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Tick-borne disease modeling: the impact of seasonality, co-feeding transmission and tick movements among patches

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Tick-borne zoonosis

- Lyme disease:
  - caused by the bacteria pathogen *Borrelia burgdorferi*
  - the most common tick-borne disease in the northern hemisphere
  - USA: the annual number of cases is 476,000 (Centers for Disease Control and Prevention, 2021)
  - Canada: 992 cases of Lyme disease were reported in 2016 compared with 114 in 2009, and the number of endemic areas is gradually increasing with the expanding range of ticks, which was attributed to climate change
  - Europe: there may be more than 200,000 cases per year
    France: annual incidence was 53/100,000 between 2009 and 2017 according to the Sentinelles network. The annual incidence of cases consulting in general medical practices in 2019 was 76 cases/100,000 population.
- tick-borne encephalitis
- babesiosis
- anaplasmosis

Transmission routes

- vector: several tick-borne diseases are mainly transmitted by *Ixodes* ticks, which are most abundant in forests, woodlands and dense bushes
- tick vector: three distinct post-egg stages (larva, nymph and adult)
- distinct hosts: the development from one stage to the next is processed by taking a blood meal. Immature ticks (larva and nymph) mainly feed on small animals such as rodents and other small vertebrates, and adult ticks prefer large mammals
- two main transmission routes:
  - systemic transmission involves three closely related paths: susceptible larvae feed on infectious rodents and get infection; infectious larvae develop into infected nymphs; infected nymphs transmit tick-borne pathogens to susceptible rodents through biting on them (most existing models are working on this aspect)
  - co-feeding transmission of a susceptible larval tick by infected nymphal ticks when they are biting on the same host individual, with transmission probability dependent on the relative location of ticks on the host and the number of infected nymphal ticks

ST: Systemic transmission

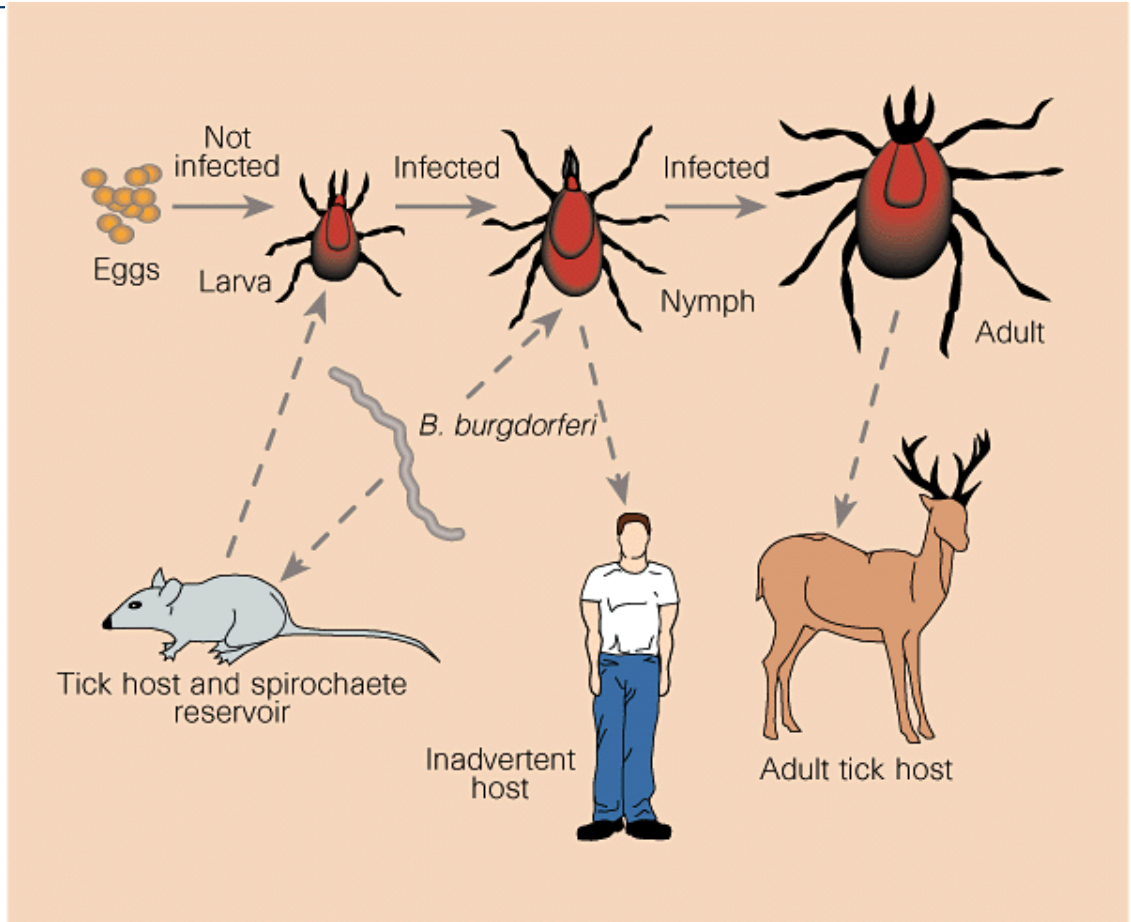

Figure: From: Alan G. Barbour & Wolfram R. Zuckert, Nature, 1997. Systemic transmission involves three closely related paths: susceptible larvae feed on infectious rodents and get infection; infectious larvae develop into infected nymphs; infected nymphs transmit tick-borne pathogens to susceptible rodents through biting on them (most existing models are working on this aspect)

