Supplementary Information for *Cocirculation of infectious diseases on networks*

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DETAILED DERIVATION OF EQUATIONS

We begin with a configuration model network, and consider two infectious diseases which infect nodes of the network. We assume infection by either disease confers immediate and complete protection from any future infection by any disease. We index the diseases by 1 and 2. Individuals infected by disease $i = 1, 2$ transmit to their partners at rate β_i, and recover at rate γ_i.

We assume that at the initial time t_0 enough individuals are infected that the disease spreads deterministically (at the aggregated population-level), and that the probability an individual of degree k is initially infected is $S(k, t_0)$. We must make an assumption about which individuals are initially infected. Namely, if we consider an initially susceptible individual u, no information we have about u at time t_0 tells us anything about the status of its partners. This assumption is satisfied if we initially infect a random subset of the population, or even if the disease has been spreading for some time before t_0. This assumption is violated if we select high-degree individuals and preferentially infect their partners.

The test individual

We now introduce the concept of a *test individual*. This concept is described in more detail in [1], and it allows us to simplify our calculations.

We modify the test individual by not permitting transmission from u to its partners. Without this assumption infection could spread from one partner v to u to another partner w. This would introduce correlation between v and w which is mediated through u. By preventing transmission from u we eliminate this correlation and we can treat the partners of u as independent. The justification for this is described below, but can be understood in part by analogy with the "price-taker" assumption of economics. A price-taker is a firm which produces insufficient amounts of some product to have any impact on the market price. As such, we can simplify a mathematical analysis of such a firm by explicitly ignoring the impact it has on the market. Here the test individual has no impact on the broader dynamics and modifying its local effect still has no impact on the broader dynamics. Thus we might as well assume that it has the simplest possible local effect for our analysis. We expand this argument below.

Whether a given individual u is infected at any given time is a random variable. However, if we make the assumption that the disease spreads deterministically at the aggregated population-level, then whether or not a given individual is infected at any given time cannot have any impact on the aggregated scale. If it did, there would be stochastic effects visible at the population scale.

This observation allows us to decouple the status of u from the dynamics of the epidemic in the sense that we can ignore any feedback from u on the epidemic. To make this mathematically rigorous, we simply allow u to become infected and for its infection to proceed as normal, but we disallow any transmission from u to its partners. This keeps the status of partners of u independent.

The probability that u is susceptible equals the probability that none of its partners has transmitted to it (under the assumption u does not transmit to its partners). To calculate the proportion of the population that is susceptible, infected, or recovered, we assume that u is randomly selected from the population and prevented from infecting its partners. We call u a *test individual*. The probability u has a given status equals the proportion of the population that has that status.

Deriving the flow diagrams

We define $\theta(t)$ to be the probability that a random neighbor of u which had not transmitted to u by time $t = t_0$ still has not transmitted by time t. Then if u has degree k, the probability it was initially susceptible is $S(k, t_0)$, and the probability it is still susceptible is $S(k, t_0)\theta(t)^k$. Averaging over all possible values of k, we have

$$S(t) = \psi(\theta(t)) = \sum_k P(k) S(k, t_0) \theta(t)^k$$

The value of S reduces over time as infections occur. Mathematically this appears as a reduction in θ. We must calculate how quickly θ changes, and how much of that change is due to each disease. This will allow us to calculate how much of the reduction in S should go into each disease's infected class.

We now look for the change in θ. We define v to be a random neighbor of u which had not transmitted to u by t_0. Then θ is the probability v has not transmitted to u by time t. As our initial condition, we have $\theta(t_0) = 1$. We divide θ into four compartments. We take ϕ_S to be the probability that v is still susceptible, $\phi_{I,1}$ the probability v is infected with disease 1 but has not transmitted to u, $\phi_{I,2}$ the probability v is infected with disease 2 but has not transmitted to u, and ϕ_R the probability that v is recovered (from either disease) and did not transmit during infection. These add up to θ: $\theta = \phi_S + \phi_{I,1} +$

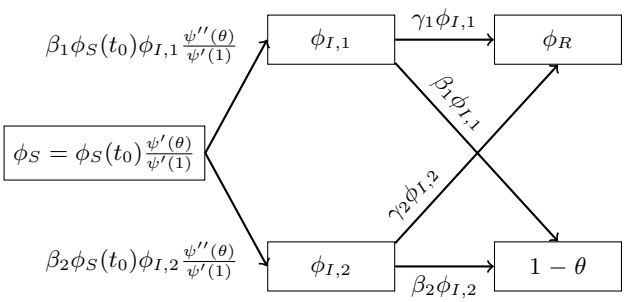

FIG. 1. Flow diagram that leads to the evolution of θ. A label along an edge gives the flux of probability along that edge.

