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Electronic Appendix A. Derivations

Derivation of SI pair density, P_{SI}^{*}

Here we present a general derivation of the steady-state SI pair density P_{SI}^{*}, including the results shown in sections 2 and 4. We begin with the standard one-sex formulation of a pair-formation/epidemic model, extended such that pair-entry rates k_y and break-up rates l_{yz} (where y,z=S or I) can vary as a function of infection status (c.f. Dietz & Hadeler 1988):

$$\begin{aligned}
\frac{dX_S}{dt} &= -k_S X_S + 2l_{SS}P_{SS} + l_{SI}P_{SI} + \sigma X_I + \lambda - \mu X_S + \mu\left(2P_{SS} + P_{SI}\right) \\
\frac{dX_I}{dt} &= -k_I X_I + 2l_{II}P_{II} + l_{SI}P_{SI} - \sigma X_I - \mu X_I + \mu\left(2P_{II} + P_{SI}\right) \\
\frac{dP_{SS}}{dt} &= \tfrac{1}{2}k_S m_{SS} X_S - l_{SS}P_{SS} + \sigma P_{SI} - 2\mu P_{SS} \qquad \text{(A1)} \\
\frac{dP_{SI}}{dt} &= \tfrac{1}{2}k_S m_{SI} X_S + \tfrac{1}{2}k_I m_{IS} X_I - l_{SI}P_{SI} - \beta_{pair}P_{SI} - \sigma P_{SI} + 2\sigma P_{II} - 2\mu P_{SI} \\
\frac{dP_{II}}{dt} &= \tfrac{1}{2}k_I m_{II} X_I - l_{II}P_{II} + \beta_{pair}P_{SI} - 2\sigma P_{II} - 2\mu P_{II}
\end{aligned}$$

Parameters and variables are defined in the caption to figure 1. The factors of ½ reflect that it takes two individuals to make a partnership (i.e. one unit of P_{yz} is equivalent to two units of X_S or X_I), and the factors of 2 in μ and σ terms reflect events that arise from transitions undergone by either member of a pair. Note that mixed partnerships (P_{SI}) are formed both by X_S individuals "choosing" X_I individuals and vice versa; the two separate terms are essential to maintaining constant population size. We assume that population density has reached equilibrium, and set $\lambda=\mu N$.

This derivation pertains to populations where pair formation and dissolution occur on faster timescales than disease and demographic processes (i.e. pairing rate parameters k_y and l_{yz} are significantly greater than epidemic rates β_{pair}, σ and μ). We therefore approximate that disease states are constant on the timescale of pairing processes, and separate the fast pairing dynamics from the slow epidemic dynamics as described in the main text and shown in figure 1. The pairing dynamics are then described by:

Fast pairing dynamics

$$\begin{cases} \dfrac{dX_{\mathrm{S}}}{dt} = -k_{\mathrm{S}} X_{\mathrm{S}} + 2l_{\mathrm{SS}} P_{\mathrm{SS}} + l_{\mathrm{SI}} P_{\mathrm{SI}} \\ \dfrac{dX_{I}}{dt} = -k_{\mathrm{I}} X_{\mathrm{I}} + 2l_{\mathrm{II}} P_{\mathrm{II}} + l_{\mathrm{SI}} P_{\mathrm{SI}} \\ \dfrac{dP_{SS}}{dt} = \frac{1}{2} k_{\mathrm{S}} m_{\mathrm{SS}} X_{\mathrm{S}} - l_{\mathrm{SS}} P_{\mathrm{SS}} \\ \dfrac{dP_{SI}}{dt} = \frac{1}{2} k_{\mathrm{S}} m_{\mathrm{SI}} X_{\mathrm{S}} + \frac{1}{2} k_{\mathrm{I}} m_{\mathrm{IS}} X_{\mathrm{I}} - l_{\mathrm{SI}} P_{\mathrm{SI}} \\ \dfrac{dP_{II}}{dt} = \frac{1}{2} k_{\mathrm{I}} m_{\mathrm{II}} X_{\mathrm{I}} - l_{\mathrm{II}} P_{\mathrm{II}} \end{cases} \tag{A2}$$

