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A MODEL OF THE ENZOOTIOLOGY OF LYME DISEASE IN THE ATLANTIC NORTHEAST OF THE UNITED STATES

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ABSTRACT. A mathematical model is presented for the dynamics of the rate of infection of the Lyme disease vector tick *Ixodes dammini* (Acari: Ixodidae) by the spirochete *Borrelia burgdorferi*, in the Atlantic Northeast of the United States. According to this model, moderate reductions in the abundance of white-tailed deer *Odocoileus virginianus* may either decrease or increase the spirochete infection rate in ticks, provided the deer are not reservoir hosts for Lyme disease. Expressions for the basic reproductive rate of the disease are computed analytically for special cases, and it is shown that as the basic reproductive rate increases, a proportional reduction in the tick population produces a smaller proportional reduction in the infection rate, so that vector control is less effective far above the threshold. The model also shows that control of the mouse reservoir hosts *Peromyscus leucopus* could reduce the infection rate if the survivorship of juvenile stages of ticks were reduced as a consequence. If the survivorship of juvenile stages does not decline as the rodent population is reduced, then rodent reduction can increase the spirochete infection rate in the ticks.

1. Introduction. Lyme disease has become the most frequently diagnosed vector-borne disease in the United States, accounting for roughly half of the diagnoses of vector-borne disease in 1983-87 (Anonymous [1989]). Lyme disease is due to infection by the spirochete *Borrelia burgdorferi* (Burgdorfer et al. [1982], Steere et al. [1983], Johnson et al. [1984]). Recently, the enzootiology of Lyme disease has been extensively reviewed (Spielman [1988]; Lane, Piesman, and Burgdorfer [1991]). The Lyme disease spirochete primarily occurs in wild animals and in the hard ticks of the genus *Ixodes* which parasitize them. Man becomes infected when he enters or resides in an area where transmission is occurring naturally and is bitten by infected ticks. To help understand the factors which lead to the spread and persistence of the

disease, I develop in this paper a simplified stage-structured transmission model of the dynamics of the spirochete infection rate of *Ixodes dammini* in the Atlantic Northeast of the United States.

2. Lyme disease enzootiology. The deer tick *Ixodes dammini* (Spielman, Clifford, Piesman and Corwin) is the main vector of Lyme disease in the northeastern United States. Like other hard ticks, *Ixodes dammini* undergoes a life cycle consisting of egg, larva, nymph, and adult (Figure 1). In the larval, nymph, and adult stages, the ticks seek hosts, attach to them, draw a blood meal, detach to digest this blood meal, and then molt to the next stage. Fully engorged females drop off of the host animal after feeding, and oviposit. *Ixodes dammini* is therefore a three-host tick. *Ixodes dammini* parasitizes many hosts, including mammals and birds (for a summary of host animals, see Anderson [1988]).

Different stages of *Ixodes dammini* are active at different times of the year, and the life cycle normally takes two years to complete. Larval ticks emerge and feed in the late summer, their peak activity being in August-September. Nymphs feed in the late spring and early summer (May-June), and adults have a bimodal feeding pattern, some feeding in late fall (November) and some in early spring (April) (Yuval and Spielman [1990]). Thus there is roughly a three month interval between the questing of nymphs, larvae, and the fall peak of adults (Godsey et al. [1987], Piesman and Spielman [1979], Schulze et al. [1985]).

The seasonal pattern of activity of *Ixodes dammini* is important in the enzootiology of Lyme disease. Because nymphs and larvae parasitize the same host animals, especially the white-footed mouse, *Peromyscus leucopus*, infected nymphs transmit the disease to host mammals which will be fed upon later in the season by larvae of the next generation. Thus, some of these larvae will become infected and maintain the infection transstadially for the next year (Habicht, Beck and Benach [1987], Piesman [1989], Yuval and Spielman [1990]).

The white-footed mouse, *Peromyscus leucopus* Rafinesque, is believed to be the main reservoir host for *B. burgdorferi* (Levine, Wilson and Spielman [1985]; Spielman [1988]; Donahue, Piesman and Spielman [1987]; Spielman et al. [1985]; Piesman and Spielman [1979]). Because of the abundance of this mouse, it is numerically the most important

host for juvenile stages of *Ixodes dammini*, though they feed on other mammals as well (Lane, Piesman and Burgdorfer [1991]; Piesman and Spielman [1979]). Also, according to Spielman [1988], the white-footed mouse displays immunotolerance for repeated feeding by *Ixodes dammini*.

The white-tailed deer is, however, believed to be the principal host for adult *Ixodes dammini* (Anderson [1988]), though some adults feed on medium-sized mammals (Lane, Piesman and Burgdorfer [1991]). It has been suggested that the presence of *O. virginianus* is one of the most important factors in determining the presence or absence of *Ixodes dammini*. The white-tailed deer has been suspected of being a reservoir host for Lyme borreliosis, but this has been challenged (see Lane, Piesman and Burgdorfer [1991]). For the purposes of the model below, it will be assumed that deer are not a reservoir host.

The factors which determine the abundance of *Ixodes dammini* are not well understood. The presence of white-tailed deer is important, as mentioned above, though it is not known how the population of *I. dammini* varies with the number of deer and mice. Also, the functional form of the increase of the death rate of feeding ticks at high concentration of ticks per host (due to increased immune reactions, competition for space, and so forth) is not known. Finally, it is unclear how the presence of the Lyme disease spirochete itself may affect the abundance of ticks. In the model below, it will be assumed that the abundance of ticks is not affected by the presence of the disease.

3. Life history model for the vector ticks. The purpose of my model is to determine how the number of vector ticks influences the spirochete infection rate in the ticks and the hosts. The model is a stage projection model, similar to that of Ginsberg [1988].

Ginsberg [1988] modeled the long-term spread of *B. burgdorferi* in a population of *Ixodes dammini* using a discrete-time model for the spirochete infection rate for each stage in the life cycle. His model looks at the effects of vertical transmission, host infectiousness, host reproductive turnover, and multiplicity of hosts on the endemic spirochete infection rate in a constant tick population.

Many other modeling studies have been undertaken previously for tick populations and tick-borne diseases. A review of the extensive lit-

erature for modeling tick populations is beyond the scope of this paper. One approach was taken by Mount and Haile [1989], who simulated the population of *Dermacentor variabilis* Say using age-structured stage-specific life tables with temperature-dependent development, survival, and fecundity rates. Their model is environmentally driven, and it includes density-dependent tick survival on hosts due to acquired immune resistance to increasing tick infestation. Cooksey, Haile and Mount [1990] modeled the transmission of Rocky Mountain Spotted Fever by *D. variabilis* using such methods. They derived transmission threshold numbers of unfed adult ticks per hectare based on their model.

In my model, a cohort of ticks is followed through its two year life cycle, with nymphs of one generation feeding in the season before larvae of the next generation. The infection rate in the ticks and hosts is projected from one season (i.e., one quarter year) to the next. Nymphs infect hosts in the spring, and these hosts maintain the infection until the larvae feed in the summer and acquire the infection.

Since the peaks of feeding of *Ixodes dammini* stages are roughly three months apart, the progress of the disease will be iterated by three-month time intervals. The structure of the life history model below will contain the feature that only one feeding stage of *I. dammini* will be active at any one time. This is a first approximation which neglects the observed temporal overlap between the feeding times of the different stages. Also, my model neglects the distribution of feeding times of ticks of the same stage, since I assume that all the ticks of a given stage emerge and find their hosts at once. This has the effect of neglecting the amplification of the infection rate within the ticks of a given stage feeding within the same season, which is the result of, say, nymph-to-host-to-nymph infection cycles within the season of feeding. An increase in the infection rate for adults is not important, since they will not feed nor transmit the disease again. For larvae, the initial infection rate is assumed to be zero, since vertical transmission has been neglected (see below). Finally, the amplification of the infection rate within a cohort of nymphs will result in a greater infection rate for feeding adults than otherwise, but this has no epizootic consequences in my model, since the adults are assumed to feed on deer, and deer are assumed to be a nontransmitting host.

I make other simplifying assumptions as well. I ignore the bimodality of the adult feeding times and assume the adults feed in the autumn

(an assumption which does not have a large effect on the disease dynamics, owing to the other assumptions of the model). I also ignore differences in emergence times, maturation delays, and the effects of temperature on tick activity and survivorship, both on a daily and a seasonal time scale. Inclusion of such refinements is only justified once an understanding of the essential dynamics has been obtained.

Let the stages in the life cycle of *Ixodes dammini* be enumerated as follows (Figure 1):

1. egg
2. a larva which has begun to seek a host (host-seeking larva)
3. a larva on a host ("feeding larva")
4. a post-feeding prenymphal larva
5. a nymph which has begun to seek a host
6. a nymph on the host
7. after nymph drops from host and before it seeks host as adult
8. an adult which has begun to seek a host
9. an adult on the host
10. an adult which has dropped off of the host
11. an ovipositing adult.

