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## CHAPTER 15

# Modeling spatial spread of communicable diseases involving animal hosts

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**Abstract.** In this chapter, we review some previous studies on modeling spatial spread of specific communicable diseases involving animal hosts. Reaction-diffusion equations are used to model these diseases due to movement of animal hosts. Selected topics include the transmission of rabies in fox populations (Källén et al., 1984; Källén et al., 1985; Murray et al., 1986), dengue (Takahashi et al., 2005), West Nile virus (Lewis et al., 2006; Ou & Wu, 2006), hantavirus spread in mouse populations (Abramson and Kenkre, 2002), Lyme disease (Caraco et al., 2002), and feline immunodeficiency virus (FIV) (Fitzgibbon et al., 1995; Hilker et al., 2007).

### 15.1 Introduction

Spatial spread of communicable diseases is closely related to the spatial heterogeneity of the environment and the spatial-temporal movement of the hosts. Mathematical modeling of disease spread normally starts with the consideration of the transmission dynamics within a population which is homogeneous in terms of host structures and environmental variation, and then follows by the examination of the impact on the transmission dynamics of the refined and detailed biological/epidemiological structures and patterns of spatial dispersal/diffusion of the hosts.

Epidemic theory for homogeneous populations has shown that the *basic reproductive number*, which may be considered as the fitness of a pathogen in a given population, must be greater than unity for the pathogen to invade a susceptible population (Anderson and May, 1991; Brauer and Castillo-Chavez, 2000; Diekmann and Heesterbeek, 2000; Edelstein-Keshet, 1988; Jones and Sleeman, 2003; Murray, 2003;

Thieme, 2003). It is natural to ask how spatial movement of the hosts affects the spatial-temporal spread pattern of the disease if the basic reproduction number for an otherwise homogeneous population exceeds unity.

Answers to the above question obviously depend on the manner in which hosts move into, out of, and within the considered geographical region. For example, adding an immigration term so that infective individuals enter the system at a constant rate clearly allows the persistence of the disease, because if it dies out in one region then the arrival of an infective from elsewhere can trigger another epidemic. Indeed, a constant immigration term has a mildly stabilizing effect on the dynamics and tends to increase the minimum number of infective individuals observed in the models (Bolker and Grenfell, 1995). Spread of diseases in a heterogeneous population has also been intensively studied using patchy or metapopulation models. These models are formulated under the assumption that the host population under consideration can be divided into multipatches so that the host population within a patch is considered as homogeneous, and the heterogeneity is associated with the rates with which individuals move from one patch to another (Arino and van den Dreissche, 2006).

Another popular way to incorporate the spatial movement of hosts into epidemic models is to assume some types of host random movements, leading to reaction-diffusion equations. See, for example, Busenberg and Travis (1983), Capasso (1978), Capasso and Wilson (1997), De Mottoni et al. (1979), Gudelj et al. (2004), Fitzgibbon et al. (2007), Webb (1981). This strand of theoretical developments built on the pioneering work of Fisher (1937), who used a logistic-based reaction-diffusion model to investigate the spread of an advantageous gene in a spatially extended population. With initial conditions corresponding to a spatially localized introduction, such models predict the eventual establishment of a well-defined invasion front which divides the invaded and uninvaded regions and moves into the uninvaded region with a constant velocity. The velocity at which an infection wave moves is set by the rate of divergence from the (unstable) disease-free state and can be determined by linear methods (Murray, 2003).

Most reaction-diffusion (or reduced/related space-dependent integral) epidemic models are space-dependent extensions of the classical Kermack-McKendrick (Kermack and McKendrick 1927) deterministic compartmental model for a directly transmitted viral or bacterial agent in a closed population consisting of susceptibles, infectives, and recovered. Their model leads to a nonlinear integral equation which has been studied extensively. The deterministic model of Bartlett (1956) predicts a wave of infection moving out from the initial source of infection. Kendall (1957) generalized the Kermack-McKendrick model to a space-dependent integro-differential equation. Aronson (1977) argued that the three-component Kendall model can be reduced to a scalar one and extended the concept of asymptotic speed of propagation developed in Aronson and Weinberger (1975) to the scalar epidemic model. The Kendall model assumes that the infected individuals become immediately infectious and does not take into account the fact that most infectious diseases have an incubation period. This incubation period was considered by Diekmann (1978, 1979) and Thieme (1977a, 1977b, 1979), using a nonlinear (double) integral equation model. For further

study on velocity of spatial spread, we refer to Mollison (1991), van den Bosch et al. (1990), the monograph of Rass and Radcliffe (2003), and references cited therein. Most of these studies concern the existence of traveling waves, and their relation to the disease propagation/spread rate. For additional studies, see Ai and Huang (2005), Cruickshank et al. (1999), Hosono and Ilyas (1995), Kuperman and Wio (1999), Zhao and Wang (2004), etc.

Despite these studies on reaction-diffusion epidemic models, however, there are very few studies on modeling spatial spread of specific diseases using partial differential equation models. In this chapter, we review some previous studies on modeling spatial spread of specific communicable diseases using reaction-diffusion equations. Selected topics include the transmission of rabies in fox population (Källén et al., 1984; Källén et al., 1985; Murray et al., 1986), dengue (Takahashi et al., 2005), West Nile virus (Lewis et al., 2006; Ou and Wu, 2006), hantavirus spread in mouse populations (Abramson and Kenkre, 2002), Lyme disease (Caraco et al., 2002), and feline immunodeficiency virus (FIV) (Fitzgibbon et al., 1995; Hilker et al., 2007).

## 15.2 Rabies

The celebrated studies by Källén (1984), Källén et al. (1985), and Murray et al. (1986) about the spatial spread of rabies among foxes show the feasibility and usefulness of utilizing a simple reaction-diffusion model for the description of transmission dynamics and spread patterns of specific diseases and for the qualitative evaluation of various space-relevant control strategies. These studies give a fine example of how to build a reaction-diffusion model based on the known ecology of the host behavior and the detailed epidemiology of the disease progression, how to use known data and facts to determine model parameter values, how to calculate the speed of propagation of the epizootic front and the threshold for the existence of an epidemic, and how to use models to quantify and evaluate space-relevant control strategies. They also demonstrate the trade-off between simplicity and the number of parameters that have to be estimated from field studies. It is therefore natural that we start with a brief introduction of these studies to illustrate some of the basic ideas and techniques involved in reaction-diffusion models for disease spread.

Rabies, a viral infection of the central nervous system, is transmitted by direct contact. The dog is the principal transmitter of the disease to man, and it is a particularly horrifying disease for which there is no known case of a recovery once the disease has reached the clinical stage. The aforementioned studies examined the rabies epidemic, which started in 1939 in Poland and moved steadily westward at a rate of 30-60 km per year. The red fox was the main carrier, and victim, of the rabies epidemic under consideration, although most mammals are thought to be susceptible to the disease and although an epidemic, which was mainly propagated by racoons, was also moving rapidly up the east coast of America during that period and subsequently.

