

Intensional infect proportion of newborn, with disease induced mortality rate

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1 Motivation

Previous analysis showed no obvious advantage for intentional infection. But those are the cases where we ignored disease induced mortality. In reality, if we are taking smallpox for example, past researches have determined the mortality rate to be 30 percent for normally infected cases, but only 1 percent for variolated cases. Thus, it is possible that intentional infection has a positive effect on disease control.

2 Introduction

Again, we consider two intentional infect strategies. One is to intentional infect newborns and the other is to intentional infect susceptible. In this document, we discuss the first strategy only.

3 System of differential equations

Since we have to consider disease induced mortality rate, we need to adjust our model by adding extra terms representing mortality rate.

The following assumptions are used:

- 19 • Birth and natural death rate are the same.
- 20 • The latent period is short enough to be ignored.
- 21 • All susceptible individuals are equally likely to be infected, and all infected individuals
- 22 are equally infectious.

$$\begin{aligned}
\frac{dS}{dt} &= \mu(1-p) - \beta S(V+I) - \mu S, \\
\frac{dV}{dt} &= \beta SV + \mu p - \gamma V - \mu V, \\
\frac{dI}{dt} &= \beta SI - \gamma I - \mu I, \\
\frac{dM}{dt} &= p_V \gamma V + p_I \gamma I, \\
\frac{dR}{dt} &= (1-p_V) \gamma V + (1-p_I) \gamma I - \mu R,
\end{aligned} \tag{1}$$

23 Here, β is the transmission rate, γ is the recovery rate, μ is the *per capita* rate of birth
 24 and death, p is the proportion of newborns that are intentionally infected.

25 We non-dimensionalize Equation 1 by scaling time, by

$$\tau = (\gamma + \mu)t, \tag{2}$$

As the result, we obtain, *<David: Do not use hard-coded specific values of case fatality proportions. Use symbols. p_V, p_I for “probability of mortality in V or I classes respectively*
>

$$\frac{dS}{d\tau} = \epsilon(1-p) - \mathcal{R}_0 S(V+I) - \epsilon S, \tag{3a}$$

$$\frac{dV}{d\tau} = \mathcal{R}_0 SV + \epsilon p - V, \tag{3b}$$

$$\frac{dI}{d\tau} = \mathcal{R}_0 SI - I, \tag{3c}$$

$$\frac{dM}{d\tau} = p_V(1-\epsilon)V + p_I(1-\epsilon)I, \tag{3d}$$

$$\frac{dR}{d\tau} = (1-p_V)(1-\epsilon)V + (1-p_I)(1-\epsilon)I - \epsilon R, \tag{3e}$$

26 where $\epsilon = \frac{\mu}{\gamma+\mu}$, $\mathcal{R}_0 = \frac{\beta}{\gamma+\mu}$.

4 Equilibria

To solve for all equilibria, we let equations Equation 3a, Equation 3b and Equation 3c equal to 0, we solve solutions.

First by letting Equation 3c equal to 0, we have either $S = \frac{1}{\mathcal{R}_0}$, $I = 0$ or both. For the case where $S = \frac{1}{\mathcal{R}_0}$, Equation 3b returns,

$$\frac{dV}{d\tau} = \epsilon p = 0, \quad (4)$$

Which has no solution if $p \neq 0$, and since we consider various possibilities where $p \neq 0$, we conclude that $S \neq \frac{1}{\mathcal{R}_0}$. Therefore, $I = 0$.

Equipped with the above condition, we now solve the other two equations and the only solution we acquire is

$$\hat{S} = \frac{1}{\mathcal{R}_0} - \frac{2p}{(\mathcal{R}_0 - 1) + \sqrt{(\mathcal{R}_0 - 1)^2 + 4\mathcal{R}_0 p}}, \quad (5a)$$

$$\hat{V} = \frac{\epsilon(\mathcal{R}_0 - 1) + \epsilon\sqrt{(\mathcal{R}_0 - 1)^2 + 4\mathcal{R}_0 p}}{2\mathcal{R}_0}, \quad (5b)$$

$$\hat{I} = 0, \quad (5c)$$

At this equilibrium, since the infected population is non-zero, this is not a disease free equilibrium. It follows that the only equilibrium we found is an endemic equilibrium, and disease free equilibrium does not exist for this model.

5 Stability of Endemic Equilibrium

Stability analysis rely on Jacobian Matrix,

$$\mathcal{J} = \begin{bmatrix} -\mathcal{R}_0(V + I) - \epsilon & -\mathcal{R}_0 S & -\mathcal{R}_0 S \\ \mathcal{R}_0 V & \mathcal{R}_0 S - 1 & 0 \\ \mathcal{R}_0 I & 0 & \mathcal{R}_0 S - 1 \end{bmatrix}. \quad (6)$$

