Uniform Asymptotic Stability of Sir Model with Distributed Delay: A Case Study of Nipha Virus

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Article Info	Abstract
Page Number: 8547-8554	This paper investigates the dynamical system of Susceptible, Infected,
Publication Issue:	Recovered (SIR) cases of Nipha Virus transmission disease. The system of
Vol. 71 No. 4 (2022)	equation incorporates the compartment SIR model with distributed delay
	from the range [0,h]. The qualitative analysis such as the expected
	existence and unique equilibrium points were performed. Uniform
	boundedness of the solved equilibrium points was examined by using
	appropriate conditions. To track the local stability of the virus free
	equilibrium and persist of the endemic equilibrium using basic
	reproduction number R_0 . If R_0 less than unity there exist a disease free
	equilibrium point which is locally asymptotically stable whereas if R_0
	greater than unity the given endemic equilibrium point is locally
	asymptotically stable. The linear matrix inequality (LMI) approach is used
	to find the uniform asymptotic stability for the constructed model. The
Article History	support of LMI Matlab toolbox, the feasibility of the solution was
Article Received: 15 September 2022	obtained. Finally the Graphical numerical simulations are investigate the
Revised: 25 October 2022	spread of the influence of the parameter through MATLAB.
Accepted: 14 November 2022	Key words: Nipha Virus, SIR model, Lyapunov function, Delay,
Publication: 21 December 2022	Boundeness, and Stability analysis.

1. Introduction

Mathematical Modeling is an emerging trend in science and engineering fields. Mathematical model help us to investigate the dynamics of the communication of infectious disease and give the appropriate strategies to control the disease. Also it is great concern of human kind since it has enormous impact of infectious disease on human and animal. The last two decades, various mathematical model have been analyzed and to study the dynamics, stability and controllability of infectious disease such as Malaria, Dengu, Chikenkunia, Ebola and Zoonotic infectious disease such as Covid 19,Nipha, brucellosis and Rabies etc. In particular the diseases were studied in both deterministic and stochastic models. Kermack and Mckendrik constructed basic and simplest model of SIR which states the theoretical total number of population infected by the disease over the time of closed population. Some basic epidemic models are SI, SIR, SEIR, which developed many mathematician and biologist [1,2]. Recently, many authors attention focus on to study the dynamical model of SI, SIR and

SEIR with time varying delay in various range. Hethcote et el. have discussed an SIS compartment model including constant delay [8]. Beretta has investigated the stability (global) of the epidemic model of SIR type for the necessary conditions with distributed delay [3]. The effect of dynamical system of the stability of the endemic point with time delay has been examined by Song and cheng [7]. The main aim in this paper is to predict and analysis the SIR infectious disease by using dynamic mathematical model. Stability of prescribed equilibrium point studied by constructing suitable Lyapunov Krovski function and through linear matrix inequality approach [6]. This work prepared as follows, section 1, gives the mathematical model of an SIR epidemic model with delay in distributed type [8]. Section 2, devoted steady states, Basic reproduction number and equilibrium point. In section 3, establishes the positivity and boundedness for the model. Section 4 analyzes the stability of the solved equilibrium point. Section 5, examined a case study of the numerical simulation via MATLAB.

2. Dynamical System with Delay

This section carried out the general form of the traditional SIR model with distributed delay. Based on the compartmental of epidemiological situations, total number of population is divided into 3 compartments "Susceptible (S(t)), Infected (I(t)), Recovered (R(t))" [10].

$$\dot{S}(t) = a - d_1 S(t) - bS(t) \int_0^h I(t - s) dk(s)$$
$$\dot{I}(t) = bS(t) \int_0^h I(t - s) dk(s) - (d_2 + c)I(t)$$

(1.1)

$$\dot{R}(t) = cI(t) - d_3R(t)$$

The parameters are:

a- natural birth ratio of the total population

b- transition rate, the No. of people infected from each infected person with the infectious period of time delay.

c- recovered rate, the infected may recovered and get full immunity.

 d_1 - the natural death rate of susceptible,

 d_2 – the natural death rate of infected and

 d_3 – the death ratio of recovered population .

h- maximum period of time taken for the infectious transmission,

s- delay parameter.