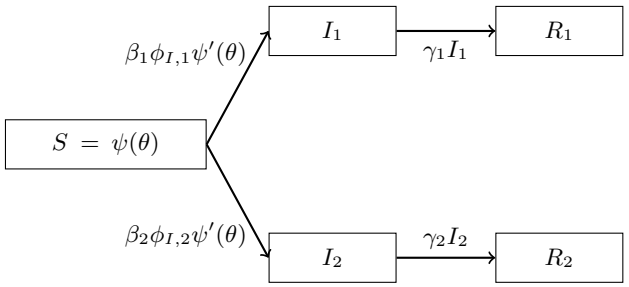

FIG. 2. Flow diagram leading to equations for the proportion of the population in each compartment.

$\phi_{I,2} + \phi_R$. The probability that v has transmitted to u is $1-\theta$. The flow between these compartments is shown in figure 1.

We first find the rate of change of θ. It is relatively straightforward to see that

$$\dot{\theta} = -\beta_1\phi_{I,1} - \beta_2\phi_{I,2}$$

This is because the only path for θ to decrease is through v transmitting to u, which requires that v be infected (and not yet transmitted to u).

At t_0, we have $\phi_S(t_0)$ is the probability a random neighbor of u is still susceptible (given that it has not transmitted to u). We take this as an input value. The value of $\phi_{I,1}$, $\phi_{I,2}$, and ϕ_R are similarly all input from the conditions at t_0. We can explicitly calculate the value of ϕ_S at later times, if we know θ. To do this, we find the probability distribution for degree of v, and then calculate the probability that no neighbor of v has transmitted to v.

At time t_0, the edge joining u to v is simply an edge from u to a random neighbor that is susceptible. The probability that edge connects to a degree k individual is proportional to the number of edges that all susceptible individuals of degree k have, $NkP(k)S(k,t_0)$. The normalization factor is the total number of all edges of susceptible individuals, $\sum_{k'} Nk'P(k')S(k',t_0)$. The probability that v is still susceptible at time t is $\theta(t)^{k-1}$. So the probability of having a degree k susceptible neighbor at time t is $NkP(k)S(k,t_0)\theta(t)^{k-1}/\sum_{k'} Nk'P(k')S(k',t_0)$. Summing over all possible k, and cancelling N, we arrive at $\sum_k kP(k)S(k,t_0)\theta(t)^{k-1}/\sum_{k'} k'P(k')S(k',t_0) = \psi'(\theta(t))/\psi'(1)$. So given that v is initially susceptible, the probability that v is susceptible at a later time t is $\psi'(\theta(t))/\psi'(1)$. Since the probability v is initially susceptible is $\phi_S(t_0)$, we conclude

$$\phi_S(t) = \phi_S(t_0)\frac{\psi'(\theta)}{\psi'(1)}$$

The rate of change of ϕ_S is simply $\phi_S(t_0)\dot{\theta}\psi''(\theta)/\psi'(1)$. It is straightforward to see that the amount that goes from ϕ_S to $\phi_{I,1}$ is $\phi_S(t_0)\beta_1\phi_{I,1}\psi''(\theta)/\psi'(1)$ and the amount going into $\phi_{I,2}$ is $\beta_2\phi_{I,2}\psi''(\theta)/\psi'(1)$.

So in figure 1, we have expressions for the flux along each edge except the edges into ϕ_R. These edges are straightforward, because the recovery rate for disease 1 is γ_1 and the recovery rate for disease 2 is γ_2. So the total flux from $\phi_{I,1}$ to ϕ_R is $\gamma_1\phi_{I,1}$ and the flux from $\phi_{I,2}$ is $\gamma_2\phi_{I,2}$.

Using the flows in figure 1, we can arrive at a coupled system for θ, $\phi_{I,1}$ and $\phi_{I,2}$. It is

$$\begin{aligned}
\dot{\theta} &= -\beta_1\phi_{I,1} - \beta_2\phi_{I,2} \\
\dot{\phi}_{I,1} &= -(\beta_1+\gamma_1)\phi_{I,1} + \beta_1\phi_{I,1}\phi_S(t_0)\frac{\psi''(\theta)}{\psi'(1)} \\
\dot{\phi}_{I,2} &= -(\beta_2+\gamma_2)\phi_{I,2} + \beta_2\phi_{I,2}\phi_S(t_0)\frac{\psi''(\theta)}{\psi'(1)}
\end{aligned}$$

with $\theta(t_0) = 1$ and $\phi_S(t_0)$, $\phi_{I,1}(t_0)$, and $\phi_{I,2}(t_0)$ given by the initial state of the population.

