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Border Screening vs. Community Level Disease Control for Infectious Diseases: Timing and Effectiveness

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Abstract. There have been many studies of the border screening using a simple math model or a statistical analysis to investigate the ineffectiveness of border screening during 2003 and 2009 pandemics. However, the use of border screening is still a controversial issue. It is due to focusing only on the functionality of border screening without considering the timing to use. In this paper, we attempt to qualitatively answer whether the use of border screening is a desirable action during a disease pandemic. Thus, a novel mathematical model with a transition probability of status change during flight and border screening is developed. A condition to check a timing of the border screening is established in terms of a lower bound of the basic reproduction number. If the lower bound is greater than one, which indicates a pandemic, then the border screening may not be effective and the disease persists. In this case, a community level control strategy should be conducted.

INTRODUCTION

In border screening, there are two types such as entry and exit screenings. The entry screening is screening incoming people to a destination. The exit screening is outgoing people from a departure. During the H1N1 pandemic in 2009, most countries pursued entry screening, i.e. screening incoming passengers to their countries in order to prevent the spread of H1N1 by air travelers.

After the H1N1 pandemic, there have been discussions on the effectiveness of the border screening as the time of SARS in 2003. For instance, Cowling *et al.* [1] compared the delayed import time of the H1N1 virus between countries with and without entry screening measures, respectively, and concluded entry screening could delay the initial introduction of the H1N1 virus to a country via a statistical analysis. However, they pointed out the potential costs of using the screening measures and suggested the balance between the implementation costs and benefits of the entry screening. Wagner *et al.* [2] investigated a within-flight transmission of H1N1 and required quarantine of almost all economy class passengers if an infectious individual was identified in the plane, which is not realistic.

In this paper, we tackle the timing issue of the border screening via mathematical modeling. In our model, two significant features are considered, namely, a transition probability and border screening measures as model parameters. The transition probability is a probability of status change from being exposed to a disease to being infectious during flight. The border screening measures are represented as parameters for entry and exit screening. We construct a condition to check whether or not the border screening is indeed effective in terms of a basic reproduction number, and provide a community level control to eradicate the disease when the border screening is not effective.

MODEL and ASSUMPTIONS

In order to investigate the efficiency and need of an exit or entry border screening in the cities to prevent the spread of a disease through a global airline transportation network, we consider a *SEIHR compartment model*. In particular, the model divides the population in a city into several classes such as susceptible (S), exposed (E), asymptomatic (A), infectious infectious (I), handled (H), and recovered (R) classes, and describes the dynamics of the population moving

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between the compartments among cities. The handled (H) class means a way of isolation or treatment of infectious people at a city. To establish a model with exit and entry border screenings, we have the following assumptions:

A-1. The transition populations, i.e. inbound and outbound passengers to each compartment except H and a part of I classes describe the spatial movement of the population in a city.
A-2. The status of exposed people during their flight can be changed, i.e. an exposed individual at departure can become sick during his or her flight so he or she can be moved to I class in the destination city. The rest of class will not change its status during flight.
A-3. Infection during border screening is not considered.
A-4. Both of exit and entry border screenings can have a detection failure.
A-5. After recovering from the disease, such people are immuned from future infection.
A-6. There is a disease induced death as well as natural death, but the natural death rate may be negligible.

To formulate the model, the n number of cities is considered. The population in each city i is divided into compartments described as above with the numbers in each compartment denoted by $S_i(t)$, $E_i(t)$, $A_i(t)$, $I_i(t)$, $H_i(t)$ and $R_i(t)$, respectively for $i = 1, \cdots, n$. The total number of individuals in city i is $N_i(t) = S_i(t) + E_i(t) + A_i(t) + I_i(t) + H_i(t) + R_i(t)$. Note that $N_i(t)$ is not constant over time since the spatial movement of passengers in each city is considered.
Thus, for city i, we have

