The Impact of Past Epidemics on Future Disease Dynamics: Supplementary Information

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1 Supplementary Methods

1.1 The Perfect Partial Immunity Model

1.1.1 Examples of the degree distribution of the extended residual network

Figure 1 shows examples of the degree distribution of the extended residual network for networks of type Poisson, exponential and scale-free at three values of α. We note that the degree distribution for $\alpha = 1$ is identical to the degree distribution for the original contact network, and that as α decreases, the population becomes more homogeneous.

1.2 The Leaky Partial Immunity Model

To find the size of an epidemic, we find the size of a cluster of infected nodes attached to a node. We define the probability generating functions for the outbreak (cluster) size distribution starting from an A and B node, respectively, as:

$$F_A(x, y; T_{AA}, T_{AB}) = \sum P_{rs} x^r y^s$$

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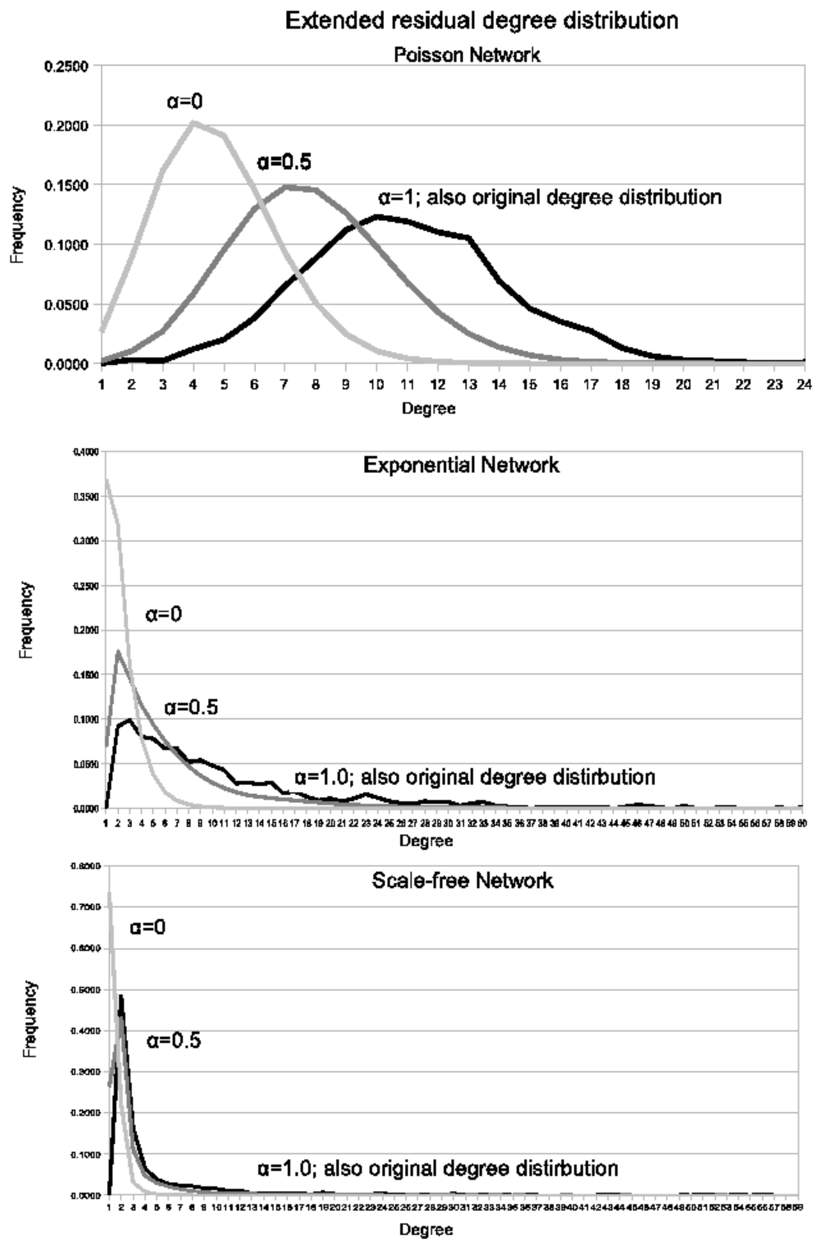

Figure 1: We show examples of the degre of the degree distribution of the extended residual network for networks of type Poisson, exponential, and scale-free at three values of α.

