In-homogeneous Virus Spread in Networks

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Abstract—Our $N$-intertwined model \cite{Ganesh2012} for virus spread in any network with $N$ nodes is extended to a full heterogeneous setting. The metastable steady-state nodal infection probabilities are specified in terms of a generalized Laplacian, that possesses analogous properties as the classical Laplacian in graph theory. The critical threshold that separates global network infection from global network health is characterized via an $N$ dimensional vector that makes the largest eigenvalue of a modified adjacency matrix equal to unity. Finally, the steady-state infection probability of node $i$ is convex in the own curing rate $\delta_i$, but concave in the curing rates $\delta_j$ of the other nodes $1 \leq j \neq i \leq N$ in the network.

Index Terms—Virus spread, epidemic threshold, generalized Laplacian

I. INTRODUCTION

This paper generalizes our $N$-intertwined model for virus spread in networks, presented in \cite{Ganesh2012}, to a heterogeneous setting. Heterogeneity rather than homogeneity abounds in real networks. For example, in data communications networks, the transmission capacity, age, performance, installed software, security level and other properties of networked computers are generally different. Social and biological networks are very diverse: a population often consists of a mix of weak and strong, or old and young species or of completely different types of species. The network topology for transport by airplane, car, train, ship is different. Many more examples can be added illustrating that homogeneous networks are the exception rather than the rule. This diversity in the “nodes” and “links” of real networks will thus likely affect the spreading pattern of viruses, that are here understood as malicious challenges of a network.

The $N$-intertwined model is a continuous-time susceptible-infected-susceptible (SIS) model for the spreading of a virus in a network with $N$ nodes, that was earlier considered by Ganesh et al. \cite{Ganesh2011} and by Wang et al. \cite{Wang2012} in discrete-time. Each node in the network is either infected or healthy. In a heterogeneous setting, an infected node $i$ can infect its neighbors with an infection rate $\beta_i$, but it is cured with curing rate $\delta_i$. Once cured and healthy, the node is again prone to the virus. Both infection and curing processes are independent.

Previously in \cite{Ganesh2012}, only a homogeneous virus spread was investigated, where all infection rates $\beta_i = \beta$ and all curing rates $\delta_i = \delta$ were the same for each node. We believe that the extension to a full heterogeneous setting is, perhaps, the best SIS model that we can achieve. The exact Markovian model, described and analyzed in \cite{Ganesh2012}, has $2^N$ states, which makes it infeasible to compute for realistic sizes of networks. Moreover, the exact Markovian model possesses as steady-state the overall healthy state, which is an absorbing state, that is, unfortunately, only reached after an extreme and unrealistically long time. The heterogeneous $N$-intertwined model makes one approximation, a mean field approximation as shown in Section \[ and in \cite{Ganesh2012}, that results in a set of $N$ non-linear equations. Hence, the $N$-intertwined model trades computational feasibility, a reduction of $2^N$ linear equations to $N$ non-linear ones, at the expense of exactness. The last point, the accuracy of the $N$-intertwined model is shown in \cite{Ganesh2012} (and further in \cite{Ganesh2013}) to be overall remarkably good, with a worst case performance near the critical threshold, which is a realistic and observable artifact of the metastable steady-state that does not exist in the exact Markovian steady-state. Below the critical epidemic threshold, infection vanishes exponentially fast in time and above the critical threshold the network stays infected to a degree determined by the effective infection vector $\tau$, with components $\tau_i = \frac{\beta_i}{\delta_i}$.

A major new insight is that the metastable steady-state can be written in terms of a generalized Laplacian matrix that bears similar deep properties as the Laplacian matrix of a graph (see e.g. \cite{VanMieghem2009} and \cite{Wang2012}). In a heterogeneous setting, the critical threshold is characterized by an effective infection vector, instead of one scalar in the homogeneous case equal to $\tau_{\text{homogeneous}} = \frac{1}{\lambda_{\text{max}}(A)}$, where $\lambda_{\text{max}}(A)$ is the largest eigenvalue of the adjacency matrix $A$ of the graph. This critical vector determines a critical surface in the $N$-dimensional space spanned by the vector components $\tau_1, \ldots, \tau_N$. We also prove that the steady-state infection probability $\tau_{\text{loc}}$ of node $i$ is convex in the curing rate $\delta_i$, given all other curing rates $\delta_j$. This convexity result is applied in a virus protection game played by the individual and selfish nodes in a network \cite{VanMieghem2013}.

II. $N$-INTERTWINED CONTINUOUS MARKOV CHAINS WITH 2 STATES

This section extends the homogeneous $N$-intertwined model in \cite{Ganesh2012} to a heterogeneous setting. Although analogous to the corresponding section in \cite{Ganesh2012}, its inclusion makes this paper self-contained.

By separately observing each node, we will model the virus spread in a bi-directional network specified by a symmetric adjacency matrix $A$. Every node $i$ at time $t$ in the network has two states: infected with probability $\Pr[X_i(t) = 1]$ and healthy with probability $\Pr[X_i(t) = 0]$. At each moment $t$, a node can only be in one of two states, thus $\Pr[X_i(t) = 1] + \Pr[X_i(t) = 0] = 1$. If we apply Markov theory, the infinitesimal generator $Q_i(t)$ of this two-state continuous Markov chain is,

$$Q_i(t) = \begin{bmatrix} -q_{1;i} & q_{1;i} \\ q_{2;i} & -q_{2;i} \end{bmatrix}$$
with \( q_{2; i} = \delta_i \) and

\[
q_{1; i} = \sum_{j=1}^{N} \beta_j a_{ij} 1(x_j(t)=1)
\]

where the indicator function \( 1_x = 1 \) if the event \( x \) is true else it is zero. The coupling of node \( i \) to the rest of the network is described by an infection rate \( q_{1; i} \) that is a random variable, which essentially makes the process doubly stochastic. This observation is crucial. For, using the definition of the infinitesimal generator \([8, p. 181]\),

\[
\Pr[X_i(t + \Delta t) = 1| X_i(t) = 0] = q_{1; i} \Delta t + o(\Delta t)
\]

the continuity and differentiability shows that this process is not Markovian anymore. The random nature of \( q_{1; i} \) is removed by an additional conditioning to all possible combinations of rates, which is equivalent to conditioning to all possible combinations of the states \( X_j(t) = 1 \) (and their complements \( X_j(t) = 0 \)) of the neighbors of node \( i \). Hence, the number of basic states dramatically increases. Eventually, after conditioning each node in such a way, we end up with a \( 2^N \)-state Markov chain, studied in \([10]\).

