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Infectious Disease Modelling In Leishmaniasis

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Abstract

We show how models detach from their implementation contexts through their connections with global narratives , and how sociological and anthropological research can help to locate models differently. In this paper we propose SEIR mathematical model to obtain stability analysis for system of non-linear differential equations. Leishmanias is disease is taken as an example. The disease free equilibrium points and pandemic equilibrium points were obtained. Our aim is to do the stability analysis for the basic reproduction number.

Keywords: Non-linear differential equation; Equilibriums points; Basic reproduction number; locally asymptotically stable.

1. Introduction

An irresistible sickness which is brought about by Leishmania parasite is called as Leishmaniasis. It also popularly known by names such as “kala azar”, “white leprosy”, “black fever” [1]. More than 90 sand-fly species are known to communicate Leishmania parasites.. An estimated 700000 to 1 million new cases occur annually [2]. Leishmaniasis is brought about by a contamination with Leishmania parasites, which are spread by the chomp of tainted female Phlebotomine sand-flies. There are three sorts of Leishmaniasis to be specific cutaneous Leshmaniasis, mucocutaneous Leishmaniaisis and visceral Leishmaniasis. This disease affects both animals and human-being. Dogs, foxes, rodents, coyotes are the animal species which are more influenced by this disease whereas cats and horse are occasionally influenced. The parasite causing this contamination is related with tropical and mild environment. This disease is mostly found in countries like Asia, Africa, South America, Central America and Middle East. It usually happens in nations with conditions like starvation, hunger absence of monetary assets, huge relocation of individuals brought about by urbanization, war, ecological changes.

Leishmaniasis is found to spread from one individual to another because of blood bonding or when shared needles are being utilized. Transmission occurs from animal to sand-flies to humans, it may also be from humans to sand-flies to leishmaniasis affect the similar cells of the immune system [Fig.1]. In the territories of Ethiopia, it is assessed however

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numerous as 35% of individuals with debilitated insusceptible frameworks may be at expanded danger of this condition [1].

Figure: 1 Disease Transmission

The indications of this illness may differ contingent upon the sort of Leishmaniasis being contaminated. There is no immunization accessible for this infection. To consider the irresistible illness numerically Kermack and McKendrick formed SIR model [3].Mathematical modeling and analysis has been at the center of infectious disease epidemiology since the classical works of Ross [4] and Macdonald [5]. There are many versions of SEIR model and treatment for the diseases can be found mathematically, for instance, in Keeling and Rohani[6], Hethcote[7],and Diekman at el.[8] among others. The model incorporated a single vector population, a human host population and a multiple animal populations that serve as reservoirs [9]. In Roy et al paper,[10] a model which focuses on human host and sand-flies is provided with single delay incorporated in human host.

The main objective of this paper is stability analysis. This paper includes 4 sections. Section 1: Introduction, Section: 2 Preliminaries, Section 3: Mathematical modelling, Section 4: Stability Analysis, Section 5: Conclusion.

2. Preliminaries:

(i) Non-linear systems:

The first-order scalar ordinary differential equation of the form $u_t = \frac{du}{dt}$ is the time-derivative , $u_t = f(u,t)$ where

$$U = \begin{bmatrix} u_1 \\ u_2 \\ . \\ . \\ . \\ u_d \end{bmatrix} \quad \text{and} \quad f(u,t) = \begin{bmatrix} f_1(u,t) \\ f_2(u,t) \\ . \\ . \\ . \\ f_d(u,t) \end{bmatrix}$$

Are now vectors with d components. We denote by u_t the component wise time derivative; that is, $u_r = f(u,t)$ can be written out explicitly

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$$u_t = \begin{bmatrix} \frac{du_1}{dt} \\ \frac{du_2}{dt} \\ . \\ . \\ . \\ \frac{du_d}{dt} \end{bmatrix} = \begin{bmatrix} f_1(u,t) \\ f_2(u,t) \\ . \\ . \\ . \\ f_d(u,t) \end{bmatrix}$$

(ii) Basic reproduction number:

Basic reproduction number is defined as the average number of secondary infectious caused by a single infectious individual during the entire infectious lifetime[11][12].The number is denoted by $R_{0.}$

3. Mathematical Model

The majority of the models are compartmental models where the population is partitioned into numerous classes [13].In this mathematical model the authors[14] considered four different compartments which includes the healthy or susceptible population (S(t)) , Exposed population (E(t)), the infected population (I(t)) and the removed population (R(t)) (either due to Leishmaniasis or natural death) at the time 't'. Figure 2 depicts the transmission cycle of the disease.

