A mathematical model for tick-borne infections: a numerical study

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Abstract. A mathematical model for tick-borne infections is presented. The conditions for parasite persistence were examined in [7]. Here we show some numerical results, using parameter estimates based on data provided by the Centre for Alpine Ecology; we study the effect of the most uncertain parameters on the endemic equilibrium of the model, and on its stability. Among other things, it is shown that increasing the disease-related host death rate may move the system to sustained oscillations.

1 Introduction

Tick-borne infections are caused by bacteria, viruses, or other pathogens, that can be transmitted to a host through the bite of an infected tick. Among the tick-borne diseases that have, in recent years, become a serious problem for human health [2], are Rickettsiosis, Lyme Disease, Ehrlichiosis, Relapsing Fever and TBE (tick-borne Encephalitis).

Because of the relevance of the problem, several recent papers have considered models for tick-borne infections. Some researchers have used complex models based solely on computer simulations (see for instance [8]), while simpler models, based on differential equations, have been studied in [5,1,4,7]. The main emphasis of these papers has been on the computation of the basic reproduction number, and so on the conditions for infection persistence. These models are rather complex, so it is difficult to study analytically their behaviour, or even their nontrivial equilibria, above the threshold for persistence. Therefore, here we study numerically, using parameter values realistic for Lyme borreliosis, how the nontrivial equilibrium changes with some parameters, and we present some numerical solutions of the system.

2 The Mathematical Model

The model studied here is a special case of the model presented in [7] which should be referred to for more details. Ticks have a life cycle of three stages: larvae, nymphs and adults (whose densities will be denoted here L, N and A), that feed on one, two or three hosts depending upon the species: we will

only consider the three-host case. Tick-borne infection are transmitted from infected ticks to susceptible hosts, and vice versa: this type of transmission is often called viraemic transmission. Recently it has been discovered that pathogens can be transmitted from an infected tick to a non-infected tick while they *co-feed* on the same host: this process is known as non-viraemic transmission, but, for the sake of simplicity and the lack of parameter estimates, will not be considered here.

Nymphs and adult ticks are divided into infected and susceptible classes. It is assumed that ticks feed on two host species, for instance mice and deer: the first one (whose size is denoted as H_1) can become infected and transmit the infection, and its dynamics is explicitly modelled; the second one (whose size is assumed to be a constant H_2) cannot transmit the infection, and is relevant only in so far as it sustains the tick population. The first population is divided into three classes, namely susceptible (H_{1s}), infected (H_{1i}) and immune (H_{1r}). The model considered here is the following:

$$
\begin{aligned}
\dot{L} &= g^A(H_1,H_2)\, a_T(T)(A_i+A_s) - d_T L - g^L(H_1,H_2)L \\
\dot{N}_s &= m^L g^L(H_1,H_2)L - m^L\beta_1^L H_{1i}\psi^L(H_1,H_2)L - d_T N_s - g^N(H_1,H_2)N_s \\
\dot{N}_i &= m^L\beta_1^L H_{1i}\psi^L(H_1,H_2)L - d_T N_i - g^N(H_1,H_2)N_i \\
\dot{A}_s &= m^N g^N(H_1,H_2)N_s - m^N\beta_1^N H_{1i}\psi^N(H_1,H_2)N_s - d_T A_s \\
&\quad - g^A(H_1,H_2)A_s \\
\dot{A}_i &= m^N\beta_1^N H_{1i}\psi^N(H_1,H_2)N_s + m^N g^N(H_1,H_2)N_i - d_T A_i \\
&\quad - g^A(H_1,H_2)A_i \\
\dot{H}_{1s} &= a_1(H_1)H_1 - d_1 H_{1s} - q^N\beta_1^N H_{1s}\psi^N(H_1,H_2)N_i \\
&\quad - q^A\beta_1^A H_{1s}\psi^A(H_1,H_2)A_i \\
\dot{H}_{1i} &= q^N\beta_1^N H_{1s}\psi^N(H_1,H_2)N_i + q^A\beta_1^A H_{1s}\psi^A(H_1,H_2)A_i - (d_1+\gamma+\alpha)H_{1i} \\
\dot{H}_{1r} &= \gamma H_{1i} - d_1 H_{1r}.
\end{aligned}
$$

All parameters are described in Table 1 together with their reference values. We only remark here that the function g^z describes the rate at which ticks in stage z encounter hosts, considering the extended feeding period [3,7], while ψ^z are auxiliary functions; their expressions are the following

$$
\psi^z(H_1,H_2) = \frac{1}{1+c_1^z H_1 + c_2^z H_2), \text{ and } g^Z(H_1,H_2) = \frac{\beta_1^z H_1 + \beta_2^z H_2}{1+c_1^z H_1 + c_2^z H_2)}
$$

where $c_i^z = \dfrac{\beta_i^z}{\sigma_i^z}$ for $z = L, N, A$ and $i = 1, 2$.