Eigenvalues of Jacobian are given as follow,

$$\lambda_1 = -1 + \mathcal{R}_0 S \quad (7a)$$

$$\lambda_2 = \frac{-1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V - \sqrt{(-1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V)^2 - 4(\mathcal{R}_0 + \epsilon - \mathcal{R}_0 S \epsilon)}}{2} \quad (7b)$$

$$\lambda_3 = \frac{-1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V + \sqrt{(-1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V)^2 - 4(\mathcal{R}_0 + \epsilon - \mathcal{R}_0 S \epsilon)}}{2} \quad (7c)$$

39 By using Equation 5a and Equation 7a, we obtain

$$-1 + \mathcal{R}_0 S = -\frac{2p\mathcal{R}_0}{(\mathcal{R}_0 - 1) + \sqrt{(\mathcal{R}_0 - 1)^2 + 4\mathcal{R}_0 p}} < 0 \quad (8)$$

40 Therefore, *⟨David: eigenvalues must be written in $a+ib$ form, where a, b are real. ⟩*
 41 *⟨David: You have not calculated the real parts of λ_2 and λ_3 . ⟩*

$$\Re(\lambda_1) = -1 + \mathcal{R}_0 S < 0, \quad (9)$$

42 To determine the real part of λ_2 and λ_3 , we need to determine the sign of the quantity under
 43 the square root.

44 By using Equation 5a again, we have

$$\mathcal{R}_0 S \epsilon < \epsilon, \quad (10)$$

45 Therefore,

$$(\mathcal{R}_0 + \epsilon - \mathcal{R}_0 S \epsilon) > \mathcal{R}_0 > 0, \quad (11)$$

46 which means, if the sign of the quantity under the square root is positive, we necessarily
 47 have

$$\sqrt{(-1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V)^2 - 4(\mathcal{R}_0 + \epsilon - \mathcal{R}_0 S \epsilon)} < |(-1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V)| \quad (12)$$

48 Therefore, $\Re(\lambda_2) < \Re(\lambda_3) < 0$.

49 Certainly, if the sign of the quantity under the square root is negative,

$$\Re(\lambda_2) = \Re(\lambda_3) = -1 + \mathcal{R}_0 S - \epsilon - \mathcal{R}_0 V < 0 \quad (13)$$

50 We are able to conclude that EE is stable.

6 Disease Free Equilibrium

As mentioned above in section 4, disease free equilibrium does not exist for this model.

7 Mortality rate at Endemic equilibrium

When performing epidemic analysis, it is important to observe the mortality rate of the population, since this parameter is crucial to the severity of this disease. Here, we emphasize the mortality rate at EE.

By substituting the corresponding values at EE into equation (3d), we obtain,

$$\frac{dM}{d\tau} = p_V(1 - \epsilon)V = \frac{p_V(1 - \epsilon)\epsilon(\mathcal{R}_0 - 1) + p_V(1 - \epsilon)\epsilon\sqrt{(\mathcal{R}_0 - 1)^2 + 4\mathcal{R}_0p}}{2\mathcal{R}_0}, \quad (14)$$

Equation 14 reveals 3 important points. First, Mortality rate does increases as proportion of intentional infection increases. It is important to notice, though it is more beneficial to increase the proportion at the beginning of epidemics to prevent a severe outbreak, it might lead to heavier casualties in the long run. Second, as expected, the probability of mortality plays a major role in the mortality rate. Meaning intentional infection is not applicable if p_V is too high. Third, mortality rate also increases as \mathcal{R}_0 increases.

More specifically, if we consider the case of smallpox, where the values in Table 1 are used.

Table 1: Model parameters and smallpox values.

Symbol	Meaning	Value
μ	Natural <i>per capita</i> death rate	$\frac{1}{50*365}$ per day
γ	Recovery rate	$\frac{1}{22}$ per day
\mathcal{R}_0	Basic reproductive number	4.5

Therefore, we can calculate $\epsilon = \frac{\mu}{\mu + \gamma} = 0.0012$

$$\frac{dM}{d\tau} = 0.00111111(0.00420902 + \frac{100375\sqrt{12.25 + 18p}}{83466496}), \quad (15)$$