$$G_B(x, y; T_{AA}, T_{AB}) = \sum Q_{rs} x^r y^s$$

where x counts the number of A nodes in the cluster and y counts the number of B nodes in the cluster. To solve for F_A and G_B,we find F_{AA}, F_{BA}, the PGFs for the size distribution of an outbreak starting from an (infected) node of type A which has been reached by following an edge from an (infected) type $A(B)$ node, G_{AB}, G_{BB}, and the PGFs for the size distribution of an outbreak starting from an (infected) node of type A which has been reached by following an edge from an (infected) type $A(B)$ node. Following the recursive logic of the derivations in [Newman, 2002], F_{AA} and the other escess cluster size PGFs are given by the self-referential equations:

$$F_{AA}(x, y; \{T\}) = x\, f_{AA}(F_{AA}(x, y; \{T\}), G_{AB}(x, y; \{T\}); T_{AA}, T_{AB}),$$

$$\begin{aligned} F_{BA}(x, y; \{T\}) &= x\, f_{BA}(F_{BA}(x, y; \{T\}), G_{BB}(x, y; \{T\}); T_{AA}, T_{AB}), \\ G_{AB}(x, y; \{T\}) &= y\, g(F_{BA}(x, y; \{T\}), G_{BB}(x, y; \{T\}); T_{BA}, T_{BB}), \\ G_{BB}(x, y; \{T\}) &= y\, g(F_{BA}(x, y; \{T\}), G_{BB}(x, y; \{T\}); T_{BA}, T_{BB}). \end{aligned}$$

Similarly, we find that

$$F_A(x, y; T_{AA}, T_{AB}) = x\, f_A(F_{AA}(x, y; \{T\}), G_{AB}(x, y; \{T\}); T_{AA}, T_{AB}),$$

$$G_B(x, y; T_{BA}, T_{BB}) = y\, g_B(F_{BA}(x, y; \{T\}), G_{BB}(x, y; \{T\}); T_{BA}, T_{BB}).$$

1.2.1 Size of a small outbreak

To find the size of an epidemic, we begin by solving for the expected outbreak size starting from an infected node. The expected number of A nodes in an outbreak starting from an A node is:

$$s_{AA} = \frac{\partial F_A}{\partial x}|_{x=1,y=1} = 1 + \left(T_{AA} \frac{\partial f_A}{\partial x}|_{x=1,y=1} \frac{\partial F_{AA}}{\partial x}|_{x=1,y=1} + T_{AB} \frac{\partial f_A}{\partial x}|_{x=1,y=1} \frac{\partial G_{AB}}{\partial x}|_{x=1,y=1} \right) \tag{1}$$

Similarly, the other three types of expected outbreak sizes can be calculated as:

$$s_{AB}=\frac{\partial F_A}{\partial y}|_{x=1,y=1}=\left(T_{AA}\frac{\partial f_A}{\partial y}|_{x=1,y=1}\frac{\partial F_{AA}}{\partial y}|_{x=1,y=1}+T_{AB}\frac{\partial f_A}{\partial y}|_{x=1,y=1}\frac{\partial G_{AB}}{\partial y}|_{x=1,y=1}\right) \tag{2}$$

$$s_{BA}=\frac{\partial G_B}{\partial x}|_{x=1,y=1}=\left(T_{BA}\frac{\partial g_B}{\partial x}|_{x=1,y=1}\frac{\partial F_{BA}}{\partial x}|_{x=1,y=1}+T_{BB}\frac{\partial g_B}{\partial x}|_{x=1,y=1}\frac{\partial G_{BB}}{\partial x}|_{x=1,y=1}\right)$$

$$s_{BAB}=\frac{\partial G_B}{\partial y}|_{x=1,y=1}=\left(T_{BA}\frac{\partial g_B}{\partial y}|_{x=1,y=1}\frac{\partial F_{BA}}{\partial y}|_{x=1,y=1}+T_{BB}\frac{\partial g_B}{\partial y}|_{x=1,y=1}\frac{\partial G_{BB}}{\partial y}|_{x=1,y=1}\right)$$

To solve for the mean outbreak sizes above, we take partial derivatives of the excess outbreak size distribution PGFs:

$$\frac{\partial F_{AA}}{\partial x}|_{x=1,y=1}=\frac{1-T_{BB}\frac{\partial g_{BB}}{\partial y}}{\chi} \tag{3}$$

$$\frac{\partial G_{AB}}{\partial x}|_{x=1,y=1}=\frac{\left(1-T_{AA}\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial g_{AB}}{\partial x}\right)\right)\left(T_{BB}T_{BA}\frac{\partial f_{BA}}{\partial y}\frac{\partial g_{BB}}{\partial x}+T_{BA}\frac{\partial f_{BA}}{\partial x}\left(1-T_{BB}\frac{\partial g_{BB}}{\partial y}\right)\right)}{\chi}$$