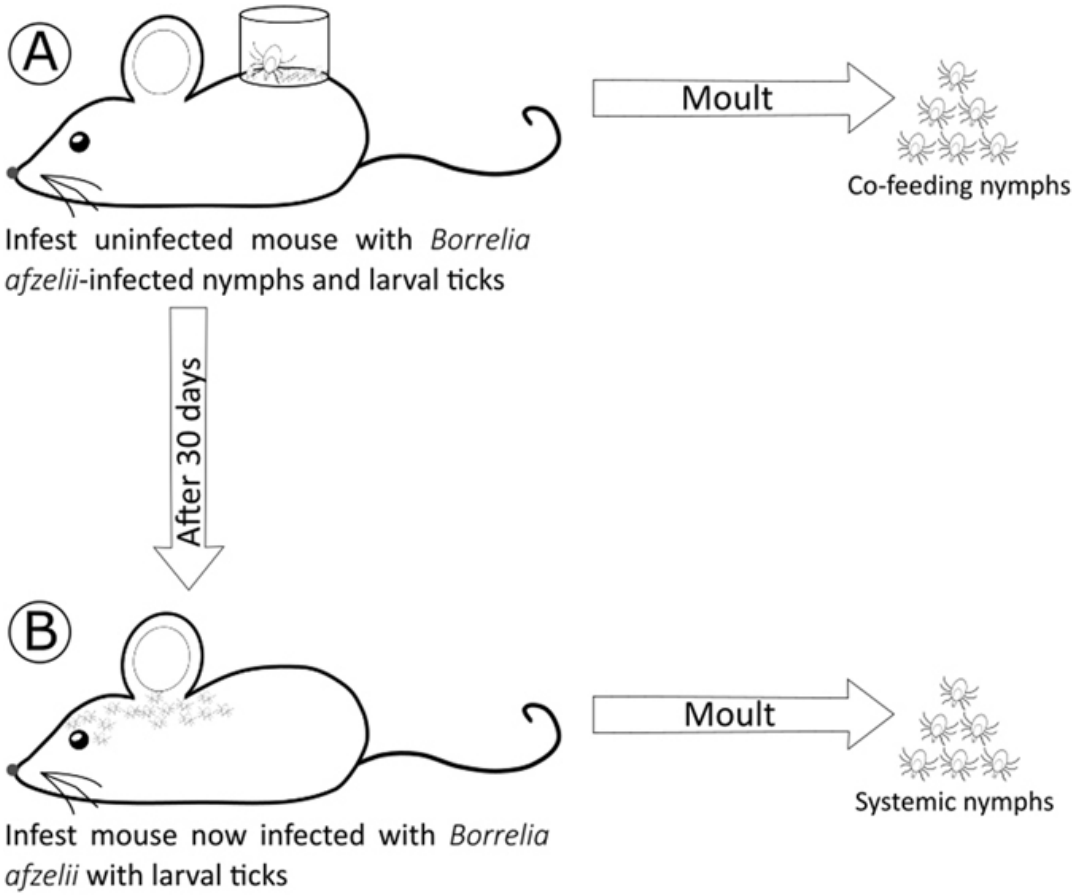

Figure: A. co-feeding transmission (CT); B. systemic transmission (ST). From: Alessandro Belli et al., Scientific Reports, 2017. Co-feeding transmission of a susceptible larval tick by infected nymphal ticks when they are biting on the same host individual, with transmission probability dependent on the relative location of ticks on the host and the number of infected nymphal ticks

Modeling various aspects

- stage-structured tick population growth
- the impact of the dynamics of tick population and host densities on the persistence of tick-borne diseases
- distinct types of host species with differential competence of transmission
- patchy/reaction-diffusion models to describe the tick dispersal due to host movement or bird migration
- seasonality of tick populations and disease risk driven by seasonal weather variations
- tick spatial invasion and disease risk under climate change
- impact of food resources of rodents on tick abundance and disease risk
- co-feeding transmission

see more details from: Yijun Lou and Jianhong Wu, Modeling Lyme disease transmission, Infectious Disease Modelling, 2017.

Key components incorporated

- patchy environment (host movement)
- systemic and co-feeding transmission routes (different transmission routes)
- seasonal variations on disease transmission (seasonal environmental variations)

Modeling notations

- an n-patch model with indexed k-th patch (subscript k)
- three stages of tick population in an indexed patch: larvae (L_k), nymphs (N_k) and adults (A_k)
- tick and host populations have two infectious status: susceptible (superscript s) and infected (superscript i)
  - two subgroups for the host population in the k-th patch H_k: susceptible hosts H_k^s and infectious hosts H_k^i
  - five subgroups for the questing tick population in the k-th patch: susceptible ticks at different stages (L_k, N_k^s and A_k^s) and infectious ticks at different stages (N_k^i and A_k^i)
  - all newly-emerged ticks are susceptible
- movements of host: $m_{ij}(t)$ as the rodent migration rate from j-th patch to i-th patch

