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A MATHEMATICAL MODEL FOR SPATIALLY EXPANDING INFECTED AREA OF EPIDEMICS TRANSMITTED THROUGH HETEROGENEOUSLY DISTRIBUTED SUSCEPTIBLE UNITS

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Little is known about the effect of environmental heterogeneity on the spatial expansion of epidemics. In this work, to focus on the question of how the extent of epidemic damage depends on the spatial distribution of susceptible units, we develop a mathematical model with a simple stochastic process, and analyze it. We assume that the unit of infection is immobile, as town, plant, etc. and classify the units into three classes: *susceptible*, *infective* and *recovered*. We consider the range expanded by infected units, the *infected range* R, assuming a certain generalized relation between R and the total number of infected units k, making use of an index, a sort of *fractal dimension*, to characterize the spatial distribution of infected units. From the results of our modeling analysis, we show that the expected velocity of spatial expansion of infected range is significantly affected by the fractal nature of spatial distribution of immobile susceptible units, and is temporally variable. When the infection finally terminates at a moment, the infected range at the moment is closely related to the nature of spatial distribution of immobile susceptible units, which is explicitly demonstrated in our analysis.

Keywords: Epidemics; Stochastic Process; SIR Model; Fractal Dimension; Velocity.

1. Introduction

A variety of infectious diseases show different seriousness in terms of the infected area expansion, depending not only on the infectivity but also on the characteristics of infected place, city, or country: the environment-dependent way of disease transmission and the sanitary/health condition determine the nature of infected area

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expansion.[1–3] However, little is known about the effect of environmental heterogeneity on the spatial expansion of epidemics. In reality, a variety of species expand their spatial distribution depending on their ecological characteristics, settling their habitats composed of patchy environments, for instance, of trees, of wetland, or of mountains.[3–13] Especially, in case of plants or crops under attack from pests and diseases, the spatial distribution of susceptible hosts is considered as important for the spread of infection.[3,14–18]

So we can regard such a spatially patchy/fragmentated habitat as the collection of immobile units for infection of an epidemic disease transmitted within a considered population which inhabits in the habitat. Jules *et al.*[17] studied an invasion of non-native root pathogen, *Phytophthora lateralis*, over a heterogeneous landscape of its host, Port Orford cedar, *Chamaecyparis lawsoniana*, the population of which is restricted to riparian zones along creeks. In human case, we may consider the town or the village as such unit. Such patchiness of population distribution can be discussed from the viewpoint of fractal, too.[12,13,19–25]

As for spatially transmitted disease dynamics, a variety of researches with mathematical model have been studied,[3,26] making use of, for instance, reaction-diffusion system,[27–32] integro-differential or integro-difference equations,[33–38] percolation theory or network theory,[18,39–46] cellular automaton or lattice dynamics.[14,47–50] Especially, mathematical models with percolation theory or network theory have been attracting researchers who are interested in the invasion threshold which is the critical condition to determine weather the infection stops in a finite period or keeps its spatial expansion.

In this paper, with a mathematical model, we consider the effect of spatial distribution of susceptible units (cities, communities, plants, nests, etc.) on the nature of spatial expansion of disease infected region. Especially we focus on the velocity of its spatial expansion, which has been theoretically discussed in various contexts mostly with mathematical models used reaction-diffusion system (for instance, see Refs. 27, 28, 30–32 and their references). In contrast, we therefore try to discuss the characteristics of velocity with a mathematical model making use of a stochastic process. The velocity of spatial expansion of disease infected region must be affected by the nature of spatial distribution of susceptible units. In our modeling, to incorporate the effect of heterogeneous spatial distribution of susceptible units on the spatial expansion of disease infected region, we characterize the spatial distribution with an index, *fractal dimension*,[22] and introduce it into our model. So our model describes the epidemic population dynamics with a stochastic process, and the spatial expansion of disease infected region with a fractal nature of spatial distribution of susceptible units. This type of combination of population dynamics and spatial expansion may be regarded as an approximation for the real inter-relationship between them. We show that our modeling would be useful to get theoretical insights or develop the more advanced or practical model about the spatial expansion of disease infected area.

2. Modeling

2.1. *Assumptions*

In our modeling, we assume that the unit of infection is immobile, as town, plant, etc. We classify the units into three classes, depending on the state in terms of the disease infection: *susceptible*, *infective* and *recovered*. Susceptible unit is not yet infected, and infective one has been transmitted the disease and is still carrying it so as to transmit the disease to another unit. Recovered unit was infected in the past but is recovered so as not to transmit the disease to any other unit. It could correspond to the unit with immunity after its recovery from the disease. So this modeling can be regarded as a kind of SIR epidemic dynamics.[27,28,30,32] Since the recovered unit has no relation to the disease transmission dynamics, we could regard it as a completed destroyed or abandoned unit due to the disease infection, though the expression "recovered" is not appropriate in this context.

We do not consider the population/epidemic dynamics within each unit, but classify the unit as mentioned above in terms of its epidemic state of the disease infection. In this sense, our model would be regarded as belonging to the *metapopulation model*.[51]

To construct our mathematical model, we assume the following:

- Infection rate depends only on the total number of infective units.
- Only susceptible unit could be infected.
- Recovered unit is never infected again.
- Infection and recovery of a unit are independent of those of any other units.

The first assumption corresponds, for instance, to the case that the epidemic vector has a high mobility to transmit the disease, or the case that the disease transmission is through the matrix environment (e.g. wind, water or soil) surrounding susceptible units.[16,18,39]

In this paper, we consider the number of *infective* units, h, and that of *infected* units which is the sum of infective and recovered, k. Infected unit is an infective or recovered one, that is, a unit which experienced the disease transmission.