FIGURE 1.

Though the life cycle could be broken down in other ways, the numbers from 1 to 11 are useful, and are here referred to as the "life-table position." Let N_j be the number of ticks in the population which are at life-table position j at a given time. It is not necessary to include all of the life-table positions in the population vector N_j specifically, as the duration of feeding is small compared with the time scale of the model (one-quarter year), so there is no need to include the number of feeding ticks in N_j. Rather, the number of feeding ticks will be calculated as an intermediate step in determining the number of engorged ticks, or the number of eggs. Let the time be denoted τ, where $\tau = 0, 1, 2, \ldots$ is the time in seasons from the beginning of the model. Thus, we let $N(\tau) = (N_1(\tau), N_2(\tau), N_4(\tau), N_5(\tau), N_7(\tau), N_8(\tau))'$ (where $'$ indicates

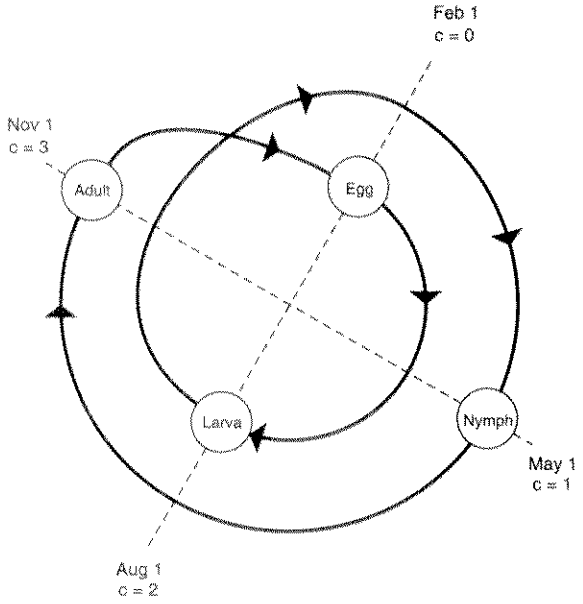

FIGURE 2. Life history of *Ixodes dammini* in relation to the interseasonal projection times $c = 0, 1, 2, 3$ (adapted from Habicht, Beck and Benach [1987]).

the list is a column vector).

Consider the feeding peaks to be on February 1, May 1, August 1, and November 1 (Figure 2). The outer circle represents one year. The feeding of larvae is taken to be concentrated in August. Next, ticks feed as nymphs in May, and then as adults in November of that same year. For "bookkeeping", eggs which will be laid in July are counted as being present in February. Indicate the times of these four feeding peaks by $c = 0, 1, 2, 3$, and the actual year u by $u = 0, 1, 2, \ldots$. Then $\tau = 4u + c$ is the total count of three-month periods from time $\tau = 0$. Specifying u and c is exactly equivalent to knowing τ.

Suppose that the population is censused at the beginning of the spring ($c = 2$), before any ticks in the nymphal stage have begun to search for hosts. The estimated density of the nymphal stage is $N_5(u, 2)$. Only a proportion of these host-seeking nymphs will feed successfully and be replete at $c = 3$. This rate of success will depend on a death rate in the field, contact rates between hosts and ticks, and host abundance. To keep the model simple, the abundance of hosts, and the infection

rate in hosts will be assumed to be constant during a single season's feeding period.

The numbers of ticks in the various stages will be projected from season to season using a projection matrix (Skellam [1967], Getz and Haight [1989]). That is, the model will have the general form

$$\mathbf{N}(\tau + 1) = \mathbf{A}(c)\mathbf{N}(\tau) \tag{1}$$

where the matrices $\mathbf{A}(0)$, $\mathbf{A}(1)$, $\mathbf{A}(2)$, and $\mathbf{A}(3)$ have the forms shown in Appendix A. Because the feeding times and field abundances for the different stages are active at different times of the year, the projection matrix $\mathbf{A}$ varies from season to season. These matrices are constructed in terms of survivorship factors from one stage to the next. Let s_j be the survivorship from stage j to stage $j+1$, or the fraction of the ticks in life-table position j who survive to reach position $j + 1$. Let b be the average number of progeny per adult tick. The survivorship factors s_j depend on the number of hosts, and a form for this dependence is discussed below.

In the model presented below, I only wish to consider the behavior of Lyme disease for equilibrium tick populations, i.e. when the total size of each cohort does not change from year to year. The model can then be used to assess the properties of the enzootic behavior around some equilibrium of a more general nonlinear, density-dependent model which incorporates the dynamics of the ticks themselves. The more general question of what determines the abundance of ticks is not considered here.

The assumption that the population of ticks has reached some equilibrium value implies a constraint on the survivorship and fecundity factors. At equilibrium, each tick in the population on average produces exactly one progeny. Let $\mathbf{N}(u, 0)$ be the number of ticks at the beginning of year u, i.e. for season $c = 0$. Then the criterion that the cohort size does not change from year to year is related to the seasonal projection matrices $\mathbf{A}(c)$; using the seasonal projection matrices to project the abundances of ticks from year to year results in the relationships

$$\begin{aligned} N_1(u + 1, 0) &= b s_{10} s_9 s_8 s_7 s_6 s_5 s_4 N_3(u, 0) \\ N_3(u + 1, 0) &= s_3 s_2 s_1 N_1(u, 0). \end{aligned}$$

Therefore, at equilibrium,

$$b\prod_{j=1}^{10} s_j = 1 \tag{2}$$

One consequence of the simplified view of the life cycle presented above is that the two cohorts in any given year are being treated as though they were demographically independent from each other. For the two independent cohorts to be the same size, assume

$$\mathbf{N}_3(0,0) = s_3 s_2 s_1 \mathbf{N}_1(0,0). \tag{3}$$

When equations (2) and (3) hold, the number of tick eggs $N_{tot} = N_1(u,0)$ each year is the same.

4. Disease transmission from ticks to hosts. The population dynamics of the rodent and deer hosts is complex, as there are seasonal changes in the breeding habits and fecundity rates of the hosts, as well as in the availability of food. There are also considerations of foraging behavior and the availability of nest sites. The populations are age-structured as well as size-structured. Animals of a given species also differ in their susceptibility to disease.

In order to consider the effects of the host population on the transmission of the disease, a simplified model of the host population is presented here. The features of the host population which are of interest here are the host recovery and mortality rates, as well as the fact that the hosts are often infected in early in the season by nymphs and then transmit the infection to larvae later that year.

Let $H_i(\tau)$ be the number of hosts of species i at time τ. The vital dynamics of the host population will be included:

$$H_i(\tau+1) = H_i(\tau)\sigma_i(c)(1+b_i(c)) \tag{4}$$

where $\sigma_i(c)$ equals the quarterly survival fraction for host species i, and $b_i(c)$ equals the quarterly birth rate. The assumption that

$$\prod_{c=1}^{4} \sigma_i(c)(1+b_i(c)) = 1 \tag{5}$$

gives a host population that varies through the course of the year, but which returns to the same value at the beginning of next year. The more restrictive assumption that

$$\sigma_i(c)(1+b_i(c)) = 1 \tag{6}$$

gives a host population that is constant from season to season, $H_i(\tau) = H_i$.

To model the infection rate of the hosts, an SIR model will be used (Kermack and McKendrick [1927], Bailey [1975], Hethcote [1976], Anderson and May [1979], and Ginsberg [1988]). Let $X_i(\tau)$ be the number of susceptible hosts, $Y_i(\tau)$ the number of infectious hosts, and $Z_i(\tau)$ the number of "removed" hosts (hosts which have recovered and are immune to reinfection), so that

$$X_i(\tau) + Y_i(\tau) + Z_i(\tau) = H_i(\tau). \tag{7}$$

Also, let $x_i(\tau) = X_i(\tau)/H_i(\tau)$ be the fraction of hosts which are susceptible, $y_i(\tau) = Y_i(\tau)/H_i(\tau)$ be the fraction of hosts which are infectious, and $z_i(\tau) = Z_i(\tau)/H_i(\tau)$ be the fraction of hosts which are removed. Thus it follows from equation (7) that $x_i + y_i + z_i = 1$ for all τ. Finally, to keep the model simple, I assume that all newborn individuals are assumed to be equally susceptible, that recovery from infection confers complete immunity, and that vertical transmission is nonexistent in the hosts. In fact, the infection process may be much more complex than this. For example, it has been suggested that there may be cyclic variation in the number of spirochetes infecting a host animal due to antigenic variation in the spirochete, similar to what occurs in relapsing fever (Burgdorfer and Schwan [1991]). The assumptions above imply that the number of infected mice would decline over time due to recovery. The same effect results from assuming a turnover in the mouse population in the absence of reinfection.

