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THE GENERALIZATION OF AN N-PATCH MODEL FOR LEISHMANIASIS

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Abstract. Leishmaniasis is a vector borne disease, which is caused by a protozoan parasite. Infected female sandflies *(Phlebotomine sp.)* are responsible for such disease transmission. People can carry some species of Leishmania for long periods and the incubation period for Leishmaniasis may be few weeks or several months. Migration depends on host immunological status also. Leishmaniasis is endemic globally in ninety eight countries. Spread of the disease is intensely dependent on migration of the disease among human and vector between various regions or countries. Here, we formulate an n-patch mathematical model (such patches can be some states, regions or countries) considering each patch have susceptible, infected human as well as susceptible and infected vector population. We have derived basic reproduction ratio for each patch as well as the general basic reproduction ratio for the system and shown that there exists a disease-free equilibrium that is locally asymptotically stable. Further, we study the system analytically and numerically when the migration between each patch of individual class of humans and vector effects the spreading of the disease. We also established the results taking into account for different number of patches for $n = 2$. Our result reveals that the movement of human and vector from each patch to another patch plays an important role for spreading of the disease.

Keywords: vector borne disease; Leishmaniasis; migration, patch; metapopulation; reproduction ratio.

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1. Introduction

Leismaniasis is a well-known tropically occurring vector borne disease spread by Phlebotomine sand flies and are the subject of renewed research interest because of the role of their females as the only proven natural vectors of Leishmania species. The parasitic protozoans that are the causative agents of this Neglected Tropical Disease (NTD), Leishmaniasis as classified by W.H.O. [1] among the listed 17 NTDs. According to the W.H.O guidelines, they are termed "neglected" because they are often hidden and remains concentrated in remote rural areas or urban slums. They are silent as the affected people have little political voices. Leishmaniasis imposes substantial distress, with many causing life-long disability and death, stigma, mental distress, and discrimination, especially among females. Economically such diseases can result in productivity loss, poverty aggravation, high health costs and presents an obstacle to socioeconomic development.

Leishmaniasis is caused by a protozoa parasite from over 20 Leishmania species and is transmitted to humans by the bite of infected female phlebotomine sandflies. Over 90 sandfly species are known to transmit Leishmania parasites. There are 3 main forms of the disease: Visceral leishmaniasis (VL), also known as kala-azar is fatal if left untreated in over 95 % of cases; Cutaneous leishmaniasis (CL) is the most common form of leishmaniasis and causes skin lesions leaving life-long scars and serious disability. Mucocutaneous leishmaniasis leads to partial or total destruction of mucous membranes of the nose, mouth and throat. A consequence of visceral leishmaniasis that appears as macular, papular or nodular rashes generally on the face, arms,trunks and other parts of the body is known as Post-kala-azar dermal leishmaniasis (PKDL). It occurs mainly in East Africa and on the Indian subcontinent. People with PKDL are considered to be a potential source of kala-azar infection. Leishmaniasis is linked to environmental changes such as deforestation, building of dams, irrigation schemes, and urbanization as well as malnutrition, population displacement (Migration), poor housing, a weak immune system and lack of financial resources [2].

The disease is endemic in many regions of Africa, South and Central America, Southern Europe, Asia and the Middle East. Leishmaniasis is endemic in ninety eight countries in the world and about 350 million people are considered at risk. An estimated 14 million people are infected, and each year about two million new cases occur, [3, 4, 5]. The disease contributes significantly to the propagation of poverty, because treatment is expensive and hence either unaffordable or it imposes a substantial economic burden, including loss of wages. Each year, there are some $5,00,000$ cases of visceral leishmaniasis (in Bangladesh, Brazil, India, Nepal and Sudan), with an estimated more than $50,000$ deaths, and $15,00,000$ cases of cutaneous leishmaniasis (in Afghanistan, Algeria, Brazil, Islamic Republic of Iran, Peru, Saudi Arabia and Sudan). The number of cases is increasing, mostly because of gradually more transmission in cities, displacement of populations, exposure of people who are not immune, [6, 7, 8, 9, 10].

There are two distinct life cycle stage of the Leishmania parasite: The mosquito cycle and the mammalian or human cycle. During the blood meal from the mammalian hosts/humans, the sandfly transmits the parasitic protozoans within the immune system of the host transforming them from susceptible to infected hosts. The vector also shares a similar fate during blood meal from a infected mammalian host/ human i.e., they too transforms from susceptible to infected and the process cycles. Further, in zoonotic transmission cycles, animals are reservoirs which maintain and disseminate the Leishmania parasites, [6, 7, 9], (see Figure 1).

Vector borne communicable diseases like Leishmaniasis can be easily transmitted from one region (or one space) to another region (or other spaces). Thus, it is important to consider the effect of vector population dispersal on spread of a disease by host density and migrations among host-vector. It remains equally daunting task to track the arthropod vectors, vertebrate mammalian reservoirs and disease in humans. Such tasks represent distinct challenges for the mapping of disease risk [11]. In case of Leismaniasis, it resembles that the disease risk or incidence is more closely correlated with the abundance of pathogen-infected vectors, rather than with simply presence of vectors, or total abundance of vectors.

