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Eigenvalue elasticity analysis of an seirc epidemic model for an infectious disease

Binuyo, Adeyemi O

Department of Physical Sciences, Ajayi Crowther University Oyo, Nigeria.

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ABSTRACT

In this paper, we have formulated a mathematical model for the transmission dynamics of an infectious disease in a certain community. The model allows for the individuals to move from the exposed phase to the infected phase. The model exhibits two equilibria, namely, the disease free equilibrium and the endemic equilibrium. The stability of these two equilibria points is controlled by the basic reproductive number R_0 which was determined using the next generation matrix approach. Using the eigenvalue elasticity analysis, it was found that the parameter denoted by β (transmission coefficient) has the greatest impact on the formulated mathematical model which must be put into consideration by the health care policy makers in order to reduce or eradicate the spread of the infectious disease in the community.

Introduction

Infectious diseases such as measles, influenza or tuberculosis are a fact of modern life. The mechanism of transmission of infections is now known for most diseases. Generally, diseases transmitted by viral agents, such as influenza, measles, rubella and chicken pox, confer immunity against re-infection while diseases transmitted by bacteria such as tuberculosis, meningitis and gonorrhea, confer no immunity against re-infection. Other diseases, such as malaria, are transmitted not directly from human to human but by vectors which are agents (usually insects) who are infected by humans and who then transmit the disease to humans [1].

In this paper, it is intended to analyze a model which incorporates the exposed individuals on the transmission dynamics [4]. We shall study an eigenvalue elasticity analysis on the SEIRC model. The name of this class of model derives from the fact that they involve equations relating the number of susceptible individuals (S), the number of exposed individuals (E), the number of infective (I), the number of recovered individuals (R) and the number of cross-immune individuals (C).

The transmission dynamics is described by a set of system of first order ordinary differential equations giving the change of population sizes of other individuals in the system [2]. Therefore, we introduce eigenvalue elasticity and sensitivity analysis in this paper to determine the parameter that has the greatest impact on the mathematical model [9].

The Mathematical Model

The SEIRC model is depicted in the compartmental diagram as shown in figure 1 and is expressed as the system of nonlinear initial value problem given in the form [2];

$$\frac{dS}{dt} = bN - \mu S + \tau C - \beta\frac{SI}{N}; \qquad S(0) = S_0 \tag{1}$$

$$\frac{dE}{dt} = \beta\frac{SI}{N} - (\mu + \varepsilon)E; \qquad E(0) = E_0 \tag{2}$$

$$\frac{dI}{dt} = \varepsilon E + \sigma\beta\frac{CI}{N} - (\mu + \alpha)I; \qquad I(0) = I_0 \tag{3}$$

$$\frac{dR}{dt} = (1-\sigma)\beta\frac{CI}{N} + \alpha I - (\mu + \delta)R; \qquad R(0) = R_0 \tag{4}$$

$$\frac{dC}{dt} = \delta R - \beta\frac{CI}{N} - (\mu + \tau)C; \qquad C(0) = C_0 \tag{5}$$

in which S = S(t), E = E(t), I = I(t), R = R(t) and C = C(t) represent the population of the susceptible, exposed, infective, recovered, and the cross-immune individuals respectively. The model assumes a population of constant size N with equal birth and death rates (b = μ) such that N(t) = S(t) + E(t) + I(t) + R(t) + C(t). The table below provides an interpretation of the model parameters.

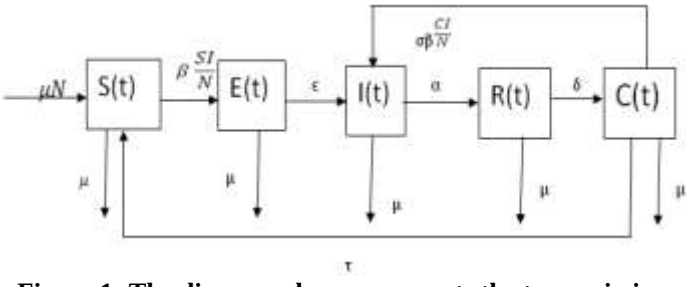

Figure 1: The diagram above represents the transmission dynamics of an SEIRC epidemic model [2]

Analysis of the Equilibrium Points

In this study, we restrict our study to the positive fractional values of the S(t), E(t), I(t), R(t) and C(t) denoted by s(t), e(t), i(t), r(t) and c(t) with equal birth and death rates which are ensuring a constant population size. We investigate the existence of equilibria of the system (1-5). System (1-5) has always a disease-free equilibrium H_0(s*, 0, 0, 0, 0) and a unique endemic equilibrium H_e(s*,e*, i*, r*, c*).

