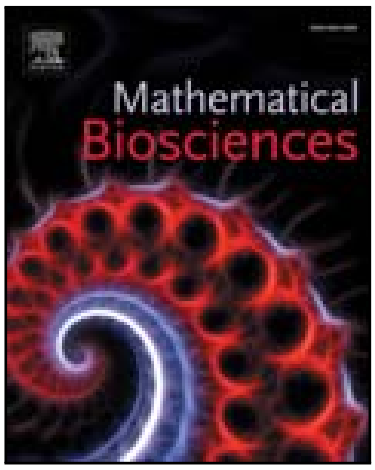

Final size of a multi-group SIR epidemic model: Irreducible and non-irreducible modes of transmission

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PII: S0025-5564(17)30347-4
DOI: 10.1016/j.mbs.2018.03.020
Reference: MBS 8053

To appear in: *Mathematical Biosciences*

Received date: 24 June 2017
Accepted date: 19 March 2018

Please cite this article as: Pierre Magal, Ousmane Seydi, Glenn Webb, Final size of a multi-group SIR epidemic model: Irreducible and non-irreducible modes of transmission, *Mathematical Biosciences* (2018), doi: 10.1016/j.mbs.2018.03.020

Final size of a multi-group SIR epidemic model: Irreducible and non-irreducible modes of transmission

March 23, 2018

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Abstract: A model of an epidemic outbreak incorporating multiple subgroups of susceptible and infected individuals is investigated. The asymptotic behavior of the model is analyzed and it is proved that the infected classes all converge to 0. A computational algorithm is developed for the cumulative final size of infected individuals over the course of the epidemic. The results are applied to the SARS epidemic in Singapore in 2003, where it is shown that the two-peak evolution of the infected population can be attributed to a two-group formulation of transmission.

Keywords: Epidemic models, final size, multi-group, irreducible and non-irreducible transmission.

1 Introduction

The evolution of an epidemic disease depends on many factors specific to the disease setting. One important factor is distinguishing the capacities of infected and susceptible subpopulations to transmit and acquire the disease. These capacities vary according to age, sex, genetic, behavioral, and many other properties of individuals. Inclusion of these factors in a mathematical model increases its utility for understanding the dynamics of the disease progression. A central issue is the prediction of the final size of the epidemic, that is, the number of susceptible individuals that ultimately acquire the disease.

The classical SIR model takes the following form (Ross [15], MacDonald [11], Anderson

and May [1]):

$$\begin{cases} \dfrac{dS(t)}{dt} = -\beta S(t)I(t) \\ \dfrac{dI(t)}{dt} = \beta S(t)I(t) - \eta I(t) \\ \dfrac{dR(t)}{dt} = \eta I(t) \end{cases} \tag{1.1}$$

with the initial distributions $S(0) = S_0 > 0, I(0) = I_0 > 0, R(0) = 0$.

At time t, $S(t)$ is the number of susceptible individuals (capable of acquiring the infection), $I(t)$ is the number of infectious individuals (capable of transmitting the disease), and $R(t)$ is the number of removed individuals (due to mortality, isolation, recovery with immunity, or other causes). The parameter $\beta > 0$ is called the infection rate and $\eta > 0$ is called the removal rate

The main tool in understanding the dynamical properties of (1.1) is the following conservation formula:

$$\frac{d}{dt}\left[S(t) + I(t) - \frac{\eta}{\beta}\ln(S(t))\right] = 0. \tag{1.2}$$

From this formula, Hethcote [9, 10] obtained a classical SIR model result. Define the basic reproduction number $R_0 = \beta S_0/\eta$, which is interpreted as the average number of infections transmitted by an infected individual through the course of the epidemic.

Theorem 1.1 *Let $(S(t), I(t))$ be a solution of (1.1). If $R_0 \leqslant 1$, then $I(t)$ decreases to zero as $t \to +\infty$. If $R_0 > 1$, then $I(t)$ first increases up to a maximum value $I_{max} = S_0 + I_0 - \frac{\eta}{\beta}\ln(S_0) - \frac{\eta}{\beta} + \frac{\eta}{\beta}\ln(\frac{\eta}{\beta})$ and then decreases to zero as $t \to +\infty$. $S(t)$ is decreasing and the limiting value $S(+\infty)$ is the unique root in $(0, \eta/\beta)$ of the equation*

$$S(+\infty) - \frac{\eta}{\beta}\ln(S(+\infty)) = S_0 + I_0 - \frac{\eta}{\beta}\ln(S_0)$$

or equivalently

$$\ln\left(\frac{S(+\infty)}{S_0}\right) = R_0\left(\frac{S(+\infty)}{S_0} - 1\right) - \frac{R_0}{S_0}I_0. \tag{1.3}$$

The final size of the epidemic, that is,, the number of susceptibles who ultimately become infected, is $S_0 + I_0 - S(+\infty)$. In [13], a method to compute the final size for a two group SIR epidemic model was developed, which for (1.1) has the following formulation: define

$$g(x) := S_0 \exp\left[\frac{\beta}{\eta}(x - S_0 - I_0)\right]. \tag{1.4}$$

$g(x)$ is positive, increasing, strictly convex, and $g(S_0) < S_0$. It follows that $S(+\infty)$ is the unique fixed point of g in $(0, S_0)$ and can be computed numerically as

$$S(+\infty) = \lim_{n\to+\infty} g^n(S_0), \tag{1.5}$$

where $g^n(x)$ is the mapping g composed n-times.

In this article we extend the ideas in [13] to develop an algorithm to compute the final size of a multi-group epidemic model. We are motivated by the limitation of Theorem 1.1 that requires $I(t)$ to have at most only one maximal value before decreasing to 0. Many epidemics show multiple peaks in the number of infected individuals as the epidemic evolves. Many reasons can explain such oscillations of $I(t)$, including multiple importation of infected individuals, changes in public health interventions (Sarakorn-Tang [16]), and consideration of geographical variations in the epidemic setting (Rass-Radcliffe [14], J. Arino, J.R. Davis, D. Hartley, *et al.* [3], G. Chowell, P. Diaz-Dueñas, J.C. Miller, *et al.* [7]). We show here that multi-group epidemic populations can also yield multiple peaks in $I(t)$.

