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Mathematical model of epidemics with intermediate classes

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Abstract

In this paper we present a Mathematical model for diseases that place some new recruits from the susceptible class into an "exposed but not yet infectious" class which we denote by E. The rest of the susceptible class can be infected directly. The model is developed and its steady state determined. The stability of the steady state was analyzed and it was found that the steady state is a saddle point. The disease free steady state was also analyzed and it was shown that it is stable if $N < \gamma/\beta$. This means that it may easy to achieve a disease free state provided the population size has a bound, ($N < \gamma/\beta$).

***Keywords*:** Mathematical model, Epidemics with intermediate class, exposed class, stead state, disease-free**.**

1.0 Introduction

The foremost S→I→R (susceptible-infective-removed) epidemic model was developed by Kermack and Mckendrick in 1927, [2,3]. This model opened the door to the involvement of many scientists in the development of a wide range of better models to describe the evolution of various types of epidemics.

Several extensions of the model have been considered, focusing on better describing many specific features of the disease kinetics, though few have focused on spatial issues.

Webb [8] proposed and analyzed a model structured by spatial position in a bounded one-dimensional environment, [0,L], L > 0. The spatial mobility is assumed in that paper to be governed by random diffusion with co-efficient k_1 and k_2 for the susceptible and infected classes, respectively, The infection is assumed to be transmitted from infected to susceptible individuals at a per capita rate $\alpha > 0$ by a "mass action" contact term, and the infected are assumed to recover at a per capita rate $\gamma > 0$. Demographic changes are neglected under the assumption that the duration of the epidemic is short in comparison with the average life span of an individual and that the disease does not affect fertility or mortality. This situation is typical, for example, of childhood diseases. Let $S = S(x,t), I = I(x,t)$ and $R = R(x,t)$ denote, respectively, the density of susceptible, infected, and removed individuals (recovered with immunity) at location x at time t. Then the evolution of the epidemic is described by the following coupled system of parabolic partial differential equations:

$$\begin{cases} S_t = k_1 S_{xx} - \alpha SI, \\ I_t = k_2 I_{xx} + \alpha SI - \gamma I \end{cases} \quad (1.1)$$

All individuals are prevented from escaping the kinetics, that is, the model is completed with homogeneous Neumann boundary conditions representing a closed environment,

$$S_X(0,t) = S_X(L,t) = I_X(0,t) = I_X(L,t) = 0. \tag{1.2}$$

It was shown in [8] that (1.1) - (1.2), complemented with appropriate initial conditions, is well-posed and has positive solutions for all time if the initial data are positive. Moreover, in the case $k_1 = k_2$ Webb has shown that the infected class dies out while the susceptibles tend to a spatially uniform steady-state. A significant limitation of this model is the fact that the spatial variable is one-dimensional, making the model of limited applicability. Moreover, the fact that the steady state in disease-free and spatially uniform leads to the conclusion that the spatial structure adds very little to the dynamics of the model, and nothing at all asymptotically.

A different extension of the Kermack-Mckendrick model was given by Gurtin and MacCamy[1]. For their model the susceptibles are assumed to move away from concentrations of infected while the disease renders these stationary. This model leads to overcrowding and, possibly to finite time blow-up. Milner, F.A. and Zhao, R [7] considered a model that incorporates spatial mobility of susceptibles away from infected regions, and of all individuals away from overcrowding. They assumed that there was no incubation or latency period for the disease, so that the terms infected and infective will be used as synonyms. For one spatial dimension, the model was first considered in [5]. They described the model in two space dimensions, analyzed some properties of its solution, and carried out numerical simulation that bring to light important epidemiological issues.

Other works on S→I→ R models can be found in [4,6]. In this paper we present an S→I→R model with intermediate class (*E*). We will formulate the model, determine the steady state and then analyze its stability. Also the disease-free steady state will be considered and analyzed. Most existing S→I→R Mathematical models lump the susceptibles into one group, but knowledge has shown that in some diseases the risk level of the susceptibles are not the same. In some S→I→R diseases, there exist intermediate classes in the susceptible group, but this has not been investigated in the literature, hence we have decided to investigate an S →I→R mathematical model with intermediate class (*E*).

2.0 The model

In this section we present the model for epidemics with intermediate classes. Some diseases place some new recruits from the susceptible class into an "exposed but not yet infectious" class which we denote by *E*, the rest of the susceptible class can be infected directly. The graph that describes this process is

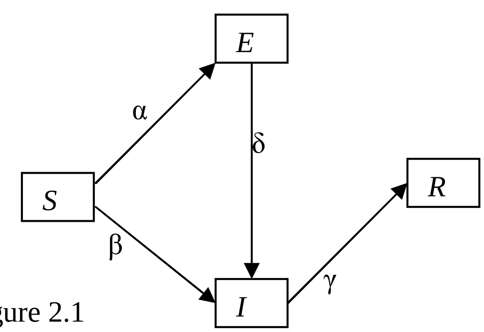

Figure 2.1

Let us define our symbols as follows

- S = the susceptible class
- E = Exposed but not yet infections class
- I = Infected and infections class
- R = Removed class, that is, those isolated or dead or recovered and immune
- μ = natural death rate for the removed class

α = the rate at which the susceptible class is exposed
β = the rate at which the susceptible class is infected
δ = the rate at which the exposed class become infectious
γ = the rate at which the infective class is removed