Tele:

E-mail addresses: binuyokay@yahoo.com

(a) Existence of disease-free equilibrium point H_0 (s*, 0, 0, 0, 0):

Here, b/μ is the solution of the system (1-5) in the absence of infections in the community (i = 0) i.e. b – μs* = 0. Clearly, s* = b/μ > 0. So the equilibrium point H_0 (b/μ, 0, 0, 0, 0) exists.

(b) Existence of endemic equilibrium points H_e (s*,e*, i*, r*, c*):

The non-trivial endemic equilibrium points H_e(s*,e*, i*, r*, c*) is the positive solution of the following algebraic equations;

$$b - \mu s(t) + \tau c(t) - \beta s(t) i(t) = 0 , \quad (6)$$

$$\beta s(t) i(t) - (\mu + \varepsilon) e(t) = 0; \quad (7)$$

$$\varepsilon e(t) + \sigma\beta c(t) i(t) - (\mu + \alpha) i(t) = 0; \quad (8)$$

$$(1 - \sigma)\beta c(t) i(t) + \alpha i(t) - (\mu + \delta) r(t) = 0; \quad (9)$$

$$\delta r(t) - \beta c(t) i(t) - (\mu + \tau) c(t) = 0; \quad (10)$$

Combining 6 and 7, we obtain,

$$e^* = \frac{b - \mu s^* + \tau c^*}{(\mu + \varepsilon)} \quad (11)$$

From equations 8, 9 and 10, we have,

$$c^* = \frac{r^*(\mu + \sigma\delta) - \alpha i^*}{\sigma(\mu + \tau) - (\mu + \tau)} \quad (12)$$

$$i^* = \frac{\varepsilon e^*}{(\mu + \alpha) - \sigma\beta c^*} \quad (13)$$

$$s^* = \frac{b + \tau c^*}{\mu + \beta i^*} \quad (14)$$

$$r^* = \frac{c^*\left(\beta i^* + (\mu + \tau)\right)}{\delta} \quad (15)$$

Now using equations 11, 12, 13, 14 and 15, we obtain,

$$A(i^*)^2 + B i^* + C = 0 \quad (16)$$

where,

$$A = \beta(\mu + \alpha)(\mu + \varepsilon)[\beta(\mu + \delta) - \delta\beta + \sigma\delta\beta] - \alpha\beta\delta\sigma\beta(\mu + \varepsilon) \quad (17)$$

$$B = (\mu + \alpha)(\mu + \varepsilon)\mu[\beta(\mu + \delta) - \delta\beta + \sigma\delta\beta] + \beta(\mu + \alpha)(\mu + \varepsilon)(\mu + \tau)(\mu + \delta) - \delta\alpha\left(\tau\beta\varepsilon + \mu\sigma\beta(\mu + \varepsilon)\right) \quad (18)$$

and

$$C = -\mu(\mu + \alpha)(\mu + \varepsilon)(\mu + \tau)(\mu + \delta) \quad (19)$$

From equation 16, we obtain i* to be two values i.e i* > 0 and i* < 0. For endemic condition, we consider i* > 0. Therefore, we obtain other results in terms of i* i.e.

$$s^* = \frac{b\left(\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)\right) + \tau\left((\mu + \alpha)(\mu + \varepsilon)(\mu + \beta i^*)\right)}{(\mu + \beta i^*)\left(\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)\right)} > 0 \quad (20)$$

$$e^* = \frac{\beta i^*\left[b\left(\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)\right) + \tau\left((\mu + \alpha)(\mu + \varepsilon)(\mu + \beta i^*)\right)\right]}{(\mu + \varepsilon)(\mu + \beta i^*)\left[\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)\right]} > 0; \quad (21)$$

$$c^* = \frac{(\mu + \alpha)(\mu + \varepsilon)(\mu + \beta i^*)}{\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)} > 0; \quad (22)$$

$$r^* = \frac{i^*\left\{\beta(1 - \sigma)[(\mu + \alpha)(\mu + \varepsilon)(\mu + \beta i^*)] + \alpha\left[\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)\right]\right\}}{(\mu + \delta)\left[\tau\beta\varepsilon + \sigma\beta(\mu + \varepsilon)(\mu + \beta i^*)\right]} > 0. \quad (23)$$

and

$R_0 = \frac{\beta\varepsilon}{(\mu + \alpha)(\mu + \varepsilon)}$ > 0 is the basic reproductive number of the mathematical model [2].