2 The SARS epidemic in Singapore in 2003

We will illustrate our results with the (SARS) epidemic in Singapore in 2003. Between February 25 and April 30 of 2003, 201 probable cases were identified ([8]). Of these cases, 153 (76%) were infections that occurred in hospitals or health-care facilities ([8]). Five patients in these facilities infected 10 or more health-care workers, family members, social contacts, or visitors to the facilities where they were hospitalized. These five cases are viewed as super spreaders, in contrast to ordinary spreaders of the infection. More examples of the role of super spreaders in epidemics are given in Stein [17]. Figure 1 diagrams the transmission network for these five cases. These five super spreaders are responsible for most of the disease transmission in the epidemic, and 81% of probable cases had no transmission to other persons ([8]). Visually we see a cascade of transmission, starting with a single individual (patient 1), and spreading out through an oriented graph of transmission.

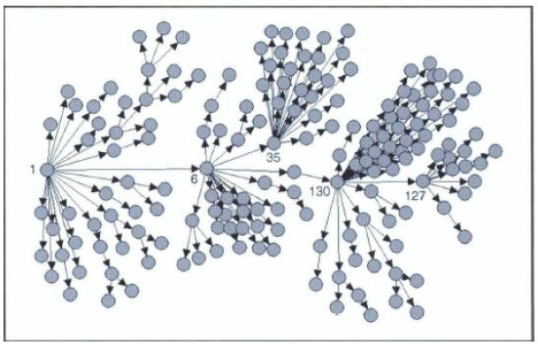

Figure 1: The contact network of the five super spreader cases in the SARS epidemic in Singapore in 2003 [8]. Patient 1, case 1; patient 6, case 2; patient 35, case 3; patient 130, case 4; and patient 127, case 5. Reference: Bogatti SP. Netdraw 1.0 Network Visualization Software. Harvard, Massachusetts: Analytic Technologies, 2002.

In Figure 2 the daily number of new infections in hospitals is represented by date of

fever onset and the reported source of infections. For the single group model (1.1), this data corresponds to newly infected individuals, namely to the mapping $t \mapsto \beta S(t)I(t)$.

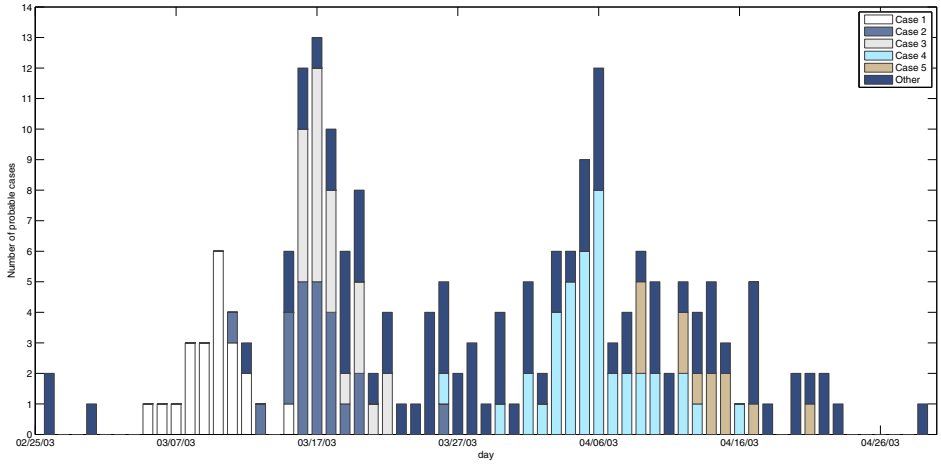

Figure 2: Case 1 generated 21 cases and 3 suspected cases, case 2 generated 23 cases and 5 suspected cases, case 3 generated 23 cases and 18 suspected cases, case 4 generated 40 cases and 22 suspected cases, case 5 generated 15 cases and 0 suspected cases [8].

We will focus here on the theoretical aspects of multi-group SIR models. We will apply our analysis to the 2003 SARS epidemic in Singapore to explain the role of super spreaders. Another goal of our investigation will be to explain the two peaks in the infected cases graph in Figure 2.

3 Formulation of a two-group SIR epidemic model

The system we consider is the following:

$$\begin{cases} \dfrac{dS(t)}{dt} = -\mathrm{diag}\,(S(t))\,B\,I(t) \\ \dfrac{dI(t)}{dt} = \mathrm{diag}\,(S(t))\,B\,I(t) - E\,I(t) \\ \dfrac{dR(t)}{dt} = E\,I(t) \end{cases} \tag{3.1}$$

with the initial distributions

$$S(0) = S_0 \in \mathbb{R}^2_+, I(0) = I_0 \in \mathbb{R}^2_+ \text{ and } R(0) = R_0 \in \mathbb{R}^2_+$$

where $S(t)$ are susceptible, $I(t)$ are infectious, and $R(t)$ are removed individuals, decomposed according to the populations 1 and 2:

$$S(t) = \begin{pmatrix} S_1(t) \\ S_2(t) \end{pmatrix}, \; I(t) = \begin{pmatrix} I_1(t) \\ I_2(t) \end{pmatrix}, \; R(t) = \begin{pmatrix} R_1(t) \\ R_2(t) \end{pmatrix} \geqslant 0.$$

The removal of individuals is described by the matrix

$$E = \begin{pmatrix} \eta_1 & 0 \\ 0 & \eta_2 \end{pmatrix},$$

while the transmission of pathogen is described by the matrix

$$B = \begin{pmatrix} \beta_{11} & \beta_{12} \\ \beta_{21} & \beta_{22} \end{pmatrix}.$$

The diagram flux of system (3.1) is described in Figure 3.