We consider the slower dynamics of disease transmission and demographic processes at the whole-population scale. First we collect the total densities (in and out of partnerships) of susceptible and infectious individuals into variables *S* and *I*:

$$\begin{aligned} S &= X_{\mathrm{S}} + 2P_{\mathrm{SS}} + P_{\mathrm{SI}} \\ I &= X_{\mathrm{I}} + 2P_{\mathrm{II}} + P_{\mathrm{SI}} \end{aligned} \tag{A3}$$

The epidemic can now be represented with a standard SEIR-type compartmental model; as an example we treat an SIS epidemic with constant recruitment rate λ. The total incidence rate is $\beta_{\mathrm{pair}} P_{\mathrm{SI}}^{*}$ (equation 2.1), the mortality rate μ is independent of disease status, and the recovery rate is σ. Thus:

Slow epidemic dynamics

$$\begin{cases} \dfrac{dS}{dt} = \lambda - \beta_{\mathrm{pair}} P_{\mathrm{SI}}^{*} + \sigma I - \mu S \\ \dfrac{dI}{dt} = \beta_{\mathrm{pair}} P_{\mathrm{SI}}^{*} - (\sigma + \mu) I \end{cases} \tag{A4}$$

As described in section 2, our goal is to find an expression for the steady-state density of mixed SI partnerships, P_{SI}^{*}, in terms of the population densities *S* and *I*. The first step is to specify the mixing matrix for pair formation. The matrix element m_{yz} is the proportion of partnerships formed by *y*-type individuals which will be with individuals of type *z*. In this study we assume proportionate mixing, hence the m_{yz} are simply the fractional contributions of each group to the total pair formation rate:

$$m_{SS} = m_{IS} = \frac{k_S X_S}{k_S X_S + k_I X_I}$$
$$m_{SI} = m_{II} = \frac{k_I X_I}{k_S X_S + k_I X_I} \qquad \text{(A5)}$$

Note that $k_S\, m_{SI}\, X_S = k_I\, m_{IS}\, X_I$ under this assumption.

Substituting equations (A3) and (A5) into system (A2) , we get:

$$\frac{dP_{SS}}{dt} = \frac{\frac{1}{2}k_S^2\left(S - 2P_{SS} - P_{SI}\right)^2}{k_S\left(S - 2P_{SS} - P_{SI}\right) + k_I\left(I - 2P_{II} - P_{SI}\right)} - l_{SS}P_{SS}$$

$$\frac{dP_{SI}}{dt} = \frac{k_S k_I\left(S - 2P_{SS} - P_{SI}\right)\left(I - 2P_{II} - P_{SI}\right)}{k_S\left(S - 2P_{SS} - P_{SI}\right) + k_I\left(I - 2P_{II} - P_{SI}\right)} - l_{SI}P_{SI} \qquad \text{(A6)}$$

$$\frac{dP_{II}}{dt} = \frac{\frac{1}{2}k_I^2\left(I - 2P_{II} - P_{SI}\right)^2}{k_S\left(S - 2P_{SS} - P_{SI}\right) + k_I\left(I - 2P_{II} - P_{SI}\right)} - l_{II}P_{II}$$

We let the pairing dynamics go to steady-state by setting the right-hand sides of (A6) equal to zero. This leads to a system of three quadratic equations in the three unknowns P_{SS}^*, P_{SI}^*, P_{II}^*, which we wish to solve for P_{SI}^*. This system was simplified using Mathematica (Wolfram Research, Champaign IL), yielding the following quadratic equation in P_{SI}^*:

$$a\left(P_{SI}^*\right)^2 + bP_{SI}^* + c = 0 \quad \text{where}$$
$$a = \frac{l_{SI}}{k_I}\left(1 - \frac{l_{SI}}{l_{SS}}\right) + \frac{l_{SI}}{k_S}\left(1 - \frac{l_{SI}}{l_{II}}\right) + \left(1 - \frac{l_{SI}^2}{l_{SS}l_{II}}\right)$$
$$b = -\left(\frac{\pi_S S + \pi_I I}{\pi_S \pi_I}\right) \qquad \text{(A7)}$$
$$c = SI$$

and $\pi_S = \frac{k_S}{k_S + l_{SI}}$ and $\pi_I = \frac{k_I}{k_I + l_{SI}}$.