Hence, the non-trivial endemic equilibrium points H_e(s*,e*, i*, r*, c*) exists if R_0 > 1.

Stability Analysis

For the stability analysis of the mathematical model, the full details shall be found in [2]. Hence, by the Routh-Hurwitz stability criteria, we can say that the endemic equilibrium point H_e(s*,e*, i*, r*, c*) is locally asymptotically stable if R_0 > 1.

Numerical Simulation

In this section, we present numerical simulation to explain the existence of equilibria of the model as well as the feasibility of stability conditions numerically for a set of parameter values given in table 1. To study the dynamical behavior of the model, numerical simulation of the system (1-5) is carried out by Maple version 15. With these values of parameters, it can be checked that the endemic equilibrium points H_e(s*,e*, i*, r*, c*) is given by s*= 0.5565564033, e*=0.2136007706, i*=0.000022388774881, r*=0.07741647125 and c*=0.01738052003. The eigenvalues of the variational matrix corresponding to the endemic equilibrium of the model are, -0.0200, -0.0306, -0.1955, -0.3997 and -111.5554. The results of numerical simulation are displayed graphically in figure 2 variation of s, e, i, r, and c with time for the consider parameters set in the table 1.

We observe from the graph that the population of the susceptible individuals decrease in the first few days and later increase due to the re infection of the infectious disease. After some days, the susceptible individuals become stable while more individuals are recovered at that time from the infective individuals.

Eigenvalue Elasticity And Sensitivity Analysis

Eigenvalue elasticities measure the transient – response sensitivities of the model to parameters [6] and since the values of elasticities are dimensionless, they can be compared with each other. This can aid us identifying the parameters which could greatly influence the system [8].

(a) Eigenvalue Sensitivity with respect to a parameter:

This is defined as the partial derivative of the eigenvalue with respect to that parameter [5]. The eigenvalue sensitivity S_i (i = 1, - - -, N and N is the dimension of the state vector) with respect to the j^{th} parameter of the system p_j is given in the form;

$$S_i(p_j) = \lim_{\Delta p_{j\to 0}} \frac{\Delta\lambda_i}{\Delta p_j} = \frac{\partial\lambda_i}{\partial p_j} = I_i^T \frac{\partial J}{\partial p_j} r_i \quad (24)$$

Eigenvalue Elasticity with respect to a parameter:

This is defined as the partial derivative of the eigenvalue with respect to that parameter normalized for the size of the parameter and the size of the eigenvalue. This could also be described as the product of the eigenvalue sensitivity and the ratio of the eigenvalue and parameter [7]. Thus, it is given in the form ;

$$E_i(p_j) = \lim_{\Delta p_{j\to 0}} \frac{\frac{\Delta\lambda_i}{\lambda_i}}{\frac{\Delta p_j}{p_j}} = \frac{\frac{\partial\lambda_i}{\lambda_i}}{\frac{\partial p_j}{p_j}} = \frac{\partial\lambda_i}{\partial p_j}.\frac{p_j}{\lambda_i} = I_i^T \frac{\partial J}{\partial p_j} r_i.\frac{p_j}{\lambda_i} \quad (25)$$

With these equations, the eigenvalue elasticity and sensitivity with respect to a parameter can be computed using the left eigenvectors (I_i) and the right eigenvectors (r_i) with the partial derivatives of the linearized Jacobian matrix (J) with respect to a parameter (p_j). Because J and $\frac{\partial J}{\partial p_j}$ can often be easily determined symbolically and because the eigenvalues can be computed for particular parameters values and points in time, both eigenvalue elasticity and sensitivity with respect to a parameter can be computed without the need to either compute closed form expressions for eigenvalues nor to perform numeric differentiation [8].