Instead of conditioning, we replace the actual, random infection rate by an effective or average infection rate, which is basically a mean field approximation,

\[
E[q_{1; i}] = E \left[ \sum_{j=1}^{N} \beta_j a_{ij} 1(x_j(t)=1) \right]
\]

(1)

In general, we may take the expectation over the rates \( \beta_i \), the network topology via the matrix \( A \) and the states \( X_j(t) \). Since we assume that both the infection rates \( \beta_i \) and the network are constant and given, we only average over the states. Using \( E[1_x] = \Pr[x] \) (see e.g. \([8]\)), we replace \( q_{1; i} \) by

\[
E[q_{1; i}] = \sum_{j=1}^{N} \beta_j a_{ij} \Pr[X_j(t) = 1]
\]

which results in an effective infinitesimal generator,

\[
\overline{Q}(t) = \left[ -E[q_{1; i}] \delta_i \right]
\]

The effective \( \overline{Q}(t) \) allows us to proceed with Markov theory. Denoting \( v_i(t) = \Pr[X_i(t) = 1] \) and recalling that \( \Pr[X_i(t) = 0] = 1 - v_i(t) \), the Markov differential equation \([8, 10, 11] \) on p. 182] for state \( X_i(t) = 1 \) turns out to be non-linear

\[
\frac{dv_i(t)}{dt} = \sum_{j=1}^{N} \beta_j a_{ij} v_j(t) - v_i(t) \left( \sum_{j=1}^{N} \beta_j a_{ij} v_j(t) + \delta_i \right)
\]

(2)

Each node obeys a differential equation as \([2]\).

\[
\frac{dv_1(t)}{dt} = \sum_{j=1}^{N} \beta_j a_{1j} v_j(t) - v_1(t) \left( \sum_{j=1}^{N} \beta_j a_{1j} v_j(t) + \delta_1 \right)
\]

\[
\frac{dv_2(t)}{dt} = \sum_{j=1}^{N} \beta_j a_{2j} v_j(t) - v_2(t) \left( \sum_{j=1}^{N} \beta_j a_{2j} v_j(t) + \delta_2 \right)
\]

\[
\vdots
\]

\[
\frac{dv_N(t)}{dt} = \sum_{j=1}^{N} \beta_j a_{Nj} v_j(t) - v_N(t) \left( \sum_{j=1}^{N} \beta_j a_{Nj} v_j(t) + \delta_N \right)
\]

Written in matrix form, with

\[
V(t) = \left[ v_1(t) \ v_2(t) \ \cdots \ v_N(t) \right]^T
\]

we arrive at

\[
\frac{dV(t)}{dt} = \text{Adiag}(\beta_j)V(t) - \text{diag}(v_i(t)) \left( \text{Adiag}(\beta_j)V(t) + C \right)
\]

(3)

where \( \text{diag}(v_i(t)) \) is the diagonal matrix with elements \( v_1(t), v_2(t), \ldots, v_N(t) \) and the curing rate vector is \( C = (\delta_1, \delta_2, \ldots, \delta_N) \).

We note that \( \text{Adiag}(\beta_i) \) is, in general and opposed to the homogeneous setting, not symmetric anymore, unless \( A \) and \( \text{diag}(\beta_i) \) commute, in which case the eigenvalue \( \lambda_i(\text{Adiag}(\beta_i)) = \lambda_i(A) \beta_i \) and both \( \beta_i \) and \( \lambda_i(A) \) have a same eigenvector \( x_i \).

III. GENERAL IN-HOMOGENEOUS STEADY-STATE

A. The steady-state equation

The metastable steady-state follows from \(3\) as

\[
\text{Adiag}(\beta_i) V_\infty - \text{diag}(v_\infty) \left( \text{Adiag}(\beta_i) V_\infty + C \right) = 0
\]

where \( V_\infty = \lim_{t \to \infty} V(t) \). We define the vector

\[
w = \text{Adiag}(\beta_i) V_\infty + C
\]

(4)

and write the steady-state equation as

\[
w - C = \text{diag}(v_\infty) w
\]

or

\[
(I - \text{diag}(v_\infty)) w = C
\]

Ignoring extreme virus spread conditions (the absence of curing \( (\delta_i = 0) \) and an infinitely strong infection rate \( \beta_i \to \infty \)), then the infection probabilities \( v_\infty \) cannot be one such that the matrix \( (I - \text{diag}(v_\infty)) = \text{diag}(1 - v_\infty) \) is invertible. Hence,

\[
w = \text{diag}\left( \frac{1}{1 - v_\infty} \right) C
\]

Invoking the definition \(4\) of \( w \), we obtain

\[
\text{Adiag}(\beta_i) V_\infty = \text{diag}\left( \frac{v_\infty}{1 - v_\infty} \right) C
\]

\[
= \text{diag}\left( \frac{\delta_i}{1 - v_\infty} \right) V_\infty
\]

(5)

The \( i \)-th row of \(5\) yields the nodal steady state equation,

\[
\sum_{j=1}^{N} a_{ij} \beta_j v_j = \frac{v_\infty \delta_i}{1 - v_\infty}
\]

(6)

Let \( V_\infty = \text{diag}(\beta_i) V_\infty \) and the effective spreading rate for node \( i \), \( \tau_i = \frac{\beta_i}{\delta_i} \), then we arrive at

\[
\text{Q} \left( \frac{1}{\tau_i (1 - v_\infty)} \right) \tilde{V}_\infty = 0
\]

(7)

where the symmetric matrix

\[
\text{Q}(q_i) = \text{diag}(q_i) - A
\]

\[
= \text{diag}(q_i - d_i) + Q
\]

(8)
can be interpreted as a generalized Laplacian because $Q(d_i) = Q = \Delta - A$, where $\Delta = \text{diag}(d_i)$. The observation that the non-linear set of steady-state equations can be written in terms of the generalized Laplacian $Q(q_i)$ is fortunate, because, as will be shown in Section III-B the powerful theory of the “normal” Laplacian $Q$ applies.

The modified steady-state vector $V_N$ is orthogonal to each row (or, by symmetry, each column) vector of $Q \left( \frac{1}{\tau_i(1-v_{i\infty})} \right)$. A non-zero modified steady-state vector $V_N$ is thus only possible provided $\det Q \left( \frac{1}{\tau_i(1-v_{i\infty})} \right) = 0$. In other words, the generalized Laplacian $Q \left( \frac{1}{\tau_i(1-v_{i\infty})} \right)$ is therefore $\text{reducible}$ [8], the Theorem 1 still applies (see e.g. [4]), however, since the modified steady-state vector $V_N$ is connected, the critical threshold on the $\tau$-vector is further explored in Section III-C while Section III-E applies the theory to the complete graph.

We also know that $\text{trace} (Q(q_i)) = \sum_{k=1}^{N} \lambda_k(Q)$. Thus, with $\lambda_N(Q) = 0$,

$$\sum_{k=1}^{N-1} \lambda_k(Q) = \sum_{i=1}^{N} \frac{1}{\tau_i(1-v_{i\infty})}$$

In addition, since

$$\text{trace} (Q^2(q_i)) = \text{trace} (\text{diag}(q_i^2)) + \text{trace} (A^2) = \sum_{i=1}^{N} \frac{1}{\tau_i^2(1-v_{i\infty})^2} + 2L$$

we have that

$$\sum_{k=1}^{N} \lambda_k^2(Q) = \sum_{i=1}^{N} \frac{1}{\tau_i^2(1-v_{i\infty})^2} + 2L$$

Right multiplication of (5) by the all one-vector $u^T = (1,1,\ldots,1)$ yields

$$u^T A \text{diag}(\beta_i) V_N = u^T \text{diag} \left( \frac{\delta_i}{1-v_{i\infty}} \right) V_N$$

With $u^T A = D^T = (d_1,d_2,\ldots,d_N)$, the degree vector, we have

$$u^T \text{diag} \left( \frac{\delta_i}{1-v_{i\infty}} \right) - D^T \text{diag}(\beta_i) V_N = 0$$
Similarly as deduced from Gershgorin’s theorem, this sum shows that, at least one \( j \) term should be negative (because \( \beta_j v_j \geq 0 \)), i.e. \( d_j \geq \frac{1}{\tau_j (1 - v_j \infty )} \). Also, in view of (9), the vector \( y \) with components \( y_j = \frac{1}{\tau_j (1 - v_j \infty )} - d_j \) is a linear combination of eigenvectors of \( Q \left( \frac{1}{\tau_j (1 - v_j \infty )} \right) \) belonging to a non-zero eigenvalue. In general, however, the vector \( y \) is not an eigenvector of \( Q \left( \frac{1}{\tau_j (1 - v_j \infty )} \right) \).