The basic model of Källén et al. (1985) is built on the assumptions that foxes are the main carriers of rabies in the rabies epizootic considered, the rabies virus is normally

transmitted by bite, and rabies is fatal in foxes. It also assumes that susceptible foxes are territorial, but once the virus enters the central nervous system it induces behavioral changes in its host and, in particular, if it enters the limbic system the foxes become aggressive, lose their sense of direction and territorial behavior, and wander about in a more or less random way.

Let  $S(x, t)$  and  $I(x, t)$  be the total number of susceptible foxes and the total number of infective foxes, respectively, in the space-time coordinate  $(x, t)$  and ignore the incubation period at the moment. Then the model formulated in a one-dimensional unbounded domain takes the form (Källén et al., 1985)

$$\begin{aligned}\frac{\partial S}{\partial t} &= -\beta S(x, t)I(x, t), \\ \frac{\partial I}{\partial t} &= D\frac{\partial^2 I}{\partial x^2} + \beta S(x, t)I(x, t) - \mu I(x, t),\end{aligned}\tag{15.1}$$

where  $\beta$  is the transmission coefficient,  $\mu^{-1}$  is the life expectancy of an infective fox, and  $D$  is the diffusion coefficient.

The basic reproduction number of the corresponding ODE model is  $R_0 = \beta S_0/\mu$ , with  $S_0$  being the initial susceptible population (with homogeneous environment). If  $R_0 < 1$  then the mortality rate is greater than the rate of recruitment of new infectives, and hence the infection is expected to die out quickly. We thus obtain the minimum fox density  $S_c := \mu/\beta$  below which rabies cannot persist. It was indeed proven (Källén, 1984) that if  $R_0 < 1$ ,  $I(\cdot, 0) \geq 0$  has bounded support, and if  $S(x, 0) = S_0$  for  $x \in R$ , then  $I(x, t) \rightarrow 0$  as  $t \rightarrow \infty$  uniformly on  $R$ .

The case where  $R_0 > 1$  indicates the persistence of the disease in a spatially homogeneous setting. The spatial diffusion then propagates the disease so that a small localized introduction of rabies evolves into a traveling wave with a certain wave speed, that is, a solution with  $I(x, t) = f(z)$ ,  $S(x, t) = g(z)$  with the wave variable  $z = x - ct$  so that the wave forms (profiles)  $f$  and  $g$  are determined by the asymptotic boundary value problem

$$\begin{aligned}Df'' + cf' + \beta fg - \mu f &= 0, cg' - \beta fg = 0; \\ f(\pm\infty) &= 0, g(+\infty) = S_0, g(-\infty) = S_\infty,\end{aligned}$$

where primes denote differentiation with respect to  $z$ ,  $S_\infty$  gives the number of susceptible foxes that remain after the infective wave has passed, and this number is found by solving the final size equation

$$S_\infty/S_0 - R_0^{-1}\ln(S_\infty/S_0) = 1.$$

The existence of traveling waves with speeds larger than  $c_0 = 2\sqrt{1 - R_0^{-1}}$  is established by Källén (1984) and Källén et al. (1985), and the importance of the traveling wave with the minimal wave speed  $c_0$  is shown by Källén (1984). Namely, it was shown that if  $I(\cdot, 0)$  has compact support, then for every  $\delta > 0$  there exists  $N$  so that  $I(x + c_0t - \ln t/c_0, t) \leq \delta$  for every  $t > 0$  and for all  $x > N$ . Therefore, if a fox travels with speed  $c(t) = c_0 - (c_0t)^{-1}\ln t$  towards  $+\infty$  (in space) to the right of the support of  $I(\cdot, 0)$ , the infection will never overtake the fox. In other words,

the asymptotic speed of the infection must be less than  $c(t)$ . As a consequence, if  $I(x, t)$  takes the form of a traveling wave for large  $t$ , it must do so for the one with the minimal speed  $c_0$ .

Estimating such a propagation speed is feasible once we know the relevant parameter values. In (Murray et al., 1986),  $R_0$  was set to 2 according to the observed mortality rate 65 – 80% during the height of the epizootic. The diffusion coefficient  $D$  is estimated to be  $60 \text{ km}^2\text{yr}^{-1}$ , using the average territory of a fox and the mean time a fox stays in its territory. This yields the minimal wave speed near 50 km per year, in good agreement with the empirical data from Europe.

The diffusion model provides a useful framework to evaluate some spatially related control measures such as the possibility of stopping the spread of the disease by creating a rabies ‘break’ ahead of the front through vaccination to reduce the susceptible population to a level below the threshold for an epidemic to occur. Based on parameter values relevant to England, the model suggests that vaccination has considerable advantages over severe culling. Using a classical logistic model for the growth of susceptible foxes, one can explain the tail part of the wave, and in particular, the oscillatory behavior. Indeed, Anderson et al. (1981) speculated that the periodic outbreak is primarily an effect of the incubation period, and Dunbar (1983) and Murray et al. (1986) obtained some qualitative results that show sustained oscillations if the classical logistic model is used and the carrying capacity of the environment is sufficiently large.

It was noted that juvenile foxes leave their home territory in the fall, traveling distances that typically may be 10 times a territory size in search of a new territory. If a fox happens to have contracted rabies around the time of such long-distance movement, it could certainly increase the rate of spread of the disease into uninfected areas (see Murray et al. (1986)). To address this impact of the age-dependent diffusion of susceptible foxes, Ou and Wu (2006) started with a general model framework in population biology and spatial ecology wherein the individual’s spatial movement behaviors depend on its maturation status, and they illustrated how delayed reaction-diffusion equations with nonlocal interactions arise naturally. For the above mentioned spatial spread of rabies by foxes, they showed how the distinction of territorial patterns between juvenile and adult foxes yields a class of partial differential equations involving delayed and non-local terms that are implicitly defined by a hyperbolic-parabolic equation. They then demonstrated how incorporating this distinction into the model leads to a formula describing the relation of the minimal wave speed and the maturation time of foxes. Their work involves  $I(t, a, x)$  and  $S(t, a, x)$  as the population density at time  $t$ , age  $a \geq 0$ , and spatial location  $x \in R$  for the infective and the susceptible foxes, respectively, and  $\tau$  as the maturation time which is assumed to be a constant. It was shown that the total population of the infective foxes  $J(t, x) = \int_0^\infty I(t, a, x) da$  and the density of the adult susceptible foxes

