



**EFFECTS OF TRAVEL UNDER GRAVITY MODEL ON
A SPATIAL SIR EPIDEMIC DYNAMIC**

สำนักวิทยาสัมถกกลาง



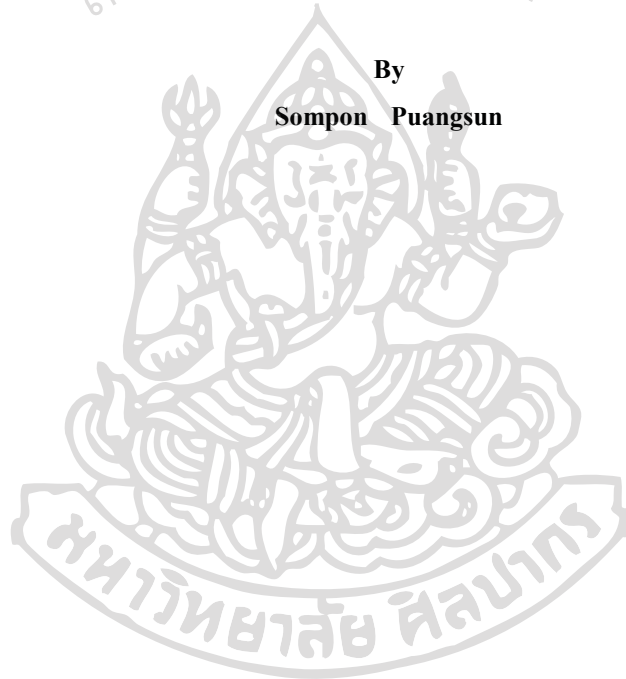
**By
Sompon Puangsun**

**A Thesis Submitted in Partial Fulfillment of the Requirements for the Degree
Master of Science Program in Mathematics
Department of Mathematics
Graduate School, Silpakorn University
Academic Year 2012
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ผลกระทบของการเดินทางภายใต้ตัวแบบแรงโน้มถ่วงต่อพลวัตการระบาดของโรคเชิงพื้นที่

สำนักหอสมุดกลาง

โดย

นายสมพล พวงสั้น



วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรปริญญาวิทยาศาสตรมหาบัณฑิต

สาขาวิชาคณิตศาสตร์

ภาควิชาคณิตศาสตร์

บัณฑิตวิทยาลัย มหาวิทยาลัยศิลปากร

ปีการศึกษา 2555

ลิขสิทธิ์ของบัณฑิตวิทยาลัย มหาวิทยาลัยศิลปากร

The Graduate School, Silpakorn University has approved and accredited the Thesis title of “Effects of travel under gravity model on a spatial SIR epidemic dynamic” submitted by Mr. Sompon Puangsun as a partial fulfillment of the requirements for the degree of Master of Science in Mathematics

.....
(Assistant Professor Panjai Tantatsanawong, Ph.D.)
Dean of Graduate School

สำนักหอสมุดกลาง

The Thesis Advisor

Klot Patanarapeelert, Ph.D.

The Thesis Examination Committee

..... Chairman

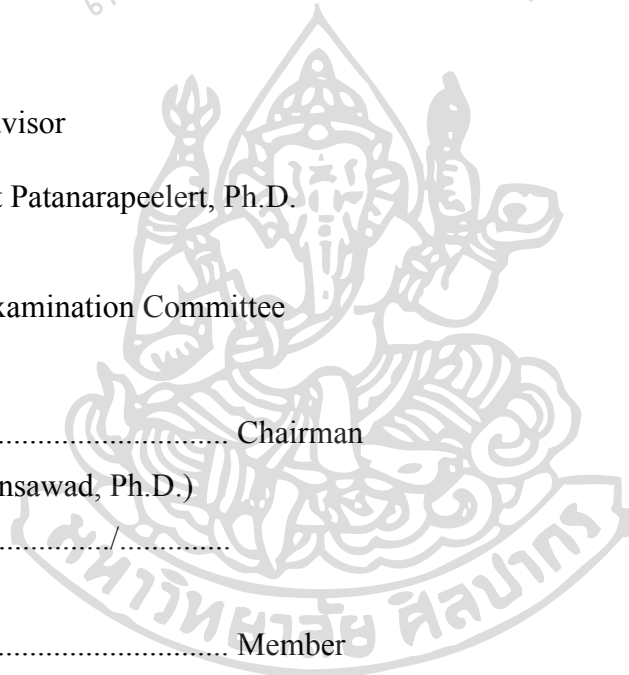
(Pornsarp Pornsawad, Ph.D.)

..... Member

(Nichaphat Boonkorkuea, Ph.D.)

..... Member

(Klot Patanarapeelert, Ph.D.)



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In this thesis, we propose an explicitly spatial SIR epidemic model with a nonlinear population travel subjected to the gravity law of movement. We analyze the model with two patches and three patches. The conditions for a stable disease-free equilibrium and the basic reproduction number of both two patches model and three patches model are derived. Moreover, we establish theorems for deciding whether an epidemic occurs or not. The numerical results are in agreement with theory. Finally, we discuss the effects of travel on the model.



Department of Mathematics

Graduate School, Silpakorn University

Student's signature.....

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Thesis Advisor's signature.....

53305209 : สาขาวิชาคณิตศาสตร์

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ในวิทยานิพนธ์นี้ เราได้เสนอแบบจำลองการระบาด SIR ที่มีการเดินทางของประชากรแบบไม่เป็นเชิงเส้น ซึ่งการเดินทางนี้อยู่ภายใต้ตัวแบบแรงโน้มถ่วง การศึกษาแบบจำลองนี้ เราได้วิเคราะห์แบบจำลองในกรณีที่มีสองพื้นที่และสามพื้นที่ โดยหาเงื่อนไขเสถียรภาพเชิงกำกับของจุดสมดุลที่ปราศจากโรค (disease-free equilibrium) และหาจำนวนการถอดแบบพื้นฐาน (basic reproduction number) ของแบบจำลองทั้งสองกรณี ยิ่งไปกว่านั้นเราได้สร้างทฤษฎีบทสำหรับการพิจารณาว่า โรคระบาดจะสามารถแพร่ระบาดไปยังประชากรได้หรือไม่ พร้อมได้แสดงการจำลองเชิงตัวเลขซึ่งสอดคล้องกับทฤษฎี สุดท้ายเราได้วิเคราะห์ผลกระทบของการเดินทางต่อแบบจำลองการระบาดนี้



ภาควิชาคณิตศาสตร์

บัณฑิตวิทยาลัย มหาวิทยาลัยศิลปากร

ลายมือชื่อนักศึกษา.....

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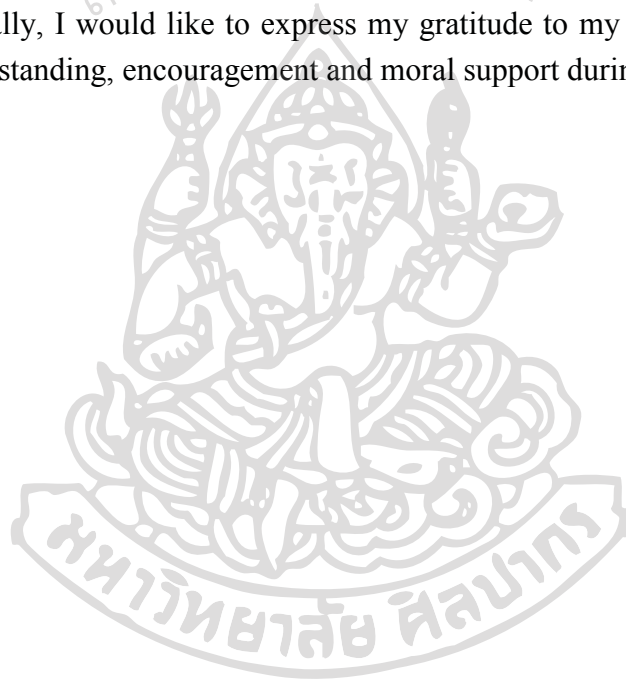
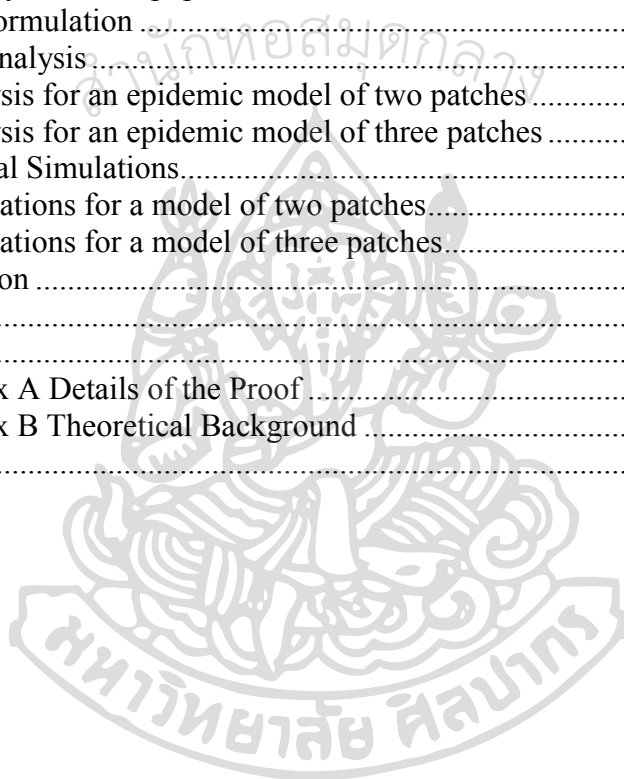


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Chapter 1

Introduction

Mathematical modeling in epidemiology is a multidisciplinary subject that stems from the need to understand underlying mechanisms and factors that influence the spread of an infectious disease. Historical background of mathematical models in studying the diseases was recognized in a defense of the practice of inoculation against smallpox in 1760 by Daniel Bernouilli [14]. For the modern mathematical epidemiology, the principle of compartmental model was first contributed by the works of McKendrick(1926) and of von Foerster(1959). As an example, it was the formulation of a simple SIR epidemic model that predicted behavior very similar to the behavior observed in epidemic curve of the Great Plague of London, which took place in 1665-1666 [15]. Basically, this kind of compartmental model divides the population into three distinct disease statuses such as susceptible individuals(S) who have not been infected but are susceptible to the disease, infectious individuals(I) who are infected and can transmit the disease and recovered individuals(R) who have recovered from the disease and have immunity. Nevertheless, with the force of globalized world, the epidemic process in the present is more complex than the past. There is a need of model development to be come up with situations that can be often observed in reality. Depending on the nature of the disease in consideration and ecological aspect in the context of study, extension of the model can be ranging from addition of compartments such as exposed class and vectors, non-homogeneous mixing, age-structured population and distributions that are spatially non-uniform, etc. For example, in the large scale of outbreak, the course of an infection of communicable disease such as measles, influenza, tuberculosis and SARS usually cannot be modeled accurately without some attention to its spatial spread.

Spatial dispersal is a key feature in modeling the spread of an infectious disease driven by human mobility. Recently, a novel influenza A (H1N1) virus has spread rapidly across many countries [16]. Spreading of cholera along the West African coast can be influenced by human movement besides hydrological transport [17]. These show that human mobility or travel allows a potentially disease agent to be introduced into a new geographic area leading to disease emergence or spread [18]. There are several ways to incorporate human mobility into the model of disease transmission. If the space is continuous, one can describe the dynamics of human mobility by using diffusion process, often in terms of partial differential

equations (for example see [19] and [20]). For discrete geographical regions, it is usual to divide the population being study into several subgroups associated with the reference area. For instance, in the regional scale, the area can be defined as district or sub-district, but in global scale, it can be defined as country or continent. In theoretical point of view, the area definition is usually abstract and being modeled in terms of *patch*. Thus, the system of this kind is referred to as a multi-patch system. Each patch may be coupled with each other through the human movement. This concept is indeed widely used in ecology for many years. The so-called *metapopulation model* [22] is termed as “*networks of idealized habitat patches in which species occur as discrete local populations connected by migration*”.

The use of metapopulation model in mathematical epidemiology has been increasing in recent years [20, 23, 24, 25, 26]. Many models of communicable diseases normally share a common basic principle on the model of infection, e.g. the standard incidence or mass action incidence [21]. For both assumptions, it must be assumed that the contact pattern is locally random mixing and homogeneous. This serves as underlying assumption for each patch in metapopulation system. However, due to the inter-patch movement, the temporal dynamics of local population is altered, so is the contact pattern within each patch. The heterogeneity of contact within patch is taking into accounted by implicit model of movement. By using this approach, the movement is embedded in the force of infection experienced by susceptible in a given patch being depicted as a weighted sum of the levels of infection in each patch [27]. Alternatively, the human movement can be modeled explicitly by adding the transportation operators being the net rate of total migrations.

In this study, we emphasize on a metapopulation model in order for studying the effects of human mobility on the transmission dynamics of an infectious disease. Here an SIR epidemic model is focused as a starting point for other possible extension along the way of specific purpose of study and for specific disease characters. We confine ourselves into the theoretical epidemic model based upon deterministic approach rather than stochastic approach. By means of theoretical aspect, we do not pay our attention on any specific infectious diseases. In literatures, an explicitly SIR model that includes the linear migration rates of population has been formulated and studied [3, 4, 5] but there is a few models that taking into account the effects of a population travel in a nonlinear fashion. The problem on choosing the model of mobility pattern for studying the impact on dynamics of communicable diseases is crucial among modelers discussion. While this problem is entangled with the accuracy of data and information in hand, the impact of the parameters and model features on the reliability of the predicted scenarios is difficult to assess. Therefore, the human movement between patch in this study is modeled explicitly by using *the gravity model*.

Gravity model is a model of population movement that is adapted from Newton’s law of gravity in physics. It characterizes the trip distribution—the number of trips between one point and another in discrete regions. In general, the gravity model considers the quantity of interaction of their economic force of at-

traction or *economic mass* and as a negative correlation with the distance between them [28]. The concept of gravity model is widely used in transportation study. For example, in 2007, T. Grosche, F. Rothlauf and A. Heinzl [6] presented a gravity model for the estimation of air passenger volume between city-pairs. In 2009, J. Alm and J. V. Winters [7] formulated a model of student migration under which the migration flows from school district to institution is subject to the gravity law. For epidemiological model, its functional form mostly represents proportionality to the population sizes of coupled *communities* and an inverse proportion to the distance between the communities. In recent years gravity models have been increasingly used in the large-scale computational models for the realistic simulation of epidemic outbreaks [29] and in agent-based micro-simulations of epidemic dynamics in synthetic networks [30]. The model calibration has been performed in predicting the spread of influenza [31] and measles outbreaks [1, 25].

In epidemiology, the main purpose of using the mathematical model is to understand how the disease evolves in communities and to indentify the impact of countermeasures those issued by model suggestions. In traditional deterministic scheme, this concept is related to the disease-free equilibrium and the most important quantity, the basic reproduction number. The **disease-free equilibrium** is defined as a steady state solution of an epidemic model at which the number of individuals in all disease stages is zero. The **basic reproduction number** [8, 9] is a measure of potential for disease spread in a population at the initial phase of epidemic. It is defined as an expected secondary infections produced by a primary index case introduced into a completely susceptible population. Thus, this quantity acts as an epidemic threshold that is, if its value is less than one, then the disease cannot be established into the community, on contrary, the epidemic occurs if its value is greater than one. Depending on the disease the derivation of the basic reproduction number from deterministic model is usually carried by using the survival function method [32]. There are complications however in the derivation when space is taken into account, and when individuals can move. A more suitable method to derive the basic reproduction number in this case is the next generation approach [32].