$$
\begin{aligned}
\frac{dS_i}{dt} &= L_i - \mu_i S_i - S_i\beta_i\left(\frac{A_i}{N_i} + \frac{I_i}{N_i}\right) + \sum_{j=1}^{n}(m_{ij}^S S_j - m_{ji}^S S_i) - S_i\sum_{j=1}^{n}\varepsilon_j\beta_j\left(m_{ij}^A\frac{A_j}{N_j} + \rho_i' m_{ij}^I \rho_j \frac{I_j}{N_j} + \rho_i' m_{ij}^E \eta_{ij}\frac{E_j}{N_j}\right)\\
\frac{dE_i}{dt} &= S_i\beta_i\left(\frac{A_i}{N_i} + \frac{I_i}{N_i}\right) - \alpha_i E_i - \alpha_i' E_i - \mu_i E_i + S_i\sum_{j=1}^{n}\varepsilon_j\beta_j\left(m_{ij}^A\frac{A_j}{N_j} + \rho_i' m_{ij}^I \rho_j \frac{I_j}{N_j} + \rho_i' m_{ij}^E \eta_{ij}\frac{E_j}{N_j}\right)\\
&\quad + \sum_{j=1}^{n}(m_{ij}^E(1-\eta_{ij})E_j - m_{ji}^E E_i)\\
\frac{dA_i}{dt} &= \alpha_i' E_i - \gamma_i A_i - \mu_i A_i + \sum_{j=1}^{n}(m_{ij}^A A_j - m_{ji}^A A_i)\\
\frac{dI_i}{dt} &= \alpha_i E_i - \gamma_i I_i - d_i I_i - \mu_i I_i - \sum_{j=1}^{n} m_{ji}^I I_i + \rho_i'\sum_{j=1}^{n}\left(m_{ij}^I \rho_j I_j + m_{ij}^E \eta_{ij} E_j\right)\\
\frac{dH_i}{dt} &= (1-\rho_i)\sum_{j=1}^{n} m_{ji}^I I_i + (1-\rho_i')\sum_{j=1}^{n}\left(m_{ij}^I \rho_j I_j + m_{ij}^E \eta_{ij} E_j\right) - \gamma_i H_i - \mu_i H_i - \delta d_i H_i\\
\frac{dR_i}{dt} &= \gamma_i A_i + \gamma_i I_i + \gamma_i H_i - \mu_i R_i + \sum_{j=1}^{n}(m_{ij}^R R_j - m_{ji}^R R_i),
\end{aligned}
\tag{1}
$$

where S_i, E_i, A_i, I_i, H_i and R_i are the susceptible, exposed, asymptomatic, symptomatic, handled and recovered population class, and

(i) L_i, is the incoming population rate, i.e. the average number of people entering airport i, μ_i is the natural death rate, and d_i is the disease induced mortality rates;
(ii) β_i is the contact rate of the infectious population;
(iii) ε_i is a positive constant indicating the strength of transmissibility or infectivity of infectious individuals;
(iv) $1/\alpha_i'$, $1/\alpha_i$ and $1/\gamma_i$ are the average incubation periods of the asymptomatic and symptomatic, infectious and transition periods, respectively;
(v) ρ_i and ρ_i' are the detection failure probabilities in the exit and entry screenings of airport i, and $\delta \in (0, 1)$;
(vi) η_{ij} is the probability of the exposed class E_j becoming infectious during their flight time T_{ij} by travelling from city j to i. In other words, it is a progression probability of the travelling exposed population of city j to become infectious during their flight.
(vii) Travelling rates m_{ij}^K of class K from city j to i are considered for $K = S$, E, A, I, and R. Note that $m_{ii}^K = 0$, i.e. no travel in its own city.

EFFECT of BORDER SCREENING

We would like observe how the border screening affects the basic reproduction number of the model in Equation 1. In order to do so, we linearize the model about the disease free equilibrium point (DFE) given by $E_i = A_i = I_i = 0$ for all i.