Out of $X_i(\tau)$ susceptibles at time τ, a proportion of these will be infected at the next time unit, because the host animals are exposed to infected ticks. The quantity $h_i(\tau)$ is the proportion of host species i inoculated with the disease at time τ, and it depends on the distribution of tick bites over the population (Goldfarb [1986], Smith and Kakoma [1989]). The proportion of susceptible hosts which do not become infected is $1-h_i(\tau)$. Assume that after the susceptible hosts are exposed

to the risk of infection from the ticks, they are then exposed to risk of mortality for the rest of the season. Since newly born hosts are assumed to enter the susceptible class, the number of susceptibles at time $\tau + 1$ is:

$$X_i(\tau + 1) = \sigma_i(c)b_i(c)H_i(\tau) + X_i(\tau)[1 - h_i(\tau)]\sigma_i(c) \tag{8}$$

The number of infected individual hosts at $\tau + 1$ can be calculated in the same way. If at time τ, $h_i(\tau)X_i$ are newly infected hosts, and ψ_i is the fraction of infectious hosts which do not recover from the disease during a season. Then, assuming that the disease causes no excess mortality in the hosts, and that the probability of recovery is independent of the probability of death, the number of infected hosts at time $\tau + 1$ is

$$Y_i(\tau + 1) = [Y_i(\tau) + h_i(\tau)X_i(\tau)]\psi_i\sigma_i \tag{9}$$

To derive a form for $h_i(\tau)$, it is necessary to know what fraction of susceptible hosts will receive infective bites (Goldfarb [1986]). This depends on the fraction of susceptible hosts which receive tick bites, and the fraction of those bites which transmit the infection. The fraction of susceptible hosts of species i which are bitten depends upon the numbers of hosts of species i which are bitten by ticks.

Feeding ticks are partitioned among hosts in a manner that depends on the number of hosts, and upon the affinity of the ticks for each host. Suppose that the number of ticks of life-table position j feeding on a host of species i over the course of one season is proportional to $\alpha_{i,j}H_i$, where $\alpha_{i,j}$ is a parameter reflecting the affinity of ticks for a given host. For convenience, the proportionality constant will be assumed to be one. Then, suppose the number of ticks of life-table position j which die during that three-month period is proportional to a mortality parameter $m_j^{(Q)}$, and it will again be assumed that the proportionality constant is one. Then let $q_{i,j+1}$ denote the fraction, out of those which feed, which feed on a given host i. Then,

$$q_{i,j+1} = \frac{\alpha_{i,j}H_i(\tau)}{\sum_{i=1}^{C}\alpha_{i,j}H_i(\tau)}, \tag{10}$$

since the denominator is the number of ticks which feed on all hosts combined. For the survivorship s_j, we need to divide the number of ticks which fed on some host over the total number of ticks, including those that fed and those that died in the course of the season:

$$s_j = \frac{\sum_{i=1}^{C}\alpha_{i,j}H_i(\tau)}{m_j^{(Q)} + \sum_{i=1}^{C}\alpha_{i,j}H_i(\tau)} \tag{11}$$

Let the proportion of questing ticks which feed on hosts of species i be denoted $p_{i,j+1}$. By definition, then,

$$p_{i,j+1} = s_j q_{i,j+1} \tag{12}$$

Thus, from equations (10), (11), (12), it follows that the proportion of ticks out of the initial cohort, before host-seeking, who end up feeding on host i is

$$p_{i,j+1} = \frac{\alpha_{i,j}H_i(\tau)}{m_j^{(Q)} + \sum_{i=1}^{C}\alpha_{i,j}H_i(\tau)}. \tag{13}$$

(Arguments similar to those used by Randolph and Steele [1985] and Plowright and Paloheimo [1977] could be employed to derive this form for the partitioning of ticks among hosts from a model of the questing and feeding within one season, but such a model will not be developed here.)

Suppose that the probability of the attachment of a tick to a host during a given season of feeding is independent of whether the host is already infected at the start of the season, and is independent of whether the tick is infected or not. Also, suppose that the numbers of ticks and hosts is large so that probabilities can be replaced by proportions (using the Law of Large Numbers). Now, suppose that the infected ticks are distributed over the susceptible hosts according to some distribution $g_i(\theta_j)$, which is the probability that a susceptible host of species i will have θ_j bites from infected ticks of life table position j during a season (for models involving a distribution of attacks over a susceptible host population, see Hassell [1978] and (Goldfarb [1986]). Let $\nu_i(\theta)$ be the proportion of hosts of species i, that become infected with the disease when bitten by θ infected ticks. In general, we expect that

$$0 \le \nu_i(1) \le \nu_i(2) \le \cdots \le \nu_i(\theta) \le \cdots.$$

Thus, it follows that the total proportion of host species i inoculated by the disease is

$$h_i(\tau) = \sum_{j=2,5,8} \sum_{\theta=0}^{\theta_{max}} \nu_i(\theta) g_i(\theta_j).$$

Here, the structure of the tick life-history model will guarantee that at most one stage of tick is questing during a given season, so the sum over questing stages ($j = 2, 5, 8$) will contain at most one term. Although the quantity $\nu_i(\theta)$ could depend on the host immunity and on seasonal susceptibility to infection for the hosts, here we assume that

$$\nu_i(\theta) = \begin{cases} 1 & \text{if } \theta > 0 \\ 0 & \text{if } \theta = 0 \end{cases}$$

that is, a single bite from an infected tick transmits the disease (Donahue, Piesman and Spielman [1987]). This implies that

$$h_i(\tau) = 1 - g_i(0).$$

Suppose that the ticks are distributed randomly over the hosts over a whole season (i.e. Poisson distributed—see Goldfarb [1986]). Let $N_j^*(\tau)$ represent the number of infected ticks in life-table position j at time τ. Then

$$g_i(0) = \exp(-a)$$

where $a = (p_{i,j+1} N_j^*(\tau))/(H_i)$ is the mean number of infected ticks per host per season. Thus, for the random or Poisson case,

$$h_i(\tau) = 1 - \exp\left(-\frac{p_{i,j+1} N_j^*}{H_i}\right) \tag{14}$$

For the negative binomial distribution, which is often used in host-parasite models to give on overdispersed distribution of parasites in or on the host population (May [1978]),

$$g_i(0) = \left(1 - \frac{a}{k}\right)^{-k},$$

where k is an aggregation parameter. Thus, in the negative binomial case,

$$h_i(\tau) = 1 - \left(1 - \frac{p_{i,j+1} N_j^*}{k H_i(\tau)}\right)^{-k} \tag{15}$$

It is not assumed in the derivation of (15) that the hosts which are "tick-prone" in one season are more likely to receive more ticks the next season, nor is it assumed that they are more or less likely to be bitten by an infected tick than an uninfected tick. However, ticks feeding on hosts have a diurnal dropping off pattern, which makes them more likely to detach in the nest of the rodent (Mather and Spielman [1986]). Furthermore, the mammals move and drop ticks off in home ranges. Thus they are more likely to be infected by such ticks again after they have molted, than they are to receive a tick in the same stage which fed on a different mammal. Some mammals may live in home ranges that have places which are more favorable to the survival of ticks than others; this could lead to an overdispersed distribution of the parasites, and yet the hosts which are prone to the most ticks would not necessarily be independent from season to season, as the above analysis assumes (Andrewartha and Birch [1954]). In fact, most studies of tick populations show an overdispersed distribution for the number of ticks per host at a certain time (for example, see Randolph [1975]).

5. Disease transmission from hosts to ticks. Let ϕ_i be the specific infectivity of hosts of species i for the ticks, i.e. the fraction of ticks which acquire the infection after feeding on hosts of species i (Mather et al. [1989]). In general, this fraction depends on the time since the beginning of the infection in a particular individual animal, as well as on the immune status of the animal (Donahue, Piesman and Spielman [1987]). For simplicity, assume that each infective at time τ has the same infectivity for the ticks, and the same constant recovery rate. Assuming that the encounter rates between hosts and ticks are in no way affected by the infection, let the fraction of ticks that feed on hosts of a given infection status, X, Y, or Z, equal the fraction of such hosts in the population. Recalling that $p_{i,j+1}$ is the proportion of ticks in the initial cohort who end up feeding on host i, the fraction of ticks

infected during feeding is

$$\lambda_j(\tau) = \sum_{i=1}^{C} p_{i,j+1}\phi_i \frac{Y_i(\tau)}{H_i(\tau)}.$$

Finally, define an infectious contact matrix $\Lambda(\tau)$, with

$$\Lambda(\tau) = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \lambda_2(\tau) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \lambda_5(\tau) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \lambda_8(\tau) \end{bmatrix}.$$

Donahue, Piesman and Spielman [1987] measured, using xenodiagnostic methods, the infection rate in white-footed mice as a function of time, following the bite of infected ticks. It took roughly one week for the infection to appear, after which time it declined due to host recovery. After one week, approximately 50% of larvae feeding on such hosts had become infected. Mather et al. [1990] measured the rate of infection in nymphs which fed on infected mice as larvae, and found a 92% infection rate. These studies give an indication of typical values of ϕ_1. (For the seasonal projection model, the time delay between the bite and the manifestation of infectiousness is neglected.)