We consider four cases, in which infection status has varying influence on pairing behaviour (i.e. different sets of the pair formation and dissolution rates k_S, k_I, l_{SS}, l_{SI} and l_{II} have distinct values). When pair dissolution rates are equal ($l_{SS}=l_{SI}=l_{II}=l$), $a=0$ in equation (A7) and $P_{SI}^* = -c/b$. Otherwise the quadratic formula was used to find P_{SI}^*. For $a<0$ there is only one positive

solution, $P_{\mathrm{SI}}^{*}=\frac{1}{2a}\left(-b-\sqrt{b^{2}-4ac}\right)$. When $0<a<b^{2}/4c$ both solutions are real and positive, but only $P_{\mathrm{SI}}^{*}=\frac{1}{2a}\left(-b-\sqrt{b^{2}-4ac}\right)$ remains bounded on the $(0,N/2)$ interval (for all numerical tests we have conducted). By reorganising terms in $b^{2}-4ac$ into a difference-of-terms squared plus some positive terms, it can be shown that $b^{2}-4ac>0$ always (for $k_{\mathrm{S}},k_{\mathrm{I}},l_{\mathrm{SS}},l_{\mathrm{SI}},l_{\mathrm{II}}>0$) so solutions are always real. Exact solutions for P_{SI}^{*} in all four cases lead to incidence rates as shown in equation (4.1), with full expressions shown in table 1. All solutions have been checked numerically to ensure their validity.

Calculation of R_0 and i_∞

The basic reproductive number, R_0, is the expected number of secondary cases caused by a typical infectious individual in a wholly susceptible population. As such, it can be calculated as the product of the total rate of transmission per I individual times the expected duration of infectiousness, in the limit $S\to N$ (Anderson & May 1991). From equation (A4), with $P_{\mathrm{SI}}^{*}=\phi_{\kappa}(s,i)\dfrac{SI}{N}$ as in equation (4.1), we find for our model:

$$\begin{aligned} R_0 &= \lim_{S\to N}\left(\text{transmission rate per I individual}\times\text{duration of infectiousness}\right) \\ &= \lim_{S\to N}\left(\beta_{\text{pair}}\phi_{\kappa}(s,i)\frac{S}{N}\times\frac{1}{\sigma+\mu}\right) \\ &= \frac{\beta_{\text{pair}}}{\sigma+\mu}\lim_{S\to N}\left(\phi_{\kappa}(s,i)\right) \end{aligned} \qquad \text{(A8)}$$

From the expressions $\phi_{\kappa}(s,i)$ in table 1, it is readily shown that $\lim_{S\to N}\left[\phi_{\kappa}(s,i)\right]=\pi_{\mathrm{I}}=\dfrac{k_{\mathrm{I}}}{k_{\mathrm{I}}+l_{\mathrm{SI}}}$ for all cases. Therefore R_0 takes the same form for all four levels of infection-induced behavioural shifts, as shown in equation (4.2).

We can also calculate the equilibrium density of infectives, I_∞, by finding the non-zero solution to $\left(\dfrac{dI}{dt}\right)_{I^{*}\neq 0}=0$. From this we can calculate the steady-state endemic prevalence, $i_\infty=\dfrac{I_\infty}{N}$. Results are shown in table 1.

Calculation of steady-state density of partnerships

When disease does not influence pair-formation dynamics, we can simply model the density of unpartnered individuals, X, and of partnerships, P:

$$\frac{dX}{dt} = -kX + 2lP$$
$$\frac{dP}{dt} = \tfrac{1}{2}kX - lP \qquad \text{(A9)}$$

Since the total population density (N) is constant, one of these equations is redundant. The steady-state is found by setting the right-hand side equal to zero and substituting $X=N-2P$. We can then solve for the steady-state density of partnerships:

$$P^* = \left(\frac{k}{k+l}\right)\frac{N}{2} \qquad \text{(A10)}$$