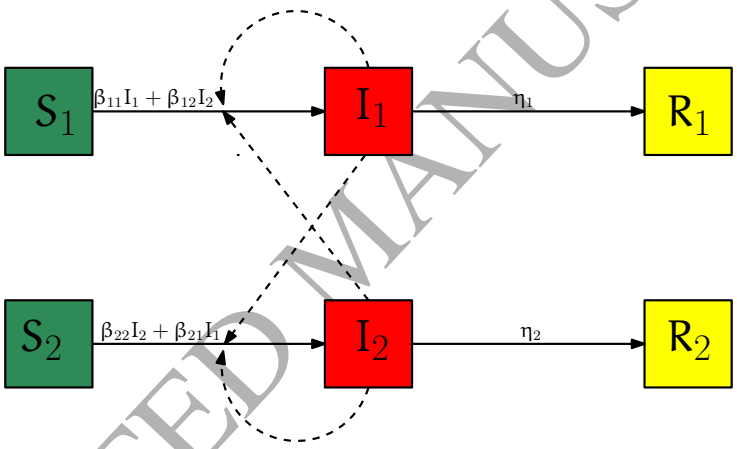

Figure 3: The figure represents a transfer diagram of the individual fluxes of system (3.1). In this diagram each solid arrow represents a flux of individuals, while the dashed arrows represent the influence of either infectious subpopulation 1 or infectious subpopulation 2.

System (3.1) can be rewritten as the following system:

$$\begin{cases} \dfrac{dS_1(t)}{dt} = -S_1(t)(\beta_{11}I_1(t) + \beta_{12}I_2(t)) \\ \dfrac{dS_2(t)}{dt} = -S_2(t)(\beta_{21}I_1(t) + \beta_{22}I_2(t)) \\ \dfrac{dI_1(t)}{dt} = S_1(t)(\beta_{11}I_1(t) + \beta_{12}I_2(t)) - \eta_1 I_1(t) \\ \dfrac{dI_2(t)}{dt} = S_2(t)(\beta_{21}I_1(t) + \beta_{22}I_2(t)) - \eta_2 I_2(t) \\ \dfrac{dR_1(t)}{dt} = \eta_1 I_1(t) \\ \dfrac{dR_2(t)}{dt} = \eta_2 I_2(t). \end{cases} \tag{3.2}$$

We make the following assumption on the parameters:

Assumption 3.1 B *is a nonnegative matrix and* $\eta_1 > 0$ *and* $\eta_2 > 0$.

Remark 3.2 *We observe that* B *irreducible is equivalent to assuming that*

$$\beta_{12} > 0 \text{ and } \beta_{21} > 0.$$

If we assume, in addition, that the transmission of pathogen occurs by criss-cross transmission only (that is,, $\beta_{11} = \beta_{22} = 0$*), it implies that* B *is invertible. The matrix* B *will be non-irreducible if and only if*

$$\beta_{12} = 0 \text{ or } \beta_{21} = 0.$$

By permuting the groups 1 *and* 2*, we can always assume that* $\beta_{12} = 0$ *and the matrix* B *becomes lower triangular.*

We observe that system (3.2) has an infinite number of equilibria. Namely, every triple of nonnegative vectors

$$\overline{S} \geqslant 0, \overline{I} = 0 \text{ and } \overline{R} \geqslant 0$$

is an equilibrium of the system. Moreover system (3.2) preserves the total number of individuals in each subpopulation. Namely, for each $t \geqslant 0$

$$S(t) + I(t) + R(t) = \begin{pmatrix} N_1 \\ N_2 \end{pmatrix} \tag{3.3}$$

where $N_1 > 0$ (respectively $N_2 > 0$) is the number of individuals in subpopulation 1 (subpopulation 2), respectively. Further, $S(t)$ and $R(t)$ are nondecreasing, and $\lim_{t\to\infty} S(t) = S^{+\infty}$ and $\lim_{t\to\infty} R(t) = R^{+\infty}$ exist, since the solutions are nonnegative.

Observe that

$$S_1(t) + S_2(t) + I_1(t) + I_2(t) + \eta_1 \int_0^\infty I_1(t)dt + \eta_2 \int_0^\infty I_2(t)dt = S_1(0) + S_2(0) + I_1(0) + I_2(0).$$

Therefore, $\lim_{t\to\infty} I(t) = I^{+\infty} = 0$, since $I(t)$ is nonnegative and the derivative of $I(t)$ is continuous and bounded. The final distribution of susceptible individuals $S^{+\infty}$ is the number of individuals who escape the epidemic. The final distribution of removed individuals $R^{+\infty}$ is the total number of individuals who have been infected during the epidemic.

The size of each group can be normalize to 1. Consider the matrix

$$D := \operatorname{diag} \begin{pmatrix} N_1 \\ N_2 \end{pmatrix}.$$

Then, the fractions of individuals in the epidemic populations are given by

$$s(t) := D^{-1}S(t), i(t) := D^{-1}I(t) \text{ and } r(t) := D^{-1}R(t)$$

and (3.1) can be rewritten as

$$\begin{cases} \dfrac{ds(t)}{dt} = -\mathrm{diag}\,(s(t))\,BD\,i(t) \\ \dfrac{di(t)}{dt} = \mathrm{diag}\,(s(t))\,BD\,i(t) - E\,i(t) \\ \dfrac{dr(t)}{dt} = E\,i(t), \end{cases} \tag{3.4}$$

where

$$BD = \begin{pmatrix} \beta_{11}N_1 & \beta_{12}N_2 \\ \beta_{21}N_1 & \beta_{22}N_2 \end{pmatrix}.$$

The existence of solutions to (3.4) is guaranteed by classical methods.

Our goal is to extend Theorem 1.1 to a n-group epidemic model. As we will see in Section 4 it is possible to extend the first part of Theorem 1.1, concerning the final size of the epidemic. But we will not be able to describe the qualitative behavior of the infected classes in the n-group case. We mention the articles of Andreasen [2], Arino *et al.* [4, 5], Ma and Earn [12], and Brauer [6] for some results in this direction. In Section 5 we will apply the two-group model to the example of SARS in Singapore 2003. This example illustrates that multi-group epidemic models reveal complexity not found in single group epidemic models.