$M(t, x) = \int_{\tau}^{\infty} S(t, a, x) da$  satisfy

$$\begin{aligned}\frac{\partial J}{\partial t} &= D_I \frac{\partial^2 J}{\partial x^2} + \beta M(t, x) J(t, x) - d_I J(t, x) + \beta J(t, x) \int_0^{\tau} S(t, a, x) da, \\ \frac{\partial M}{\partial t} &= -\beta M(t, x) J(t, x) - d_S M(t, x) + S(t, \tau, x),\end{aligned}$$

where  $D_I$  is the diffusive coefficient,  $d_I$  is the death rate for the infective foxes,  $\beta$  is the transmission rate, the constant  $d_S$  is the death rate for the susceptible foxes, and  $S(t, a, x)$  with  $0 \leq a \leq \tau$  can be solved implicitly in terms of  $(J, M)$  by considering

$$\begin{cases} \left( \frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) S(t, a, x) = D_Y \frac{\partial^2}{\partial x^2} S(t, a, x) - \beta S(t, a, x) J(t, x) - d_Y S(t, a, x), \\ S(t, 0, x) = b(M(t, x)), \end{cases}$$

where  $D_Y$  and  $d_Y$  are the diffusive and death coefficients for the immature susceptible foxes and  $b(\cdot)$  is the birth function of the susceptible foxes.

It was shown in Ou and Wu (2006) that some of the key issues related to the spatial spread can be addressed, despite the difficulty in obtaining an explicit analytic formula of  $S(t, a, x)$  in terms of the historical values of  $M$  at all spatial locations. For example, the minimal wave speed can be shown to be a decreasing function of the maturation period. This result coincides in principle with the speculation by Anderson et al. (1981) and Murray et al. (1986), and gives a more precise qualitative description of the influence of maturation time on the propagation of the disease in space.

### 15.3 Dengue

Dengue fever (DF) and dengue hemorrhagic fever (DHF) are caused by one of four closely related, but antigenically distinct, virus serotypes (DEN-1, DEN-2, DEN-3, and DEN-4) of the genus *Flavivirus*. Infection by one of these serotypes provides immunity to only that serotype for life, so persons living in a dengue-endemic area can have more than one dengue infection during their lifetime. DF and DHF are primarily diseases of tropical and sub-tropical areas, and the four different dengue serotypes are maintained in a cycle that involves humans and the *Aedes* mosquito. Here, *Aedes aegypti*, a domestic, day-biting mosquito that prefers to feed on humans, is the most common *Aedes* species. Infections produce a spectrum of clinical illness ranging from a nonspecific viral syndrome to severe and fatal hemorrhagic disease. Important risk factors for DHF include the strain of the infecting virus, as well as the age, and especially the prior dengue infection history of the patient (CDC, 2007a).

Winged female *Aedes aegypti* in search of human blood or places for oviposition are the main reason for local population dispersal and the slow advance of a mosquito infestation. On the other hand, wind currents may also result in an advection movement of large masses of mosquitoes and consequently cause a quick advance of infestation. The study (Takahashi et al., 2005) we describe here focuses on an urban scale of space, wherein a (local) diffusion process due to autonomous and random

search movements of winged *Aedes aegypti* is coupled to constant advection which may be interpreted as the result of wind transportation.

Takahashi et al. (2005) considered only two sub-populations: the winged form (mature female mosquitoes) and an aquatic population (including eggs, larvae and pupae), with mortality rates  $\mu_1$  and  $\mu_2$ . The spatial density of the winged *A. aegypti* and aquatic population at point  $x$  and time  $t$  are denoted by  $M(x, t)$  and  $A(x, t)$ , respectively. The specific maturation rate of the aquatic form into winged female mosquitoes is  $\gamma$ , which is saturated by a term describing a carrying capacity  $K_1$ ; that is,  $\gamma A(1 - M/K_1)$ . Similarly, the rate of oviposition by female mosquitoes, which is the only source of the aquatic form, is proportional to their density but is also regulated by a carrying capacity effect dependent on the occupation of the available breeders; that is,  $rM(1 - A/K_2)$ . Since the focus is on the *A. aegypti* dispersal as a result of a random (and local) flying movement, macroscopically represented by a diffusion process with coefficient  $D$ , coupled to a wind advection caused by a constant velocity flux  $\nu$ , we obtain naturally the coupled system of reaction-diffusion equations

$$\begin{aligned}\frac{\partial M}{\partial t} &= D \frac{\partial^2 M}{\partial x^2} - \frac{\partial(\nu M)}{\partial x} + \gamma A \left(1 - \frac{M}{K_1}\right) - \mu_1 M, \\ \frac{\partial A}{\partial t} &= rM \left(1 - \frac{A}{K_2}\right) - (\mu_2 + \gamma)A.\end{aligned}\tag{15.2}$$

Traveling wave solutions representing an invasion process (linking two stationary and spatially homogeneous solutions) were formally investigated under the assumption that the invasion speeds obtained for the two sub-populations are equal. This assumption was justified by the following biological argument: Suppose that there are distinct subpopulations linked with the wave speed for the winged population larger than that for the aquatic population. If we wait long enough there will be some distant interval where the (faster) mosquito population will reach values close to the saturation level with practically no aquatic population for as long as we want. That would contradict the vital dynamics, since in that interval a large population of mosquitoes would lay eggs at an enormous rate because (almost) no saturation effect exists without a sizable aquatic population. A similar argument works if the wave speed for the winged population is smaller than that for the aquatic population. Consequently, from a practical point of view, we should only expect a time delay between the wavefronts and a constant spatial gap, not an expanding one.

Existence and uniqueness of a positive spatially homogeneous equilibrium is guaranteed if the mortality rate  $\mu_1$  is less than the oviposition rate  $r$  and if the basic reproduction number  $R_0 = \frac{r\gamma}{(\gamma + \mu_2)\mu_1}$  is larger than 1. The traveling wave with the minimal wave speed was shown numerically to have the strong stability and attractivity property, and hence an effective strategy for controlling the *A. aegypti* dispersal based on the above model is to ensure the minimal wave speed is as small as possible. In relation to this containment strategy, a numerical examination of dependence of the wave speed on a few vital model parameters was carried and it was shown that an application of insecticide against the winged (mosquito) phase is much more effective as an infestation containment strategy than insecticide application against its aquatic

phase. This should not be surprising, since the winged form is the one responsible for the *A. aegypti* movement. However, it was also shown that a saturation effect is very apparent and massive insecticide application to increase the mosquito mortality rate beyond a certain value will show very little improvement in wave speed reduction. In addition, it was shown that insecticide application against the aquatic form is not very effective for wave control, but if a chemical attack against the winged form is coupled with the elimination of infested water-holding containers, the results are surprisingly effective.