Lemma 2: If \( q_i^* > q_i \) for all \( 1 \leq i \leq N \), then \( Q(q_i^*) \) is positive definite.

Proof: For any non-zero vector \( x \), consider the quadratic form

\[
x^T Q(q_i^*) x = x^T Q(q_i) x + x^T \text{diag}(q_i^* - q_i) x
\]

Theorem 1 implies that \( x^T Q(q_i) x \geq 0 \), i.e. that \( Q(q_i) \) is semi-definite. Since \( q_i^* > q_i \) for all \( 1 \leq i \leq N \), \( x^T \text{diag}(q_i^* - q_i) x > 0 \), which demonstrates the lemma.

Lemma 2 indicates that the matrix \( T = Q \left( \frac{1}{\tau_i (1 - v_i \infty )} \right) \), defined in (23) below, is positive definite, because \( Q \left( \frac{1}{\tau_i (1 - v_i \infty )} \right) \) defines the vector \( V_\infty = (v_{1 \infty}, v_{2 \infty}, \ldots, v_{N \infty}) \) via (1).

C. The critical threshold

We known that the exact steady-state is \( V_\infty = 0 \), but the metastable steady-state (see [10] for a deeper discussion) is characterized by a second solution, the eigenvector of (7).

Theorem 3: The critical threshold is determined by vectors \( \tau_c = (\tau_{1c}, \tau_{2c}, \ldots, \tau_{Nc}) \) that obey \( \lambda_{\max}(R) = 1 \), where \( \lambda_{\max}(R) \) is the largest eigenvalue of the symmetric matrix

\[
R = \text{diag} \left( \frac{1}{\tau_i} \right) A \text{diag} \left( \frac{1}{\tau_i} \right)
\]

whose corresponding eigenvector has positive components if the graph \( G \) is connected.

Proof: At the critical threshold, the second, non-zero solution is \( V_\infty = \varepsilon x \), where \( x \) is a vector with non-negative components and where \( \varepsilon \) is arbitrary small. This property allows us to approximate the generalized Laplacian \( Q(q) \) as

\[
Q \left( \frac{1}{\tau_i (1 - v_i \infty )} \right) = \text{diag} \left( \frac{\delta_i}{\beta_i (1 - \varepsilon x_1)} \right) - A = \text{diag} \left( \frac{\delta_i}{\beta_i} \right) (I - \varepsilon \text{diag}(x_1)) - A + O(\varepsilon^2)
\]

such that (11) becomes first order in \( \varepsilon \)

\[
Q \left( \frac{1}{\tau_i} \right) \text{diag} (\beta_i) x = 0
\]

2The result [10] also follows by adding all rows in (7)

\[
Q(q_i) V_\infty = \text{diag}(q_i - d_i) V_\infty + QV_\infty
\]

and using the basic fact that the row sum of the Laplacian \( Q \) is zero, which can be rewritten as an eigenvalue equation for the adjacency matrix,

\[
\text{diag} \left( \frac{1}{\beta_i} \right) A \text{diag}(\beta_i) x = x
\]

Hence, \( x \) is the eigenvector of \( \bar{A} = \text{diag} \left( \frac{1}{\beta_i} \right) A \text{diag}(\beta_i) \) belonging to the eigenvalue 1. Since \( \bar{A} \) is a non-negative, irreducible matrix, the Perron-Frobenius Theorem ([8] p. 451) states that \( A \) has a positive largest eigenvalue \( \lambda_{\max}(A) \) with a corresponding eigenvector whose elements are all positive and that there is only one eigenvector of \( A \) with non-negative components. Since any scaled vector \( V_\infty = \varepsilon x \) must have non-negative components (because they represent scaled probabilities), we find that \( \lambda_{\max}(A) = 1 \). Hence, for the given vectors \( B = (\beta_1, \beta_2, \ldots, \beta_N) \) and \( C = (\delta_1, \delta_2, \ldots, \delta_N) \), there are three possibilities:

\[
\begin{cases}
  \lambda_{\max}(\bar{A}) < 1 & \text{not infected network} \\
  \lambda_{\max}(\bar{A}) = 1 & \text{critical threshold} \\
  \lambda_{\max}(\bar{A}) > 1 & \text{infected network}
\end{cases}
\]

where the inequalities sign are deduced by relating the largest eigenvalue to the norm of the matrix \( A \); higher eigenvalues correspond to a larger norm (see e.g. [8] Section A.3.1). Of course, only case \( \lambda_{\max}(\bar{A}) = 1 \), the eigenvector equation has a non-zero solution. If \( \lambda_{\max}(\bar{A}) > 1 \), then the first order expansion is inadequate and the full non-linear equation (7) needs to be solved.

The first order expansion process has caused \( \bar{A} \) to be not symmetric, while \( Q \left( \frac{1}{\tau_i (1 - v_i \infty )} \right) \) is symmetric in general. Fortunately, there exist a similarity transform \( H = \text{diag} \left( \sqrt{\beta_i} \right) \) which symmetrizes \( A \).

\[
R = H \bar{A} H^{-1} = \text{diag} \left( \frac{\beta_i}{\beta_i} \right) \text{diag} \left( \frac{\beta_i}{\beta_i} \right)
\]

and \( R = R^T \) has the same real eigenvalues as \( \bar{A} \) (see [8] p. 438)). The matrix \( R \) also demonstrates that only an effective rate per node, \( \tau_i = \frac{\beta_i}{\beta_i} \), is needed. Thus, the equation that characterizes the critical threshold is

\[
Ry = y
\]

where \( y = Hx \). The eigenvalue \( \lambda_{\max}(\bar{A}) = \lambda_{\max}(R) = 1 \) determines the critical vectors \( \tau_c = (\tau_{1c}, \tau_{2c}, \ldots, \tau_{Nc}) \). In general, there can be more than one critical vector because \( \lambda_{\max}(R) = 1 \) is a map of \( \mathbb{R}^N \rightarrow \mathbb{R} \).

We remark that, since \( \text{trace}(R) = \text{trace}(A) = 0 \), that \( \lambda_{\max}(R) = \lambda_1(R) = -\sum_{j=2}^{N} \lambda_j(R) \), where the eigenvalues are ordered as \( \lambda_N \leq \lambda_{N-1} \leq \cdots \leq \lambda_1 \).

1) Special cases: We illustrate that more than one critical vector obeys \( \lambda_{\max}(R) = 1 \). The particular example of the complete graph is discussed in Section III-E.

I. The homogeneous threshold \( \gamma_{\text{hom}} \) is found when \( \tau_i = \tau \), in which case \( \lambda_{\max}(R) = 1 \) reduces to \( \frac{1}{\gamma_{\text{hom}}} = \lambda_{\max}(A) \), a basic result in [10].
2. When \( \frac{\Delta}{\beta} = \frac{1}{\tau_i} = d_i \) for all \( 1 \leq i \leq N \), we observe that \( Q(d_i) = Q \) if \( v_{i \infty} = \varepsilon > 0 \), where \( \varepsilon \) is arbitrary small. In that case, the steady-state vector is \( V_{i \infty} \rightarrow \varepsilon u \), thus \( V_{i \infty} = \varepsilon (\beta_1, \beta_2, \ldots, \beta_N) \) and the critical vector \( \tau_c = \left( \frac{\tau_1}{\tau_1, \frac{\tau_2}{
abla}, \ldots, \frac{\tau_N}{\tau_N} \right) \). In that case, \( R = \text{diag} \left( \sqrt{\frac{1}{\tau_i}} \right) \text{Adiag} \left( \sqrt{\frac{1}{\tau_i}} \right) \) and after a similarity transform \( H_1 = \text{diag} \left( \frac{1}{\tau_i} \right) \), we obtain the stochastic matrix [8 p. 484-486]

\[ H_1 R H_1^{-1} = \Delta^{-1} A \]

whose largest eigenvalue is, indeed, equal to one.

