KMITL Sci. Tech. J. Vol. 12 No. 2 Jul.-Dec. 2012

# An SIR Epidemic Model with Gravity in Patchy Environment: Analyses for Two Patches System

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## Abstract

In this study, we propose an explicitly spatial SIR epidemic model under which a population travel is subject to the gravity law. Namely, the migration rates are assumed to be increased with the populations between coupled patches and decreased with the distance. We analyze the model simplified into two patches. The conditions for a stable disease-free equilibrium are derived. Moreover, we show that the derived basic reproduction number corresponds with such conditions. The numerical results shown are in agreement with theory.

**Keywords:** SIR epidemic model, Gravity model, Asymptotic stability

## 1. Introduction

The spatial heterogeneity has been recognized as a key issue in dynamical modeling of communicable infectious diseases such as measles, SARS, influenza and several vector borne diseases (e.g., Dengue and Malaria). A susceptible individual who live far away from an infective may has a lower risk of infection than who live in close proximity to the disease [1]. In recent years, several mathematical models have been developed to investigate an impact of human movement on the disease transmission dynamics [2-7]. For large scale movement, the network structure is incorporated together with the information of geographic region into the model. The difficulty arises when attempt to determine the traveling rates between locations. By lacking of precise data, most studies usually assume that the travel frequency depends on the community sizes and the distance between them [3, 8]. This kind of assumption leads to the so-called gravity model of movement [3, 8-10].

In this paper, we propose an SIR epidemic metapopulation model subject to the assumption of gravity law of movement. The objective is to provide a preliminary analytic framework that facilitates an investigation of the influence of travel on the presence of epidemic. Due to complexity, we analyze a simplifying two-patch model. In the following sections, we derive the conditions for stability of the disease-free equilibrium. The results will be compared with the derived basic reproduction number. Finally, the numerical results will be used to assure the theoretical predictions.

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## 2. Model Formulation

We begin with the formulation of an epidemic SIR metapopulation model. Assume that a population is divided into *n* distinct geographical regions. Throughout the paper the region is referred to as *patch*. The inter-connecting between patch is determined by the travel of population. According to a generalized gravity model [9], the rate that population of patch *i* moves to patch *j* is proportional to $N_j^{\tau_2} N_i^{\tau_1} / D_{ij}^{\rho}$ where $N_i$ is the population size of patch *i*, $D_{ij}$ is the distance between patch *i* and patch *j*, and $\rho, \tau_1, \tau_2 > 0$ are parameters. Thus, we have a metapopulation model with *n* patches in the form

$$\frac{dN_i}{dt} = \sum_{j=1, j\neq i}^{n} w_0 \frac{N_i^{\tau_2} N_j^{\tau_1}}{D_{ij}^{\rho}} - \sum_{j=1, j\neq i}^{n} w_0 \frac{N_j^{\tau_2} N_i^{\tau_1}}{D_{ij}^{\rho}}, \; i = 1,...,n \tag{2.1}$$

where $w_0$ is a proportionality constant. The parameter $\tau_1$ and $\tau_2$ indicate the dependency of travel on the *donor* and *recipient* population sizes, whereas, $\rho$ quantifies how the travel rate decays with the distance.

For the transmission of a communicable disease among *n* subpopulations the number of susceptible, infectious and recovered individuals in patch *i* at time *t* are denoted by $S_i(t)$, $I_i(t)$ and $R_i(t)$, respectively. We now assume that the rates that susceptible, infectious and recovered individuals move from patch *i* to patch *j* are proportional to $N_j^{\tau_2} S_i^{\tau_1} / D_{ij}^{\rho}$, $N_j^{\tau_2} I_i^{\tau_1} / D_{ij}^{\rho}$ and $N_j^{\tau_2} R_i^{\tau_1} / D_{ij}^{\rho}$, respectively. Since the spatial coupling is explicitly determined, the contact occurs only within patch which is assumed to be homogeneous mixing. We then have an SIR epidemic model with *n* patches under the gravity law of movement of the form