In this study, we propose an explicitly SIR epidemic model under which a population travel is subjected to the gravity law that modified from previous work [2]. In order to study the effect of travel under gravity law on a SIR epidemic model in a patchy environment, we analytically derive the disease-free equilibrium and the basic reproduction number using the next generation method. Our aim is to determine the conditions in which the disease dies out in the metapopulation system. In doing this, we work on simplest network topology, that is two patches and consider the impact on an extendable three-patch system. As far as the stability of the disease-free stage is concerned, we will show that the stability condition for disease-free stage is agree with the below epidemic threshold derived from the basic reproduction number.

This thesis is organized as follows. In Chapter 2, we give some important basic knowledge about an SIR epidemic model, a gravity model of population movement and the next generation method which is the method for computing

the basic reproduction number. We note that some theoretical background will be given in appendix. In Chapter 3, we discuss the results from [2] and formulation of a new explicitly SIR epidemic model under which a population travel is subject to the gravity law. We remark also that analysis under the new model has technically advantage over the previous model [2] since it can get rid of a weak constraint. In Chapter 4, we analyze the new model given in Chapter 3 for two patches and three patches. We determine the conditions for the stability of the disease-free equilibrium and derive the threshold condition in terms of travel on the basic reproduction number. The method used for two patch analysis is employed from previous work [33]. In Chapter 5, we give the numerical simulations to verify our hypotheses given in Chapter 4. Finally, conclusion and discussion will be given in Chapter 6.



Chapter 2

Theoretical Background

In this chapter, we briefly review a nonspatial SIR epidemic model and a gravity model of population movement. Also, the method for computing the basic reproduction number will be given.

2.1 Nonspatial SIR epidemic model

A basic SIR epidemic model [10] is the deterministic compartmental model for the disease transmission. It composes of three compartments such as S -compartment, I -compartment and R -compartment. The variables $S(t)$, $I(t)$ and $R(t)$ denote the number of susceptible, infectious and recovered individuals at time t . A basic SIR model with the standard incidence is given by the following system of ordinary differential equations:

$$\frac{dS}{dt} = \mu N - \mu S - \frac{\beta SI}{N} \quad (2.1)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \mu I - \gamma I \quad (2.2)$$

$$\frac{dR}{dt} = \gamma I - \mu R. \quad (2.3)$$

Here $N(t) = S(t) + I(t) + R(t)$ is the number of total population at time t . The model parameters are described as follows: μ denotes the birth rate and natural death rate, whereas β is an average number of effective contacts of an infectious individual per unit time (effective contact rate) and γ is the recovery rate. Note that it is assumed that all parameters are positive constants. The total population size is constant since

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0. \quad (2.4)$$

In this model, it is assumed to be homogeneous mixing, i.e. each individual have the same probability to encounter another individual. Since β is the effective contact rate of an infectious individual and a fraction $\frac{S}{N}$ is a proportion to contact susceptible individuals by one infected individual, the rate of new infections per infection is $\frac{\beta S}{N}$. Thus the number of new infections per unit time is $\frac{\beta SI}{N}$. In other

words, the rate that susceptible individuals encounter infectious individuals and become infected is equal to $\frac{\beta SI}{N}$. This incidence is called the *standard incidence*.

Definition 2.1. A *disease-free equilibrium* is a steady state solution of an epidemic model at which the number of individuals in all disease stages are zero.

We first find a disease-free equilibrium of an SIR epidemic models.

Example 2.2. Consider an SIR model given by system (2.1)-(2.3). Setting the RHS of the system (2.1)-(2.3) to be equal to zero and let $I(t) = 0$. Then it is obvious that $R(t) = 0$ which implies $S(t) = N$. Thus the disease-free equilibrium point for this model is $(N, 0, 0)$.

2.2 Next generation method

The next generation method [9, 11] is the method for computing the basic reproduction number for which the population is structured.

Definition 2.3. The *basic reproduction number* denoted by \mathcal{R}_0 is an expected secondary infections produced by a primary index case introduced into a completely susceptible population.

In epidemic models, if $\mathcal{R}_0 < 1$, then the disease cannot invade the population. On the other hand, if $\mathcal{R}_0 > 1$, then the disease can invade a susceptible population.

Consider the compartmental models for disease transmission. A compartment is called a *disease compartment* if the individuals therein are infected.

Suppose there are p disease compartments and q non-disease compartments. Let $x = (x_1, \dots, x_p) \in \mathbb{R}^p$ be the subpopulations in each of disease compartments and $y = (y_1, \dots, y_q) \in \mathbb{R}^q$ be the subpopulations in each of non-disease compartments. Let \mathcal{F}_i be the rate of appearance of new infections in the i -th disease compartment and \mathcal{V}_i be the rate of transfer of individuals (disease progression, death and recovery rates) in the i -th disease compartment. Then the compartmental model can be written in the following form:

$$\frac{dx_i}{dt} = \mathcal{F}_i(x, y) - \mathcal{V}_i(x, y), \quad i = 1, \dots, p \quad (2.5)$$

$$\frac{dy_j}{dt} = g_j(x, y), \quad j = 1, \dots, q \quad (2.6)$$

where g_j is the rate of transfer of individuals in the j -th non-disease compartment.

By the linearization of (2.5) about the disease-free equilibrium $(0, y_0)$ with the assumptions given in [9], we have a linearized system

$$\frac{dx}{dt} = (F - V)x$$

where $F = \left[\frac{\partial \mathcal{F}_i}{\partial x_j}(0, y_0) \right]$ and $V = \left[\frac{\partial \mathcal{V}_i}{\partial x_j}(0, y_0) \right]$ are the $p \times p$ matrices for all $i, j = 1, \dots, p$.

Following Diekmann and Heesterbeek [11], the matrix $K = FV^{-1}$ is referred to as the *next generation matrix* for the system at the disease-free equilibrium.

Suppose that $K = [k_{ij}]$. The element k_{ij} means the expected number of secondary infections in compartment i produced by individuals initially in compartment j , during its entire period of infectiousness. Let $\phi = (\phi_1, \dots, \phi_p)$ be the vector describing the infecteds, that is, ϕ_i is the number of infected individuals in compartment i . In deterministic description we can then say that, if ϕ^0 describes the initial distribution of infecteds, the vector describing the first generation reads

$$\phi_i^1 = \sum_{j=1}^p k_{ij} \phi_j^0,$$

and then

$$\phi^1 = K\phi^0.$$

Continuing in this manner we get the n -th generation of infected as

$$\phi^n = K\phi^{n-1} = \dots = K^n\phi^0.$$

By using the average per-generation multiplication factor in the long run, \mathcal{R}_0 can be defined as

$$\mathcal{R}_0 := \lim_{n \rightarrow \infty} \|K^n\|^{\frac{1}{n}} = \rho(K) = \rho(FV^{-1}) \quad (2.7)$$

where $\|\cdot\|$ is any matrix norm and $\rho(\cdot)$ is the spectral radius of a square matrix.

The next example will demonstrate how to derive \mathcal{R}_0 using the next generation method.

Example 2.4. Consider an SIR model given by system (2.1)-(2.3). By Example 2.2, the disease-free equilibrium of this model is $(S^*, I^*, R^*) = (N, 0, 0)$ where N is the total population size(constant). From (2.1)-(2.3), we have the 1×1 matrices

$$[\mathcal{F}_I] = \left[\frac{\beta SI}{N} \right] \text{ and } [\mathcal{V}_I] = [(\mu + \gamma)I].$$

Then

$$F = \left[\frac{\beta S^*}{N} \right] = [\beta] \text{ and } V = [\mu + \gamma]$$

which are 1×1 matrices. Thus, the next generation matrix is $FV^{-1} = \left[\frac{\beta}{\mu + \gamma} \right]$. Hence, the basic reproduction number for an SIR model given by (2.1)-(2.3) is

$$\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\beta}{\mu + \gamma}. \quad (2.8)$$

We remark that although the next generation method is suitable for structured population, above example showed that it also works well for simple model.

2.3 Gravity model of population movement

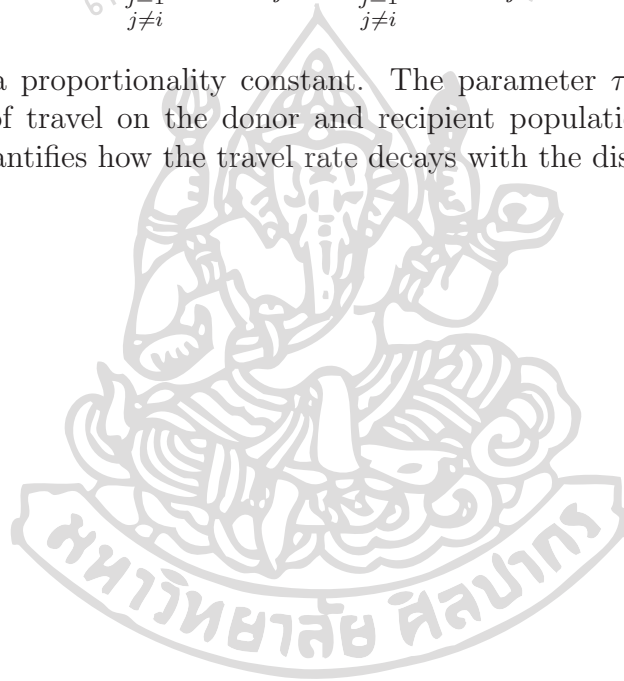
According to a generalized gravity model [1, 12], the rate that population of patch i moves to patch j is increased with the population size of coupled patches and decreased with the distance between patch i and patch j . That is, it is proportional to

$$\frac{N_j^{\tau_2} N_i^{\tau_1}}{D_{ij}^\theta} \quad (2.9)$$

where N_i is the population size of patch i , D_{ij} is the distance between patch i and patch j , and τ_1 , τ_2 , θ are positive parameters. Thus, we have a metapopulation model with n patches of the form

$$\frac{dN_i}{dt} = \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} N_j^{\tau_1}}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} N_i^{\tau_1}}{D_{ij}^\theta}, \quad i = 1, \dots, n \quad (2.10)$$

where w_0 is a proportionality constant. The parameter τ_1 and τ_2 indicate the dependency of travel on the donor and recipient population sizes, respectively, whereas θ quantifies how the travel rate decays with the distance.



Chapter 3

Model Formulation

In this chapter, we formulate an explicitly spatial SIR epidemic metapopulation model with a nonlinear travel subjected to the gravity law. The model used in this study is modified from that proposed in previous study [2]. The modification is due to the presence of a weak constraint. In order to be clear, we will begin the first part by reviewing the result from previous work.

Let us assume that the population travel subjected to the gravity law of movement and a population is divided into n distinct patches. For the transmission of a communicable disease among n patches 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. According to the gravity law of movement in section 2.3, we have the rate that population of patch i moves to patch j depends on the patch size and distance between patches. S. Puangsun and K. Patanarapeelert [2] assumed that the trip originating for each disease compartment is proportional to the number of individuals in that compartment. This results in the rate that susceptible, infectious and recovered individuals move from patch i to patch j are proportional to $\frac{N_j^{\tau_2} S_i^{\tau_1}}{D_{ij}^\theta}$, $\frac{N_j^{\tau_2} I_i^{\tau_1}}{D_{ij}^\theta}$ and $\frac{N_j^{\tau_2} R_i^{\tau_1}}{D_{ij}^\theta}$, respectively. Since the spatial coupling is explicitly determined, the contact occurs only within patch which is assumed to be homogeneous mixing. The heterogeneity of contact is the result from mixing that govern by the transport operator. An SIR epidemic model with n patches under the gravity law of movement proposed by S. Puangsun and K. Patanarapeelert [2] is given by

$$\frac{dS_i}{dt} = \mu_i N_i - \mu_i S_i - \frac{\beta_i S_i I_i}{N_i} + \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} S_j^{\tau_1}}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} S_i^{\tau_1}}{D_{ij}^\theta} \quad (3.1)$$

$$\frac{dI_i}{dt} = \frac{\beta_i S_i I_i}{N_i} - \mu_i I_i - \gamma_i I_i + \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} I_j^{\tau_1}}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} I_i^{\tau_1}}{D_{ij}^\theta} \quad (3.2)$$

$$\frac{dR_i}{dt} = \gamma_i I_i - \mu_i R_i + \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} R_j^{\tau_1}}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} R_i^{\tau_1}}{D_{ij}^\theta} \quad (3.3)$$

with $i = 1, \dots, n$. Here $N_i(t) = S_i(t) + I_i(t) + R_i(t)$ is the number of total population

in patch i at time t and w_0 is a proportionality constant. The model parameters are described as follows: μ_i denotes the birth rate and natural death rate in patch i , whereas β_i is an average number of effective contacts of infectious individual per unit time within patch i and γ_i is the recovery rate in patch i . The total population size, denoted by N is constant since

$$\frac{dN}{dt} = \frac{d}{dt} \left(\sum_{i=1}^n N_i \right) = \sum_{i=1}^n \frac{dN_i}{dt} = \sum_{i=1}^n \left(\frac{dS_i}{dt} + \frac{dI_i}{dt} + \frac{dR_i}{dt} \right) = 0. \quad (3.4)$$

In previous work, they focus on analyzing the model given by system (3.1)-(3.3) for $n = 2$, that is

$$\frac{dS_1}{dt} = \mu_1 N_1 - \mu_1 S_1 - \frac{\beta_1 S_1 I_1}{N_1} + \frac{w_0}{d_{12}} N_1^{\tau_2} S_2^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} S_1^{\tau_1} \quad (3.5)$$

$$\frac{dS_2}{dt} = \mu_2 N_2 - \mu_2 S_2 - \frac{\beta_2 S_2 I_2}{N_2} + \frac{w_0}{d_{12}} N_2^{\tau_2} S_1^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} S_2^{\tau_1} \quad (3.6)$$

$$\frac{dI_1}{dt} = \frac{\beta_1 S_1 I_1}{N_1} - \mu_1 I_1 - \gamma_1 I_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} I_2^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} I_1^{\tau_1} \quad (3.7)$$

$$\frac{dI_2}{dt} = \frac{\beta_2 S_2 I_2}{N_2} - \mu_2 I_2 - \gamma_2 I_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} I_1^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} I_2^{\tau_1} \quad (3.8)$$

$$\frac{dR_1}{dt} = \gamma_1 I_1 - \mu_1 R_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} R_2^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} R_1^{\tau_1} \quad (3.9)$$

$$\frac{dR_2}{dt} = \gamma_2 I_2 - \mu_2 R_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} R_1^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} R_2^{\tau_1} \quad (3.10)$$

where $d_{ij} = D_{ij}^\theta$. For this model, the disease-free equilibrium is denoted by $(S_1^*, S_2^*, I_1^*, I_2^*, R_1^*, R_2^*)$ with $I_1^* = I_2^* = 0$. Setting all infected variables equal to zero at steady state, it is easy to see that $R_1^* = R_2^* = 0$ from equations (3.9)-(3.10). It follows that $S_1^* = N_1^*$ and $S_2^* = N_2^*$ where (N_1^*, N_2^*) is an equilibrium point of the model (2.10) with $n = 2$. The disease-free equilibrium can be derived directly from the equilibrium point of the model (2.10) with $n = 2$. It is easy to see that there are four disease-free equilibrium points such as $(0, 0, 0, 0, 0, 0)$, $(N, 0, 0, 0, 0, 0)$, $(0, N, 0, 0, 0, 0)$ and $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$. Since the first three equilibrium points are nothing to do with disease transmission in metapopulation dynamics, it is reasonable to focus on stability of the last equilibrium. In order for the Jacobian matrix for (3.4)-(3.9) at the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ to exist, it is necessary to assume that $\tau_1 > 1$ which is a weak constraint since a parameter travel τ_1 should be arbitrary.

