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Behavior Stability in two SIR-Style Models for HIV

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Abstract

In this article we want to compare the SIR model with the modified SIR model for HIV describing behavioral. In the modified SIR model for HIV we assume that high-infective and higher-infective individuals in infective class I to inter I_1 and I_2 classes. At last, we can say that the modified SIR model have bigger or equal stability region in comparison with the SIR model.

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1 Introduction

In figure 1 we consider an SIR model for HIV transmission in a population of individuals who are at high-risk for HIV [2]. In this population let S denote the

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susceptible, I denote the infectives and R denote the individuals removed from the infective class. Not that $S, I, R \geq 0$ because they are represent numbers of people. Assume a constant migration of individuals into high-risk population as new susceptible, that is into S, $\mu S^0 > 0$. Assume that the number of people removed from each group due to natural causes such as death or leaving the high-risk population (not HIV or AIDS related) is proportional to the number of individuals in the group, μS, μI and μR, where $\mu > 0$ will be called the natural death rate for historical reasons, which is constant. Additionally the number of individuals removed from the infective class into the removed class (by progression from HIV to AIDS) is proportional to the number of individuals in the infective class, γI, where $\gamma > 0$ is the removal rate which is a constant. The infection rate, λ, depends on the number of partners per individual per unit time, $r > 0$, the transmission probability per partner, $\beta > 0$, which are both taken to be constants, and the proportion of infected individuals to sexually active individuals, $I/(S + I)$ [1,2,3]. The following system of ODEs

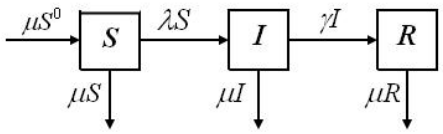


Figure 1: A schematic of system (1.1). Here S is the susceptibles, I is the infectives, R is the removeds, $\mu > 0$, a constant, is the death rate, $\mu S^0 > 0$, a constant, is the migration term, γ, a constant, is the removal rate from I to R and $\lambda = r\beta\frac{I}{S+I}$ is the infection rate.

describes this SIR model,

$$\begin{cases} \frac{dS}{dt} = \mu(S^0 - S(t)) - \lambda(t)S(t), \\ \frac{dI}{dt} = \lambda(t)S(t) - \mu I(t) - \gamma I(t), \\ \frac{dR}{dt} = \gamma I(t) - \mu R(t), \end{cases} \tag{1.1}$$

Figure 1 illustrates the system (1.1). This system is nonlinear due to the form of λ.

The reproductive number, disease-free equilibrium and endemic equilibrium

for Eq.(2.1) are, $R_0 = \frac{r\beta}{\mu+\gamma}$, $E_0 = (S^0, 0)$ and $E_e = (S^*, I^*)$, where,

$$S^* = \frac{S^0}{1 + (R_0 - 1)(1 + \gamma/\mu)} \text{ and } I^* = (R_0 - 1)S^*. \tag{1.2}$$

2 Modified SIR Model for HIV

In figure 2 we consider an modified SIR model for HIV transmission in a population of individuals who are at high-risk for HIV. The modified SIR model is same the SIR model, but, in modified SIR model high-infectives and higher-infectives individuals in class I to inter I_1 and I_2 classes.
The following system of ODEs describes this modified SIR model,

$$\begin{cases} \frac{dS}{dt} = \mu(S^0 - S(t)) - \lambda(t)S(t), \\ \frac{dI}{dt} = \lambda(t)S(t) - (\mu + \gamma + \alpha_1 + \alpha_2)I(t), \\ \frac{dI_1}{dt} = \alpha_1 I(t) - (\mu + \gamma_1)I_1(t), \\ \frac{dI_2}{dt} = \alpha_2 I(t) - (\mu + \gamma_2)I_2(t), \\ \frac{dR}{dt} = \gamma I(t) + \gamma_1 I_1(t) + \gamma_2 I_2(t) - \mu R(t), \end{cases} \tag{2.1}$$

Figure 2 illustrates the system (2.1). This system is nonlinear due to the form of λ.