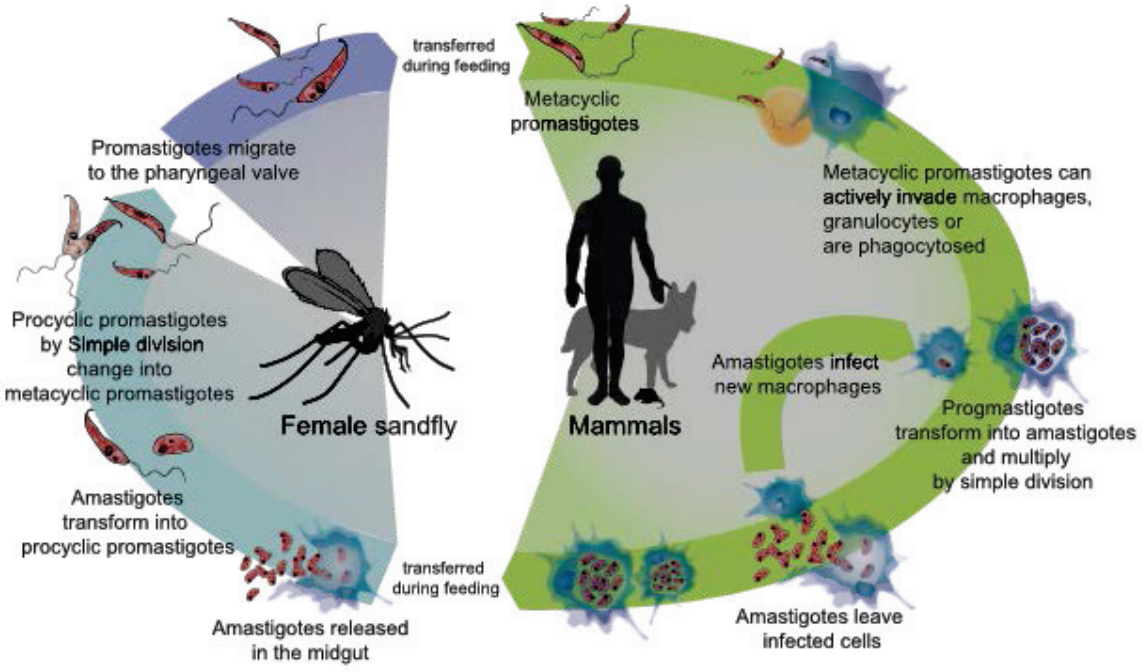

FIGURE 1. Life cycle of Leishmaniasis

Metapopulation was initially originated from ecological concepts notwithstanding any epidemiological interests, however recently its application in disease dynamics is very popular in epidemiologists universally. The concept of metapopulation was introduced by Rich- ard Levin's (an American ecologist) in 1969. The Levin's model is based on a population in which individuals reproduce and die within local patches of the habitat, and their offspring disperse into other patches. Metapopulation dynamics in a general sense are not restricted to systems with population turnover, extinctions and colonizations, but the concept developed is based on Levin's classic metapopulation notion with extinction-prone populations in discrete habitat patches [12, 13]. The basis of the current metapopulation perception is in Levin's visualization of a metapopulation as a population of locally unstable population, inhabiting discrete habitat patches. Effects of inhabited patch area and isolation on migration, colonization and population extinction became integrated with classic metapopulational dynamics from the former two decades. This has generated various models which can be used to predict the movement patterns of individuals, the dynamics of species, and the distributional patterns in multi-species

communities in real fragmented landscapes.

Vector borne communicable diseases like Leishmaniasis can be easily transmitted from one country (or one region) to other countries (or other regions). Thus, it is important to consider the effect of population dispersal on spread of a disease. Hethcote [14] proposed an epidemic model with population dispersal between two patches. Brauer and van den Driessche, [15] proposed a model with migration of infectives. Metapopulation biology is the dynamic consequences of migration among local populations and the conditions of regional persistence of species with unstable local populations, [16]. Effects of habitat patch area and isolation on migration, colonization and population extinction become integrated with classic metapopulation dynamics. This has led to models that can be used to predict the movement patterns of individuals, the dynamics of species, and the distributional patterns in multi-species communities in real fragmented landscapes, [13].

Metapopulation models have been studied a lot, in particular to understand the dynamics of infectious diseases [17, 18]. Many authors have revisited how metapopulation processes operate at various spatial scales (individual level, local, and regional epidemics). More recently, patch models have been applied to Malaria disease indicating clearly that human population movement is an important component to understand the time course of an epidemic situation, [19, 20].

In this present research work, we have tried to understand the complex dynamics of the role of migration patterns on the spread of epidemics in Leishmaniasis among two patches. We enhance the SIS model on metapopulations grounds and we assume that the human (host) migration has a crucial role on the spread of the epidemics among connected local patches and individual patches in absence of migration. Specifically, individuals move freely over the patches but at a rate depending on the population of the departure patch. Based on this we have formulated a four dimensional mathematical model to observe the effect of the migration behavior of the human (host) among the patches with infection and the resultant spread of the epidemics within

the patch network.

The outline of the paper is as follows. In section 2 , we present the migration model and in in section 3 the full epidemiological model for n cities. In section 3, we also analyse the full epidemiological model and compute the Disease free equilibrium, and the general basic reproduction ratio, R_0, and show that the Disease free equilibrium is locally asymptotically stable. In section 4, we study the two patch model and spreading of the disease in that model with migration and without migration. Finally, we validate our theoretical results numerically in two patches model.

2. Formulation of the Human Migration Model

We consider a variant of an Human *SI* model with n patches, each with populations of susceptible and infected human denoted by S_i , I_i for each patch $1 \leq i \leq n$. All the groups migrate from patch i to patch j at the rates m_{ij}^S, m_{ij}^I.
Figure 2 describes the general topological connections among the n-patch model.

We assume that the total population in each patch is denoted by N_i where $N_i = S_i + I_i$ for $1 \leq i \leq n$ and the total population is $N = N_1 + N_2 + ... + N_n$. For each patch i, we consider the following migration model :

$$\begin{aligned} \frac{dS_i}{dt} &= \sum_{j=1}^{n} m_{ij}^S S_j - \sum_{j=1}^{n} m_{ji}^S S_i, \\ \frac{dI_i}{dt} &= \sum_{j=1}^{n} m_{ij}^I I_j - \sum_{j=1}^{n} m_{ji}^I I_i. \end{aligned} \tag{1}$$

Now considering $S = (S_1, S_2, ..., S_n)^T$,
$I = (I_1, I_2, ..., I_n)^T$ we derive that $\frac{dS}{dt} = M^S S, \frac{dI}{dt} = M^I I$ where M^X is given by