2.2. *Model construction*

2.2.1. *Probability for infection*

With the assumptions given in the previous section, we consider events occurring in sufficiently short time interval $(t, t + \Delta t]$ when h infective units exist at time t.

Probability that a susceptible unit has been transmitted the disease by an infective unit is assumed to be given by $\beta\Delta t + o(\Delta t)$ independently of the distance between them, where β is a positive constant, the infection rate. Since we assume that the infection of a susceptible unit by an infective unit is independent of that by

any other infective one, the probability that a susceptible unit has been transmitted the disease by h infective units becomes

$$\beta h\Delta t + o(\Delta t). \tag{2.1}$$

Probability that more than one susceptible units have been transmitted the disease during sufficiently small period Δt is assumed to be $o(\Delta t)$. Hence, the probability that none of the susceptible units has been transmitted the disease during sufficiently small period Δt is given by

$$1 - [\beta h\Delta t + o(\Delta t)] - o(\Delta t) = 1 - \beta h\Delta t - o(\Delta t). \tag{2.2}$$

2.2.2. *Probability for recovery*

Probability that an infective unit recovers during sufficiently small period Δt is assumed to be given by

$$\gamma\Delta t + o(\Delta t), \tag{2.3}$$

where γ is a positive constant, the recovery rate.

When there are h infective units, the probability that only one infective unit recovers is given by the probability for the case when the recovery of an infective unit occurs with probability given by (2.3) and at the same time the other $h-1$ infective units do not recover with probability given by $[1-\{\gamma\Delta t+o(\Delta t)\}]^{h-1}$. This is because the probability that an infective unit does not recover is $1-\{\gamma\Delta t+o(\Delta t)\}$, and the epidemic state of each unit is assumed to be independent of that of any other unit.

Therefore, taking account of which infective unit of h recovers, the required probability is obtained as follows:

$$\begin{aligned} &h \cdot \{\gamma\Delta t + o(\Delta t)\} \cdot [1 - \{\gamma\Delta t + o(\Delta t)\}]^{h-1} \\ &\quad = h \cdot \{\gamma\Delta t + o(\Delta t)\} \cdot \{1 - (h-1)\gamma\Delta t + o(\Delta t)\} \\ &\quad = \gamma h\Delta t + o(\Delta t). \end{aligned} \tag{2.4}$$

Probability that more than one infective units recover is assumed to be $o(\Delta t)$. Thus, from (2.4), the probability that none of the infective units recovers during sufficiently small period Δt is given by

$$1 - \gamma h\Delta t - o(\Delta t). \tag{2.5}$$

From the assumption of independence between infection and recovery, the probability that both infection and recovery occur during the time period Δt is given by $o(\Delta t)$, because the probability for each of them has the order Δt at the highest.

2.2.3. *Probability distribution for epidemic state*

We denote by $P(k,h,t)$ the probability of epidemic state such that there are k *infected* units and h *infective* units at time t in the considered system. To determine the probability $P(k,h,t)$, we consider the transition of state in sufficiently small time interval $(t, t+\Delta t]$, and derive the system of differential equations that govern the temporal variation of probability $P(k,h,t)$.

With transition probabilities for possible transitions of epidemic state in sufficiently small time interval $(t, t+\Delta t]$ as derived in Appendix A, we can get the following differential equations for $P(k,h,t)$ (Appendix B):

$$\begin{aligned}\frac{dP(k,h,t)}{dt} &= -(\beta+\gamma)hP(k,h,t) + \gamma(h+1)P(k,h+1,t) \\ &\quad + \beta(h-1)P(k-1,h-1,t),\end{aligned} \tag{2.6}$$

for $k \geq 2,\ h \geq 1,\ k \geq h+1$, and

$$\frac{dP(k,0,t)}{dt} = \gamma P(k,1,t), \tag{2.7}$$

$$\frac{dP(k,k,t)}{dt} = -k(\beta+\gamma)P(k,k,t) + (k-1)\beta P(k-1,k-1,t) \tag{2.8}$$

for $k \geq 1$.

2.2.4. *Initial condition*

We assume that the epidemic begins at a unit, so that the initial condition is given by

$$P(k,h,0) = \begin{cases} 1 & \text{if } k=h=1, \\ 0 & \text{otherwise.} \end{cases} \tag{2.9}$$

2.2.5. *Expansion of infected range*

Next, we consider the range expanded by infected units, say, the *infected range*. We characterize the infected range by the minimal diameter R which includes all infected units.

In the case when the infected range expands in every direction with the same probability, the shape of infected region can be approximated by the disc, and therefore, the range R approximately has the following relation with the number of infected units k: $k \propto R^2$. However, the expansion of infected range is constrained by the spatial distribution of potential carriers for the considered disease, which could be in general heterogeneous. So the shape of infected region is possibly inhomogeneous in direction, and could be characterized by its *fractal* nature (for the concept of "fractal" (see Refs. 22 and 52). To deal with such a case, we assume the following generalized relation between the infected range and the total number of infected units:

