Type reproduction number for epidemic models on heterogeneous networks

Satoru Morita
Department of Mathematical and Systems Engineering, Shizuoka University, Hamamatsu, 432-8561, Japan
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Infection can spread easily on networks with heterogeneous degree distribution. Here, we considered targeted immunization on such networks, wherein a fraction of individuals with the highest connectivity are immunized. To quantify the effect of this targeted immunization approach on population immunity, we proposed a method using the type reproduction number. Consequently, we derived a precise and simple formula that can yield the immunization threshold, which, to the best of our knowledge, is the first such result presented in the literature.

In the previous works [8, 9], a simple method for deriving the type reproduction number using the next-generation matrix has been proposed: if the next-generation matrix \( A \) is decomposed into the target matrix \( C \) of the terms subject to be immunized and residual matrix \( A - C \) of the terms not subject to be immunized, then we have

\[
T_C = \rho(C(I - A + C)^{-1})
\]

if \( A \) is irreducible and \( \rho(A - C) < 1 \) [8, 9].

Considering the spread of infections in social networks, an important property of networks that should not be overlooked is its degree heterogeneity, where the degree \( k \) is defined as the number of connections each node has with other nodes [10–12]. It is well-known that the degree distribution often follows a power law for large values of \( k \):

\[
P(k) \sim k^{-\gamma}.
\]

In this case, the network is called a scale-free network [12, 13]. For example, it has been reported that the networks of human sexual contact are scale-free [14, 16]. On the contrary, some other studies on the subject have rejected this notion [17, 18]. While it is still being debated whether real sexual networks are strictly scale-free, it is clear that they are highly heterogeneous; this is because only a few individuals tend to have a large number of sexual partners, while most individuals only have a few sexual partners.

In the popular susceptible-infected-susceptible (SIS) model in networks [19, 21], the basic reproduction number is given as follows:

\[
R_0 = \lambda \langle k^2 \rangle / \langle k \rangle,
\]

where \( \lambda \) represents the infection rate, which is defined later. A similar formula for \( R_0 \) has long been known in the field of epidemiology [1, 22]. If the degree distribution follows Eq. (2) and \( \gamma \leq 3 \), then the second moment \( \langle k^2 \rangle \) diverges in the large-size limit. Thus, \( R_0 \) can diverge if \( \lambda \) is finite. Conversely, even if \( \lambda \) is considerably small, the infection can become widespread. While real social networks might not be strictly scale-free networks, typically, they have high \( \langle k^2 \rangle \).
In this study, to develop efficient herd immunity, we considered the case wherein only a fraction of individuals in a population with the highest connectivity ($k \geq k_{\text{max}}$) are immunized; this is because it is expected that targeting individuals that act as hubs effectively reduces ($k^2$). Though this case has been analyzed in previous works [21, 23], unlike those studies, herein, we quantify the effect of target immunization by using the type reproduction number. Furthermore, we also derive a new formula to calculate the immunization threshold.

To account for the effect of heterogeneity in the degree distribution of a population, it is appropriate to consider the density $\rho_k(t)$ of infected nodes within each degree class $k$. Based on the previously proposed SIS model [24, 27], the mean-field rate equation can be obtained as

$$\frac{d\rho_k(t)}{dt} = -\rho_k(t) + \lambda k[1 - \rho_k(t)]\Theta_k(t). \quad (4)$$

In this equation, the first term on the right-hand side represents recovery, wherein the average duration of infection is set to one, while the second term represents transmission, which is proportional to the combined product of infection rate ($\lambda$), density of susceptible nodes ($1 - \rho_k(t)$), number of neighboring vertices ($k$), and probability that any neighbor is infected ($\Theta_k(t)$). In particular, the probability $\Theta_k(t)$ is the average of the probabilities that a connection from a node with degree $k$ exists to an infected node with degree $k'$ over all degrees:

$$\Theta_k(t) = \frac{1}{\langle k \rangle} \sum_k k P(k') P_k(t), \quad (5)$$

where $P(k'|k)$ represents the conditional probability that a node of degree $k$ is connected to a node of degree $k'$. Assuming that there is no degree-degree correlation [13, 20], $\Theta_k(t)$ could be considered independent of $k$, and thus, can be given as

$$\Theta(t) = \frac{1}{\langle k \rangle} \sum_k k P(k) P_k(t). \quad (6)$$

This is because, here

$$P(k'|k) = k' P(k')/(k). \quad (7)$$

If the degree distribution has the maximum value $k_{\text{max}}$, then the next-generation matrix of eq. (4) is as follows:

