Intentional infect susceptible with disease induced mortality rate

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1 Introduction

We also have to consider intentionally infect susceptible individuals with disease induced mortality rate being considered.

2 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:

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

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \mu - \beta S(V+I) - rS - \mu S\,, \tag{1a}$$
$$\frac{\mathrm{d}V}{\mathrm{d}t} = \beta SV + rS - \gamma V - \mu V\,, \tag{1b}$$
$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \gamma I - \mu I\,, \tag{1c}$$
$$\frac{\mathrm{d}M}{\mathrm{d}t} = p_V\gamma V + p_I\gamma I\,, \tag{1d}$$
$$\frac{\mathrm{d}R}{\mathrm{d}t} = (1-p_V)\gamma V + (1-p_I)\gamma I - \mu R\,, \tag{1e}$$

Where β is transmission rate, γ is recovery rate, μ is the *per capita* rate of birth and death, r is the rate of intensional infection on susceptible individuals.

We non-dimensionalize Equation 1 by scaling time, by

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

As the result, we obtain,

$$\frac{\mathrm{d}S}{\mathrm{d}\tau} = \epsilon - \eta S - \mathcal{R}_0 S(V+I) - \epsilon S\,, \tag{3a}$$
$$\frac{\mathrm{d}V}{\mathrm{d}\tau} = \mathcal{R}_0 SV + \eta S - V\,, \tag{3b}$$
$$\frac{\mathrm{d}I}{\mathrm{d}\tau} = \mathcal{R}_0 SI - I\,, \tag{3c}$$
$$\frac{\mathrm{d}M}{\mathrm{d}\tau} = p_V(1-\epsilon)V + p_I(1-\epsilon)I\,, \tag{3d}$$
$$\frac{\mathrm{d}R}{\mathrm{d}\tau} = (1-p_V)(1-\epsilon)V + (1-p_I)(1-\epsilon)I - \epsilon R\,, \tag{3e}$$

Where $\epsilon = \frac{\mu}{\gamma+\mu}$, $\mathcal{R}_0 = \frac{\beta}{\gamma+\mu}$, $\eta = \frac{r}{\gamma+\mu}$

3 Equilibria

To solve for all equilibria for this system of ODEs, we let Equation 3a, Equation 3b and Equation 3c equal to 0 and solve for solutions.

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,

$$\frac{\mathrm{d}V}{\mathrm{d}\tau} = \eta S = 0\,, \tag{4}$$

Since we consider a non-zero rate of intentional infection, we could conclude that $I = 0$.

Therefore, by substituting back into Equation 3a and Equation 3b, we get

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

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

$$\hat{I} = 0\,, \tag{5c}$$

Clearly $\hat{V}$ is non-zero, therefore this equilibrium is not a disease free equilibrium. It follows that it is the endemic equilibrium.

4 Stability of Endemic Equilibrium

The Jacobian matrix of this system is,

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

Eigenvalues of Jacobian are ,

$$\lambda_1 = -1 + \mathcal{R}_0 S \tag{7a}$$

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

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

By using Equation 5a and Equation 7a, we get

$$\Re(\lambda_1) = -1 + \mathcal{R}_0 S = -\frac{2\eta}{(-(\eta + \epsilon - \epsilon\mathcal{R}_0) + \sqrt{(\eta + \epsilon - \epsilon\mathcal{R}_0)^2 + 4\mathcal{R}_0\epsilon\eta} + 2\eta)} < 0 \tag{8}$$

To decide the real parts of λ_2 and λ_3, we need to determine the sign of the quantity under the square root.

By using Equation 5a again, we have

$$\mathcal{R}_0 S\epsilon < \epsilon\,, \tag{9}$$

Therefore

$$(\eta + \mathcal{R}_0 V + \epsilon - \mathcal{R}_0 S\epsilon) > 0\,, \tag{10}$$

It follows that

$$\sqrt{(-1 + \mathcal{R}_0 S - \eta - \epsilon - \mathcal{R}_0 V)^2 - 4(\eta + \mathcal{R}_0 V + \epsilon - \mathcal{R}_0 S\epsilon)} < |(-1 + \mathcal{R}_0 S - \eta - \epsilon - \mathcal{R}_0 V)|\,. \tag{11}$$

It follows that we have two cases, if the quantity under square root is negative, then

$$\Re(\lambda_2) = \Re(\lambda_3) = -1 + \mathcal{R}_0 S - \eta - \epsilon - \mathcal{R}_0 V < 0\,, \tag{12}$$

Otherwise, we have

$$\Re(\lambda_3) < \Re(\lambda_2) < 0 \tag{13}$$

We are able to conclude that EE is stable.

5 Disease Free Equilibrium

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

6 Disease induced mortality rate at Endemic Equilibrium

By using Equation 3 and Equation 5b, we can find the mortality rate at EE,

$$\frac{\mathrm{d}M}{\mathrm{d}\tau} = p_V(1-\epsilon)V = \frac{p_V(1-\epsilon)\epsilon(\mathcal{R}_0 - 1) + p_V(1-\epsilon)\epsilon\sqrt{(\mathcal{R}_0 - 1)^2 + 4\mathcal{R}_0 p}}{2\mathcal{R}_0}, \tag{14}$$

