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

Shweta Bansal*†,Lauren Ancel Meyers‡§

May 17, 2012

1 Supplementary Methods

1.1 Polarized Immunity Model Details

1.1.1 Structural Properties of the Residual Network

In Figure 1, we compare additional structural properties of the residual network to those of the original contact network. In particular, we consider transitivity, or the propensity of triangles in the network, and the degree correlation coefficient. To consider the structural impact of the epidemic process in the most extreme situations, we focus on two sets of parameter values: (a) $\alpha = 0, T_1 \in [0, 1]$, (b) $T_1 = 1, \alpha \in [0, 1]$ for two sets of average degrees (3, 10) in random networks distributed with Poisson, exponential and scale-free degree distributions. The residual network is attained by performing 500 Monte Carlo SIR percolation simulations on each original random network. As shown below, for all parameter values, absolute values of clustering and degree correlations in the residual network remain small (or decrease) compared to the original network, and thus the assumptions of bond percolation still apply. The scale-free distributed network has large transitivity and disassortativity originally, but absolute values of both measures are reduced due to the infection process.

1.1.2 Derivation of u_1, u_2

Let $u_1$be the probability that an individual at the end of a random contact is uninfected. Then, the probability that a random individual with degree k remains uninfected during the first epidemic,$\eta_1(k)$, is equal to the probability

*Center for Infectious Disease Dynamics, The Pennsylvania State University, 208 Mueller Lab, University Park PA 16802

†Fogarty International Center, National Institutes of Health, Bethesda, MD 20892, USA

‡Section of Integrative Biology and Institute for Cellular and Molecular Biology, University of Texas at Austin, 1 University Station, C0930, Austin, TX 78712, USA

§Santa Fe Institute, 1399 Hyde Park Road, Santa Fe, NM 87501, USA

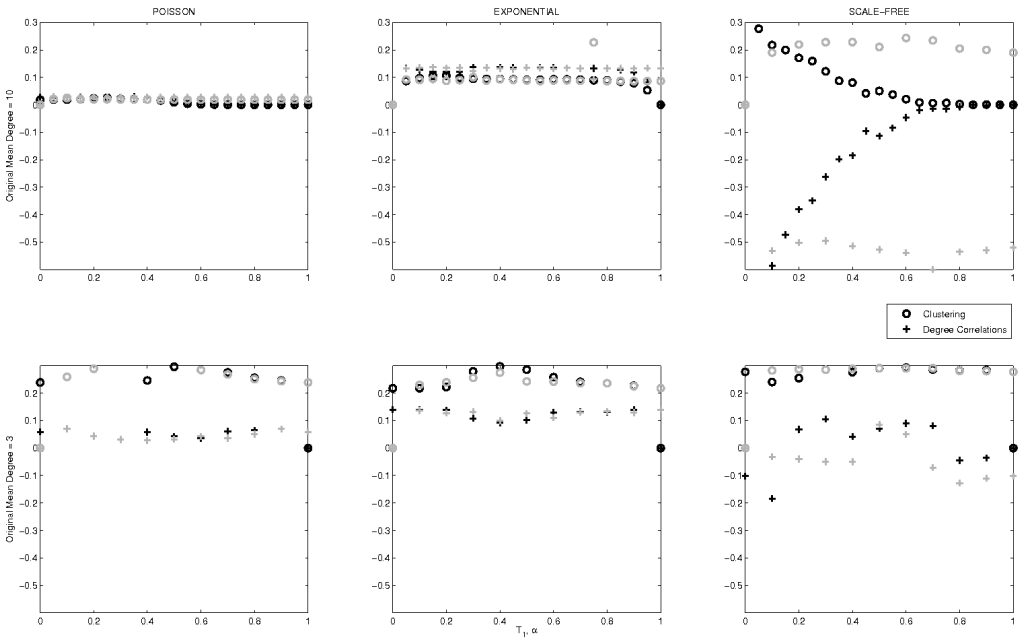

Figure 1: We consider the average clustering coefficient (o) and the degree correlation coefficient (+) in the (largest component of the) residual network, for Poisson (left panels), exponential (center panels), scale-free (right panels) original random networks, of average degree 10 (upper panels) and average degree 3 (lower panels), for $\alpha = 0, T_1 \in [0,1]$ (black) and $T_1 = 1, \alpha \in [0,1]$ (gray). The values of each structural characteristic shown for the case of $T_1 = 0$ are those of the original network.

that none of its k neighbors infected it. This occurs when each of its k edges either : (a) leads to a node that is uninfected (with probability u_1) or (b) leads to a node that was infected in the previous epidemic (with probability $(1-u_1)$) but was unsuccessful at transmitting the infection to the node in question (with probability $(1-T_1)$),where T_1 is the transmissibility or the per-contact probability that a node will be infected. Thus, accounting for all k independent edges, we have:

$$\eta_1(k) = (u_1 + (1-u_1)\cdot(1-T_1))^k = (1 - T_1 + T_1 u_1)^k \tag{1}$$

Then the probability that a node at the end of a random edge is uninfected is $\sum_k q(k)\,\eta(k)$where $q(k)$ is the excess degree distribution, and this value is equal to u_1. The derivation for u_2 follows a similar argument.