Transition diagram

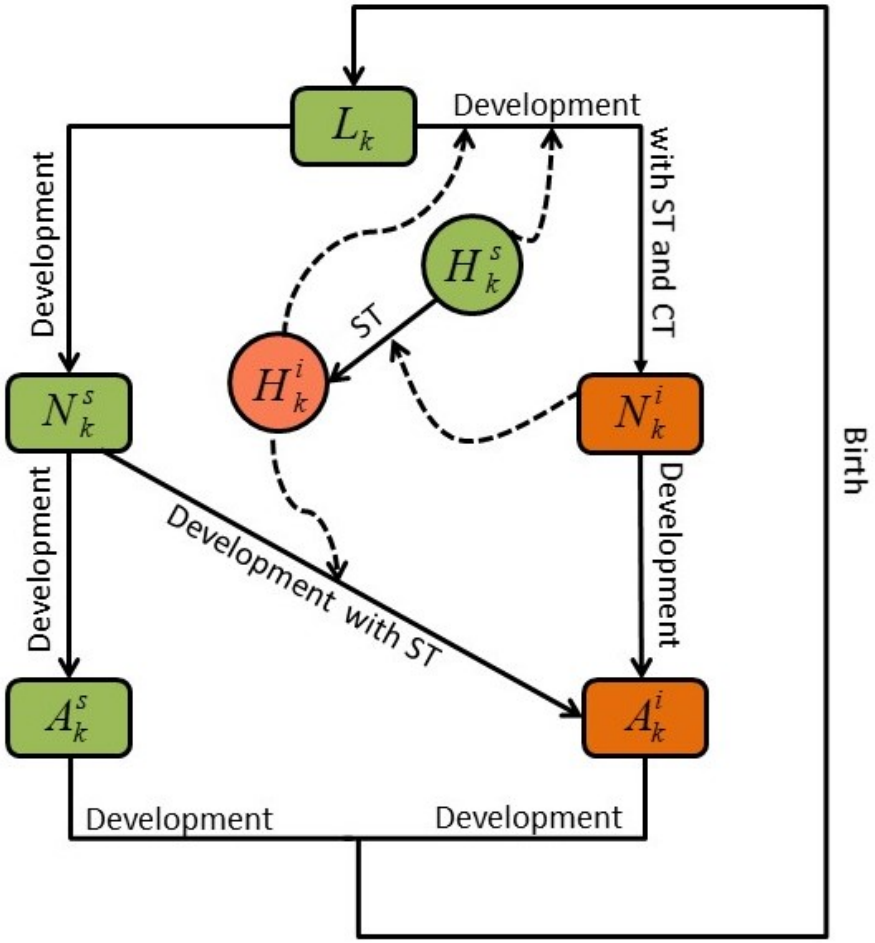

Figure: A schematic illustration of tick-borne disease dynamics with both systemic and co-feeding transmissions. ST: systematic transmission; CT: co-feeding transmission. Please note that in this diagram, L_k and N_k should be regarded as questing ticks looking for host for blood meal.

Co-feeding transmission term

- η_k: the probability that a susceptible larva gets infection from a co-feeding infected nymph through co-feeding transmission
- $(1-\eta_k)^N$: the probability that a susceptible larva will not get infection through co-feeding transmission when N infected nymphs are biting on the same host
- $1-(1-\eta_k)^N$: the probability that a susceptible larva becomes infected through co-feeding with N number of infectious nymphs
- Assume that feeding nymphs are evenly distributed in all rodent, at time t, there are $N_k^i(t)$ infected nymphs in patch k with the rodent population size $H_k(t)$, then $N = N_k^i(t)/H_k(t)$
- Ref: Nah et al., PloS One, 2019
- Remark: Actually, the distributions of ticks on hosts may obey other complicated forms, such as a Poisson distribution, which may derive other incidence terms

The model (tick equations)

$$\frac{dL_k(t)}{dt} = \rho_k(t)A_k(t) - d_k^L(t)L_k(t) - \mu_k^L(t)L_k^2(t) - \beta_k^L(t)H_k(t)L_k(t), \textbf{(larvae)}$$

$$\begin{aligned}\frac{dN_k^s(t)}{dt} = {} & m_k^L(t)\beta_k^L(t)H_k(t)L_k(t) - d_k^N(t)N_k^s(t) - \mu_k^N(t)N_k(t)N_k^s(t) - \beta_k^N(t)H_k(t)N_k^s(t) \\ & -\zeta_k^L m_k^L(t)\beta_k^L(t)H_k^i(t)L_k(t) - \left(1-(1-\eta_k)^{N_k^i(t)/H_k(t)}\right)m_k^L(t)\beta_k^L(t)H_k^s(t)L_k(t) \\ & -\left(1-(1-\eta_k)^{N_k^i(t)/H_k(t)}\right)(1-\zeta_k^L)m_k^L(t)\beta_k^L(t)H_k^i(t)L_k(t), \textbf{(susceptible nymph}\end{aligned}$$

$$\begin{aligned}\frac{dN_k^i(t)}{dt} = {} & \zeta_k^L m_k^L(t)\beta_k^L(t)H_k^i(t)L_k(t) + \left(1-(1-\eta_k)^{N_k^i(t)/H_k(t)}\right)m_k^L(t)\beta_k^L(t)H_k^s(t)L_k(t) \\ & +\left(1-(1-\eta_k)^{N_k^i(t)/H_k(t)}\right)(1-\zeta_k^L)m_k^L(t)\beta_k^L(t)H_k^i(t)L_k(t) - d_k^N(t)N_k^i(t) \\ & -\mu_k^N(t)N_k(t)N_k^i(t) - \beta_k^N(t)H_k(t)N_k^i(t), \textbf{(infected nymphs)}\end{aligned}$$

$$\begin{aligned}\frac{dA_k^s(t)}{dt} = {} & m_k^N(t)\beta_k^N(t)H_k(t)N_k^s(t) - d_k^A(t)A_k^s(t) - \mu_k^A(t)A_k(t)A_k^s(t) \\ & -\beta_k^A(t)D_kA_k^s(t) - \zeta_k^N m_k^N(t)\beta_k^N(t)H_k^i(t)N_k^s(t), \textbf{(susceptible adults)}\end{aligned}$$

$$\begin{aligned}\frac{dA_k^i(t)}{dt} = {} & m_k^N(t)\beta_k^N(t)H_k(t)N_k^i(t) + \zeta_k^N m_k^N(t)\beta_k^N(t)H_k^i(t)N_k^s(t) - d_k^A A_k^i(t) \\ & -\mu_k^A(t)A_k(t)A_k^i(t) - \beta_k^A(t)D_kA_k^i(t). \textbf{(infected adults)}\end{aligned}$$