$$k \propto R^d \quad (1 \leq d \leq 2), \tag{2.10}$$

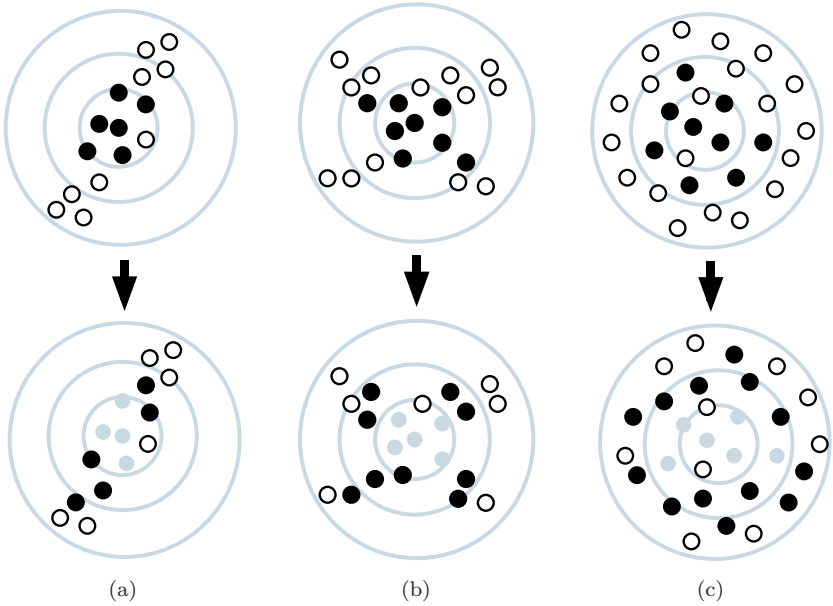


Fig. 1. Illustrative explanation of the relation of the fractal dimension d to the spatial pattern of unit distribution. Schematic procedure of disease transmission is also shown: White disc indicates susceptible unit, black infective, and grey recovered. (a) $d \approx 1$; (b) $1 < d < 2$; and (c) $d \approx 2$.

where the power d characterizes the spatial pattern of infected region occupied by infected units (Fig. 1). Power d is called *cluster dimension* or *mass dimension*, which is a sort of *fractal dimension*.[22,52] When $d \approx 2$, the spatial distribution of infected units has approximately a disc shape of its envelope. When $d \approx 1$, the distribution can be approximately regarded as one-dimensional, that is, the infected units can be regarded to be arrayed along a curve.

For instance, Port Orford cedar, *Chamaecyparis lawsoniana*, is the host for the root pathogen, *Phytophthora lateralis*, and has a heterogeneous population distribution, because it is restricted to riparian zones along creeks.[17] The population distribution of Port Orford cedar, *Chamaecyparis lawsoniana*, would be characterized with the fractal dimension d such that $1 < d < 2$ (see Fig. 1).

This idea of introduction of fractal nature into the mathematical model for the spatial distribution of units is the same as that in Seno.[53] This modeling may be regarded as a sort of mean-field approximation for the percolation process on a fractal lattice or the growing network. However, we focus on the temporal variation of the spatial range spanned by infected susceptible units, differently from most of previous works with the percolation theory or the growing network theory.[18,39,40,42–46]

Some percolation models for the epidemic dynamics considered the fractal nature of susceptible unit distribution, too.[46] In such previous models, the main problem was the invasion threshold which is the critical condition to determine

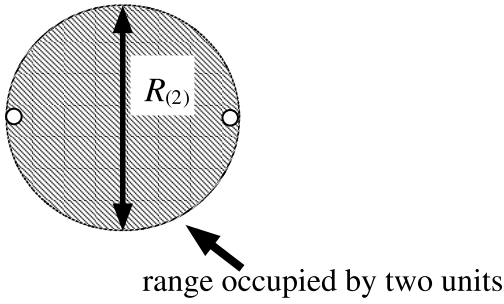


Fig. 2. Illustrative explanation of range $R_{(2)}$.

whether the infection stops in a finite period or keeps its spatial expansion. In contrast, we are going to focus on the velocity of spatial expansion of infected range.

For convenience to apply the relation (2.10) for our modeling, we now define the proportional constant C:

$$k = CR^d \quad (1 \leq d \leq 2). \tag{2.11}$$

Then, we define the mean distance $\bar{R}_{(2)}$ from one unit to the nearest neighbor (Fig. 2). In our modeling, $\bar{R}_{(2)}$ is assumed to correspond to the expected infected range expanded by two infected units, that is, $k = 2$. Therefore, from (2.11), we assume that

$$2 = C\bar{R}^d_{(2)}. \tag{2.12}$$

Hence, from (2.11), for the *expected* number of infected units $\langle k \rangle_t$ at time t, we assume the following relation with the *expected* infected range $\bar{r}_t$ at time t:

$$\langle k \rangle_t = 2\bar{r}_t^d \quad (1 \leq d \leq 2), \tag{2.13}$$

where $\bar{r}_t$ is the expected infected range at time t, measured in the mean distance $\bar{R}_{(2)}$: $\bar{r}_t \equiv \bar{R}_t / \bar{R}_{(2)}$.

Further, we define the *expected* velocity $\bar{V}_t$ of the expansion of *infected* range at time t as follows:

$$\bar{V}_t = \frac{d\bar{r}_t}{dt}.$$

From (2.13), we can obtain the following relation between the expected velocity $\bar{V}_t$ and the expected number $\langle k \rangle_t$ of infected units at time t:

$$\bar{V}_t = \frac{1}{d}\left(\frac{1}{2}\right)^{1/d} \langle k \rangle_t^{1/d-1} \cdot \frac{d\langle k \rangle_t}{dt}. \tag{2.14}$$

3. Analysis

3.1. *Expected number of infective units*

We denote by $\langle h \rangle_t$ the *expected* number of infective units at time t. It is defined by

$$\langle h \rangle_t = \sum_{k=1}^{\infty} \sum_{h=1}^{k} hP(k, h, t). \tag{3.1}$$

Hence, from (2.6) and (2.8), we can obtain the following:

$$\frac{d}{dt}\langle h \rangle_t = (\beta - \gamma)\langle h \rangle_t,$$

that gives

$$\langle h \rangle_t = e^{(\beta-\gamma)t}, \tag{3.2}$$

where we used the initial condition (2.9) for (3.1): $\langle h \rangle_0 = 1$.

