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Stability Analysis of the Transmission Dynamic and Control of Infectiousrate under Treatment

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Abstract: ***On account of the effect of limited treatment resources on the control of epidemic disease, the transmission dynamic and control of infectious rate under treatment is incorporated. The stability analysis of the disease-free equilibrium and the endemic equilibrium are discussed with treatment rate.***

Keywords: Basic Reproduction Number, Disease-free equilibrium, Endemic equilibrium

1. Introduction

Kermack and McKendrick divided the total population (P_t) into three compartments such as susceptible (S_t), Infective (I_t) and Removable (R_t) individuals, so that:

$$P_t = S_t + I_t + R_t \quad (1)$$

Where

$$\frac{dS_t}{dt} = iS_tI_t \quad (2)$$

$$\frac{dI_t}{dt} = iS_tI_t - gI_t \quad (3)$$

$$\frac{dR_t}{dt} = gI_t \quad (4)$$

2. Model Formulation

In this model, we divide the total population into four compartments such as Susceptible, Infective, Hospitalized and Recovered individuals. We assume that:

- *S* is the number of susceptible individuals who are not infected but could become infected.
- *I*is the number of infective individuals who are infected by the disease and can transmit it to the susceptible.
- H is the number of individuals who are admitted in the hospital to take treatment for a specified period.
- *R* is the number of recovered or removed individuals. These may or may not have the disease, but they can't become infected and they can't transmit the disease to others.

A susceptible, infective or hospitalized individual can willingly become recovered or removed.

The model variables and parameters are defined as follows

$N(t)$ Total population individual at time t

$S(t)$ Susceptible individual at time t

$I(t)$ Infective individual at time t

$H(t)$ Hospitalized individual at time t

$R(t)$ Recovered individual at time t

A Recruitment rate of the population

μ Death removal rate

p Infection transmission probability per contact

τ Effort rate against infection and thus

$\beta = p(1-\tau)$ is the effective infectious contact rate

ϕ Rate at which infective individual are admitted as a patient

$\frac{1}{\psi}$ Average period of the infected individual spent in the hospital

θ Proportion of individuals that leaves S, I or A compartment to R

The susceptible sub-population S(t) is generated from constant recruitment of individual at a rate A. They acquired infection via horizontal transfers from individual in the infective class, I(t) at a rate $\beta = p(1-\tau)$ and thus become infective individual in the susceptible infective and admitted class become removed due to treatment on the danger of infection at the rate θ $(0 < \theta < 1)$. Infective individuals are admitted and treated at the rate ∅ admitted individuals stay in hospital for an average period of $\frac{1}{\psi}$ after which a proportion θ become recovery while (1-θ) go back to infective class and not due to the fear of the consequence of being admitted. Thus as the admitted individual spent an average period of $\frac{1}{\psi}$ in the hospital then $\Psi\theta$ and $\Psi(1-\theta)$ are the transition rates from H compartment to R compartment and back to I compartment respectively.

Furthermore, natural death occurs in all classes at a rate ⍰. The corresponding mathematical equation of model can be

described by a system of ordinary differential equations given in (5)

$$\frac{dS}{dt} = A - \frac{\beta I}{N} S - K_1 S$$
$$\frac{dI}{dt} = \frac{\beta I}{N} S + \psi(1-\theta)H - K_2 I$$
$$\frac{dH}{dt} = \phi I - K_3 H + T(I)$$
$$\frac{dR}{dt} = \theta(S + I + \psi H) - \mu R - T(I)$$

where $T(I) = rI$. Now

$$\frac{dS}{dt} = A - \frac{\beta I}{N} S - K_1 S$$
$$\frac{dI}{dt} = \frac{\beta I}{N} S + \psi(1-\theta)H - K_2 I$$
$$\frac{dH}{dt} = \phi I - K_3 H + rI \qquad (5)$$
$$\frac{dR}{dt} = \theta(S + I + \psi H) - \mu R - rI$$
$$K_1 = (\theta + \mu)$$
$$K_2 = (\phi + \theta + \mu) \quad (6)$$
$$K_3 = (\psi + \mu)$$