These equations govern the spread of the disease through the network. However, they are not the usual variables of interest. Typically we want to know the proportion susceptible, infected, or recovered. Figure 2 shows a flow diagram governing the proportion of the population in each state. We can use this to recover S, I_1, I_2, R_1, and R_2. As we noted above, $S(t) = \psi(\theta)$. The flux into I_1 can be calculated to be $\beta_1\phi_{I,1}\psi'(\theta)$, and the flux into I_2 is $\beta_2\phi_{I,2}\psi'(\theta)$. The fluxes from each of these into the recovered states are $\gamma_1 I_1$ and $\gamma_2 I_2$. We distinguish the two recovered states because we will frequently be interested in the total proportion infected by each disease. We could have similarly subdivided ϕ_R into two compartments, but it would not provide any information that is useful here.

Thus our final system of equations is

$$\begin{aligned}
\dot{\theta} &= -\beta_1\phi_{I,1} - \beta_2\phi_{I,2} \\
\dot{\phi}_{I,1} &= -(\beta_1+\gamma_1)\phi_{I,1} + \beta_1\phi_{I,1}\phi_S(t_0)\frac{\psi''(\theta)}{\psi'(1)} \\
\dot{\phi}_{I,2} &= -(\beta_2+\gamma_2)\phi_{I,2} + \beta_2\phi_{I,2}\phi_S(t_0)\frac{\psi''(\theta)}{\psi'(1)} \\
S &= \psi(\theta) \\
\dot{I}_1 &= \beta_1\phi_{I,1}\psi'(\theta) - \gamma_1 I_1 \\
\dot{I}_2 &= \beta_2\phi_{I,2}\psi'(\theta) - \gamma_2 I_2 \\
\dot{R}_1 &= \gamma_1 I_1 \\
\dot{R}_2 &= \gamma_2 I_2
\end{aligned}$$

REGIME ANALYSIS

There are several regimes that can be identified. When the cumulative number of infections is small enough that S and ϕ_S are approximately 1, then we can neglect nonlinear terms. Which regime is observed is determined by the relative sizes of the two epidemics when the linear approximation breaks down. We focus our attention on regimes for which the linear approximation is valid at the initial time.

When the initial condition is small, the linear terms dominate and the epidemics grow (or decay) exponentially. The equations governing the epidemics are uncoupled in this regime. Physically, this means that competition for nodes is so weak that it can be neglected. In fact a stronger statement is true: in addition to not having inter-disease competition, there is no intra-disease competition: a transmission path is very unlikely to encounter a node infected along another transmission path.

Assume that the exponential growth rates of the two diseases are r_1 and r_2, with $r_1 \geq r_2$. This continues until one of them becomes large enough that competition begins to appear. At this point the growth of both epidemics starts to slow. If the difference in epidemic sizes is large enough at this point, then this first epidemic will not be slowed by the much smaller other epidemic. The dynamics will proceed as if there were just one disease spreading. Eventually the susceptible population will decrease, the disease will peak and eventually decay away, all with the second disease negligible. Once this decay has occurred, there will be a "residual" network. The second disease will continue to spread along this network. If the residual network is well enough connected (and the second disease sufficiently infectious), the second disease can continue to grow, and then it experiences its own epidemic.

If the diseases are close enough in size when nonlinear terms become important, then both diseases contribute a nonnegligible amount to reduction in S and ϕ_S at the same time. Thus they interact dynamically. Each disease contributes in a nonnegligible way to hindering the spread of the other. To determine whether this can happen, we use a simple balance based on the initial sizes and the early growth rates. Typically we might expect that one disease becomes large while the other is still exponentially small.

If one disease is sufficiently small when the other disease becomes large, then the larger disease will spread and cause an epidemic that is effectively the same size as it would be in the absence of the smaller disease. Using the initial sizes and growth rates, it is straightforward to calculate the sizes of the two diseases once nonlinearities begin to be significant. For the two diseases to not interact, the "smaller" disease must remain negligibly small until the "larger" disease has finished its epidemic. We derive slightly different thresholds for the case where the smaller disease is the fast-growing disease or the slow-growing disease. To derive the threshold condition, we make a crude assumption that the two diseases continue spreading according to the exponential growth rate. In the nonoverlapping regimes, the smaller disease must remain small throughout the spread of the larger disease. We crudely choose to apply our conditions when the exponential growth implies that the larger disease would have reached size 1. We look at the size of the smaller disease (assuming exponential growth) at this time. For a given observed size for the smaller disease, we reach different conclusions if it is the fast or the slow growing disease. If it is the fast-growing disease, and we observe 0.05, then that means that at previous times it was much smaller, and so we would not expect to observe any impact. On the other hand if it is the slower-growing disease, and we observe 0.05, that means for much of the spread of the larger disease it was at about that size, and so we would expect to observe some impact. So if the fast-growing disease is the small disease, we allow it to be as large as 0.05 when the slow disease would reach 1. If the slow-growing disease is the small disease, we require that it be much smaller, choosing $0.0025 = 0.05^2$ instead. Our choice of threshold is somewhat arbitrary, and influenced by the fact that $\ln 0.05 \approx -3$ giving a simple expression for our thresholds. Taking this, we can derive the $C_{\min} \approx -6$ and $C_{\max} \approx 3r_2/r_1$ thresholds in the text.