$$\frac{dS_i}{dt} = \mu_i N_i - \mu_i S_i - \frac{\beta_i S_i I_i}{N_i} + \sum_{j=1, j\neq i}^{n} w_0 \frac{N_i^{\tau_2} S_j^{\tau_1}}{D_{ij}^{\rho}} - \sum_{j=1, j\neq i}^{n} w_0 \frac{N_j^{\tau_2} S_i^{\tau_1}}{D_{ij}^{\rho}}, \tag{2.2}$$

$$\frac{dI_i}{dt} = \frac{\beta_i S_i I_i}{N_i} - \mu_i I_i - \gamma_i I_i + \sum_{j=1, j\neq i}^{n} w_0 \frac{N_i^{\tau_2} I_j^{\tau_1}}{D_{ij}^{\rho}} - \sum_{j=1, j\neq i}^{n} w_0 \frac{N_j^{\tau_2} I_i^{\tau_1}}{D_{ij}^{\rho}}, \tag{2.3}$$

$$\frac{dR_i}{dt} = \gamma_i I_i - \mu_i R_i + \sum_{j=1, j\neq i}^{n} w_0 \frac{N_i^{\tau_2} R_j^{\tau_1}}{D_{ij}^{\rho}} - \sum_{j=1, j\neq i}^{n} w_0 \frac{N_j^{\tau_2} R_i^{\tau_1}}{D_{ij}^{\rho}}, \tag{2.4}$$

with $N_i(t) = S_i(t) + I_i(t) + R_i(t)$ and $i = 1,...,n$. The model parameters are described as follows: $\mu_i$ denotes the birth rate and natural death rate in patch *i*, whereas $\beta_i$ is an average number of effective contacts of infectious individual per unit time and $\gamma_i$ is the recovery rate in patch *i*. The total population size, denoted by $N$ is constant since

$$\frac{dN}{dt} = \frac{d}{dt}\left(\sum_{i=1}^{n} N_i\right) = \sum_{i=1}^{n} \frac{dN_i}{dt} = \sum_{i=1}^{n}\left(\frac{dS_i}{dt} + \frac{dI_i}{dt} + \frac{dR_i}{dt}\right) = 0. \tag{2.5}$$

We assume that the initial conditions are satisfied $S_i(0) > 0$, $I_i(0) > 0$ and $R_i(0) \geq 0$ for all $i = 1,...,n$. It is easy to show that $S_i(t)$, $I_i(t)$ and $R_i(t)$ are nonnegative for all *t*.

## 3. Analyses for Two Patches Model

In this section, we analyze the model (2.2) - (2.4) for $n = 2$. The simplification allows us to examine the stability of the disease-free equilibrium. The stability condition will be determined and compared with the derived basic reproduction number.

We first consider an SIR epidemic model for two patches

$$\frac{dS_1}{dt} = \mu_1 N_1 - \mu_1 S_1 - \frac{\beta_1 S_1 I_1}{N_1} + \frac{w_0}{d_{12}} N_1^{\tau_2} S_2^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} S_1^{\tau_1}, \tag{3.1}$$

$$\frac{dS_2}{dt} = \mu_2 N_2 - \mu_2 S_2 - \frac{\beta_2 S_2 I_2}{N_2} + \frac{w_0}{d_{12}} N_2^{\tau_2} S_1^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} S_2^{\tau_1}, \tag{3.2}$$

$$\frac{dI_1}{dt} = \frac{\beta_1 S_1 I_1}{N_1} - \mu_1 I_1 - \gamma_1 I_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} I_2^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} I_1^{\tau_1}, \tag{3.3}$$

$$\frac{dI_2}{dt} = \frac{\beta_2 S_2 I_2}{N_2} - \mu_2 I_2 - \gamma_2 I_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} I_1^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} I_2^{\tau_1}, \tag{3.4}$$

$$\frac{dR_1}{dt} = \gamma_1 I_1 - \mu_1 R_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} R_2^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} R_1^{\tau_1}, \tag{3.5}$$

$$\frac{dR_2}{dt} = \gamma_2 I_2 - \mu_2 R_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} R_1^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} R_2^{\tau_1}. \tag{3.6}$$

Note: that $d_{ij} = D_{ij}^{\rho}$ and since the distance between two patches is constant, we have $d_{12} = d_{21}$ The model of two patches eliminates the effects of distance on infection rates.