4 The final size for a n–group SIR model

Let us consider a multi-group epidemic model with a mass action law incidence function. More precisely we consider the following system

$$\begin{cases} \dfrac{dS(t)}{dt} = -\mathrm{diag}(S(t))BI(t),\ t > 0 \\ \dfrac{dI(t)}{dt} = \mathrm{diag}(S(t))BI(t) - EI(t),\ t > 0 \\ \dfrac{dR(t)}{dt} = EI(t),\ t > 0 \end{cases} \tag{4.1}$$

Subjected to the following initial conditions

$$S(0) = S_0 \in \mathbb{R}^n_+,\ I(0) = I_0 \in \mathbb{R}^n_+ \text{ and } R(0) = R_0 \in \mathbb{R}^n_+$$

where $n \geqslant 2$ is a positive integer. Here $S(t)$ denotes the susceptible individuals, $I(t)$ the infectious individuals, and $R(t)$ the removed individuals at time t. Each state $S(t)$, $I(t)$ and $R(t)$ consists of a vector

$$S(t) = (S_1(t), \ldots, S_n(t))^T,\ I(t) = (I_1(t), \ldots, I_n(t))^T,\ R(t) = (R_1(t), \ldots, R_n(t))^T.$$

The removal rates are given by the matrix

$$E = \mathrm{diag}\,(\eta_1, \ldots, \eta_n)$$

and the transmission of pathogens is described by the nonnegative matrix

$$B = (\beta_{ij})_{1\leqslant i,j\leqslant n}\,.$$

We make the following assumption.

Assumption 4.1 $\eta_i > 0$ *for each* $i = 1,\dots,n$.

Therefore the explicit form of our system is given for $i = 1,\dots,n$ by

$$\begin{cases} \dfrac{dS_i(t)}{dt} = -S_i(t)\displaystyle\sum_{j=1}^{n}\beta_{ij}I_j(t),\ t>0 \\ \dfrac{dI_i(t)}{dt} = S_i(t)\displaystyle\sum_{j=1}^{n}\beta_{ij}I_j(t) - \eta_i I_i(t),\ t>0 \\ \dfrac{dR_i(t)}{dt} = \eta_i I_i(t),\ t>0 \end{cases} \tag{4.2}$$

with initial conditions

$$S_i(0) = S_{i0} \in \mathbb{R}_+,\ I_i(0) = I_{i0} \in \mathbb{R}_+ \text{ and } R_i(0) = R_{i0} \in \mathbb{R}_+.$$

4.1 Derivation of the final size equations

In this section we will derive the final size relation for system (4.2). By using the S_i-equations of (4.2) we obtain for each $t \geqslant 0$ and $i = 1,\dots,n$,

$$\frac{d\ln(S_i(t))}{dt} = -\sum_{j=1}^{n}\beta_{ij}I_j(t)$$

so that

$$\ln(S_i(t)) - \ln(S_i(0)) = -\sum_{j=1}^{n}\beta_{ij}\int_0^t I_j(s)ds. \tag{4.3}$$

The sum of the S-equation and the I-equation of system (4.1) yields

$$\frac{d(S_i+I_i)(t)}{dt} = -\eta_i I_i(t),\ t>0$$

and we deduce that

$$(S_i+I_i)(t) - (S_i+I_i)(0) = -\eta_i\int_0^t I_i(s)ds,\ t>0. \tag{4.4}$$

Hence by combining (4.3) and (4.4) we obtain

$$\ln(S_i(t)) - \ln(S_i(0)) = \sum_{j=1}^{n}\frac{\beta_{ij}}{\eta_j}(S_j(t)+I_j(t)-S_j(0)+I_j(0)),\ t>0$$

or equivalently

$$\sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j}(S_j(t) + I_j(t)) - \ln(S_i(t)) = \sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j}(S_j(0) + I_j(0)) - \ln(S_i(0)),\ t > 0.$$

Therefore we obtain the following conservation law for each subgroup $i = 1, \dots, n$

$$\frac{d}{dt}\left[\sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j}(S_j(t) + I_j(t)) - \ln(S_i(t))\right] = 0,\ \forall t > 0. \tag{4.5}$$

Next, integrating (4.5) between 0 and $+\infty$ yields for $i = 1, \dots, n$,

$$\ln(S_i(\infty)) = \sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j} S_j(\infty) - \sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j}(S_j(0) + I_j(0)) + \ln(S_i(0))$$

and we derive the following system that will be referred as the final size relation:

$$\begin{cases} S_1(\infty) = S_1(0) \exp\left(\displaystyle\sum_{j=1}^{n} \frac{\beta_{1j}}{\eta_j}(S_j(\infty) - S_j(0)) - \sum_{j=1}^{n} \frac{\beta_{1j}}{\eta_j} I_j(0)\right) \\ \vdots \\ S_n(\infty) = S_n(0) \exp\left(\displaystyle\sum_{j=1}^{n} \frac{\beta_{nj}}{\eta_j}(S_j(\infty) - S_j(0)) - \sum_{j=1}^{n} \frac{\beta_{nj}}{\eta_j} I_j(0)\right) \end{cases} \tag{4.6}$$

Note that system (4.6) can be rewritten in the following more compact form

$$S(\infty) = \exp\left(\mathrm{diag}[BE^{-1}(S(\infty) - S(0) - I(0))]\right) S(0). \tag{4.7}$$

Motivated by system (4.6) we consider the map $F : \mathbb{R}^n \to \mathbb{R}^n$ defined by

$$F(X) = \exp\left(\mathrm{diag}[BE^{-1}(X - S(0) - I(0))]\right) S(0).$$

More precisely F is given by

$$F(X) = (F_1(X), \dots, F_n(X))^T,\ X \in \mathbb{R}^n$$

with

$$F_i(X) = S_i(0) \exp\left(\sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j}(X_j - S_j(0)) - \sum_{j=1}^{n} \frac{\beta_{ij}}{\eta_j} I_j(0)\right),\ i = 1, \dots, n. \tag{4.8}$$

In what follows we will use the following notations. For $X, Y \in \mathbb{R}^n$ we define

$$\begin{array}{lcll} X \leqslant Y & \iff & X_i \leqslant Y_i & \text{for} \quad i = 1, \dots, n \\ X < Y & \iff & X \leqslant Y \text{ and } X_i < Y_i & \text{for some} \quad i = 1, \dots, n \\ X \ll Y & \iff & X_i < Y_i & \text{for} \quad i = 1, \dots, n. \end{array}$$