By linearizing Equation 1 with respect to only E_i, A_i, and I_i about the DEF with the variables in the order $E_1, \cdots, E_n, A_1, \cdots, A_n, I_1 \cdots, I_n$ the Jacobian matrix can be written as $F - V \in \mathbb{R}^{3n\times 3n}$ where F specifies new infections and V includes transfers in and out of the classes, and they are given by

$$F = \begin{bmatrix} F_{11} & \vdots & F_{12} & \vdots & F_{13} \\ .... & & .... & & .... \\ 0 & \vdots & 0 & \vdots & 0 \\ .... & & .... & & .... \\ 0 & \vdots & 0 & \vdots & 0 \end{bmatrix}, \quad V = \begin{bmatrix} V_{11} & \vdots & 0 & \vdots & 0 \\ .... & & .... & & .... \\ V_{21} & \vdots & V_{22} & \vdots & 0 \\ .... & & .... & & .... \\ V_{31} & \vdots & 0 & \vdots & V_{33} \end{bmatrix}, \tag{2}$$

where $0 \in \mathbb{R}^{n\times n}$ is a matrix whose entries are all zero, F_{11}, F_{12}, F_{13}, V_{11}, V_{21}, V_{22}, V_{31}, $V_{33} \in \mathbb{R}^{n\times n}$, and

$$F_{11} = \begin{bmatrix} 0 & \epsilon_2\beta_2\rho_1' m_{12}^E \eta_{12} & \cdots & \cdots & \cdots & \epsilon_n\beta_n\rho_1' m_{1n}^E \eta_{1n} \\ \epsilon_1\beta_1\rho_2' m_{21}^E \eta_{21} & 0 & \cdots & \cdots & \cdots & \epsilon_n\beta_n\rho_2' m_{2n}^E \eta_{2n} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \epsilon_1\beta_1\rho_n' m_{n1}^E \eta_{n1} & \cdots & \cdots & \cdots & \cdots & 0 \end{bmatrix}, \tag{3}$$

$$F_{12} = \begin{bmatrix} \beta_1 & \epsilon_2\beta_2 m_{12}^A & \cdots & \epsilon_n\beta_n m_{1n}^A \\ \epsilon_1\beta_1 m_{21}^A & \beta_2 & \cdots & \epsilon_n\beta_n m_{2n}^A \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \epsilon_1\beta_1 m_{n1}^A & \cdots & \cdots & \beta_n \end{bmatrix}, F_{13} = \begin{bmatrix} \beta_1 & \epsilon_2\beta_2\rho_1' m_{12}^I \rho_2 & \cdots & \epsilon_n\beta_n\rho_1' m_{1n}^I \rho_n \\ \epsilon_1\beta_1\rho_2' m_{21}^I \rho_1 & \beta_2 & \cdots & \epsilon_n\beta_n\rho_2' m_{1n}^I \rho_n \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \epsilon_1\beta_1\rho_n' m_{n1}^I \rho_1 & \cdots & \cdots & \beta_n \end{bmatrix}, \tag{4}$$

$$V_{11} = \begin{bmatrix} \alpha_1 + \alpha_1' + \mu_1 + \sum_{j=1}^n m_{j1}^E & -m_{12}^E(1-\eta_{12}) & \cdots & -m_{1n}^E(1-\eta_{1n}) \\ -m_{21}^E(1-\eta_{21}) & \alpha_2 + \alpha_2' + \mu_2 + \sum_{j=1}^n m_{j2}^E & \cdots & -m_{2n}^E(1-\eta_{2n}) \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ -m_{n1}^E(1-\eta_{n1}) & \cdots & \cdots & \alpha_n + \alpha_n' + \mu_n + \sum_{j=1}^n m_{jn}^E, \end{bmatrix}, V_{22} = \begin{bmatrix} \gamma_1 + \mu_1 + \sum_{j=1}^n m_{j1}^A & \cdots & -m_{1n}^A \\ -m_{21}^A & \cdots & -m_{2n}^A \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \\ -m_{n1}^A & \cdots & \gamma_n + \mu_n + \sum_{j=1}^n m_{jn}^A \end{bmatrix}, \tag{5}$$

