a_{22}),$$
(6a)
$$\gamma_k = D_1 D_2 k^4 - (D_2 a_{11} + D_1 a_{22} - D a_{21})k^2$$

$$+ a_{11}a_{22} - a_{12}a_{21}. (6b)$$

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. This situation occurs only when the diffusion vanishes.^[14,15] Mathematically speaking, the Hopf bifurcation occurs when

$$\operatorname{Im}(\lambda_k) \neq 0, \quad \operatorname{Re}(\lambda_k) = 0, \quad \text{at} \quad k = 0, \quad (7)$$

where λ_k is the root of Eq. (5). Then we can obtain the critical value of the transition, the Hopf bifurcation parameter, i.e. β , equal to

$$\beta_H = \frac{1}{\mu A^2} (d^4 + 4d^3\mu + 6d^2\mu^2 + 4d\mu^3 + \mu^4).$$
 (8)

The system (1) will be unstable if at least one of the roots of Eq. (5) is positive. By straightforward analysis we find that γ_k is a quadratic polynomial with respect to k^2 . Its extremum is a minimum at some k^2 .^[16,17] From Eq. (6b), elementary differentiation with respect to k^2 shows

$$k_{\min}^2 = \frac{a_{11}D_2 + a_{22}D_1 - Da_{21}}{2D_1D_2}.$$
 (9)

By substituting $k = k_{\min}$ into Eq. (6b), we have

$$\gamma_{k_{\min}} = D_1 D_2 k_{\min}^4 - (D_2 a_{11} + D_1 a_{22} - D a_{21}) k_{\min}^2 + a_{11} a_{22} - a_{12} a_{21}.$$
(10)

By setting $\gamma_{k_{\min}} = 0$, we can obtain the critical value of Turing bifurcation parameter β_T , equal to

$$\begin{split} \beta_T &= A^2 \left[2(-12d^6D_2^2D_1^4D^2 - 20d^6D_2^4D_1^3D + 32d^6D_2^3D_1^2D^3 - 16d^6D_2^3D_1^4D + 10d^6D_2^2D_1^2D^4 \\ &\quad - d^6D_2D_1^5D^2 + 30d^4D_1^6\mu^2D_2^2 + 30d^5D_1^5\mu D_2^3 - 24d^5D_2^5D_1^3\mu - 8d^6D_2^5D_1D^2 - 20d^6D_2^4D_1D^3 \\ &\quad - 8d^6D_2^5D_1^3 + 6d^6D_2^3D_1^5 + 2D_1^6D_2^2\mu^6 + 2d^6D_1^6D_2^2 + 10d^4D_2^2D_1^5D\mu^2 + 10d^3D_2^2D_1^5D\mu^3 \\ &\quad - 10d^3D_2D_1^5D^2\mu^3 + 20d^3D_1^6\mu^3D_2D + 15d^2D_1^6\mu^4D_2D + 5d^5D_2^2D_1^5D\mu - 5d^5D_2D_1^5D^2\mu \\ &\quad + 6d^5D_2D_1^3D^4\mu - 60d^5D_2^4D_1^3D\mu - 8d^5D_2D_1^4D^3\mu - 12d^5D_2^3D_1^3D^2\mu + 18d^5D_2^2D_1^3D^3\mu \\ &\quad + 15d^4D_1^6\mu^2D_2D - 12d^4D_1^4\mu^2D_2D^3 - 10d^4D_1^5\mu^2D_2D^2 + 6d^5D_1^6\mu D_2D - 96d^4D_1^4\mu^2D_2^3D \\ &\quad - 72d^4D_1^4\mu^2D_2^2D^2 - 64d^5D_1^4\mu DD_2^3 + 32d^4D^3\mu^2D_1^2D_2^3 + 64d^5D^3\mu D_1^2D_2^3 - 7d^5D^5\mu D_1D_2^2 \\ &\quad - d^5D^6\mu D_1D_2 + 10d^4D^4\mu^2D_1^2D_2^2 + d^4D^5\mu^2D_1^2D_2 - 12d^4D_2^3D_1^3\mu^2D^2 - 8d^5D_2^5D_1\mu D^2 \\ &\quad - 20d^5D_2^4D_1\mu D^3 + 16d^4D_2^5D_1^2\mu^2D + 40d^4D_2^4D_1^2\mu^2D^2 + 20d^5D_2^5D_1^2\mu D + 80d^5D_2^4D_1^2D^2 \mu \\ &\quad + 40d^6D^2D_2^4D_1^2 + 6d^6D^3D_2^2D_1^3 + d^6D_2^2D_1^5D + 2d^6D^4D_2D_1^3 - 2d^6D_2D_1^4D^3 - 4d^6D_2^3D_1^3D^2 \end{split}$$