3.2. *Expected number of infected units*

We denote by $\langle k \rangle_t$ the *expected* number of infected units at time t, defined by

$$\langle k \rangle_t = \sum_{k=1}^{\infty} k \left\{ \sum_{h=0}^{k} P(k, h, t) \right\}. \tag{3.3}$$

From (2.6), (2.7) and (2.8), we can obtain the following:

$$\frac{d}{dt}\langle k \rangle_t = \beta \langle h \rangle_t.$$

With (3.2), we can solve this differential equation and get the following:

$$\langle k \rangle_t = \frac{\beta}{\beta - \gamma}\{e^{(\beta-\gamma)t} - 1\} + 1, \tag{3.4}$$

where we used the initial condition (2.9) for (3.3): $\langle k \rangle_0 = 1$.

We can get the saturated value for $\langle k \rangle_t$. From (3.4), for $\beta \geq \gamma$ when the infection rate is not less than the recovery rate, the saturate value becomes positively infinite, that is, any saturation to a finite value does not occur. On the other hand, for $\beta < \gamma$ when the recovery rate is greater than the infection rate, the saturated value is finite, and is given by

$$\langle k \rangle_{t\to\infty} = \frac{\gamma}{\gamma - \beta}. \tag{3.5}$$

3.3. *Expected infected range*

Since, from (2.13),

$$\bar{r}_t = \left(\frac{\langle k \rangle_t}{2} \right)^{1/d}, \tag{3.6}$$

we can consider how the expected infected range $\bar{r}_t$ depends on the fractal dimension d for the spatial distribution of susceptible units, making use of (3.4). For $0 < \beta/\gamma < 1/2$, when the recovery rate is sufficiently greater than the infection rate, the expected infected range $\bar{r}_t$ gets larger as d is larger (Fig. 3a). This means that the infected range is expected to become wider as the susceptible units are more uniformly distributed. In contrast, for $\beta/\gamma \geq 1/2$, the expected infected range gets smaller as d is larger (Figs. 3b–3d). In this case, the infected range is expected to be narrower as the susceptible units are more uniformly distributed. Therefore, in our model, only if the infection rate is smaller than half of the recovery rate, the more uniform distribution of susceptible units causes the wider expected infected range (see Fig. 4).

Now, we consider the saturated value of expected infected range as $t \to \infty$. From (3.4) and (3.6), for $\beta > \gamma$ when the infection rate is greater than the recovery

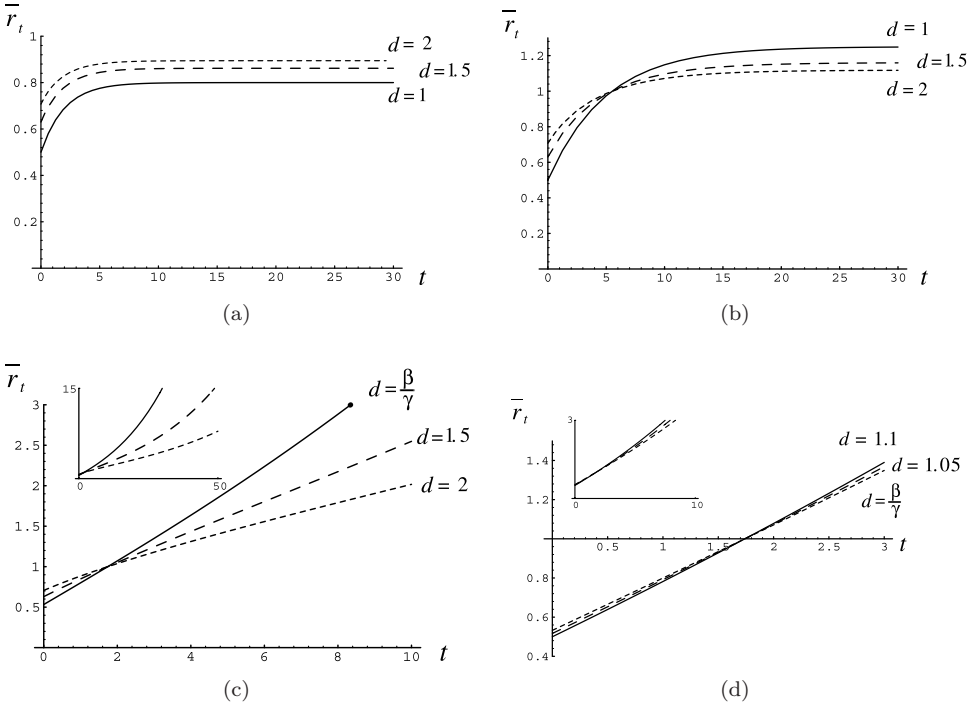
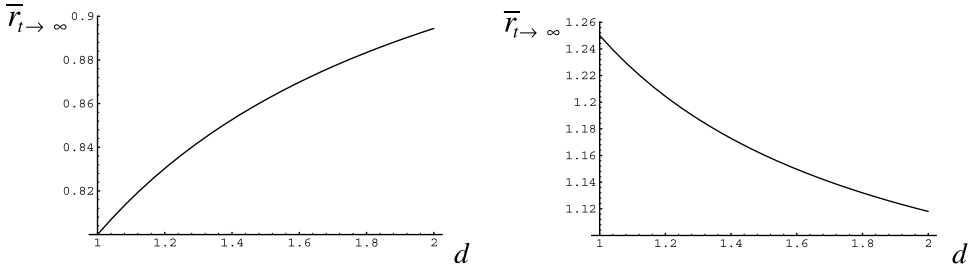
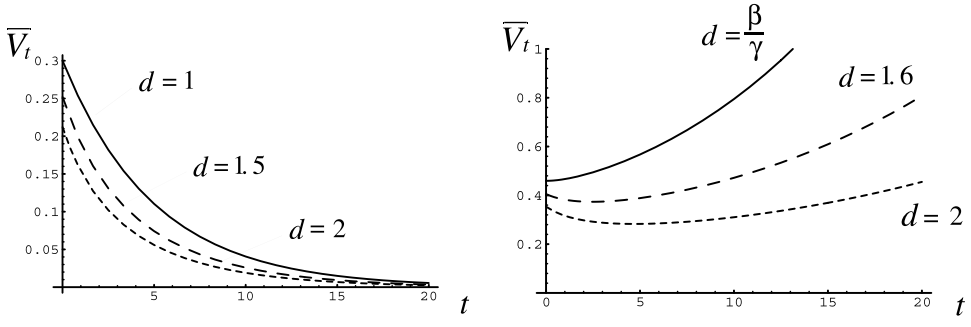