D. Bounding \( \lambda_{\max} (R) \)

Applying the general Rayleigh formulation for any matrix \( M \),

\[ \lambda_{\max} = \sup_{x \neq 0} \frac{x^T M x}{x^T x} \]

and, knowing that all components of the eigenvector belonging to the largest eigenvalue are non-negative, we obtain

\[ \lambda_{\max} (R) = \sup_{z \neq 0} \frac{z^T R z}{z^T x} \]

Let \( z = \text{diag} \left( \frac{1}{\tau_i} \right) x \), then

\[ \lambda_{\max} (R) = \sup_{z \neq 0} \frac{z^T A z}{z^T \text{diag} \left( \frac{1}{\tau_i} \right) z} \]

(12)

If \( x \) is the eigenvector of \( R \) belonging to the largest eigenvalue \( \lambda_{\max} (R) = 1 \), then (12) implies that the vector \( z \) satisfies

\[ z^T \text{diag} \left( \frac{1}{\tau_i} \right) z = z^T A z \]

which shows that \( z \) (with positive vector components) cannot be an eigenvector of \( A \), unless all \( \tau_i = \tau \). Indeed, suppose that \( z \) is an eigenvector of \( A \) belonging to \( \lambda (A) \), then \( z^T A z = \lambda (A) z^T z \), which can only be equal to \( z^T \text{diag} \left( \frac{1}{\tau_i} \right) z \) if all \( \tau_i = \tau \) and \( \lambda (A) = \lambda_{\max} (A) = \frac{1}{\tau} \); thus, only in the homogeneous case. In the sequel, we deduce several bounds from (12).

First, we rewrite (12) as

\[ \lambda_{\max} (R) = \sup_{z \neq 0} \frac{z^T A z}{z^T \text{diag} \left( \frac{1}{\tau_i} \right) z} \]

\[ \geq \sup_{z \neq 0} \frac{z^T A z}{z^T \text{diag} \left( \frac{1}{\tau_i} \right) z} \]

\[ = \lambda_{\max} (A) \min_{1 \leq j \leq N} \tau_i \]

Thus,

\[ \lambda_{\max} (A) \min_{1 \leq j \leq N} \tau_i \leq \lambda_{\max} (R) \leq \lambda_{\max} (A) \max_{1 \leq j \leq N} \tau_i \]

(13)

where the upper bound follows similarly from

\[ \sup_{z \neq 0} \frac{z^T A z}{z^T \text{diag} \left( \frac{1}{\tau_i} \right) z} \leq \frac{\lambda_{\max} (R)}{\lambda_{\min} (R)} \frac{\max_{z \neq 0} z^T A z}{\min_{z \neq 0} z^T A z} \]

At the critical threshold where \( \lambda_{\max} (R) = 1 \), the bounds reduce, with \( \tau_{\min} = \min_{1 \leq j \leq N} \tau_i \) and \( \tau_{\max} = \max_{1 \leq j \leq N} \tau_i \), to the inequality for the minimum and maximum component of the critical \( \tau \)-vector,

\[ \tau_{\min} \leq \frac{1}{\lambda_{\max} (A)} \leq \tau_{\max} \]

Hence, there is always at least one \( \tau \)-component below and one \( \tau \)-component above the critical threshold of the homogeneous case \( \tau_{\text{hom;c}} = \frac{1}{\lambda_{\max} (A)} \).

Next, a common lower bound (see e.g. [9, 11]) is obtained by letting \( z = u \), the all-one vector, in (12). Equality in (12) is only achieved when \( z \) is the eigenvector such that, in all other cases,

\[ \lambda_{\max} (R) \geq \frac{u^T A u}{u^T \text{diag} \left( \frac{1}{\tau_i} \right) u} = \frac{2L}{\sum_{j=1}^{N} \frac{1}{\tau_j}} \]

(14)

For all regular graphs \(G\), the bound (14) is very sharp, because \( u \) is the largest eigenvector of \( A \) belonging to \( \lambda_{\max} (A) = d \). However, all eigenvectors of \( \left( \frac{1}{\tau_i} \right) \) are the basic vectors \( e_j \) with all components equal to zero, except for the \( j \)-th one that is equal to one. Written in terms of the average degree \( E [D] = \frac{1}{N} \sum_{j=1}^{N} \frac{d_j}{\tau_j} \) and the harmonic mean \( E \left[ \frac{1}{\tau} \right] = \frac{1}{N} \sum_{j=1}^{N} \frac{1}{\tau_j} \)

yields

\[ \lambda_{\max} (R) \geq \frac{E [D]}{E \left[ \frac{1}{\tau} \right]} \]

such that at the critical threshold, where \( \lambda_{\max} (R) = 1 \), there holds that \( E \left[ \frac{1}{\tau} \right] \geq E [D] \). Unfortunately, the harmonic, geometric and arithmetic mean inequality\(^3\) that leads to \( \frac{1}{N} \sum_{j=1}^{N} \frac{1}{\tau_j} \geq \frac{1}{N} \sum_{j=1}^{N} \frac{d_j}{\tau_j} = E \left[ \frac{1}{\tau} \right] \), prevents us to clearly upper bound the average zero infection \( \tau \)-region, \( [0, E \left[ \frac{1}{\tau} \right] \). Approximative, by assuming \( \frac{1}{N} \sum_{j=1}^{N} \frac{1}{\tau_j} \approx E \left[ \frac{1}{\tau} \right] \), the average zero infection \( \tau \)-region is upper bounded by the mean degree \( E [D] \). Notice that, in the homogeneous case \( (\tau_j = \tau) \), the approximation is exact, leading to \( \tau_{\text{hom;c}} \leq \frac{E [D]}{E \left[ \frac{1}{\tau} \right]} \).

There are several other interesting choices. A first alternative choice is \( z = D \), where \( D = (d_1, d_2, \ldots, d_N) \) is the degree vector. The Rayleigh expression (12) becomes

\[ \lambda_{\max} (R) \geq \frac{D^T A D}{D^T \text{diag} \left( \frac{1}{\tau_i} \right) D} = \frac{\sum_{k=1}^{N} \sum_{j=1}^{N} d_k a_{kj} d_j}{\sum_{j=1}^{N} \frac{d_j}{\tau_j}} \]

With \( d_j = \sum_{l=1}^{N} a_{lj} \), and using symmetry, \( a_{ij} = a_{ji} \),

\[ D^T A D = \sum_{k=1}^{N} \sum_{l=1}^{N} \sum_{q=1}^{N} \sum_{j=1}^{N} a_{kj} a_{kj} d_k \]

\[ = N \sum_{j=1}^{N} \sum_{l=1}^{N} \sum_{q=1}^{N} a_{kj} a_{kj} d_k \]

\[ = N \sum_{j=1}^{N} \sum_{l=1}^{N} \sum_{q=1}^{N} a_{kj} \left( A^2 \right) \]

\[ = N \sum_{j=1}^{N} \sum_{l=1}^{N} \sum_{q=1}^{N} \left( A^3 \right) \]

\[ = N \sum_{j=1}^{N} \sum_{l=1}^{N} \sum_{q=1}^{N} \left( A^3 \right) \]

\[ = N \]

\[ \frac{1}{\tau_j} \]

\[ \leq \frac{1}{n} \sum_{j=1}^{N} \frac{1}{\tau_j} \]

\[ \leq \frac{1}{n} \sum_{j=1}^{N} a_{ij} \]

(15)

\(^3\) A regular graph is a graph where all degree \( d_i = d \).