$$A = \begin{pmatrix}
\lambda P(1|1) & \lambda P(2|1) & \cdots & \lambda P(k_{\text{max}}|1) \\
2\lambda P(1|2) & 2\lambda P(2|2) & \cdots & 2\lambda P(k_{\text{max}}|2) \\
\cdots & \cdots & \cdots & \cdots \\
k_{\text{max}} \lambda P(1|k_{\text{max}}) & k_{\text{max}} \lambda P(2|k_{\text{max}}) & \cdots & k_{\text{max}} \lambda P(k_{\text{max}}|k_{\text{max}})
\end{pmatrix}, \quad (8)$$

where $A_{ij}$ represents the rate of infection for nodes of degree $i$ due to spread of the infection from infectious nodes of degree $j$. The complete derivation of the matrix in Eq. (8) was performed using the method proposed by Diekmann et al. [4]; we decomposed the Jacobian of Eq. (4) into $T + \Sigma$, where $T_{ij} = i P(j|i)$ represents the transmission part, describing the production of new infections, and $\Sigma_{ij} = -\delta_{ij}$ is the transition part, describing changes in state, and computed $A = -T \Sigma^{-1}$.

If we target nodes with $k$ larger than $k_t$, the target matrix can be written as follows:

$$C = \begin{pmatrix}
0 & 0 & \cdots & 0 \\
\vdots & \vdots & \cdots & \vdots \\
0 & 0 & \cdots & 0 \\
k_t \lambda P(1|k_t) & k_t \lambda P(2|k_t) & \cdots & k_t \lambda P(k_{\text{max}}|k_t) \\
\vdots & \vdots & \cdots & \vdots \\
k_{\text{max}} \lambda P(1|k_{\text{max}}) & k_{\text{max}} \lambda P(2|k_{\text{max}}) & \cdots & k_{\text{max}} \lambda P(k_{\text{max}}|k_{\text{max}})
\end{pmatrix}. \quad (9)$$

Then, the type reproduction number $T_{\geq k_t}$ is determined using Eq. (10). In the absence of degree-degree correlation (i.e., Eq. (7)), by using Eq. (10), the type reproduction number can be obtained as follows:

$$T_{\geq k_t} = \frac{\lambda}{\langle k \rangle} \sum_{k=k_t}^{k_{\text{max}}} k^2 P(k) \frac{1}{1 - \lambda \sum_{k=1}^{k_{\text{max}}} k^2 P(k)}. \quad (10)$$
can survive even if all nodes of $k$ is obvious from Eq. (10) that can be calculated as.

The infection is targeted ($t$, it means the divergence of $P(k)$ of $k$ which coincides with the formula for the basic reproduction number $T_{r,1}$, (b) plot for required fraction of immunized nodes with degree $k \geq k_t$, and (c) plot of total amount of vaccine given by Eq. (14). Here, the degree distribution $P(k) \propto k^{-3}$ for $2 \leq k \leq 10^4$ and the infection rate is set to $\lambda = 0.22$ (such that $R_0 = 3$).

if the denominator is positive. If the denominator is negative, it means the divergence of $T_{r,k_t}$, i.e., the infection can survive even if all nodes of $k \geq k_t$ have immunity. It is obvious from Eq. (11) that $T_{r,k_t}$ increases monotonically with respect to $k_t$. Furthermore, if the entire population is targeted ($k_t=1$), the type reproduction number can be calculated as

$$T_{r,1} = \frac{\lambda}{k(t)} \sum_{k=1}^{k_{max}} k^2 P(k),$$

which coincides with the formula for the basic reproduction number $R_0$ given by Eq. (3). For a general case, it can be mathematically confirmed that $T_{r,k_t} > 1 \Leftrightarrow R_0 > 1$ and $T_{r,k_t} < 1 \Leftrightarrow R_0 < 1$.

We examine the characteristics of the type reproduction number $T_{r,k_t}$, using the example shown in Fig. 1, where the degree distribution $P(k) \propto k^{-3}$ for $k_{min} \leq k \leq k_{max}$ with $k_{min} = 2$ and $k_{max} = 10^4$. It should be noted that $k_{max}$ is an artificially introduced cutoff; however, a system with a finite size always has a similar cutoff. The value of $\lambda$ is set such that $R_0 = 3$; consequently, more than $1 - 1/R_0 = 2/3$ of the total population would have to be randomly immunized to prevent the spread of the infection. Fig. 1(a) shows the dependency of $T_{r,k_t}$ on $k_t$; in this case, because Eq. (10) is well-defined for $k_t \leq 29$, the infection cannot be eradicated by immunizing only nodes with degrees $k > 29$. Thus, this critical value is based on the maximum value $k_t$ and satisfies:

$$\frac{\lambda}{k(t)} \sum_{k=1}^{k_{min}-1} k^2 P(k) < 1.$$ (12)