Density-dependence is assumed, for the sake of simplicity, to occur only in two quantities: the production of larvae per feeding adult tick $a_T(T)$ and the birth rate for host $a_1(H_1)$. Note however that there is some evidence for density-dependence in all moulting probabilities [6].

We only report here the formula for R_0 found in [7] in the special case of only viraemic transmission and setting equal to 1 the probability of becoming

Table 1. Notation used to denote the various variable and parameters included in the model

Symbol	Description	Value
L	Larval density	variable
N	Nymph density	variable
A	Adult density	variable
T	Total tick density	$= L + N + A$
H_{1s}	Density of susceptible hosts 1	variable
H_{1i}	Density of infected hosts 1	variable
H_{1r}	Density of immune hosts 1	variable
H_1	Total density of host species 1	$= H_{1s} + H_{1i} + H_{1r}$
H_2	Non-viraemic host density	0.1 $(\text{ha})^{-1}$
a_T	Number of larvae produced by an adult tick	$1{,}300 - 0.1 \cdot T$
d_T	Natural death rate of ticks (the same for all stages)	0.06688 $(\text{days})^{-1}$
a_1	Birth rate of hosts 1	$\frac{5}{365} - \frac{4}{365}\frac{H1}{30}$ $(\text{d.})^{-1}$
d_1	Natural death rate of hosts 1	$1/365$ $(\text{d.})^{-1}$
α	Disease related death rate of hosts 1	?
γ	Recovery rate of viraemic host	0–0.7 $(\text{d.})^{-1}$
β_1^z	Encounter rate between questing ticks in stage z $(z = L, N, A)$ and hosts H_i $(i = 1, 2)$	see below
σ_i^z	Detachment rate of ticks in stage z $(z = L, N, A)$ feeding on hosts H_i $(i = 1, 2)$	0.4 $(\text{d.})^{-1}$
m^z	Moulting success probability for ticks in stage z $(z = L, N)$	0.15
q^z	Probability of becoming infected for a host 1 bitten by an infectious tick in stage z $(z = N, A)$	?

infected for a susceptible tick feeding on an infected host:

$$R_0 = \frac{m^L \beta_1^L \psi^L L}{d_1 + \gamma + \alpha} \cdot \frac{q^N \beta_1^N H_1 \psi^N}{d_T + g^N} + \frac{m^L \beta_1^L \psi^L L}{d_1 + \gamma + \alpha} \cdot \frac{m^N g^N}{d_T + g^N} \cdot \frac{q^A \beta_1^A H_1 \psi^A}{d_T + g^A} + \frac{m^N \beta_1^N \psi^N N}{d_1 + \gamma + \alpha} \cdot \frac{q^A \beta_1^A H_1 \psi^A}{d_T + g^A} \quad (1)$$

where all quantities L, N, A and H_1 are computed at the pathogen-free equilibrium. Recall that $R_0 > 1$ is the condition for pathogen persistence.

3 Choice of Functions and Parameters

Our parameter choice has been tuned towards the dynamics of Lyme borreliosis in the province of Trento, Italy, where the relevant tick species is *Ixodes ricinus* while H_1 represent small rodents (especially *Apodemus* spp. and *Clethrionomys glareolus*) and H_2 roe deer. As far as possible, we used

parameter estimates taken from the literature or derived, according to procedures that will be described elsewhere, from data collected by researchers of the Centre for Alpine Ecology (CEA); however, for some parameters we could produce only educated guesses. All the parameter values used are listed in Table 1, except for the contact rates β_i^z which are estimated as follows:

	L	N	A
on host 1	0.028402	0.000887	0
on host 2	0.048798	0.028779	0.12849

As for the functional form of density dependence, we chose the simplest: $a_T(T) = r_T - s_T\, T$ and $a_1(H_1) = r_1 - (r_1 - d_1)\frac{H_1}{K_1}$, where r_1 and d_1 are the natural birth and death rate of hosts 1, and K_1 is their carrying capacity; r_T is the average egg production per fed adult tick, and s_T is related to ticks' carrying capacity.

Some parameters for which there exist no sensible estimates are q^N, q^A and α, which we will vary in the simulations. As for γ, while it is known that infected mice remain positive for a couple of weeks ($\gamma \approx \frac{1}{15}$ (days)$^{-1}$), it is generally thought that infected mice remain infectious, although perhaps to a lesser degree, forever ($\gamma \approx 0$); thus, we will also let γ vary.