6. Seasonal projection model. Let $\mathbf{N}^*$ be a vector of the numbers of infected ticks, and let $\hat{\mathbf{N}} = \mathbf{N} - \mathbf{N}^*$ be a vector of numbers of the uninfected ticks. With these definitions, and assuming that the life table for infected ticks is the same as for uninfected ticks, except for vertical transmission, the change in the number of ticks infected by spirochetes is described by the equation (see Appendix 1)

$$\mathbf{N}^*(\tau + \mathbf{1}) = \mathbf{A}(c)[\mathbf{N}^*(\tau) + \Lambda(\tau)\hat{\mathbf{N}}(\tau)] \tag{16}$$

Vertical transmission in ticks is taken to be zero. Field studies have found only about 1% of unfed larvae to have the infection (Piesman et al. [1986]). Also, Magnarelli, Anderson and Fish [1987] reared larval ticks from eggs deposited by field collected females, and found only 1.9% of the larvae had acquired the infection transovarially.

For each set of values of the parameters of the system, the model predicts a particular equilibrium infection rate, both in the hosts and in the ticks. When the infection rates do not equal this equilibrium value, they increase or decrease until this equilibrium is reached.

In the simulations below, parameter values were chosen based on available data. However, accurate field measurements of the parameters of interest are not available.

Telford et al. [1988] estimated the density of deer on Hog Island, Massachusetts at roughly 1 deer per hectare, and the number of mice at 75 per hectare. This has been used as an approximate guide in choosing the values below, where an area of 10 hectares has been arbitrarily chosen. Falco and Fish [1988] estimated the number of *Ixodes dammini* adults on lawns in Westchester County, New York, at approximately 1 adult per square meter. If the average number of progeny per adult tick is approximately 1000, there must be on the order of 10^8 larval ticks in a ten-hectare area. The average population density in the endemic foci is not known. The model below gives high infection rates for far fewer ticks; it is possible that the homogeneous mixing assumption is inadequate, and Telford, Mather, Moore et al. [1988] suggest that there may be a reduction in survival of infected ticks.

In the seasonal projection model, the fraction of hosts infected drops due to recovery and turnover, and under the assumptions that the number of hosts is not changing and that the turnover rate is constant from season to season, the recovery rate and the turnover rate have the same effect on the dynamics of the disease. (This is shown by the symmetry with which these terms appear in equation (27), below.) The population dynamics of mice are discussed by Terman [1968]; in his Table 8 are listed the results of studies on the force of increase of populations of *Peromyscus*. Females typically have 3–5 young per litter and 3–5 litters per year.

6.1 First scenario: Mice as sole host for juvenile ticks. Suppose that the larvae and nymphs are restricted to mice as the sole host, i.e. H_1, which is *Peromyscus leucopus*. Adult ticks are also restricted to a single host, i.e. H_2, which is the white-tailed deer *Odocoileus*

virginianus. This implies that

$$q_{1,2}=1,\quad q_{2,2}=0,\quad q_{1,5}=1,\quad q_{2,5}=0,\quad q_{1,8}=0,\quad \text{and}\quad q_{2,8}=1 \tag{17}$$

Finally, assume a constant host population per season, i.e., assume that equation (6) holds, and furthermore that both $\sigma_i(c)$ and $b_i(c)$ are constants, not depending on c.

It will be useful to derive a set of difference equations for the change in the infection rate from year to year. Let $n^*(u)$ be the proportion of replete larvae or unfed nymphs who have the infection before questing in the early spring ($c=0$); that is, $n^*(u)=(N_4^*(u,0))/(N_4(u,0))$. In the remainder of what follows, $x(u)$ and $y(u)$ denote the susceptible and infectious proportion of hosts of species 1 respectively, taken at $c=0$. Then

$$n^*(u+1)=F_1(n^*(u),x(u),y(u)) \tag{18}$$

$$x(u+1)=F_2(n^*(u),x(u),y(u)) \tag{19}$$

$$y(u+1)=F_3(n^*(u),x(u),y(u)) \tag{20}$$

Using the seasonal projection equations (1) and (16), together with (17), it is possible to project the infection around four full seasons beginning from $n^*(u)$, $x(u)$, and $y(u)$, to arrive at corresponding values for $n^*(u+1)$, $x(u+1)$, and $y(u+1)$, evaluated for $c=0$ of the following year. The nontrivial equilibrium values of these quantities will be denoted $\bar{n}^*$, $\bar{x}$, $\bar{y}$. Using the Poisson form (14) for the distribution of ticks over hosts, the equations are

(21)
$$n^*(u+1)=\phi_1\left[y(u)\psi_1^2\sigma_1^2+(\mu_1+x(u)\sigma_1)\psi_1\sigma_1\left(1-\exp\left(\frac{-N_{tot}s_{1,5}n^*(u)}{H_1}\right)\right)\right]$$

(22)
$$x(u+1)=\mu_1+\left[\mu_1+\left[\mu_1+(\mu_1+x(u)\sigma_1)\sigma_1\exp\left(\frac{-N_{tot}s_{1,5}n^*(u)}{H_1}\right)\right]\sigma_1\right]\sigma_1$$

(23)
$$y(u+1)=y(u)\psi_1^4\sigma_1^4+(\mu_1+x(u)\sigma_1)\psi_1^3\sigma_1^3\left(1-\exp\left(\frac{-N_{tot}s_{1,5}n^*(u)}{H_1}\right)\right)$$

where $s_{1,5}=s_1s_2s_3s_4s_5$, and $\mu_1=1-\sigma_1$.

Here, the first and third equations are not independent; specifically,

$$n^*(u+1)=\frac{\psi_1^2\sigma_1^2}{\phi_1}y(u+1). \tag{24}$$

(This is a consequence of the assumption that the survivorship does not differ for infected ticks and uninfected ticks.)

First, I will examine the stability properties of the equilibrium corresponding to the absence of disease, in order to derive a threshold expression for the disease to be able to invade a region. Then, I will consider the values of the nontrivial equilibrium infection rates, $\bar{n}^*$, $\bar{x}$, and $\bar{y}$.

The steady state of equations (21), (22), and (23) which corresponds to the absence of disease is $n^*=0$, $x=1$, and $y=0$. This corresponds to the situation where there is no disease in the host or the vector population, and all of the hosts are susceptible. The stability of this steady state indicates whether the disease can invade the population; only when the steady state is unstable are outbreaks of the disease possible. The stability of this steady state can be evaluated by computing the Jacobian **J** of the system evaluated at the steady state $n^*=0$, $y=0$, $x=1$. The condition for stability is that the eigenvalues all have magnitudes less than 1. When this steady state is stable, the disease would not persist if it were introduced. When this steady state is unstable, the introduction of the disease results in the persistence of the disease.

The eigenvalues of **J** were computed using Mathematica (Wolfram [1988]), and the following expressions for the eigenvalues were obtained: $\lambda_1=0$, $\lambda_2=\sigma_1^4$, and

$$\lambda_3=\psi_1^4\sigma_1^4+\phi_1\psi_1\sigma_1\frac{N_{tot}s_{1,5}}{H_1} \tag{25}$$

Thus, λ_3 is the only eigenvalue that can be greater than 1. So the condition for an outbreak of disease to be possible in a disease-free population is

$$\psi_1^4\sigma_1^4 + \phi_1\psi_1\sigma_1\frac{N_{tot}s_{1,5}}{H_1} > 1 \tag{26}$$

This result can be interpreted as follows. The first term of equation (26), representing the contribution to disease persistence due to the hosts alone, is the proportion of hosts infected this year who will be alive and infected next year. The second term of (26) represents the amplification of the disease due to the host-tick interaction. Suppose that an infected questing nymph bites a host rodent at $c = 1$ this year. This host would become infected, but to transmit the disease, would have to survive and not recover for one quarter year, which it would do with probability $\psi_1\sigma_1$, but next season the number of ticks has been multiplied by $r_1 = \sigma_1(1 + b_1)$ according to equation (4); the ticks will be distributed over a different number of hosts. If the fraction of hosts of species i which have the disease is $x_i(\tau)$, then the fraction which have the disease at $\tau + 1$ in the absence of reinfection can be shown to be $x_i(\tau)/(1 + b_i(c))$. When the population is assumed to be constant using equation (6), then the fraction of hosts that have the disease becomes $x_i(\tau)\sigma_i(c)$. Thus the number of infected mice is reduced each season by the fraction $\sigma_1(c)$, provided the host population is constant. In the summer, larvae would feed on the host, and on each host; the number of larvae that successfully completed feeding is $N_{tot}s_1s_2s_3/H_1$ on average. Of these, a fraction ϕ_1 become infected. Finally, these larvae would have to survive molting (s_4) and survive questing to feed on another host (s_5). So the second term in inequality (26) represents the number of infected nymphs next year which would result from a single infected nymph this year, in an otherwise uninfected population (i.e. the basic reproductive rate).