Define

$$\mathcal{R}_0^{(i)} = \frac{\beta_i}{\mu_i + \gamma_i} \quad (3.11)$$

as the basic reproduction number in patch i when there is no travel between the patches. This parameter describes the transmission potential within patch in isolation.

In order to derive \mathcal{R}_0 of the model given by system (3.5)-(3.10), we use the next generation method in section 2.2. The next generation matrix of this model

is

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

under a constraint $\tau_1 > 1$. Hence, the basic reproduction number for model (3.4)-(3.9) is

$$\mathcal{R}_0 = \rho(FV^{-1}) = \max_{i=1,2} \frac{\beta_i}{\mu_i + \gamma_i} = \max_{i=1,2} \mathcal{R}_0^{(i)}. \quad (3.12)$$

Clearly, the basic reproduction number for this model depends on the basic reproduction number in patch i when there is no travel between the patches. It is not allow us to understand how the term of travel affects the basic reproduction number in anyway.

We remark that, for applying the gravity law to this model, travel for each subpopulation, which is divided by disease states, is considered to depend on a recipient total population size and a donor subpopulation size. But the gravity law is increased with the total size of both patches, thus its travel should be depend on the total population size of both patches.

In this research, we modify an SIR epidemic model with applying the gravity law for the term of travel as the following.

By the gravity law in section 2.3, we observe that if the rate that the population of patch i moves to patch j is proportional to $\frac{N_j^{\tau_2} N_i^{\tau_1}}{D_{ij}^\theta}$, then the rate that an individual of patch i moves to patch j must proportional to

$$\frac{N_j^{\tau_2} N_i^{\tau_1 - 1}}{D_{ij}^\theta}. \quad (3.13)$$

This is a key element that leads to the new model. When the population is divided into three disease-state compartments, we have the rate that susceptible, infectious and recovered individuals move from patch i to patch j are proportional to $\frac{N_j^{\tau_2} N_i^{\tau_1 - 1} S_i}{D_{ij}^\theta}$, $\frac{N_j^{\tau_2} N_i^{\tau_1 - 1} I_i}{D_{ij}^\theta}$ and $\frac{N_j^{\tau_2} N_i^{\tau_1 - 1} R_i}{D_{ij}^\theta}$, respectively. For a new model, it is assumed that $\mu_i = \mu$ and $\gamma_i = \gamma$ for all $i = 1, \dots, n$ since the birth(death) rate for each patch should be equal in metapopulation and each patch have the same disease. Then we have a new explicitly SIR model with a gravity travel in a patchy environment of the form

$$\frac{dS_i}{dt} = \mu N_i - \mu S_i - \frac{\beta_i S_i I_i}{N_i} + \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} N_j^{\tau_1 - 1} S_j}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} N_i^{\tau_1 - 1} S_i}{D_{ij}^\theta} \quad (3.14)$$

$$\frac{dI_i}{dt} = \frac{\beta_i S_i I_i}{N_i} - \mu I_i - \gamma I_i + \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} N_j^{\tau_1 - 1} I_j}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} N_i^{\tau_1 - 1} I_i}{D_{ij}^\theta} \quad (3.15)$$

$$\frac{dR_i}{dt} = \gamma I_i - \mu R_i + \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} N_j^{\tau_1 - 1} R_j}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} N_i^{\tau_1 - 1} R_i}{D_{ij}^\theta} \quad (3.16)$$

where $i = 1, \dots, n$. We note that the model given by system (3.14)-(3.16) can get rid of a constraint $\tau_1 > 1$ and the basic reproduction number of this model depends on the travel term which will be presented in the next chapter. Moreover, D. Brockmann, V. David and A.M. Gallardo [13] showed that the rate that individuals of an SIS epidemic model move from a node i to a node j is directly proportional to $C_j^\xi C_i^{\xi-1}$ with $0 \leq \xi \leq 1$, where C_i and C_j are the capacity of the stationary population size of nodes i and j , respectively. That is, $C_i = P_i^k$ for some positive k and P_i is the stationary population size of nodes i . Thus, the rate that individuals of an SIS epidemic model move between nodes depends on the (stationary) population size of both nodes and we see that ξ is referred to as τ_1 and τ_2 which correspond to the movement rate of our model.

Next, we will firstly analyze and consider the new model to obtain its basic properties. The total population size N of the model (3.14)-(3.16) is also constant since it is satisfied equation (3.4). We assume that the initial conditions are satisfied $S_i(0) > 0$, $I_i(0) > 0$ and $R_i(0) \geq 0$ for all $i = 1, \dots, n$. According to the proof from [3], it is easy to show that $S_i(t)$, $I_i(t)$ and $R_i(t)$ are nonnegative for all t . For example, if I_i becomes zero at a time t_1 before I_k , S_j and R_j become zero for all $j = 1, \dots, n$ and $k = 1, \dots, n$ with $i \neq k$, then

$$\frac{dI_i}{dt} = \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} N_j^{\tau_1-1} I_j}{D_{ij}^\theta} \geq 0$$

at a time t_1 . Thus I_i is non-decreasing function of t at t_1 . Therefore, I_i is non-negative. Similarly, we have S_i and R_i are nonnegative for all $i = 1, \dots, n$. Moreover, provided that $N_i(t) > 0$ for all i , this model is well-posed since the RHS of the system (3.14)-(3.16) is continuous and continuously differentiable (see Picard-Lipschitz fundamental theorem of ordinary differential equations).

Finally, we consider the model given by (3.14)-(3.16) with $\tau_1 = \tau_2$. Then, when $\tau_1 = \tau_2$, we have

$$\frac{dN_i}{dt} = \frac{dS_i}{dt} + \frac{dI_i}{dt} + \frac{dR_i}{dt} = \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_i^{\tau_2} N_j^{\tau_1}}{D_{ij}^\theta} - \sum_{\substack{j=1 \\ j \neq i}}^n w_0 \frac{N_j^{\tau_2} N_i^{\tau_1}}{D_{ij}^\theta} = 0$$

for all $i = 1, \dots, n$ which implies that N_i is constant for all $i = 1, \dots, n$. Thus we have the rate that individual moves between patches given by (3.13) becomes constant in this case. Then an SIR model given by (3.14)-(3.16) will be the model with a linear travel which is not the goal of this research. Hence, throughout this research we consider the model given by (3.14)-(3.16) with $\tau_1 \neq \tau_2$ for studying an SIR epidemic model with a nonlinear travel under the gravity law.

Chapter 4

Model Analysis

To obtain some useful analytical results, we focus on the simplest network structure for (3.14)-(3.16). We begin by considering two patch model. The key feature of analysis is the conditions for which the disease dies out and spreads. We will derive the disease-free equilibrium and the basic reproduction number for two patch model. Usually, the stability condition for the disease-free equilibrium is associated with the basic reproduction number below unity. We will show that this is true for our case. Since such derived conditions depend on travel rates, we will examine in terms of the parameters τ_1 and τ_2 for the threshold condition of epidemic. Then, the three patch model will be analyzed analogously.

4.1 Analysis for an epidemic model of two patches

Consider an SIR epidemic model given by (3.14)-(3.16) for $n = 2$,

$$\frac{dS_1}{dt} = \mu N_1 - \mu S_1 - \frac{\beta_1 S_1 I_1}{N_1} + \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} S_2 - \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} S_1 \quad (4.1)$$

$$\frac{dS_2}{dt} = \mu N_2 - \mu S_2 - \frac{\beta_2 S_2 I_2}{N_2} + \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} S_1 - \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} S_2 \quad (4.2)$$

$$\frac{dI_1}{dt} = \frac{\beta_1 S_1 I_1}{N_1} - \mu I_1 - \gamma I_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} I_2 - \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} I_1 \quad (4.3)$$

$$\frac{dI_2}{dt} = \frac{\beta_2 S_2 I_2}{N_2} - \mu I_2 - \gamma I_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} I_1 - \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} I_2 \quad (4.4)$$

$$\frac{dR_1}{dt} = \gamma I_1 - \mu R_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} R_2 - \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} R_1 \quad (4.5)$$

$$\frac{dR_2}{dt} = \gamma I_2 - \mu R_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} R_1 - \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} R_2 \quad (4.6)$$

with $d_{ij} = D_{ij}^\theta$ and since the distance between two patches is constant, we have $d_{12} = d_{21}$.

Let us begin by finding a disease-free equilibrium which is denoted by $(S_1^*, S_2^*, I_1^*, I_2^*, R_1^*, R_2^*)$ with $I_1^* = I_2^* = 0$. Setting the right-hand side of the system (4.1)-(4.6) equal to zero with $I_1 = I_2 = 0$, we have a following system of algebraic

equations for S_1^* , S_2^* , R_1^* and R_2^* ,

$$\mu N_1^* - \mu S_1^* + \frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1-1} S_2^* - \frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1-1} S_1^* = 0 \quad (4.7)$$

$$\mu N_2^* - \mu S_2^* + \frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1-1} S_1^* - \frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1-1} S_2^* = 0 \quad (4.8)$$

$$-\mu R_1^* + \frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1-1} R_2^* - \frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1-1} R_1^* = 0 \quad (4.9)$$

$$-\mu R_2^* + \frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1-1} R_1^* - \frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1-1} R_2^* = 0 \quad (4.10)$$

where N_i^* is the total population of patch i at a disease-free state. From equations (4.9) and (4.10), we have $\mu(R_1^* + R_2^*) = 0$. Since μ is positive and the number of individuals must be nonnegative, $R_1^* = R_2^* = 0$. It implies that $S_i^* = N_i^*$ for all $i = 1, 2$. Thus equations (4.7) and (4.8) becomes

$$\frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1} - \frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1} = 0 \quad (4.11)$$

$$\frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1} - \frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1} = 0. \quad (4.12)$$

So, we are dealing with the steady state for the population model (2.10) with $n = 2$. Hence, the disease-free equilibrium can be derived directly from the equilibrium point of the model (2.10) with $n = 2$. Consequently, we see that there are four disease-free equilibrium points such as $(0, 0, 0, 0, 0, 0)$, $(N, 0, 0, 0, 0, 0)$, $(0, N, 0, 0, 0, 0)$ and $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$.

Since the first three disease-free equilibrium points are not relevant in the context of disease transmission in metapopulation dynamics, we focus on stability of the last disease-free equilibrium point $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$. The following theorem gives the conditions for stability of the disease-free equilibrium point which depends on travel parameters and the basic reproduction number of both patches in which there is no travel between patches.

Theorem 4.1. *A disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ of a model given by (4.1)-(4.6) is locally asymptotically stable if $\tau_2 < \tau_1$ and $\mathcal{R}_0^{(i)} < 1$ for all $i \in \{1, 2\}$.*

Proof. Note that the disease-free equilibrium is locally asymptotically stable if all eigenvalues of the Jacobian matrix for system (4.1)-(4.6) at the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ have negative real parts. The Jacobian matrix for system (4.1)-(4.6) at the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ is given by

$$J^* = \begin{bmatrix} A & B & C \\ \mathbf{0} & X & \mathbf{0} \\ \mathbf{0} & Y & Z \end{bmatrix}$$

where A , B , C , X , Y and Z are 2×2 matrices defined by

$$A = \begin{bmatrix} 2(\tau_2 - \tau_1)m & 0 \\ 0 & 2(\tau_2 - \tau_1)m \end{bmatrix}, B = \begin{bmatrix} \mu - \beta_1 + cm & -m \\ -m & \mu - \beta_2 + cm \end{bmatrix},$$

$$C = \begin{bmatrix} \mu + cm & -m \\ -m & \mu + cm \end{bmatrix}, X = \begin{bmatrix} \beta_1 - \mu - \gamma - m & m \\ m & \beta_2 - \mu - \gamma - m \end{bmatrix},$$

$$Y = \begin{bmatrix} \gamma & 0 \\ 0 & \gamma \end{bmatrix} \text{ and } Z = \begin{bmatrix} -\mu - m & m \\ m & -\mu - m \end{bmatrix}$$

with

$$m = \frac{w_0}{d_{12}} \left(\frac{N}{2} \right)^{\tau_1 + \tau_2 - 1}, \quad (4.13)$$

$c = 2\tau_2 - 2\tau_1 + 1$ and \mathbf{O} is a 2×2 zero matrix (see Appendix for detailed derivation). The eigenvalues of J^* compose of the eigenvalues of A , the eigenvalues of X and the eigenvalues of Z , respectively.

First, we will consider the eigenvalues of Z . The characteristic equation in variable λ for Z is

$$0 = \det(Z - \lambda I) = \lambda^2 + 2(\mu + m)\lambda + \mu^2 + 2\mu m.$$

So, two eigenvalues of Z are

$$\lambda_{1,2} = \frac{-2(\mu + m) \pm \sqrt{4(\mu + m)^2 - 4(\mu^2 + 2\mu m)}}{2}$$

$$= -(\mu + m) \pm m.$$

That is, $\lambda_1 = -\mu$ and $\lambda_2 = -\mu - 2m$ which are real and are always negative. Hence, the local stability of the disease-free equilibrium depends on the eigenvalues of both A and X . It is easy to see that two eigenvalues of A are

$$\lambda_{3,4} = 2(\tau_2 - \tau_1)m.$$

which are real. Thus, it is seen that λ_3 and λ_4 are negative if $\tau_2 < \tau_1$. Next, we consider the eigenvalues of X and begin by letting $a = \beta_1 - \mu - \gamma$ and $b = \beta_2 - \mu - \gamma$. The characteristic equation in variable λ for X is

$$0 = \det(X - \lambda I) = (a - m - \lambda)(b - m - \lambda) - m^2$$

$$= \lambda^2 - (a + b - 2m)\lambda + ab - (a + b)m.$$

Thus, the two eigenvalues of X are

$$\lambda_{5,6} = \frac{(a + b - 2m) \pm \sqrt{(a + b - 2m)^2 - 4ab + 4(a + b)m}}{2}.$$

Since

$$(a + b - 2m)^2 - 4ab + 4(a + b)m$$

$$= (a + b)^2 - 4(a + b)m + 4m^2 - 4ab + 4(a + b)m$$

$$= (a - b)^2 + 4m^2$$

$$= (\beta_1 - \beta_2)^2 + 4m^2$$

which is always positive, we have λ_5 and λ_6 are real. Next, we consider the sign of eigenvalues λ_5 and λ_6 provided the conditions $a < 0$ and $b < 0$.