Considering Figure 2.1 and using the above symbols, the model is as follows:

$$\frac{dS}{dt} = -\beta SI - \alpha S = -S(\beta I + \alpha),\ \frac{dE}{dt} = -\delta E + \alpha S,\ \frac{dI}{dt} = \beta SI + \delta E - \gamma I$$
$$\frac{dR}{dt} = \gamma I - \mu R,\ N = S + E + I + R \qquad (2.1)$$

3.0 Steady state and its stability

Steady state occurs at $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$. This implies that

$$-\beta S^0 I^0 - \alpha S^0 = 0 \qquad (ii)$$
$$-\delta E^0 + \alpha S^0 = 0 \qquad (ii)$$
$$\beta S^0 I^0 + \delta E^0 - \gamma I^0 = 0 \qquad (iii)$$
$$\gamma I^0 - \mu = 0 \qquad (iv)$$

where S^0, E^0, I^0, R^0 are the steady state values of S, E, I, R. From (i) $S^0(\beta I^0 + \alpha) = 0 \Rightarrow$ $S^0 = 0$ and $I^0 = -\alpha/\beta$. From (iii) $(\beta S^0 - \gamma)I_0 + \delta E^0 = 0 \Rightarrow \frac{\gamma\alpha}{\beta} + \delta E^0 = 0$, since $S^0 = 0$ and $I^0 = \frac{-\alpha}{\beta} \Rightarrow E^0 = -\frac{\gamma\alpha}{\beta\delta}$, hence the steady state is $(S^0, E^0, I^0, R^0) = (0, \frac{-\gamma\alpha}{\beta\delta}, \frac{-\alpha}{\beta}, 0)$.

3.1 Stability

To discuss the stability of the steady state, we first linearize (2.1) to get

$$J = -\begin{bmatrix} \beta I^0 - \alpha & 0 & -\beta S^0 \\ \alpha & -\delta & \gamma \\ \beta I^0 & \delta & \beta S^0 \end{bmatrix} \qquad (3.1)$$

$$|J - I\lambda| = \begin{bmatrix} -\beta I^0 - \alpha - \lambda & 0 & -\beta S^0 & 0 \\ \alpha & -\delta - \lambda & 0 & 0 \\ \beta I^0 & \delta & \beta S^0 - \gamma - \lambda & 0 \\ 0 & 0 & \gamma & -\mu - \lambda \end{bmatrix} = 0 \qquad (3.2)$$

$\Rightarrow \quad (\beta I^0 + \alpha + \lambda)(\delta + \lambda)(\beta S^0 - \gamma - \lambda)(-\mu - \lambda) = 0 \Rightarrow \quad \lambda = -\beta I^0 - \alpha,\ -\delta, -\gamma + \beta S^0,\ -\mu$. Since $I^0 = -\alpha/\beta$, $E^0 = -\frac{\gamma\alpha}{\delta\beta}$, $S^0 = R^0 = 0$, $\lambda_1 = 0$, $\lambda_2 = -\delta$, $\lambda_3 = -\gamma$, $\lambda_4 = -\mu$. Since $\lambda_1 = 0$, the steady state $(S^0, E^0, I^0, R^0) = (0, \frac{-\gamma\alpha}{\delta\beta}, \frac{-\alpha}{\beta}, 0)$ is not stable but is a saddle point.

3.2 Disease free population

There is a disease free equilibrium point where the point is $(S^0, E^0, I^0, R^0) = (N,0,0,$

$0,)$. The question now is assume that a small number of infections come into a community, what will happen to the community? Will the disease free state be achieved? To provide answer to these questions, we carry out the stability analysis for the steady state. For the point $(S^0, E^0, I^0, R^0) = (N,0,0,0,)$, the Jacobian (*J*) of the system results into the following matrix below.

$$J_1 = \begin{bmatrix} -\alpha & 0 & -\beta N & 0 \\ \alpha & -\delta & 0 & 0 \\ 0 & \delta & \beta N - \gamma & 0 \\ 0 & 0 & \gamma & -\mu \end{bmatrix} \quad (3.3)$$

The eigenvalues of the Jacobian is found to be $\lambda_1 = -\alpha\, \lambda_2 = -\delta, \lambda_3 = \beta N - \gamma, \lambda_4 = -\mu..$ Since all the eigenvalues are negative if $\beta\mu - \gamma < 0$, the steady state is stable. This means that disease free state may be achieved. The disease may easily be eradicated after some time and the condition for this to happen is that N < γ/β, which means that there is a bound on the population size.

4.0 Conclusion and recommendation

We have formulated a mathematical model for diseases that place some new recruits from the susceptible class into an "exposed but not yet infectious" class. The model was analyzed using method of dynamical systems theory. The steady state was determined to be (S^0, E^0, I^0, R^0) = $(0, \frac{-\gamma\alpha}{\beta\delta}, \frac{-\gamma}{\beta}, 0)$. Analysis of the stability showed that the steady state is not stable but a saddle point. The disease free steady state was investigated and found to be $S^0, E^0, I^0 R^0) = (N,0,\ 0,0)$. It was shown that this steady state is stable provided there is a bound on the population size ($N < \gamma/\beta$) . This means that it is easy to achieve a disease free state, which means that the disease may easily be eradicated after some time. This simply means that the disease is not endemic and more effort should be made to reduce its spread. This is unlike the Webb's model where the disease free steady state was not stable. Serious campaigns should be mounted and efforts should be made to provide vaccination against the disease.

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