So we plot $\frac{dM}{d\tau}$ as a function of p ,

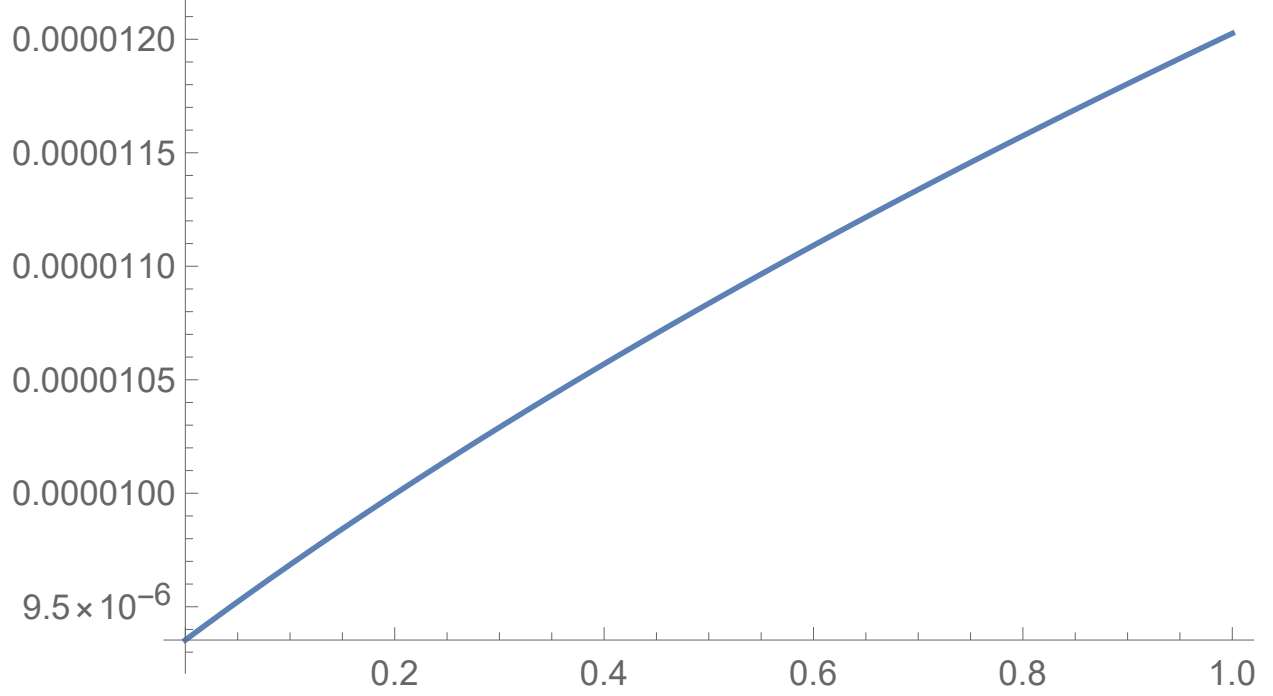


Figure 1: $\frac{dM}{d\tau}$ at EE as a function of p .

68 A major observation from this plot is, the magnitude of mortality rate at endemic
69 equilibrium is far less than natural death rate. That is,

$$\frac{dM}{dt}|_{EE} \ll \epsilon \quad (16)$$

70 Therefore, such an insignificant rate of death at EE can give us a conclusion that the total
71 disease induced mortality may eventually be close to not increasing anymore. We demon-
72 strate the total mortality counts as a function of time, using parameters from [Table 1](#).

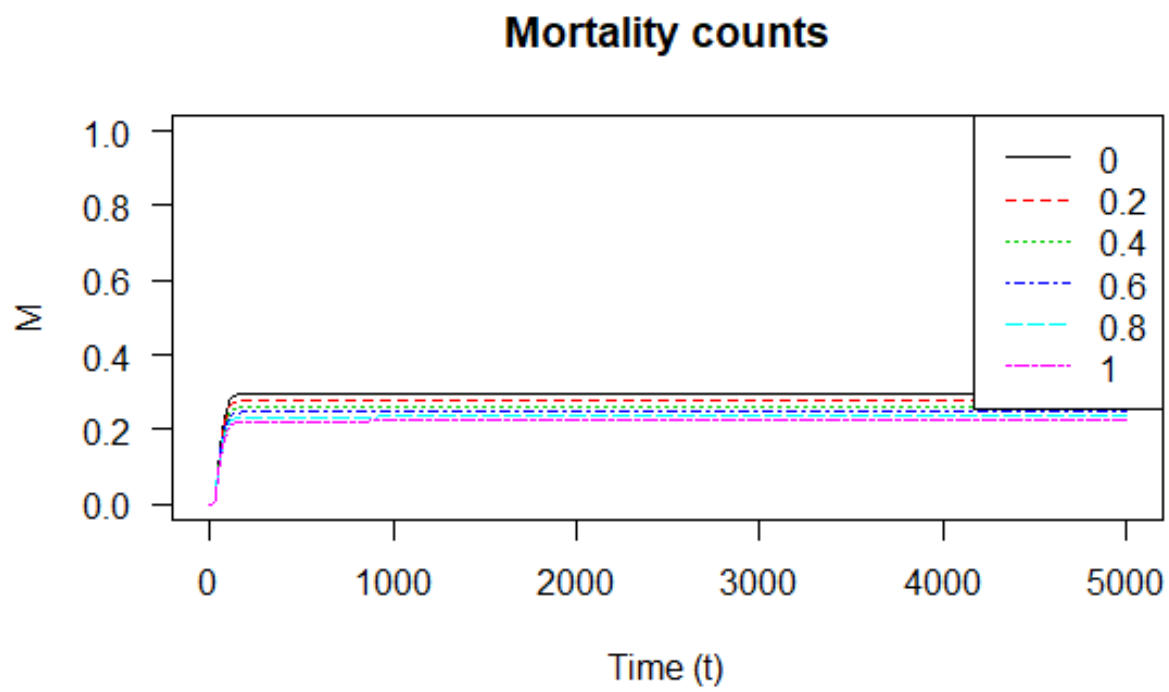


Figure 2: $\frac{dM}{d\tau}$ at EE as a function of p .