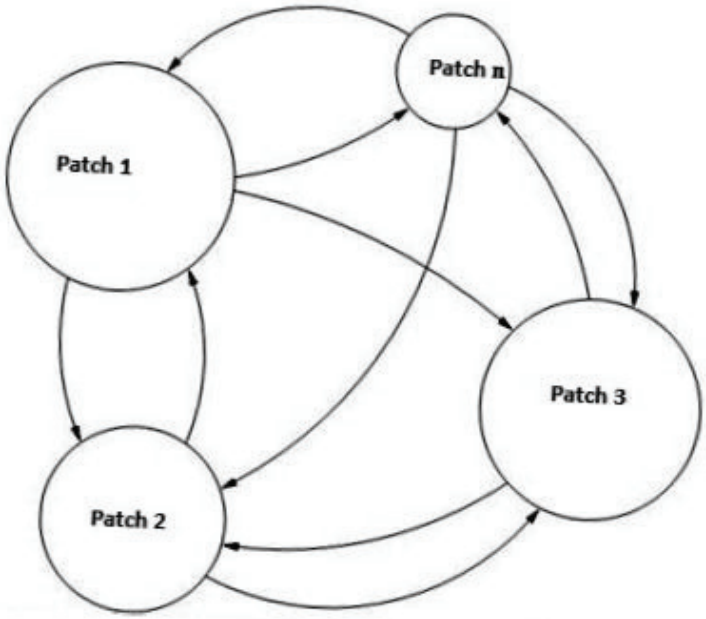

FIGURE 2. Diagram of an n - patch model.

$$M^X = \begin{pmatrix} -\sum_{j=2}^{n} m_{j1}^X & m_{12}^X & \dots & m_{1n}^X \\ m_{21}^X & -\sum_{j=1}^{n} m_{j2}^X & \dots & m_{2n}^X \\ \dots & \dots & \dots & \dots \\ m_{n1}^X & m_{n2}^X & \dots & -\sum_{j=1}^{n-1} m_{jn}^X \end{pmatrix}, \text{ where } X \in \{S, I\}.$$

3. Formulation of Full Mathematical Model

We consider that in each patch i, the human population is constant and equal to N_i and is divided into two compartments S_i, I_i and the vector population is divided into two compartments, susceptible vector (S_i^*) and infected vector (I_i^*). Π_i and d_i^* are the constant birth rate and death rate of vector respectively in each patch i. d_i is the death rate of human population in patch i. As the total human population in each patch is considered as constant, this parameter is also assumed to be the birth rate of humans in the susceptible population. β_i is the infection rate of susceptible human by infected sandfly and β_i^* is the infection rate of susceptible sandfly by infected human. Thus the epidemiological mathematical model in each patch i is given by

$$
\begin{aligned}
\frac{dS_i}{dt} &= d_i N_i - \beta_i S_i I_i^* + \sum_{j=1}^{n} m_{ij}^S S_j - (\sum_{j=1}^{n} m_{ji}^S) S_i - d_i S_i, \\
\frac{dI_i}{dt} &= \beta_i S_i I_i^* + \sum_{j=1}^{n} m_{ij}^I I_j \lambda_j - (\sum_{j=1}^{n} m_{ji}^I) I_i \lambda_i - d_i I_i, \\
\frac{dS_i^*}{dt} &= \Pi_i - \beta_i^* S_i^* I_i - d_i^* S_i^*, \\
\frac{dI_i^*}{dt} &= \beta_i^* S_i^* I_i - d_i^* I_i^*.
\end{aligned} \tag{2}
$$

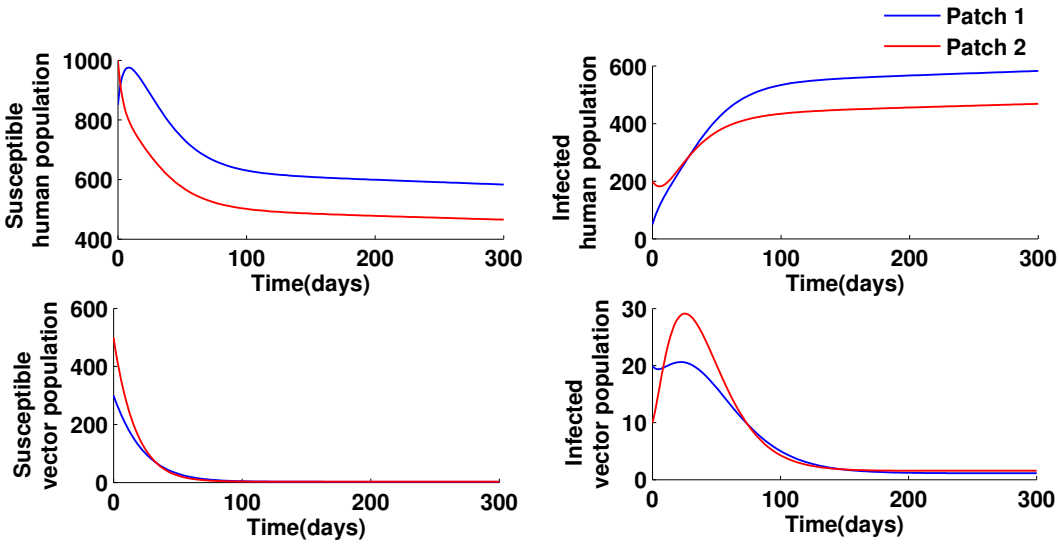

FIGURE 3. Time series solution of 2-patch model is shown with parameter as given in Table 1.

3.1. Mathematical Analysis of the Model

Setting $S = (S_1, S_2, ..., S_n)^T$, $I = (I_1, I_2, ..., I_n)^T$, $S^* = (S_1^*, S_2^*, ..., S_n^*)^T$, $I^* = (I_1^*, I_2^*, ..., I_n^*)^T$ we will assume that the migration rate models for the states S, $M^S = M$. However, Leishmaniasis is a disease which causes irregular fever, swelling of the spleen and liver, skin ulcers so sometimes it is really very difficult for infected people to move from one patch to another patch. Thus, we will assume that $M^I = \Lambda M$, with $\Lambda = diag(\lambda_i)$, where $i \in [0,1]$. λ_i indicates the proportion of infected people that were able to move from patch i to the other patches. After simplification

the model becomes:

$$\begin{aligned}
\frac{dS}{dt} &= dI - diag(\beta_i I_i^*)S + MS, \\
\frac{dI}{dt} &= diag(\beta_i I_i^*)S + \Lambda MI - dI, \\
\frac{dS^*}{dt} &= \Pi - diag(\beta_i^* I_i)S^* - d^* S^*, \\
\frac{dI^*}{dt} &= diag(\beta_i^* I_i)S^* - d^* I^*. \qquad (3)
\end{aligned}$$

where $d = diag(d_i)$, $d^* = diag(d_i^*)$.