1.1.3 Deviations of $p_2(l|k, uninfected), p_2(l|k, re-susceptible)$

As described in the main text, the conditional probability distributions for l residual contacts, given k original contacts, for nodes of uninfected and re-susceptible status, respectively, is the following:

$$p_2(l|k,\text{uninfected}) = \binom{k}{l}(u_1 + (1-u_1)\,\alpha)^l\,((1-u_1)\,(1-\alpha))^{k-l}$$

$$p_2(l|k,\text{re-susceptible}) = \begin{cases} (1-\alpha)\,\tau^{(k-1)} & l = 0 \\ \alpha\left(\binom{k-1}{l-1}\sigma^{(l-1)}\tau^{(k-1)-(l-1)}\right) + (1-\alpha)\left(\binom{k-1}{l}\sigma^{l}\tau^{(k-1)-l}\right) & l \in [1, k-1] \\ \alpha\sigma^{(k-1)} & l = k \end{cases}$$

where, $\sigma = (u_1(1-T_1)(1-\alpha)+\alpha)$ is the probability of being connected to a residual edge, and $\tau = ((1-u_1+T_1u_1)(1-\alpha))$ is the probability of being connected to a non-residual edge.

These distributions can be derived using the following arguments:

1. An uninfected node with k original contacts will have l residual contacts leading to:
   (a) other uninfected nodes, with probability u_1
   (b) re-susceptible nodes, with probability $(1-u_1)\,\alpha$, because they are previously infected $(1-u_1)$, have lost immunity α
2. An uninfected node with k original contacts will have $(k-l)$ non-residual contacts leading to:

(a) immune nodes, with probability $(1-u_1)(1-\alpha)$, because they are previously infected $(1-u_1)$, have not lost immunity $(1-\alpha)$.

3. An re-susceptible node with k original contacts will have l residual contacts leading to:

   (a) uninfected nodes, with probability $u_1(1-T_1)$, because they are uninfected u_1, and have not been infected by the focal node $(1-T_1)$,

   (b) other re-susceptible nodes, with probability $(1-u_1)\alpha + u_1 T_1 \alpha$, because they are previously infected $(1-u_1)$ and have lost immunity α. Or, because, they were uninfected otherwise u_1, were infected by the focal node T_1, and have lost immunity α.

4. An re-susceptible node with k original contacts will have $(k-l)$ non-residual contacts leading to:

   (a) immune nodes, with probability $((1-u_1)(1-\alpha) + u_1 T_1 (1-\alpha))$, because they are previously infected $(1-u_1)$ and have not lost immunity $(1-\alpha)$. Or, because they were uninfected otherwise u_1, were infected by the node in question T_1, and have not lost immunity $(1-\alpha)$.

Also, in the derivation of $p_2(l|k, re-susceptible)$, we know that

1. the focal node (which was infected and has lost immunity) was infected by one of its neighbors, and that the focal node cannot have infected this neighbor. Thus we only count $(k-1)$ original edges.

2. the neighbor will count as a residual edge of the focal node if it has lost immunity (with probability α) and not count as a residual edge if it has no lost immunity (with probability $(1-\alpha)$).

1.2 Leaky Immunity Model Details

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:

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

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

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 excess cluster size PGFs are given by the self-referential equations:

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

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

$$G_{AB}(x, y; \{T\}) = y\, g(F_{BA}(x, y; \{T\}), G_{BB}(x, y; \{T\}); T_{BA}, T_{BB}),$$

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

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:

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

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

$$s_{AB} = \frac{\partial F_A}{\partial y}|_{x=1,y=1} = \left(T_{AA}\frac{\partial f_A}{\partial y}|_{x=1,y=1}\frac{\partial F_{AA}}{\partial y}|_{x=1,y=1} + T_{AB}\frac{\partial f_A}{\partial y}|_{x=1,y=1}\frac{\partial G_{AB}}{\partial y}|_{x=1,y=1}\right) \tag{3}$$

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

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

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

$$\frac{\partial F_{AA}}{\partial x}|_{x=1,y=1} = \frac{1 - T_{BB}\frac{\partial g_{BB}}{\partial y}}{\chi} \tag{4}$$

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

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

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

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

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

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

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

where,

$$\chi = \alpha\beta + \gamma \tag{5}$$

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:

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

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

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 $I\sum_k k\left(1-\left(1-T_1+T_1u_1\right)^k\right)$, where $\left(1-T_1+T_1u_1\right)^k$ 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

$$\sigma_{polar} = \left(\alpha m + (1-m)\right)1 + (1-\alpha)\,m0 = \alpha m + (1-m)$$

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,

$$\tau_{leaky} = m\left(T\alpha\right) + (1-m)T = T - mT + mT\alpha$$

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

$$\tau_{polar} = \left(\alpha m + (1-m)\right)T + (1-\alpha)m0 == T - mT + mT\alpha$$

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.)