It is clear from (4.8) that F is monotone increasing. This means that

$$X \leqslant Y \Longrightarrow F(X) \leqslant F(Y). \tag{4.9}$$

Hence if $0 \ll S_0$ and $0 \leqslant I_0$ then

$$0 \ll F(0) \leqslant F(S_0) \leqslant S_0.$$

Therefore by using induction arguments we obtain for each $k \geqslant 1$

$$0 \ll F(0) \leqslant \cdots \leqslant F^k(0) \leqslant F^{k+1}(0) \leqslant F^{k+1}(S_0) \leqslant \cdots \leqslant F(S_0) \leqslant S_0$$

so that by taking the limit when k goes to $+\infty$ we obtain

$$0 \ll \lim_{k\to+\infty} F^k(0) =: S^- \leqslant S^+ := \lim_{k\to+\infty} F^k(S_0) \leqslant S_0.$$

Then by the continuity of F we have

$$0 \ll F(S^-) = S^- \quad \text{and} \quad F(S^+) = S^+.$$

The following lemma holds:

Lemma 4.2 *Let Assumption 4.1 be satisfied. Assume in addition that* $0 \ll S_0$ *and* $0 \leqslant I_0$. *Then, all the fixed points of* F *in* $[0, S_0]$ *lie in the interval* $[S^-, S^+]$.

Let us note that F is continuously differentiable and by using (4.8) we obtain

$$\frac{\partial F_i(X)}{\partial X_j} = \frac{\beta_{ij}}{\eta_j} F_i(X), \ \forall X \in \mathbb{R}^n, \ i, j = 1, \ldots, n$$

so that

$$DF(X) = \operatorname{diag}(F(X))BE^{-1}, \ X \in \mathbb{R}^n. \tag{4.10}$$

Therefore the monotony of DF follows from the monotony of F. More precisely, for each $0 \leqslant X \leqslant Y \leqslant S_0$ and $H \geqslant 0$

$$DF(X)H \leqslant DF(Y)H.$$

Furthermore, recalling that

$$F(S^+) = S^+ \quad \text{and } F(S^-) = S^-$$

we obtain

$$DF(S^+) = \operatorname{diag}(S^+)BE^{-1} \quad \text{and } DF(S^-) = \operatorname{diag}(S^-)BE^{-1}.$$

4.2 Irreducible modes of transmission

In this section we will prove that if B is a nonnegative nonzero irreducible matrix, then (4.7) has a unique solution in $[0, S_0]$.

Definition 4.3 *The matrix B is irreducible if and only if one of the following equivalent conditions is satisfied*

i) The matrix $\varepsilon I + B$ (for $\varepsilon > 0$) is primitive. that is, to say, that there exists an integer $n \geqslant 1$ such that $(\varepsilon I + B)^n \gg 0$ (that is, all the components of $(\varepsilon I + B)^n$ are strictly positive).

ii) For each $i, j \in \{1, \dots, n\}$, there exists an integer $m := m(i, j) > 0$ such that

$$\langle e_j, B^m e_i \rangle > 0$$

where $\{e_1, \dots, e_n\}$ is the canonical basis of $\mathbb{R}^n$.

Theorem 4.4 *Let Assumption 4.1 be satisfied. Assume in addition B is a nonnegative irreducible matrix. Assume in addition that $0 \ll S_0$ and $0 \leqslant I_0$. Then we have the following properties*

i) $F(S_0) = S_0 \Longleftrightarrow I_0 = 0$;

ii) If $0 < I_0$ then F has a unique fixed point $S(\infty)$ satisfying $0 \ll S(\infty) < S_0$.

Remark 4.5 *From the above theorem we deduce that the final size of the epidemic can be computed numerically as follows:*

$$R(\infty) = N - S(\infty)$$

and

$$N = S_0 + I_0 + R_0.$$

The final size of the susceptible population is given by

$$S(\infty) = \lim_{k \to +\infty} F^k(S_0)$$

for any given initial distribution of the infectious population I_0. Furthermore, when $0 < I_0$, the formula

$$S(\infty) = \lim_{k \to +\infty} F^k(0)$$

may also be used to compute the final distribution of the susceptible population.

Proof. Before proceeding to the proof note that since B is a nonnegative irreducible matrix, $0 \ll S^+$ and

$$E^{-1} = \operatorname{diag}\left(\frac{1}{\eta_1}, \dots, \frac{1}{\eta_n}\right),$$

it follows that $DT(S^+) = \operatorname{diag}(S^+)BE^{-1}$ is a nonnegative irreducible matrix.
Proof of i) : Next we prove that $S_0 \gg 0$ is a fixed point of F if and only if $I_0 = 0$. In fact $F(S_0) = S_0$ is explicitly given by

$$\begin{cases} S_1(0) = S_1(0) \exp\left(-\sum_{j=1}^{n} \frac{\beta_{1j}}{\eta_j} I_j(0)\right) \\ \vdots \\ S_n(0) = S_n(0) \exp\left(-\sum_{j=1}^{n} \frac{\beta_{nj}}{\eta_j} I_j(0)\right) \end{cases}$$

which holds if and only if

$$\sum_{j=1}^{n} \frac{\beta_{1j}}{\eta_j} I_j(0) = 0, \ i = 1, \dots, n \Longleftrightarrow BE^{-1} I_0 = 0,$$

and by using the fact that BE^{-1} is an irreducible matrix and $0 \leqslant I_0$, we obtain

$$BE^{-1} I_0 \Longleftrightarrow I_0 = 0.$$

Proof of ii) : Assume that $0 < I_0$. Therefore we have

$$0 \ll F(S_0) < S_0 \ \text{ and } S^+ < S_0, \tag{4.11}$$

and by the monotony of F we also have

$$F(S^+) = S^+ \leqslant F(S_0).$$

To prove that F has a unique fixed point whenever $0 < I_0$ it is sufficient to show that $S^- = S^+$. In what follows we will argue by contradiction, that is, we assume that $S^- < S^+$. Then we have

$$S^+ - S^- = F(S^+) - F(S^-) = \int_0^1 DF(S^- + l(S^+ - S^-))(S^+ - S^-) dl$$

and since for all $l \in [0, 1]$

$$DF(S^- + l(S^+ - S^-))(S^+ - S^-) \leqslant DF(S^+)(S^+ - S^-)$$

we obtain

$$S^+ - S^- \leqslant DF(S^+)(S^+ - S^-). \tag{4.12}$$

By the Perron-Frobenius theorem there exists a left eigenvector $W \gg 0$ of $DT(S^+)$ associated to the spectral radius $r(DT(S^+))$, and

$$W^T(S^+ - S^-) \leqslant W^T DF(S^+)(S^+ - S^-) = r(DT(S^+))W^T(S^+ - S^-),$$

and since by assumption $S^+ > S^-$, it follows that

$$r(DF(S^+)) \geqslant 1.$$

Next note that

$$\begin{aligned} F(S_0) - S^+ &= F(S_0) - F(S^+) \\ &= \int_0^1 DF(S^+ + l(S_0 - S^+))(S_0 - S^+)dl \\ &\geqslant DF(S^+)(S_0 - S^+). \end{aligned}$$