3.2. Disease Free Equilibrium

We consider the system (3). At the disease free equilibrium, let $I = 0, I^* = 0$. Then the system (3) gives $E_0 = (S_0, 0, S_0^*, 0) = (N_0, 0, \frac{\Pi}{d^*}, 0)$. To find the basic reproduction ratio, two compartments I and I^* have been considered here. Now we have

$$\begin{aligned}
\frac{dI}{dt} &= diag(\beta_i I_i^*)S + \Lambda MI - dI, \\
\frac{dI^*}{dt} &= diag(\beta_i^* I_i)S^* - d^* I^*. \qquad (4)
\end{aligned}$$

The above equation can be simplified as

$$\begin{aligned}
\frac{dI}{dt} &= diag(\beta_i S_i)I^* - (\Lambda M - D)I, \\
\frac{dI^*}{dt} &= diag(\beta_i^* S_i^*)I^* - d^* I^*. \qquad (5)
\end{aligned}$$

Using the Next Generation Matrix method we have,

$$F = \begin{pmatrix} O_{n,n} & diag(\beta_i S_{0i}) \\ diag(\beta_i^* S_{0i}^*) & O_{n,n} \end{pmatrix}$$

and

$$V = \begin{pmatrix} d - \Lambda M & O_{n,n} \\ O_{n,n} & d^* \end{pmatrix}.$$

Thus the next generation matrix is given by

$$FV^{-1} = \begin{pmatrix} O_{n,n} & a_{12} \\ a_{21} & O_{n,n} \end{pmatrix},$$

where $a_{12} = diag(\beta_i S_{0i})(d^*)^{-1}$

and

$$a_{21} = diag(\beta_i^* S_{0i}^*)(d - \Lambda M)^{-1}.$$

The reproduction ratio

$$R_0 = \rho(FV^{-1}) = \rho(diag(\beta_i \beta_i^*) diag(S_{0i}) diag(d_i^*)^{-1} \times diag(S_{0i}^*)(d - \Lambda M)^{-1}).$$

Here R_0 is the general basic reproduction ratio related to the whole system.

Now,

$$\rho(diag(S_{0i}) diag(d_i^*)^{-1} diag(S_{0i}^*)) \leq \max(\tfrac{S_{0i} S_{0i}^*}{d_i^*}) \rho(I_n),$$

where I_n is the identity matrix of order n and $\rho(I_n) = 1$.

Thus we have,

$$\begin{aligned} & \rho(FV^{-1}) \\ & = \rho(diag(\beta_i \beta_i^*) diag(S_{0i}) diag(d_i^*)^{-1} \times \\ & diag(S_{0i}^*)(d - \Lambda M)^{-1}) \\ & \leq \max(\frac{\beta_i \beta_i^* S_{0i} S_{0i}^*}{d_i^*}) \rho(d - \Lambda M)^{-1}). \end{aligned} \tag{6}$$

Again, as $(d + \mu - \Lambda M)$ is an M matrix, its inverse $(d - \Lambda M)^{-1}$ is a positive matrix. Also the stability modulus of M is equal to zero. So, $\rho = (d - \Lambda M)^{-1} = \frac{1}{d_i}$.

Thus we have

$$\begin{aligned} R_0 &= \rho(FV^{-1}) \\ &= \rho(diag(\beta_i\beta_i^*)diag(S_{0i})diag(d_i^*)^{-1} \times \\ &\quad diag(S_{0i}^*)(d-\Lambda M)^{-1}). \\ &\leq \max(\frac{\beta_i\beta_i^* S_{0i}S_{0i}^*}{d_i^* d_i}). \end{aligned} \tag{7}$$

Similarly, we can show that

$$R_0 \geq \min(\frac{\beta_i\beta_i^* S_{0i}S_{0i}^*}{d_i^* d_i}) \tag{8}$$

Thus from the equations (6) and (7) we have the following proposition:

proposition 1.1. *The basic reproduction number of whole system satisfies*

$$\min(\tfrac{\beta_i\beta_i^* S_{0i}S_{0i}^*}{d_i^* d_i}) \leq R_0 \leq \max(\tfrac{\beta_i\beta_i^* S_{0i}S_{0i}^*}{d_i^* d_i}).$$

Now, we have the following theorem:

Theorem 1.1. *If $R_0 < 1$, infection-free equilibrium is stable, while if $R_0 > 1$, the infection-free equilibrium is unstable and the infected state equilibrium exists.*

However the basic reproduction in patch i can be defined when $\Lambda = 0$. In ith patch the disease free equilibrium is given by $E_{0i} = (N_{0i}, 0, \frac{\Pi_i}{d_i^*}, 0)$ which is obtained from

$$\begin{aligned} \frac{dI_i}{dt} &= \beta_i S_i I_i^* - d_i I_i, \\ \frac{dI_i^*}{dt} &= \beta_i^* S_i^* I_i - d_i^* I_i^*. \end{aligned} \tag{9}$$

In this case $F = \begin{pmatrix} 0 & \beta_i S_{0i} \\ \beta_i^* S_{0i}^* & 0 \end{pmatrix} = \begin{pmatrix} 0 & \beta_i N_{0i} \\ \frac{\beta_i^*\Pi_i}{d_i^*} & 0 \end{pmatrix}$

and $V = \begin{pmatrix} d_i & 0 \\ 0 & d_i^* \end{pmatrix}$.

Thus, the next generation matrix is:

$FV^{-1} = \begin{pmatrix} 0 & \frac{\beta_i N_{0i}}{d_i^*} \\ \frac{\beta_i^*\Pi_i}{d_i^* d_i} & 0 \end{pmatrix}$.

So the basic reproduction ratio in patch i is given by:

$R_{0i} = \rho(FV^{-1}) = \frac{\Pi_i \beta_i \beta_i^* N_{0i}}{(d_i^*)^2 d_i}$.