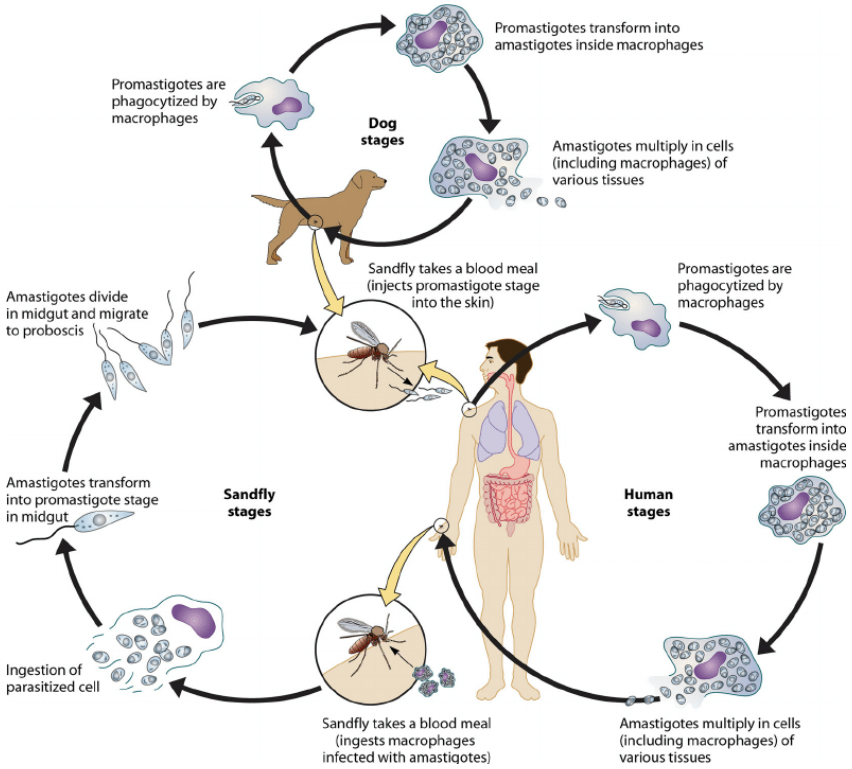

Fig. 2: Transmission cycle

In the SEIR model, it has been described that the susceptible population becomes exposed to the disease when the female sand-fly bites the person. The person gets infected if person has been bitten by an infected sand-fly (Leishmaniasis parasite) and becomes an infected person. The person may undergo few treatments after the diagnosis of the disease or may die.

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The following is the system of four differential equations which describes the proposed model.

$$\frac{dS}{dt} = \alpha - KI(t)S(t)\,(1+a\,I(t)) - d_0\,S(t)$$

$$\frac{dE}{dt} = KI(t)\,S(t)\,(1+a\,I(t)) - (d_0+\kappa)\,E(t) \qquad (1)$$

$$\frac{dI}{dt} = \beta + aE(t) - (d + d_0 + b)I(t)$$

$$\frac{dR}{dt} = b\,I(t) - d_0\,R(t)$$

NOTATION	DESCRIPTION
α	Population whose Leishmaniasis test is found to be negative
d_0	Natural death
β	Population whose Leishmaniasis test is found to be positive
d	Death due to Leishmaniasis
K	Proportionality constant
κ	Infected rate
a	Rate at which recovered individuals lose immunity
b	Recovered rate

TABLE 1: Description of parameters

4. Stability Analysis

In this section, we do the stability analysis. To perform the stability analysis, we require the equilibrium points.