If we assume that $a < 0$ and $b < 0$, then we have $(a + b)m < ab$ and $2m - a - b > 0$. It follows that

$$\begin{aligned} 4(a + b)m - 4ab &< 0 \\ (a + b - 2m)^2 + 4(a + b)m - 4ab &< (2m - a - b)^2. \end{aligned}$$

Since $(a + b - 2m)^2 + 4(a + b)m - 4ab > 0$ and $2m - a - b > 0$, we have

$$\sqrt{(a + b - 2m)^2 + 4(a + b)m - 4ab} < 2m - a - b$$

which implies that λ_5 is negative. And we also have λ_6 is negative since

$$a + b - 2m < \sqrt{(a + b - 2m)^2 - 4ab + 4(a + b)m}.$$

Therefore, if $a < 0$ and $b < 0$, then λ_5 and λ_6 are negative. Since $a < 0$ and $b < 0$ if and only if $\mathcal{R}_0^{(1)} < 1$ and $\mathcal{R}_0^{(2)} < 1$, respectively, we have λ_5 and λ_6 are negative if $\mathcal{R}_0^{(1)} < 1$ and $\mathcal{R}_0^{(2)} < 1$.

In sum, if $\tau_2 < \tau_1$, $\mathcal{R}_0^{(1)} < 1$ and $\mathcal{R}_0^{(2)} < 1$, then all eigenvalues of the Jacobian matrix J^* have negative real parts which implies that the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ is locally asymptotically stable. \square

We remark that, in the absence of the disease, the system (4.1)-(4.6) reduces to the model (2.10) 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, otherwise, the extinction may be observed.

In order to derive the basic reproduction number for two patches, we use the next generation method given in section 2.2. Here, the last disease-free equilibrium point is considered. From system (4.1)-(4.6), infected variables are I_1 and I_2 , we then have

$$\begin{bmatrix} \mathcal{F}_{I_1} \\ \mathcal{F}_{I_2} \end{bmatrix} = \begin{bmatrix} \frac{\beta_1 S_1 I_1}{N_1} \\ \frac{\beta_2 S_2 I_2}{N_2} \end{bmatrix}$$

and

$$\begin{bmatrix} \mathcal{V}_{I_1} \\ \mathcal{V}_{I_2} \end{bmatrix} = \begin{bmatrix} \mu I_1 + \gamma I_1 - \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} I_2 + \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} I_1 \\ \mu I_2 + \gamma I_2 - \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1-1} I_1 + \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1-1} I_2 \end{bmatrix}.$$

Therefore, we have matrices F and V defined in section 2.2. at the disease-free equilibrium $(S_1^*, S_2^*, I_1^*, I_2^*, R_1^*, R_2^*)$ as follows

$$F = \begin{bmatrix} \frac{\beta_1 S_1^* (N_1^* - I_1^*)}{N_1^{*2}} & 0 \\ 0 & \frac{\beta_2 S_2^* (N_2^* - I_2^*)}{N_2^{*2}} \end{bmatrix} \text{ and } V = \begin{bmatrix} V_1 & V_2 \end{bmatrix}$$

where

$$V_1 = \begin{bmatrix} \mu + \gamma - \frac{w_0}{d_{12}}\tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* + \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) \\ -\frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \end{bmatrix}$$

and

$$V_2 = \begin{bmatrix} -\frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\ \mu + \gamma - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* + \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) \end{bmatrix}.$$

Hence, at the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ we obtain

$$F = \begin{bmatrix} \beta_1 & 0 \\ 0 & \beta_2 \end{bmatrix} \text{ and } V = \begin{bmatrix} \mu + \gamma + m & -m \\ -m & \mu + \gamma + m \end{bmatrix}$$

with m is defined by (4.13). According to the next generation method, we define $\mathcal{R}_0 = \rho(FV^{-1})$. Since $\det V = (\mu + \gamma + m)^2 - m^2 = (\mu + \gamma)(\mu + \gamma + 2m) > 0$, V is nonsingular matrix. Then the next generation matrix for this model is

$$FV^{-1} = \begin{bmatrix} \beta_1 & 0 \\ 0 & \beta_2 \end{bmatrix} \begin{bmatrix} \frac{\mu + \gamma + m}{(\mu + \gamma)(\mu + \gamma + 2m)} & \frac{m}{(\mu + \gamma)(\mu + \gamma + 2m)} \\ \frac{m}{(\mu + \gamma)(\mu + \gamma + 2m)} & \frac{\mu + \gamma + m}{(\mu + \gamma)(\mu + \gamma + 2m)} \end{bmatrix} \quad (4.14)$$

$$= \begin{bmatrix} \frac{\beta_1(\mu + \gamma + m)}{(\mu + \gamma)(\mu + \gamma + 2m)} & \frac{\beta_1 m}{(\mu + \gamma)(\mu + \gamma + 2m)} \\ \frac{\beta_2 m}{(\mu + \gamma)(\mu + \gamma + 2m)} & \frac{\beta_2(\mu + \gamma + m)}{(\mu + \gamma)(\mu + \gamma + 2m)} \end{bmatrix}. \quad (4.15)$$

The characteristic equation in variable λ for the next generation matrix FV^{-1} is

$$(\mu + \gamma)(\mu + \gamma + 2m)\lambda^2 - (\beta_1 + \beta_2)(\mu + \gamma + m)\lambda + \beta_1\beta_2 = 0$$

which comes from the equation $\det(FV^{-1} - \lambda I) = 0$. Thus we obtain two eigenvalues of FV^{-1} ,

$$\lambda_{\pm} = \frac{(\beta_1 + \beta_2)(\mu + \gamma + m) \pm \sqrt{(\beta_1 + \beta_2)^2(\mu + \gamma + m)^2 - 4\beta_1\beta_2(\mu + \gamma)(\mu + \gamma + 2m)}}{2(\mu + \gamma)(\mu + \gamma + 2m)}.$$

Since

$$\begin{aligned} & (\beta_1 + \beta_2)^2(\mu + \gamma + m)^2 - 4\beta_1\beta_2(\mu + \gamma)(\mu + \gamma + 2m) \\ &= (\beta_1^2 + 2\beta_1\beta_2 + \beta_2^2)(\mu + \gamma + m)^2 - 4\beta_1\beta_2[(\mu + \gamma + m)^2 - m^2] \\ &= (\beta_1 - \beta_2)^2(\mu + \gamma + m)^2 + 4\beta_1\beta_2m^2, \end{aligned}$$

λ_{\pm} are real. Therefore,

$$\begin{aligned}\mathcal{R}_0 &= \rho(FV^{-1}) = \lambda_+ \\ &= \frac{(\beta_1 + \beta_2)(\mu + \gamma + m) + \sqrt{(\beta_1 - \beta_2)^2(\mu + \gamma + m)^2 + 4\beta_1\beta_2m^2}}{2(\mu + \gamma)(\mu + \gamma + 2m)}\end{aligned}$$

which is the basic reproduction number for two patches. It describes the average of secondary infection given by an index case who is introduced into the completely susceptible population of two patches. As far as the value of all parameters are known, we will obtain directly the basic reproduction number for describing the spread of the disease from above expression.

For a 2×2 matrix A with $\text{tr}(A) > 0$ and $\text{tr}(A)^2 - 4\det(A) > 0$, the following lemma gives the conditions for which the spectral radius of a matrix A is less than one.

Lemma 4.2. *Let A be a 2×2 matrix. If $\text{tr}(A) > 0$ and $\text{tr}(A)^2 - 4\det(A) > 0$, then $\rho(A) < 1$ if and only if $\text{tr}(A) < 2$ and $\text{tr}(A) - \det(A) < 1$.*

Proof. Suppose that A is a 2×2 matrix with $\text{tr}(A) > 0$ and $\text{tr}(A)^2 - 4\det(A) > 0$. The characteristic equation in variable λ of A is $\lambda^2 - \tau\lambda + \delta = 0$ where $\tau = \text{tr}(A)$ and $\delta = \det(A)$. Thus eigenvalues of A are

$$\lambda_{\pm} = \frac{\tau \pm \sqrt{\tau^2 - 4\delta}}{2}.$$

Since $\tau^2 - 4\delta > 0$, all eigenvalues are real. So

$$\rho(A) = \frac{\tau + \sqrt{\tau^2 - 4\delta}}{2}.$$

Then we have

$$\begin{aligned}\rho(A) < 1 &\iff \tau + \sqrt{\tau^2 - 4\delta} < 2 \\ &\iff \sqrt{\tau^2 - 4\delta} < 2 - \tau \\ &\iff \tau^2 - 4\delta < (2 - \tau)^2 \text{ and } \tau < 2 \\ &\iff -\delta < 1 - \tau \text{ and } \tau < 2 \\ &\iff \tau - \delta < 1 \text{ and } \tau < 2\end{aligned}$$

which completes the proof. \square

We now rewrite the matrix FV^{-1} given by (4.15) as

$$FV^{-1} = \begin{bmatrix} \mathcal{R}_0^{(1)}\epsilon & \mathcal{R}_0^{(1)}\eta \\ \mathcal{R}_0^{(2)}\eta & \mathcal{R}_0^{(2)}\epsilon \end{bmatrix} \quad (4.16)$$

where

$$\epsilon = \frac{\mu + \gamma + m}{\mu + \gamma + 2m} \quad (4.17)$$

and

$$\eta = \frac{m}{\mu + \gamma + 2m}. \quad (4.18)$$

Since μ , γ and m are positive, it is easy to see that $0 < \epsilon < 1$, $0 < \eta < 1$ and $\epsilon + \eta = 1$. In particular, $0.5 < \epsilon$. Note that by (4.16) we have $tr(FV^{-1}) = (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon > 0$ and

$$\begin{aligned} \det(FV^{-1}) &= \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(\epsilon^2 - \eta^2) \\ &= \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(\epsilon - \eta)(\epsilon + \eta) \\ &= \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(\epsilon - \eta). \end{aligned}$$

Furthermore, we have

$$\begin{aligned} tr(FV^{-1})^2 - 4\det(FV^{-1}) &= (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})^2\epsilon^2 - 4\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(\epsilon - \eta) \\ &= \frac{(\beta_1 + \beta_2)^2(\mu + \gamma + m)^2 - 4\beta_1\beta_2(\mu + \gamma)(\mu + \gamma + 2m)}{(\mu + \gamma)^2(\mu + \gamma + 2m)^2} \\ &> 0 \end{aligned}$$

which corresponds to the assumption of Lemma 4.2. Hence, we can apply Lemma 4.2 to the matrix FV^{-1} .

The three following theorems describe the criterion for the disease can invade or cannot invade the population for two patches by applying Lemma 4.2. The first theorem shows that if the disease cannot invade the population in both patches in which there is no travel between patches, then the disease also cannot invade the population although there is travelling between patches.

Theorem 4.3. *For the model given by a system (4.1)-(4.6), if $\mathcal{R}_0^{(i)} < 1$ for all $i \in \{1, 2\}$, then $\mathcal{R}_0 < 1$.*

Proof. Assume that $\mathcal{R}_0^{(1)} < 1$ and $\mathcal{R}_0^{(2)} < 1$. From the bound of ϵ which is defined by (4.17), we have $tr(FV^{-1}) = (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon < \mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} < 2$. Therefore, by Lemma 4.2, it suffices to show that $1 - tr(FV^{-1}) + \det(FV^{-1}) > 0$. Consider

$$\begin{aligned} 1 - tr(FV^{-1}) + \det(FV^{-1}) &= 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(\epsilon - \eta) \\ &= 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(2\epsilon - 1) \end{aligned}$$

which is a function of ϵ , denoted by $f(\epsilon)$. Then we have $f(0.5) = 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})(0.5) > 0$ and $f(1) = 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)}) + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} = (1 - \mathcal{R}_0^{(1)})(1 - \mathcal{R}_0^{(2)}) > 0$. That is, f is linear function with $f(0.5) > 0$ and $f(1) > 0$. It implies that f is a positive function for all $0.5 < \epsilon < 1$. That is, $1 - tr(FV^{-1}) + \det(FV^{-1}) > 0$. By Lemma 4.2, we have $\mathcal{R}_0 = \rho(FV^{-1}) < 1$ which completes the proof. \square

On the other hand, the following theorem shows that if the disease can invade a susceptible in both patches in which there is no travel between patches, then the disease also can invade a susceptible although there is travelling between patches.

Theorem 4.4. *For the model given by a system (4.1)-(4.6), if $\mathcal{R}_0^{(i)} > 1$ for all $i \in \{1, 2\}$, then $\mathcal{R}_0 > 1$.*

Proof. Assume that $\mathcal{R}_0^{(1)} > 1$ and $\mathcal{R}_0^{(2)} > 1$. By Lemma 4.2, we have

$$\text{tr}(FV^{-1}) > 2 \text{ or } \text{tr}(FV^{-1}) - \det(FV^{-1}) > 1 \longrightarrow \rho(FV^{-1}) > 1.$$

By the first condition, it implies directly that $\mathcal{R}_0 > 1$ if $\epsilon > \epsilon^0$ where

$$\epsilon^0 = \frac{2}{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)}}. \quad (4.19)$$

Next, we use the second condition to show that $\mathcal{R}_0 > 1$ for some interval of ϵ . Recall the function f which is defined in the proof of Theorem 4.3, we have $f(0.5) = 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})(0.5) < 0$ and $f(1) = (1 - \mathcal{R}_0^{(1)})(1 - \mathcal{R}_0^{(2)}) > 0$. By the linearity of a function f , we have f is an increasing function for all $0.5 < \epsilon < 1$ with $f(0.5) < 0$ and $f(1) > 0$. Thus there exist a unique point $\epsilon^* \in (0.5, 1)$ such that $f(\epsilon^*) = 0$. By calculating, we obtain

$$\epsilon^* = \frac{\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - 1}{2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - \mathcal{R}_0^{(1)} - \mathcal{R}_0^{(2)}}. \quad (4.20)$$

It follows that f is a negative function on $\epsilon < \epsilon^*$. That is, $\text{tr}(FV^{-1}) - \det(FV^{-1}) > 1$ if $\epsilon < \epsilon^*$. Therefore, $\mathcal{R}_0 > 1$ if $\epsilon < \epsilon^*$.

Next, we will show that $\epsilon^* > \epsilon^0$. From the fact that $(\mathcal{R}_0^{(i)} - 1)^2 > 0$ and $\mathcal{R}_0^{(i)} > 0$ for all $i = 1, 2$, we have

$$((\mathcal{R}_0^{(1)})^2 - 2\mathcal{R}_0^{(1)} + 1)\mathcal{R}_0^{(2)} > 0 \text{ and } ((\mathcal{R}_0^{(2)})^2 - 2\mathcal{R}_0^{(2)} + 1)\mathcal{R}_0^{(1)} > 0.$$

So,

$$\mathcal{R}_0^{(1)}((\mathcal{R}_0^{(2)})^2 + 1) > 2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} \text{ and } \mathcal{R}_0^{(2)}((\mathcal{R}_0^{(1)})^2 + 1) > 2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}.$$

It follows that

$$\begin{aligned} \mathcal{R}_0^{(1)}((\mathcal{R}_0^{(2)})^2 + 1) + \mathcal{R}_0^{(2)}((\mathcal{R}_0^{(1)})^2 + 1) &> 2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} + 2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} \\ (\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} + 1)(\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)}) &> 4\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} \\ (\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - 1)(\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)}) &> 4\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - 2(\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)}) \end{aligned}$$

In particular, $\mathcal{R}_0^{(1)} > 1$ and $\mathcal{R}_0^{(2)} > 1$, we have $2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - \mathcal{R}_0^{(1)} - \mathcal{R}_0^{(2)} > 0$. Thus

$$\frac{\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - 1}{2\mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)} - \mathcal{R}_0^{(1)} - \mathcal{R}_0^{(2)}} > \frac{2}{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)}}.$$

That is, $\epsilon^* > \epsilon^0$, as required. Hence, $\mathcal{R}_0 > 1$ for all $0.5 < \epsilon < 1$. \square

The next theorem gives the conditions that the disease can or cannot invade the population for the model that have an epidemic patch and a nonepidemic patch when there is no travel between patches.