$$\frac{\partial F_{BA}}{\partial x}|_{x=1,y=1}=\frac{\left(1-T_{AA}\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial g_{AB}}{\partial x}\right)\right)\left(1-T_{BB}\frac{\partial g_{BB}}{\partial y}\right)}{\chi}$$

$$\frac{\partial G_{BB}}{\partial x}|_{x=1,y=1}=\frac{\left(1-T_{AA}\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial g_{AB}}{\partial x}\right)\right)\left(T_{BA}\frac{\partial g_{BB}}{\partial x}\right)}{\chi}$$

$$\frac{\partial F_{AA}}{\partial y}|_{x=1,y=1}=\frac{T_{AB}\frac{\partial f_{AA}}{\partial y}\left(1-T_{BB}\left(\frac{\partial g_{BB}}{\partial y}-\frac{\partial f_{BA}}{\partial y}\right)\right)}{\chi}$$

$$\frac{\partial G_{AB}}{\partial y}|_{x=1,y=1}=\frac{\left(1-T_{AA}\frac{\partial f_{AA}}{\partial x}\right)\left(1-T_{BB}\left(\frac{\partial g_{BB}}{\partial y}-\frac{\partial f_{BA}}{\partial y}\right)\right)}{\chi}$$

$$\frac{\partial F_{BA}}{\partial y}|_{x=1,y=1} = \frac{\left(T_{AB}\frac{\partial f_{AA}}{\partial y}\right)\left(1-T_{AA}\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial g_{AB}}{\partial x}\right)\right)\left(1-T_{BB}\left(\frac{\partial g_{BB}}{\partial y}-\frac{\partial f_{BA}}{\partial y}\right)\right)}{\chi}$$

$$\frac{\partial G_{BB}}{\partial y}|_{x=1,y=1} = \frac{\left(1-T_{AA}\frac{\partial f_{AA}}{\partial x}\right)-\left(T_{AB}\frac{\partial f_{AA}}{\partial y}\right)\left(T_{BA}\left(\frac{\partial f_{BA}}{\partial x}+\frac{\partial g_{BB}}{\partial x}\right)\left(1-T_{AA}\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial f_{AA}}{\partial y}\right)\right)\right)}{\chi}$$

where,

$$\chi = \alpha\beta + \gamma \tag{4}$$

with

$$\alpha = \left(1-T_{AA}\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial g_{AB}}{\partial x}\right)\right)\left(-T_{AB}T_{BA}\frac{\partial f_{AA}}{\partial y}\right)$$

$$\beta = \left(T_{BB}\frac{\partial f_{BA}}{\partial y}\frac{\partial g_{BB}}{\partial x}-\frac{\partial f_{BA}}{\partial x}\left(1-T_{AA}\frac{\partial g_{BB}}{\partial y}\right)\right)$$

$$\gamma = \left(1-T_{AA}\frac{\partial f_{AA}}{\partial x}\right)\left(1-T_{BB}\frac{\partial g_{BB}}{\partial y}\right)$$

Then, substituting the set of partial derivatives above (equations # 8) into equation 6 and 7 above yields equations for the expected small outbreak sizes.

1.2.2 Threshold Conditions

The expected small outbreak sizes above all diverge when $\chi = 0$. Thus this is a divergence condition that can be used to solve for threshold values on T_{AA}, T_{AB}, T_{BA}, and T_{BB}. In our partial immunity model, we assume that $T_{AA} = T_2$, $T_{AB} = T_{BA} = T_2\alpha$, and $T_{BB} = T_2\alpha^2$. Combining the threshold condition $\chi = 0$ with equation 9 above as well as the values for $T_{AA}, T_{AB}, T_{BA}$and T_{BB} in terms of $T_2$and α, we use numerical polynomial root finding to solve for T^*, the root of the following equation:

$$\alpha\beta + \gamma = 0$$

$$\left(1-T^*\left(\frac{\partial f_{AA}}{\partial x}-\frac{\partial g_{AB}}{\partial x}\right)\right)\left(-T^{*2}\alpha^2\frac{\partial f_{AA}}{\partial y}\right)\left(T^*\alpha^2\frac{\partial f_{BA}}{\partial y}\frac{\partial g_{BB}}{\partial x}-\frac{\partial f_{BA}}{\partial x}\left(1-T^*\frac{\partial g_{BB}}{\partial y}\right)\right)+...$$

$$...\left(1-T^*\frac{\partial f_{AA}}{\partial x}\right)\left(1-T^*\alpha^2\frac{\partial g_{BB}}{\partial y}\right)\quad=0$$