\(^4\) For real positive numbers \( a_1, a_2, \ldots, a_n \), the harmonic, geometric and arithmetic mean inequality is

\[ \frac{1}{n} \sum_{j=1}^{n} \frac{1}{a_j} \leq \frac{1}{n} \sum_{j=1}^{n} a_j \]
where $N_3$ equals the total number of walks of length 3 in the graph. Thus, at the critical threshold where $\lambda_{\text{max}}(R) = 1$,

$$
\sum_{j=1}^{N} \frac{d_j^2}{\tau_j} \geq N_3
$$

(16)

Invoking the Cauchy-Schwarz inequality (see e.g. [8], p. 90]), we further obtain

$$
\sum_{j=1}^{N} \frac{\tau_j^2}{\tau_j} = \sum_{j=1}^{N} \frac{q_j^2}{\tau_j} \geq \frac{N^2}{\sum_{j=1}^{N} \tau_j^4}
$$

$$
\sum_{j=1}^{N} \frac{1}{\tau_j} \geq \frac{N_2^2}{\sum_{j=1}^{N} \tau_j^4}
$$

A second alternative choice is to choose the components of the vector $z$ equal to a row vector of $A$, i.e. $z_j = a_{qj}$, such that

$$
\lambda_{\text{max}}(R) \geq \frac{\sum_{k=1}^{N} \sum_{j=1}^{N} a_{kj} a_{qj}}{\sum_{j=1}^{N} a_{qj}^2} = (A^2)_{qq}
$$

and $\sum_{j=1}^{N} \frac{a_{qj}^2}{\tau_j} = \sum_{j=1}^{N} \frac{a_{qj}}{\tau_j}$, we obtain at the critical threshold where $\lambda_{\text{max}}(R) = 1$,

$$
\sum_{j=1}^{N} \frac{a_{qj}}{\tau_j} \geq (A^3)_{qq}
$$

Summing over all $q$ leads to

$$
\sum_{j=1}^{N} \frac{d_j}{\tau_j} \geq \text{trace} (A^3)
$$

(17)

E. Computation of $\lambda_{\text{max}}(R)$ in $K_N$

The adjacency matrix of the complete graph $K_N$ is $A_{K_N} = J - I$, where $J = u_1 u_1^T$ is the all-one matrix. Then, the $R$ matrix defined in (11) is

$$
R_{K_N} = \text{diag} (\sqrt{\tau_1}) (J - I) \text{diag} (\sqrt{\tau_1}) = \text{diag} (\sqrt{\tau_1}) u_1 u_1^T \text{diag} (\sqrt{\tau_1}) - \text{diag} (\tau_1) = (u_1^T \text{diag} (\sqrt{\tau_1}) u_1)^T \cdot u_1 u_1^T \text{diag} (\sqrt{\tau_1}) - \text{diag} (\tau_1) = \sqrt{T} \cdot \sqrt{T}^T - \text{diag} (\tau_1)
$$

where the square root vector of $\tau$ is $\sqrt{T} = (\sqrt{\tau_1}, \sqrt{\tau_2}, \ldots, \sqrt{\tau_N})$. The eigenvalues are determined by the zeros of the characteristic polynomial $p_N(\lambda) = \det (R - \lambda I)$,

$$
p_N(\lambda) = \det \left( \sqrt{T} \cdot \sqrt{T}^T - \text{diag} (\tau_1 + \lambda) \right) = \det (-\text{diag} (\tau_1 + \lambda)) \times \det \left( I - \frac{1}{\tau_1 + \lambda} \right) \sqrt{T} \cdot \sqrt{T}^T
$$

After using the one-rank update formula (see e.g. [5]),

$$
\det (I + c d^T) = 1 + d^T c,
$$

we obtain

$$
p_N(\lambda) = (-1)^N \left( 1 - \sqrt{\tau i + \lambda} \right) \sqrt{T} \prod_{i=1}^{N} (\tau_i + \lambda) = (-1)^N \left( 1 - \sum_{j=1}^{N} \frac{\tau_j}{\tau_j + \lambda} \right) \prod_{i=1}^{N} (\tau_i + \lambda)
$$

Let us order the non-negative vector components of $\tau$ as $0 \leq \tau_{(N)} \leq \tau_{(N-1)} \leq \cdots \leq \tau_1$. The rational function $r(\lambda) = 1 - \sum_{j=1}^{N} \frac{\tau_j}{\tau_j + \lambda}$ has simple poles at $\lambda = -\tau_j$ and is increasing between two consecutive poles. Moreover, $\lim_{\lambda \to \pm \infty} r(\lambda) = 1$. This implies that $r(\lambda)$ has simple zeros between each pair $(-\tau_{(j-1)}, -\tau_{(j)})$ and those zeros are the zeros of the characteristic polynomial $p_N(\lambda) = r(\lambda) \prod_{i=1}^{N} (\tau_i + \lambda)$ provided

$$
p_N(-\tau_j) = -\tau_j \prod_{i=1}^{N} (\tau_i - \tau_j) \neq 0, \text{ i.e. provided all } \tau_i \text{ are different. The largest zero of } p_N(\lambda) \text{ exceeds } \lambda = -\tau_{(N)} \leq 0. \text{ Even much sharper, since } \text{trace}(A) = \sum_{i=1}^{N} \lambda_i = 0, \text{ we know that}
$$

$$
\lambda_{\text{max}} = \lambda_1 = -\sum_{i=1}^{N} \frac{\tau_i}{\tau_i - \tau_{\text{min}}}
$$

from which the largest zero of $(-1)^N p_N(\lambda)$ is the only positive solution in $\lambda$ of

$$
\sum_{j=1}^{N} \frac{1}{\tau_j + \lambda} = \frac{N - 1}{\lambda}
$$

(18)

By iteration of the rewritten equation as $\lambda = \frac{1}{\sum_{j=1}^{N} \frac{1}{\tau_j + \lambda} - \frac{N - 1}{\lambda}}$, we obtain the continued fraction

$$
\lambda_{\text{max}} = \frac{1}{\sum_{j=1}^{N} \frac{1}{\tau_j + \lambda} + \frac{1}{\sum_{j=1}^{N} \frac{1}{\tau_j + \lambda} + \cdots}}
$$

from which the following convergents are deduced,

$$
\frac{N - 1}{\sum_{j=1}^{N} \frac{1}{\tau_j + \lambda}} < \cdots < \frac{N - 1}{\sum_{j=1}^{N} \frac{1}{\tau_j + \sum_{k=1}^{N} \frac{1}{\tau_k + \lambda}}}
$$

Notice that these convergents for $K_N$ show that, indeed, (14) is a sharp bound for regular graphs. Lagrange expansion of (18) is also possible, but we omit this analysis.