Theorem 4.5. *For a model given by a system (4.1)-(4.6) with $\mathcal{R}_0^{(i)} < 1$ and $\mathcal{R}_0^{(j)} > 1$ for some $i, j \in \{1, 2\}$ and $i \neq j$. Suppose that $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} < 2$. Then*

- (i). $\mathcal{R}_0 < 1$ if $\epsilon < \epsilon^*$
- (ii). $\mathcal{R}_0 > 1$ if $\epsilon > \epsilon^*$

where ϵ and ϵ^* are defined by (4.17) and (4.20), respectively.

Proof. Without loss of generality, we assume that $\mathcal{R}_0^{(1)} < 1$ and $\mathcal{R}_0^{(2)} > 1$ with $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} < 2$. From the bound of ϵ defined by (4.17), we obtain

$$\text{tr}(FV^{-1}) = (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon < \mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} < 2.$$

Thus, by applying Lemma 4.2, we have that

$$\mathcal{R}_0 < 1 \iff 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(2\epsilon - 1) > 0.$$

Recall the function f which is defined in the proof of Theorem 4.3, we have $f(0.5) = 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})(0.5) > 0$ and $f(1) = (1 - \mathcal{R}_0^{(1)})(1 - \mathcal{R}_0^{(2)}) < 0$. Therefore, f is a linear function of ϵ with $f(0.5) > 0$ and $f(1) < 0$. Thus f is a decreasing function with respect to ϵ . It follows that f is a positive function on $\epsilon < \epsilon^*$ where ϵ^* is defined by (4.20) with $f(\epsilon^*) = 0$. That is, $1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(2\epsilon - 1) > 0$ if $\epsilon < \epsilon^*$. Hence, $\mathcal{R}_0 < 1$ if $\epsilon < \epsilon^*$. Conversely, f is a negative function on $\epsilon > \epsilon^*$ which implies that $1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(2\epsilon - 1) < 0$ if $\epsilon > \epsilon^*$. Consequently, $\mathcal{R}_0 > 1$ if $\epsilon > \epsilon^*$. \square

We remark that if $\mathcal{R}_0^{(1)} < 1$ and $\mathcal{R}_0^{(2)} > 1$ with $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} > 2$, then $f(0.5) < 0$ and $f(1) < 0$. By the linearity of a function f , we have f is a negative function for all $0.5 < \epsilon < 1$ which implies that $1 - \text{tr}(A) + \det(A) = 1 - (\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)})\epsilon + \mathcal{R}_0^{(1)}\mathcal{R}_0^{(2)}(2\epsilon - 1) < 0$ for all $0.5 < \epsilon < 1$. Thus, by Lemma 4.2, we have $\mathcal{R}_0 > 1$ for all $0.5 < \epsilon < 1$.

In Theorem 4.5, we have the condition for which the disease spread depending on the parameter ϵ . When we expand the parameter ϵ , we see that the spread of the disease depends on the parameters m which is the term of travel parameters τ_2 and τ_1 . Thus, in this case, the travel subject to the gravity law affects the spread of the disease, whereas it does not affect the spread of the disease in case of Theorem 4.3 and Theorem 4.4.

Next, we derive the equilibrium point of the model at which the number of infectious individual is not equal to zero, this is called *an endemic equilibrium point*.

Let $(\hat{S}_1, \hat{S}_2, \hat{I}_1, \hat{I}_2, \hat{R}_1, \hat{R}_2)$ with $\hat{I}_1 > 0$ or $\hat{I}_2 > 0$ be an endemic equilibrium point of the model given by (4.1)-(4.6) and let $\hat{N}_i = \hat{S}_i + \hat{I}_i + \hat{R}_i$ be the total population number of patch i at an endemic state. We have that (\hat{N}_1, \hat{N}_2) is an equilibrium point of the population model (2.10) with $n = 2$. Thus $(\hat{N}_1, \hat{N}_2) = (\frac{N}{2}, \frac{N}{2})$ which is a unique positive equilibrium point of the population model. Therefore,

$$\hat{S}_1 = \frac{N}{2} - \hat{I}_1 - \hat{R}_1 \quad \text{and} \quad \hat{S}_2 = \frac{N}{2} - \hat{I}_2 - \hat{R}_2.$$

For deriving $\hat{I}_1, \hat{I}_2, \hat{R}_1$ and \hat{R}_2 , we can solve from the following system,

$$\frac{2\beta_1\hat{S}_1\hat{I}_1}{N} - \mu\hat{I}_1 - \gamma\hat{I}_1 + m\hat{I}_2 - m\hat{I}_1 = 0 \quad (4.21)$$

$$\frac{2\beta_2\hat{S}_2\hat{I}_2}{N} - \mu\hat{I}_2 - \gamma\hat{I}_2 + m\hat{I}_1 - m\hat{I}_2 = 0 \quad (4.22)$$

$$\gamma\hat{I}_1 - \mu\hat{R}_1 + m\hat{R}_2 - m\hat{R}_1 = 0 \quad (4.23)$$

$$\gamma\hat{I}_2 - \mu\hat{R}_2 + m\hat{R}_1 - m\hat{R}_2 = 0 \quad (4.24)$$

with m is defined by (4.13). From equations (4.23) and (4.24), we have

$$\hat{R}_1 = \frac{\gamma\hat{I}_1 + m\hat{R}_2}{\mu + m} \quad \text{and} \quad \hat{R}_2 = \frac{\gamma\hat{I}_2 + m\hat{R}_1}{\mu + m},$$

respectively. By eliminating variables \hat{R}_1 and \hat{R}_2 in the RHS, we obtain

$$\hat{R}_1 = \frac{\gamma\hat{I}_1 + m\left(\frac{\gamma\hat{I}_2 + m\hat{R}_1}{\mu + m}\right)}{\mu + m} = \frac{\gamma(\mu + m)\hat{I}_1 + m\gamma\hat{I}_2 + m^2\hat{R}_1}{(\mu + m)^2}$$

and

$$\hat{R}_2 = \frac{\gamma\hat{I}_2 + m\left(\frac{\gamma\hat{I}_1 + m\hat{R}_2}{\mu + m}\right)}{\mu + m} = \frac{\gamma(\mu + m)\hat{I}_2 + m\gamma\hat{I}_1 + m^2\hat{R}_2}{(\mu + m)^2}$$

which implies that

$$\hat{R}_1 = \frac{\gamma(\mu + m)\hat{I}_1 + m\gamma\hat{I}_2}{(\mu + m)^2 - m^2}$$

and

$$\hat{R}_2 = \frac{\gamma(\mu + m)\hat{I}_2 + m\gamma\hat{I}_1}{(\mu + m)^2 - m^2}.$$

Now, we have both \hat{R}_1 and \hat{R}_2 are expressed in terms of \hat{I}_1 and \hat{I}_2 . Next, we derive \hat{I}_1 and \hat{I}_2 . From (4.21), we have

$$\frac{2}{N}\beta_1\left(\frac{N}{2} - \hat{I}_1 - \hat{R}_1\right)\hat{I}_1 - (\mu + \gamma + m)\hat{I}_1 + m\hat{I}_2 = 0$$

$$\beta_1N\hat{I}_1 - 2\beta_1\hat{I}_1^2 - 2\beta_1\hat{R}_1\hat{I}_1 - (\mu + \gamma + m)N\hat{I}_1 + mN\hat{I}_2 = 0$$

$$\beta_1N\hat{I}_1 - 2\beta_1\hat{I}_1^2 - 2\beta_1\left(\frac{\gamma(\mu + m)\hat{I}_1 + m\gamma\hat{I}_2}{(\mu + m)^2 - m^2}\right)\hat{I}_1 - (\mu + \gamma + m)N\hat{I}_1 + mN\hat{I}_2 = 0.$$

Simplifying the last equation and letting $k = (\mu + m)^2 - m^2$, we have

$$k(\beta_1 - \mu - \gamma - m)N\hat{I}_1 - 2\beta_1(k + \gamma\mu + m\gamma)\hat{I}_1^2 = (2\beta_1m\gamma\hat{I}_1 - kmN)\hat{I}_2.$$

In the same argument, from (4.22), we have

$$k(\beta_2 - \mu - \gamma - m)N\hat{I}_2 - 2\beta_2(k + \gamma\mu + m\gamma)\hat{I}_2^2 = (2\beta_2m\gamma\hat{I}_2 - kmN)\hat{I}_1.$$

We remark that $\hat{I}_1 = 0$ if and only if $\hat{I}_2 = 0$. Thus, $\hat{I}_1 > 0$ and $\hat{I}_2 > 0$ at an endemic state. Next, we can distinguish four cases as follows.

Case I. $\hat{I}_1 = \frac{kN}{2\beta_1\gamma}$ and $\hat{I}_2 = \frac{kN}{2\beta_2\gamma}$. Observe that $\hat{I}_1 = \frac{kN}{2\beta_1\gamma}$ occurs when $\beta_1 = \frac{k}{\gamma} + 2(\mu + m) + \gamma$ and $\hat{I}_2 = \frac{kN}{2\beta_2\gamma}$ occurs when $\beta_2 = \frac{k}{\gamma} + 2(\mu + m) + \gamma$. It follows that $\beta_1 = \beta_2$ which implies that $\hat{I}_1 = \hat{I}_2$.

Case II. $\hat{I}_1 = \frac{kN}{2\beta_1\gamma}$ and $\hat{I}_2 \neq \frac{kN}{2\beta_2\gamma}$. We can derive \hat{I}_2 from a quadratic equation

$$2\beta_2(k + \gamma\mu + m\gamma)\hat{I}_2^2 + kN\left(\frac{\beta_2m}{\beta_1} - \beta_2 + \mu + \gamma + m\right)\hat{I}_2 - \frac{k^2mN^2}{2\beta_1\gamma} = 0.$$

Note that this quadratic equation has only one positive real root since the last term is negative.

Case III. $\hat{I}_1 \neq \frac{kN}{2\beta_1\gamma}$ and $\hat{I}_2 = \frac{kN}{2\beta_2\gamma}$. We can derive \hat{I}_1 from a quadratic equation

$$2\beta_1(k + \gamma\mu + m\gamma)\hat{I}_1^2 + kN\left(\frac{\beta_1m}{\beta_2} - \beta_1 + \mu + \gamma + m\right)\hat{I}_1 - \frac{k^2mN^2}{2\beta_2\gamma} = 0.$$

On the same note in previous case, this quadratic equation has only one positive real root since the last term is negative.

Case IV. $\hat{I}_1 \neq \frac{kN}{2\beta_1\gamma}$ and $\hat{I}_2 \neq \frac{kN}{2\beta_2\gamma}$. We have

$$\hat{I}_2 = \frac{k(\beta_1 - \mu - \gamma - m)N\hat{I}_1 - 2\beta_1(k + \gamma\mu + m\gamma)\hat{I}_1^2}{2\beta_1m\gamma\hat{I}_1 - kmN} \quad (4.25)$$

and

$$\hat{I}_1 = \frac{k(\beta_2 - \mu - \gamma - m)N\hat{I}_2 - 2\beta_2(k + \gamma\mu + m\gamma)\hat{I}_2^2}{2\beta_2m\gamma\hat{I}_2 - kmN}. \quad (4.26)$$

After substituting \hat{I}_2 given by equation (4.25) into equation (4.26), we can obtain \hat{I}_1 from a cubic equation

$$c_3\hat{I}_1^3 + c_2\hat{I}_1^2 + c_1\hat{I}_1 + c_0 = 0$$

where c_0 , c_1 , c_2 and c_3 are coefficients. We will not expand the coefficients due to the complexity. Hence, we can derive the endemic equilibrium point for this model.

4.2 Analysis for an epidemic model of three patches

In this section, we consider an SIR epidemic model given by (3.14)-(3.16) for $n = 3$. The three patches model is given by

$$\frac{dS_1}{dt} = \mu N_1 - \mu S_1 - \frac{\beta_1 S_1 I_1}{N_1} + m_{21} S_2 + m_{31} S_3 - m_{12} S_1 - m_{13} S_1 \quad (4.27)$$

$$\frac{dS_2}{dt} = \mu N_2 - \mu S_2 - \frac{\beta_2 S_2 I_2}{N_2} + m_{12} S_1 + m_{32} S_3 - m_{21} S_2 - m_{23} S_2 \quad (4.28)$$

$$\frac{dS_3}{dt} = \mu N_3 - \mu S_3 - \frac{\beta_3 S_3 I_3}{N_3} + m_{13} S_1 + m_{23} S_2 - m_{31} S_3 - m_{32} S_3 \quad (4.29)$$

$$\frac{dI_1}{dt} = \frac{\beta_1 S_1 I_1}{N_1} - \mu I_1 - \gamma I_1 + m_{21} I_2 + m_{31} I_3 - m_{12} I_1 - m_{13} I_1 \quad (4.30)$$

$$\frac{dI_2}{dt} = \frac{\beta_2 S_2 I_2}{N_2} - \mu I_2 - \gamma I_2 + m_{12} I_1 + m_{32} I_3 - m_{21} I_2 - m_{23} I_2 \quad (4.31)$$

$$\frac{dI_3}{dt} = \frac{\beta_3 S_3 I_3}{N_3} - \mu I_3 - \gamma I_3 + m_{13} I_1 + m_{23} I_2 - m_{31} I_3 - m_{32} I_3 \quad (4.32)$$

$$\frac{dR_1}{dt} = \gamma I_1 - \mu R_1 + m_{21} R_2 + m_{31} R_3 - m_{12} R_1 - m_{13} R_1 \quad (4.33)$$

$$\frac{dR_2}{dt} = \gamma I_2 - \mu R_2 + m_{12} R_1 + m_{32} R_3 - m_{21} R_2 - m_{23} R_2 \quad (4.34)$$

$$\frac{dR_3}{dt} = \gamma I_3 - \mu R_3 + m_{13} R_1 + m_{23} R_2 - m_{31} R_3 - m_{32} R_3 \quad (4.35)$$

where $m_{ij}(t) = \frac{w_0}{d_{ij}} N_j(t)^{\tau_2} N_i(t)^{\tau_1 - 1}$ with $N_i = S_i + I_i + R_i$ and $N_j = S_j + I_j + R_j$.