Theorem 1.2. *For $1 \leq i \leq n$, if $R_{0i} < 1$, infection-free equilibrium is stable, while if $R_{0i} > 1$, the infection-free equilibrium is unstable and the infected state equilibrium exists.*

4. The Two Patch Model

In this section we formulate 2-patch model as an application of above theory. The mathematical model for $n = 2$ can be given as:

$$
\begin{aligned}
\frac{dS_1}{dt} &= d_1 N_1 - \beta_1 S_1 I_1^* + m_{12} S_2 - m_{21} S_1 - d_1 S_1, \\
\frac{dI_1}{dt} &= \beta_1 S_1 I_1^* + \lambda_2 m_{12} I_2 - \lambda_1 m_{21} I_1 - d_1 I_1, \\
\frac{dS_1^*}{dt} &= \Pi_1 - \beta_1^* S_1^* I_1 - d_1^* S_1^*, \\
\frac{dI_1^*}{dt} &= \beta_1^* S_1^* I_1 - d_1^* I_1^*, \qquad (10)
\end{aligned}
$$

$$
\begin{aligned}
\frac{dS_2}{dt} &= d_2 N_2 - \beta_2 S_2 I_2^* + m_{21} S_1 - m_{12} S_2 - d_2 S_2, \\
\frac{dI_2}{dt} &= \beta_2 S_2 I_2^* + \lambda_1 m_{21} I_1 - \lambda_2 m_{12} I_2 - d_2 I_2, \\
\frac{dS_2^*}{dt} &= \Pi_2 - \beta_2^* S_2^* I_2 - d_2^* S_2^*, \\
\frac{dI_2^*}{dt} &= \beta_2^* S_2^* I_2 - d_2^* I_2^*. \qquad (11)
\end{aligned}
$$

Here system (9) and (10) represent patch-1 and patch-2 respectively.

4.1. Analysis of the System

Here, we will consider two cases. In first case we choose $\Lambda = 0$ i.e. there is no migration between infected people and in later case we choose $\Lambda \neq 0$.

Case 1: $\Lambda = 0$

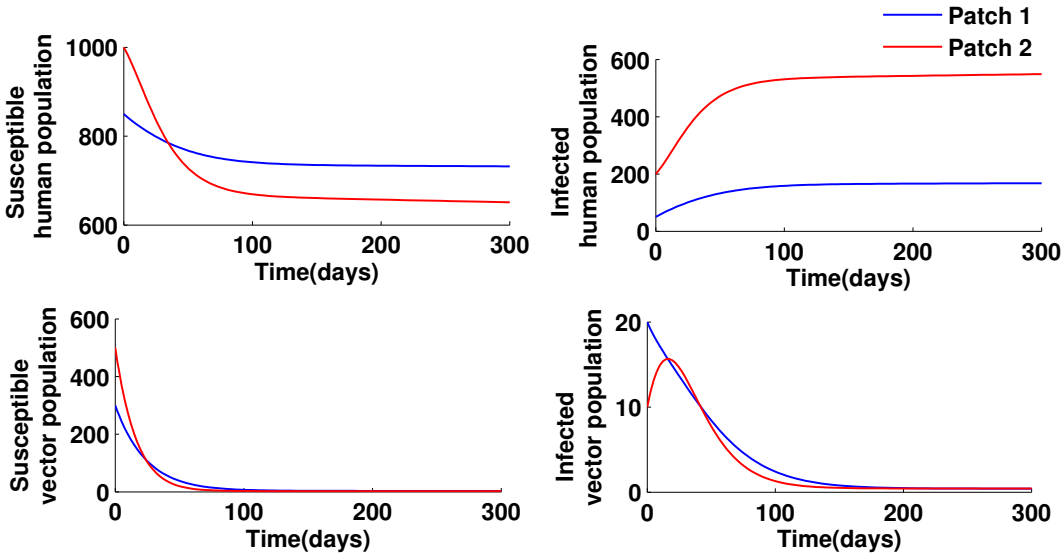

FIGURE 4. Time series solution of our 2-patch model is shown with $m_{12} = m_{21} = 0$ and other parameters as given in Table 1.

When $\Lambda = 0$, each patch is disjoint. So there is no connection between two patches. In this case, we can find the basic reproduction ration in each patch independently. We have already derived the basic reproduction ratio R_{0i} in each patch i in the section 3 when $\Lambda = 0$. So the basic reproduction ratio in patch-1 is given by

$$R_{01} = \frac{\Pi_1 \beta_1 \beta_1^* N_{01}}{(d_1^*)^2 d_1}. \tag{12}$$

In patch-2 is given by

$$R_{02} = \frac{\Pi_2 \beta_2 \beta_2^* N_{02}}{(d_2^*)^2 d_2}. \tag{13}$$

In this case human movements has no impact on the basic reproduction ratio. Thus, for cities of equal size, and with the same biological parameters whatever the migration, local risks are the same.

Now, a question may arise whether it is possible to have one patch with disease free equilibrium and one patch with endemic equilibrium at the same time. If we consider this two patch model assuming that $R_{01} < 1$ and $R_{02} > 1$ i.e. in patch-1 disease free equilibrium exists and in the 2nd patch equilibrium is endemic. So we have $I_1 = 0, I_1^* = 0$. From patch-1 the for the disease free

equilibrium point, we have the equations

$$\begin{aligned} d_1N_1 + m_{12}^S S_2 - m_{21}S_1 - d_1S_1 = 0, \\ \Pi_1 - d_1^* S_1^* = 0. \end{aligned} \tag{14}$$

and from patch-2, we get

$$\begin{aligned} \beta_2 S_2 I_2^* - \lambda_2 m_{12} I_2 - d_2 I_2 = 0, \\ d_2^* I_2^* = 0. \end{aligned} \tag{15}$$

Equation (12) gives $I_2^* = 0$, $I_2 = 0$ in patch-2. This implies that it is not possible to have disease free equilibrium in one patch and endemic equilibrium in another patch at the same time.

Case 2: $\Lambda \neq 0$

When $\Lambda \neq 0$, there is a connection between the two patches and the disease free equilibrium point as well as the basic reproduction ratio has been affected by Λ. At the disease free equilibrium:

$$\begin{aligned} d_1N_1 + m_{12}S_2 - m_{21}S_1 - d_1S_1 = 0, \\ d_2N_2 + m_{21}S_1 - m_{12}S_2 - d_2S_2 = 0, \\ \Pi_1 - d_1^* S_1^* = 0, \\ \Pi_2 - d_2^* S_2^* = 0. \end{aligned} \tag{16}$$

Thus $E_0^* = (N_{01}, 0, \frac{m_{21}N_{01}}{m_{12}}, 0, \frac{\Pi_1}{d_1^*}, 0, \frac{\Pi_2}{d_2^*}, 0)$.

