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Stability analysis of an Seirc epidemic model for an infectious disease

A.O. Binuyo[1] and O. Komolafe[2]

[1]Department of Physical Sciences, Ajayi Crowther University Oyo, Nigeria

[2]Engineering Materials Development Institute, Akure, Nigeria.

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ABSTRACT

In this paper, we consider a deterministic mathematical model for the transmission dynamics of an infectious disease in a community. Although, the equilibria of the model could not be expressed analytically, their existence and the threshold conditions for their stability are theoretically and numerically investigated. We analyzed the stability of the model using the linearization techniques via the Jacobian matrix approach and the Routh-Hurwitz stability criteria to determine the equilibria for the model. The basic reproductive number of the model was determined using the next generation matrix operator. Their numerical results were shown in graphical forms using some hypothetical values for the parameters used in the model. It was shown graphically that the mathematical model produced asymptotically stable population when the parameter values are perturbed to a certain degree.

Introduction

Wirawan (2007) estabilished and analyzed a deterministic mathematical model on the transmission dynamics of influenza [5]. However, the integration of the exposed individuals to the population was not incorporated into the mathematical model. In this paper, it is intended to analyze a model which incorporates the exposed individuals on the transmission dynamics [2]. Therefore, we shall study a stability analysis on an 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 infectives (I), the number of recovered individuals (R) and the number of cross-immuned 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 [1]. It is much more complicated to know more from the qualitative structure of the isoclines that whether the system is stable or unstable after the change in any of the population size. Therefore, we introduce stability analysis in this paper to find out whether the system is stable or not when individuals in each subclass is in competition [3].

The SEIRC model is depicted in the compartmental diagram as shown in figure 1.1 and is expressed as the system of nonlinear initial value problem given in the form;

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

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

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

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

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

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, infectives, recovered, and the cross-immuned individuals respectively. The model assumes a population of constant size N with equal birth and death rates such that N(t) = S(t) + E(t) + I(t) + R(t) + C(t) [2]. The table below provides an interpretation of the model parameters.

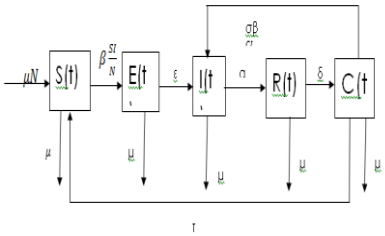

Figure 1.1: The diagram above represents the transmission dynamics of an SEIRC epidemic model

Basic Reproductive Number

One extremely useful concept that may be used on more complicated system is to find the threshold values to describe in what situation an outbreak will develop into an epidemic. A threshold value is often a bifurcation point as it is the position the steady state (equilibrium) solutions exchange stability [1]. The most commonly used threshold value is called the basic reproductive number denoted by R_0 and it is defined as the average number of secondary infectives produced when a single infected individual is introduced into a population consisting entirely of susceptible [3]. It is obviously the case that if $R_0 > 1$, the infected individual is infecting more than one further person, so the number of infectives will exponentially increase and an epidemic will occur. If however $R_0 < 1$, the infective is not passing the infection on to enough people to replace itself so the disease dies out and not persist in the community. There may be some secondary cases, but these will decrease with time and eventually the infection will become extinct.

Tele:

E-mail addresses: binuyokay@yahoo.com, fepraise@yahoo.com

If $R_0 \approx 1$, the infection just barely succeeds in reproducing itself and there will be a similar number of cases at any later time [6]. In this paper, the basic reproductive number for the model is obtained using the next generation matrix operator. This method is proposed by [8] and it is given in the form

$R_0 = \rho(FV^{-1})$ (6)

where R_0 denotes the basic reproductive number, F represents the matrix of the rate secondary infections are produced and V represents the matrix of the expected time an individual initially introduced into disease compartment.

Forming the matrices for F and V at the disease free equilibrium of the form $H_0 = (1, 0, 0, 0, 0)$ such that there is no infection in the population,

$$F = \begin{pmatrix} 0 & \beta S_0 \\ \varepsilon & \sigma\beta C_0 \end{pmatrix} \quad (7)$$

$$V = \begin{pmatrix} \mu + \varepsilon & 0 \\ 0 & \mu + \alpha \end{pmatrix} \quad (8)$$

$$FV^{-1} = \begin{pmatrix} 0 & \frac{\beta}{\mu+\alpha} \\ \frac{\varepsilon}{\mu+\varepsilon} & 0 \end{pmatrix} \quad (9)$$

The method was used and the basic reproductive number is obtained as

$$R_0 = \frac{\beta\varepsilon}{(\mu+\varepsilon)(\mu+\alpha)} \quad (10)$$

In the context of epidemiology modeling, it is generally known that if $R_0 < 1$, then the disease free equilibrium is locally asymptotically stable and the disease will be eradicated from the community.