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$$\begin{split} &+ 60d^4D_1^5\mu^2D_2^3 + 60d^3D_1^5\mu^3D_2^3 + 40d^3D_1^6\mu^3D_2^2 + 30d^2D_1^6\mu^4D_2^2 + 12d^5D_1^6\mu D_2^2 - 24d^4D_2^5D_1^3\mu^2 \\ &- 8d^3D_2^5D_1^3\mu^3 + 16d^6D_2^5D_1^2D - 7d^6D^5D_2^2D_1 - 18d^6D^4D_2^3D_1 + d^6D^5D_2D_1^2 - d^6D^6D_2D_1 \\ &- 18d^5D^4D_2^3\mu D_1 + 5d^2D_2^2D_1^5\mu^4D - dD_1^5\mu^5D^2D_2 + 6d^3D^3\mu^3D_1^3D_2^2 + 2d^3D^4\mu^3D_1^3D_2 \\ &- 8d^3D^3\mu^3D_1^4D_2 - 2d^2D^3\mu^4D_1^4D_2 - 4d^3D_2^3D_1^3\mu^3D^2 - 60d^4D_2^4D_1^3\mu^2D - 20d^3D_2^4D_1^3\mu^3D \\ &- 64d^3D_2^3D_1^4\mu^3D - 16d^2D_2^3D_1^4\mu^4D + d^6D_1^6DD_2 - 48d^3D_1^4D^2\mu^3D_2^2 - 5d^2D_1^5D^2\mu^4D_2 \\ &+ 30d^2D_2^3D_1^5\mu^4 + 6dD_2^3D_1^5\mu^5 + 12dD_1^6\mu^5D_2^2 + D_1^6D_2\mu^6D - 12d^2D_2^2D_1^4\mu^4D^2 + dD_2^2D_1^5\mu^5D \\ &+ 6dD_1^6\mu^5D_2D)^{(1/2)} + 5d^3D_2D_1^2D + 9d^2D_1^3\mu D_2 + 3d^2D_1^3\mu D + d^2D^3\mu D_1 + 8d^2D_2^3D_1\mu \\ &+ 4d^2D_1^2D^2\mu + 8d^3D_2^3D_1 - d^3D^2D_2^2 + 7d^3D_2^2D_1^2 - d^3D^3D_2 + d^3D_1^3D + 14d^2D_2^2D_1\mu D \\ &+ 9d^2D^2\mu D_2D_1 + 14d^2D_2^2D_1^2\mu + 2dD_1^2\mu^2D^2 + 7dD_2^2D_1^2\mu^2 + 10d^2D_2D_1^2D\mu + 5dD_1^2D\mu^2D_2 \\ &+ 9dD_1^3\mu^2D_2 + 3dD_1^3\mu^2D + 3D_1^3D_2\mu^3 + D_1^3\mu^3D + 3d^3D_1^3D_2 + 2d^3D_1^2D^2 + d^3D_1D^3 \\ &+ 14d^3D_1DD_2^2 + 9d^3D_2D_1D^2\Big] / \Big[(d^2D_1^2D^2 + 2dD_2^2D_12\mu + 4dD_2D_1^2\mu D + 2dD_2^3D_1\mu \\ &+ 2dD_1^2D^2\mu + d^2D^2D_2^2 + d^2D_1^2D_2^2 + 2d^2D_1^2D_2 + 4dD_2D_1\mu D + 2dD_2^3D_1\mu \\ &+ 2dD_1D^2\mu + d^2D^2D_2^2 + d^2D_1^2D_2^2 + 2d^2D_1^2D_2 + 2d^2D_1D^2 + d^2D_2^2D_1\mu D + 2dD_2^3D_1\mu \\ &+ 2dD_1D^2\mu + d^2D^2D_2^2 + d^2D_1^2D_2^2 + 2d^2D_1^2D_2 + 2d^2D_1D^2 + d^2D_2^2D_1\mu D + 2dD_2^3D_1\mu \\ &+ 2dD_1D^2\mu + d^2D^2D_2^2 + d^2D_1^2D_2^2 + 2d^2D_1^2D_2 + 2d^2D_1D^2 + d^2D_2^2D_1\mu + 2dD_2^3D_1\mu \\ &+ 2dD_1D^2\mu + d^2D^2D_2^2 + d^2D_1^2D_2^2 + 2d^2D_1^2D_2 + 2d^2D_1D^2 + d^2D_2^2 + d^2D_2^4 + d^2D_2^2D_1 + 2d^2D_1D^2 + d^2D_2^2 + d^2D_2^4 + d^2D_2^2D_1 + 2d^2D_1D^2 + d^2D_2^2 + d^2D_2^4 + d^2D_2^2 + d^2D_2^4 + d^2D_2^2 + d^2D_2^2$$