First, we will determine the disease-free equilibrium $(S_1^*, S_2^*, S_3^*, I_1^*, I_2^*, I_3^*, R_1^*, R_2^*, R_3^*)$ with $I_1^* = I_2^* = I_3^* = 0$ of the presented model. Setting the right-hand side of the system (4.27)-(4.35) equal to zero with $I_1 = I_2 = I_3 = 0$, we can derive $S_1^*, S_2^*, S_3^*, R_1^*, R_2^*$ and R_3^* by solving the following system

$$\mu N_1^* - \mu S_1^* + m_{21}^* S_2^* + m_{31}^* S_3^* - m_{12}^* S_1^* - m_{13}^* S_1^* = 0 \quad (4.36)$$

$$\mu N_2^* - \mu S_2^* + m_{12}^* S_1^* + m_{32}^* S_3^* - m_{21}^* S_2^* - m_{23}^* S_2^* = 0 \quad (4.37)$$

$$\mu N_3^* - \mu S_3^* + m_{13}^* S_1^* + m_{23}^* S_2^* - m_{31}^* S_3^* - m_{32}^* S_3^* = 0 \quad (4.38)$$

$$-\mu R_1^* + m_{21}^* R_2^* + m_{31}^* R_3^* - m_{12}^* R_1^* - m_{13}^* R_1^* = 0 \quad (4.39)$$

$$-\mu R_2^* + m_{12}^* R_1^* + m_{32}^* R_3^* - m_{21}^* R_2^* - m_{23}^* R_2^* = 0 \quad (4.40)$$

$$-\mu R_3^* + m_{13}^* R_1^* + m_{23}^* R_2^* - m_{31}^* R_3^* - m_{32}^* R_3^* = 0 \quad (4.41)$$

where $m_{ij}^* = \frac{w_0}{d_{ij}} N_j^{*\tau_2} N_i^{*\tau_1 - 1}$ with N_i^* is the total population number of patch i at a disease-free state. Summing equations (4.39), (4.40) and (4.41), we have $\mu(R_1^* + R_2^* + R_3^*) = 0$. By the same reasons with two patches model, μ is positive and the number of individuals must be nonnegative, we then have $R_1^* = R_2^* = R_3^* = 0$. It implies that $S_i^* = N_i^*$ for all $i \in \{1, 2, 3\}$. Then equations (4.36), (4.37) and

(4.38) become

$$\begin{aligned} m_{21}^* N_2^* + m_{31}^* N_3^* - m_{12}^* N_1^* - m_{13}^* N_1^* &= 0 \\ m_{12}^* N_1^* + m_{32}^* N_3^* - m_{21}^* N_2^* - m_{23}^* N_2^* &= 0 \\ m_{13}^* N_1^* + m_{23}^* N_2^* - m_{31}^* N_3^* - m_{32}^* N_3^* &= 0. \end{aligned}$$

We observe that (N_1^*, N_2^*, N_3^*) is an equilibrium point of the model (2.10) with $n = 3$, that is

$$\frac{dN_1}{dt} = \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1} + \frac{w_0}{d_{13}} N_1^{\tau_2} N_3^{\tau_1} - \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1} - \frac{w_0}{d_{13}} N_3^{\tau_2} N_1^{\tau_1} \quad (4.42)$$

$$\frac{dN_2}{dt} = \frac{w_0}{d_{12}} N_2^{\tau_2} N_1^{\tau_1} + \frac{w_0}{d_{23}} N_2^{\tau_2} N_3^{\tau_1} - \frac{w_0}{d_{12}} N_1^{\tau_2} N_2^{\tau_1} - \frac{w_0}{d_{23}} N_3^{\tau_2} N_2^{\tau_1} \quad (4.43)$$

$$\frac{dN_3}{dt} = \frac{w_0}{d_{13}} N_3^{\tau_2} N_1^{\tau_1} + \frac{w_0}{d_{23}} N_3^{\tau_2} N_2^{\tau_1} - \frac{w_0}{d_{13}} N_1^{\tau_2} N_3^{\tau_1} - \frac{w_0}{d_{23}} N_2^{\tau_2} N_3^{\tau_1} \quad (4.44)$$

with the constant total population N . Thus the equilibrium point (N_1^*, N_2^*, N_3^*) must satisfy with following equations

$$\frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1} + \frac{w_0}{d_{13}} N_1^{*\tau_2} N_3^{*\tau_1} = \frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1} + \frac{w_0}{d_{13}} N_3^{*\tau_2} N_1^{*\tau_1} \quad (4.45)$$

$$\frac{w_0}{d_{12}} N_2^{*\tau_2} N_1^{*\tau_1} + \frac{w_0}{d_{23}} N_2^{*\tau_2} N_3^{*\tau_1} = \frac{w_0}{d_{12}} N_1^{*\tau_2} N_2^{*\tau_1} + \frac{w_0}{d_{23}} N_3^{*\tau_2} N_2^{*\tau_1} \quad (4.46)$$

$$\frac{w_0}{d_{13}} N_3^{*\tau_2} N_1^{*\tau_1} + \frac{w_0}{d_{23}} N_3^{*\tau_2} N_2^{*\tau_1} = \frac{w_0}{d_{13}} N_1^{*\tau_2} N_3^{*\tau_1} + \frac{w_0}{d_{23}} N_2^{*\tau_2} N_3^{*\tau_1}. \quad (4.47)$$

Obviously, the trivial equilibrium point is $(0, 0, 0)$. For the boundary equilibrium point such that only one patch has zero population, for example, if $N_1^* = 0$, then we will derive (N_2^*, N_3^*) from equations

$$\begin{aligned} \frac{w_0}{d_{23}} N_2^{*\tau_2} N_3^{*\tau_1} &= \frac{w_0}{d_{23}} N_3^{*\tau_2} N_2^{*\tau_1} \\ \frac{w_0}{d_{23}} N_3^{*\tau_2} N_2^{*\tau_1} &= \frac{w_0}{d_{23}} N_2^{*\tau_2} N_3^{*\tau_1}. \end{aligned}$$

It is clear that we retrieve the steady state of the model of two patches. It follows that the boundary equilibrium points of three patches model are $(0, N, 0)$, $(0, 0, N)$ and $(0, \frac{N}{2}, \frac{N}{2})$. Hence, all equilibrium point of three patches model are $(0, 0, 0)$, $(0, N, 0)$, $(0, 0, N)$, $(N, 0, 0)$, $(0, \frac{N}{2}, \frac{N}{2})$, $(\frac{N}{2}, 0, \frac{N}{2})$, $(\frac{N}{2}, \frac{N}{2}, 0)$ and (N_1^*, N_2^*, N_3^*) with $N_i^* > 0$ for all $i \in \{1, 2, 3\}$. The last point is referred to as a positive equilibrium point.

In the following theorem, we show that the model has a unique positive equilibrium point, in particular, we find $(N_1^*, N_2^*, N_3^*) = (\frac{N}{3}, \frac{N}{3}, \frac{N}{3})$.

Theorem 4.6. *For the population model given by (2.10) with $n = 3$, if $N_i > 0$ for all $i \in \{1, 2, 3\}$, then there exists a unique equilibrium point. Moreover, this equilibrium point is $(\frac{N}{3}, \frac{N}{3}, \frac{N}{3})$.*

Proof. Consider the model given by (4.42)-(4.44) which is the population model given by (2.10) with $n = 3$. Since the total population number N is constant, we can consider this model from equations (4.42) and (4.43) with $N_3(t) = N - N_1(t) - N_2(t)$. Assume that $N_1(t) > 0$, $N_2(t) > 0$ and $N_3(t) > 0$ for all t . Let (N_1^*, N_2^*, N_3^*) be the positive equilibrium point of this model. It is clear that (N_1^*, N_2^*, N_3^*) satisfy the system (4.45)-(4.46) with $N_3^* = N - N_1^* - N_2^*$. Rewrite the system as following

$$N_1^{*\tau_2} \left(\frac{N_2^{*\tau_1}}{d_{12}} + \frac{N_3^{*\tau_1}}{d_{13}} \right) = N_1^{*\tau_1} \left(\frac{N_2^{*\tau_2}}{d_{12}} + \frac{N_3^{*\tau_2}}{d_{13}} \right) \quad (4.48)$$

$$N_2^{*\tau_2} \left(\frac{N_1^{*\tau_1}}{d_{12}} + \frac{N_3^{*\tau_1}}{d_{23}} \right) = N_2^{*\tau_1} \left(\frac{N_1^{*\tau_2}}{d_{12}} + \frac{N_3^{*\tau_2}}{d_{23}} \right). \quad (4.49)$$

Multiplying (4.48) by $\frac{1}{N_1^{*\tau_1+\tau_2}}$, we have

$$\frac{1}{d_{12}} \left(\frac{N_2^*}{N_1^*} \right)^{\tau_1} + \frac{1}{d_{13}} \left(\frac{N_3^*}{N_1^*} \right)^{\tau_1} = \frac{1}{d_{12}} \left(\frac{N_2^*}{N_1^*} \right)^{\tau_2} + \frac{1}{d_{13}} \left(\frac{N_3^*}{N_1^*} \right)^{\tau_2}. \quad (4.50)$$

Multiplying (4.49) by $\frac{1}{N_2^{*\tau_1+\tau_2}}$, we have

$$\frac{1}{d_{12}} \left(\frac{N_1^*}{N_2^*} \right)^{\tau_1} + \frac{1}{d_{23}} \left(\frac{N_3^*}{N_2^*} \right)^{\tau_1} = \frac{1}{d_{12}} \left(\frac{N_1^*}{N_2^*} \right)^{\tau_2} + \frac{1}{d_{23}} \left(\frac{N_3^*}{N_2^*} \right)^{\tau_2}. \quad (4.51)$$

Let $p = \frac{N_1^*}{N_2^*}$, $q = \frac{N_2^*}{N_3^*}$ and $r = \frac{N_3^*}{N_1^*}$, they are satisfied $pqr = 1$. We will show that $p = q = r = 1$ which implies that $N_1^* = N_2^* = N_3^*$. From equation (4.50), we can write

$$\begin{aligned} \frac{1}{d_{12}} p^{-\tau_1} + \frac{1}{d_{13}} (pq)^{-\tau_1} &= \frac{1}{d_{12}} p^{-\tau_2} + \frac{1}{d_{13}} (pq)^{-\tau_2} \\ p^{-\tau_1} \left(\frac{1}{d_{12}} + \frac{1}{d_{13}} q^{-\tau_1} \right) &= p^{-\tau_2} \left(\frac{1}{d_{12}} + \frac{1}{d_{13}} q^{-\tau_2} \right) \\ p^{\tau_1-\tau_2} &= \frac{\frac{1}{d_{12}} + \frac{1}{d_{13}} q^{-\tau_1}}{\frac{1}{d_{12}} + \frac{1}{d_{13}} q^{-\tau_2}} = \frac{1 + \frac{d_{12}}{d_{13}} q^{-\tau_1}}{1 + \frac{d_{12}}{d_{13}} q^{-\tau_2}}. \end{aligned}$$

By assumption, we remark that $\tau_1 - \tau_2 \neq 0$.

We then let $\Delta = \frac{1 + \frac{d_{12}}{d_{13}} q^{-\tau_1}}{1 + \frac{d_{12}}{d_{13}} q^{-\tau_2}}$ for convenience. Therefore, $p^{\tau_1} = \Delta^{\frac{\tau_1}{\tau_1-\tau_2}}$ and

$$p^{\tau_2} = \Delta^{\frac{\tau_2}{\tau_1-\tau_2}}.$$

From equation (4.51), we have

$$\begin{aligned}\frac{1}{d_{12}}p^{\tau_1} + \frac{1}{d_{23}}q^{-\tau_1} &= \frac{1}{d_{12}}p^{\tau_2} + \frac{1}{d_{23}}q^{-\tau_2} \\ \frac{1}{d_{12}}(p^{\tau_1} - p^{\tau_2}) &= \frac{1}{d_{23}}(q^{-\tau_2} - q^{-\tau_1}) \\ \Delta^{\frac{\tau_1}{\tau_1 - \tau_2}} - \Delta^{\frac{\tau_2}{\tau_1 - \tau_2}} &= \frac{d_{12}}{d_{23}}(q^{-\tau_2} - q^{-\tau_1}).\end{aligned}$$

Since $\frac{\tau_1}{\tau_1 - \tau_2} = 1 + \frac{\tau_2}{\tau_1 - \tau_2}$, it follows that

$$\begin{aligned}\Delta^{\frac{\tau_2}{\tau_1 - \tau_2}}(\Delta - 1) &= \frac{d_{12}}{d_{23}}(q^{-\tau_2} - q^{-\tau_1}) \\ \Delta^{\frac{\tau_2}{\tau_1 - \tau_2}} \left(\frac{\frac{d_{12}}{d_{13}}q^{-\tau_1} - \frac{d_{12}}{d_{13}}q^{-\tau_2}}{1 + \frac{d_{12}}{d_{13}}q^{-\tau_2}} \right) &= \frac{d_{12}}{d_{23}}(q^{-\tau_2} - q^{-\tau_1}) \\ \Delta^{\frac{\tau_2}{\tau_1 - \tau_2}} \left(\frac{q^{-\tau_1} - q^{-\tau_2}}{1 + \frac{d_{12}}{d_{13}}q^{-\tau_2}} \right) &= \frac{d_{13}}{d_{23}}(q^{-\tau_1} - q^{-\tau_2}).\end{aligned}$$

If $q^{-\tau_1} - q^{-\tau_2} \neq 0$, then

$$\frac{\Delta^{\frac{\tau_2}{\tau_1 - \tau_2}}}{1 + \frac{d_{12}}{d_{13}}q^{-\tau_2}} = \frac{d_{13}}{d_{23}}$$

which is contradictory because the LHS is always positive. Thus $q^{-\tau_1} - q^{-\tau_2} = 0$. Then $q^{\tau_1 - \tau_2} = 1$ which implies that $q = 1$. By the definition of Δ , we have $\Delta = 1$ which implies that $p^{\tau_1} = 1$. Thus $p = 1$. Hence, $p = q = 1$. It follows that $N_1^* = N_2^* = N_3^*$. So, $N = 3N_1^* = 3N_2^* = 3N_3^*$. Consequently, $(N_1^*, N_2^*, N_3^*) = (\frac{N}{3}, \frac{N}{3}, \frac{N}{3})$. Finally, it is easy to see that there is unique disease-free equilibrium point such that the population number in each patch is positive because if there is another equilibrium point (N_1^0, N_2^0, N_3^0) with $N_i^0 > 0$ for all $i \in \{1, 2, 3\}$, then $N_1^0 = N_2^0 = N_3^0$. We also have $N = 3N_1^0 = 3N_2^0 = 3N_3^0$. \square

In summary, we have eight disease-free equilibrium points of the model given by (4.27)-(4.35) as follows

$$\begin{aligned}P_1(0, 0, 0, 0, 0, 0, 0, 0, 0), P_2(0, N, 0, 0, 0, 0, 0, 0, 0), P_3(0, 0, N, 0, 0, 0, 0, 0, 0), \\ P_4(N, 0, 0, 0, 0, 0, 0, 0, 0), P_5(0, \frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0, 0, 0), P_6(\frac{N}{2}, 0, \frac{N}{2}, 0, 0, 0, 0, 0, 0), \\ P_7(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0, 0, 0, 0) \text{ and } P_8(\frac{N}{3}, \frac{N}{3}, \frac{N}{3}, 0, 0, 0, 0, 0, 0).\end{aligned}$$

Since we are not concern with the extinction of the patch due to the movement of individuals during the initial phase of epidemic, we focus on the last disease-free equilibrium point P_8 .

Next, we consider the stability of the last disease-free equilibrium point P_8 . We begin by giving the following lemma which will be used in the proof of the next theorem.

Let M be a 3×3 matrix in the form

$$M = \begin{bmatrix} u - a - b & a & b \\ a & y - a - c & c \\ b & c & z - b - c \end{bmatrix} \quad (4.52)$$

where u, y, z, a, b and c are real with $a > 0, b > 0$ and $c > 0$. The following lemma shows that all eigenvalues of M have negative real parts when u, y and z are negative.