4. i. Disease free equilibrium:

The disease free equilibrium is obtained as $E_0 = (\frac{\alpha}{d0},0,0,0)$

4. ii. Basic Reproduction Number:

Theorem 1:

The basic reproduction number is $R_0 = \frac{aK\alpha}{d_0\ (d_0+\kappa)(d+d_0+B)}$

Proof:

To find R_0, let us consider second and third equation of (1)

(i.e) $$\frac{dE}{dt} = KI(t)\,S(t)\,(1+a\,I(t)) - (d_0+\kappa)\,E(t)$$

$$\frac{dI}{dt} = \beta + aE(t) - (d + d_0 + b)I(t)$$

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Let us consider X= $\begin{bmatrix} E \\ I \end{bmatrix}$ then

$$\frac{dX}{dt} = \begin{bmatrix} KIS(1 + aI - (d_0 + \kappa)E \\ \beta + aE - (d + d_0 + b)I \end{bmatrix}$$

$$F = \begin{bmatrix} KIS(1 + aI) \\ 0 \end{bmatrix} \qquad V = \begin{bmatrix} (d_0 + \kappa)E \\ -(\beta + aE) + (d + d_0 + b)I \end{bmatrix}$$

To obtain the next generation matrix [15] we need to take Jacobian for both F and V. Thus, we get the following matrices.

$$F = \mathcal{F} = \begin{bmatrix} 0 & KS + 2aKSI \\ 0 & 0 \end{bmatrix}$$

$$V = \upsilon = \begin{bmatrix} (d_0 + \kappa) & 0 \\ -a & (d + d_0 + b) \end{bmatrix}$$

Therefore, the next generation matrix is

$$\mathcal{F}\upsilon^{-1} = \begin{bmatrix} \frac{a(KS+2aKSI)}{(d+d_0+b)(d_0+\kappa)} & \frac{KS+2aKSI}{d+d_0+b} \\ 0 & 0 \end{bmatrix}$$

At disease free equilibrium point $E_0 = (\frac{\alpha}{d_0},0,0,0)$

$$\rho\,(\mathcal{F}\upsilon^{-1}) = \begin{bmatrix} \frac{aK\alpha}{d_0(d_0+\kappa)(d+d_0+b)} & \frac{a(K+2aKSI)}{d_0(d+d_0+b)} \\ 0 & 0 \end{bmatrix}$$

Thus, we obtain the basic reproduction number as

$$R_0 = \frac{aK\alpha}{d_0(d_0+\kappa)(d+d_0+b)}$$

Theorem: 2

The pandemic free equilibrium point of (1) is locally asymptotically stable as $R_0 < 1$.

Proof:

Let us consider (1) and assume the right hand side of the equations to be Ω_1 , Ω_2 , Ω_3 , Ω_4 respectively. The Jacobian matrix of (1) is as follows,

$$J = \begin{bmatrix} \frac{\partial}{\partial S}\Omega 1 & \frac{\partial}{\partial E}\Omega 1 & \frac{\partial}{\partial I}\Omega 1 & \frac{\partial}{\partial R}\Omega 1 \\ \frac{\partial}{\partial S}\Omega 2 & \frac{\partial}{\partial E}\Omega 2 & \frac{\partial}{\partial I}\Omega 2 & \frac{\partial}{\partial R}\Omega 2 \\ \frac{\partial}{\partial S}\Omega 3 & \frac{\partial}{\partial E}\Omega 3 & \frac{\partial}{\partial I}\Omega 3 & \frac{\partial}{\partial R}\Omega 3 \\ \frac{\partial}{\partial S}\Omega 4 & \frac{\partial}{\partial E}\Omega 4 & \frac{\partial}{\partial I}\Omega 4 & \frac{\partial}{\partial R}\Omega 4 \end{bmatrix}$$

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$$J = \begin{bmatrix} -d_0 & 0 & \frac{-k\alpha}{d_0} & 0 \\ 0 & -(d_0+\kappa) & \frac{k\alpha}{d_0} & 0 \\ 0 & a & -(d+d_0+b) & 0 \\ 0 & 0 & b & -d_0 \end{bmatrix}$$

The characteristic equation can be obtained as,

$$\text{Det } (J - \lambda) = \begin{vmatrix} -d_0-\lambda & 0 & \frac{-K\alpha}{d_0} & 0 \\ 0 & -(d_0+\kappa)-\lambda & \frac{K\alpha}{d_0} & 0 \\ 0 & a & -(d+d_0+b)-\lambda & 0 \\ 0 & 0 & b & -d_0-\lambda \end{vmatrix} = 0$$

Thus, all the Eigen values are negative and the system of equations is locally asymptotically stable as $R_0 < 1$.

5. Conclusion:

A compartmental SEIR model for the Leishmaniasis disease is studied. The next generation matrix method was used to obtain basic reproduction number. We proved that the stability of the equilibrium points depends on the nature of the basic reproduction number.

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