Thus, we obtain

$$W^T(F(S_0) - S^+) \geqslant r(DF(S^+))W^T(S_0 - S^+),$$

which means

$$W^T(F(S_0) - S^+) \geqslant W^T(S_0 - S^+) \Longrightarrow W^T F(S_0) \geqslant W^T S_0,$$

which contradicts (4.11). ∎

4.3 An algorithm to compute the final size of a multi-group epidemic for non-irreducible modes of transmission

We provide an algorithm for computation of the final size of the epidemic whenever the pathogen transmission matrix B is non-irreducible and nonnegative. A case with cascade contamination in three groups is illustrated in the following diagram:

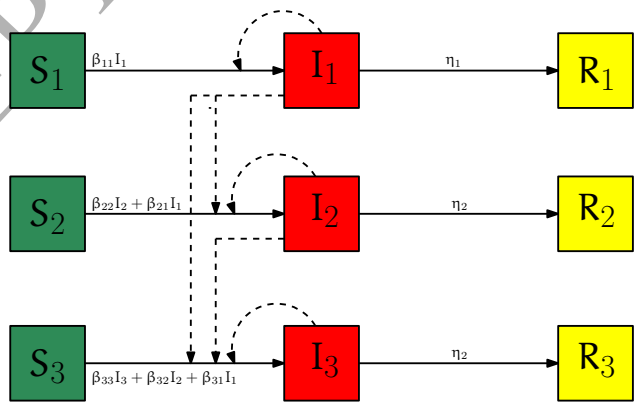

Figure 4: The figure represents a transfer diagram of the individual fluxes with a cascade transmission into three groups. Each solid arrow represents a flux of individuals, while the dashed arrows represent the influence of infectious of subpopulation 1, infectious of subpopulation 2 or infectious of subpopulation 3.

More generally we assume we have l subgroups and that B has the following form

$$B = \begin{pmatrix} B_{11} & 0 & \cdots & 0 \\ B_{21} & B_{22} & \ddots & 0 \\ \vdots & & \ddots & 0 \\ B_{l1} & \cdots & \cdots & B_{ll} \end{pmatrix}$$

where each B_{ii}, $1 \leqslant i \leqslant l$ is an irreducible nonnegative nonzero square matrix of dimension n_i with $n_1 + n_2 + \cdots + n_l = n$. Moreover each bloc matrix B_{ij}, $1 \leqslant i, j \leqslant l$ is a $n_i \times n_j$ nonnegative matrix. Let the removal matrix E be given by

$$E = \mathrm{diag}(E_1, \ldots, E_l)$$

where each E_j is a n_j square diagonal matrix with strictly positive diagonal entries. Therefore, the susceptible, infectious and removed individuals are divided into l subgroups and the n dimensional SIR epidemic model takes the following form for each subgroup $i \in \{1, \ldots, l\}$

$$\begin{cases} S_i'(t) = -\mathrm{diag}(S_i(t)) \displaystyle\sum_{j=1}^{i} B_{ij} I_j(t) \\ I_i'(t) = \mathrm{diag}(S_i(t)) \displaystyle\sum_{j=1}^{i} B_{ij} I_j(t) - E_i I_i \\ R_i'(t) = E_i I_i \end{cases} \tag{4.13}$$

where $S_i(t) =$

$(S_{i1}(t), \ldots, S_{in_i}(t))^T$, $I_i(t) = (I_{i1}(t), \ldots, I_{in_i}(t))^T$ and $R_i(t) = (R_{i1}(t), \ldots, R_{in_i}(t))^T$.

By proceeding as in Section 4.1 we obtain the following system of final size relations for the subgroups

$$\begin{cases} S_1(\infty) = \\ \exp\left(\mathrm{diag}\left[B_{11}E_1^{-1}(S_1(\infty) - S_1(0)) - B_{11}E_1^{-1}I_1(0)\right]\right) S_1(0) \\ \\ S_2(\infty) = \\ \exp\left(\mathrm{diag}\left[B_{22}E_2^{-1}(S_2(\infty) - S_2(0)) - B_{21}E_2^{-1}(S_1(0) - S_1(\infty)) - B_{22}E_2^{-1}I_1(0)\right]\right) S_2(0) \\ \\ \vdots \\ S_l(\infty) = \\ \exp\left(\mathrm{diag}\left[B_{ll}E_l^{-1}(S_l(\infty) - S_l(0)) - \displaystyle\sum_{i=1}^{l-1} B_{li}E_i^{-1}(S_i(0) - S_i(\infty)) - B_{ll}E_l^{-1}I_l(0)\right]\right) S_l(0) \end{cases}$$

that is for each $i = 1, \ldots, l$, $S_i(\infty) =$

$$\exp\left(\mathrm{diag}\left[B_{ii}E_i^{-1}(S_i(\infty) - S_i(0)) - \sum_{j=1}^{i-1} B_{ij}E_j^{-1}(S_j(0) - S_j(\infty)) - B_{ii}E_j^{-1}I_j(0)\right]\right) S_i(0).$$

Observe that we have

$$\sum_{j=1}^{i-1} B_{ij}E_j^{-1}(S_j(0)-S_j(\infty)) + B_{ii}E_j^{-1}I_j(0) \geqslant 0,\ \forall i = 2,\dots,l.$$