Therefore, the disease is able to invade a region when

$$\frac{N_{tot}}{H_1} > \frac{1 - \psi_1^4\sigma_1^4}{\phi_1\psi_1\sigma_1 s_{1,5}} \tag{27}$$

It is difficult to solve analytically for the nontrivial steady states of equations (21), (22), and (23), so in order to determine this equilibrium,

equation (1) was simulated according to the assumptions of the first scenario, with juveniles feeding only on mice. Curves of constant equilibrium infection rate in ticks ($\bar{n}^*$) were derived (Figure 3), as functions of the number of hosts and ticks. Different values of the tick cohort size N_{tot} and of H_1 were chosen, and the model was simulated until the infection rate was close to equilibrium. In this simulation, the survivorship factors s_2, s_5, and s_8 are held constant, so that the questing mortalities are assumed to vary by equation (11). For low values of tick density, the disease does not persist at all. Above a threshold value of the ticks per host (equation (27)), the infection rate rapidly rises, but for large values of the tick density, the infection rate is determined by the turnover rates of hosts, recovery rates, and the infectivity to ticks (compare with Ginsberg [1988]). In Figure 3, the isoclines slope upward. The level of disease rises with the number of ticks, and falls with the number of rodents. The isoclines are linear, indicating that the dependence on the number of hosts and ticks is a dependence on the number of ticks per host only. For the first scenario, it is sufficient to show how the equilibrium infection rate depends on N_{tot}/H_1. (The linearity of the isoclines in Figure 3 can be shown from equations (21), (22), and (23)).

Isoclines of the infection rate in ticks with respect to the number of hosts and ticks were calculated (Figure 4), except that here, the questing mortality of the ticks was assumed constant, so that the survivorship parameters varied with the number of hosts according to equation (11). The comparison of the equilibria of these models leads to entirely different results. In both Figure 3 and Figure 4, the infection rate in ticks increases with the number of ticks. But in Figure 4, the dependence on the number of hosts is different. In Figure 3, fewer hosts mean more ticks per host, increasing greatly the transmission of the disease. In Figure 4, fewer hosts lead to reduced survivorship of ticks, as more ticks die before finding hosts. In the latter, very low levels of hosts prevent the disease from establishing itself at all; at higher levels of ticks, for moderate to high levels of hosts, the infection rate is nearly independent of the numbers of host. The isoclines are closest together near the boundary separating the allowable region from the nonallowable region. When the number of mice is relatively large, a given drop in the number of ticks (all else remaining equal) has a smaller effect on the spirochete infection rate than the same drop in the number of ticks would have if there were fewer mice. When the

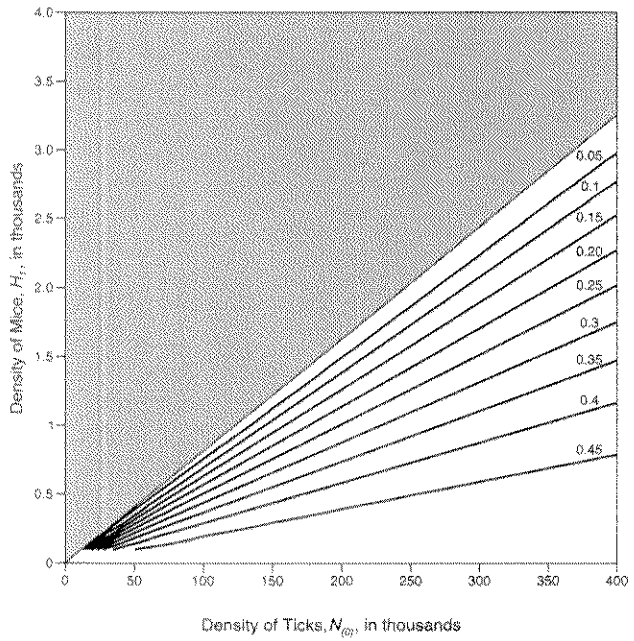

FIGURE 3. Curves of constant equilibrium infection rate in ticks $\bar{n}^*$ as a function of the number of ticks $N_{(0)}$ and the number of individual hosts of species 1, H_1. The survivorship values for questing ticks were held constant. Parameters were chosen as follows: $\sigma_1 = 0.8, \psi_1 = 1, \phi_1 = 0.6, H_2 = X_2 = 10, \alpha_{1,2} = \alpha_{1,5} = 0.001, \alpha_{1,8} = \alpha_{2,2} = \alpha_{2,5} = 0, \alpha_{2,8} = 0.1, b = 1000, s_j = 1$ for $j \neq 2, 5, 8$, $s_2 = s_5 = s_8 = 0.1$, and the initial number of infected questing nymphs $N_5^*(0,0) = 50$. Values of $N_{(0)}$ and H_1 which lie below the threshold for disease invasion are shown in gray.

system is farther above the threshold, tick reduction is less effective. In Figure 4, the infection rates in ticks increase with the number of hosts due to improved survivorship of ticks. This effect is most important at high levels of ticks. To the extent that rodent control decreases the survivorship of infected ticks, it is possible that it may reduce disease levels. Related to this is the strategy of applying acaricide to rodents, thus targeting infected ticks (Mather, Ribiero and Spielman [1987]; Deblinger and Rimmer [1991]; Stafford [1991]).

Curves of constant infection rate in ticks were calculated as functions of the ratio of ticks to host over the season, and the infectivity (Figure 5). In the simulations presented in Figure 5, the number of hosts was kept constant, while the number of ticks varied. For a given specific

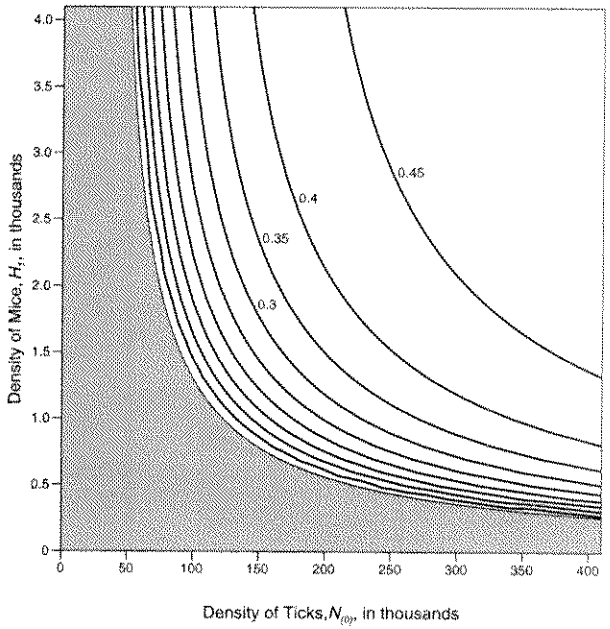

FIGURE 4. Curves of constant equilibrium infection rate in ticks $\bar{n}^*$ as a function of the number of ticks $N_{(0)}$ and the number of individual hosts of species 1, H_1. The values for the mortality rates for questing ticks were held constant. Parameters were chosen as follows: $\sigma_1 = 0.8, \psi_1 = 1, \phi_1 = 0.6, H_2 = X_2 = 10, \alpha_{1,2} = \alpha_{1,5} = 0.001, \alpha_{1,8} = \alpha_{2,2} = \alpha_{2,5} = 0, \alpha_{2,8} = 1.0, b = 1000, s_j = 1$ for $j \neq 2, 5, 8$, $m_j^{(Q)} = 9.0$ for $j \neq 2, 5, 8$, and the initial number of infected questing nymphs $N_5^*(0,0) = 50$. Values of $N_{(0)}$ and H_1 which lie below the threshold for disease invasion are shown in gray.

infectivity, increasing the number of ticks increases the spirochete infection rate in ticks at equilibrium. The curves in Figure 5 indicate the extent to which increasing infectivity ϕ_1 in rodents reduces the number of ticks required to achieve the same level of disease.

