1 PMoveSTIR in continuous space

In the main text, we derive PMoveSTIR assuming that hosts are moving and contacting each other within some area A_x, which we can conceptually think about as a grid cell on a gridded landscape. While this conceptually simplifies the problem, it is more general to consider the case of continuous space where we define contact as potentially happening when present or past host j is (was) within some distance r of host i at its present location (Wilber et al., 2022). The output we want from this alternative version of PMoveSTIR is the function $\hat{h}^*(x,t)$, which is the force of infection *per unit area* at point x on the landscape (e.g., $\hat{h}^*(x,t)$ might have units $\text{day}^{-1}\text{m}^{-2}$). Integrating this function over different areas will yield estimates of force of infection felt by host i from host j for any area of interest on the landscape.

Let's start with the situation where a host i is occupying some circular area $A_{x,\rho}$ where x is the center of the area and ρ is the radius of the area. A contact can occur when host j (past or present) is in the area $A_{x,\rho+r}$ where r is our epidemilogically relevant contact distance and $r >> \rho$. The force of infection felt by host i from host j as time t in area $A_{x,\rho}$ is given by

$$h_{i \leftarrow j}(t, A_{x,\rho}) = \int_{-\infty}^{t} \beta' \lambda \delta'_{x_i(t)}(A_{x,\rho}) \delta'_{x_j(u)}(A_{x,\rho+r}) e^{-\nu(t-u)} du. \tag{1}$$

where, consistent with the main text, $\delta'_{x_i(t)}(A_{x,\rho})$ is a Bernoulli random variable that determines whether or not host i is located in area $A_{x,\rho}$ at time t and $\delta'_{x_j(u)}(A_{x,\rho+r})$ is a Bernoulli random variable that determines whether or not host j is in area $A_{x,\rho+r}$ at time u. The variables $x_i(t)$ and $x_j(u)$ indicate the locations of host i and j at time t and u, respectively. The parameter $\beta' = \frac{\tilde{\beta}}{A_{x,\rho+r}}$ and indicates our assumption that encounters are equally likely within an area $A_{x,\rho+r}$. The parameter λ is the pathogen shedding rate of host j and ν is the pathogen decay rate once deposited in the environment. As in the main text, we are computing maximum transmission risk and assuming that host j is always infected at any time u.

As we did in the main text, we can envision simulating many different movement trajectories for host i and j and take the expectation of $h_{i \leftarrow j}(t, A_{x,\rho})$. We obtain

$$h^*_{i \leftarrow j}(t, A_{x,\rho}) = \int_{-\infty}^{t} \beta' \lambda E[\delta'_{x_i(t)}(A_{x,\rho}) \delta'_{x_j(u)}(A_{x,\rho+r})] e^{-\nu(t-u)} du. \tag{2}$$

We can rewrite equation 2 as

$$h^*_{i \leftarrow j}(t, A_{x,\rho}) = \frac{\tilde{\beta}}{A_{x,\rho+r}} \lambda \int_{-\infty}^{t} [p_i(A_{x,\rho}, t) p_j(A_{x,\rho+r}, u) + Cov(\delta'_{x_i(t)}(A_{x,\rho}), \delta'_{x_j(u)}(A_{x,\rho+r}))] e^{-\nu(t-u)} du, \tag{3}$$

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where the force of infection felt by host i from host j is the related to the utilization distributions of the two hosts and their covariance within an area (in actuality, two nested areas).

For simplicity, let's consider hosts moving independently. In this case, we can write

$$h_{i\leftarrow j}^*(t, A_{x,\rho}) = \beta'\lambda \int_{-\infty}^{t} [p_i(A_{x,\rho}, t)p_j(A_{x,\rho+r}, u)]e^{-\nu(t-u)}du \tag{4}$$

where $p_i(A_{x,\rho}, t)$ is the probability of host i being in area $A_{x,\rho}$ at time t and $p_j(A_{x,\rho+r}, u)$ is the probability of host j being in area $A_{x,\rho+r}$ at time u.

Now we want to calculate $h_{i\leftarrow j}^*(t, A_{x,\rho})$ in the limit as $\rho \to 0$. For equation 4, we can divide both sides by $A_{x,\rho}$ and take the limit as $\rho \to 0$ (such that $A_{x,\rho} \to 0$). Doing this we obtain

$$\hat{h}_{i\leftarrow j}^*(t, x) = \beta'\lambda \int_{-\infty}^{t} [f_i(x, t)p_j(A_{x,r}, u)]e^{-\nu(t-u)}du = \beta'\lambda \int_{-\infty}^{t} [f_i(x, t)\int_{s\in A_{x,r}} f_j(s, u)ds]e^{-\nu(t-u)}du \tag{5}$$

where $f_i(x, t)$ and $f_j(x, t)$ are the probability density functions of space use for host i and host j, respectively. Note that the units on $f_i(x, t)$ or $f_j(x, t)$ are per area, such that the force of infection $\hat{h}_{i\leftarrow j}^*(t, x)$ has units per time per area as opposed to $h_{i\leftarrow j}^*(t, A_{x,\rho})$ which has units per time. Conceptually, for $h_{i\leftarrow j}^*(t, A_{x,\rho})$ we have already integrated over area so we cancel out the per area units.