### 3.1 Disease-free equilibrium

The disease-free equilibrium is defined as an equilibrium point of epidemic model at which the number of individuals in all disease stages are zero. For system (3.1) - (3.6) it is denoted by $(S_1^*, S_2^*, I_1^*, I_2^*, R_1^*, R_2^*)$ with $I_1^* = I_2^* = 0$ .Setting the RHS. of the system (3.1) - (3.6) equal to zero, we solve a system of algebraic equations for $S_1^*, S_2^*, R_1^*$ and $R_2^*$.From Eqs. (3.5) - (3.6), it is obvious that $R_1^* = R_2^* = 0$. Suppose that $(N_1^*, N_2^*)$ is an equilibrium point of the model (2.1) with $n = 2$. It follows that $S_1^* = N_1^*$ and $S_2^* = N_2^*$. The disease-free equilibrium can be derived directly from the equilibrium point of the model (2.1) with $n = 2$. It is easy to see that there are four points such as (i) $(0,0,0,0,0,0)$, (ii) $(N,0,0,0,0,0)$, (iii) $(0,N,0,0,0,0)$, and (iv) $(\frac{N}{2}, \frac{N}{2}, 0,0,0,0)$.

### 3.2 Stability Analysis

Since the first three equilibrium points are not relevant in the context of disease transmission in metapopulation dynamics, we focus on stability of the last equilibrium that is $(\frac{N}{2}, \frac{N}{2}, 0,0,0,0)$.

The Jacobian matrix for (3.1) - (3.6) at the disease free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0,0,0,0)$ is given by

$$J=\left[\begin{array}{cc|cc|cc} 2a & 0 & \mu_1-\beta_1+a+c & -b & \mu_1+a+c & -b \\ 0 & 2a & -b & \mu_2-\beta_2+a+c & -b & \mu_2+a+c \\ \hline 0 & 0 & \beta_1-\mu_1-\gamma_1 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2-\mu_2-\gamma_2 & 0 & 0 \\ \hline 0 & 0 & \gamma_1 & 0 & -\mu_1 & 0 \\ 0 & 0 & 0 & \gamma_2 & 0 & -\mu_2 \end{array}\right]$$

where $a=\frac{w_0}{d_{12}}(\tau_2-\tau_1)\left(\frac{N}{2}\right)^{\tau_1+\tau_2-1}$, $b=\frac{w_0}{d_{12}}\tau_1\left(\frac{N}{2}\right)^{\tau_1+\tau_2-1}$ and $c=\frac{w_0}{d_{12}}\tau_2\left(\frac{N}{2}\right)^{\tau_1+\tau_2-1}$. Note that in order for the Jacobian matrix to exist it is necessary to assume that $\tau_1>1$. Since the matrix $J$ represents block structure, its eigenvalues, denoted by $\lambda$ can be computed according to three diagonal submatrices. They are $\lambda_1=\lambda_2=2a$, $\lambda_3=\beta_1-\mu_1-\gamma_1$, $\lambda_4=\beta_2-\mu_2-\gamma_2$, $\lambda_5=-\mu_1$ and $\lambda_6=-\mu_2$.

It is seen that all eigenvalues are real and only $\lambda_1$ and $\lambda_2$ are concerned with travel parameters. Define

$$R_0^{(i)}=\frac{\beta_i}{\mu_i+\gamma_i},\ i=1,2, \tag{3.7}$$

as the basic reproduction number in patch *i* when there is no travel between patches. This parameter describes the transmission potential within patch in isolation. Since all disease parameters are positive, the disease-free equilibrium is locally asymptotically stable if

$$R_0^{(1)},R_0^{(2)}<1 \text{ and } \tau_2<\tau_1, \tag{3.8}$$

and unstable if at least one of the above conditions are not satisfied.