Consider the closed set:

$$\Omega = \left\{ (S, \mathrm{I}, H, \mathrm{R}) \in : S + I + H + R \le \frac{A}{\mu} \right\} \quad (7)$$

In order to study the dynamics of the system (5) in Ω, the positive-invariance and attractiveness of Ω with respect to the system(5) is established as follows now the rate of change of the total population, obtained by adding all the equation in the system (5) is given by

$\frac{dN}{dt} = A - \mu N$ (8) It follows from (8) that whenever $N > \frac{A}{\mu}$ then $\frac{dN}{dt} = 0$ implying $\frac{dN}{dt}$ is bounded by $A - \mu N$. Thus a standard comparison theorem can be used to show that $N(t) \le N(0)e^{-\mu t} + \frac{A}{\mu}(1 - e^{-\mu t})$, thus Ω is positively-invariant (i.e. all solution in Ω remain in Ω for all time).

Furthermore, if $N(t) > \frac{A}{\mu}$ then either the solution enters Ω in finite time or N(t) approaches $\frac{A}{\mu}$ and the infected variables (i.e., all solution in eventually enters Ω). Therefore the model is well-posed epidemiologically and mathematically (Hetthcote, 2000). And hence it is sufficient to study the dynamics of the system (5) in Ω.

3. Model Analysis

3.1 Existence and Local Stability of Disease-Free Equilibrium

The disease-free equilibrium is the state in which the population is free of disease, so that we have only susceptible and recovered individuals. Thus the model has a disease–free equilibrium, obtained by setting the right-hand side of (5) to zero given by

$A - \frac{\beta I}{N} S - K_1 S = 0$ & Put I=0, we get

$$S = \frac{A}{K_1} \quad \& \quad R = \frac{\theta(S + I + \psi H) - rI}{\mu}$$

$$Put \ \mathrm{H}{=}0 \Rightarrow R = \frac{\theta S}{\mu}$$

$$i.e., \ R = \frac{\theta A}{\mu K_1}$$

$$E_0 : (S^*, \mathrm{I}^*, H^*, \mathrm{R}^*) = \left(\frac{A}{K_1}, 0, 0, \frac{\theta A}{\mu K_1} \right) (9)$$

Using the next generation operator technique described by Diekmann and Heesterbeek (2000) and subsequently analyzed by Van Den Driessche and Watmough (2002), we obtained the basic reproduction number R_0 of the model equation (5) which is the spectral radius (ρ) of the next generation matrix K.

That is $R_0 = \rho K$, where $K = FV^{-1}$ the matrix of F (for the new infection terms) are obtained from the infected compartment (i.e., I and H) at disease-free equilibrium and are given respectively by

$$\frac{dS}{dt} = A - \frac{\beta I}{N} S - K_1 S$$
$$\frac{dH}{dt} = \phi I - K_3 H + rI$$

$$F = \begin{pmatrix} -\frac{\beta S}{N} & 0 \\ \phi + r & -K_3 \end{pmatrix}$$

$$F = \frac{\beta K_3 S^*}{N^*}$$

$$\frac{dI}{dt} = \frac{\beta I}{N} S + \psi(1-\theta)H - K_2 I$$

$$\frac{dH}{dt} = \phi I - K_3 H + rI$$

$$V = \begin{pmatrix} -K_2 & \psi(1-\theta) \\ \phi + r & -K_3 \end{pmatrix}$$

$$V = K_2 K_3 - (\phi + r)\psi(1-\theta)$$

$$F = \begin{pmatrix} \frac{\beta S^*}{N^*} & 0 \\ -(\phi + r) & K_3 \end{pmatrix} \quad (10)$$

and

$$V = \begin{pmatrix} K_2 & -\psi(1-\theta) \\ -(\phi + r) & K_3 \end{pmatrix} \quad (11)$$

The basic reproduction number is then given as:

$$R_0 = FK = FV^{-1} = \frac{F}{V}$$

$$R_0 = \frac{\beta K_3 S^*}{(K_2 K_3 - (\phi + r)\psi(1-\phi))N^*} \quad (12)$$

Theorem:

The disease-free equilibrium E_0 of the model is locally asymptotically stable (LAS) if $R_0 < 1$.