Assuming a stationary process, we can write equation 5 as

$$\hat{h}_{i\leftarrow j}^*(t, x) = \frac{\beta'\lambda}{\nu}[f_i(x)\int_{s\in A_{x,r}} f_j(s)ds] \tag{6}$$

Furthermore, if we assume that the space use of host j is relatively uniform within the contact area $A_{x,r}$ we can simplify to

$$\hat{h}_{i\leftarrow j}^*(t, x) = \frac{\beta'\lambda}{\nu}[f_i(x)f_j(x)\pi r^2] \tag{7}$$

Remembering that $\beta' = \tilde{\beta}/A_{x,r} = \tilde{\beta}/\pi r^2$, we get

$$\hat{h}_{i\leftarrow j}^*(t, x) = \frac{\tilde{\beta}\lambda}{\nu}[f_i(x)f_j(x)] \tag{8}$$

Integrating $\hat{h}_{i\leftarrow j}^*(t, x)$ over some area of interest centered at x would yield $h_{i\leftarrow j}^*(t, A_{x,d}) = \frac{\tilde{\beta}\lambda}{\nu}\int_{A_{x,d}}[f_i(s)f_j(s)ds]$. This is reminiscent of the equation 17 in Martinez-Garcia et al. (2020) where a limiting case of the mean encounter rate of two individuals moving according to an Ornstein-Uhlenbeck movement process is proportional to the inner product of their utilization distributions.

Including correlation in movement into this formulation of PMoveSTIR is more theoretically and empirically challenging, and we leave this task for a later paper.

2   Deriving PMoveSTIR given an assumption of statistical stationarity

To derive equation 6 in the main text that assumes stationarity in utilization distributions, we start with equation 4 in the main text

$$h_{i \leftarrow j}^*(t, x) = \frac{\tilde{\beta}}{A_x} \lambda \int_{-\infty}^t [p_i(x, t) p_j(x, u) + Cov(\delta'_{x_i(t)}(x), \delta'_{x_j(u)}(x))] S(t - u) du. \tag{9}$$

Here, $p_i(x, t)$ and $p_j(x, u)$ represent the probabilities of host i and j using location x at time t and u, respectively. The parameters $\tilde{\beta}$ and λ are the acquisition and deposition rates respectively, and A_x is the area of location x. $Cov(\delta'_{x_i(t)}(x), \delta'_{x_j(u)}(x))$ gives the covariance in how host i and j at time t and u are using area x. Finally, $S(t - u)$ gives the survival probability of a pathogen at time t that was deposited at time u.

If we now assume a stationary utilization distribution, the time indexes on $p_i(x, t)$ and $p_j(x, u)$ are irrelevant – the logic here is that, by definition, the mean of a stationary distribution is independent of time so $p_i(x, t) = p_i(x)$ and $p_j(x, u) = p_j(x)$. Therefore, we can write

$$h_{i \leftarrow j}^*(t, x) = \frac{\tilde{\beta}}{A_x} \lambda \left[p_i(x) p_j(x) \int_0^\infty S(\tau) d\tau + \int_{-\infty}^t Cov(\delta'_{x_i(t)}(x), \delta'_{x_j(u)}(x)) S(t - u) du \right].$$

In addition, given stationarity, $h_{i \leftarrow j}^*(t, x)$ does not depend on time, such that

$$h_{i \leftarrow j}^*(x) = \frac{\tilde{\beta}}{A_x} \lambda \left[p_i(x) p_j(x) \int_0^\infty S(\tau) d\tau + \int_{-\infty}^t Cov(\delta'_{x_i(t)}(x), \delta'_{x_j(u)}(x)) S(t - u) du \right].$$

Moreover, given stationarity, we know that $Cov(\delta'_{x_i(t)}(x), \delta'_{x_j(u)}(x))$ just depends on the time lag $\tau = t - u$ and not specific time stamps. Thus, we can write

$$h_{i \leftarrow j}^*(x) = \frac{\tilde{\beta}}{A_x} \lambda \left[p_i(x) p_j(x) \int_0^\infty S(\tau) d\tau + \int_0^\infty Cov(\delta_{i \in x}, \delta_{j \in x} | \tau) S(\tau) d\tau \right]. \tag{10}$$

By replacing $S(\tau)$ with the exponential survival function $e^{-\nu \tau}$ we obtain equation 6 in the main text.

References

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