Taking ρ_1 and ρ_2 to be the proportions initially infected with each disease (at random). So long as $C = \ln\rho_2 - (r_2/r_1)\ln\rho_1$ is not between -6 and $3r_2/r_1$, then the two diseases will not interact dynamically. One disease will become large and run through its entire epidemic prior to the other disease (possibly) having its own epidemic. This defines the "nonoverlapping" epidemic regimes. If C lies within this range, then we have the overlapping epidemic regime.

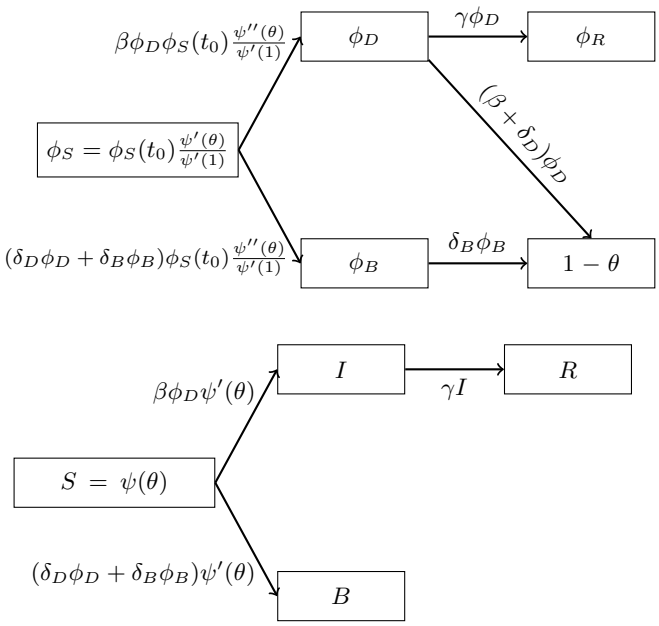

FIG. 3. The flow diagrams underlying the spread of an infectious disease in the presence of a behavior change. We assume behavior change can be triggered by contact with an infected individual or with an individual who has already adopted the change. We assume behavior change provides complete immunity to disease.

IMPACT OF BEHAVIOR CHANGE

We now consider the spread of a single disease through a network, which can be prevented with a behavior change. We assume that the behavior change gives complete protection from infection. Once an individual has adopted the behavior change, the change is permanent. An individual who has changed behavior will transmit that behavior change to partners.

The disease transmits at rate β and recovery occurs at rate γ. Contact with an infected individual causes behavior change at rate δ_D. Contact with an individual whose behavior has changed causes behavior change at rate δ_B. The flow diagrams are shown in figure 3. The resulting equations are

$$\begin{aligned}
\dot{\theta} &= -(\beta_D + \delta_D)\phi_D - \delta_B\phi_B \\
\dot{\phi}_B &= (\delta_B\phi_B + \delta_D\phi_D)\phi_S(t_0)\frac{\psi''(\theta)}{\psi'(1)} \\
\dot{\phi}_D &= \beta_D\phi_D\phi_S(t_0)\frac{\psi''(\theta)}{\psi'(1)} - (\beta_D + \delta_D + \gamma)\phi_D \\
\dot{I} &= \beta_D\phi_D\psi'(\theta) - \gamma I \\
\dot{B} &= (\delta_B\phi_B + \delta_D\phi_D)\psi'(\theta) \\
\dot{R} &= \gamma I \\
S &= \psi(\theta)
\end{aligned}$$

The early growth of ϕ_D is exponential with rate $\beta_D\phi_S(t_0)\psi''(1)/\psi'(1) - (\beta_D + \delta_D + \gamma)$. If δ_D is sufficiently large, the infection decays. This corresponds to a balance between transmitting disease prior to either recovering or transmitting behavior change. When the transmission probability is small enough a typical infected individual causes fewer than 1 new infection and the disease must die out.

Changing δ_B does not alter the early growth rate of the disease. So we might anticipate that the disease will be able to cause a large scale epidemic. However, if $\delta_B > 0$, the behavior change itself also leads to an "epidemic". If the behavior growth rate is sufficiently large, its "epidemic" occurs while the disease epidemic is still exponentially small. In this limit, the behavior change will dominate the population, and the disease remains exponentially small. We do not see the complementary case in which the disease becomes large while the behavior change is exponentially small, because as disease incidence increases it directly induces behavior changes. So either the behavior change has its "epidemic" first, or the two have overlapping "epidemics".

[1] J. C. Miller, Bulletin of Mathematical Biology **74**, 2125 (2012).