At the critical point, we have $\gamma_k = 0$ when $k = k_c$.^[16] For fixed kinetics parameters, this defines a critical cross-diffusion coefficient D_c as the appropriate root of

$$(a_{11}D_2 + a_{22}D_1 - Da_{21})^2 - 4D_1D_2(a_{11}a_{22} - a_{12}a_{21}) = 0.$$
(11)

Then critical wavenumber k_c is then given by

$$k_c^2 = \frac{a_{11}D_2 + a_{22}D_1 - D_c a_{21}}{2D_1D_2} = \sqrt{\frac{a_{11}a_{22} - a_{12}a_{21}}{D_1D_2}}.$$
(12)

Note that the critical wavenumber of the crossdiffusion system is the same as the non-cross-diffusion system. That is to say, cross-diffusion has no effect on the critical wavenumber but has effect on the roots of Eq. (5).



Fig. 1. Bifurcation diagram for system (1). We set the parameter values A = 1, d = 1, $\mu = 1.8$ and $D_1 = D_2 = 1$.

Now, let us discuss the bifurcations represented by these formulas in the parameter space spanned by the parameters β and D which can be seen from Fig. 1. The whole class of spatial model is included in this parameter space. The upper part of the displayed parameter space (where is marked by IV) corresponds to systems with homogeneous equilibria, which is unconditionally stable. If this region is left via a bifurcation (Turing or Hopf), the qualitative behaviour of such equilibria changes. If an equilibrium is represented by a point in the part of the parameter space, where is marked by III, it can be destabilized by a homogeneous oscillations. In domain II, both Hopf and Turing instability occur. The equilibria that can be found in the area, where is marked by I, are stable with respect to homogeneous perturbations but loose their stability with respect to perturbations of specific wave numbers k. In this region, stationary inhomogeneous patterns can be observed.

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 Fig. 2. Here, we set A = 1, d = 1, $\mu = 1.8$, $\beta = 35$ and $D_1 = D_2 = 1$. It can be seen from Fig. 2 that when D is increased, Turing modes [Re(λ) > 0] can be available.



Fig. 2. Dispersion relation of system (1). (a) D = 1 and (b) D = 0.5.

The dynamics behaviour of the spatial model can not be studied by using analytical methods or normal forms. Thus we have to perform numerical simulations by computer. To solve differential equations by computers, one has to discretize the space and time of the problem. In practice the continuous problem defined by the reaction-diffusion system in 2D is solved in a discrete domain with $M \times N$ lattice sites. The spacing between the lattice points is defined by the lattice constant Δh . In the discrete system the Laplacian describing diffusion is calculated using finite differences, i.e., the derivatives are approximated by differences over Δh . The time evolution is also discrete, i.e., the time goes in steps of Δt . The time evolution can be solved by using the Euler method. In the present study, we set $\Delta h = 1$, $\Delta t = 0.01$ and M = N = 200. It is checked that a further decrease of the step values does not lead to any significant modification of the results.



Fig. 3. Snapshots of contour pictures of the infected at 100000 iterations with (a) D = 1, (b) D = 1.3, (c) D = 1.5.

We keep A = 1, d = 1, $\mu = 1.8$, $\beta = 35$, $D_1 = D_2 = 1$ and vary parameter D for simulations. Figure 3 shows the evolution of the spatial pattern of infected population with small random perturbation of the stationary solution S^* and I^* of the spatially homogeneous systems when the parameter values are in the domain of Turing space. As D increases, stripe only, coexistence of stripe and spotted, and spotted only pattern emerge successively.

In summary, spatial pattern of an epidemic model with both self- and cross-diffusion has been investigated. The numerical results correspond perfectly to our theoretical findings that there are a range of parameters in $\beta - D$ plane where the different spatial patterns can be obtained. The influence of crossdiffusion on the pattern formation is revealed. More specifically, when there is no cross-diffusion, there is no Turing pattern. However, combing with crossdiffusion, we obtain stripe-like, spotted or coexistence of both patterns as D increases. Although more work is needed, in principle, it seems that cross-diffusion is able to generate many different kinds of spatiotemporal patterns. For such reason, we can predict that the interaction of self- and cross-diffusion can be considered as an important mechanism for the appearance of complex spatiotemporal dynamics in epidemic models.

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