We remark that, in the absence of the disease, the system (3.1)-(3.6) reduces to

$$\frac{dN_1}{dt}=\frac{w_0}{d_{12}}N_1^{\tau_2}N_2^{\tau_1}-\frac{w_0}{d_{12}}N_2^{\tau_2}N_1^{\tau_1}, \tag{3.9}$$

$$\frac{dN_2}{dt}=\frac{w_0}{d_{12}}N_2^{\tau_2}N_1^{\tau_1}-\frac{w_0}{d_{12}}N_1^{\tau_2}N_2^{\tau_1}, \tag{3.10}$$

which is the model (2.2) - (2.3) for $n=2$. For this model, it can be verified that a nontrivial equilibrium point, i.e., $(\frac{N}{2},\frac{N}{2})$ is stable if $\tau_2<\tau_1$ and unstable if $\tau_2>\tau_1$. The stability condition for pure mobility model implies that the degree of recipient population must be lower than the degree of donor population in order to maintain the two patch sizes in balance. It is intuitive that if $\tau_2>\tau_1$, then one of the two subpopulations must be extinct in the future.

The conditions in (3.8) tell us that if the two populations (in the absence of the disease) are in balance, then it can be viewed as static population. In this case, if the transmission of the disease from an index case cannot be successful for both patches, the epidemic will not be happen.

### 3.3 The Basic Reproduction Number

In the context of epidemiology, it is necessary to inspect whether an infectious disease persists or dies out at the initial phase. This concept is laid on the basic reproduction number, $R_0$ which is defined as an expected secondary infections produced by a primary index case introduced into a completely susceptible population [11, 12]. As state earlier, $R_0$ can be used to determine the threshold behavior. For example, if $R_0<1$, then the disease cannot invade the population. On the other hand, if $R_0>1$, then the disease can invade a susceptible population.

In order to derive $R_0$ of the system (3.1) - (3.6), we employ the next generation method [11, 12] (The reader who interested in detail analysis for this method see [12, 13]). In short, it is given by the spectral radius of the so-called *next generation matrix*

$$FV^{-1} = \begin{bmatrix} \dfrac{\beta_1}{\mu_1+\gamma_1} & 0 \\ 0 & \dfrac{\beta_2}{\mu_2+\gamma_2} \end{bmatrix} \tag{3.11}$$

Hence, the basic reproduction number for model (3.1) - (3.6) is

$$R_0 = \rho\left(FV^{-1}\right) = \max_{i=1,2} R_0^{(i)} \tag{3.12}$$

where $\rho(\cdot)$ denotes the spectral radius of a matrix $\cdot$, and $R_0^{(i)}$ is given by Eq. (3.7). It is clear that, if $R_0^{(i)} < 1$ for all *i*, then $R_0 < 1$, on the other hand, if $R_0^{(i)} > 1$ for some *i*, then $R_0 > 1$.

### 3.4 Numerical Results

To verify our hypotheses, we solve system (3.1) - (3.6) numerically. The parameters used are set as follows: $w_0 = 0.05\times10^{-5}$, $N = 10^5$, $d = 10$, $\mu_1 = \mu_2 = 3.91\times10^{-5}$ and $\gamma_1 = \gamma_2 = 0.143$. Figure 1 shows the changes of susceptible, infective and recovery classes with time. In this case $\tau_2 = 1$, $\tau_1 = 1.2$, $\beta_1 = 0.09$ and $\beta_2 = 0.06$. In order to check whether the stability conditions (3.8) are satisfied, we calculated the parameters $R_0^{(1)}$ and $R_0^{(2)}$ as given in Eq. (3.7). We also calculate $R_0$ by using Eq. (3.12). The results are given in table 1.

As opposed, Fig. 2 demonstrates a large outbreak in both communities. To simulate this, we use $\tau_2 = 1$, $\tau_1 = 1.2$, $\beta_1 = 0.17$ and $\beta_2 = 0.2$. Again, the stability conditions are tested, and the basic reproduction number is also calculated in this case. The results are illustrated in table 1. It is remarked that due to the lack of vital effects the disease is no longer exist after some period. These results strongly agree with theoretical conjectures either via stability analysis or the derived basic reproduction number.