6.2 Second scenario: Host infections limited to one year. In this second scenario, all of the assumptions of the first scenario are held. In addition, I assume that all of the hosts eventually recover by next year, or that the rodents never live more than one year. The duration of host infections is thus limited to one year. This implies that equations (21),

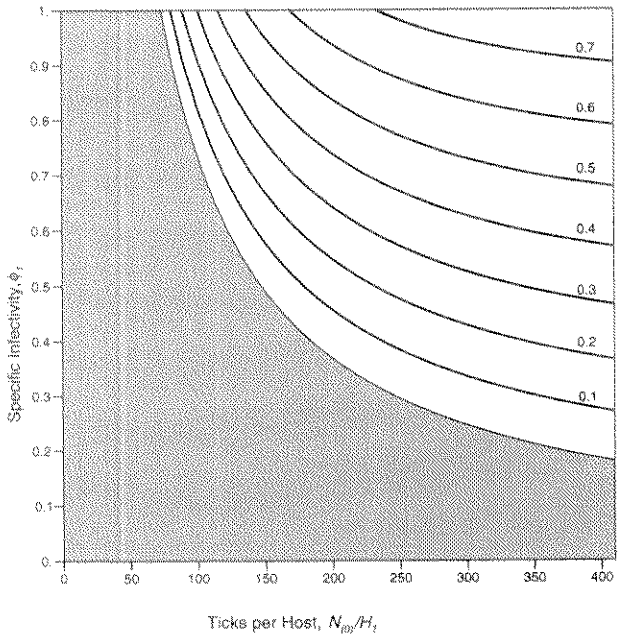

FIGURE 5. Curves of constant equilibrium infection rate in ticks $\bar{n}^*$ as a function of the ratio of ticks to the number of hosts of $N_{(0)}/H_1$, and the specific infectivity ϕ_1. The values for the mortality rates for questing ticks were held constant. Parameters were chosen as follows: $\sigma_1 = 0.8, \psi_1 = 1, H_2 = X_2 = 10, \alpha_{1,2} = \alpha_{1,5} = 0.001, \alpha_{1,8} = \alpha_{2,2} = \alpha_{2,5} = 0, \alpha_{2,8} = 1.0, m_j^{(Q)} = 9.0$ for $j \neq 2, 5, 8$, $b = 1000, s_j = 1$ for $j \neq 2, 5, 8$, and the initial number of infected questing nymphs $N_5^*(0,0) = 50$. Values of $N_{(0)}/H_1$ and ϕ_1 which lie below the threshold for disease invasion are shown in gray.

(22), and (23) can be reduced to

$$n^*(u+1) = \phi_1\sigma_1\psi_1\left(1 - \exp\left(\frac{-N_{tot}s_{1,5}n^*(u)}{H_1}\right)\right) \tag{28}$$

Figure 6 is a graph of $n^*(u+1)$, plotted as a function of $n^*(u)$, with values of $a_1 = \phi_1\sigma_1\psi_1$ and $a_2 = N_{tot}s_{1,5}/H_1$ chosen as indicated. By differentiating the right-hand side of the equation and evaluating the derivative at $n^*(u) = 0$ (Edelstein-Keshet [1988]), the condition for stability in this special case is found to be

$$\phi_1\psi_1\sigma_1\frac{N_{tot}s_{1,5}}{H_1} > 1 \tag{29}$$

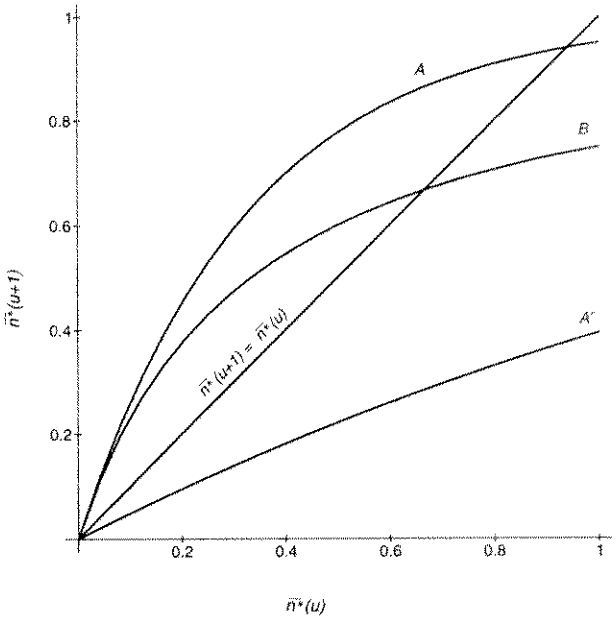

FIGURE 6. The infection rate in ticks depends on the infection rate the previous year, under the second and fourth scenarios (see text for details). For lines A and B, $\alpha_1 = 1$ and $\alpha_2 = 3$; for line A', $\alpha_1 = 1$ and $\alpha_2 = 0.5$ Lines A and A' are based on the Poisson distribution; line B is based on the negative binomial distribution with aggregation parameter $k = 1$.

This is the second term of the threshold equation (26). When the host turnover rate is high or the recovery rate is high, equation (29) and equation (26) give practically the same result.

Equation (29) can be interpreted as the basic reproductive rate. If the basic reproductive rate is large, a given proportional reduction in the vector population will not produce as large a proportional reduction in the infection rate as if the basic reproductive rate is small. This is similar to what occurs in other vector borne diseases (for example, see Smith and Kakoma [1989]).

6.3 Third scenario: Nonrandom distribution. The effect of a "non-random" distribution of ticks over their hosts can be seen by taking the distribution of ticks over hosts to be negative binomial. Figure 7

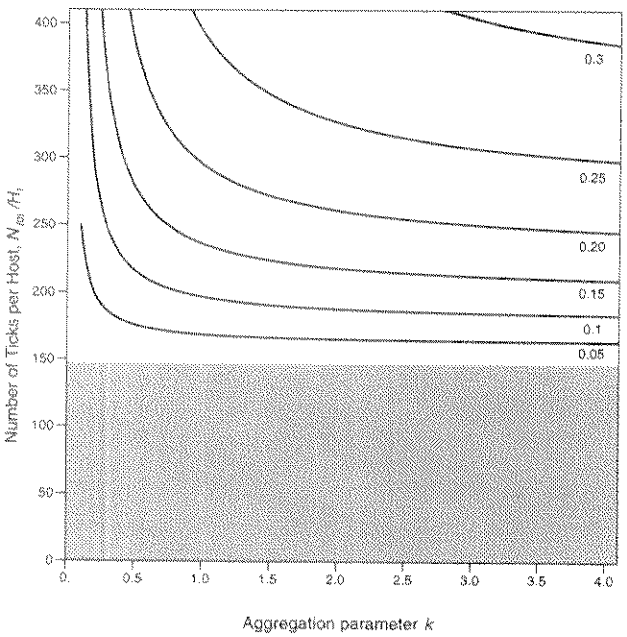

FIGURE 7. Isoclines of the infection rate in ticks $\bar{n}^*$ vary with respect to the aggregation parameter of the negative binomial k and the number of ticks per host $N_{(0)}/H_1$. The values for the mortality rates for questing ticks were held constant. Parameters were chosen as follows: $\sigma_1 = 0.8, \psi_1 = 1, H_2 = X_2 = 10, \alpha_{1,2} = \alpha_{1,5} = 0.001, \alpha_{1,8} = \alpha_{2,2} = \alpha_{2,5} = 0, \alpha_{2,8} = 0.1, m_j^{(Q)} = 9.0$ for $j \neq 2, 5, 8$, $b = 1000, s_j = 1$ for $j \neq 2, 5, 8$, and the initial number of infected questing nymphs $N_5^*(0,0) = 50$. Values of k and $N_{(0)}/H_1$ which lie below the threshold for disease invasion are shown in gray.

shows isoclines of the infection rate for different values of the aggregation parameter k and the density of ticks, with the number of hosts held constant. As the aggregation parameter declines (representing further departure from randomness), it requires more and more ticks to achieve the same level of disease.