The study of the wavefront speed dependence on advection, i.e., wind transportation, is interesting from a prediction point of view, and numerical analysis shows that the wavefront speed varies linearly with the advection velocity but not in the same way as in the classical Fisher model. Since the advection only carries the winged form, and the mosquitoes need some time to oviposit, the dependence of the wavefront speed in the model on the advection velocity is not as strong as in Fisher's model. Although advection by natural causes cannot be controlled, the above discussion may be useful for the prediction of patterns of *A. aegypti* invasion in urban areas exposed to strong and constant winds.

Notice that model (15.2) only considers mosquito movement. More realistic models need to include both host and vector populations. Some related models can be found in Favier et al. (2005) and Tran and Raffy (2006).

#### 15.4 West Nile virus

West Nile virus (WNV) was first isolated from a febrile adult woman in the West Nile District of Uganda in 1937. The ecology was characterized in Egypt in the 1950s. The virus became recognized as a cause of severe human meningitis or encephalitis (inflammation of the spinal cord and brain) in elderly patients during an outbreak in Israel in 1957. Equine disease was first noted in Egypt and France in the early 1960s. WNV first appeared in North America in 1999, with encephalitis reported in humans and horses. The subsequent spread in North America is an important milestone in the evolving history of this virus (CDC, 2007b).

West Nile virus belongs to a family of viruses called Flaviviridae. It is spread by mosquitoes that have fed on the blood of infected birds. West Nile virus is closely related to the viruses that cause Dengue fever, Yellow fever, and St. Louis encephalitis. People, horses, and most other mammals are not known to develop infectious-level viremias very often, and thus are probably "dead-end" or incidental-hosts (CDC, 2007b; PHAC, 2007).

Lewis et al. (2006) investigated the spread of WNV by spatially extending the non-spatial dynamical model of Wonham et al. (2004) to include diffusive movements of birds and mosquitoes, resulting in a system of 7 reaction-diffusion equations. A



reduced 2-equation model takes the form

$$\begin{aligned}\frac{\partial I_V}{\partial t} &= \epsilon \frac{\partial^2 I_V}{\partial x^2} + \alpha_V \beta_R \frac{I_R}{N_R} (A_V - I_V) - d_V I_V, \\ \frac{\partial I_R}{\partial t} &= D \frac{\partial^2 I_R}{\partial x^2} + \alpha_R \beta_R \frac{N_R - I_R}{N_R} I_V - \gamma_R I_R,\end{aligned}\tag{15.3}$$

where  $d_V$  is the adult female mosquito death rate,  $\gamma_R$  is the bird recovery rate from WNV,  $\beta_R$  is the biting rate of mosquitoes on birds,  $\alpha_V$  and  $\alpha_R$  are the WNV transmission probability per bite to mosquitoes and birds, respectively,  $\epsilon$  and  $D$  are the diffusion coefficients for mosquitoes and birds, respectively,  $I_V(x, t)$  and  $I_R(x, t)$  are the numbers of infectious (infective) female mosquitos and birds at time  $t$  and spatial location  $x \in R$ ,  $N_R$  is the number of live birds, and  $A_V$  is the number of adult mosquitoes.

Phase-plane analysis of the spatially homogeneous system shows that a positive (endemic) equilibrium  $(I_V^*, I_R^*)$  exists if and only if the basic reproduction number  $R_0$  is larger than 1, where

$$R_0 = \sqrt{\frac{\alpha_V \alpha_R \beta_R^2 A_V}{d_V \gamma_R N_R}}.$$

Moreover, this endemic equilibrium, if it exists, is globally asymptotically stable in the positive quadrant.

For the spatially varying model, the vector field is cooperative, therefore an application of the general result in (Li et al., 2005) ensures that there exists a minimal speed of traveling fronts  $c_0$  such that for every  $c \geq c_0$ , the system has a non-increasing traveling wave solution  $(I_V(x - ct), I_R(x - ct))$  with speed  $c$ , linking  $(I_V^*, I_R^*)$  to  $(0, 0)$ . The cooperative nature of the vector field ensures that the minimal wave speed  $c_0$  coincides with the spread rate in the sense that if the initial values of  $(I_V(\cdot, 0), I_R(\cdot, 0))$ ,  $I_V(\cdot, 0) + I_R(\cdot, 0) > 0$ , have compact support and are not identical to either equilibrium, then for small  $\epsilon > 0$ ,

$$\begin{aligned}\lim_{t \rightarrow \infty} \left\{ \sup_{|x| \geq (c_0 + \epsilon)t} \|(I_V(x, t), I_R(x, t))\| \right\} &= 0, \\ \lim_{t \rightarrow \infty} \left\{ \sup_{|x| \leq (c_0 - \epsilon)t} \|(I_V(x, t), I_R(x, t)) - (I_V^*, I_R^*)\| \right\} &= 0.\end{aligned}$$

In addition, this  $c_0$  is linearly determined and thus could be explicitly calculated from model parameters. In particular, using real data estimated from Wonham et al. (2004) on the original 7-dimensional system, it was shown that a diffusion coefficient of about 5.94 is needed in the model to achieve the observed spread rate of about 1000km/year in North America.

The work in Liu et al. (2006), using a patchy model based on the framework of Bowman et al. (2004), seems to indicate the spread speed may be different if the movement of birds has a preference direction.

One important biological aspect of the hosts in many epidemiological models, namely the stage structure, seems to have received little attention, although structured population models have been intensively studied in the context of population dynamics and spatial ecology, and the interaction of stage-structure with spatial dispersal has

drawn considerable attention in association with the theoretical development of the so-called reaction-diffusion equations with nonlocal delayed feedback (see the survey of Gourley and Wu (2006) and the references therein). The developmental stages of hosts have a profound impact on the transmission dynamics of vector borne diseases. In the case of West Nile virus the transmission cycle involves both mosquitoes and birds, the crow species being particularly important. Nestling crows are crows that have hatched but are helpless and stay in the nest, receiving more-or-less continuous care from the mother for up to two weeks and less continuous care thereafter. Fledgling crows are old enough to have left the nest (they leave it after about five weeks), but they still cannot fly very well. After three or four months these fledglings will be old enough to obtain all of their food by themselves. Consequently, adult birds, fledglings, and nestlings are all very different from a biological and an epidemiological perspective, and a realistic model needs to take these different stages into account. For example, in comparison with grown birds, the nestlings and fledglings have much higher disease induced death rate, much poorer ability to avoid being bitten by mosquitoes, and much less spatial mobility.

Gourley et al. (2007) derived a structured population model in terms of a system of delay differential equations describing the interaction of five subpopulations, namely susceptible and infected adult and juvenile reservoirs and infected adult vectors, for a vector borne disease with particular reference to West Nile virus. Spatial movement was then incorporated into this model to yield an analogue reaction-diffusion system with nonlocal delayed terms. This permits a consideration of some specific conditions for the disease eradication and sharp conditions for the local stability of the disease-free equilibrium, as well as a formal calculation of the minimal wave speed for the traveling waves and subsequent comparison with field observation data.

