Notes on a Simple Epidemic Model

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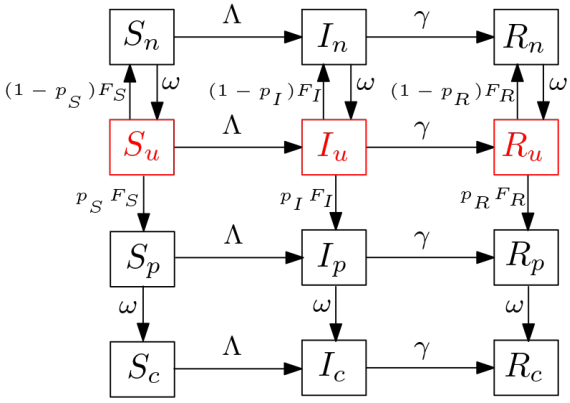
1 Method

1.1 model and parameters



The model is

$$dS_u/dt = -\Lambda S_u - F_S S_u + \omega S_n, \tag{1}$$
$$dS_n/dt = -\Lambda S_n + (1-p_S) F_S S_u - \omega S_n, \tag{2}$$
$$dS_p/dt = -\Lambda S_p + p_S F_S S_u - \omega S_p, \tag{3}$$
$$dS_c/dt = -\Lambda S_c + \omega S_p, \tag{4}$$
$$dI_u/dt = \Lambda S_u - F_I I_u + \omega I_n - \gamma I_u, \tag{5}$$
$$dI_n/dt = \Lambda S_n + (1-p_I) F_I I_u - \omega I_n - \gamma I_n, \tag{6}$$
$$dI_p/dt = \Lambda S_p + p_I F_I I_u - \omega I_p - \gamma I_p, \tag{7}$$
$$dI_c/dt = \Lambda S_c + \omega I_p - \gamma I_c, \tag{8}$$
$$dR_u/dt = \gamma I_u - F_R R_u + \omega R_n, \tag{9}$$
$$dR_n/dt = \gamma I_n + (1-p_R) F_R R_u - \omega R_n, \tag{10}$$
$$dR_p/dt = \gamma I_p + p_R F_R R_u - \omega R_p, \tag{11}$$
$$dR_c/dt = \gamma I_c + \omega R_p, \tag{12}$$
$$dN/dt = \omega(S_n + I_n + R_n), \tag{13}$$
$$dP/dt = \omega(I_p + R_p), \tag{14}$$

Symbol	Description	Unit	Value
N_0	Total population size	people	10^6
ω	Rate of onward flow from the awaiting to reported or untested compartments	1/day	-
γ	Recovery rate	1/day	1/3
ρ	Per capita testing intensity	1/day	0.01
η_w	Relative probability of transmission for isolated awaiting individuals	-	-
η_c	Relative probability of transmission for isolated confirmed individuals	-	-
Λ	Force of infection	1/day	-
p_S	Probability of false positive for susceptible	-	0
p_I	Probability of being infected and tested positive	-	1
p_R	Probability of being recovered and tested positive	-	0.5
W_S, W_I, W_R	Relative testing weight	-	Random testing: $W_S = W_I = W_R = 1$, Non-random testing: $W_S = 0.3, W_I = W_R = 1$

Table 1: The underlying parameters of model, Eqs. (1) to (12).

2 Results

2.1 On the calculation of $\mathcal{R}_0$

- **DFE** is given by solving the following system [1]

$$\begin{aligned} S_u + S_n &= N_0 \\ F_S S_u - \omega S_n &= 0 \end{aligned}$$

- **DFE:**

$$\begin{aligned} &S_u = (1 - \tfrac{\rho}{\omega})N_0, \\ &S_n = \tfrac{\rho}{\omega}N_0, \\ &I_j = R_j = 0 \quad \text{for all} \quad j. \end{aligned}$$

- At the DFE, $F_I^* = \frac{\rho}{(1-\rho/\omega)} W_I/W_S$ also note that $\partial F_I^*/\partial\rho > 0$.

$$F = \beta/N_0 \begin{bmatrix} S_u & \eta_w S_u & \eta_w S_u & \eta_c S_u \\ S_n & \eta_w S_n & \eta_w S_n & \eta_c S_n \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \tag{15}$$

$$V = \begin{bmatrix} F_I + \gamma & -\omega & 0 & 0 \\ -(1-p_I)F_I & \omega + \gamma & 0 & 0 \\ -p_I F_I & 0 & \omega + \gamma & 0 \\ 0 & 0 & -\omega & \gamma \end{bmatrix}. \tag{16}$$