The critical vector components thus satisfy, with $\lambda_{\text{max}}(R) = 1$, the equation

$$
\sum_{j=1}^{N} \frac{1}{\tau_j + 1} = N - 1
$$

(19)
A critical \( \tau \)-vector must have bounded components. For, if \( \tau_k \to \infty \), then (19) implies that all other \( \tau_j = 0 \), which leads to a physically uninteresting situation. Let \( \tau_j = \tau_{\text{hom}} + h_j \), where \( \tau_{\text{hom}} = \frac{1}{N - 1} \) as shown below, then (19) can be rewritten as

\[
\sum_{j=1}^{N} \frac{1}{1 + \frac{N-1}{N} h_j} = N
\]

For small \( h_j \) where \( (1 + \frac{N-1}{N} h_j)^{-1} = 1 - \frac{N-1}{N} h_j + O(h_j^2) \), we have that \( \sum_{j=1}^{N} h_j \approx 0 \). Hence, the small deviations \( h_j \) from the homogeneous case are balanced, in the sense that the net or average deviation is about zero. Suppose that all \( h_j = 0 \) for \( 3 \leq j \leq N \), then \( h_1 \) and \( h_2 \) obey a hyperbolic relation

\[
h_1 = \frac{-h_2}{1 + 2\frac{N-1}{N} h_2}
\]

Small negative values for \( h_2 \) correspond on the critical threshold, to large positive values for \( h_1 \) (and vice versa).

Finally, the homogeneous case, where \( \tau_j = \tau_{\text{hom}} \), considerably simplifies to the characteristic polynomial

\[
p_N(\lambda) = (-1)^N (\lambda - \tau_{\text{hom}} (N - 1)) (\tau_{\text{hom}} + \lambda)^{N-1}
\]

whose zeros are \( \lambda = \tau_{\text{hom}} (N - 1) \) and \( \lambda = -\tau_{\text{hom}} \) with multiplicity \( N - 1 \). This example illustrates that, although heterogeneity is much more natural, it complicates analysis seriously.

### F. Additional properties

We list here additional properties that have been proved in (10), and whose extension to the inhomogeneous setting is rather straightforward.

**Lemma 4:** In a connected graph, either \( v_{t\infty} = 0 \) for all \( i \) nodes, or none of the components \( v_{t\infty} \) is zero.

**Lemma 4** also follows from the Perron-Frobenius theorem as shown in the proof of Theorem 1.

**Theorem 5:** The non-zero steady-state infection probability of any node \( i \) in the \( N \)-intertwined model can be expressed as a continued fraction

\[
v_{t\infty} = 1 - \frac{1}{1 + \frac{2\gamma_i - \delta_i^{-1} \sum_{j=1}^{N} \beta_j a_{ij}}{\sum_{j=1}^{N} \beta_j a_{ij}}}
\]

where the total infection rate of node \( i \), incurred by all neighbors towards node \( i \), is

\[
\gamma_i = \sum_{j=1}^{N} a_{ij} \beta_j = \sum_{j \in \text{neighbor}(i)} \beta_j
\]

Consequently, the exact steady-state infection probability of any node \( i \) is bounded by

\[
0 \leq v_{t\infty} \leq 1 - \frac{1}{1 + \frac{2\gamma_i - \delta_i^{-1} \sum_{j=1}^{N} \beta_j a_{ij}}{\sum_{j=1}^{N} \beta_j a_{ij}}}
\]

As explained in (19), the continued fraction stopped at iteration \( k \) includes the effect of virus spread up to the \((k-1)\)-hop neighbors of node \( i \). In the homogeneous case where \( \beta_j = \beta \) for all \( 1 \leq j \leq N \), we have that \( \gamma_i = \beta d_i \) is proportional to the degree of node \( i \). The ratio \( \tau_i = \frac{\gamma_i}{\delta_i} \) is the total effective infection rate of node \( i \).

**Lemma 6:** In a connected graph \( G \) above the critical threshold, a lower bound of \( v_{t\infty} \) for any node \( i \) equals

\[
v_{t\infty} \geq 1 - \frac{1}{1 + \delta_i^{-1} \sum_{j=1}^{N} a_{ij} \beta_j v_{t\infty}} \geq 1 - \frac{1}{1 + \frac{1}{\gamma_i} v_{t\infty}}
\]

where we have used the definition (21). From the last inequality, it follows that

\[
v_{t\infty} \geq 1 - \frac{\delta_i}{\gamma_i}
\]

such that (23) is proved. \( \Box \)

By combining (22) and (23), the total fraction of infected nodes \( y_{t\infty} = \frac{1}{N} \sum_{k=1}^{N} v_{t\infty} \) in steady-state is bounded by

\[
1 - \frac{1}{\min_{1 \leq k \leq N} \frac{\gamma_i}{\delta_i}} \leq y_{t\infty} \leq 1 - \frac{1}{\sum_{i=1}^{N} \frac{1}{1 + \frac{2\gamma_i - \delta_i^{-1} \sum_{j=1}^{N} \beta_j a_{ij}}{\sum_{j=1}^{N} \beta_j a_{ij}}}}
\]

### IV. The convexity of \( v_{t\infty} \) as a function of \( \delta_i \)

It is of interest (e.g. in game theory (2)) to know whether the steady-state infection probability \( v_{t\infty} \) is convex in the own curing rate \( \delta_i \), given that all other curing rates \( \delta_j \) for \( 1 \leq j \neq i \leq N \) are constant. In many infection situations, the node \( i \) cannot control the spreading process, but it can protect itself better by increasing its own curing rate \( \delta_i \), for example, by installing more effective antivirus software in computer networks, or by vaccinating people against some diseases.

**Theorem 7:** Given that all curing rates \( \delta_j \) for \( 1 \leq j \neq i \leq N \) are constant and independent from the infection rates \( \beta_j \), the non-zero steady-state infection probability \( v_{t\infty}(\delta_1, \ldots, \delta_i, \ldots, \delta_N) > 0 \) is strict convex in \( \delta_i \), while all other non-zero steady-state infection probabilities \( v_{t\infty}(\delta_1, \ldots, \delta_i, \ldots, \delta_N) > 0 \) are concave in \( \delta_i \).

**Proof:** We operate above the critical threshold specified by \( \lambda_{\text{max}}(R) = 1 \), where the vector \( V_{t\infty} > 0 \) and start from the steady-state equation (6) for node \( i \). Differentiation with respect to \( \delta_i \) results in

\[
\sum_{k=1}^{N} a_{ik} \beta_k \frac{\partial v_{t\infty}}{\partial \delta_i} = \frac{v_{t\infty}}{1 - v_{t\infty}} + \frac{\delta_i}{(1 - v_{t\infty})^2} \frac{\partial v_{t\infty}}{\partial \delta_i}
\]