### 15.5 Hantavirus

Hantaviruses are rodent-borne zoonotic agents that result in hemorrhagic fever with renal syndrome or hantavirus pulmonary syndrome. Hemorrhagic fever with renal syndrome was first reported in 1951 when an outbreak occurred among military personnel involved in the Korean War (Lee and van der Groen, 1989) and now has been identified in Asia and Europe (Shi, 2007). In 1993, hantavirus pulmonary syndrome was identified from an outbreak in New Mexico, USA (Schmaljohn and Hjelle, 1997). Since then, it has been discovered in various regions of southwestern US and in other countries in the Americas. Each hantavirus is generally associated with a primary rodent host. Human infection occurs primarily through the inhalation of aerosolized saliva and excreta of infected rodents. The case fatality rate for hantavirus pulmonary syndrome in the United States is 37% (CDC, 2002a). Hantaviruses pathogenic to humans in the United States include Sin Nombre virus hosted by the deer mouse (*Peromyscus maniculatus*) (Mills et al., 1999), New York virus hosted by the white-footed mouse (*Peromyscus leucopus*) (Song et al., 1994), Black Creek Canal virus hosted by the cotton rat (*Sigmodon hispidus*) (Glass et al., 1998), and Bayou virus hosted by the rice rat (*Oryzomys palustris*) (McIntyre et al., 2005).

In the last few years, several mathematical models have been used to investigate the temporal and spatial dynamics of various hantavirus reservoir species and their relation to the human population. Allen et al. (2003) proposed ordinary differential equation models to study hantavirus infection (Black Creek Canal virus) and arenavirus infection (Tamiami virus) in cotton rats. The two viruses differ in their modes of infection; the first virus is horizontally transmitted, whereas the second is primarily vertically transmitted. Sauvage et al. (2003) considered Puumala virus infection in bank voles (*Clethrionomys glareolus*). Their model is a system of ordinary differential equations for rodents infected with hantavirus in two different habitats: optimal and suboptimal. The population is subdivided into susceptible and infected juveniles and adults. Allen et al. (2006) developed two new mathematical models for hantavirus infection in male and female rodents. The first model is a system of ordinary differential equations while the second model is a system of stochastic differential equations.

Taking the random movement of the rodent population into account, Abramson and Kenkre (2002) and Abramson et al. (2003) used partial differential equation models to study Sin Nombre virus in deer mice. Suppose that the whole mice population is composed of two classes, susceptible and infected, represented by  $M_S$  and  $M_I$ , respectively, with  $M_S + M_I = M$ . Since the virus does not affect properties such as the mortality of the mice, the death rate is assumed to be the same for both susceptible and infected mice. It is also not transmitted to newborns, so that no mice are born in the infected state. The infection is transmitted from mouse to mouse through individual contacts, such as fights. The dispersal of mice is modeled as a diffusion process. Finally, intra-species competition for resources indicates a logistic population growth. The model is described by the following equations:

$$\begin{aligned}\frac{\partial M_S}{\partial t} &= D \frac{\partial^2 M_S}{\partial x^2} + bM - cM_S - \frac{M_S M}{K} - aM_S M_I, \\ \frac{\partial M_I}{\partial t} &= D \frac{\partial^2 M_I}{\partial x^2} - cM_I - \frac{M_I M}{K} + aM_S M_I.\end{aligned}\quad (15.4)$$

All parameters characterizing the different processes affecting the mice are supposed constant, except the carrying capacity  $K$  of the mouse population, which we will sometimes write  $K = K(x, t)$  explicitly to indicate the dependence on the location and time which allows for diversity in habitats and temporal phenomena. The birth rate  $b$  characterizes a source of susceptible mice only. The death rate, common to both subpopulations, is  $c$ . The contagion rate is the parameter  $a$ . Finally, a diffusion coefficient  $D$  characterizes a diffusive transport mechanism for the mice.

The sum of the two equations in (15.4) reduces to a Fisher type equation for the whole population

$$\frac{\partial M}{\partial t} = D \frac{\partial^2 M}{\partial x^2} + (b - c)M \left[ 1 - \frac{M}{(b - c)K} \right]. \quad (15.5)$$

Abramson and Kenkre (2002) showed that, as a function of  $K$ , the system undergoes a bifurcation between a stable state with only susceptible mice (and  $M_I = 0$ ) to a stable state with both subpopulations positive. The value of the critical carry-

ing capacity is a function of other parameters and is given by  $K_c = \frac{b}{a(b-c)}$ . This critical value does not depend on  $D$ , and the same bifurcation is observed either in a spatially independent system ( $D = 0$ ) or in a homogeneous extended one in the presence of diffusion. In a nonhomogeneous situation, for moderate values of the diffusion coefficient, the infected subpopulation remains restricted to those places where  $K(x, t) > K_c$ , becoming extinct in the rest.

Yates et al. (2002) found that the outbreaks of hantavirus pulmonary syndrome in southwest US in 1993 and again in 1998-2000 were associated with the El Niño-southern oscillation phenomenon, which produced increased amounts of fall-spring precipitation in the arid and semi-arid regions of New Mexico and Arizona and in turn initiated greater production of rodent food resources. Consequently, rodent population increased dramatically, and at high densities, rodents began dispersing across the landscape and coming into contact with humans in homes and businesses. This suggests that a 'wave' of virus infection was following the 'wave' of rodent dispersal.

Let  $z_1 = x - v_S t$  and  $z_2 = x - v_I t$ , where  $v_S$  and  $v_I$  are the speeds of the susceptible and infected waves, respectively. The wave form equations are

$$\begin{aligned} D \frac{d^2 M_S}{dz_1^2} + v_S \frac{dM_S}{dz_1} + bM - cM_S - \frac{M_S M}{K} - aM_S M_I &= 0, \\ D \frac{d^2 M_I}{dz_2^2} + v_I \frac{dM_I}{dz_2} - cM_I - \frac{M_I M}{K} + aM_S M_I &= 0. \end{aligned} \quad (15.6)$$

There are two interesting scenarios.

(i) Initially the system is at a state of low carrying capacity (below  $K_c$ ) and the population consists of uninfected mice only at the stable equilibrium. When the environment changes so that  $K > K_c$ , the population will be out of equilibrium: the susceptible mice population will evolve towards a new equilibrium and a wave of infected mice will invade the susceptible population. Analysis at the unstable equilibrium  $(K(b-c), 0)$  implies that traveling wave speed satisfies  $v \geq 2\sqrt{D[-b + aK(b-c)]}$ .