6.4 Fourth scenario: Nonrandom distribution and host infection limited to one year. For the fourth scenario, suppose that everything were identical to the second scenario, except that the negative binomial had been used for the distribution of ticks over hosts instead of the Poisson distribution. (The fourth scenario will combine the features of the second and third scenarios.) Then, the expression (28) becomes

$$n^*(u+1) = \phi_1\sigma_1\psi_1\left(1 - \left(1 - \frac{-N_{tot}s_{1,5}n^*(u)}{kH_1}\right)^{-k}\right) \tag{30}$$

Differentiating the right-hand side of (30) with respect to n^* and substituting in the value of $n^* = 0$ gives the same threshold condition (29) for the number of ticks per host on average as in the third scenario (see Figure 6). In Figure 6, curve B is drawn using the same parameter values as curve A, except that the negative binomial distribution is used with aggregation parameter $k = 1$. The slope of the curve B is the same as the slope of the curve A at the origin, illustrating that the threshold condition for invasion is the same, and that the equilibrium $n^* = 0$ is unstable. But the point of intersection of the curve B with the line $\bar{n}^*(u) = \bar{n}^*(u+1)$ is lower than for line A, showing that the infection rate is smaller when there is aggregation of ticks on hosts. For very small numbers of infected ticks, the effect of this aggregation is small, since it is then extremely unlikely for a host to get two infected ticks; so the curves A and B are very similar at small $\bar{n}^*$. For larger $\bar{n}^*$, the aggregation increases the likelihood of a host which has one infected tick to get another, over what it would be in the "random" (Poisson) case. In this case, more infected ticks feed on hosts which are already infected, and final equilibrium infection rate is lower. Aggregation of ticks on hosts, when there is no dependence from stage to stage, reduces the infection rate without lowering the invasion threshold. So the threshold condition is the same when the negative binomial (overdispersed) distribution is used, but the steady state spirochete infection rate occurs at a smaller value. Attempts to estimate the basic reproductive rate or the threshold condition based on endemic spirochete infection rate data are dependent to some extent on the form of the distribution of the number of ticks over the hosts.

6.5 Fifth scenario: Juvenile ticks feeding on deer. Although the role of mice as the chief reservoir of Lyme disease has been emphasized in the literature and forms the basis of this model, it is known that deer are host to a significant proportion of juvenile ticks. It is assumed that the deer can be host to a considerable number of juvenile ticks. It has been argued that the deer are not a significant reservoir host; accordingly, suppose that the deer do not transmit the disease to the

ticks. Then, equation (17) is replaced by

$$q_{2,2}=1-q_{1,2},\qquad q_{2,5}=1-q_{1,5},\qquad q_{1,8}=0,\quad \text{and}\quad q_{2,8}=1 \tag{31}$$

Equations analogous to equations (21), (22), and (23) can be found, and their Jacobian computed as before. The significant eigenvalue is determined to be:

$$\lambda_3=\psi_1^4\sigma_1^4+\phi_1\psi_1\sigma_1 q_{1,2}q_{1,5}\frac{N_{tot}s_{1,5}}{H_1} \tag{32}$$

When the hosts of species 2 (deer) feed a large portion of juvenile ticks, the effect of this is to greatly increase the number of ticks per mouse needed for the disease to be able to invade a region:

$$\frac{N_{tot}}{H_1}>\frac{1-\psi_1^4\sigma_1^4}{q_{1,2}q_{1,5}\phi_1\psi_1\sigma_1 s_{1,5}} \tag{33}$$

where s_2 and s_5 also depend on H_2.

In Figure 8, isoclines of the equilibrium infection rate in ticks are plotted as a function of the number of deer (horizontal) and the number of ticks (vertical). The isoclines slope upward, showing that if the number of deer is larger, it takes more ticks to achieve the same infection rate. This is because the deer (assumed not to be transmitting the disease) divert juvenile ticks away from the mice, as discussed by Spielman [1988]. Conversely, for a given number of ticks, an increase in the number of deer results in a decrease in the infection rate for this reason. However, the number of deer affects the equilibrium number of ticks, presumably, and this will happen independently of whether or not Lyme disease is present. Therefore,

$$N_{(0)}=f_1(H_2) \tag{34}$$

This means that out of the plane shown in Figure 8, only the points satisfying (34) are actually realized. In general, (34) must cross the isoclines of the infection rate from below for a reduction in the number of deer to reduce the infection rate. When this occurs, the reduction in the number of ticks would outweigh the increased fraction of ticks

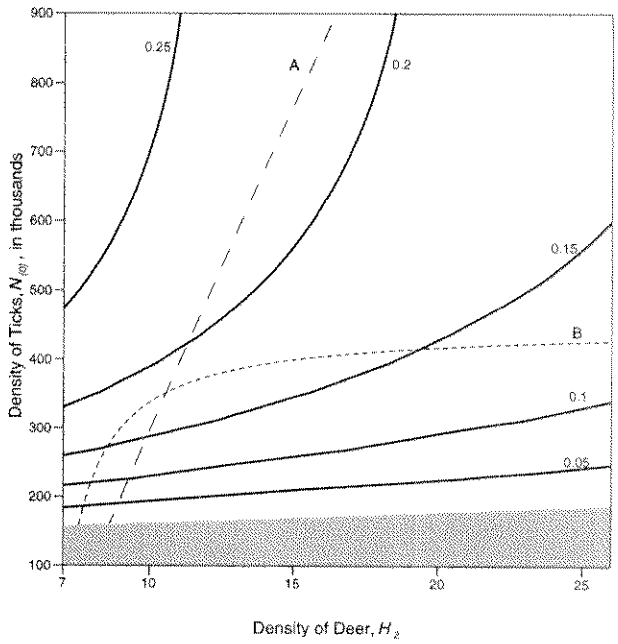

FIGURE 8. Isoclines of the infection rate in ticks $\bar{n}^*$, shown in solid lines, vary with respect to the the number of hosts of species 2 (deer) and the number of ticks $N_{(0)}$. The values for the mortality rates for questing ticks were held constant. Parameters were chosen as follows: $\sigma_1=0.8, \psi_1=1, H_1=X_1=1000, \phi_1=.5, \alpha_{1,2}=\alpha_{1,5}=0.001, \alpha_{1,8}=0, \alpha_{2,2}=\alpha_{2,5}=0.05, \alpha_{2,8}=0.1, m_j^{(Q)}=9.0$ for $j\neq 2,5,8$, $b=1000, s_j=1$ for $j\neq 2,5,8$, and the initial number of infected questing nymphs $N_5^*(0,0)=50$. For curve A, e_1 is 20 000 000 and e_2 is 200; for curve B, e_1 is 450 000, and e_2 is 1. Parameter values which lie below the threshold for disease invasion are shown in gray.

which would feed on mice. For instance, suppose the relationship (34) is

$$N_{(0)}=\frac{e_1(H_2-H_2^{crit})}{e_2+(H_2-H_2^{crit})}, \tag{35}$$

provided the equilibrium exists. This form is arbitrary, but something like it could arise when, for example, the ticks are unable to persist at all when H_2 is below H_2^{crit}, but when H_2 rises above this value, the number of ticks begins to rise, finally leveling off for high deer densities where, perhaps, the ticks are limited by something else. Two curves of

this form are plotted in dashed lines on Figure 8. Depending on the particular parameter values, a decrease in the number of deer could either decrease or increase the infection rate. (For very large values of H_2, (35) flattens out, and so when the number of deer is very large, this predicts that a decrease in the number of deer will always reduce the infection rate. However, such large values of H_2 may be biologically unrealistic.) Finally, it is possible that the reduction in the number of ticks may outweigh the increase in the infection rate, so that the total number of infected ticks—and thus the risk of disease—is reduced anyway.

Although moderate deer curtailment may increase or decrease the infection rate in the ticks, severe curtailment such as was undertaken by Wilson et al. [1988] leads to such great reduction in the number of ticks that the disease cannot persist.

6.6 Sixth scenario: Seasonally-varying mouse population. In this scenario, everything is identical to the fifth scenario, where juvenile ticks were considered to feed on deer, except that the assumption of a constant host population is relaxed. That is, equation (5) is used instead of equation (6), and in this way the effect of a mouse population which varies throughout the course of the year can be examined. The significant eigenvalue was determined to be:

$$\lambda_3 = \frac{\psi_1^4}{\prod_{c=0}^{4}(1+b_1(c))} + \frac{N_{tot}\phi_1\psi_1 q_{1,2}q_{1,5}s_{1,5}\sigma_1(1)}{H_1(0)r_1(0)r_1(1)} \tag{36}$$

where $r_1(c) = \sigma_1(c)(1+b_1(c))$ for $c = 0,1,2,3$, which comes from equation (4). Each season the reduction of the infection due to host turnover is found by dividing by $1+b_1(c)$ (see discussion of equation (26) above). The interpretation of this is similar, except that instead of dividing by $H_1(0)$, it is the number of hosts at season $c = 2$, when larvae are questing, that occurs in the denominator, reflecting the distribution of the infected ticks over more hosts.

One effect of the nonconstant host population is to reduce the transmission from spring to summer; as the number of hosts increases, there are more hosts competing for the same number of ticks, so the number of ticks per infected host is reduced. This is a consequence of the assumption of the relative separation of feeding times of nymphs and larvae. If the overlap is great, then the effect cannot be explored within this model. Under these circumstances, the increasing host population may favor increased transmission. Equation (36) does indicate that it is the size of the host population during the time of year that transmission is occurring that is important in calculating the threshold.

