Some effects of host movement in vector-borne disease systems

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Single Patch Model (Ross-Macdonald type)

\[ \frac{dx}{dt} = Mabz(1 - x) - rx, \]

\[ \frac{dz}{dt} = acx(e^{-mn} - z) - mz. \]

\( x \) fraction of infectious individuals in human population
\( y \) fraction of infectious individuals in mosquito population
\( a \) human feeding rate of mosquitoes (number of bites on humans, per mosquito, per unit time),
\( b \) transmission efficiency from infectious mosquitoes to humans,
\( c \) transmission efficiency from infected humans to mosquitoes,
\( m \) mortality rate of mosquitoes,
\( r \) recovery rate of humans,
\( n \) incubation period from the time a mosquito becomes infected until it becomes infectious,
\( M \) ratio of mosquitoes to humans.
Spatial Models

Two approaches:

1. Describe interactions as local. Track densities of individuals at each location ("Eulerian"). Movement changes density until density equilibrates ("migration"). These sorts of models include reaction-diffusion equations, discrete diffusion systems, and integro-differential equations.

2. Allow interactions between individuals with different locations (think of “location” as “home address”). Track interactions between individuals from different locations, based on time budgets and movement patterns or other factors affecting contact between individuals. ("Lagrangian"). Movement does not directly change density associated with a given location ("commuting"). These sorts of models are mathematically similar to multi-group epidemiological models or Levins-Hanski type metapopulation models.

Either type of model can be formulated in discrete or continuous space, as a matrix model or integro-differential model respectively. The “Eulerian” models can also be formulated as reaction-diffusion systems in continuous space.
Eulerian Models in Discrete Space

Since movement may change population densities in this modeling framework, we will work with populations instead of proportions of populations:

- $H_i$ represents the total human population in patch $i$,
- $X_i$ represents the number of infected humans in patch $i$,
- $V_i$ represents the total mosquito population in patch $i$,
- $Y_i$ represents the number of infected mosquitoes in patch $i$.

The basic movement models on a network of $N$ patches take the form

$$\frac{dH_i}{dt} = \sum_{j=1, j \neq i}^{N} C_{ij}H_j - (\sum_{j=1, j \neq i}^{N} C_{ji})H_i,$$

$$\frac{dV_i}{dt} = \sum_{j=1, j \neq i}^{N} D_{ij}V_j - (\sum_{j=1, j \neq i}^{N} D_{ji})V_i, \quad i = 1, \ldots, N.$$  

where $C_{ij}$ and $D_{ij}$ are movement rates from patch $i$ to patch $j$. 

Eulerian Models in Continuous Space

Let \( \Omega \subseteq \mathbb{R}^n \) denote a spatial domain and \( x \) a point in \( \Omega \). The human movement model for discrete space

\[
\frac{dH_i}{dt} = \sum_{j=1\atop j\neq i}^{N} C_{ij} H_j - \left( \sum_{j=1\atop j\neq i}^{N} C_{ji} \right) H_i
\]

would be replaced by the nonlocal model

\[
\frac{\partial H(x,t)}{\partial t} = \int_{\Omega} C(x,y)H(y,t)dy - \int_{\Omega} C(y,x)dyH((x,t)
\]

or the diffusion-advection model (with diffusion rate \( d(x) \) and advection \( p(x) \))

\[
\frac{\partial H}{\partial t} = \nabla \cdot [d(x)\nabla H - H p(x)]
\]

Movement models of the first and third type with the same SIS dynamics were studied using similar methods by LJS Allen, BM Bolker, Y Lou, and AL Nevai:


Eulerian Models with Epidemiology

Fact: In the Eulerian movement models above, population densities approach a spatial equilibrium if there are no population dynamics:

Total human population in patch $i = H_i$, with $H_i \to H_i^*$ as $t \to \infty$.
Similarly, total mosquito population in patch $i = V_i$ with $V_i \to V_i^*$ as $t \to \infty$.

$X_i =$ number of infected humans in patch $i$,
$Y_i =$ number of infected mosquitoes in patch $i$.

A simple model is

$$\frac{dX_i}{dt} = A_i Y_i (H_i^* - X_i) - r_i X_i + \sum_{j=1, j \neq i}^{N} C_{ij} X_j - (\sum_{j=1, j \neq i}^{N} C_{ji}) X_i,$$

$$\frac{dY_i}{dt} = B_i X_i (V_i^* - Y_i) - m_i Y_i + \sum_{j=1, j \neq i}^{N} D_{ij} Y_j - (\sum_{j=1, j \neq i}^{N} D_{ji}) Y_i, \quad i = 1, \ldots, N,$$

Eulerian Models with Epidemiology, Continued

This type of model can also allow population growth or decline, and can be extended to cover more complicated disease dynamics such as SEIR:


Such models can be analyzed by using the celebrated matrix-theoretic formula for $R_0$ developed in


The analogous formulation extended to the reaction-diffusion case is given in


There are results on traveling waves for Eulerian models; see for example

S Ruan and J Wu, Modeling the spatial spread of communicable diseases with animal hosts, p. 293-315 in Spatial Ecology (eds. RS Cantrell, C Cosner and S Ruan), Chapman Hall/CRC, 2010.
Lagrangian Models in Discrete Space

These models assume constant numbers of individuals with “home address” in each patch, allow individuals to visit other patches, and track their contacts. As before, $H_i$ and $X_i$ are total numbers of humans and infected humans, and $V_i$ and $Y_i$ are total numbers of mosquitoes and infected mosquitoes, with “addresses” in patch $i$.