Then by using the same arguments in the proof of Theorem 4.4, one obtains the following algorithm to compute the final size of the susceptible populations for the subgroups $i \geqslant 1$:
Step 1: If $i = 1$ then define $F_1 : \mathbb{R}^{n_1} \to \mathbb{R}^{n_1}$ by

$$F_1(X_1) = \exp\left(\operatorname{diag}\left[B_{11}E_1^{-1}(X_1 - S_1(0)) - B_{11}E_1^{-1}I_1(0)\right]\right) S_1(0)$$

so that the final size of susceptibles for subgroup 1 is given by

$$S_1(\infty) = \lim_{k\to+\infty} F_1^k(S_1(0)).$$

Step 2: If $i = 2$ then define the map $F_2 : \mathbb{R}^{n_2} \to \mathbb{R}^{n_2}$ by

$$F_2(X_2) = \exp\left(\operatorname{diag}\left[B_{22}E_2^{-1}(X_2 - S_2(0)) - B_{21}E_2^{-1}(S_1(0) - S_1(\infty)) - B_{22}E_2^{-1}I_1(0)\right]\right) S_2(0)$$

and we obtain the final size of susceptibles for subgroup 2 by

$$S_2(\infty) = \lim_{k\to+\infty} F_2^k(S_2(0)).$$

Induction: If $i > 2$ then by induction we obtain the final size of susceptible poppulations $S_1(\infty),\dots,S_{i-1}(\infty)$. The final size for susceptibles for subgroup i is then obtained by defining the map $F_i : \mathbb{R}^{n_i} \to \mathbb{R}^{n_i}$ by

$$F_i(X_i) = \exp\left(\operatorname{diag}\left[B_{ii}E_i^{-1}(X_i - S_i(0)) - \sum_{j=1}^{i-1} B_{ij}E_j^{-1}(S_j(0)-S_j(\infty)) - B_{ii}E_i^{-1}I_i(0)\right]\right) S_i(0)$$

and

$$S_i(\infty) = \lim_{k\to+\infty} F_i^k(S_i(0)).$$

5 Application to the SARS Singapore outbreak in 2003

In an earlier work [13] we showed that a two-group model can be used to distinguish the role of super spreaders and ordinary spreaders in the 2003 SARS epidemic in Singapore. Here we will use the two-group analysis above to again connect super spreaders to this epidemic, and also to connect their role to the two peaks occurring in the graph in Figure 2.

Consider the system (3.1) with group 1 transmissions preceding and initiating group 2 transmissions:

$$\begin{cases} \dfrac{dS_1(t)}{dt} = -\beta_{11} S_1(t) I_1(t) \\ \dfrac{dS_2(t)}{dt} = -S_2(t)(\beta_{21} I_1(t) + \beta_{22} I_2(t)) \\ \dfrac{dI_1(t)}{dt} = \beta_{11} S_1(t) I_1(t) - \eta_1 I_1(t) \\ \dfrac{dI_2(t)}{dt} = S_2(t)(\beta_{21} I_1(t) + \beta_{22} I_2(t)) - \eta_2 I_2(t) \\ \dfrac{dR_1(t)}{dt} = \eta_1 I_1(t) \\ \dfrac{dR_2(t)}{dt} = \eta_2 I_2(t). \end{cases} \tag{5.1}$$

Then by using the same arguments as in section 2.3, the final size relation is given by the following system

$$\begin{aligned} S_1(\infty) &= S_1(0) \exp\left(\frac{\beta_{11}}{\eta_1}(S_1(\infty) - S_1(0)) - \frac{\beta_{11}}{\eta_1} I_1(0) \right) \\ S_2(\infty) &= S_2(0) \exp\left(\frac{\beta_{21}}{\eta_1}(S_1(\infty) - S_1(0)) + \frac{\beta_{22}}{\eta_2}(S_2(\infty) - S_2(0)) - \sum_{j=1}^{2} \frac{\beta_{2j}}{\eta_j} I_j(0) \right) \end{aligned} \tag{5.2}$$

Then by using the same argument as before in (1.5) we have

$$S_1(\infty) = \lim_{n \to +\infty} g_1^n(S_1(0)), \tag{5.3}$$

where g_1 is the map defined by

$$g_1(x) := S_1(0) \exp\left(\frac{\beta_{11}}{\eta_1}(x - S_1(0)) - \frac{\beta_{11}}{\eta_1} I_1(0) \right).$$

Once the final size in the first group has been computed by using the iteration procedure (5.3), the final size for the second group can be computed by using the following iteration procedure:

$$S_2(\infty) = \lim_{n \to +\infty} g_2^n(S_2(0)), \tag{5.4}$$

where g_2 is the map defined by

$$g_2(x) := S_2(0) \exp\left(\frac{\beta_{22}}{\eta_2}(x - S_2(0)) - V(S_1(\infty)) \right).$$

with

$$V(S_1(\infty)) := \frac{\beta_{21}}{\eta_1} \left[(S_1(0) - S_1(\infty)) + I_1(0) \right] + \frac{\beta_{22}}{\eta_2} I_2(0) \geqslant 0.$$

We set group 1 to be infected individuals with average lower infection rates and shorter periods of infectiousness. Super spreader cases 1,2, and 3 belong to group 1, as well as cases

that generated no secondary cases and the few cases that generated a very small number of secondary cases (see Figure 2). We set group 2 to be the cases resulting from infected individuals with average higher infection rates and longer periods of infectiousness. Super spreader cases 4 and 5 belong to group 2 (see Figure 2). We merge case 4 and case 5 and their secondary cases in the group 2. The epidemic began with 3 non-super spreader group 1 cases, which generated the first super spreader case in the hospital (patient 1). The first group 2 case (patient 4) appeared approximately 4 weeks later. The parameter values for group 1 and group 2 are given in Table 1.