Lemma 4.7. *Consider a matrix M given by (4.52), if $u < 0, y < 0$ and $z < 0$, then all eigenvalues of M have negative real parts.*

Proof. Assume that $u < 0, y < 0$ and $z < 0$. The characteristic equation with λ as an eigenvalue of a matrix M is $\det(M - \lambda I) = 0$. That is,

$$\lambda^3 + k_2\lambda^2 + k_1\lambda + k_0 = 0$$

where k_2, k_1 and k_0 are defined as follows

$$\begin{aligned} k_2 &= 2a + 2b + 2c - u - y - z, \\ k_1 &= (b + c - u - y)a + (a + c - u - z)b + (a + b - y - z)c \\ &\quad + (b - u)(c - y) + (a - u)(c - z) + (a - y)(b - z) \quad \text{and} \\ k_0 &= (ab + bc + ac)(-u - y - z) + (a + c)uz + (b + c)uy + (a + b)yz - uyz. \end{aligned}$$

According to the Routh-Hurwitz criteria, all eigenvalues of M have negative real parts if $k_2 > 0, k_0 > 0$ and $k_2k_1 > k_0$. By the assumption, it implies directly that $k_2 > 0$ and $k_0 > 0$. So, it remains to show that $k_2k_1 > k_0$. Since

$$\begin{aligned} (-u - y - z)k_1 &> (-u - y - z) \left((b + c - u - y)a + (a + c - u - z)b + (a - y)(b - z) \right) \\ &> (-u - y - z)(ab + bc + ac + yz) \\ &= (ab + bc + ac)(-u - y - z) + (-u - y - z)yz \\ &> (ab + bc + ac)(-u - y - z) - uyz \end{aligned}$$

and

$$\begin{aligned} (2a + 2b + 2c)k_1 &> (2a + 2b + 2c) \left((b - u)(c - y) + (a - u)(c - z) + (a - y)(b - z) \right) \\ &> (a + b + c)(uy + uz + yz) \\ &= (a + b + c)uy + (a + b + c)uz + (a + b + c)yz \\ &> (b + c)uy + (a + c)uz + (a + b)yz, \end{aligned}$$

we have

$$\begin{aligned} k_2k_1 &= (2a + 2b + 2c - u - y - z)k_1 \\ &= (2a + 2b + 2c)k_1 + (-u - y - z)k_1 \\ &> (ab + bc + ac)(-u - y - z) - uyz + (b + c)uy + (a + c)uz + (a + b)yz \\ &= k_0 \end{aligned}$$

as required. \square

The following theorem shows the conditions for the local stability of the positive disease-free equilibrium point.

Theorem 4.8. *For the model given by (4.27)-(4.35), if $\tau_2 < \tau_1$ and $\mathcal{R}_0^{(i)} < 1$ for all $i \in \{1, 2, 3\}$, then a disease-free equilibrium P_8 is locally asymptotically stable.*

Proof. Assume that $\tau_2 < \tau_1$ and $\mathcal{R}_0^{(i)} < 1$ for all $i \in \{1, 2, 3\}$. Note that the disease-free equilibrium P_8 is locally asymptotically stable if all eigenvalues of the Jacobian matrix for system (4.27)-(4.35) at P_8 have negative real parts. The Jacobian matrix for system (4.27)-(4.35) denoted by G is derived in Appendix. We now calculate the Jacobian matrix at the disease-free equilibrium P_8 as

$$G^* = \begin{bmatrix} A & B & C \\ \mathbf{0} & X & \mathbf{0} \\ \mathbf{0} & Y & Z \end{bmatrix}$$

where A , B , C , X , Y and Z are 3×3 matrices given by

$$A = \begin{bmatrix} \left(\frac{x}{d_{12}} + \frac{2x}{d_{13}}\right)\kappa & \left(\frac{x}{d_{13}} - \frac{x}{d_{12}}\right)\kappa & 0 \\ 0 & \left(\frac{x}{d_{23}} + \frac{2x}{d_{12}}\right)\kappa & \left(\frac{x}{d_{12}} - \frac{x}{d_{23}}\right)\kappa \\ \left(\frac{x}{d_{23}} - \frac{x}{d_{13}}\right)\kappa & 0 & \left(\frac{x}{d_{13}} - \frac{2x}{d_{23}}\right)\kappa \end{bmatrix},$$

$$B = \begin{bmatrix} \mu - \beta_1 + \frac{x}{d_{12}}\kappa_1 + \frac{x}{d_{13}}\kappa_2 & \frac{x}{d_{13}}\kappa - \frac{x}{d_{12}}\kappa_1 & -\frac{x}{d_{13}} \\ -\frac{x}{d_{12}} & \mu - \beta_2 + \frac{x}{d_{23}}\kappa_1 + \frac{x}{d_{12}}\kappa_2 & \frac{x}{d_{12}}\kappa - \frac{x}{d_{23}}\kappa_1 \\ \frac{x}{d_{23}}\kappa - \frac{x}{d_{13}}\kappa_1 & -\frac{x}{d_{23}} & \mu - \beta_3 + \frac{x}{d_{13}}\kappa_1 - \frac{x}{d_{23}}\kappa_2 \end{bmatrix},$$

$$C = \begin{bmatrix} \mu + \frac{x}{d_{12}}\kappa_1 + \frac{x}{d_{13}}\kappa_2 & \frac{x}{d_{13}}\kappa - \frac{x}{d_{12}}\kappa_1 & -\frac{x}{d_{13}} \\ -\frac{x}{d_{12}} & \mu + \frac{x}{d_{23}}\kappa_1 + \frac{x}{d_{12}}\kappa_2 & \frac{x}{d_{12}}\kappa - \frac{x}{d_{23}}\kappa_1 \\ \frac{x}{d_{23}}\kappa - \frac{x}{d_{13}}\kappa_1 & -\frac{x}{d_{23}} & \mu + \frac{x}{d_{13}}\kappa_1 - \frac{x}{d_{23}}\kappa_2 \end{bmatrix},$$

$$X = \begin{bmatrix} \beta_1 - \mu - \gamma - \frac{x}{d_{12}} - \frac{x}{d_{13}} & \frac{x}{d_{12}} & \frac{x}{d_{13}} \\ \frac{x}{d_{12}} & \beta_2 - \mu - \gamma - \frac{x}{d_{12}} - \frac{x}{d_{23}} & \frac{x}{d_{23}} \\ \frac{x}{d_{13}} & \frac{x}{d_{23}} & \beta_3 - \mu - \gamma - \frac{x}{d_{13}} - \frac{x}{d_{23}} \end{bmatrix},$$

$$Y = \begin{bmatrix} \gamma & 0 & 0 \\ 0 & \gamma & 0 \\ 0 & 0 & \gamma \end{bmatrix}$$

and

$$Z = \begin{bmatrix} -\mu - \frac{x}{d_{12}} - \frac{x}{d_{13}} & \frac{x}{d_{12}} & \frac{x}{d_{13}} \\ \frac{x}{d_{12}} & -\mu - \frac{x}{d_{12}} - \frac{x}{d_{23}} & \frac{x}{d_{23}} \\ \frac{x}{d_{13}} & \frac{x}{d_{23}} & -\mu - \frac{x}{d_{13}} - \frac{x}{d_{23}} \end{bmatrix}$$

with

$$x = w_0 \left(\frac{N}{3} \right)^{\tau_1 + \tau_2 - 1}, \quad (4.53)$$

$\kappa = \tau_2 - \tau_1$, $\kappa_1 = \tau_2 - \tau_1 + 1$, $\kappa_2 = 2\tau_2 - 2\tau_1 + 1$ and \mathbf{O} is a 3×3 zero matrix. Since G^* is a diagonal block matrix, it is easy to see that the eigenvalues of G^* compose of the eigenvalues of A , the eigenvalues of X and the eigenvalues of Z .

First, we consider the eigenvalues of the matrix X and of the matrix Z . Observe that both matrices X and Z have the same pattern as a matrix M given by (4.52). By the assumption $\mathcal{R}_0^{(i)} < 1$ for all $i \in \{1, 2, 3\}$, it implies that $\beta_i - \mu - \gamma < 0$ for all $i \in \{1, 2, 3\}$. Moreover, we know that $-\mu$ is always negative. Thus by Lemma 4.7, we have all eigenvalues of both matrices X and Z with negative real parts. So, it remains to show that all eigenvalues of A have negative real parts.

The characteristic equation in variable λ of a matrix A is

$$\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0$$

where

$$\begin{aligned} a_2 &= -3x(\tau_2 - \tau_1) \left(\frac{1}{d_{12}} + \frac{1}{d_{13}} + \frac{1}{d_{23}} \right), \\ a_1 &= x^2(\tau_2 - \tau_1)^2 \left(\frac{2}{d_{12}^2} + \frac{2}{d_{13}^2} + \frac{2}{d_{23}^2} + \frac{7}{d_{12}d_{13}} + \frac{7}{d_{13}d_{23}} + \frac{7}{d_{12}d_{23}} \right) \text{ and} \\ a_0 &= -3x^3(\tau_2 - \tau_1)^3 \left(\frac{1}{d_{12}^2d_{13}} + \frac{1}{d_{12}^2d_{23}} + \frac{1}{d_{12}d_{13}^2} + \frac{1}{d_{13}^2d_{23}} \right. \\ &\quad \left. + \frac{1}{d_{12}d_{23}^2} + \frac{1}{d_{13}d_{23}^2} + \frac{3}{d_{12}d_{13}d_{23}} \right). \end{aligned}$$

According to the Routh-Hurwitz criteria, all eigenvalues of A have negative real parts if $a_2 > 0$, $a_0 > 0$ and $a_2a_1 > a_0$. By the first assumption $\tau_2 < \tau_1$, it implies directly that $a_2 > 0$, $a_0 > 0$. It is easy to see that

$$\begin{aligned} &\left(\frac{1}{d_{12}} + \frac{1}{d_{13}} + \frac{1}{d_{23}} \right) \left(\frac{2}{d_{12}^2} + \frac{2}{d_{13}^2} + \frac{2}{d_{23}^2} + \frac{7}{d_{12}d_{13}} + \frac{7}{d_{13}d_{23}} + \frac{7}{d_{12}d_{23}} \right) > \\ &\left(\frac{1}{d_{12}^2d_{13}} + \frac{1}{d_{12}^2d_{23}} + \frac{1}{d_{12}d_{13}^2} + \frac{1}{d_{13}^2d_{23}} + \frac{1}{d_{12}d_{23}^2} + \frac{1}{d_{13}d_{23}^2} + \frac{3}{d_{12}d_{13}d_{23}} \right) \end{aligned}$$

which implies that $a_2a_1 > a_0$. Hence, all eigenvalues of A have negative real parts which completes the proof. \square

In order to derive the basic reproduction number for three patches model, we use the next generation method given in section 2.2. For system (4.27)-(4.35), all infected variables are I_1 , I_2 and I_3 . Then we have

$$\begin{bmatrix} \mathcal{F}_{I_1} \\ \mathcal{F}_{I_2} \\ \mathcal{F}_{I_3} \end{bmatrix} = \begin{bmatrix} \frac{\beta_1 S_1 I_1}{N_1} \\ \frac{\beta_2 S_2 I_2}{N_2} \\ \frac{\beta_3 S_3 I_3}{N_3} \end{bmatrix}$$

and

$$\begin{bmatrix} \mathcal{V}_{I_1} \\ \mathcal{V}_{I_2} \\ \mathcal{V}_{I_3} \end{bmatrix} = \begin{bmatrix} \mu I_1 + \gamma I_1 - m_{21} I_2 - m_{31} I_3 + m_{12} I_1 + m_{13} I_1 \\ \mu I_2 + \gamma I_2 - m_{12} I_1 - m_{32} I_3 + m_{21} I_2 + m_{23} I_2 \\ \mu I_3 + \gamma I_3 - m_{13} I_1 - m_{23} I_2 + m_{31} I_3 + m_{32} I_3 \end{bmatrix}.$$

Therefore, we have matrices F and V defined in section 2.2. at the disease-free equilibrium $(S_1^*, S_2^*, S_3^*, I_1^*, I_2^*, I_3^*, R_1^*, R_2^*, R_3^*)$ as follows

$$F = \begin{bmatrix} \frac{\beta_1 S_1^* (N_1^* - I_1^*)}{N_1^{*2}} & 0 & 0 \\ 0 & \frac{\beta_2 S_2^* (N_2^* - I_2^*)}{N_2^{*2}} & 0 \\ 0 & 0 & \frac{\beta_3 S_3^* (N_3^* - I_3^*)}{N_3^{*2}} \end{bmatrix}$$

and

$$V = \begin{bmatrix} v_{11} & v_{12} & v_{13} \\ v_{21} & v_{22} & v_{23} \\ v_{31} & v_{32} & v_{33} \end{bmatrix}$$

where v_{ij} are given as follows

$$\begin{aligned} v_{11} &= \mu + \gamma - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* + \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} \right. \\ &\quad \left. + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) + \frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) \\ v_{21} &= -\frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\ v_{31} &= -\frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\ v_{12} &= -\frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \end{aligned}$$

$$\begin{aligned}
v_{22} &= \mu + \gamma - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* + \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} \right. \\
&\quad \left. + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) + \frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) \\
v_{32} &= -\frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
v_{13} &= -\frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
v_{23} &= -\frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
v_{33} &= \mu + \gamma - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* + \frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} \right. \\
&\quad \left. + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) + \frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right).
\end{aligned}$$

At the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0, 0)$ we obtain

$$F = \begin{bmatrix} \beta_1 & 0 & 0 \\ 0 & \beta_2 & 0 \\ 0 & 0 & \beta_3 \end{bmatrix} \quad (4.54)$$

and

$$V = \begin{bmatrix} \mu + \gamma + \frac{x}{d_{12}} + \frac{x}{d_{13}} & -\frac{x}{d_{12}} & -\frac{x}{d_{13}} \\ -\frac{x}{d_{12}} & \mu + \gamma + \frac{x}{d_{12}} + \frac{x}{d_{23}} & -\frac{x}{d_{23}} \\ -\frac{x}{d_{13}} & -\frac{x}{d_{23}} & \mu + \gamma + \frac{x}{d_{13}} + \frac{x}{d_{23}} \end{bmatrix}$$

where

$$x = w_0 \left(\frac{N}{3} \right)^{\tau_1 + \tau_2 - 1}. \quad (4.55)$$

Consider the determinant of the matrix V ,

$$\det V = (\mu + \gamma)^3 + 2(\mu + \gamma)^2 \left(\frac{1}{d_{12}} + \frac{1}{d_{13}} + \frac{1}{d_{23}} \right) x + 3(\mu + \gamma) \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2$$

which is always positive. Thus, V is nonsingular which the inverse is in the form

$$V^{-1} = \frac{1}{\det V} [V_3 \quad V_4 \quad V_5] \quad (4.56)$$

where

$$V_3 = \begin{bmatrix} (\mu + \gamma)^2 + (\mu + \gamma) \left(\frac{1}{d_{12}} + \frac{1}{d_{13}} + \frac{2}{d_{23}} \right) x + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \\ (\mu + \gamma) \frac{x}{d_{12}} + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \\ (\mu + \gamma) \frac{x}{d_{13}} + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \end{bmatrix},$$

$$V_4 = \begin{bmatrix} (\mu + \gamma) \frac{x}{d_{12}} + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \\ (\mu + \gamma)^2 + (\mu + \gamma) \left(\frac{1}{d_{12}} + \frac{2}{d_{13}} + \frac{1}{d_{23}} \right) x + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \\ (\mu + \gamma) \frac{x}{d_{23}} + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \end{bmatrix}$$

and

$$V_5 = \begin{bmatrix} (\mu + \gamma) \frac{x}{d_{13}} + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \\ (\mu + \gamma) \frac{x}{d_{23}} + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \\ (\mu + \gamma)^2 + (\mu + \gamma) \left(\frac{2}{d_{12}} + \frac{1}{d_{13}} + \frac{1}{d_{23}} \right) x + \left(\frac{1}{d_{12}d_{13}} + \frac{1}{d_{13}d_{23}} + \frac{1}{d_{12}d_{23}} \right) x^2 \end{bmatrix}$$

The detailed derivation for these is given in Appendix. Due to the complexity, it is almost impossible to derive analytic expression of \mathcal{R}_0 for three patches model. Instead, \mathcal{R}_0 can be obtained implicitly or numerically via the formula

$$\mathcal{R}_0 = \rho(FV^{-1})$$

where matrices F and V^{-1} is given by (4.54) and (4.56), respectively.