Then, the required fraction of the targeted nodes $k \geq k_t$ that need to be immunized can be obtained as follows:

$$1 - \frac{1}{T_{r,k_t}} = \frac{R_0 - 1}{\lambda} \frac{\sum_{k=k_t}^{k_{max}} k^2 P(k)}{\sum_{k=1}^{k_{max}} k^2 P(k)};$$ (13)

and tends to a value of one when $k_t$ approaches the critical value of 29 as shown in Fig. 1(b). In particular, this figure can be used to obtain the required value of $k_t$ based on public health constraints. For example, if only 80% of the target population can be vaccinated, or the effective rate of vaccination is 80%, then, to eradicate the infection, $k_t \leq 7$ because $1 - T_{r,8} > 0.8$.

When all nodes with $k \geq k_t$ are immunized, the proportion of the population that receives immunity from the infection is $\sum_{k_t} P(k)$. Because the total amount of vaccine is $\sum_{k_t} P(k)$ multiplied by $1 - 1/T_{r,k_t}$, it is calculated as

$$g_c = (R_0 - 1) \frac{\langle k \rangle \sum_{k=k_t}^{k_{max}} P(k)}{\lambda} \frac{\sum_{k=1}^{k_{max}} k^2 P(k)}{\sum_{k=1}^{k_{max}} k^2 P(k)}.$$ (14)

It can be easily proved that $g_c$ is a decreasing function of $k_t$, regardless of the degree distribution $P(k)$ (see also Fig. 1(c)). Therefore, it was confirmed that the critical value of $k_t$ obtained via Eq. (12) or using its plot (such as in Fig. 1(b)) yields the optimal value for $k_t$.

In summary, we formulated an optimal immunization strategy, which is given by Eq. (12), based on the degree and using the type reproduction number. The same immunization strategy has already been studied by Pastor-Satorras and Vespignani [21, 22]. However, their reported formula for calculating the immunization threshold is different from the formula we obtained in this study, because they focused on the number of links that disappeared when the higher-degree nodes were removed, where the fraction of disappearing links is given as follows:

$$p = \frac{\sum_{k=k_t}^{k_{max}} k P(k)}{\sum_{k=1}^{k_{max}} k P(k)}. $$ (15)

Then, they gave the immunization threshold as follows:

$$\frac{\langle k^2 \rangle_{g_c}}{\langle k \rangle_{g_c}} = \frac{\sum_{k=1}^{k_{min}-1} k^2 P(k)}{\sum_{k=1}^{k_{min}-1} k P(k)} (1 - p) + p < \frac{1}{\lambda}. $$ (16)
where $\langle \cdot \rangle_k$ represents the average of residual degrees after the links disappears. In contrast, Eq. (12) can be rewritten as

$$\frac{\sum_{k=1}^{k_{\ast}-1} k^2 P(k)}{\sum_{k=1}^{k_{\ast}-1} k P(k)} (1 - p) < \frac{1}{\lambda}. \quad (17)$$

The reason for this discrepancy between the previous work and current study is that, in the former case, it was assumed that links between nodes with $k < k_{\ast}$ can also disappear with the probability given by Eq. (15); however, their assumption is not accurate because all links between nodes with $k \geq k_{\ast}$ must disappear too. Thus, the authors of this previous study underestimated the critical value of $k_{\ast}$. Accordingly, Eq. (12) provides a precise and simple formula to calculate the immunization threshold.

Furthermore, while we considered the SIS model in our study, it is easy to extend our result to susceptible-infected-recovered (SIR) models for infections as well. For the SIR model, the equation reported in Ref. [26] can be used instead of Eq. (5), i.e.,

$$\Theta_{k}(t) = \sum_{k'} k'^{-1} P(k') \rho_{k'}(t). \quad (18)$$

Consequently, Eq. (12) is replaced by

$$\frac{\lambda}{\langle k \rangle} \sum_{k=1}^{k_{\ast}-1} (k^2 - k) P(k) < 1. \quad (19)$$

In conclusion, we showed that the type reproduction number is a considerably useful metric to devise an optimal immunization strategy for a population. It should be noted that the main result of this study, i.e., Eq. (12), was obtained assuming no degree-degree correlation. However, if degree-degree correlation is considered, it is necessary to numerically calculate the type reproduction number using the two matrices given by Eqs. (8) and (9). Lastly, the proposed method to calculate immunization threshold could also be used for various other extended epidemic models, such as in [27].

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* morita.satoru@shizuoka.ac.jp

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