Fig. 3. Temporal development of the expected infected range. (a) $0 < \beta/\gamma < 1/2$, calculated for $\beta = 0.3$ and $\gamma = 0.8$; (b) $1/2 \leq \beta/\gamma \leq 1$, calculated for $\beta = 0.3$ and $\gamma = 0.5$; (c) $1 < \beta/\gamma < d$, calculated for $\beta = 0.55$ and $\gamma = 0.5$; and (d) $\beta/\gamma \geq d$, calculated for $\beta = 0.55$ and $\gamma = 0.5$.



(a) (b)

Fig. 4. d-dependence of the saturated value of expected infected range. (a) $0 < \beta/\gamma < 1/2$, calculated for $\beta = 0.3$ and $\gamma = 0.8$ and (b) $\beta/\gamma \geq 1/2$, calculated for $\beta = 0.3$ and $\gamma = 0.5$.



(a) (b)

Fig. 5. Temporal variation of the expected expansion velocity of infected range. (a) $0 < \beta/\gamma \leq 1$, calculated for $\beta = 0.3$ and $\gamma = 0.5$; (b) $1 < \beta/\gamma < d$, calculated for $\beta = 0.5$ and $\gamma = 0.4$; and (c) $\beta/\gamma \geq d$, calculated for $\beta = 0.5$ and $\gamma = 0.4$.

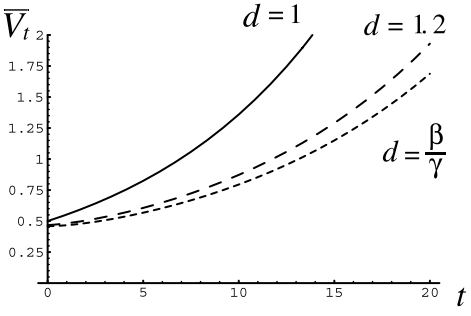
rate, the value becomes positively infinite as $t \to \infty$ (Figs. 3c and 3d). On the other hand, for $\beta < \gamma$ when the recovery rate is greater than the infection rate, it is saturated to the following value as $t \to \infty$ (Figs. 3a and 3b):

$$\begin{aligned} \bar{r}_{t\to\infty} &= \left(\frac{\langle k \rangle_{t\to\infty}}{2} \right)^{1/d} \\ &= \left(\frac{1}{2} \cdot \frac{\gamma}{\gamma - \beta} \right)^{1/d}. \end{aligned} \tag{3.7}$$

3.4. *Expected expansion velocity of infected range*

When $\beta/\gamma \leq 1$, that is, when the recovery rate is not less than the infection rate, the expected velocity $\bar{V}_t$ given by (2.14) monotonically decreases in time (Fig. 5a).

When $1 < \beta/\gamma < d$, the expected velocity $\bar{V}_t$ decreases in the earlier period and then turns to increase monotonically (Fig. 5b). We denote by t_c the time when the expected velocity turns from decreasing to increasing. From (2.14), we can



(c)

Fig. 5. (*Continued*).

explicitly get

$$t_c = \frac{1}{\beta - \gamma} \ln \frac{\gamma}{\beta} d. \tag{3.8}$$

When $\beta/\gamma \geq d$, the expected velocity $\bar{V}_t$ monotonically increases in time (Fig. 5c).

At last, we can see how the expected velocity $\bar{V}_t$ depends on the fractal dimension d for the spatial distribution of susceptible units. The expected velocity gets smaller as d is larger (Figs. 5a–5c) for any value of β/γ. Therefore, in our model, the more uniform distribution of susceptible units causes the slower expansion of infected range.

3.5. *Probability of termination of infection*

We denote by $P_{h=0}$ the probability of termination of infection. Once an infective unit disappears in space because of recovery, the infection can no longer continue and restart. If the infection terminates at time t, for sufficiently small Δt, the epidemic state should be with only one infective unit at time $t - \Delta t$, and the infective unit should recover during Δt without causing any new infection. When the number of infected units is k at time t, from (2.2) and (2.3), the probability for this event is given by

$$P(k, 1, t)[1 - \beta\Delta t - o(\Delta t)] \cdot [\gamma\Delta t + o(\Delta t)] = \gamma P(k, 1, t)\Delta t + o(\Delta t). \tag{3.9}$$

Therefore, the probability for the termination of infection between $t - \Delta t$ and t is given by the sum of (3.9) over any possible k.