Symbol	Description	Value	Units
$S_1(0)$	Number of Susceptible individuals in group 1	350	individuals
$S_2(0)$	Number of Susceptible individuals in group 2	90	individuals
$I_1(0)$	Number of Infectious individuals in group 1	1	individuals
$I_2(0)$	Number of Infectious individuals in group 2	0	individuals
$R_1(0)$	Number of Removed individuals in group 1	0	individuals
$R_2(0)$	Number of Removed individuals in group 2	0	individuals
N_1	Total number of individuals in group 1	351	individuals
N_2	Total number of individuals in group 2	90	individuals
β_{11}	Infection rate	0.002	dimensionless
β_{21}	Infection rate	$6.3\ 10^{-7}$	dimensionless
β_{22}	Infection rate	0.0042	dimensionless
η_1	Removal rate	0.475	day^{-1}
η_2	Removal rate	0.091	day^{-1}

Table 1: List of the model parameters used for simulations

By using the algorithm (5.3)-(5.4), with the parameter values in Table 1, we compute $S_1(\infty) = 150.4013$ and $S_2(\infty) = 1.5153$. Therefore, the total number of infected individuals in each group is $R_1(\infty) = N_1 - 150.4013 = 200.5987$ and $R_2(\infty) = N_2 - 1.5153 = 88.4847$. In Figure 5 we graph the model simulation of the flux of new cases over the course of the epidemic and compare to data from [8]. The two peaks in the graph and in the data coincide. In Figure 6 we graph the total number of cases, each week and the cumulative number of cases over the course of the epidemic. In Figure 7 we plot these graphs separately for groups 1 and 2. We conclude that an explanation of the bi-modality of peaks in the flux of infected cases is due to the distinctions of infectiousness in the parameters of groups 1 and 2.

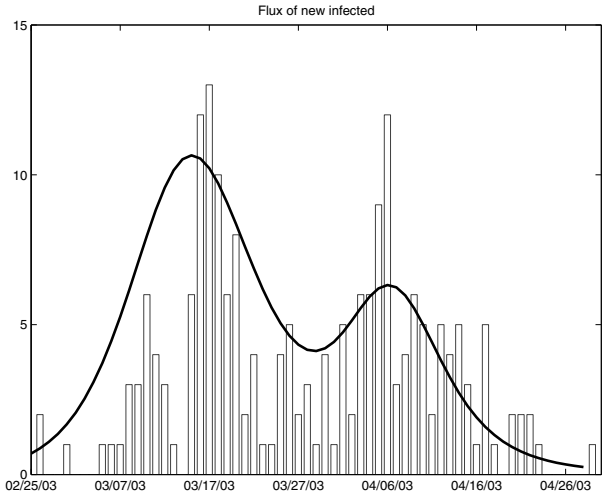

Figure 5: Comparison of the data from [8] and the model (5.1). The parameters values are listed in Table 1. The black curve is the function $t \mapsto \beta_{11} S_1(t) I_1(t) + S_2(t) (\beta_{21} I_1(t) + \beta_{22} I_2(t))$ which is the flux of new infected at time t.

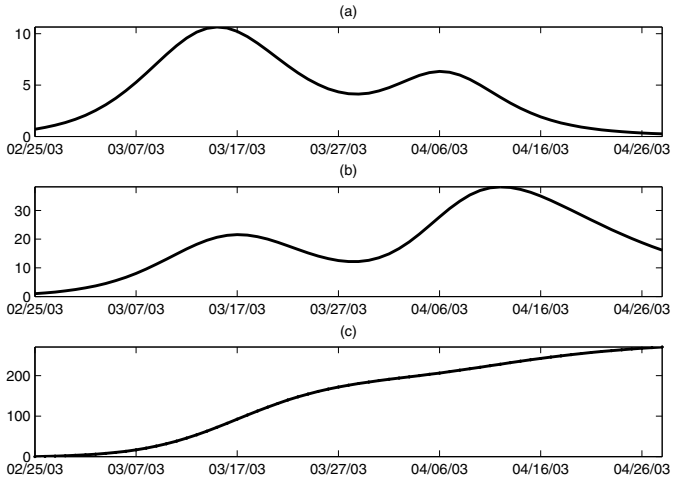

Figure 6: (a) the flux of new infected $t \mapsto \beta_{11} S_1(t) I_1(t) + S_2(t) (\beta_{21} I_1(t) + \beta_{22} I_2(t))$, (b) the total number of infected $t \mapsto I_1(t) + I_2(t)$, and (c) the total number of removed individuals $t \mapsto R_1(t) + R_2(t)$.

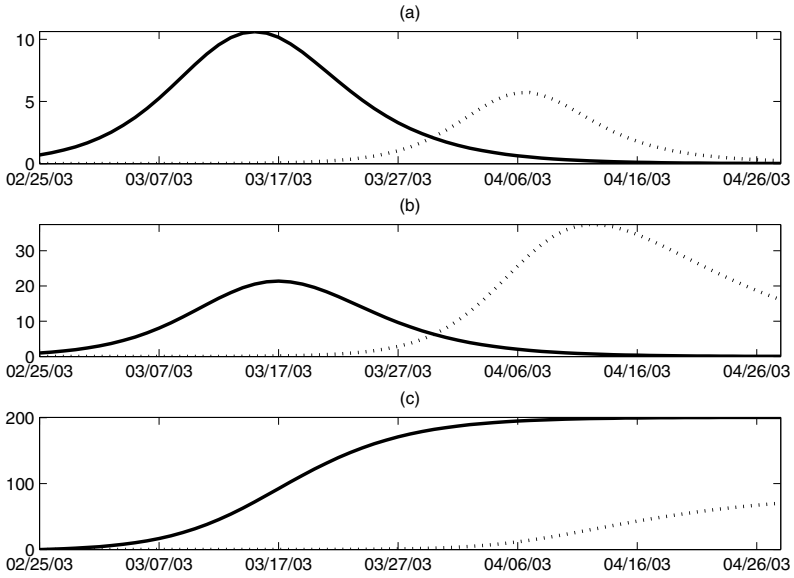

Figure 7: (a) the flux of new infected individuals in each group $t \mapsto \beta_{11} S_1(t) I_1(t)$ for the group 1 and $t \mapsto S_2(t)\left(\beta_{21} I_1(t) + \beta_{22} I_2(t)\right)$ for the group 2, (b) the number of infected $t \mapsto I_1(t)$ and $t \mapsto I_2(t)$, and (c) the total number of removed individuals $t \mapsto R_1(t)$ and $t \mapsto R_2(t)$. In each subfigure (a) (b) (c), the solid line corresponds to the first group and the dash line correspond to the second group.

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