(ii) Initially the system is empty of mice. Consider a system with  $K > K_c$  and with  $M_S = M_I = 0$  in almost all of its range, but with a small region where  $M_S > 0$  and  $M_I > 0$ . A wave of both mouse populations will develop and invade the empty region. The wave speed of the susceptible is  $v_S \geq 2\sqrt{D(b-c)}$  and the wave speed of the infected  $v_I \geq 2\sqrt{D[-b + aK(b-c)]}$ .

The density of susceptible mice rises from zero and lingers near the positive unstable equilibrium before tending to the stable one.

Barbera et al. (2008) generalized the Abramson-Kenkre reaction-diffusion model to a hyperbolic reaction-diffusion model for the hantavirus infection in mouse populations and investigated traveling wave solutions related to the spread of the infection in the landscape. For further studies on modeling spatial spread of hantavirus, we refer to Giuhhioli et al. (2005), Kenkre et al. (2007), and the references cited therein.

### 15.6 Lyme disease

In 1975, a group of children in the Lyme, Connecticut, area were originally diagnosed as having juvenile rheumatoid arthritis (Steere et al., 1977). Subsequently it became apparent that this occurrence was actually a delayed manifestation of a tick-transmitted multisystem disease for which some manifestations had been reported previously in Europe (Steere et al., 2004). In 1976, the disease was recognized as a separate entity and named Lyme disease (Steere, 1989). In 1981 the spirochetal bacterium *Borrelia burgdorferi* from the deer tick *Ixodes scapularis* was identified (Burgdorfer et al., 1982) and cultured from patients with early Lyme disease (Steere et al., 1983). Lyme disease is now the most commonly reported tick-borne illness in the US, Europe, and Asia (Dannis et al., 2002; CDC, 2002b; Zhang et al., 1998).

New cases of Lyme disease appear at unabated rates in endemic regions, the geographic distribution of the incidence of Lyme disease has expanded rapidly, and the spread of the disease involves direct interactions among no fewer than four species (Ostfeld et al., 1995). The hematophagous vector is the deer tick *Ixodes scapularis*. Larval and nymphal ticks feed primarily on the white-footed mouse *Peromyscus leucopus* but will attack a variety of hosts; inadvertent nymph bites can infect humans with the spirochete. Adult ticks feed preferentially on white-tailed deer *Odocoileus virginianus*.

Caraco et al. (1998) proposed an ODE model focusing on these four species and let infection in humans follow as a consequence of the community's population dynamics. According to Caraco et al. (1998), *Ixodes scapularis* exhibits a two-year life cycle. 89% of newly hatched larvae attack white-footed mice. Larvae that obtain a blood meal drop off their host and then overwinter as nymphs. At the beginning of the second year, nymphs quest for a blood meal (the second of the life cycle). If they succeed, the nymphs mature to the adult stage. Adult females feed almost exclusively on white-tailed deer and mate there. Females eventually drop off the deer they have parasitized, lay about 2000 fertile eggs nearby, and die. It is estimated that 20 – 33% of nymphs in infected areas (ticks that have previously taken a single blood meal) are infected, and that 50% of questing adults (those that have already taken two blood meals) are infected with the spirochete. Interestingly, it is the tick to mouse to tick enzootic cycle of infection that maintains the spirochete. Seasonality helps drive the cycle. Nymphs infected last year appear first as warmer weather begins; these ticks pass the spirochete to susceptible mice. After summer has arrived larvae hatch, quest for a blood meal, and acquire the spirochete when they attack an infected mouse. These individuals then become quiescent as infected nymphs, completing the cycle of infection.

Since deer move fecund adult ticks, their dispersal influences the spatial pattern of tick larvae. But deer cannot be infected and do not disperse the pathogen. Furthermore, *Borrelia* cannot survive outside of its hosts. Mice usually disperse juvenile ticks, and dispersal of infectious mice can introduce the spirochete into tick populations. So the spatial advance of infection must be driven by dispersal of mice and other hosts to juvenile ticks (Van Buskirk and Ostfeld, 1998). Caraco et al. (2002)

modeled the advance of the natural infection cycle as a reaction-diffusion process. The model may help identify factors influencing the rate at which the disease spreads and predict the velocity at which spirochete infection advances spatially.

The model treats population densities at locations  $(x, y)$  in a two-dimensional domain  $\Omega$ . Parameters for birth, death, infection, and developmental advance do not depend on spatial location. Diffusion approximates dispersal via random motion. It is assumed that the dynamics and dispersal of mice are independent of infestation/infection status. To limit the number of variables, dispersal of nymphs is ignored. At equilibrium population densities, nymph dispersal does not affect the spread of Lyme disease. Dispersal of larvae is important; spatial dispersion of replete larvae governs the pattern in the risk of Lyme disease when these animals quest as nymphs. Therefore, dispersal of larvae while they feed on mice is considered. Adult ticks reproduce and disperse diffusively; dispersal of adults mimics movements of deer while ticks mate (deer are not modeled explicitly). Natality and mortality among black-legged ticks are apparently independent of *Borrelia* infection (Van Buskirk and Ostfeld, 1998). The model requires six state variables for the reaction-diffusion dynamics; among them, three subsidiary variables are required to model the tick's population structure.

Mice reproduce in a density-dependent manner and incur density-independent mortality. Since mice are born uninfected, the equation for susceptible-mouse density  $M(x, y, t)$  includes birth, death, acquisition of the spirochete from infectious-nymph bites, and dispersal:

$$\frac{\partial M}{\partial t} = D_M \left( \frac{\partial^2 M}{\partial x^2} + \frac{\partial^2 M}{\partial y^2} \right) + r_M (M + m) \left( 1 - \frac{M + m}{K_M} \right) - \mu_M M - \alpha \beta M n, \quad (15.7)$$

where  $D_M$  is the diffusion coefficient for mice with unit (distance)<sup>2</sup>/time;  $r_M$  is the intrinsic birthrate;  $K_M$  is the spatially homogeneous carrying capacity;  $\mu_M$  is the individual mortality rate among mice;  $\alpha$  is the attack rate of juvenile ticks questing for mice;  $\beta$  ( $0 < \beta < 1$ ) is a mouse's susceptibility to pathogen infection when bitten by an infectious nymph.