Making use of the probability generating function (p.g.f.) defined by

$$f(x, y, t) = \sum_{k=1}^{\infty} \sum_{h=0}^{k} P(k, h, t) x^k y^h, \tag{3.10}$$

we can derive the probability for the termination of infection (as for the p.g.f., see Appendix C):

$$\begin{aligned} P_{h=0} &= \int_0^\infty \gamma \sum_{k=1}^\infty P(k,1,t)dt \\ &= \int_0^\infty \gamma \cdot \left.\frac{\partial f}{\partial y}\right|_{x=1,y=0} dt \\ &= \int_0^\infty \gamma \cdot \frac{e^{-(\beta-\gamma)t}\{(\beta-\gamma)/\beta\}^2}{1-e^{-(\beta-\gamma)t}\gamma/\beta} dt \\ &= \min\left\{\frac{\gamma}{\beta}, 1\right\}. \end{aligned} \tag{3.11}$$

The probability $P_{h=0}$ is 1 for $\beta \leq \gamma$ when the recovery rate is greater than the infection rate (Fig. 6). This case is when the infection certainly terminates in a finite time. When the infection rate is greater than the recovery rate, the probability $P_{h=0}$ is proportional to the recovery rate and inversely proportional to the infection rate (Fig. 6).

3.6. *Expected time for the termination of infection*

We denote by $\langle t \rangle_{h=0}$ the expected time for the termination of infection. From the arguments in the previous section, we can explicitly obtain

$$\begin{aligned} \langle t \rangle_{h=0} &= \int_0^\infty t\gamma \sum_{k=1}^\infty P(k,1,t)dt \\ &= \begin{cases} +\infty & \text{if } \beta \geq \gamma; \\ \dfrac{1}{\beta} \ln \dfrac{\gamma}{\gamma-\beta} & \text{if } \beta < \gamma. \end{cases} \end{aligned} \tag{3.12}$$

For $\beta < \gamma$ when the recovery rate is greater than the infection rate, we can expect that the infection terminates at a finite time. In this case, the expected time gets

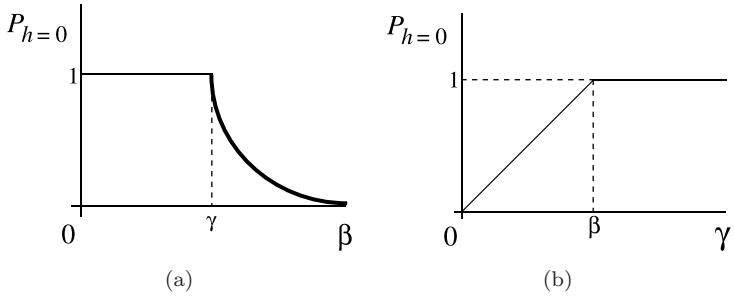


Fig. 6. Parameter dependence of the probability for the termination of infection, $P_{h=0}$. (a) β-dependence and (b) γ-dependence.

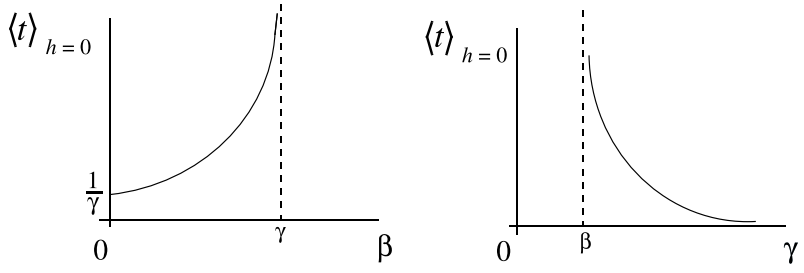


Fig. 7. Parameter dependence of the expected time for the termination of infection $\langle t \rangle_{h=0}$. (a) β-dependence and (b) γ-dependence.

longer as the infection rate is greater, and shorter as the recovery rate is greater (Fig. 7).

3.7. *Expected number of infected units at the termination of infection*

We denote by $\langle k \rangle_{h=0}$ the expected number of infected units at the termination of infection. Integral $\int_0^\infty \gamma P(k,1,t)dt$ gives the probability that the number of infected units is k at the moment when the infection terminates. Therefore, making use of the p.g.f. (3.10) and (4.4) in Appendix C, we can get

$$\begin{aligned}
\langle k \rangle_{h=0} &= \sum_{k=1}^{\infty} k \int_0^\infty \gamma P(k,1,t)dt \\
&= \gamma \int_0^\infty \sum_{k=1}^{\infty} kP(k,1,t)dt \\
&= \gamma \int_0^\infty \frac{\partial}{\partial y} \left(\frac{\partial f}{\partial x} \right) \Big|_{x=1,y=0} dt \\
&= \gamma \int_0^\infty \frac{\partial}{\partial x} \left(\frac{\partial f}{\partial y} \Big|_{y=0} \right) \Big|_{x=1} dt \\
&= \frac{\gamma}{\gamma - \beta}. \qquad (3.13)
\end{aligned}$$

From (3.5) and (3.13), we can see that the expected number of infected units at the termination of infection, $\langle k \rangle_{h=0}$ is identical to the saturated value of $\langle k \rangle_t$, that is, $\langle k \rangle_{t\to\infty}$:

$$\langle k \rangle_{h=0} = \langle k \rangle_{t\to\infty}.$$

Therefore, $\langle k \rangle_{h=0}$ has the characteristics same as for $\langle k \rangle_{t\to\infty}$. The expected range at the termination of infection is also identical to the saturated range of $\bar{r}_t$, that is, $\bar{r}_{t\to\infty}$.

4. Discussion

In this work, to focus on the question of how the extent of epidemic damage depends on the spatial distribution of susceptible units, we constructed a mathematical model with a simple stochastic process, and analyzed it.