Equations for hosts for immature ticks

(susceptible hosts)

$$\frac{dH_k^s(t)}{dt} = d_k^H H_k(t) - d_k^H H_k^s(t) - \zeta_k^H \beta_k^N(t) H_k^s(t) N_k^i(t) + \sum_{j=1, j\neq k}^{n} m_{kj}(t) H_j^s(t) - \sum_{j=1, j\neq k}^{n} m_{jk}(t) H_k^s(t),$$

(infected hosts)

$$\frac{dH_k^i(t)}{dt} = \zeta_k^H \beta_k^N(t) H_k^s(t) N_k^i(t) - d_k^H H_k^i(t) + \sum_{j=1, j\neq k}^{n} m_{kj}(t) H_j^i(t) - \sum_{j=1, j\neq k}^{n} m_{jk}(t) H_k^i(t)$$

- $\zeta_k^L m_k^L(t) \beta_k^L(t) H_k^i(t) L_k(t)$ and $\zeta_k^H \beta_k^N(t) H_k^s(t) N_k^i(t)$: the incidence term of systemic transmission route
- $\left(1 - (1-\eta_k)^{N_k^i(t)/H_k(t)}\right) m_k^L(t) \beta_k^L(t) H_k^s(t) L_k(t)$ and $\left(1 - (1-\eta_k)^{N_k^i(t)/H_k(t)}\right)(1-\zeta_k^L) m_k^L(t) \beta_k^L(t) H_k^i(t) L_k(t)$: the incidence rates of co-feeding transmission routes when larvae biting susceptible and infectious hosts, respectively
- All parameters are positive. All time-dependent parameters are continuous and $\omega = 1$ year-periodic functions

the host population in k-th patch:

$$\frac{dH_k(t)}{dt} = \sum_{j=1, j\neq k}^{n} m_{kj}(t)H_j(t) - \sum_{j=1, j\neq k}^{n} m_{jk}(t)H_k(t),$$

which can be rewritten into

$$\frac{dH(t)}{dt} = M(t)H(t),$$

where $H(t) = (H_1(t), H_2(t), \cdots, H_n(t))^T$ and the mobility matrix

$$M(t) = \begin{bmatrix} -\sum_{j=1, j\neq 1}^{n} m_{j1}(t) & m_{12}(t) & \dots & m_{1n}(t) \\ & & \ddots & \vdots \\ m_{n1}(t) & m_{n2}(t) & \dots & -\sum_{j=1, j\neq n}^{n} m_{jn}(t) \end{bmatrix}$$

Assumption: the mobility matrix $M(t)$ consisting of the migration rates among various patches is irreducible. That is, the patches as vertices following the matrix $M(t)$ as arcs of a directed digraph are strongly connected under the migration of host population

Theorem

Assume that the mobility matrix $M(t)$ is irreducible in the host migration model. Then it has a unique positive ω-periodic solution $H^*(t) = (H_1^*(t), H_2^*(t), \cdots, H_n^*(t))$ which is globally asymptotically stable to any positive solution.

Remark: (i) Without loss of generality, assume $H_k^s(t) + H_k^i(t) = H_k^*(t)$, $k = 1, 2, \cdots, n$; (ii) $A_k(t) = A_k^s(t) + A_k^i(t)$ admits:

$$\frac{dA_k(t)}{dt} = m_k^N(t)\beta_k^N(t)H_k(t)N_k(t) - d_k^A(t)A_k(t) - \mu_k^A(t)A_k^2(t) - \beta_k^A(t)D_kA_k(t)$$

Using population densities of nymphs $N_k^s(t) = N_k(t) - N_k^i(t)$, adult ticks $A_k^s(t) = A_k(t) - A_k^i(t)$ and rodents $H_k^s(t) = H_k(t) - H_k^i(t)$ to replace susceptibles (7 equations model to 5 equations system):

$$\frac{dL_k(t)}{dt} = \rho_k(t)A_k(t) - d_k^L(t)L_k(t) - \mu_k^L(t)L_k^2(t) - \beta_k^L(t)H_k(t)L_k(t),$$

$$\frac{dN_k(t)}{dt} = m_k^L(t)\beta_k^L(t)H_k(t)L_k(t) - d_k^N(t)N_k(t) - \mu_k^N(t)N_k^2(t) - \beta_k^N(t)H_k(t)N_k(t),$$

$$\frac{dA_k(t)}{dt} = m_k^N(t)\beta_k^N(t)H_k(t)N_k(t) - d_k^A(t)A_k(t) - \mu_k^A(t)A_k^2(t) - \beta_k^A(t)D_kA_k(t),$$

$$\begin{aligned}\frac{dN_k^i(t)}{dt} =& \zeta_k^L m_k^L(t)\beta_k^L(t)H_k^i(t)L_k(t) + \left(1-(1-\eta_k)^{N_k^i(t)/H_k(t)}\right)\left(H_k(t) - \zeta_k^L H_k^i(t)\right) \\ & \cdot m_k^L(t)\beta_k^L(t)L_k(t) - d_k^N(t)N_k^i(t) - \mu_k^N(t)N_k(t)N_k^i(t) - \beta_k^N(t)H_k(t)N_k^i(t),\end{aligned}$$

$$\begin{aligned}\frac{dH_k^i(t)}{dt} =& \zeta_k^H\beta_k^N(t)(H_k(t) - H_k^i(t))N_k^i(t) - d_k^H H_k^i(t) + \sum_{j=1,j\neq k}^{n} m_{kj}(t)H_j^i(t) \\ & - \sum_{j=1,j\neq k}^{n} m_{jk}(t)H_k^i(t)\end{aligned}$$