Stability analysis of the model

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. The model equations (1 - 5) will be qualitatively analyzed to investigate the existence and stability of its associated equilibria.

In order to know the asymptotical behavior of the system (1- 5), we set in the form of :

$$f_1(s(t),e(t),i(t),r(t),c(t)) = \mu - \mu s(t) + \tau c(t) - \beta s(t) i(t), \quad s(0) = s_0 \quad (11)$$

$$f_2(s(t),e(t),i(t),r(t),c(t)) = \beta s(t) i(t) - (\mu+\varepsilon) e(t); \quad e(0) = e_0 \quad (12)$$

$$f_3(s(t),e(t),i(t),r(t),c(t)) = \varepsilon e(t) + \sigma\beta c(t) i(t) - (\mu+\alpha) i(t); \quad i(0) = i_0 \quad (13)$$

$$f_4(s(t),e(t),i(t),r(t),c(t)) = (1-\sigma)\beta c(t) i(t) + \alpha i(t) - (\mu+\delta) r(t); \quad r(0) = r_0 \quad (14)$$

$$f_5(s(t),e(t),i(t),r(t),c(t)) = \delta r(t) - \beta c(t) i(t) - (\mu+\tau) c(t); \quad c(0) = c_0 \quad (15)$$

To investigate the possible equilibria of the system (11 - 15), we consider the Jacobian matrix $\frac{\partial(f_1 f_2 f_3 f_4 f_5)}{\partial(s,e,i,r,c)}$ and impose the restriction on the equilibrium points; $s_\infty(t) > 0, e_\infty(t) > 0, i_\infty(t) > 0, r_\infty(t) > 0$ and $c_\infty(t) > 0$.

By differentiating the system (11 - 15) with respect to the state variables and with the parameter values in the table above, we obtain the Jacobian matrix as follows:

$$J(H_0) = \begin{pmatrix} -\mu-\beta i & 0 & -\beta s & 0 & \tau \\ \beta i & -(\mu+\varepsilon) & \beta s & 0 & 0 \\ 0 & \varepsilon & \sigma\beta c-(\mu+\alpha) & 0 & \sigma\beta i \\ 0 & 0 & (1-\sigma)\beta c+\alpha & -(\mu+\delta) & (1-\sigma)\beta i \\ 0 & 0 & -\beta c & \delta & -(\mu+\tau) \end{pmatrix} \quad (16)$$

at the disease – free equilibrium with $H_0 = (1, 0, 0, 0, 0)$), we obtain

$$J(H_0) = \begin{pmatrix} -\mu & 0 & -\beta & 0 & \tau \\ 0 & -(\mu+\varepsilon) & \beta & 0 & 0 \\ 0 & \varepsilon & -(\mu+\alpha) & 0 & 0 \\ 0 & 0 & \alpha & -(\mu+\delta) & 0 \\ 0 & 0 & 0 & \delta & -(\mu+\tau) \end{pmatrix} \quad (17)$$

with eigenvalues obtained as

$\lambda_1 = -\mu, \quad \lambda_2 = -(\mu+\varepsilon), \quad \lambda_3 = -(\mu+\alpha), \quad \lambda_4 = -(\mu+\delta)$ and $\lambda_5 = -(\mu+\tau)$

Since λ_i, i = 1, 2, 3, 4, 5 are negative with all the parameters are assumed to be positive, then the disease – free equilibrium H_0 is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

In the presence of infection ($i \neq 0$), the mathematical model (11 – 15) has a unique endemic equilibrium given by $H^* = (s^*, e^*, i^*, r^*, c^*)$ which are determined from the system as follows. The associated Jacobian matrix is obtained as:

$$J(H^*) = \begin{pmatrix} -\mu-\beta i^* & 0 & -\beta s^* & 0 & \tau \\ \beta i^* & -(\mu+\varepsilon) & \beta s^* & 0 & 0 \\ 0 & \varepsilon & \sigma\beta c^*-(\mu+\alpha) & 0 & \sigma\beta i^* \\ 0 & 0 & (1-\sigma)\beta c^*+\alpha & -(\mu+\delta) & (1-\sigma)\beta i^* \\ 0 & 0 & -\beta c^* & \delta & -\beta i^*-(\mu+\tau) \end{pmatrix} \quad (18)$$