$$V_{21} = diag\{-\alpha_1', \cdots, -\alpha_n'\}, \tag{6}$$

$$V_{31} = \begin{bmatrix} -\alpha_1 & -\rho_1' m_{12}^E \eta_{12} & \cdots & -\rho_1' m_{1n}^E \eta_{1n} \\ -\rho_2' m_{21}^E \eta_{21} & -\alpha_2 & \cdots & -\rho_2' m_{2n}^E \eta_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ -\rho_n' m_{n1}^E \eta_{n1} & \cdots & \cdots & -\alpha_n \end{bmatrix}, V_{33} = \begin{bmatrix} \gamma_1 + d_1 + \mu_1 + \sum_{j=1}^n m_{j1}^I & -\rho_1' m_{12}^I \rho_2 & \cdots & -\rho_1 m_{1n}^I \rho_n \\ -\rho_2' m_{21}^I \rho_1 & \gamma_2 + d_2 + \mu_2 + \sum_{j=1}^n m_{j2}^I & \cdots & -\rho_2' m_{2n}^I \rho_n \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ -\rho_n' m_{n1}^I \rho_1 & \cdots & \cdots & \gamma_n + d_n + \mu_n + \sum_{j=1}^n m_{jn}^I \end{bmatrix}. \quad (7)$$

Note that V_{11}, V_{22} and V_{33} are irreducible non-singular M-matrices with positive column sums. Thus have positive inverses. All eigenvalues of $F - V$ have negative real parts if and only if $\rho(FV^{-1}) < 1$, where ρ denotes the spectral radius and FV^{-1} is the next generation matrix [3, 4]. The product FV^{-1} is given by

$$FV^{-1} = \begin{bmatrix} F_{11} & \vdots & F_{12} & \vdots & F_{13} \\ .... & & .... & & .... \\ 0 & \vdots & 0 & \vdots & 0 \\ .... & & .... & & .... \\ 0 & \vdots & 0 & \vdots & 0 \end{bmatrix} \times \begin{bmatrix} V_{11}^{-1} & \vdots & 0 & \vdots & 0 \\ .... & & .... & & .... \\ X & \vdots & V_{22}^{-1} & \vdots & 0 \\ .... & & .... & & .... \\ Y & \vdots & 0 & \vdots & V_{33}^{-1} \end{bmatrix} = \begin{bmatrix} F_{11}V_{11}^{-1} + F_{12}X + F_{13}Y & \vdots & F_{12}V_{22}^{-1} & \vdots & F_{13}V_{33}^{-1} \\ .... & & .... & & .... \\ 0 & \vdots & 0 & \vdots & 0 \\ .... & & .... & & .... \\ 0 & \vdots & 0 & \vdots & 0 \end{bmatrix}, \quad (8)$$

where $X = V_{22}^{-1}(-V_{21})V_{11}^{-1}$ and $Y = V_{33}^{-1}(-V_{31})V_{11}^{-1}$. Thus, the basic reproduction number $\mathcal{R}_o$ is obtained as

$$\mathcal{R}_o = \rho(FV^{-1}) = \rho(F_{11}V_{11}^{-1} + F_{12}X + F_{13}Y). \quad (9)$$

If $\mathcal{R}_o < 1$, the DFE is locally asymptotically stable, and if $\mathcal{R}_o > 1$, the DFE is unstable. Then, there is a possibility of the existence of stable endemic equilibria.

Border Screening and Community Level Treatment

In the midst of epidemic, border screening itself may not be enough to stop the epidemic. Then, other control measure such as community level treatment might be used along with the border screening. Here, the community level treatment means any types of treating infectious people in each city so that the number of infectious people is reduced inside the city. We will establish conditions to check the effectiveness of the border screening and the quantity of community level treatment in each city in terms of the upper and lower bounds of $\mathcal{R}_o$.

Note that the fact that the basic reproduction number is greater than 1 for all t when border screening is not applied means that there is an outbreak, i.e. the disease free equilibrium point is not stable and hence the disease spreads over the whole network. So, when border screening is applied, the question is whether the border screening can reduce $\mathcal{R}_o$ below 1. We would like to investigate such an effect in terms of a lower bound of $\mathcal{R}_o$. Before we carry on the lower bound of $\mathcal{R}_o$ we need the following propositions:

Proposition 1 *For an M-matrix $A = [a_{ij}]_{n\times n}$,*

$$\det(A) \le a_{ii} \det(A[i']), \quad (10)$$

where $A[i']$ is the matrix A with row and column i deleted.

Proof It follows the Fischer's inequality and Theorem 2.5.4 in Horn and Johnson (1991) [5].