and

\[
\sum_{k=1}^{N} a_{ik} \beta_k \frac{\partial^2 v_{t\infty}}{\partial^2 \delta_i} = \frac{2}{(1 - v_{t\infty})^2} \frac{\partial v_{t\infty}}{\partial \delta_i} + \frac{2\delta_i}{(1 - v_{t\infty})^3} \left( \frac{\partial v_{t\infty}}{\partial \delta_i} \right)^2 + \frac{\delta_i}{(1 - v_{t\infty})^2} \frac{\partial^2 v_{t\infty}}{\partial^2 \delta_i}
\]
Differentiating any other row \( j \neq i \) in (5) with respect to \( \delta_i \) results in
\[
\sum_{k=1}^{N} a_{jk} \beta_k v_{k\infty} = \frac{v_{j\infty}}{1 - v_{j\infty}} \delta_j
\]
and
\[
\sum_{k=1}^{N} a_{jk} \beta_k \frac{\partial^2 v_{k\infty}}{\partial \delta_i^2} = \frac{2 \delta_j}{(1 - v_{j\infty})^2} \left( \frac{\partial v_{j\infty}}{\partial \delta_i} \right)^2 + \frac{\delta_j}{(1 - v_{j\infty})^2} \frac{\partial v_{j\infty}}{\partial \delta_i} \frac{\partial^2 v_{j\infty}}{\partial \delta_i^2}
\]
Written in matrix form, we have
\[
\text{Adiag} (\beta_k) \frac{\partial V_{\infty}}{\partial \delta_i} = \text{diag} \left( \frac{\delta_j}{(1 - v_{j\infty})^2} \right) \frac{\partial V_{\infty}}{\partial \delta_i} + \frac{v_{i\infty}}{1 - v_{i\infty}} e_i
\]
where the basisvector \( e_i \) has all zero components, except for the component \( i \) that equals 1. The second order derivatives are, in matrix form,
\[
\text{Adiag} (\beta_k) \frac{\partial^2 V_{\infty}}{\partial \delta_i^2} = W_{\infty} + \text{diag} \left( \frac{\delta_i}{(1 - v_{i\infty})^2} \right) \frac{\partial^2 V_{\infty}}{\partial \delta_i^2} + \frac{2}{(1 - v_{i\infty})^2} \frac{\partial v_{i\infty}}{\partial \delta_i} e_i
\]
where
\[
W_{\infty} = \left[ \frac{2 \delta_1 \left( \frac{\partial v_{1\infty}}{\partial \delta_1} \right)^2}{(1 - v_{1\infty})^2} \ldots \frac{2 \delta_N \left( \frac{\partial v_{N\infty}}{\partial \delta_N} \right)^2}{(1 - v_{N\infty})^2} \right]^T
\]
We rewrite the matrix equations as
\[
T \frac{\partial V_{\infty}}{\partial \delta_i} = -\frac{v_{i\infty}}{1 - v_{i\infty}} e_i
\]
where the symmetric matrix
\[
T = \text{diag} \left( \frac{\delta_j}{(1 - v_{j\infty})^2} \right) - \text{Adiag} (\beta_k)
\]
is written in terms of the generalized Laplacian \( Q (q_i) \), defined in (5), as
\[
T = \text{diag} (\beta_j) Q \left( \frac{1}{\tau_j (1 - v_{j\infty})^2} \right)
\]
Lemma 2 shows that \( T \) is positive definite, which implies that also \( T^{-1} \) is positive definite because \( T = U \text{diag} (\lambda_j) U^T \) shows that \( T^{-1} = U \text{diag} (\lambda_j^{-1}) U^T \) and, thus, that the inverse \( T^{-1} \) exists. The vector \( \frac{\partial V_{\infty}}{\partial \delta_i} \) is solved from (27) explicitly as
\[
\frac{\partial V_{\infty}}{\partial \delta_i} = -\frac{v_{i\infty}}{1 - v_{i\infty}} \frac{T^{-1}}{T^{-1}} e_i = -\frac{v_{i\infty}}{1 - v_{i\infty}} \frac{T^{-1}}{T^{-1}} \text{column } i = -\frac{v_{i\infty}}{1 - v_{i\infty}} \frac{T^{-1}}{T^{-1}} \text{row } i
\]
Increasing the virus curing rate cannot increase the virus infection probability, such that \( \frac{\partial v_{i\infty}}{\partial \delta_i} \leq 0 \) for all \( 1 \leq k \leq N \). This implies that all elements of \( T^{-1} \) are non-negative. Only at the critical threshold, derivatives do not exist because the left- and right derivative at that point are not equal. Below the critical threshold, where \( V_{\infty} = 0 \), (30) does not yield information about the existence of \( T^{-1} \). However, the definition shows that \( T = \text{diag} (\delta_j) - \text{Adiag} (\beta_j) \). Hence, if \( \frac{\delta_j}{\beta_j} = d_j \) for each node \( j \), then \( \text{diag} (\beta_j^{-1}) T \) equals the Laplacian \( Q \) and \( T^{-1} \) does not exist. In general, it is difficult to conclude for which vector \( C = (\delta_1, \delta_2, \ldots , \delta_N) \) that \( T^{-1} \) exists below the critical threshold. But, below the critical threshold, \( V_{\infty} = 0 \) such that both convexity and concavity hold. In the sequel, we ignore further considerations about this sub-threshold regime.
We recast the second order derivatives in terms of the matrix \( T \),
\[
T \frac{\partial^2 V_{\infty}}{\partial \delta_i^2} = -W_{\infty} - \frac{2}{(1 - v_{i\infty})^2} \frac{\partial v_{i\infty}}{\partial \delta_i} e_i
\]
Introducing (30) in \( W_{\infty} \) yields
\[
W_{\infty} = \frac{2 v_{i\infty}^2}{(1 - v_{i\infty})^2} \left[ \frac{\delta_1 ((T^{-1})_{11})^2}{(1 - v_{1\infty})^2} \ldots \frac{\delta_N ((T^{-1})_{NN})^2}{(1 - v_{N\infty})^2} \right]^T
\]
and
\[
\frac{2}{(1 - v_{i\infty})^2} \frac{\partial v_{i\infty}}{\partial \delta_i} e_i = -\frac{2 v_{i\infty}}{(1 - v_{i\infty})^3} (T^{-1})_{ii} e_i
\]
which shows that the right hand side vector \( \tilde{W} = W_{\infty} + \frac{2}{(1 - v_{i\infty})^2} \frac{\partial v_{i\infty}}{\partial \delta_i} e_i \) has all positive elements, except possibly for the \( i \)-th component which is
\[
\tilde{W}_i = \frac{2 \delta_i (v_{i\infty} (T^{-1})_{ii})^2}{(1 - v_{i\infty})^3} - \frac{2 v_{i\infty} (T^{-1})_{ii}}{(1 - v_{i\infty})^3}
\]
\[
= \frac{2 v_{i\infty} (T^{-1})_{ii}}{(1 - v_{i\infty})^3} \left( \delta_i (v_{i\infty} (T^{-1})_{ii})^2 - 1 \right)
\]
Now, \( \tilde{W}_i < 0 \) provided
\[
\delta_i \frac{v_{i\infty} (T^{-1})_{ii}}{(1 - v_{i\infty})^3} < 1
\]
Above the critical threshold, \( T^{-1} \) exists such that
\[
\frac{\partial^2 v_{i\infty}}{\partial \delta_i^2} = -T^{-1} \tilde{W}
\]
Since all elements of \( T^{-1} \) are positive, we conclude that, for all \( 1 \leq k \neq i \leq N \),
\[
\frac{\partial^2 v_{i\infty}}{\partial \delta_i^2} \leq 0
\]
and that
\[
\frac{\partial^2 v_{i\infty}}{\partial \delta_i^2} > 0 \text{ provided } \frac{v_{i\infty} \delta_i (T^{-1})_{ii}}{(1 - v_{i\infty})^2} < 1
\]
We rewrite the steady-state equation (5) as
\[
\text{Adiag} (\beta_i) V_{\infty} = \text{diag} \left( \frac{\delta_i}{(1 - v_{i\infty})^2} \right) V_{\infty} = \text{diag} \left( \frac{\delta_i}{(1 - v_{i\infty})^2} \right) \text{diag} (1 - v_{i\infty}) V_{\infty} = \text{diag} \left( \frac{\delta_i}{(1 - v_{i\infty})^2} \right) V_{\infty}
\]
In terms of the $T$-matrix \(^{(25)}\),
\[
TV_{\infty} = \text{diag} \left( \frac{\delta_i v_{i\infty}}{(1-v_{i\infty})^2} \right) V_{\infty}
\]
and, since above the critical threshold the inverse $T^{-1}$ exists, we arrive at
\[
V_{\infty} = T^{-1} \text{diag} \left( \frac{\delta_i v_{i\infty}}{(1-v_{i\infty})^2} \right) V_{\infty}
\]
The $i$-th row is
\[
v_{i\infty} = \sum_{k=1}^{N} (T^{-1})_{ik} \frac{\delta_k v_{k\infty}^2}{(1-v_{k\infty})^2} - \delta_i v_{i\infty} \left( T^{-1} \right)_{ii} \sum_{k=1; k \neq i}^{N} (T^{-1})_{ik} \frac{\delta_k v_{k\infty}^2}{(1-v_{k\infty})^2}
\]
Thus,
\[
1 = \frac{\delta_i v_{i\infty} (T^{-1})_{ii}}{(1-v_{i\infty})^2} + \sum_{k=1; k \neq i}^{N} (T^{-1})_{ik} \frac{\delta_k v_{k\infty}^2}{(1-v_{k\infty})^2} v_{i\infty} \frac{\delta_k v_{k\infty}^2}{(1-v_{k\infty})^2}
\]
Since all elements of $T^{-1}$ are positive, we verify that the condition for strict convexity in \(^{(21)}\)
\[
\frac{\delta_i v_{i\infty} (T^{-1})_{ii}}{(1-v_{i\infty})^2} < 1
\]
holds, because by Lemma \(^{(4)}\) all $v_{i\infty} > 0$ above the critical threshold. \(\Box\)