Also,

$$V^{-1} = \begin{bmatrix} \frac{\omega+\gamma}{\hat{F}_I} & \frac{\omega}{\hat{F}_I} & 0 & 0 \\ \frac{(1-p_I)F_I}{\hat{F}_I} & \frac{F_I+\gamma}{\hat{F}_I} & 0 & 0 \\ \frac{p_I F_I}{\hat{F}_I} & \frac{\omega p_I F_I}{(\omega+\gamma)\hat{F}_I} & \frac{1}{\omega+\gamma} & 0 \\ \frac{\omega\, F_I\, p_I}{\gamma \hat{F}_I} & \frac{\omega^2\, F_I\, p_I}{\gamma(\omega+\gamma)\hat{F}_I} & \frac{\omega}{\gamma(\omega+\gamma)} & \frac{1}{\gamma} \end{bmatrix}, \tag{17}$$

where $\hat{F}_I = \gamma(\omega + \gamma) + (\gamma + \omega p_I)F_I$.

[1] Note when $I_u = R_u = 0$, $F_S = \frac{\rho N_0}{W_S S_u}$.

The particular form of F with two rows of zeros at the bottom, simplifies G as

$$G = \begin{bmatrix} G_{11} & G_{12} \\ 0 & 0 \end{bmatrix}, \text{ where } G_{11} = C \begin{bmatrix} A\,S_u & B\,S_u \\ A\,S_n & B\,S_n \end{bmatrix}. \tag{18}$$

The Disease-Free Equilibrium (DFE) for the SIR model, Eqs. (1) to (12), is given by solving the coupled system including $S_u + S_n = N_0$ and $F_S S_u - \omega S_n = 0$. The DFE is

$$S_n^* = \frac{\rho}{\omega} N_0,\ S_u^* = N_0 - S_n^*, \text{and} I_j = R_j = 0 \text{ for all j.} \tag{19}$$

The basic reproduction number, $\mathcal{R}_0$, was calculated by using the next generation matrix method developed by Van den Driessche and Watmough (2002). $\mathcal{R}_0$ is

$$\mathcal{R}_0 = (A \times S_u^* + B \times S_n^*) \times C, \tag{20}$$

where

$$\begin{aligned} A =& \gamma(\omega + \gamma) + (\gamma\eta_w + \omega\eta_c p_I)F_I, \\ B =& \big(\omega + (F_I + \gamma)\eta_w\big)\gamma + \frac{(\eta_w\gamma + \eta_c\omega)\omega p_I F_I}{\omega + \gamma}, \\ C =& \frac{\beta/\gamma}{N_0(\gamma(\omega + \gamma) + F_I(\gamma + \omega p_I))}. \end{aligned}$$

Note that the block matrix G_{12} does not influence $\mathcal{R}_0$ defined as the spectral radius of G. All matters here are the eigenvalues of G_{11}, which are 0 and $\mathcal{R}_0$ (20).

2.2 Sensitivity of $\mathcal{R}_0$ with respect to the underlying parameters

note 1. The tricky one is the $\partial\mathcal{R}_0/\partial\rho$; Following JD comment and some analysis, we can prove that analytically.

Jonathan's comment: "There should be a logical route to a clear proof about ρ. The total amount of time spent in I_x when starting from a given starting point should not depend on ρ (or anything but γ). And this should be reflected in the column sums of V^{-1}. Since both of the η's are < 1, all we should then need to prove is that the (nonzero) values on the first row of V^{-1} decrease with ρ to show that the elements of FV^{-1} decrease with ρ, which presumably shows that $\mathcal{R}_0$ decreases as well. This needs to be filled ink but should work."

note 2. Notice that matrix F is a rank one matrix, thus FV^{-1} is of a rank one. This is why FV^{-1} has only one non-zero eigenvalue. Specifically, F is a rank one means that it can be written as matrix product of a column vector and a row vector as follows

$$F = \beta/N_0 \begin{bmatrix} S_u \\ S_n \\ 0 \\ 0 \end{bmatrix} \begin{bmatrix} 1\eta_w\eta_w\eta_c \end{bmatrix}.$$

note 3. The enteries in the first row of matrix V^{-1} are decreasing wrt ρ, which represents that individuals are spending less time in average in untested compartment, I_u, as testing intensity increases. On the other hand, the enteries in the other rows of V^{-1} are increasing wrt ρ. Thus, the more testing the more waiting or reporting time.5

References

Van den Driessche, P. and Watmough, J. (2002). Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission. *Mathematical biosciences*, 180(1-2):29–48.