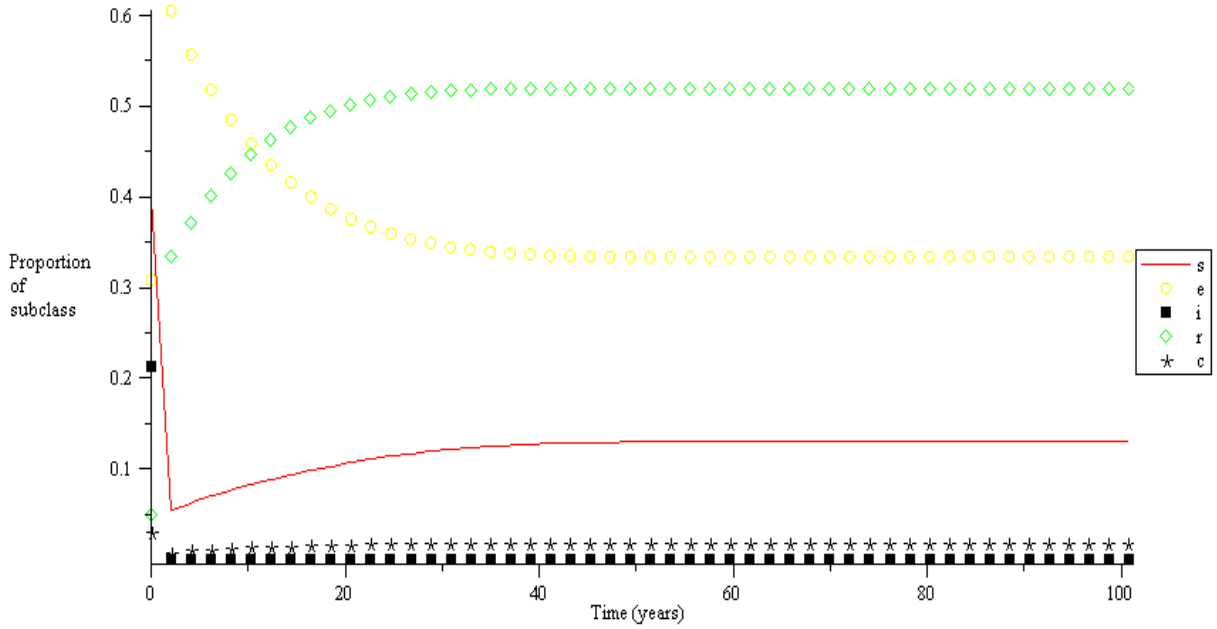

Figure 2: The numerical result of the stable system investigated by the stability analysis

Table 1: Parameter values in the mathematical model

Parameters	Definitions	Hypothetical values
b	birth rate	$0.02yr^{-1}$
μ	Mortality rate	$0.02yr^{-1}$
τ	Rate of progression from cross-immune to susceptible	$0.35yr^{-1}$
β	Transmission coefficient	1200
ε	Rate of progression from exposed to infective	$0.05yr^{-1}$
σ	Rate of re infection	$0 < \sigma < 1$
α	Rate of progression from infective to recovered	$365/3yr^{-1}$
δ	Rate of progression from recovered to cross-immune	$0.0182yr^{-1}$
S(0)	Initial values of the susceptible individuals	0.3982
E(0)	Initial values of the exposed individuals	0.3086
I(0)	Initial values of the infective individual	0.2131
R(0)	Initial values of the recovered individuals	0.0502
C(0)	Initial values of the cross-immune individuals	0.0299

Table 2: The values of the eigenvalue sensitivity and elasticity analysis

Parameters	Eigenvalue Sensisvity	Eigenvalue Elasticity
b	0	0
μ	-1.0000	-0.00017928
τ	0.00069621	0.0000021843
β	0.00024876	0.0027
ε	4.9743	0.0022
σ	0.0557	0.00024986
α	-0.0027	-0.0030
δ	0.05	0.0000081650

Using the MATLAB software package, the computer program was written for the evaluation of the values of eigenvalue elasticity and sensitivity of the mathematical model given in equations (1-5). The results obtained are shown in the table below.

With the above table, it was shown that the parameter β which is the transmission coefficient has the highest positive eigenvalue elasticity value. This means that the parameter has the greatest impact on the formulated mathematical model of the infectious disease. This is to show that the parameter should be thoroughly investigated as a possible policy lever such that the rate of transmission should be reduced to the bearest minimum by public health officials and the government at large.

Conclusion

In this paper, we develop a mathematical model to explore the parameter with the greatest impact on the model using the eigenvalue elasticity analysis. From the analysis, we obtained that parameter β has the greatest impact such that the health policy makers will take into consideration such that the rate of the transmission of the infectious disease can be greatly reduced or eradicated from the community.

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