Proposition 2 *(Corollary 8.1.20 in Horn and Johnson (1985) [6])*
For $A = [a_{ij}]_{n\times n} \geq 0$, let $\tilde{A}$ be any principle submatrix of A. Then, $\rho(\tilde{A}) \leq \rho(A)$ and $\max_{i=1,\cdots,n} a_{ii} \leq \rho(A)$.

Recall $\mathcal{R}_o = \rho(FV^{-1})$ in Equation 9 and $V_{ii}^{-1} > 0$ for $i = 1, 2, 3$ since it is an irreducible and nonsingular with positive column sums. Let $S = [s_{ij}] = A + B + C$, where

$$A = [a_{ij}] = F_{11}V_{11}^{-1},\ B = [b_{ij}] = F_{12}V_{22}^{-1}(-V_{21})V_{11}^{-1}, \text{ and } C = [c_{ij}] = F_{13}V_{33}^{-1}(-V_{31})V_{11}^{-1}. \tag{11}$$

Then, $\mathcal{R}_o$ can be written as

$$\rho(FV^{-1}) \quad = \rho(F_{11}V_{11}^{-1} + F_{12}V_{22}^{-1}(-V_{21})V_{11}^{-1} + F_{13}V_{33}^{-1}(-V_{31})V_{11}^{-1}) = \rho(A + B + C) = \rho(S). \tag{12}$$

Since A, B, and $C \geq 0$, $FV^{-1} \geq 0$ and hence by Proposition 2,

$$\rho(FV^{-1}) \geq \max_{i=1,\cdots,n} s_{ii} = \max_{i=1,\cdots,n}\{a_{ii} + b_{ii} + c_{ii}\}. \tag{13}$$

If $a_{ii} + b_{ii} + c_{ii}$ is obtained, then we determine the lower bound for the basic reproduction number.

Proposition 3 *Let $\mathcal{R}_o^{lower}$ be*

$$\mathcal{R}_o^{lower} = \max_{i=1}^{n}\{\frac{\beta_i\alpha_i'}{(\gamma_i + \mu_i' + \sum_{j=1}^n m_{ji}^A)(\alpha_i + \alpha_i' + \mu_i + \sum_{j=1}^n m_{ji}^E)} + \frac{\beta_i\alpha_i}{(\gamma_i + \mu_i' + d_i + \sum_{j=1}^n m_{ji}^I)(\alpha_i + \alpha_i' + \mu_i + \sum_{j=1}^n m_{ji}^E)}\}. \tag{14}$$

Then,

$$\mathcal{R}_o^{lower} \leq \mathcal{R}_o \text{ for all } \rho_i, \text{ and } \rho_i',$$

for $i = 1, \cdots, N$.

Proof See the proof in [7].

Theorem 4 *If $\mathcal{R}_o^{lower} > 1$, then the basic reproduction number $\mathcal{R}_o$ in Equation 9 will not be reduced below 1 by any exit and entry screenings.*

Proof In fact, the lower bound $\mathcal{R}_o^{lower}$ of $\mathcal{R}_o$ from Proposition 3 is obtained at $\rho_i = \rho_i' = 0$ for all $i = 0, \cdots, n$. However, $\rho_i = \rho_i' = 0$ for all i means that the detection failure rates of the exit and entry screenings are zero, i.e. the exit and entry screenings can detect the infectious travellers close to 100%. If, even under this situation, $\mathcal{R}_o^{lower} > 1$, this implies $\mathcal{R}_o > 1$ and $\rho_i, \rho_i' > 0$, $i = 1, \cdots, n$. Thus, the border screenings are not effective. ∎

Remark Theorem 4 implies that in the middle of outbreak when $\mathcal{R}_o^{None} > 1$, the border screenings alone will not be able to reduce $\mathcal{R}_o$ below 1. This result suggests that another disease control measure other than border screening is needed such as community level treatment in order to directly decrease the number of the infectious in each city.