Proof.

We used the Jacobean stability approach to prove the local stability of the disease-free equilibrium state. Now, we observed that the variable R does not appear in the first three (3) equations of the system (5).

Thus, using the relation

$$S + I + H + R = N$$
$$R = N - (S + I + H) \quad (13)$$

Linearization at E_0, gives the Jacobian matrix:

$$\frac{dS}{dt} = A - \frac{\beta I}{N} S - K_1 S$$
$$\frac{dI}{dt} = \frac{\beta I}{N} S + \psi(1-\theta)H - K_2 I$$
$$\frac{dH}{dt} = \phi I - K_3 H + rI$$

$$H(E_0) = \begin{pmatrix} -K_1 & -\frac{\beta S^*}{N^*} & 0 \\ 0 & -\left(K_2 - \frac{\beta S^*}{N^*}\right) & \psi(1-\theta) \\ 0 & \phi + r & -K_3 \end{pmatrix} \quad (14)$$

Considering (5) at E_0, we can deduced that

$$\frac{dS}{dt} = A - \frac{\beta I}{N} S - K_1 S$$
$$\frac{dI}{dt} = \frac{\beta I}{N} S + \psi(1-\theta)H - K_2 I$$
$$\frac{dH}{dt} = (\phi + r)I - K_3 H$$
$$\frac{dR}{dt} = \theta(S + I + \psi H) - \psi R - rI$$

$$A - \frac{\beta I^*}{N} - K_1 S^* = 0$$
$$\Rightarrow A = \frac{\beta I^* S^*}{N^*} + K_1 S^*$$
$$\frac{\beta I^*}{N^*} S^* + \psi(1-\theta)H^* - K_2 I^* = 0$$
$$\Rightarrow K_2 = \frac{\beta S^*}{N^*} + \frac{\psi(1-\theta)H^*}{I^*}$$
$$(\phi + r)I^* - K_3 H^* = 0$$
$$\Rightarrow K_3 = \frac{(\phi + r)I^*}{H^*}$$
$$\theta(S^* + I^* + \mu H^*) - \mu R^* - rI^* = 0$$
$$\Rightarrow \mu = \frac{\theta(S^* + I^* + \mu H^*) - rI^*}{R^*}$$

Therefore

$$A = \frac{\beta I^* S^*}{N^*} + K_1 S^*$$
$$K_2 = \frac{\beta S^*}{N^*} + \frac{\psi(1-\theta)H^*}{I^*}$$
$$K_3 = \frac{(\phi + r)I^*}{H^*} \quad (15)$$
$$\mu = \frac{\theta(S^* + I^* + \psi H^*) - rI^*}{R^*}$$

Using elementary row transformation, equation (14) becomes

$$R_1 \to R_1$$

$$R_2 \to R_2$$

$$R_3 \to R_3\left(K_2 - \frac{\beta S^*}{N^*}\right) + (\phi + r)R_2$$

$$H(E_0) = \begin{bmatrix} -K_1 & -\frac{\beta S^*}{N^*} & 0 \\ 0 & -\left(K_2 - \frac{\beta S^*}{N^*}\right) & \psi(1-\theta) \\ 0 & \phi & -K_3 + \frac{(\phi+r)\psi(1-\theta)}{\left(K_2 - \frac{\beta S^*}{N^*}\right)} \end{bmatrix} \quad (16)$$

And clearly, the eigen values are

$$\lambda_1 = -K_1 < 0$$

$$\lambda_2 = -(K_2 - \frac{\beta S^*}{N^*}) < 0$$

Since from equation (15)

$$K_2 = \frac{\beta S^*}{N^*} + \frac{\psi(1-\theta)H^*}{I^*}$$

$$K_2 > \frac{\beta S^*}{N^*}$$

and $K_2 N^* - \beta S^* > 0$

$$\lambda_3 = -(K_3 - \frac{(\phi + r)\psi(1-\theta)N^*}{K_2 N^* - \beta S^*}) \quad (17)$$

Now λ_3 to be negative, we must have

$$-K_3(K_2 N^* - \beta S^*) + (\phi + r)\psi(1-\theta)N^* < 0$$

$$i.e.,\ \beta K_3 S^* < K_3 K_2 N^* - (\phi + r)\psi(1-\theta)N^*$$

$$\frac{\beta K_3 S^*}{(K_2 K_3 - (\phi + r)\psi(1-\theta)N^*} < 1$$

Thus $\lambda_3 < 0$ if $R_0 < 1$ implying all the eigen values have negative real parts and by Jacobean stability E_0 is LAS. This completes the proof.