Using the next generation matrix method, from the equation (15), we have:

$$F = \begin{pmatrix} 0 & 0 & \beta_1 S_{01} & 0 \\ 0 & 0 & 0 & \beta_2 S_{02} \\ \beta_1^* S_{01}^* & 0 & 0 & 0 \\ 0 & \beta_2^* S_{02}^* & 0 & 0 \end{pmatrix}$$

$$= \begin{pmatrix} 0 & 0 & \beta_1 N_{01} & 0 \\ 0 & 0 & 0 & \frac{\beta_2 m_{21} N_{01}}{m_{12}} \\ \frac{\beta_1^* \Pi_1}{d_1^*} & 0 & 0 & 0 \\ 0 & \frac{\beta_2^* \Pi_2}{d_2^*} & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \lambda_1 m_{21} + d_1 & -\lambda_2 m_{12} & 0 & 0 \\ -\lambda_1 m_{21} & \lambda_2 m_{12} + d_2 & 0 & 0 \\ 0 & 0 & d_1^* & 0 \\ 0 & 0 & 0 & d_2^* \end{pmatrix}$$

and

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

$$= \frac{N_{01}[(d_1^*)^2 m_{21}\beta_2\beta_2^*\pi_2(d_1+\lambda_1 m_{21}+(d_2^*)^2 m_{12}\beta_1\beta_1^*\pi_1(d_2+\lambda_2 m_{12})]}{m_{12}(d_1^*)^2(d_2^*)^2(d_1 d_2+d_1\lambda_2 m_{12}+d_2\lambda_1 m_{21})}.$$

5. Numerical Simulation

In this section, the dynamics of the model system are analyzed using numerical methods in MATLAB. The numerical results of the model system (equation (9) & (10)) are obtained to verify the analytical predictions obtained in the previous sections.

Figure 3 is the time series solution of the 2-patch model (eq. 9 & 10). Here, in patch-2, $R_{02} > 1$, has a large population compared to patch-1. Thus the flow of infected people from patch-2 to patch-1, will increase the number of infected people in patch-1, as long as the epidemic occurs in patch-1. There is a constant reduction among the vector population as they are assumed to be constant in the patches without migration. So, the conversion of the susceptible to infected vectors are general feature due to high host migration among the patches converting the vector population to infected class with a sustainable low population. Infected humans host were prevalent in both the patches due to high migration and it seems that the density of the infected

TABLE 1. List of parameters used in the models (eq. 9, 10) simulations [4, 21].

Parameter	Definition	Value
d_1	Death rate of human population in patch-1	0.002 day^{-1}
d_2	Death rate of human population in patch-2	0.0015 day^{-1}
d_1^*	Death rate of sandfly population in patch-1	0.4 day^{-1}
d_2^*	Death rate of sandfly population in patch-2	0.6 day^{-1}
Π_1	Constant birth rate of sandfly in patch-1	1 - 15 day^{-1}
Π_2	Constant birth rate of sandfly in patch-2	1 - 15 day^{-1}
β_1	Infection rate of human by sandfly	0.0015 day^{-1}
β_2	Infection rate of human by sandfly	0.005 day^{-1}
m_{12}	Migration rate from patch-2 to patch-1	1.5 day^{-1}
m_{21}	Migration rate from patch-1 to patch-2	1.2 day^{-1}
β_1^*	Infection rate of susceptible sandfly by infected human	0.0003 day^{-1}
β_2^*	Infection rate of susceptible sandfly by infected human	0.0005 day^{-1}
λ_1	Proportion of infected human that are moved from patch-2 to patch-1	0 - 1 day^{-1}
λ_2	Proportion of infected human that are moved from patch-1 to patch-2	0 - 1 day^{-1}

class is almost equivalent at some time scale. However patch-1 is contained with more infectives due to high emigration rate from patch-2 to patch-1 as well as high population density in patch-2. Thus disease control is necessary in both patches in order to avoid the risk of disease spreading.

In Figure 4, when there is no active migration among the patches the infections assumes epidemic in the patch-2 due to density dependent factors and also the force of infection ($\beta_2 = 0.005$) within the patch being more intense. In figure 4, we observe that the populations within the disconnected patch structure is different where Patch-1 has low intensity epidemic with lower population but Patch-2 has high intensity epidemic with the basic reproduction ratios

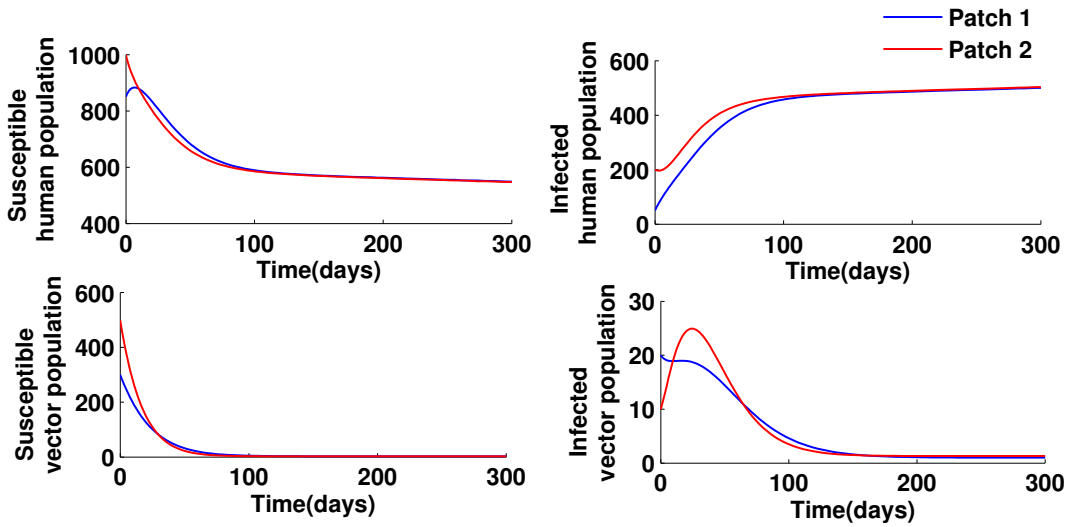

FIGURE 5. Time series solution of our 2-patch model is shown with $m_{12} = m_{21} = 1$ and other parameter as given in Table 1.