The density of pathogen-infected mice  $m(x, y, t)$  increases as susceptible mice are bitten by infectious nymphs and decreases through mortality. The equation for infected mice includes infection, death, and dispersal:

$$\frac{\partial m}{\partial t} = D_M \left( \frac{\partial^2 m}{\partial x^2} + \frac{\partial^2 m}{\partial y^2} \right) - \mu_M m + \alpha \beta M n. \quad (15.8)$$

The subsidiary variable  $L(A, a)$  is the density of questing larvae which declines through mortality and attacks on mice, where  $A(x, y, t)$  and  $a(x, y, t)$  are density of uninfected adult ticks and pathogen-infected adult ticks, respectively. It is assumed that larval hatching rate depends nonlinearly on adult tick density. Then, at each point  $(x, y)$  :

$$\frac{dL}{dt} = r(A + a)[1 - c(A + a)] - \mu_L L - \alpha L(M + m), \quad (15.9)$$

where  $r$  is the tick's per capita reproduction at low density;  $\mu_L$  is the mortality rate among questing larvae; and  $c$  represents crowding among reproducing ticks. Larvae must hatch at a positive rate when  $(A+a) > 0$ , so  $c$  is small. Essentially,  $c$  is inversely proportional to deer density, which is assumed a constant and treated implicitly.

The density of larvae infesting susceptible mice  $V(x, y, t)$  varies in successful attack, completion of the first blood meal, death, and dispersal while they infest mice:

$$\frac{\partial V}{\partial t} = D_M \left( \frac{\partial^2 V}{\partial x^2} + \frac{\partial^2 V}{\partial y^2} \right) - (\sigma + \mu_V)V + \alpha ML, \quad (15.10)$$

where  $\sigma$  is the rate at which larvae infesting mice complete their meal, and  $\mu_V$  is the mortality rate among larvae infesting mice. Since the duration of a larval meal seldom exceeds a few days,  $\sigma > \mu_V$ . The assumptions concerning the density of larvae infesting pathogen-infected mice,  $v(x, y, t)$ , are similar. We substitute the density of infectious mice ( $m$ ) for susceptible-mouse density ( $M$ ) and obtain  $\partial v / \partial t$ .

The subsidiary variable  $N(V, v)$  is the density of susceptible questing nymphs at  $(x, y, t)$ , which increases as larvae complete their first meal without acquiring the spirochete. The larvae may have infested a susceptible mouse or attacked an infectious mouse and avoided infection. As they die, bite humans, and attack mice,  $N(V, v)$  decreases. Combining processes yields

$$\frac{dN}{dt} = \sigma[V + (1 - \beta_T)v] - N[\gamma + \alpha(M + m) + \mu_N], \quad (15.11)$$

where  $\beta_T$  ( $0 < \beta_T < 1$ ) is a tick's susceptibility to infection when feeding on an infected mouse. The mortality rate among questing nymphs is  $\mu_N$ , and  $\gamma$  is the rate at which nymphs bite humans.

The subsidiary variable  $n(v)$  is the density of questing infectious nymphs at  $(x, y, t)$ . Infectious nymphs must have attacked a mouse infected with *Borrelia* as larvae and then acquired the pathogen. Their density at any location  $(x, y)$  varies as

$$\frac{dn}{dt} = \beta_T \sigma v - n[\gamma + \alpha(M + m) + \mu_N], \quad (15.12)$$

where the term  $\gamma n$  represents the local risk of Lyme disease to humans.

The density of uninfected adult ticks  $A(x, y, t)$  changes through attacks of those nymphs on mice, death of adults, and dispersal:

$$\frac{\partial A}{\partial t} = D_H \left( \frac{\partial^2 A}{\partial x^2} + \frac{\partial^2 A}{\partial y^2} \right) - \mu_A A + \alpha N[M + (1 - \beta_T)m], \quad (15.13)$$

where  $\mu_A$  is the density-independent mortality rate among adult ticks. The diffusion coefficient  $D_H$  models dispersal of adult ticks while they infest deer.

The density of pathogen-infected adult ticks  $a(x, y, t)$  increases as infected nymphs attack any mouse and as susceptible nymphs attack infected mice and acquire *Borrelia* during their second blood meal. Adding death and dispersal yields

$$\frac{\partial a}{\partial t} = D_H \left( \frac{\partial^2 a}{\partial x^2} + \frac{\partial^2 a}{\partial y^2} \right) - \mu_A a + \alpha[(M + m)n + \beta_T m N]. \quad (15.14)$$

To analyze this model, Caraco et al. (2002) first identified three aspatial equilibria: extinction of the system, positive abundance of ticks and mice in the absence of spirochete, and proportional infection of both mice and ticks. Then they studied how adult tick mortality and juvenile attack rate influence the velocity at which infection spreads in the diffusion model. Their results indicate that as vector mortality rates vary, the disease spread velocity is roughly proportional to the density of infectious vectors, and thus proportional to the local risk of zoonotic infection. However, as the rate at which juvenile ticks attack hosts varies, the spread velocity of infection may increase or decrease. In both cases, the disease spread velocity remains proportional to the frequency of infection among hosts.

### 15.7 Feline immunodeficiency virus (FIV)

In 1987, the isolation of a T-lymphotropic virus possessing the characteristics of a lentivirus from pet cats in Davis, California was reported (Pedersen et al., 1987). The virus is a member of the family of retroviruses and causes an acquired immunodeficiency syndrome in cats. It shares many physical and biochemical properties with human immunodeficiency virus (HIV) and was therefore named feline immunodeficiency virus (FIV). Today FIV has been detected worldwide. The prevalences vary, ranging from 2% in Germany and 16% in the United States to 33% in the United Kingdom and 44% in Japan (Hartmann, 1998).

FIV can be isolated from blood, serum, plasma, cerebrospinal fluid, and saliva of infected cats. The infection is much more common in males than females since the transmission mode is through bites inflicted during fights and biting is more apt to occur between male cats (Yamamoto et al., 1989). Veneral transmission from infected males to females is possible. In experimental studies, infection has been shown to occur not only via a vaginal route, but also via rectal mucous membrane (Moench et al., 1993).

Though there is no evidence that FIV can spread to humans, it is important to study its epidemiology for a variety of reasons. Its spread mimics the spread of HIV within the human population and it is possible that subsequent mutations of FIV could produce a virus capable of infecting humans. Courchamp et al. (1995) constructed a deterministic model to study the circulation of FIV within populations of domestic cats. Since all sexually transmitted diseases can be transferred from males to males, from females to females, and from males to females and vice versa, Fitzgibbon et al. (1995) proposed a criss-cross infection model to describe the spread of FIV. Their model uses Fickian diffusion to account for the geographic spread of the disease and introduces age of the disease within an individual as a structural variable.