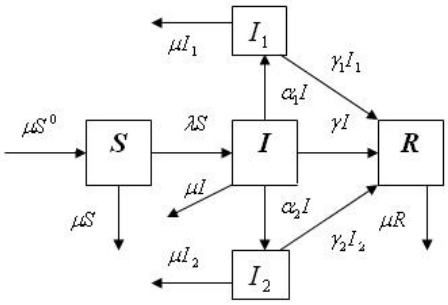


Figure 2: A schematic of system (2.1). Here S is the susceptibles, I is the infectives, I_1 is the high-infectives, I_2 is the higher-infectives, R is the removeds, $\mu > 0$, a constant, is the death rate, α_1 a constant, is removal rate high-infective individuals from I to I_1, α_2 a constant, is removal rate higher-infective individuals from I to I_2, $\mu S^0 > 0$, a constant, is the migration term, γ, γ_1, γ_2 constants, is the removal rate from I, I_1, I_2 to R and $\lambda = r\beta\frac{I}{S+I}$ is the infection rate.

2.1 The Reproductive Number

We derive an explicit formula for the reproductive number of infection by determining the spectral radius of the next generation operator of system (2.1) with $\lambda = r\beta\frac{I}{S+I}$, as follows,
System (2.1) has an infection-free equilibrium, given by $(S^0, 0, 0, 0)$, linearizing system (2.1) around the infection-free equilibrium, we have the following Jacobian matrix,

$$J = \begin{pmatrix} -\mu & r\beta & 0 & 0 \\ 0 & r\beta - \mu - \gamma - \alpha_1 - \alpha_2 & 0 & 0 \\ 0 & \alpha_1 & -\mu - \gamma_1 & 0 \\ 0 & \alpha_2 & 0 & -\mu - \gamma_2 \end{pmatrix}$$

Define matrixes F and V as,

$$F = \begin{pmatrix} r\beta & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} -\mu - \gamma - \alpha_1 - \alpha_2 & 0 & 0 \\ \alpha_1 & -\mu - \gamma_1 & 0 \\ \alpha_2 & 0 & -\mu - \gamma_2 \end{pmatrix}$$

Then F is a nonnegative matrix and V is a nonsingular matrix. Hence the reproductive number,$\Re_0$, is equal to the spectral radius $\rho(FV^{-1})$ [6].

$$\Re_0{=}\rho(FV^{-1}).$$

Now, we are ready to derive an explicit formula for the reproductive number $\Re_0$. Since matrix F has rank 1, the spectral radius $\rho(FV^{-1})$ is equal to the trace of matrix FV^{-1}. Therefore we have,

$$\Re_0 = trace(FV^{-1}) = r\beta\tfrac{1}{\mu+\gamma+\alpha_1+\alpha_2}.$$

2.1.1 Theorem

Define the reproductive number $\Re_0$ as,

$$\Re_0 = r\beta\tfrac{1}{\mu+\gamma+\alpha_1+\alpha_2}.$$

If $\Re_0 < 1$ the infection free equilibrium is locally asymptotically stable for the modified SIR model, and if $\Re_0 > 1$ the infection equilibrium is unstable for the modified SIR model.

2.1.2 Theorem

If R_0 to be the reproductive number for the SIR model and $\Re_0$ to be the reproductive number for the modified SIR model, then,

$$R_0 = \Re_0(1 + \tfrac{\alpha_1+\alpha_2}{\mu+\gamma}) \ .$$

Proof.

$$R_0 = r\beta\frac{1}{\mu+\gamma} \implies r\beta = (\mu+\gamma)R_0 \tag{2.2}$$

$$\begin{aligned}
\Re_0 &= r\beta\frac{1}{\mu+\gamma+\alpha_1+\alpha_2}\\
\overset{(2.2)}{\Longrightarrow} \Re_0 &= (\mu+\gamma)R_0\frac{1}{\mu+\gamma+\alpha_1+\alpha_2},\\
\Longrightarrow \frac{\Re_0}{R_0} &= \frac{\mu+\gamma}{\mu+\gamma+\alpha_1+\alpha_2},\\
\Longrightarrow \frac{R_0}{\Re_0} &= \frac{\mu+\gamma+\alpha_1+\alpha_2}{\mu+\gamma},\\
\Longrightarrow \frac{R_0}{\Re_0} &= (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}),\\
\Longrightarrow R_0 &= \Re_0(1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}). \qquad (2.3)
\end{aligned}$$

2.1.3 Theorem

Let R_0 to be the reproductive for the SIR model, then if $R_0 < (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma})$ the infection free equilibrium is locally asymptotically stable for the modified SIR model, and if $R_0 > (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma})$ the infection equilibrium is unstable for the modified SIR model.