The initial condition for the system $\varphi \in [-h, 0]$, by $S(\varphi) = \theta_1(\varphi), I(\varphi) = \theta_2(\varphi), R(\varphi) = \theta_3(\varphi)$ with $\theta = (\theta_1, \theta_2, \theta_3) \in C([-h, 0], R^+)$ is the nonnegative Banach space from [-h,0] to R^+ and is defined based on standard theory of functional differential equation. The death

rates d_1, d_2, d_3 are positive constant and assume that $d_1 \le \min\{d_1, d_2\}$. Without loss of generality, let us considered that,

$$\int_0^h dk(s) = 1.$$
(1.2)

Steady States and Equilibrium points

Let us take the total population as N(t) = S(t) + I(t) + R(t). Assume the following condition,

$$\lim_{t \to \infty} I(t) = \lim_{t \to \infty} I(t-s) = I^*(t)$$
(2.1)

Equation (1.1) has a virus free equilibrium point at the steady state (2.1) we have

$$C_0 = \left(\frac{a}{d_1}, 0, 0\right)$$

Equation (1.1) has a endemic equilibrium point,

$$S^* = \frac{d_2 + c}{b},$$
 $I^* = \frac{a - d_1 S^*}{bS^*},$ $R^* = \frac{c(a - d_1 S^*)}{d_2 bS^*}$

(2.2)

Basic Reproduction Number (BRN):

The BRN rate is a expected number of secondary infection directly caused by the completely infected population to susceptible population. The use of Next Generating Matrix (NGM) the necessary BRN is obtain[4]. The dynamic equation in the form state is as follows,

$$X' = \frac{dX}{dt} = F(X) - V(X)$$

(2.3)

where $F(X) = {\binom{bS^*I^*}{0}}, V(X) = {\binom{-(d_2 + c)I^*}{-d_1S^*}}$, The spectral radius is known as basic reproduction number, Therefore

$$R_0 = \rho(FV^{-1}) = \frac{ab}{(d_2 + c)d_1^2}$$

3. Positivity and Boundeness

In this section we study the positivity and uniform boundeness of equation (1.1)

Lemma 3.1: If the existence of the initial conditions for the solution of the equation (1.1) and is positive for $s \ge 0$, then (S(t), I(t), R(t)) are bounded uniformly on [0,h] if $\lim_{n\to\infty} \sup N(t) \le \frac{a}{d_1}$.

Proof:

Consider the R.H.S of equation (1.1) is locally Lipschitzian and completely continuous on the domain C [12]. Hence, from the existence and uniqueness theorem, we observed that the solution of equation (1.1), there exist (S(t), I(t), R(t)) and its unique on [0,h) in some h>0.

Here, for all $t \in [0, h)$, the given S(t) > 0 when S(t) = 0, $\dot{S}(t) = b > 0$ for any $t \in [0, h)$, which contradiction, therefore S(t) is positive. Now show that I(t) > 0 for all $t \in [0, h)$. Let us assume that there exist another time $t_1 \in [0, h)$ such that $I(t_1) = 0$ and I(t) > 0 for all t in $[0, t_1)$. but $I(t_1)$ greater than 0 for all $t_1 \in [0, h)$. Which is contradicts $I(t_1)$ equal to 0. Therefore I(t) > 0 for all $t \in [0, h)$. Similarly R(t)>0 for all $t \in [0, h)$.

This implies that, $\dot{N}(t) = \dot{S}(t) + \dot{I}(t) + \dot{R}(t) \le -d_1 N(t) + a$

$$\lim_{t\to\infty}\sup N(t)\leq \frac{a}{d_1}$$

Therefore (S(t), I(t), R(t)) is uniformly bonded on [0,h).

4. Stability analysis of delay system

Lemma 4.1:

If BRN is less than unity ($R_0 < 1$) then the Virus (disease) free equilibrium $C_0(\frac{a}{d_1}, 0, 0)$ is local asymptotically stable.