The epidemiological implication of the theorem is that infection can be under control in the population (when $R_0 < 1$) if the initial sizes of the sub-populations of the model are in the basis of attraction of DFE (E_0). In order to ensure that corruption is independent of the initial sizes of the sub-populations of the model, it is necessary to show that $E_0$is globally-asymptotically stable.

3.2 Global Stability of Disease–Free Equilibrium

Theorem:

The disease-free equilibrium E_0 of (5) is globally asymptotically stable (GAS) in Ω if $R_0 \leq 1$.

Proof.

One common approach in studying the global asymptotic stability of the DFE is to construct an appropriate Lyapunov function. Consider the Lyapunov function

$$L = K_3 I + \psi(1-\theta)H \quad (18)$$

It's derivative along the solutions of the model equation is

$$L' = K_3 I' + \psi(1-\theta)H'$$

$$= K_3\left(\frac{\beta I}{N} S + \psi(1-\theta)H - K_2 I\right) + \psi(1-\theta)[(\phi + r)I - K_3 H]$$

$$= K_3 I\left(\frac{\beta S}{N}\right) - I[K_2 K_3 - (\phi + r)\psi(1-\theta)]$$

$$= I[K_2 K_3 - (\phi + r)\psi(1-\theta)]$$

$$\mathrm{X}\left(\frac{K_3 \beta S}{[K_2 K_3 - (\phi + r)\psi(1-\theta)]N} - 1\right)$$

Since $\frac{S}{N} \leq \frac{S^*}{N^*}$, we have

$$L' \leq I[K_2 K_3 - (\phi + r)\psi(1-\theta)]$$

$$\mathrm{X}\left(\frac{K_3 \beta S^*}{[K_2 K_3 - (\phi + r)\psi(1-\theta)]N^*} - 1\right)$$

i.e., $L' \leq I[K_2 K_3 - (\phi + r)\psi(1-\theta)](R_0 - 1)$ where

$$R_0 = \frac{K_3 \beta S^*}{[K_2 K_3 - (\phi + r)\psi(1-\theta)]N^*} \quad (19)$$

Since all model parameters are non-negative and from (15), we have

$$K_2 = \frac{\beta S^*}{N^*} + \frac{\psi(1-\theta)H^*}{I^*}$$

$$K_3 = \frac{(\phi + r)I^*}{H^*}$$

$$K_2 K_3 = \left(\frac{\beta S^*}{N^*} + \frac{\psi(1-\theta)H^*}{I^*}\right)\left(\frac{(\phi + r)I^*}{H^*}\right)$$

$$= \frac{\beta S^*(\phi + r)I^*}{N^* H^*} + \frac{(\phi + r)\psi(1-\theta)H^* I^*}{H^* I^*}$$

$$K_2 K_3 = \frac{\beta S^* I^*(\phi + r)}{N^* H^*} + (\phi + r)\psi(1-\theta)$$

$$K_2 K_3 > (\phi + r)\psi(1-\theta)$$

It follows that when$R_0 \leq 1, L' \leq 0$, the equality is zero holds when R_0 =1 and I=0.

Therefore, the largest compact invariant set $\{(S, I, H, R) \in L' = 0\}$ is the singleton $\{E_0\}$. Hence, by the LaSalle invariance principle, E_0 is overall globally asymptotically stable and hencethe proof is complete.

The above theorem shows that infection will be under control regardless of the initial profile of the sub-population in the community if R_0 can be brought down to a level less than unity.