4 Simulations

In this Section we show some numerical results: we study the effect of some parameters on the endemic equilibrium of the model, and on its stability (using software CONTENT and XPP). We let one parameter vary at a time, while all other parameters are set at the values listed in Table 1; for the uncertain ones we used:

$$q^N = 0.5 = q^A, \gamma = 0.01, \alpha = 0.0005.$$

For this set of parameters we find the reproduction number $R_0 \approx 17.09$ and a positive equilibrium point at:

$$L \approx 862,\ N_s \approx 345,\ N_i \approx 85.3, A_s \approx 14.8,$$
$$A_i \approx 7.69,\ H_{1s} \approx 2.19,\ H_{1i} \approx 5.92,\ H_{1r} \approx 21.6.$$

Effect of H_2: It was found [4] that an increase of H_2 may decrease R_0, hence act against parasite persistence, since, when H_2 is large, many bites of infected ticks get "wasted" on incompetent hosts: this was named the "dilution effect". Here we see (Fig. 1a) that this effect occurs at unrealistically high population densities: there is a branching point (B.P.) slightly above 100, meaning that, beyond that value, $R_0 < 1$. Another branching point is at $H_2 \approx 0.089$. In between these values, there exists an infected equilibrum; it can be seen that the equilibrium density of infected hosts is almost independent of the value of H_2 over the range 0.1–10.

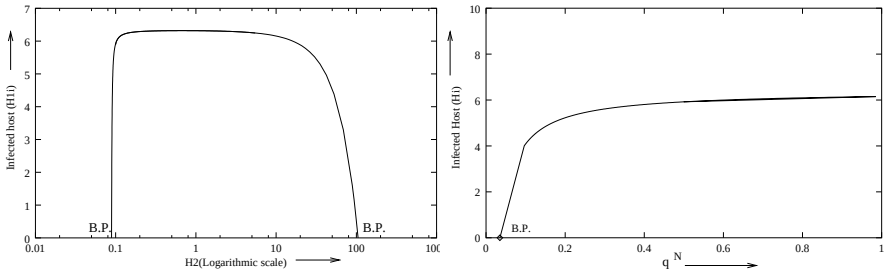

Fig. 1. Variation of equilibrium level of infected hosts with H_2 (left part) or q^N (right part).

Effect of $\mathbf{q^N}$: As expected, the equilibrium density of infected hosts increases with increasing q^N, first sharply, then more moderately. The threshold value (B.P.) is at $q^N \approx 0.035$ (see Fig. 1b).

Effect of γ: With increasing γ, the density of infected hosts decreases (see Fig. 2a) and at $\gamma \approx 0.186$ we get a branching point. When γ approaches 0, the density of infected hosts greatly increases.

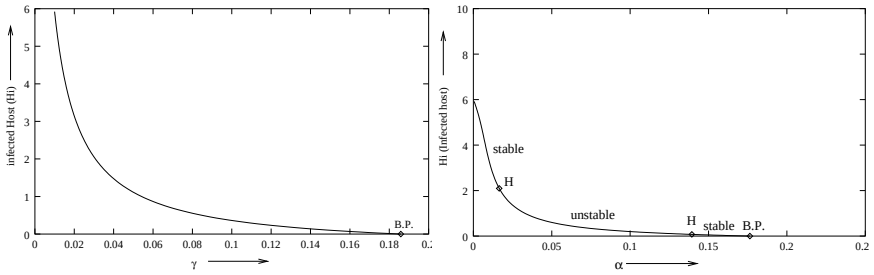

Fig. 2. Variation of equilibrium level of infected host with γ (left part) or α (right part).

Effect of α: The parameter α (disease-induced death rate of mice) has a more complex effect. While the density of infected hosts decreases monotonically with increasing α up to the branching point at $\alpha \approx 0.176$, there are two Hopf points, the first at $\alpha \approx 0.0165$ and the second at $\alpha \approx 0.139$ (see Fig. 2b). Presumably, when α is between the two Hopf points, the system will exhibit oscillations. Two simulations, with α below and above the first Hopf point, are shown in Fig. 3.

To conclude, we remark that this preliminary study has provided some intuition about the behaviour of this model for realistic parameter values. Certainly, much more research is required on parameter estimates and on the properties of this system of equations, before being able to apply reliably this (or similar) model to our case study.

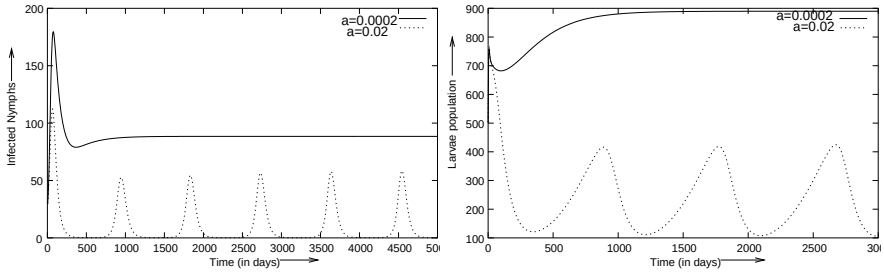

Fig. 3. Numerical solutions of the system with $\alpha = 0.0002$ (solid line) and $\alpha = 0.02$ (dashed line). In the left part, number of infected nymphs against time; in the right, total number of larvae

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