A decoupled system for tick growth in patch $k = 1, 2, \ldots, n$:

$$\begin{aligned}
\frac{dL_k(t)}{dt} &= \rho_k(t)A_k(t) - d_k^L(t)L_k(t) - \mu_k^L(t)L_k^2(t) - \beta_k^L(t)H_k^*(t)L_k(t),\\
\frac{dN_k(t)}{dt} &= m_k^L(t)\beta_k^L(t)H_k^*(t)L_k(t) - d_k^N(t)N_k(t) - \mu_k^N(t)N_k^2(t) - \beta_k^N(t)H_k^*(t)N_k(t),\\
\frac{dA_k(t)}{dt} &= m_k^N(t)\beta_k^N(t)H_k^*(t)N_k(t) - d_k^A(t)A_k(t) - \mu_k^A(t)A_k^2(t) - \beta_k^A(t)D_kA_k(t)
\end{aligned}$$

- $\mathcal{R}_T^{(k)}$: Net reproduction number of ticks in k-th patch
- reordering: Without loss of generality, by relabelling each patch, assume $\mathcal{R}_T^{(i)} \geq \mathcal{R}_T^{(j)}$ whenever $i < j$
- maximum and minimum net reproduction number for all patches:

$$\mathcal{R}_T^{max} = \max_{1\leq k\leq n} \mathcal{R}_T^{(k)} = \mathcal{R}_T^{(1)} \quad \text{and} \quad \mathcal{R}_T^{min} = \min_{1\leq k\leq n} \mathcal{R}_T^{(k)} = \mathcal{R}_T^{(n)}$$

Theorem

(i) *If* $\mathcal{R}_T^{max} \leq 1$, *the tick-free equilibrium is globally asymptotically stable (no ticks in all patches)*

(ii) *If* $\mathcal{R}_T^{min} > 1$, *the system has a unique* ω*-periodic solution*

$$(L^*(t), N^*(t), A^*(t)) = (L_1^*(t), \cdots, L_n^*(t), N_1^*(t), \cdots, N_n^*(t), A_1^*(t), \cdots, A_n^*(t))$$

which is globally asymptotically attractive for each positive solution. (ticks establish in all patches)

(iii) *If* $\mathcal{R}_T^{min} \leq 1 < \mathcal{R}_T^{max}$, *there exists a unique* K *with* $0 < K < n$ *such that* $\mathcal{R}_T^{(K)} > 1$ *while* $\mathcal{R}_T^{(K+1)} \leq 1$. *Moreover,*

$$\lim_{t\to\infty} (L_k(t), N_k(t), A_k(t)) = (L_k^*(t), N_k^*(t), A_k^*(t))$$

$$\text{and } \lim_{t\to\infty} (L_p(t), N_p(t), A_p(t)) = (0, 0, 0)$$

for $1 \leq k \leq K$ *and* $K+1 \leq p \leq n$. *(ticks establish in some, but not all, patches)*

The pathogen transmission described by infected ticks and hosts:

$$\frac{dN_k^i(t)}{dt} = \zeta_k^L m_k^L(t)\beta_k^L(t)H_k^i(t)L_k^*(t) + \left(1-(1-\eta_k)^{N_k^i(t)/H_k^*(t)}\right)\left(H_k^*(t)-\zeta_k^L H_k^i(t)\right)$$
$$\cdot m_k^L(t)\beta_k^L(t)L_k^*(t) - d_k^N(t)N_k^i(t) - \mu_k^N(t)N_k^*(t)N_k^i(t) - \beta_k^N(t)H_k^*(t)N_k^i(t),$$
$$\frac{dH_k^i(t)}{dt} = \zeta_k^H\beta_k^N(t)(H_k^*(t)-H_k^i(t))N_k^i(t) - d_k^H H_k^i(t) + \sum_{j=1,j\neq k}^{n} m_{kj}(t)H_j^i(t)$$
$$- \sum_{j=1,j\neq k}^{n} m_{jk}(t)H_k^i(t)$$

- For a patch with the net reproduction number smaller than or equal to unity, that is $\mathcal{R}_T^{(k)} \leq 1$, there will be no ticks. For this unfavorable patch for ticks, we have $\lim_{t\to\infty} N_k^i(t) = \lim_{t\to\infty} N_k(t) = 0$ as $N_k^i(t) \leq N_k(t)$
- The scenario $\mathcal{R}_T^{min} > 1$: the tick population in patch k will eventually follow the seasonal pattern $(L^*(t), N^*(t), A^*(t))$. Then we can define the basic reproduction number $\mathcal{R}_0$ for disease transmission
- The scenario $\mathcal{R}_T^{max} \leq 1$: it makes no sense to define the basic reproduction number $\mathcal{R}_0$ for disease transmission (the disease free-state is zero)
- The scenario $\mathcal{R}_T^{min} \leq 1 < \mathcal{R}_T^{max}$: ticks establish in the first K patches while the remaining $n-K$ patches are unfavorable. patches for ticks. basic reproduction number, denoted as $\tilde{\mathcal{R}}_0$.

1. If $\mathcal{R}_T^{max} \le 1$, the zero equilibrium is globally attractive. (no pathogen in all patches)
2. When $\mathcal{R}_T^{min} > 1$
   - 2.1 If $\mathcal{R}_0 \le 1$, the disease-free state $(L^*(t), N^*(t), A^*(t), 0, 0)$ is globally attractive. (no pathogen in all patches)
   - 2.2 If $\mathcal{R}_0 > 1$, the unique positive ω-periodic solution $(L^*(t), N^*(t), A^*(t), N^{i*}(t), H^{i*}(t))$ is globally attractive. (pathogen invades successfully in all patches)
3. When $\mathcal{R}_T^{max} > 1 \ge \mathcal{R}_T^{min}$, then

$$\lim_{t\to\infty}(N_k(t) - N_k^*(t)) = 0 \text{ and } \lim_{t\to\infty} N_p^i(t) = \lim_{t\to\infty} N_p(t) = 0$$

for $1 \le k \le K$ and $K+1 \le p \le n$. Furthermore, we have

- 3.1 If $\tilde{\mathcal{R}}_0 \le 1$, then $\lim_{t\to\infty} N_k^i(t) = 0$ and $\lim_{t\to\infty} H_q^i(t) = 0$ for $1 \le k \le K$ and $1 \le q \le n$; (no pathogen in all patches)
- 3.2 If $\tilde{\mathcal{R}}_0 > 1$, then there are unique positive ω-periodic functions $N_k^{i*}(t)$ and $H_q^{i*}(t)$ such that $\lim_{t\to\infty}(N_k^i(t) - N_k^{i*}(t)) = 0$ and $\lim_{t\to\infty}(H_q^i(t) - H_q^{i*}(t)) = 0$ for $1 \le k \le K$ and $1 \le q \le n$. (pathogen invades successfully in some, but not all, patches)