Then, the epidemic threshold for the individual-level immunity model is:

$$(T_{2_c})_{leaky}=T^*\left(e_{UU}+\frac{e_{UI}}{\alpha}+\frac{e_{IU}}{\alpha}+\frac{e_{II}}{\alpha^2}\right)$$

where, e_{UU},e_{UI},$e_{IU}$and e_{II} are the proportion of all edges in the network that are from uninfected (infected) to infected (uninfected) nodes, respectively, and can be calculated as

$$e_{UU}=U\frac{\frac{\partial f_A}{\partial x}}{\sum kp_k},$$

$$e_{UI}=U\frac{\frac{\partial f_A}{\partial y}}{\sum kp_k},$$

$$e_{IU}=I\frac{\frac{\partial g_B}{\partial x}}{\sum kp_k},$$

$$e_{II}=I\frac{\frac{\partial g_B}{\partial y}}{\sum kp_k}.$$

Here, U and I are the fraction of uninfected and infected nodes in the previous epidemic, respectively, and can be calculated as $U=\sum p_k\left(1-T_1+T_1u_1\right)^k$and $I=1-U$, where p_k is the degree distribution of the original contact network, T_1 is the transmissibility of the pathogen from the first epidemic, and u_1 is the probability of following a random edge in the network after the first epidemic and reaching an uninfected node.

For Figure 6 of the main text, we show a curve for $T_1=T_{2_c}$, which can be found my numerically finding roots (α):

$$\left(T_1-T^*e_{UU}\right)\alpha^2-\left(T^*\left(e_{UI}+e_{IU}\right)\right)\alpha-T^*e_{II}=0$$

1.3 Total Susceptibility/Transmissibility

Here we calculate the total susceptibility (σ) and transmissibility (τ) over all edges (in both directions) in the network under both immunity models. We denote m as the fraction of edges in the population emanating from infected individuals. (m can be calculated as $I\sum_k k\left(1-(1-T_1+T_1u_1)^k\right)$, where $(1-T_1+T_1u_1)^k$ is the probability that an individual of degree k is uninfected.) Then,

$$\sigma_{leaky} = m\alpha + (1-m)\,1 = \alpha m + (1-m)$$

because all the infected edges (m) have susceptibility α and all the uninfected edges (1-m) have susceptibility 1; and

$$\sigma_{polarized} = (\alpha m + (1-m))\,1 + (1-\alpha)\,m0 = \alpha m + (1-m)$$

because a fraction α of the infected edges (m) and all the uninfected edges (1-m) have susceptibility 1, while the remaining $(1-\alpha)$ of the infected edges (m) have susceptibility 0.

Similarly,

$$\tau_{leaky} = m\,(T\alpha) + (1-m)T$$

as all infected edges have transmissibility $T\alpha$ and all uninfected edges have transmissibility T; and

$$\tau_{polarized} = (\alpha m + (1-m))\,T + (1-\alpha)m0$$

as a fraction α of the infected edges and all uninfected edges have transmissibility T, while the remaining $(1-\alpha)$ of the infected edges have transmissibility 0.

Thus, the total infectivity ($\sigma+\tau$) is equal in both models.

2 Supplementary Analysis

2.1 Results on a Demographic Contact Network

In Figure 2, we compare the predictions for size of second epidemic from our two analytical models to simulations for a network with non-random structure. The network is made up of 2500 nodes that represent individuals and edges represent disease-causing contacts, and is generated by an activity-based contact network generator for data from the urban area of Vancouver, Canada (Meyers et al, 2005.)

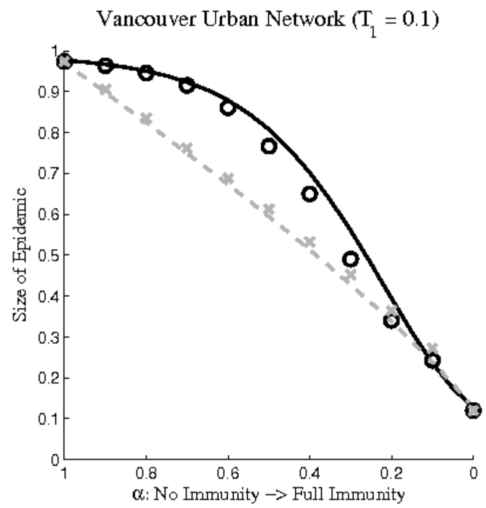

Figure 2: Expected size of second epidemic for the pefect and leaky partial immunity analytical models (lines) and simulations (markers) for a realistic network based on empirical contact patterns in the urban area of Vancouver, Canada.