Proof.

$$\begin{aligned}
R_0 &< (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}) \overset{2.3}{\Longrightarrow} \Re_0(1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}) < (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}),\\
&\Longrightarrow \Re_0 < 1(\texttt{Since } (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}) > 0). \qquad (2.4)
\end{aligned}$$

$$\begin{aligned}
R_0 &> (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}) \overset{2.3}{\Longrightarrow} \Re_0(1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}) > (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}),\\
&\Longrightarrow \Re_0 > 1(\texttt{Since } (1+\frac{\alpha_1+\alpha_2}{\mu+\gamma}) > 0). \qquad (2.5)
\end{aligned}$$

2.2 The Endemic Equilibrium

For $\Re_0 > 1$ we have an equilibrium where $I \neq 0$. This is the so called Endemic Equilibrium, $E_e = (S^*, I^*, I_1^*, I_2^*)$, where,

$$\begin{aligned}
S^* &= \frac{\mu S^0/(\mu+\gamma)}{((\alpha_1+\alpha_2)/(\mu+\gamma))(\Re_0-1)+\Re_0-\gamma/(\mu+\gamma)},\\
I^* &= (\Re_0-1)S^*,\\
I_1^* &= (\alpha_1/(\mu+\gamma_1))(\Re_0-1)S^*,\\
I_2^* &= (\alpha_2/(\mu+\gamma_2))(\Re_0-1)S^*,
\end{aligned}$$

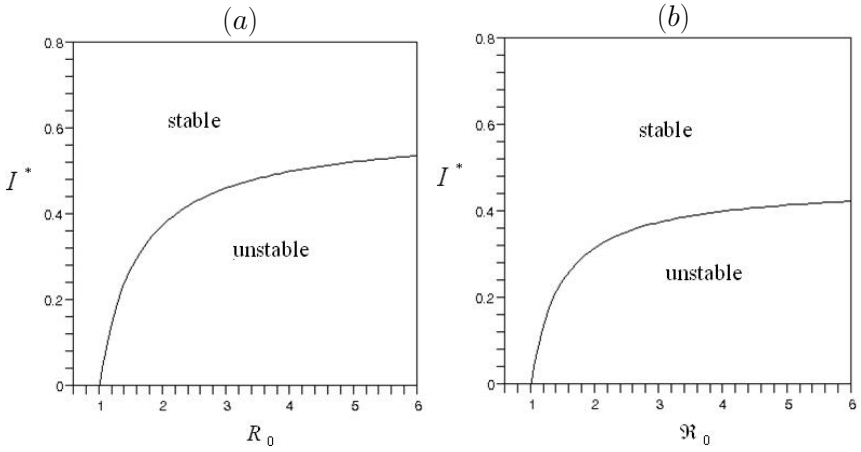
3 Conclusions

When $\alpha_1, \alpha_2 = 0$ then the SIR model and the modified SIR model are same. But, when $\alpha_1 \neq 0$ or $\alpha_2 \neq 0$ or $\alpha_1, \alpha_2 \neq 0$ then I think that the modified SIR model is better than the SIR model, because in the modified SIR model we can keep my system stable with go out the high-infective and higher-infective individuals from infective class.

3.1 Numerical Simulations

For draw the bifurcation diagram [4] for find the stable and unstable region [4,5], we use the following model parameters,

$$S^0 = 1, \mu = 0.6; \alpha_1 = 0.1, \alpha_2 = 0.2, \gamma = 0.4; \gamma_1 = 0.1, \gamma_2 = 0.05.$$



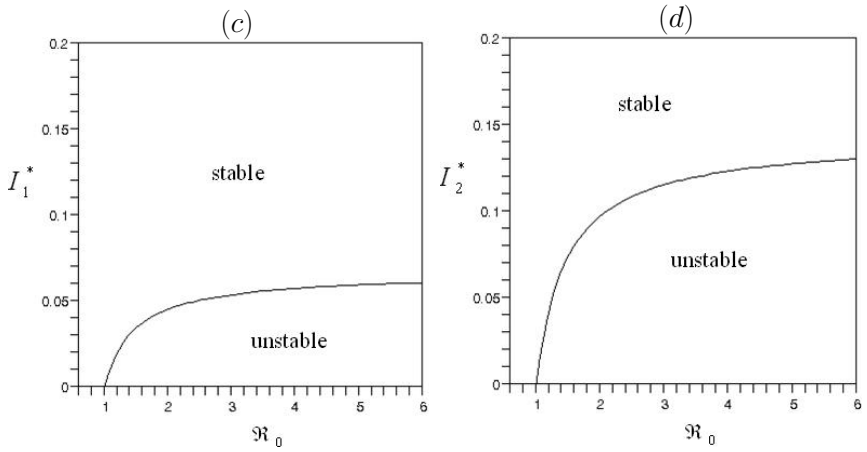


Figure 3: Bifurcation diagram

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