Table: Different parameter values of the model with 2 patches. Please note that parameter values of $\rho_k(t)$ and $d_k^N(t)$ in k-th patch ($k = 1, 2$) are set to be out of phase, which implies mortality rate of nymphs is high only sometimes after the recruitment rate of larvae is high.

Parameter	Patch 1 ($k = 1$)	Patch 2 ($k = 2$)
$\rho_k(t)$	$0.45 - 0.1\cos(\frac{2\pi t}{365})$ (day^{-1})	$0.41 - 0.1\cos(\frac{2\pi t}{365})$ (day^{-1})
$d_k^N(t)$	$0.035 - 0.02\sin(\frac{2\pi t}{365})$ (day^{-1})	$0.03 - 0.01\sin(\frac{2\pi t}{365})$ (day^{-1})
d_k^H	0.01 (day^{-1})	0.03 (day^{-1})
D_k	15	20
ζ_k^L	0.5	0.25
ζ_k^N	0.5	0.25
ζ_k^H	0.5	0.3
$H_k(0)$	250	180

Solution simulation

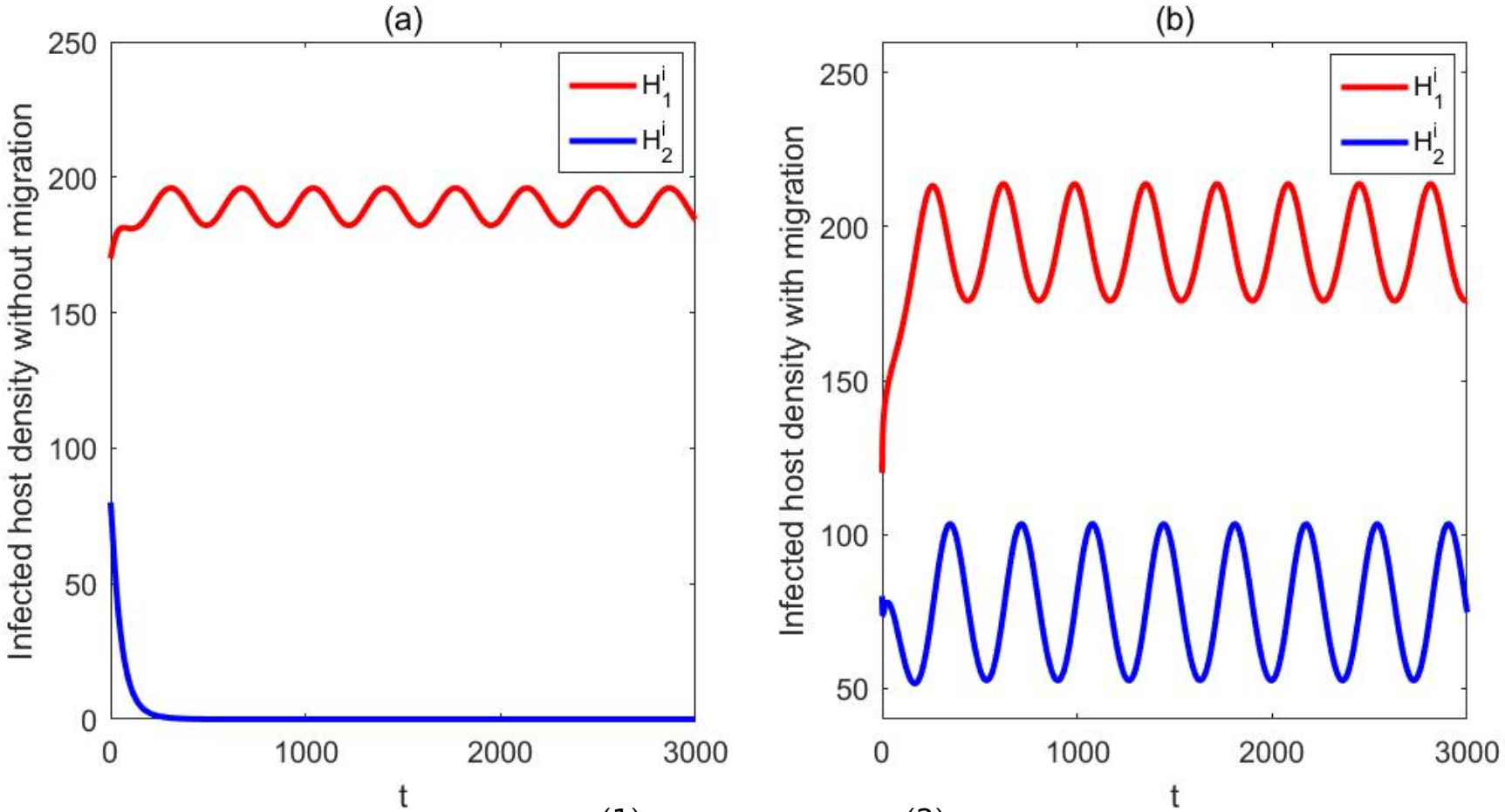

Figure: (a) Without host migration, $R_T^{(1)} = 1.56$ and $R_T^{(2)} = 1.27$, $\mathcal{R}_0^1 = 1.88$, $\mathcal{R}_0^2 = 0.61$; (b) When hosts are allowed to move between patches ($m_{12}(t) = 0.5$ and $m_{21}(t) = 0.2$), $\mathcal{R}_0 = 1.43$.