Hence, let the community level treatment rate be w_i for $i = 1, \cdots, n$. Then, we have some modifications in I and H classes such that

$$\frac{dI_i}{dt} = \alpha_i E_i - \gamma_i I_i - d_i I_i - \mu_i I_i - w_i I_i - \sum_{j=1}^n m_{ji}^I I_i + \rho_i' \sum_{j=1}^n \left(m_{ij}^I \rho_j I_j + m_{ij}^E \eta_{ij} E_j\right) \tag{15}$$

$$\frac{dH_i}{dt} = (1-\rho_i)\sum_{j=1}^n m_{ji}^I I_i + (1-\rho_i')\sum_{j=1}^n \left(m_{ij}^I \rho_j I_j + m_{ij}^E \eta_{ij} E_j\right) - \gamma_i H_i - \mu_i H_i - \delta d_i H_i + w_i I_i, \tag{16}$$

where $w_i \in [0,1]$ is a constant. Thus, V_{33} in Equation 7 can be written as

$$V_{33}^{Control} = \begin{bmatrix} \gamma_1 + d_1 + \mu_1 + w_1 + \sum_{j=1}^{n} m_{j1}^I & -\rho_1' m_{12}^I \rho_2 & \cdots & \cdots & -\rho_1 m_{1n}^I \rho_n \\ -\rho_2' m_{21}^I \rho_1 & \gamma_2 + d_2 + \mu_2 + w_2 + \sum_{j=1}^{n} m_{j2}^I & \cdots & \cdots & -\rho_2' m_{2n}^I \rho_n \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ -\rho_n' m_{n1}^I \rho_1 & \cdots & \cdots & \cdots & \gamma_n + d_n + \mu_n + w_n + \sum_{j=1}^{n} m_{jn}^I \end{bmatrix}. \tag{17}$$

Then, we obtain the controlled basic reproduction number $\mathcal{R}_o^{Control}$ as

$$\mathcal{R}_o^{Control} = \rho(F_{11}V_{11}^{-1} + F_{12}V_{22}^{-1}(-V_{21})V_{11}^{-1} + F_{13}(V_{33}^{Control})^{-1}(-V_{31})V_{11}^{-1}). \tag{18}$$

When $\mathcal{R}_o^{lower}$ in Proposition 3 is greater than 1, we try to reduce $\mathcal{R}_o^{Control}$ below 1 by controlling the community treatment rate w_i.

DISCUSSION

We have developed a mathematical model to investigate the effectiveness and timing of border screening in the time of an epidemic. Our model includes a transition probability of status change during flight and a border screening measure as model parameters. Such a modeling detail has provided more realistic and qualitative answer to the timing and effectiveness of the border screening via the checking condition in Proposition 3 and Theorem 4 in terms of a lower bound of the basic reproduction number. If the lower bound is greater than one, the disease will persist for all time even with any border screening. In other words, in the middle of an outbreak, a border screening will not be effective. Thus, community level treatment should be proceeded with a top priority. This result clearly shows that a community level disease control such as treatment of local infectious people is more important than border screening during a pandemic. Thus, during the SARS and H1N1 pandemics in 2003 and 2009, respectively, border screening was conducted at a wrong timing to prevent the spread of such viruses.

Our result has practical significance since the lower bound that we developed can be explicitly obtained with model parameters and is independent of border screening measures. Hence, the lower bound can enable one to check the effectiveness of border screening even before implementing it during an epidemic. For the future work, we would like to implement our result on global airline transportation networks and to establish feasible predictions to prevent the spread of a disease.

REFERENCES

[1] B. J. Cowling, L. L. Lau, P. Wu, H. W. Wong, V. J. Fang, S. Riely, and H. Nishiura, BMC Infectious Diseases **10** (2010).

[2] B. G. Wagner, B. J. Coburn, and S. Blower, BMC Med. **7** (2009).

[3] P. van den Driessche and J. Watmough, Math. Biosci. **180**, 221–236 (2002).

[4] J. Arino and P. van den Driessche, in *Lecture Notes in Control and Information Sciences*, Vol. 294, edited by L. Benvenuti, A. D. Santis, and L. Farina (Springer-Verlag, Berlin Heidelberg, 2003), pp. 818–820.

[5] R. A. Horn and C. R. Johnson, *Topics in matrix analysis* (Cambridge University Press, 1991).

[6] R. A. Horn and C. R. Johnson, *Matrix analysis* (Cambridge University Press, 1985).

[7] S. Kim, A. Tridane, and D. E. Chang, Mathematical Population Studies **23**, 123–146 (2016).