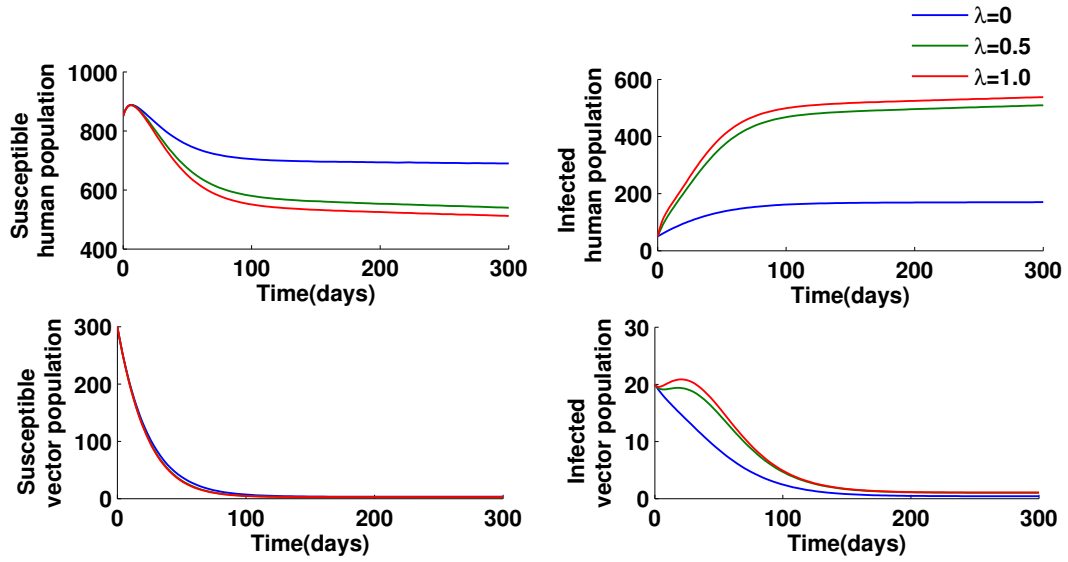

FIGURE 6. Time series solution of patch-1 is shown for different values of λ parameter as given in Table 1.

$R_{01} = 1.4766$ and $R_{02} = 20$.

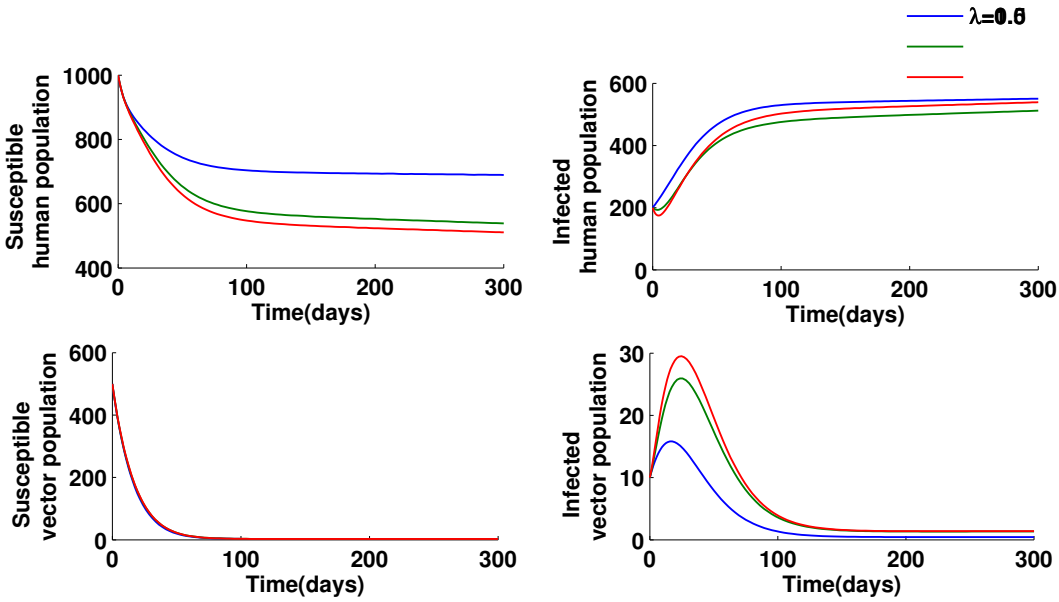

FIGURE 7. Time series solution of patch-2 (system (10)) is shown with parameter as given in Table 1.

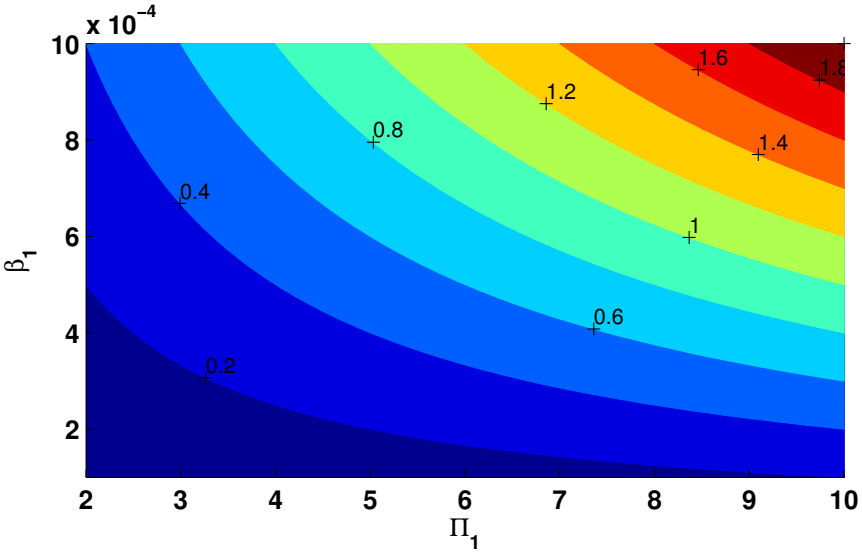

FIGURE 8. Graphical representation of R_{01} is shown as function of β_1 and Π_1 with parameter as given in Table 1.