Obtaining the eigenvalues as usual form from the formula $|J(H^* - \lambda I)| = 0$, the results in characteristic polynomial are given in the form

$\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5 = 0$ (19)

where,

$a_0 = 1$, $a_1 = 615.3082$, $a_2 = 123028.2888$, $a_3 = 0.7949220698*10^7$, $a_4 = 714958.7442$ and $a_5 = 11096.92577$ with $s(0) = s^* = 0.3982$, $e(0) = e^* = 0.3086$, $i(0) = i^* = 0.2131$, $r(0)=r^*=0.0502$ and $c(0) = c^* = 0.0299$. Since all the values are positive and by the Routh-Hurwitz stability criteria [4], the systems (11 – 15) are locally asymptotically stable provided that;

$a_i > 0$, for i = 1, 2, 3, 4, 5; (20)

$a_1a_2 - a_3 > 0$; (21)

$a_1a_2a_3 - a_1^2a_4 - a_3^2 > 0$; (22)

$(a_1a_2 - a_3)(a_3a_4 - a_2a_5) - (a_1a_4 - a_5)^2 > 0$ (23)

The figure 3.1 represents the asymptotically stable model in which the numerical results of the stable system (11 - 15) were investigated by the stability analysis. We observe from the graph that the population of the susceptible individuals decrease in the first few days and later increase due to the reinfection. After some days, the susceptible individuals becomes stable while more individuals are recovered at that time from the infective individuals. Also, the rate of recovered individuals is much faster than the rate of infected in the first few days. Furthermore, we note here that a small change in parameters μ, τ, β, ε, σ, α, and δ bring a sensitive change in each individual while keeping the initial conditions constant.

For instance, if we consider ten percent increase or decrease in the parameter values, the model will still be asymptotically stable as represented in the figure 3.2 below.

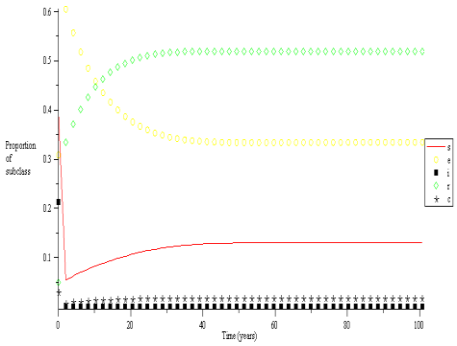

Figure 3.1: The SEIRC asymptotically stable model. This plot is the numerical result of the stable system investigated by the stability analysis

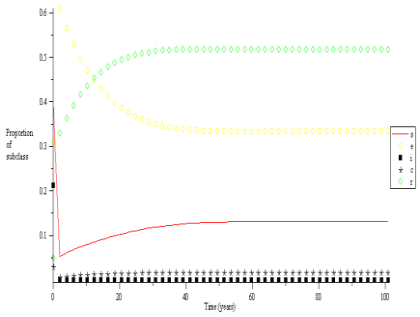

Figure 3.2: The plot shows the SEIRC stable model. The proportion of each subclass were shown when the parameter values were perturbed by ten percent.

Conclusion

In this paper, we have analyzed the stability of the SEIRC epidemic model using the linearization technique via Jacobian matrix and the Routh-Hurwitz stability criteria. We observed that the mathematical model produced the asymptotically stable population such that the infectious disease dies out from the population as time increases.

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Table 1: Parameter values in the mathematical model

Parameters	Definitions	Hypothetical values
μ	birth and mortality rates	$0.02yr^{-1}$
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 reinfection	$0 < \sigma < 1$
α	Rate of progression from infective to recovered	$365/3yr^{-1}$
δ	Rate of progression from recovered to cross-immuned	$0.0182yr^{-1}$
S(0)	Initial values of the susceptibles	0.3982
E(0)	Initial values of the exposed	0.3086
I(0)	Initial values of the infectives	0.2131
R(0)	Initial values of the recovered	0.0502
C(0)	Initial values of the cross-immuned	0.0299