3.3 Existence of Disease-Endemic Equilibrium

At the disease endemic equilibrium we have persistence of infection. Thus at least one of the infected class is greater than zero. In order to find the positive endemic equilibrium of the system (5), denoted by

$$E^* = (S^{**}, \mathrm{I}^{**}, H^{**}, \mathrm{R}^{**}) \quad (20)$$

The equations in the system (5) are solved as explained in Gumel (2007) in terms of the associated force of infection at steady-state, given by

$$\lambda^{**} = \frac{\beta I^{**}}{N^{**}} \quad (21)$$

$$A - \frac{\beta I^{**}}{N^{**}} S^{**} - K_1 S^{**} = 0$$

$$\Rightarrow S^{**} = \frac{A}{K_1 + \lambda^{**}}$$

$$\lambda^{**} S^{**} + \psi(1-\theta) H^{**} - K_2 I^{**} = 0$$

$$\frac{\lambda^{**} A}{K_1 + \lambda^{**}} + \frac{(\phi + r)\psi(1-\theta)\mathrm{I}^{**}}{K_3} - K_2 I^{**} = 0$$

$$\frac{\lambda^{**} A}{K_1 + \lambda^{**}} = \left(K_2 - \frac{(\phi + r)\psi(1-\theta)}{K_3} \right) I^{**}$$

$$\frac{\lambda^{**} A}{K_1 + \lambda^{**}} = \left(\frac{K_2 K_3 - (\phi + r)\psi(1-\theta)}{K_3} \right) I^{**}$$

$$I^{**} = \frac{\lambda^{**} A K_3}{(K_1 + \lambda^{**})(K_2 K_3 - (\phi + r)\psi(1-\theta)}$$

$$(\phi + r) I^{**} = K_3 H^{**}$$

$$H^{**} = \frac{A(\phi + r)\lambda^{**}}{(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$\mu R^{**} = \theta(S^{**} + I^{**} + \psi H^{**}) - r I^{**}$$

$$\mu R^{**} = \theta\{\frac{A}{K_1 + \lambda^{**}} + \frac{\lambda^{**} A K_3}{(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$+ \frac{\psi A(\phi + r)\lambda^{**}}{(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}\} - \frac{\lambda^{**} A K_3 r}{(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$R^{**} = \frac{A\theta[K_2 K_3 - (\phi + r)\psi(1-\theta)] + \{A\theta[K_3 - (\phi + r)\psi] - A r K_3\}\lambda^{**}}{\mu(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

Solving the equations of the model (5) at steady-state gives

$$S^{**} = \frac{A}{K_1 + \lambda^{**}}$$

$$I^{**} = \frac{\lambda^{**} A K_3}{(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$H^{**} = \frac{\lambda^{**} A(\phi + r)}{(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$R^{**} = \frac{A\theta[K_2 K_3 - (\phi + r)\psi(1-\theta)] + \{A\theta[K_3 - (\phi + r)\psi] - A r K_3\}\lambda^{**}}{\mu(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

(22)

Using the second equation of system (22) in (21) and simplifying it gives

$$I^{**} = \frac{\beta K_3 A}{N^{**}(K_1 + \lambda^{**})[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$K_1 + \lambda^{**} = \frac{\beta K_3 A}{N^{**}[K_2 K_3 - (\phi + r)\psi(1-\theta)]}$$

$$\lambda^{**} = \frac{\beta K_3 A}{N^{**}[K_2 K_3 - (\phi + r)\psi(1-\theta)]} - K_1$$

$$\lambda^{**} = K_1 \left(\frac{\beta K_3}{\mathrm{K}_1[K_2 K_3 - (\phi + r)\psi(1-\theta)]\mathrm{N}^{**}} - 1 \right)$$

i.e., $\lambda^{**} = K_1(R_0 - 1)$ (23)

Since all model parameters are assumed and non-negative with $\mu > 0$, it follows that $\lambda^{**} > 0$, whenever $R_0 > 1$. The components of E^* are then determined by substituting (23) into (22), given by:

$$S^{**} = \frac{A}{K_1 + K_1(R_0 - 1)} = \frac{A}{K_1 R_0} = \frac{A}{K_1 R_0}$$

$$I^{**} = \frac{(R_0 - 1)AK_3}{R_0[K_2K_3 - (\phi + r)\psi(1-\theta)]}$$

$$H^{**} = \frac{A(\phi + r)(R_0 - 1)}{R_0[K_2K_3 - (\phi + r)\psi(1-\theta)]} \quad (24)$$

$$R^{**} = \frac{(A\theta\{[K_2K_3 - (\phi + r)\psi(1-\theta)] + [K_3 - (\phi + r)\psi]\} - ArK_3)(R_0 - 1)}{\mu R_0[K_2K_3 - (\phi + r)\psi(1-\theta)]}$$