V. THE DERIVATIVES $\frac{\partial v_{i\infty}}{\partial \delta_i}$

Our starting point is the matrix equation \(^{(27)}\), which we solve here by using Cramer’s rule.
\[
\frac{\partial v_{i\infty}}{\partial \delta_i} = -v_{i\infty} \frac{\det (T_{G \backslash \{i\}})}{1-v_{i\infty}} \frac{\det (T)}{\det (T)}
\]
where $G \backslash \{i\}$ denotes the graph $G$ from which the node $i$ is removed (together with all its incident links). Using the definition \(^{(29)}\) of $T$ shows that
\[
\frac{\partial v_{i\infty}}{\partial \delta_i} = -v_{i\infty} \frac{\det \left( Q_{G \backslash \{i\}} \left( \frac{1}{\tau_j (1-v_{i\infty})^2} \right) \right)}{\beta_i (1-v_{i\infty})^2} \frac{\det Q}{\det (T)}
\]
A determinant is unchanged by interchanging two rows and two columns. This means that we can write the matrix
\[
\frac{1}{\tau_j (1-v_{i\infty})^2} = \left[ \frac{Q_{G \backslash \{i\}} \left( \frac{1}{\tau_j (1-v_{i\infty})^2} \right)}{\tau_i (1-v_{i\infty})^2} - a_i^T \right]
\]
where the vector $a_i$ is the relabeled connection vector of node $i$ to all other nodes in $G$ and $a_i^T a_i = d_i$. Invoking
\[
\det \left[ \begin{array}{cc} A & B \\ C & D \end{array} \right] = \det A \det (D - CA^{-1}B)
\]
where $D - CA^{-1}B$ is called the Schur complement of $A$ (see e.g. \(^{(5)}\)), we find that
\[
\frac{\det Q}{\det Q_{G \backslash \{i\}}} = \frac{1}{\tau_i (1-v_{i\infty})^2} - f
\]
where the quadratic form is
\[
a_i^T Q_{G \backslash \{i\}}^{-1} \left( \frac{1}{\tau_j (1-v_{i\infty})^2} \right) a_i = f
\]
Whence,
\[
\frac{\partial v_{i\infty}}{\partial \delta_i} = -\frac{(1-v_{i\infty}) v_{i\infty}}{\delta_i - \beta_i (1-v_{i\infty})^2}
\]
The quadratic form $f$ does not depend on $v_{i\infty}$. Moreover, Lemma \(^{(2)}\) implies that $Q_{G \backslash \{i\}}^{-1} \left( \frac{1}{\tau_j (1-v_{i\infty})^2} \right)$ is positive definite (for $V_{\infty} > 0$). Hence, $f > 0$. The fact that $\frac{\partial v_{i\infty}}{\partial \delta_i} < 0$ implies $1 \geq \tau_i (1-v_{i\infty})^2 f$ and because the inequality holds for all $v_{i\infty}$, we also have that $1 \geq \tau_i f$.

The optimization of an utility or cost function of the type, that, for example, appears in game theory (see \(^{(7)}\)),
\[
J_i = c_i \delta_i + v_{i\infty}
\]
where $c_i$ is price to protect a node $i$ against the spread of infections, requires to compute the optimum $\frac{\partial J_i}{\partial \delta_i} = c_i + \frac{\partial v_{i\infty}}{\partial \delta_i} = 0$ for all $1 \leq i \leq N$. With \(^{(33)}\), this equation is solved explicitly as
\[
\frac{(1-v_{i\infty}) v_{i\infty}}{\delta_i} + \beta_i (1-v_{i\infty})^2 = f = \delta_i^*
\]
Thus, the optimal value of $\delta_i^* > \frac{(1-v_{i\infty}) v_{i\infty}}{c_i}$. An exact computation of $\delta_i^*$ is generally complex because $f = f(\tau_1, \ldots, \tau_{i-1}, \tau_{i+1}, \ldots, \tau_N)$ is a non-linear function that couples all the $\tau_j$ (and $\delta_i$).

VI. SUMMARY

The heterogeneous $N$-intertwined virus spread model has been described and analyzed in the steady-state. Since it applies to any network and any combination of node infections and curing vectors, $B$ and $C$, we believe that the heterogeneous $N$-intertwined virus spread model is useful for a wide range of practical infection scenarios in networks, from computer viruses to epidemics in social networks and in nature. The critical threshold regime is investigated, bounds are presented and the metastable steady-state infection probabilities are shown to be convex in the own curing rate, but concave in another node’s curing rate.

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REFERENCES

[1] N. Biggs. Algebraic Graph Theory. Cambridge University Press, Cambridge, U.K., second edition, 1996.
[2] D. M. Cvetković, M. Doob, and H. Sachs. Spectra of Graphs, Theory and Applications. Johann Ambrosius Barth Verlag, Heidelberg, third edition, 1995.
[3] A. Ganesh, L. Massoulié, and D. Towsley. The effect of network topology on the spread of epidemics. IEEE INFOCOM05, 2005.
[4] F. R. Gantmacher. The Theory of Matrices, volume II. Chelsea Publishing Company, New York, 1959.
[5] C. D. Meyer. Matrix Analysis and Applied Linear Algebra. Society for Industrial and Applied Mathematics (SIAM), Philadelphia, 2000.
[6] J. Omić and P. Van Mieghem. The metastable state of a SIS model. Journal of computer and system science, submitted 2008.
[7] J. Omic, P. Van Mieghem, and A. Orda. Game Theory and Computer Viruses. IEEE InfoCom09, 2009.
[8] P. Van Mieghem. Performance Analysis of Communications Systems and Networks. Cambridge University Press, Cambridge, U.K., 2006.
[9] P. Van Mieghem. A new type of lower bound for the largest eigenvalue of a symmetric matrix. Linear Algebra and its Applications, 427(1):119–129, November 2007.
[10] P. Van Mieghem, J. Omic, and R. E. Kooij. Virus spread in networks. IEEE/ACM Transactions on Networking, 17(1):1–14, February 2009.
[11] S. G. Walker and P. Van Mieghem. On Lower Bounds for the Largest Eigenvalue of a Symmetric Matrix. Linear Algebra and its Applications, 429(2-3):519–526, July 2008.
[12] Y. Wang, D. Chakrabarti, C. Wang, and C. Faloutsos. Epidemic spreading in real networks: An eigenvalue viewpoint. 22nd International Symposium on Reliable Distributed Systems (SRDS’03)- IEEE Computer, pages 25–34, October 2003.
[13] J. H. Wilkinson. The Algebraic Eigenvalue Problem. Oxford University Press, New York, 1965.