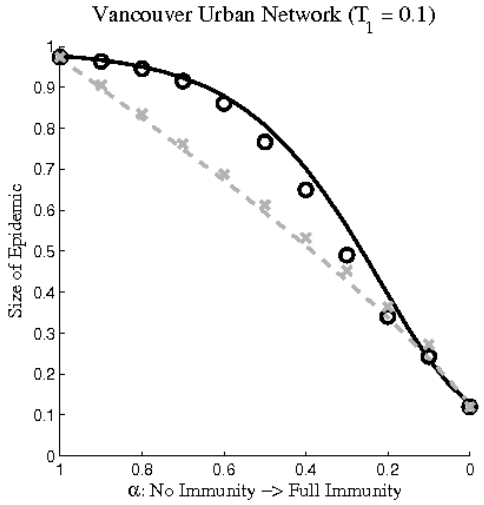

Figure 2: Expected size of second epidemic for the polarized and leaky partial immunity analytical models (lines) and simulations (markers) for a realistic network based on empirical contact patterns in the urban area of Vancouver, Canada.

2.2 Differences between Polarized and Leaky Immunity Models

As discussed in the main text, the polarized 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 polarized 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 $(S_2)_{polar}$, whereas the blue parts represent areas of the parameter space

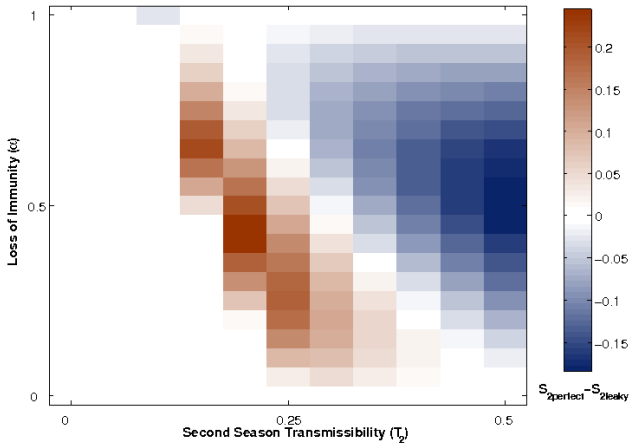

Figure 3: Differences in the expected size of a subsequent epidemic for the polarized and leaky immunity models in the ranges $T_2 \in [0.0, 0.5]$ and $\alpha \in [0.0, 1.0]$ for a Poisson network of mean degree 10.

where $(S_2)_{polar}$ is smaller.

2.3 Reinvasion Criteria for the Polarized Immunity Model

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

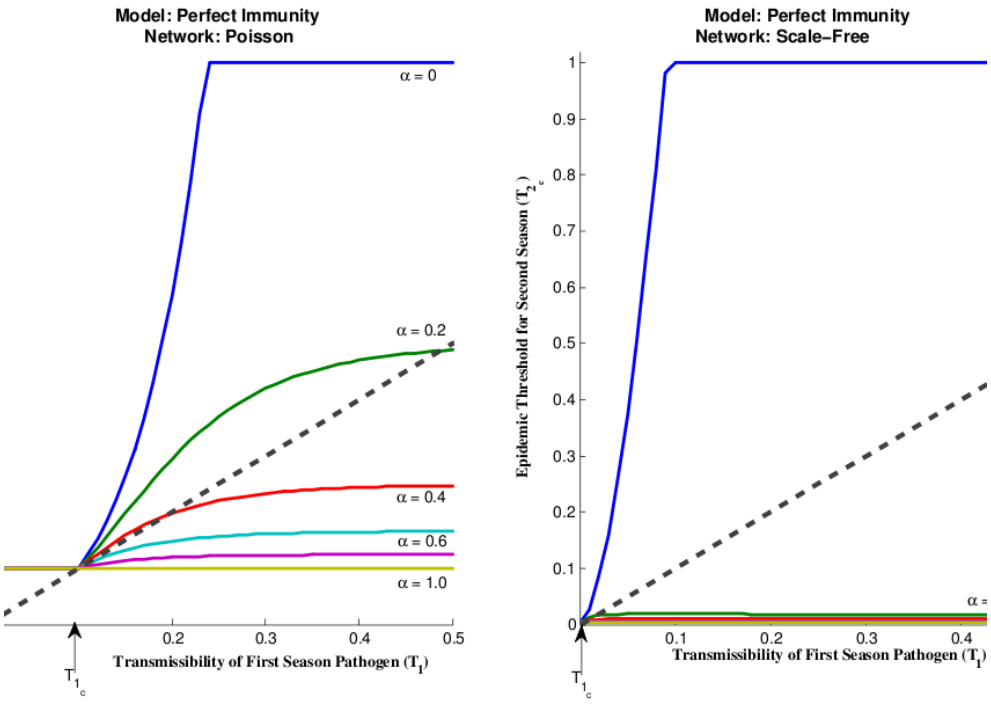

Figure 4: The reinvasion threshold for a second pathogen into a population with polarized partial immunity for a Poisson-distributed and power law-distributed random network of mean degree 10.