We assumed that the unit of infection is immobile, as town, plant, etc. and classify the units into three classes: *susceptible*, *infective* and *recovered*. This modeling can be regarded as a kind of SIR epidemic dynamics.[27,28,30,32] We do not consider the population/epidemic dynamics within each unit, but classify the unit as mentioned above in terms of its epidemic state in terms of the disease infection. In this sense, our model would be regarded as belonging to the *metapopulation model*.[51]

Our modeling is not always unrealistic or over-idealized. In reality, a variety of species expand their spatial distributions, settling their habitats composed of patchy environments, for instance, of trees, of wetland, or of mountains.[3,8,10–16,18] So we can regard each patch of such spatially fragmentated habitats as the immobile unit of infection for an epidemic disease transmitted within the population. In human case, we may consider the town or the village as such unit.

In our model, we considered the probability for the state such that k *infected* and h *infective* units exist at time t. Infected unit is an infective or recovered one, that is, a unit which experienced the disease transmission. Infective unit has been transmitted the disease and is still carrying it so as to transmit the disease to another unit. Recovered unit was transmitted the disease in the past and has recovered so as not to transmit the disease to any other unit. So it could correspond to the unit with immunity after its recovery from the disease. Since the recovered unit has no relation to the disease transmission dynamics, we could regard it as a completely destroyed or abandoned unit due to the disease infection, though the expression "recovered" is not appropriate in this context.

We derived the system of differential equations to describe the temporal variation of the probability distribution in terms of the numbers of infected and infective units. Furthermore, we considered the mathematical modeling for the range expanded by infected units in space ,the *infected range* R, which can be characterized by the *expected* minimal diameter R which includes all infected units. In our modeling, we assumed a generalized relation between R and the total number of infected units k, making use of an index called *cluster dimension* or *mass dimension*, that is a sort of *fractal dimension*, which characterizes the spatial distribution of susceptible units. With the generalized relation, we can develop the mathematical model for the temporal variation of expected infected range and of expected expansion velocity of infected range. From our analysis of the model, we showed that the expected velocity is significantly affected by the nature of spatial distribution of immobile susceptible units, and is temporally variable, differently from those typical results derived for the mathematical model with the reaction-diffusion system in continuous space.

Consequently we found three types of temporal variation of expected velocity of infected range expansion, depending on the fractal dimension of spatial

distribution of susceptible units: monotonically decreasing, monotonically decreasing, and increasing after initially decreasing. The last case implies that we have to pay attention to the expansion of infected area even if the velocity of its spatial expansion is observed to decrease in the early period of disease transmission process.

In our modeling, a susceptible unit has been transmitted the disease and becomes infective with probability proportional to the *total number* of infective units, that is, the total number of patchy habitats with active disease carriers, as in Seno and Matsumoto[54] who analyzed a mathematical model for population dynamics to expand its spatial distribution with patch creation by the existing whole population. This assumption corresponds, for instance, to the case that the epidemic vector has a high mobility to transmit the disease, or the case that the disease transmission is through the matrix environment (e.g. wind, water or soil) surrounding susceptible units.[16,18,39]

It may be more realistic that a susceptible unit would have transmitted the disease via some *spatially neighbor* infective units. This assumption requires another modeling and would make the model more difficult to be mathematically analyzed. Some cellular automaton models or lattice models have been considered such disease transmission in space. Computer-aided numerical analysis has always been useful in the analysis of such models, whereas numerical calculations could not derive the general result about the nature of spatial disease transmission. To consider only a specific disease transmission in space, it might be satisfactory with some specific parameter values. However, as indicated in some well-known mathematical works about epidemics, for example, the Kermack-McKendrick model,[55] this does not mean less evaluation of theoretically/mathematically general results from mathematical models in mathematical biology. Only a few mathematical methods could reach some general features of such models, for instance, the mean field approximation and the pair approximation, etc.[15,48,50,56]

In this paper, we consider our mathematical model in the context of spatial expansion of infected range of epidemic disease transmitted via immobile susceptible units. However, our modeling is easily applied in the case of the spatially expanding population distribution through patchy/fragmentated habitats in space. In this context, the parameter β can be regarded as the settlement rate from an established habitat to another newly immigrated one, and γ as the rate to abandon or destroy a settled habitat. If the considered population is of a harmful insect to be exterminated, γ may be regarded as the exterminated rate for a unit aggregated by the insect.

For the spatial expansion of population distribution, some well-known mathematical models are of reaction-diffusion system in spatially continuous space.[30–32,57] However, in general, it is not easy or is more tactical to introduce the nature of spatial heterogeneity of habitat distribution into such models with reaction-diffusion system. In contrast, in the case of spatially discrete models, frequently constructed by cellular automaton or lattice space,[18,39,50,58] introduction of spatial

heterogeneity is relatively easy, whereas mathematical analysis is rarely easy and becomes harder as the number of factors governing the dynamics increases, so that a number of numerical calculations are required. Stochastic model like ours is another way for the theoretical study that could give some new insights, as indicated in some papers of landscape ecology.[59–61] Our model could be regarded as one that is between a non-spatial population dynamics model and a numerical one, and may be termed a *semi-spatial model* as called by Filipe *et al.*[48] Since there has been few models to consider the velocity of spatial expansion of infected region with such spatially discrete susceptible units, we hope that our modeling consideration would be a pioneer approach to the problem.

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Appendix A

To determine the probability $P(k, h, t)$, we consider respectively the following transitions of state in sufficiently small time interval $(t, t + \Delta t]$.