Sensitivity analysis

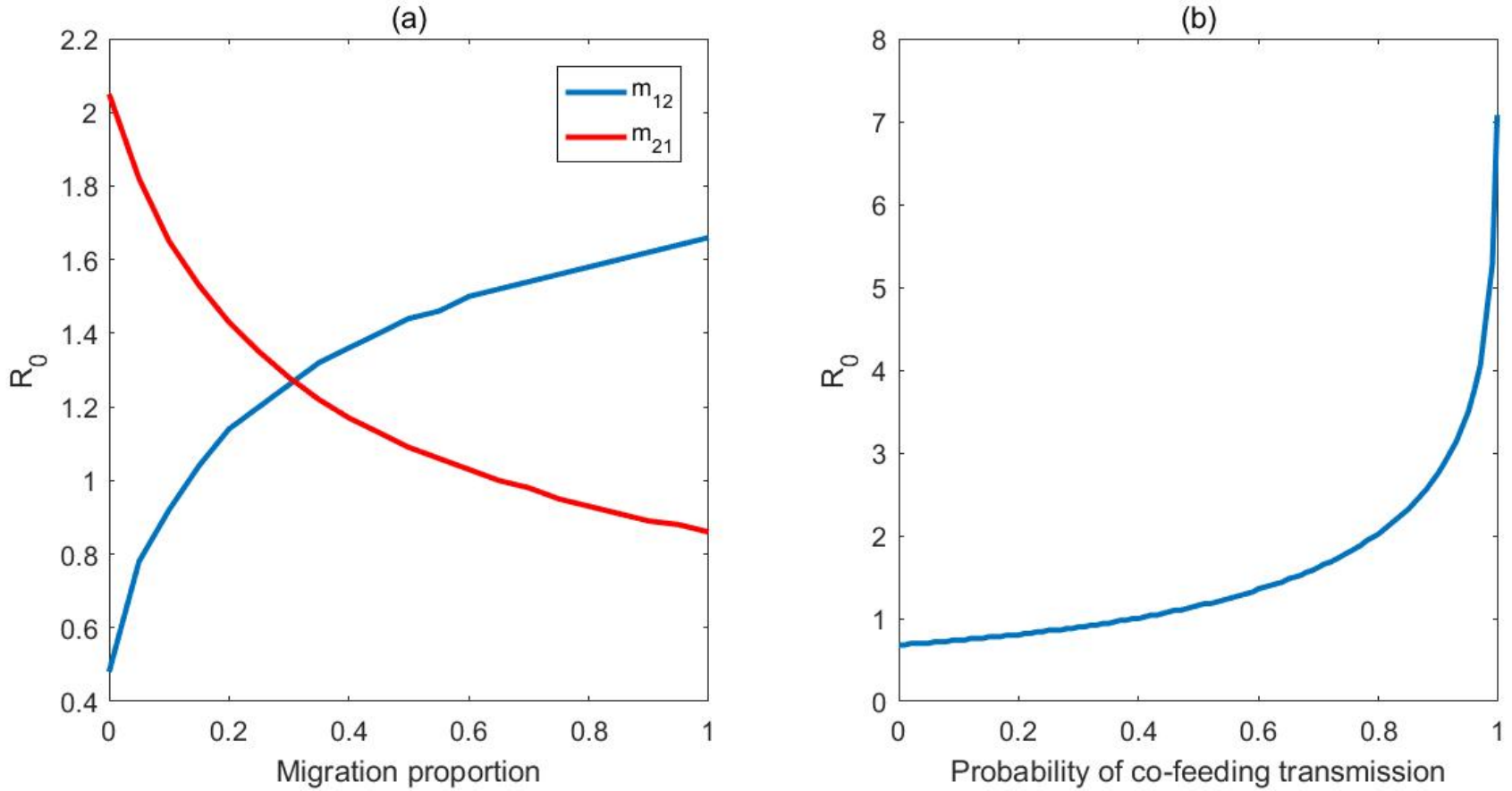

Figure: The basic reproduction numbers vary with the host migration proportions and probability of co-feeding transmission. (a) The blue (red) curve shows the basic reproduction number is increasing (decreasing) with respect to $m_{12} \in [0, 1]$ ($m_{21} \in [0, 1]$) when $m_{21} = 0.2$ ($m_{12} = 0.5$), $\eta_k = 0.04$; (b) The basic reproduction number is increasing with respect to $\eta_k \in [0, 1]$ when $m_{12} = 0.15$, $m_{21} = 0.6$.

Table: Different parameter values of model with 9 patches.

Patch	ρ_k	η_k^L	β_k^L	β_k^N	$H_k(0)$
P_1	$0.6-0.04\cos(2\pi t/365)$	0.45	0.0015	0.0015	230
P_2	$0.51-0.06\cos(2\pi t/365)$	0.35	0.0012	0.0012	250
P_3	$0.46-0.1\cos(2\pi t/365)$	0.4	0.0009	0.0009	220
P_4	$0.43-0.1\cos(2\pi t/365)$	0.28	0.00087	0.00087	250
P_5	$0.45-0.1\cos(2\pi t/365)$	0.3	0.0012	0.0012	230
P_6	$0.38-0.1\cos(2\pi t/365)$	0.32	0.00039	0.00039	230
P_7	$0.42-0.05\cos(2\pi t/365)$	0.2	0.0006	0.0006	200
P_8	$0.21-0.05\cos(2\pi t/365)$	0.1	0.0009	0.0009	180
P_9	$0.25-0.05\cos(2\pi t/365)$	0.05	0.00045	0.00045	200

Table: Net reproduction numbers and basic reproduction numbers for 9 patches.