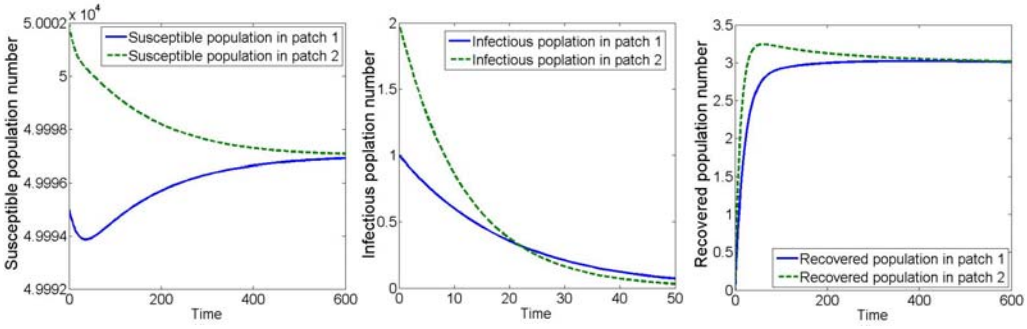


**Figure 1** SIR model with 2 patches in case $\tau_2 < \tau_1$ and $R_0 < 1$.

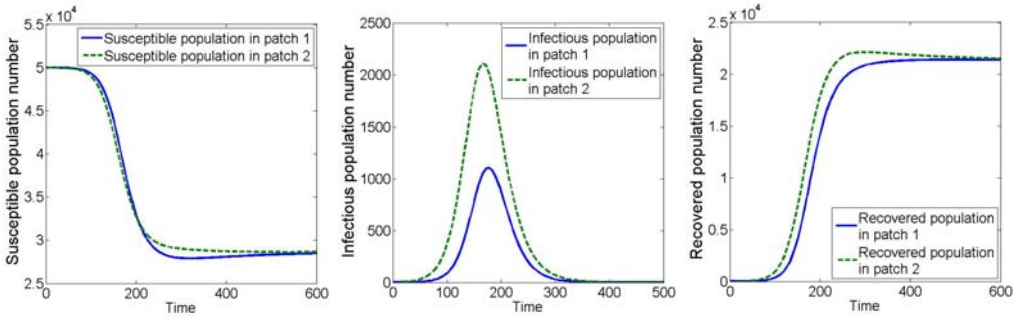


**Figure 2** SIR model with 2 patches in case $\tau_2 < \tau_1$ and $R_0 > 1$.

**Table 1** Summary of numerical results under two different criteria

| Numerical examples | Threshold Criteria | | Results |
|---|---|---|---|
| | **Stability analysis (Eq. (3.8))** | **Basic reproduction number (Eq. (3.12) and $\tau_1 > \tau_2$)** | |
| Figure 1 | $\tau_1 = 1.2, \tau_2 = 1$<br>$R_0^{(1)} = 0.63$, $R_0^{(2)} = 0.42$ | $\tau_1 = 1.2, \tau_2 = 1$<br>$R_0 = R_0^{(1)} = 0.63$ | Epidemic dies out |
| Figure 2 | $\tau_1 = 1.2, \tau_2 = 1$<br>$R_0^{(1)} = 1.19$, $R_0^{(2)} = 1.40$ | $\tau_1 = 1.2, \tau_2 = 1$<br>$R_0 = R_0^{(2)} = 1.40$ | Epidemic occurs |

## 4. Conclusions

We have formulated a gravity SIR epidemic model with *n* patches. Analysis for two patches provided the preliminary conditions for which the disease dies out. It is remarked that throughout linear stability analysis we needs $\tau_1 > 1$ as a necessary constraint for the Jacobian matrix to exist since the presence of dividing by zero of derivatives of migration terms with respect to the infective variable. The conditions for stable disease-free equilibrium correspond with the basic reproduction number. Yet, the correspondence has not been guaranteed in general. For the present model the dependence on travel is only $\tau_1 > \tau_2$. These two parameters play an important role in the mobility process with $n \geq 2$. Indeed, the next generation method requires that the system must be at equilibrium so that the susceptible populations can be viewed as static [14]. Since we dealt with two-patch model, the dependence of travel is implicit and the effect of distance is eliminated. In the higher system components, the basic reproduction number is expected to be explicitly dependent on such parameters.

The possible extension is twofold: on the one hand, we can look at the model with $n > 2$, on the other hand, one can develop method for analyzing the unstable system. It is interesting that how the basic reproduction number can be derived under the fluctuating population.

## 5. Acknowledgements

This research is (partially) supported by the Centre of Excellence in Mathematics, the Commission on Higher Education, Thailand.

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