Figure 5 describes the similar system behavior as in figure 4 but here the migration rates being equal, it validates that after the initial $90-100$ days approximately, the two patch assumes homogeneity in terms of epidemic spread and the infected host are equivalent in nature.

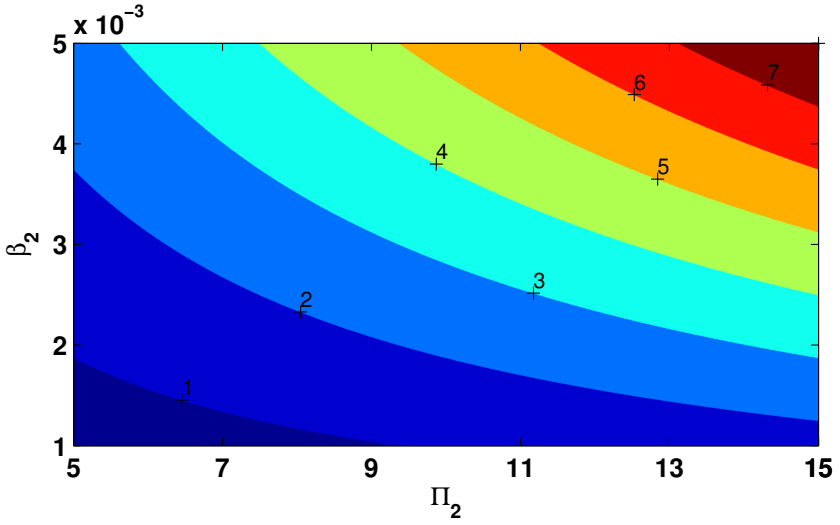

FIGURE 9. Graphical representation of R_{02} is shown as function of β_2 and Π_2 with parameter as given in Table 1.

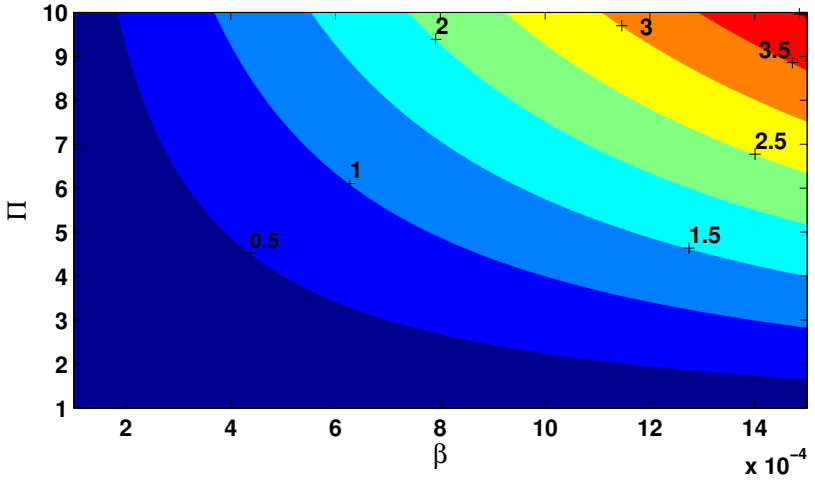

FIGURE 10. Graphical representation of R_0 is shown with parameter as given in Table 1. Here, we have taken $\Pi_1 = \Pi_2 = \Pi$ and $\beta_1 = \beta_2 = \beta$.

In Figure 6, the populations are compared with the range of λ from $0-1$. As λ assumes maximum value i.e $\lambda = 1$, it is observed that the infected population is maximize with high mixing among the susceptible and infected populations, but when $\lambda = 0$, the migration between the infected people cannot occur. So the infective people in patch-1 remains at low level as the initial infected population is considered low in patch-1. This suggests the here migration has a

crucial role if every other parameters were assumed to be constant. It is also to be noted that in low density population structure high migration from epidemic patch may bring an infection cascade which may turn the population to become intense epidemic from a state of endemic or low epidemic state.

In Figure 7, the similar analysis done numerically for patch-2 with densely populated structure than patch-1 and comparatively here we find that here in this local patch high immigration from the other patch has no role on the magnitude of intensity of the infection whether the migration assumes a high, moderate or low value.

Figure 8 is the contour plot of R_{01} as a function of Π_1 and β_1, it shows that when the value of Π_1 lies between $1-15$ the system becomes stable ($R_{01} < 1$) with increasing value of the infection rate. However, if we increase the value of π_1 beyond this value the system loses its stability. Also, In Figure 9 and 10, The contour plot exhibits the R_{02} and R_0 as a function of Π_2, β_2 and Π, β respectively. It also show that for different ranges of Π, $\beta 2$, Π and β the systems become stable with increasing value of the infection rate.

6. Discussion and Conclusion

In this research article, our analytical and numerical analysis reveals that the migration of the host in a vector borne disease has a significant contribution in the spread of the disease when the host population migrates among the two distinct patches with different demographic structures. It is observed through our numerical analysis that the connected patches attains homogeneity when the migration rates are equal. The opposite behavior is observed within the disconnected patch system. Local dynamic reflects differences in disconnected patches compared to connected patches bridged by the migratory behavior of the human host. As our main emphasis is on the migratory role of the humans among the patch system which shares endemic infections, the host-vector interaction and infection process is not thoroughly emphasized and generalized as density dependent process. However, it may be pragmatic to consider the infection among

the vector is a critical factor that may initially affects the demographics of the vector population. Further, if one incorporates habitat fragmentation and the frequency dependent transmission of disease within vector than density dependent transmission it may add a new dimension to the studied system. Also, the vector prevalence and force of infection is environmentally dependent which we have not considered here for simplicity. Another unchallenged issue is, considering breeding sites within the patches. They can also restructure the R_0 with enhanced vector recruitment. There are several factors which may change the demographic risk of disease invasion among connected patches. We simply assumed that irrespective of all operating factors, if we want of observe the changes in demographics of a population with unrestricted and free migration, then the local dynamics of the discrete patch becomes inseparable as the population is homogeneously mixed with progressing time scale. Our study shows that if such case arise where the populations have local epidemic then a connected system with high migration among the host population is a key factor in dispersal of the disease both among the host and vector population under certain constant density dependence factors. In absence of migration the local patch dynamics can be either epidemic, endemic or may be disease free depending on the demographic structure.

Conflict of Interests

The authors declare that there is no conflict of interests.

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