Divide the feline population sexually into male and female classes. Each of these classes is in turn subdivided into susceptible and infective subclasses. Consider four state variables  $u, w, v, z$  representing population densities of susceptible males, infective males, susceptible females, and infective females, respectively. Assume that the infection spreads from infective males to susceptible males and females and from



infective females to susceptible males and females, with different infection rates. Let  $\Omega \subset R^n (1 \leq n \leq 3)$  be a bounded region which lies locally on one side of its boundary  $\partial\Omega$ , which is sufficiently smooth. The criss-cross epidemic model without age structure is, for  $x \in \Omega, t > 0$  :

$$\begin{aligned} \frac{\partial u}{\partial t} &= d_1 \Delta u - k_1 u w - k_2 u z, \\ \frac{\partial w}{\partial t} &= d_2 \Delta w + k_1 u w + k_2 u z - \lambda_1 w, \\ \frac{\partial v}{\partial t} &= d_3 \Delta v - k_3 v w - k_4 v z, \\ \frac{\partial z}{\partial t} &= d_4 \Delta z + k_3 v w + k_4 v z - \lambda_2 z \end{aligned} \tag{15.15}$$

with Neumann boundary conditions

$$\frac{\partial u}{\partial n} = \frac{\partial w}{\partial n} = \frac{\partial v}{\partial n} = \frac{\partial z}{\partial n} = 0, \quad x \in \partial\Omega, \quad t > 0 \tag{15.16}$$

and initial conditions

$$\begin{aligned} u(x, 0) = u_0(x) \geq 0, \quad v(x, 0) = v_0(x) \geq 0, \\ w(x, 0) = w_0(x) \geq 0, \quad z(x, 0) = z_0(x) \geq 0, \quad x \in \Omega, \end{aligned} \tag{15.17}$$

where  $k_i (i = 1, \dots, 4)$  are the infection rates of the four subclasses;  $\lambda_1$  and  $\lambda_2$  are the removal rate of the infective males and females, respectively;  $d_i (i = 1, \dots, 4)$  are the diffusion rates of the four subclasses. All parameters are positive constants. The Neumann boundary conditions imply that all populations remain confined to the region  $\Omega$  for all time.

The analysis of Fitzgibbon et al. (1995) indicates that the infective population is always ultimately extinguished. Thus, the model applies to a short term development of FIV, which extinguishes because of a lack of new susceptibles. From their ODE model, Courchamp et al. (1995) claim that FIV is endemic in domestic feline populations. The reason is that the model of Courchamp et al. incorporates a logistic growth nonlinearity for the total population, whilst the the model of Fitzgibbon et al. does not include demographic population dynamics of the feline population.

Hilker et al. (2007) extended the model of Courchamp et al. (1995) to the reaction-diffusion system version. Let  $S(x, t)$  and  $I(x, t)$  denote the densities of susceptible and infectious cats in the location  $x \in \Omega$  (in km) and at time  $t > 0$  (in years), so that  $P(x, t) = S + I$  is the density of the cat population (in number of individuals per km<sup>2</sup>). The model takes the form

$$\begin{aligned} \frac{\partial S}{\partial t} &= D_S \Delta S - \sigma \frac{SI}{P} + \beta(P)P - \mu(P)S, \\ \frac{\partial I}{\partial t} &= D_I \Delta I + \sigma \frac{SI}{P} - \mu(P)I - \alpha I, \end{aligned} \tag{15.18}$$

where  $D_S$  and  $D_I$  (km<sup>2</sup> per year) are the diffusion rates of the susceptibles and infectives, respectively;  $\sigma$  is the transmission coefficient; and  $\alpha$  is the disease related death rate. The fertility function  $\beta(P) \geq 0$  and the mortality function  $\mu(P) \geq 0$  are assumed to be density-dependent; the intrinsic per-capita growth rate is  $g(P) =$

$\beta(P) - \mu(P)$ . If  $\beta(P) = b > 0$ ,  $\mu(P) = m + rP/K$ ,  $r = b - m$ ,  $m > 0$ , one obtains the well-known logistic per-capita growth rate  $g(P) = r(1 - P/K)$ . If

$$\beta(P) = \begin{cases} a[-P^2 + (K_+ + K_- + e)P + c], & 0 \leq P \leq K_+ + K_- \\ \text{nonnegative and nonincreasing,} & \text{otherwise} \end{cases}$$

and  $\mu(P) = a(eP + K_+K_- + c)$ , then the per-capita growth rate

$$g(P) = a(K_+ - P)(P - K_-)$$

describes the strong Allee effect in the vital dynamics. This type of function can be used to model the fact that cat is a very opportunistic predator and is one of the worst invasive species threatening many indigenous species.

For the model with logistic growth, numerical simulation indicates that a traveling infection wave emerges and advances with a constant speed. In its wake, the population settles down to the endemic state. In the model with Allee effect, the emergence and propagation of a traveling wave can be observed as well. However, if the transmission coefficient is further increased so that the nontrivial state disappears, two different scenarios are possible: (a) front reversal with eventual host extinction (see Fig. 2c, Hilker et al. 2007) and (b) a transient (and spatially restricted) epidemic before disease-induced extinction (see Fig. 10, Hilker et al. 2007). In both cases, the propagation of traveling pulse-like epidemics will wipe out the host population.

Recently, the spatial spread of some infectious diseases, including FIV and FeLV (Feline Leukemia Virus), among animal populations distributed on heterogeneous habitats has been extensively studied. We refer to Fitzgibbon et al. (2001), Fitzgibbon and Langlais (2008), Malchow et al. (2008), and the references cited therein.

## 15.8 Summary

We have summarized a few models developed for specific diseases which involve animal hosts and have significant implication to human health: rabies, dengue, West Nile virus, hantavirus, Lyme disease, and feline immunodeficiency virus. A common feature of these diseases is the involvement of a certain animal carrier and at least a subgroup of individuals in the animal population that may move more or less randomly in space. This feature leads naturally to the addition of diffusion and perhaps advection terms to classical compartmental models.

Most studies introduced here started with the assumption that the disease is capable of invading the susceptible population in a spatially homogeneous environment, and these studies then considered the issue of spatial spread patterns and disease propagation speeds under various conditions of spatial movement of the host population. A particular object is the existence of traveling wave fronts and the minimal wave speed of such fronts that is believed to coincide with the disease spread speed.

Spatial diffusion may interact with structural heterogeneity, for example, maturation status of the host population. How this interaction leads to particular spatio-temporal

patterns of disease spread and the implication for the design of containment strategies was a key issue of some of the studies discussed here. Further work in this area is discussed in two other recent review articles (Ruan, 2007; Gourley et al., 2008).

Diseases involving multiple species or higher dimensional space may also permit different propagation speeds for different species and dimensions, and pose great mathematical challenges for analysis. Furthermore, parameterizing spatial models from epidemiological or biological data (Noble, 1974; Murray et al., 1986) is difficult but crucial in studying the spatial spread of diseases.

So, despite the substantial recent progress in the study of spatial spread of diseases using reaction-diffusions equations, the implications of spatial structure in epidemiological models are still far from clear, and the statement in Murray (2003) remains: “the geographic spread of epidemics is less well understood and much less well studied than the temporal development and control of diseases and epidemics.”

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