2.2 Differences between Partial and Leaky Immunity Models

As discussed in the main text, the perfect and leaky models of partial immunity lead to differing epidemic consequences (as measured by the expected size of a large epidemic in a subsequent season). In Figure 3, we consider the difference in S_2, the size of the second season epidemic, as predicted by the perfect immunity model and the leaky immunity model for the Poisson network type. The figure shows the equivalence of the predictions for $\alpha = 0$ and $\alpha = 1$. The red parts of the plots represent areas where $(S_2)_{leaky}$ is smaller than $(S_2)_{perfect}$, whereas the blue parts represent areas of the parameter space where $(S_2)_{perfect}$ is smaller.

2.3 Reinvasion Criteria for the Perfect Immunity Model

In Figure 4 we consider the reinvasion threshold as measured by T_{2_c} for the perfect partial immunity model in terms of T_1 and α.

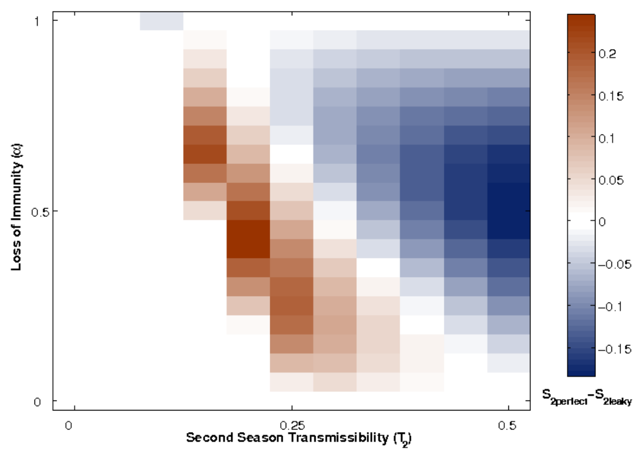

Figure 3: Differences in the expected size of a subsequent epidemic for the perfect and leaky immunity models in the ranges $T_2 \in [0.0, 0.5]$ and $\alpha \in [0.0, 1.0]$ for a Poisson network of mean degree 10.

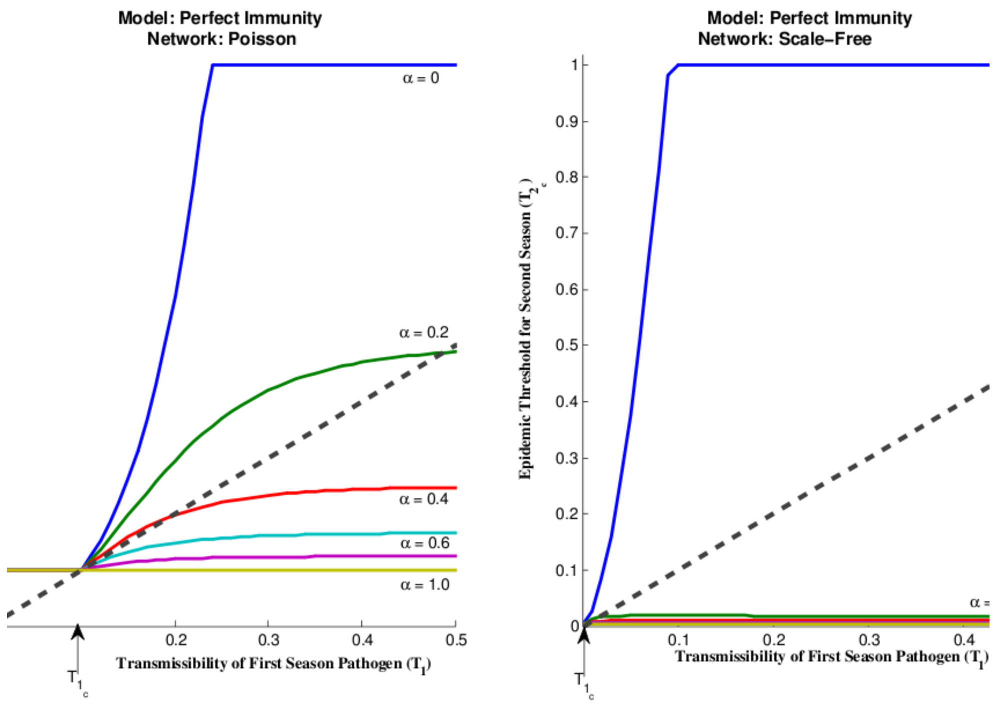

Figure 4: The reinvasion threshold for a second pathogen into a population with perfect partial immunity for a Poisson-distributed and power law-distributed random network of mean degree 10.