Proof:

Consider equation (1.1) at the steady states,

$$\dot{S}(t) = a - d_1 S^*(t) - b S^*(t) I^*(t)$$
$$\dot{I}(t) = b S^*(t) I^*(t) - (d_2 + c) I^*(t)$$
$$\dot{R}(t) = c I^*(t) - d_3 R^*(t)$$

The Jacobian matrix is given for the given equilibrium point is follows,

$$J[x(t)]_{C_0} = \begin{bmatrix} -d_1 & -\frac{ba}{-d_1} & 0\\ 0 & \frac{ba}{d_1 - d_2 + c} & 0\\ 0 & c & -d_3 \end{bmatrix}$$

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The eigen values of the Jacobian matrix, $\lambda_1 = -d_1$, $\lambda_2 = -d_3$, $\lambda_3 = \frac{ab}{d_1} - d_2 + c$. As per Ruth Hurwitz criteria for the stability all eigen values must be negative real values, here λ_1 and λ_2 are negative. So it is necessary to prove λ_3 should be negative. The eigen value is negative only if $\frac{ab}{d_1} - d_2 + c < 0$, that is $R_0 < 1$. Therefore, the condition is true and hence it is locally asymptotically stable for the given system (1.1). Also if $S_0 < S^*$ the system is locally asymptotically stable.

Lemma 4.2

If the BRN is greater than unity $(R_0 > 1)$ then the endemic equilibrium (2.2) is locally asymptotically stable, if not the solved equilibrium is unstable.

Proof:

The Jacobian matrix at the given endemic point,

$$J[x(t)]_{C_0} = \begin{bmatrix} -d_1 - (\frac{b - d_1 S^*}{S^*}) & d_2 + c & 0\\ \frac{b - d_1 S^*}{S^*} & 0 & 0\\ 0 & c & -d_3 \end{bmatrix}$$

The characteristic equation for the given system is,

$$(-\lambda - d_3)\left(-d - \left(\frac{a - d_1 S^*}{S^*}\right) - \lambda\right)(-\lambda) - (d_2 + c)\left(\frac{b - d_1}{S^*}\right) = 0$$

Solving this, we get $\lambda^2 + a_1\lambda + a_2 = 0$. Where $a_1 = \frac{ab}{d_2+C}$ and $a_2 = ab - d_1(d_2 + \lambda)$. For locally asymptotically stable it is necessary $a_1 > 0$ and $a_2 > 0$. Here $a_2 > 0$ only if $R_0 > 1$. Hence the proof is complete.

Uniform asymptotically Stable:

Definition: 4.1 [9] Shur Complements: It is used to transforming nonlinear inequalities to convex type into LMI $\begin{bmatrix} A(x) & B(x) \\ * & C(x) \end{bmatrix} < 0$, where $A(x) = A(x)^T$, $C(x) = C(x)^T$ and B(x)depends on x, equivalent to C(x) < 0, $A(x) - B(x)C(x)^{-1}B(x)^T < 0$.

Definition: 4.2: [9] If there exists a continuous differentiable function for the system of equation is uniformly stable that is, V(x(t)), V(0)=0 such that, $a(||x(t)||) \le V(x(t)) \le$ b(||x(t)||) and $\dot{V}(x(t)) \leq -c(||x(t)||)$, with the initial a(0) = b(0) = c(0) where a, b and c are continuous non decreasing function (scalar). If c(r) > 0 for r > 0 then it is uniform asymptotically stable.

Substitute the variables $x_1(t) = S(t) - S^*$, $x_2(t) = I(t) - I^*$, $x_1(t) = R(t) - R^*$ in equation (1.1) then the transformed equations are,

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$$\dot{x}_1(t) = (-a(S^*)^{-1})x_1(t) - bS^*J(x_{2t}) - bx_1(t)J(x_{2t})$$
$$\dot{x}_2(t) = bI^*x_1(t) - (d_2 + c)x_2(t) + bS^*J(x_{2t}) + bx_1(t)J(x_{2t})$$
$$\dot{x}_3(t) = cx_2(t) - d_3x_3(t)$$

For proving the zero solution for nonlinear system, it is enough to prove uniform asymptotic stability of zero solution of linear system [8].