Noting that $R_0 < 1$ implies that the force of infection at steady state (λ^{**}) negative (which is biologically meaningless). Hence the model has no positive equilibria in this case. Thus, we established the following result.

3.4 Local Stability of Disease Endemic Equilibrium

Similarly, as in local stability of disease–free equilibrium, we used the Jacobian stability approach to prove the stability of the disease endemic equilibrium state. Noting the relation R=*N-(S+I+H)*, the Jacobian matrix of system (5) at E^* is given by

$$H(E^*) = \begin{pmatrix} -\left(\frac{\beta I^{**}}{N^{**}} + K_1\right) & -\frac{\beta S^{**}}{N^{**}} & 0 \\ \frac{\beta I^{**}}{N^{**}} & -\left(K_2 - \frac{\beta S^{**}}{N^{**}}\right) & \psi(1-\theta) \\ 0 & \phi + r & -K_3 \end{pmatrix} \quad (25)$$

From (5) at E^*, we have

$$A = \frac{\beta I^{**} S^{**}}{N^{**}} + K_1 S^{**}$$

$$K_2 = \frac{\beta S^{**}}{N^{**}} + \frac{\psi(1-\theta)H^{**}}{I^{**}}$$

$$K_3 = \frac{(\phi + r)I^{**}}{H^{**}}$$

$$\mu = \frac{\theta(S^{**} + I^{**} + \psi H^{**}) - rI^{**}}{R^{**}} \quad (26)$$

Using elementary row operation (25) becomes:

$$H(E^*) = \begin{pmatrix} -\left(\frac{\beta I^{**} + K_1 N^{**}}{N^{**}}\right) & -\frac{\beta S^{**}}{N^{**}} & 0 \\ 0 & -M & \psi(1-\theta) \\ 0 & 0 & -K_3 + \frac{(\phi + r)\psi(1-\theta)}{M} \end{pmatrix} \quad (27)$$

where $M = \left(K_2 - \frac{\beta S^{**}}{N^{**}} + \frac{\beta^2 S^{**} I^{**}}{(\beta I^{**} K_1 N^{**})N^{**}}\right)$ (28)

Thus, clearly the eigen values are:

$$\lambda_1 = -\left(\frac{\beta I^{**} + K_1 N^{**}}{N^{**}}\right) < 0$$

Since from (26) $K_2 > \frac{\beta S^{**}}{N^{**}}$ and

$$\lambda_3 = -\left(K_3 - \frac{(\phi + r)\psi(1-\theta)}{M}\right) \quad (29)$$

Now for λ_3 to be negative, we must have

$$\frac{-K_3 M + (\phi + r)\psi(1-\theta)}{M} < 0$$

i.e., $K_3\left\{K_2 - \frac{\beta S^{**}}{N^{**}} + \frac{\beta^2 S^{**} I^{**}}{(\beta I^{**} + K_1 N^{**})}\right\} > (\phi + r)\psi(1-\theta)$

Simplifying this, we obtain $\beta I^{**} > 0$

Substituting (24) and simplifying, we obtain $(R_0 - 1) > 0$.

Thus $\lambda_3 < 0$. If $R_0 > 1$ implies that, all the eigen values has negative real parts.

4. Conclusion

A mathematical model with constant recruitment rate and standard incidence for the transmission dynamics of infection as a disease was proposed. The basic reproduction number (R_0)was obtained and the analysis revealed that for $R_0 \leq 1$, the disease-free equilibrium is globally asymptotically stable. Although, the illicit and secretive nature of infection can never allow for its total eradication, but it can be curbed (reduced) to a bearable level. And for whatever reason if $R_0 > 1$ the disease-free equilibrium point is unstable and the endemic equilibrium emerges.

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