$\boldsymbol{(k, h, t) \to (k, h, t + \Delta t)}$: In this case, since there is no change in the number of infected units and that of infective ones, neither infection nor recovery occurs during time period Δt. Therefore, from (2.2) and (2.5), the transition probability is given by

$$[1 - \beta h \Delta t - o(\Delta t)] \cdot [1 - \gamma h \Delta t - o(\Delta t)] = 1 - (\beta + \gamma) h \Delta t + o(\Delta t). \tag{4.1}$$

$\boldsymbol{(k - 1, h, t) \to (k, h, t + \Delta t)}$: Since only the number of infected units increases by one, one infection and one recovery should occur during time period Δt. To increase the number of infected units by one, the number of infective units must increase by one. Hence, in order that the number of infective units at $t + \Delta t$ is simultaneously h, the number of infective units must decrease by one during Δt. From the assumption given in the previous section, both infection and recovery occur during Δt with probability $o(\Delta t)$, so that the considered transition probability is $o(\Delta t)$, too.

$\boldsymbol{(k, h + 1, t) \to (k, h, t + \Delta t)}$: In this case, only one recovery occurs during time period Δt with no change in the number of infected units, when any new infection does not occur. Therefore, from (2.2) and (2.4), the transition probability is given by

$$[1 - \beta(h + 1)\Delta t - o(\Delta t)] \cdot [\gamma(h + 1)\Delta t + o(\Delta t)] = \gamma(h + 1)\Delta t + o(\Delta t). \tag{4.2}$$

$\boldsymbol{(k - 1, h - 1, t) \to (k, h, t + \Delta t)}$: In this case, one infection occurs without any recovery during time period Δt. Therefore, from (2.1) and (2.5), the transition probability is given by

$$[\beta(h - 1)\Delta t + o(\Delta t)] \cdot [1 - \gamma h \Delta t - o(\Delta t)] = (h - 1)\beta \Delta t + o(\Delta t). \tag{4.3}$$

$\boldsymbol{(k - l, h - l, t) \to (k, h, t + \Delta t)\ (l \geq 2)}$: In this case, infection occurs l times without any recovery during time period Δt. Since more than one infection occurs during Δt, the transition probability is $o(\Delta t)$.

$\boldsymbol{(k, h + m, t) \to (k, h, t + \Delta t)\ (m \geq 2)}$: In this case, recovery occurs m times without any infection during Δt. Since more than one recovery occurs during Δt, the transition probability is $o(\Delta t)$.

$\boldsymbol{(k - l, h + n, t) \to (k, h, t + \Delta t)\ (n \geq 0; 1 \leq l \leq k - 1)}$: In this case, infection and recovery occur l and $n + l$ times, respectively during Δt. Since more than one infection and recovery occurs during Δt, the transition probability is $o(\Delta t)$.

Appendix B

With transition probabilities (4.1), (4.2) and (4.3) for possible transitions of state in sufficiently small time interval $(t, t+\Delta t]$, we can derive the following equation from the definition of $P(k,h,t)$ for $k \geq 1,\ h \geq 0,\ k \geq h+1$:

$$\begin{aligned} P(k,h,t+\Delta t) = {} & P(k,h,t)\cdot[1-(\beta+\gamma)h\Delta t + o(\Delta t)] \\ & + P(k,h+1,t)\cdot[\gamma(h+1)\Delta t + o(\Delta t)] \\ & + P(k-1,h-1,t)\cdot[(h-1)\beta\Delta t + o(\Delta t)] \\ & + \sum_{l=2}^{\infty} P(k-l,h-l,t)\cdot o(\Delta t) \\ & + \sum_{m=2}^{\infty} P(k,h+m,t)\cdot o(\Delta t) \\ & + \sum_{l=1}^{k-1}\sum_{n=0}^{\infty} P(k-l,h+n,t)\cdot o(\Delta t). \end{aligned}$$

Therefore, we can obtain the equation for $\{P(k,h,t+\Delta t) - P(k,h,t)\}/\Delta t]$, and then as $\Delta t \to 0$, we can get the differential equation (2.6).

Appendix C

From (3.10), applying (2.6) to (2.8) with a cumbersome and careful calculation, we can derive the following partial differential equation for the probability generating function (p.g.f.) $f(x,y,t)$ defined by (3.10):

$$\frac{\partial f(x,y,t)}{\partial t} = \{-(\beta+\gamma)y + \gamma + \beta x y^2\}\frac{\partial f(x,y,t)}{\partial y}. \tag{4.1}$$

From (2.9), the initial condition is given by

$$\begin{aligned} f(x,y,0) &= \sum_{k=1}^{\infty}\sum_{h=0}^{k} P(k,h,0)x^k y^h \\ &= P(1,1,0)xy \\ &= xy. \end{aligned} \tag{4.2}$$

In addition, the following condition can be derived:

$$f(1,1,t) = \sum_{k=1}^{\infty}\sum_{h=0}^{k} P(k,h,t) = 1, \tag{4.3}$$

because the sum of probability for any possible k and h corresponds to the occurrence of any event.

With condition (4.2) and (4.3), we can directly solve (4.1) as follows:[62]

$$f(x, y, t) = x \cdot \left[v_+(x) - \frac{\hat{v}(x)\{v_+(x) - y\}}{\Phi(x)} \right], \tag{4.4}$$

where

$$\Phi(x) = \{v_+(x) - y\} + \{y - v_-(x)\} e^{-\beta x \hat{v}(x) t};$$
$$\hat{v}(x) = v_+(x) - v_-(x),$$

and $v_+(x)$ and $v_-(x)$ are functions of x, given by two distinct roots of the following equation in terms of ξ:

$$\beta x \xi^2 - (\beta + \gamma)\xi + \gamma = 0.$$