By plotting it, we obtain the following graph,

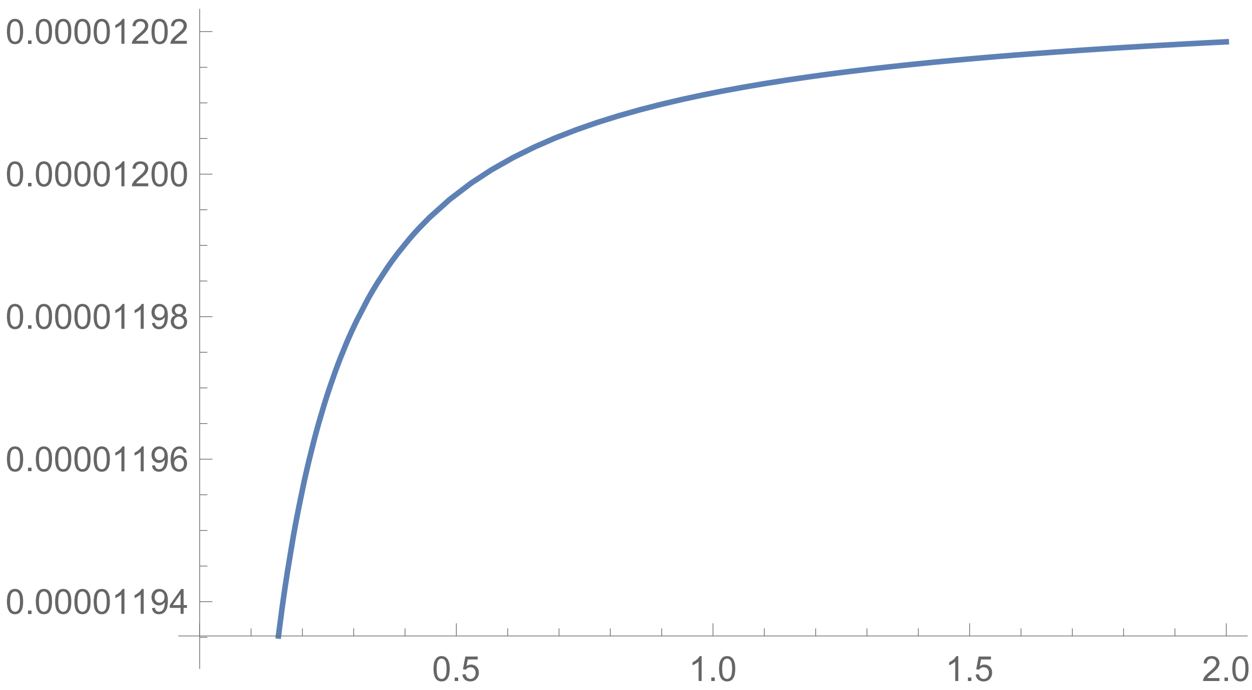

Figure 1: $\frac{\mathrm{d}M}{\mathrm{d}\tau}$ at EE as a function of η.

Again, the magnitude of this mortality rate at EE is way smaller than natural death rate, which has similar result in comparison with newborn model.

The significant difference between two models would be the total mortality count, parameters from Table 1 are used to plot the total mortality counts for this model.

Table 1: Model parameters and smallpox values.

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

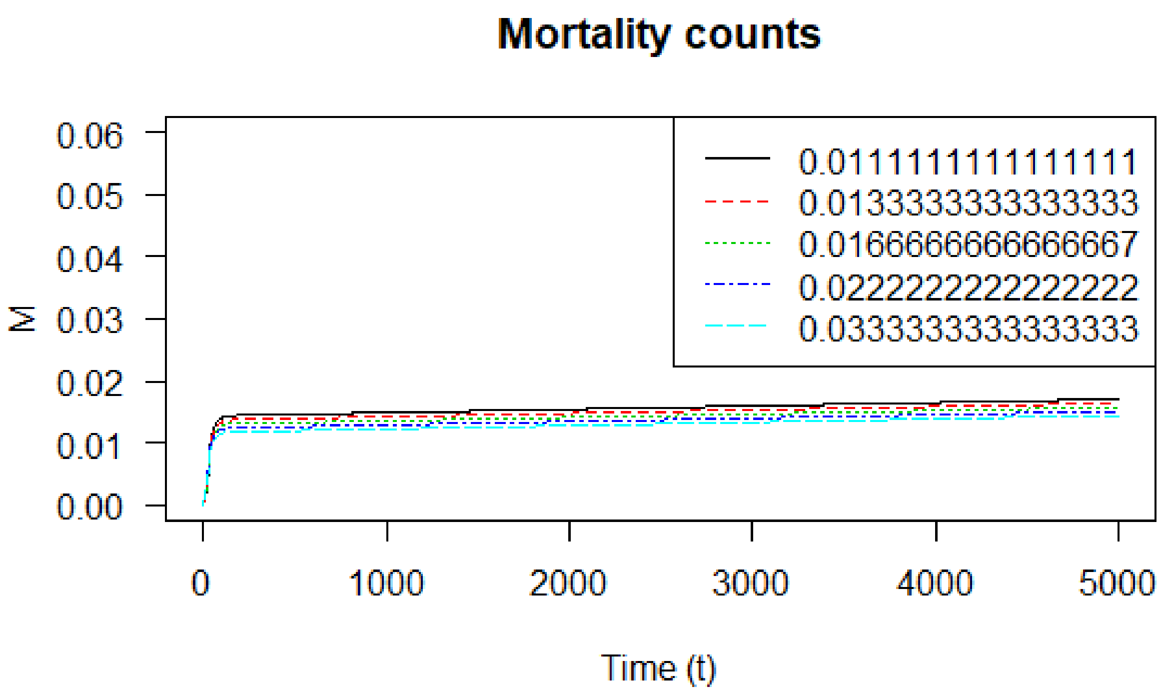

Figure 2: $\frac{\mathrm{d}M}{\mathrm{d}\tau}$ at EE as a function of p.

From the scale of the graph, the total mortality count is much lower for this model in comparison with newborn model, this is also why each solution in the figure above has an incline.