	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8	P_9
$\mathcal{R}_T$	2.12	1.83	1.61	1.44	1.48	1.34	1.34	0.65	0.86
$\mathcal{R}_0$	2.47	1.92	1.64	1.36	1.8	0.88	0.95	not defined	not defined

Disease risk in a patch network

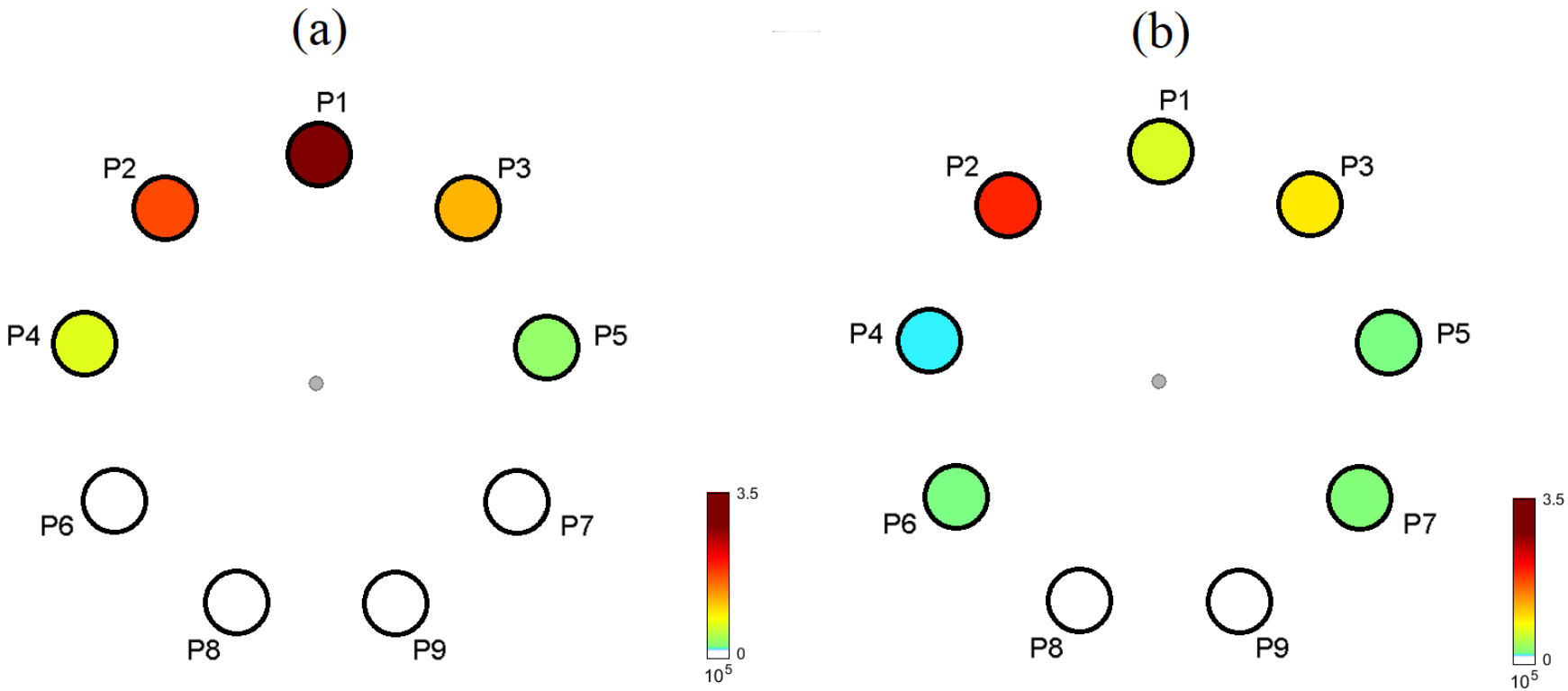

Figure: The comparison of accumulated infected nymph density in a year: (a) 9 patches are isolated from each other; (b) host population can move freely among 9 patches.

Table: Accumulated yearly nymphal ticks (AYNT) and accumulated yearly infected nymphal ticks (AYINT) with and without migration, and their comparisons for 9 patches ($\times 10^5$). TN: total number.

	Without migration		With migration		Comparisons	
	AYNT	AYINT	AYNT	AYINT	AYNT	AYINT
P_1	3.6599	3.5098	0.5973	0.5694	−3.0626	−2.9404
P_2	2.3746	1.7109	2.4389	1.8927	0.0643	0.1818
P_3	1.7637	1.1409	1.7451	0.8656	−0.0186	−0.2753
P_4	1.0794	0.2164	0.8644	0.0773	−0.2150	−0.1391
P_5	1.2771	0.6064	1.0947	0.4834	−0.1824	−0.1230
P_6	0.8382	0.0000	0.8194	0.1034	−0.0188	0.1034
P_7	0.9296	0.0000	0.8208	0.1261	−0.1088	0.1261
P_8	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
P_9	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TN	11.9225	7.1844	8.3806	4.1179	−3.5419	−3.0665

Discussion

- Migration can help/inhibit the tick establishment and disease persistence in more patches
- Migration can not guarantee a larger total tick population size and total infected ticks
- Migration may increase/decrease the reproduction numbers
- The relationship is very complicated: Migration may increase/decrease the tick population sizes in some patches, while decrease/increase the infected ticks

This talk is based on joint work:

- Yijun Lou and Jianhong Wu, Modeling Lyme disease transmission, Infectious Disease Modelling, 2017.
- Xue Zhang, Bei Sun and Yijun Lou, Dynamics of a periodic tick-borne disease model with co-feeding and multiple patches, Journal of Mathematical Biology, 2021.

Thank you!