The transformed system in matrix form is,

$$\dot{x}(t) = Ax(t) + B \int_0^h y(t-s)dk(s)$$

(5.1)

Where
$$A = \begin{bmatrix} -d_1 & 0 & 0 \\ bI^* & -(d_2 + c) & 0 \\ 0 & c & -d_3 \end{bmatrix}$$
, $B = \begin{bmatrix} 0 & -bS^* & 0 \\ 0 & bS^* & 0 \\ 0 & 0 & 0 \end{bmatrix}$

Lemma: 4.3

The (S^*, I^*, R^*) uniformly asymptotical stability for any delay satisfying $h \ge 0$ if the existence of a matrix P > 0 and R > 0 such that the following inequalities hold,

$$\phi_0 = \begin{bmatrix} PA + A^T P & PB \\ * & -R \end{bmatrix} < 0.$$

Proof: Consider the following Lyapunov krasovskii function (LKF) for the system (5.1),

$$V(t) = x^{T}(t)Px(t) + \int_{0}^{h} \int_{t-s}^{t} x^{T}(\tau)Rx(\tau)dk(s)$$

Take a derivative,

$$\dot{V}(t) = 2x^{T}(t)P(Ax(t) + BJ(x_{t}))x(t) + x^{T}(t)Rx(t) - \int_{0}^{h} x^{T}(t-s)Rx(t-s)dk(s)$$

$$\leq x^{T}(t)(PA + A^{T}P)x(t) + 2x'(t)PBJ(x_{t}) + x^{T}(t)R(t)x(t) - J'(x_{t})RJ'(x_{t})$$

Since $J'(x_t)RJ(x_t) \le \int_0^\infty x'(t-s)Rx(t-s)dk(s)$

$$\leq x^{T}(t)(PA + A^{T}P + R)x(t) + 2x^{T}(t)PBJ(x_{t}) - J^{T}(x_{t})RJ(x_{t})$$

From the schur complements and uniform stability condition we obtain,

$$\dot{V}(t) \le Z^{T}(t) \begin{bmatrix} PA + A'P & PB \\ * & -R \end{bmatrix} Z(t)$$

where, $Z(t) = (x(t), J^T(x_t))^T$, and the matrix is less than zero. So the constructed LK function satisfies the condition of uniform asymptotic condition. Therefore the system of zero solution is uniformly asymptotically stable. Hence the proof.

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Numerical Simulation:

This section studies the numerical simulation for the case study of Nipha virus using real time data, so that our model will be more realistic. Nipha virus is a new class and member of Henipavirus. It is an emerging Zoonotic type of virus, that is spread from animal to human and then remains spread from human to human. Now we take the following data is plotted in the graph using MATLAB.

Case 1: For a = 0.1, b = 0.75, c = 0.002, h = 10 d_1 = 0.02, d_2 = 0.01, d_3 =0.03 in (1.1), we get the figure 1 which shows that at this transition rate the disease start from 12th week onwards and peak at 27th week and recovered will increase.

Case 2: For a = 0.1, b = 0.5, c = 0.002, h = 10 d_1 =0.02, d_2 =0.01, d_3 =0.03 in (1.1), we get figure 2 which show that at this transition rate the recovered start form 15th week onwards. So avoiding conduct between person to person, the disease will reduced.

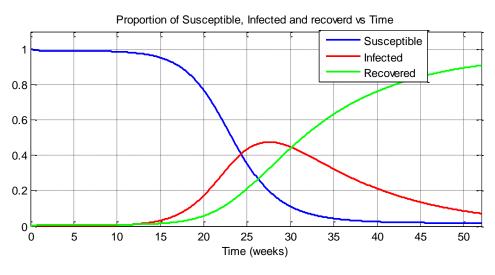


Figure	(a)
	···/

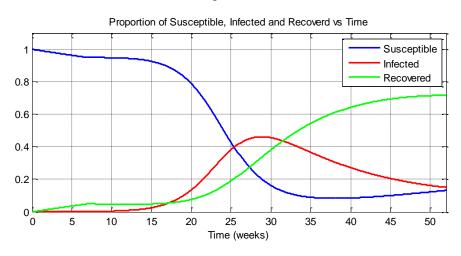


Figure (b)

5. Conclusion

In this paper, the system of equation of SIR model with distributed delay from the range [0,h] were carried out. The persistence of uniqueness and existence of the equilibrium points for the proposed model has been proved. The local and uniform asymptotic stability for the virus free equilibrium and uniqueness of the endemic equilibrium was proved. If the BRN is less than unity then the virus free equilibrium point is locally asymptotically stable, greater than 1 then the endemic equilibrium is locally asymptotically stable were studied. By using the Lyapunov Krosovskii function approach, the uniform asymptotic stability was found for the proposed model. The Matlab LMI Toolbox helps us to get the feasibility of the matrix. Finally the numerical simulation is illustrated through MATLAB.

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