$p_{ij}$ represents the fraction of time a human from patch $i$ spends in patch $j$

$q_{ij}$ represents the fraction of time a mosquito from patch $i$ spends in patch $j$.

Note that $\sum_{j=1}^{N} p_{ij} = \sum_{j=1}^{N} q_{ij} = 1$. Let $A_{ij} = \frac{a_j b_j p_{ij} e^{-m_j n_j}}{H_j}$ and $B_{ij} = \frac{a_j c_j q_{ij}}{H_j}$.

(Transmission rates weighted by time schedule.) The models then have the form

$$\frac{dX_i}{dt} = \left( \sum_{j=1}^{N} A_{ij} Y_j \right) (H_i - X_i) - r_i X_i,$$

$$\frac{dY_i}{dt} = \left( \sum_{j=1}^{N} B_{ij} X_j \right) (V_i - Y_i) - m_i Y_i, \quad i = 1, \ldots, N.$$
More on Lagrangian Models

Discrete case

\[
\begin{align*}
\frac{dX_i}{dt} &= (\sum_{j=1}^{N} A_{ij}Y_j)(H_i - X_i) - r_iX_i, \\
\frac{dY_i}{dt} &= (\sum_{j=1}^{N} B_{ij}X_j)(V_i - Y_i) - m_iY_i, \quad i = 1, \ldots, N.
\end{align*}
\]


For \( \Omega \subseteq \mathbb{R}^n \), using \( \rho, \sigma \in \Omega \) instead of \( i, j \), a continuum version is

\[
\begin{align*}
\frac{\partial X(\rho)}{\partial t} &= (H(\rho) - X(\rho)) \int_{\Omega} A(\rho, \sigma)Y(\sigma)d\sigma - r(\rho)X(\rho), \\
\frac{\partial Y(\rho)}{\partial t} &= (V(\rho) - Y(\rho)) \int_{\Omega} B(\rho, s)X(\sigma)d\sigma - m(\rho)Y(\rho).
\end{align*}
\]


More on Lagrangian Models

Discrete case again:

\[
\frac{dX_i}{dt} = \left( \sum_{j=1}^{N} A_{ij} Y_j \right) (H_i - X_i) - r_i X_i, \\
\frac{dY_i}{dt} = \left( \sum_{j=1}^{N} B_{ij} X_j \right) (V_i - Y_i) - m_i Y_i, \quad i = 1, \ldots, N.
\]

Compare to Hanski-type metapopulation models: \( P_i \) = probability patch \( i \) is occupied, \( c_{ij} \) = colonization rate from patch \( i \) to patch \( j \), \( e_i \) = extinction rate on patch \( i \).

\[
\frac{dP_i}{dt} = \left( \sum_{j=1}^{N} c_{ij} P_j \right) (1 - P_i) - e_i P_i,
\]

This is mathematically identical to one of the models in

Models of this general type can describe populations with various types of heterogeneity, spatial or otherwise.
Some results: Eulerian Models

Two patches, transmission in only one:

\[
\frac{dX_1}{dt} = A_1 Y_1 (H_1^* - X_1) - r_1 X_1 + C_{12} X_2 - C_{21} X_1 \\
\frac{dX_2}{dt} = -C_{12} X_2 + C_{21} X_1 \\
\frac{dY_1}{dt} = B_1 X_1 (V_1^* - Y_1) - m_1 Y_1
\]

For this model,

\[
R_0^2 = \frac{A_1 B_1 H_1^* V_1^*}{m_1} \cdot \frac{C_{12} + r_2}{C_{12} r_1 + C_{21} r_2 + r_1 r_2}
\]

Increasing \(C_{12}\) (movement rate of infectious humans from no transmission patch 2 to high transmission patch 1) increases \(R_0\). Increasing \(C_{21}\) (movement rate of infectious humans from high transmission patch 1 to no transmission patch 2) decreases \(R_0\). Thus, depending on the details of the remaining coefficients, changing human movement rates can shift the disease from endemicity to extinction or vice-versa.
Some results: Lagrangian Models

Again, two patches, transmission in only one:

\[
\begin{align*}
\frac{dX_1}{dt} &= A_{11}Y_1(H_1 - X_1) - r_1X_1 \\
\frac{dX_2}{dt} &= A_{21}Y_1(H_2 - X_2) - r_2X_2 \\
\frac{dY_1}{dt} &= (B_{11}X_1 + B_{12}X_2)(V_1 - Y_1) - m_1Y_1.
\end{align*}
\]

In this case

\[ R_0^2 = \frac{A_{11}B_{11}H_1V_1}{r_1m_1} + \frac{A_{21}B_{21}H_2V_1}{r_2m_1}. \]

The first term is the value for $R_0^2$ for the first patch in isolation. Clearly “movement” can increase $R_0$. In cases with transmission in both patches, in some cases the disease is not endemic in either patch in isolation but is with contact. An important idea in this context is “activity space”, a description of the space-time budget of individuals.

Some related work


A broader survey:
What about mosquito movement?

Some references:


(Eulerian models for mosquito movement in patchy environments; humans don’t move, mosquito movement rates decrease in patches with humans and/or water.)


(Model for the trajectories of individual mosquitoes seeking and/or odor plumes.)
References