6.7 Seventh scenario: Deer as reservoir host. When the deer are also transmitters of the infection to ticks, then the equations become analytically intractable, although they can be solved numerically. When deer are assumed to be reservoir hosts for the spirochete, then transmission by adults becomes important. The infection rate in adults is dependent on the infection rate in nymphs *after* feeding. Since the ticks do not lose the infection, the infection rate in adults is at least as great as the infection rate in questing nymphs. However, in the field, the nymphal feeding times are spread out, rather than simultaneous. Thus, nymphs that feed early infect more hosts. Consequently, nymphs that feed later are exposed to a higher force of infection than would be assumed. The seasonal projection model formulated here does not include this effect.

Conclusion. The model presented above illustrates the overall pattern of persistence of Lyme disease (and other *Ixodes dammini*-borne infections such as babesiosis).

The model suggests that moderate reductions in the number of deer can lead to an increase in the infection rate in ticks due to increased aggregation of the ticks on the reservoir hosts, the mice. The model shows that this possibility depends on the fraction of ticks which feed on the deer, on the functional dependence of the tick population size on the number of deer, and on the assumption that the white tailed deer does not transmit the disease as efficiently as mice. The model suggests therefore the possibility that moderate deer curtailment strategies may have the opposite effect that they are intended to have. However, the reduction in the number of ticks may outweigh the increase in the spirochete infection level in those that remain, so that the number of infected questing ticks is reduced.

The model also shows that control of the rodent reservoir hosts could reduce the infection rate if the survivorship of juvenile stages of ticks were reduced as a consequence. If the survivorship of juvenile stages

does not decline as the rodent population is reduced, then rodent reduction can increase the spirochete infection rate in the ticks.

The model shows that the upper limit of the infection rate in ticks rises with the transmission rate to ticks and decreases with the recovery and turnover rates in the hosts for the time of year that the hosts are important as a reservoir.

Expressions for the basic reproductive rate of the disease are computed analytically for special cases, and it is shown that as the basic reproductive rate increases, a proportional reduction in the tick population produces a smaller proportional reduction in the infection rate, so that vector control is less effective far above the threshold.

Finally, the model shows that the infection rate rises with the number of ticks in a manner which depends on whether the distribution of ticks over the host individuals is random or not. When the distribution is random, the endemic spirochete infection rate is higher than when the distribution of ticks is clumped, but the threshold number of ticks per host which is required for the disease to invade is the same. However, this conclusion assumes that the probability that a tick in one stage will attach to a given host individual is independent of the probability that tick will attach to that host individual in a later stage of its life.

The model depicts some of the overall features of the enzootic, though a number of simplifying assumptions have been made, and this must be kept in mind when interpreting the results. Models which are relatively simple, or which are built up from general principles, often aid in understanding a system. Further, the addition of more detail to a model does not always improve its accuracy. Simplified or "top-down" models, such as the one presented here, thus have played a complementary role to models which seek for increased realism by including greater amounts of detail (Getz and Haight [1989]).

However, the nature of the simplifying assumptions of the model, the uncertainties in the population estimates of the animals involved, and the gaps in our knowledge of the factors which regulate the abundance of ticks make it difficult to predict infection rates quantitatively. A crucial parameter in the dynamics is the number of ticks which feed on a given host throughout the season, and this parameter is not known well. It is also important to know how the ticks that feed on a given host are distributed among other hosts after they molt to the

next stage. For a more complete understanding of the dynamics of Lyme disease and other tick-borne diseases, it is necessary to have an understanding of density-dependent mortality factors acting on the tick populations. These include predation, host grooming, and host immunologic reactions. It is important to understand how the tick population responds to increased host abundance, in terms of increased chance of host finding, increased death rates (due, for example, to trampling of ticks), as well as the Allee effect resulting from the dispersion of male and female ticks so thinly over the host population that a significant proportion of females fail to mate and hence to lay eggs (Plowright and Paloheimo, [1977]). The role of climatic and meteorological factors must be examined, because these factors influence the death rates of ticks, the time of year that the ticks quest, the type and abundance of vegetation, and affects the host population levels. The role of other organisms must be known as well; Mather, Piesman and Spielman [1987] discuss the role of a parasitoid wasp of *Ixodes dammini* on the presence of infection by *Borrelia burgdorferi* and *Babesia microti*. In many ways, tick infestations are similar to macroparasitic infections, which have been discussed by Anderson and May [1978], but ticks are vectors of a microparasitic infection as well, and the effect that the presence of this infection itself has on ticks must be known. Does the disease reduce their survival through certain stages, or alter their feeding behavior? Are infected ticks more susceptible to adverse climate or to predation? Is the number of ticks reduced to any significant degree by the disease?

An important conclusion to be drawn from the model presented here is that there is a need for more data about Lyme disease, and the model helps show how such data could help in planning control strategies. The model also shows the need for caution in planning control strategies. Further field and laboratory studies are needed before predictive models of Lyme disease will be feasible.

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Appendix A
Seasonal Projection Matrices

The seasonal projection matrices can be taken as:

$$\mathbf{A}(0) = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & s_4 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$\mathbf{A}(1) = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ s_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & s_6 s_5 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

$$\mathbf{A}(2) = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & s_3 s_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & s_7 & 0 \end{bmatrix}$$

$$\mathbf{A}(3) = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & s_{10} s_9 s_8 b \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Appendix B

Notation

j	the life table position of a tick
N_j	the number of ticks at j at a given season
$\mathbf{N}(\tau)$	vector of numbers of ticks for $j = 1, 2, 4, 5, 7, 8$
c=0, 1, 2, 3	seasons of the year, spring = 0
u	year, starting with zero at the beginning of the model
τ	is the total count of three-month seasons from beginning of model
$\mathbf{A}(i)$	for $i = 0, 1, 2, 3$ the seasonal projection matrices
s_j	survivorship from stage j to stage $j + 1$
$s_{1,5}$	the product $s_1 s_2 s_3 s_4 s_5$
b	the average number of progeny per adult tick
$m_j^{(Q)}$	daily mortality rate of a questing tick, stage j
c	the number of possible host species
i	denotes a given species of host animal
H_i	numerical abundance of hosts of species
$\alpha_{i,j}$	the affinity of stage j ticks for hosts of species i.
$q_{i,j+1}$	proportion of feeding ticks which fed on species i
$p_{i,j+1}$	proportion of ticks out of the initial cohort N_j which fed on a host of species i
N_{tot}	the number of tick eggs at the beginning of the life cycle of each cohort
$H_i(\tau)$	number of hosts of species i at time τ
$X_i(\tau)$	number of susceptible hosts of species i at time τ
$Y_i(\tau)$	number of infectious hosts of species i at time τ
$Z_i(\tau)$	number of removed hosts of species i at time τ
$x_i(\tau)$	fraction of susceptible hosts of species i at time τ
$y_i(\tau)$	fraction of infectious hosts of species i at time τ
$z_i(\tau)$	fraction of removed hosts of species i at time τ
$\mu_i(\tau)$	the quarterly mortality fraction for host species i
$\sigma_i(\tau)$	the quarterly survival fraction for host species i
$b_i(\tau)$	equals the quarterly birth rate for host species i
h_i	proportion of hosts of species i inoculated with disease at time τ
ψ_i	the fraction of hosts which do NOT recover from the disease during a season

$g_i(\theta_j)$	probability distribution of tick bites over susceptible hosts, where
θ_j	the number of bites from infected ticks of life table position j during a season
$\nu_i(\theta)$	proportion of hosts of species i, bitten by θ infected ticks, who receive the infection
$N_j^*(\tau)$	number of infected ticks in position j at time τ
a	mean number of infected ticks per host per season
k	an aggregation parameter for the negative binomial
ϕ_i	fraction of ticks becoming infected after feeding on hosts of species i
$\lambda_j(\tau)$	fraction of ticks of stage j infected during feeding
$\Lambda(\tau)$	infectious contact matrix
$\mathbf{N}^*$	vector of the numbers of infected ticks (stages 1,2,4,5,7,8)
$\hat{\mathbf{N}}$	vector of numbers of the uninfected ticks (stages 1,2,4,5,7,8)
$n^*(u)$	proportion of unfed nymphs who have the infection at $c = 0$
a_1	$= \phi_1\sigma_1\psi_1$
a_2	$N_{tot}s_{1,5}/H_1$
e_1	in equation (35), the limiting number of ticks for large host populations
e_2	in equation (35), related to the host density at half-maximum tick abundance
H_2^{crit}	in equation (35), the threshold number of hosts for a ticks to persist
$\mathbf{J}$	the Jacobian of the system of difference equations (21), (22) and (23)

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