Since we cannot analyze \mathcal{R}_0 directly, it is reasonable to consider its boundary and looking for the possibility for threshold under the variation of travel parameters. The following Theorem gives bounds on the basic reproduction number of the model given by (4.27)-(4.35) in terms of the basic reproduction number in which there is no travel between patches.

Theorem 4.9. *For the model given by (4.27)-(4.35), we have*

$$\min_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} \leq \mathcal{R}_0 \leq \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}.$$

Proof. Without loss of generality, we assume that $\beta_1 \leq \beta_2 \leq \beta_3$. It follows that

$$\frac{\beta_1}{\mu + \gamma} \leq \frac{\beta_2}{\mu + \gamma} \leq \frac{\beta_3}{\mu + \gamma}.$$

That is,

$$\min_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} = \mathcal{R}_0^{(1)} \leq \mathcal{R}_0^{(2)} \leq \mathcal{R}_0^{(3)} = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}.$$

For convenience, we take $Z = FV^{-1}$ and let $V^{-1} = [y_{ij}]_{3 \times 3}$ with $y_{ij} > 0$ for all $i, j \in \{1, 2, 3\}$ where the metrics F and V^{-1} defined by (4.54) and (4.56), respectively. Then, we have

$$\begin{aligned} Z = FV^{-1} &= \begin{bmatrix} \beta_1 & 0 & 0 \\ 0 & \beta_2 & 0 \\ 0 & 0 & \beta_3 \end{bmatrix} \begin{bmatrix} y_{11} & y_{12} & y_{13} \\ y_{21} & y_{22} & y_{23} \\ y_{31} & y_{32} & y_{33} \end{bmatrix} \\ &= \begin{bmatrix} \beta_1 y_{11} & \beta_1 y_{12} & \beta_1 y_{13} \\ \beta_2 y_{21} & \beta_2 y_{22} & \beta_2 y_{23} \\ \beta_3 y_{31} & \beta_3 y_{32} & \beta_3 y_{33} \end{bmatrix}. \end{aligned}$$

We will first show that each column sum of $Z = FV^{-1}$ is bounded by the basic reproduction number in which there is no travel between patches and then apply Theorem B.2. Let $[Z]_j$ be the sum of entries in j -th column of Z . Then

$$\begin{aligned} [Z]_j &= \beta_1 y_{1j} + \beta_2 y_{2j} + \beta_3 y_{3j} \\ &\leq \beta_3 y_{1j} + \beta_3 y_{2j} + \beta_3 y_{3j} \\ &= \beta_3 (y_{1j} + y_{2j} + y_{3j}) \end{aligned}$$

for all $j \in \{1, 2, 3\}$. By the form of V^{-1} given by (4.56), it can be seen that each column sum of V^{-1} is $\frac{1}{\mu + \gamma}$. That is, $y_{1j} + y_{2j} + y_{3j} = \frac{1}{\mu + \gamma}$ for all $j \in \{1, 2, 3\}$. Therefore,

$$\begin{aligned} [Z]_j &\leq \beta_3 (y_{1j} + y_{2j} + y_{3j}) \\ &= \frac{\beta_3}{\mu + \gamma} = \mathcal{R}_0^{(3)} = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} \end{aligned}$$

for all $j \in \{1, 2, 3\}$. Similarly, we have $\min_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} = \mathcal{R}_0^{(1)} = \frac{\beta_1}{\mu + \gamma} \leq [Z]_j$ for all $j \in \{1, 2, 3\}$. Consequently,

$$\min_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} \leq [Z]_j \leq \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} \quad (4.57)$$

for all $j \in \{1, 2, 3\}$. By Theorem B.2, we obtain

$$\min_{1 \leq j \leq 3} [Z]_j \leq \rho(Z) \leq \max_{1 \leq j \leq 3} [Z]_j.$$

By equation (4.57), it implies that

$$\min_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} \leq \rho(FV^{-1}) \leq \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}.$$

Hence, $\min_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} \leq \mathcal{R}_0 \leq \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}$ which completes the proof. \square

As a consequence from Theorem 4.9, we have directly two results

- (a). if $\mathcal{R}_0^{(i)} < 1$ for all $i \in \{1, 2, 3\}$, then $\mathcal{R}_0 < 1$,
- (b). if $\mathcal{R}_0^{(i)} > 1$ for all $i \in \{1, 2, 3\}$, then $\mathcal{R}_0 > 1$

which implies the global epidemic threshold will be dominated by the transmission in each patch if they are all below or above the local threshold regardless of the effect of travel although there are travels between patches. An interesting case occurs when $\min \mathcal{R}_0^{(i)} < 1$ and $\max \mathcal{R}_0^{(i)} > 1$. That is, what happens when there exist $i, j \in \{1, 2, 3\}$ and $i \neq j$ such that $\mathcal{R}_0^{(i)} < 1$ and $\mathcal{R}_0^{(j)} > 1$.

The following theorem estimates the limit of the basic reproduction number of the model given by (4.27)-(4.35) when there is a lot of travel. It would be found that \mathcal{R}_0 approaches the average of the basic reproduction number in each isolated patch.

Theorem 4.10. For the model given by (4.27)-(4.35), if $\tau_1 + \tau_2 \rightarrow \infty$, then

$$\mathcal{R}_0 \rightarrow \frac{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} + \mathcal{R}_0^{(3)}}{3}.$$

Proof. Assume that $\tau_1 + \tau_2$ tends to infinity. It implies that x defined by (4.55) tends to infinity. By the definition of \mathcal{R}_0 in sense of the next generation method and Theorem B.5, we have

$$\begin{aligned} \lim_{\tau_1 + \tau_2 \rightarrow \infty} \mathcal{R}_0 &= \lim_{x \rightarrow \infty} \mathcal{R}_0 = \lim_{x \rightarrow \infty} \rho(FV^{-1}) \\ &= \lim_{x \rightarrow \infty} \lim_{k \rightarrow \infty} \|(FV^{-1})^k\|^{\frac{1}{k}} \\ &= \lim_{k \rightarrow \infty} \|(\lim_{x \rightarrow \infty} FV^{-1})^k\|^{\frac{1}{k}} \\ &= \rho(\lim_{x \rightarrow \infty} FV^{-1}) \end{aligned}$$

with matrices F and V^{-1} given by (4.54) and (4.56), respectively. Since F does not depend on x , we focus on $\lim_{x \rightarrow \infty} V^{-1}$. By the form of V^{-1} , each element of V^{-1} is a fraction with a maximum degree of x in both numerator and denominator are equal to two. By L' Hospital's rule, we find

$$\lim_{x \rightarrow \infty} V^{-1} = \frac{1}{3(\mu + \gamma)} \begin{bmatrix} 1 & 1 & 1 \\ 1 & 1 & 1 \\ 1 & 1 & 1 \end{bmatrix}.$$

Therefore,

$$\lim_{x \rightarrow \infty} FV^{-1} = \begin{bmatrix} \frac{\beta_1}{3(\mu + \gamma)} & \frac{\beta_1}{3(\mu + \gamma)} & \frac{\beta_1}{3(\mu + \gamma)} \\ \frac{\beta_2}{3(\mu + \gamma)} & \frac{\beta_2}{3(\mu + \gamma)} & \frac{\beta_2}{3(\mu + \gamma)} \\ \frac{\beta_3}{3(\mu + \gamma)} & \frac{\beta_3}{3(\mu + \gamma)} & \frac{\beta_3}{3(\mu + \gamma)} \end{bmatrix}.$$

The characteristic equation in variable λ for the matrix $\lim_{x \rightarrow \infty} FV^{-1}$ is

$$0 = \det \left(\lim_{x \rightarrow \infty} FV^{-1} - \lambda I \right) = \left(\frac{\beta_1}{3(\mu + \gamma)} + \frac{\beta_2}{3(\mu + \gamma)} + \frac{\beta_3}{3(\mu + \gamma)} - \lambda \right) \lambda^2.$$

Thus, all eigenvalues of $\lim_{x \rightarrow \infty} FV^{-1}$ are $\frac{\mathcal{R}_0^{(1)}}{3} + \frac{\mathcal{R}_0^{(2)}}{3} + \frac{\mathcal{R}_0^{(3)}}{3}$, 0 and 0. Hence,

$$\lim_{\tau_1 + \tau_2 \rightarrow \infty} \mathcal{R}_0 = \rho(\lim_{x \rightarrow \infty} FV^{-1}) = \frac{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} + \mathcal{R}_0^{(3)}}{3} \text{ as required.} \quad \square$$

We remark that if we change the assumption of Theorem 4.9 to be τ_1 tends to infinity or τ_2 tends to infinity, then we also have the same result.

In contrast to the condition of the previous theorem, when there is no travel, the following theorem shows that the basic reproduction number of three patches is a maximum of $\mathcal{R}_0^{(i)}$, where $\mathcal{R}_0^{(i)}$ is the basic reproduction number of patch i in isolation.

Theorem 4.11. *For an SIR epidemic model with three patches, if there is no travel between patches, then $\mathcal{R}_0 = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}$.*

Proof. Assume that there is no travel between patches of an SIR epidemic model with three patches. The dynamic of this model is given by the following system of nine ordinary differential equations which is reduced from system (4.27)-(4.35),

$$\begin{aligned}\frac{dS_i}{dt} &= \mu N_i - \mu S_i - \frac{\beta_i S_i I_i}{N_i} \\ \frac{dI_i}{dt} &= \frac{\beta_i S_i I_i}{N_i} - \mu I_i - \gamma I_i \\ \frac{dR_i}{dt} &= \gamma I_i - \mu R_i\end{aligned}$$

with $i = 1, 2, 3$. First, we will find the disease-free equilibrium for this model. we see that parameters of each patch dose not depend on parameters of other patch and the dynamic of each patch is similarly to a basic SIR epidemic model given in section 2.1. By Example 2.1, we have the disease-free equilibrium of patch i is $(N_i, 0, 0)$ where N_i is the total population number of patch i and N_i is constant. Hence, the disease-free equilibrium $(S_1^0, S_2^0, S_3^0, I_1^0, I_2^0, I_3^0, R_1^0, R_2^0, R_3^0)$ of this model is $(N_1, N_2, N_3, 0, 0, 0, 0, 0, 0)$. To derive \mathcal{R}_0 for this model by the next generation method, we let $F_0 V_0^{-1}$ be the next generation matrix to avoid a confusion with the next generation matrix of the model given by (4.21)-(4.29). The infected variables are I_1, I_2 and I_3 . By the concept of the next generation method, we have matrices F_0 and V_0 at $(N_1, N_2, N_3, 0, 0, 0, 0, 0, 0)$ as follows

$$F_0 = \begin{bmatrix} \beta_1 & 0 & 0 \\ 0 & \beta_2 & 0 \\ 0 & 0 & \beta_3 \end{bmatrix}$$

and

$$V_0 = \begin{bmatrix} \mu + \gamma & 0 & 0 \\ 0 & \mu + \gamma & 0 \\ 0 & 0 & \mu + \gamma \end{bmatrix}.$$

It is obvious to see that V_0 is nonsingular. We obtain

$$V_0^{-1} = \begin{bmatrix} \frac{1}{\mu + \gamma} & 0 & 0 \\ 0 & \frac{1}{\mu + \gamma} & 0 \\ 0 & 0 & \frac{1}{\mu + \gamma} \end{bmatrix}.$$

Therefore,

$$F_0 V_0^{-1} = \begin{bmatrix} \frac{\beta_1}{\mu + \gamma} & 0 & 0 \\ 0 & \frac{\beta_2}{\mu + \gamma} & 0 \\ 0 & 0 & \frac{\beta_3}{\mu + \gamma} \end{bmatrix}.$$

So, it can be seen that all eigenvalues are $\frac{\beta_i}{\mu + \gamma}$ for all $i \in \{1, 2, 3\}$. Thus, the basic reproduction number of this model is

$$\mathcal{R}_0 = \rho(F_0 V_0^{-1}) = \max_{1 \leq i \leq 3} \frac{\beta_i}{\mu + \gamma} = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}$$

as required. \square

The next theorem estimates the limit of the basic reproduction number of the model given by (4.27)-(4.35) with $\frac{w_0}{N}$ tends to zero when $\tau_1 + \tau_2$ tends to zero. It shows that the basic reproduction number of this model approaches a maximum of $\mathcal{R}_0^{(i)}$ which equal to the basic reproduction number in which there is no travel.

Theorem 4.12. *For the model given by (4.27)-(4.35), if $\tau_1 + \tau_2 \rightarrow 0$ and $\frac{w_0}{N} \rightarrow 0$, then*

$$\mathcal{R}_0 \rightarrow \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}.$$

Proof. Assume that $\tau_1 + \tau_2$ tends to zero and $\frac{w_0}{N}$ tends to zero. Recall the parameter x defined by (4.55), we have

$$\lim_{\substack{\tau_1 + \tau_2 \rightarrow 0 \\ \frac{w_0}{N} \rightarrow 0}} x = \lim_{\frac{w_0}{N} \rightarrow 0} \lim_{\tau_1 + \tau_2 \rightarrow 0} \left(w_0 \left(\frac{N}{3} \right)^{\tau_1 + \tau_2 - 1} \right) = \lim_{\frac{w_0}{N} \rightarrow 0} \frac{3w_0}{N} = 0.$$

That is, x tends to zero as $\tau_1 + \tau_2 \rightarrow 0$ and $\frac{w_0}{N} \rightarrow 0$. By the same argument in the proof of Theorem 4.10, we have

$$\lim_{\substack{\tau_1 + \tau_2 \rightarrow 0 \\ \frac{w_0}{N} \rightarrow 0}} \mathcal{R}_0 = \lim_{x \rightarrow 0} \mathcal{R}_0 = \lim_{x \rightarrow 0} \rho(FV^{-1}) = \rho(\lim_{x \rightarrow 0} FV^{-1}) = \rho(F \lim_{x \rightarrow 0} V^{-1})$$

with matrices F and V^{-1} given by (4.54) and (4.56), respectively. By the form of matrix V^{-1} , we have

$$\lim_{x \rightarrow 0} V^{-1} = \begin{bmatrix} 1 & 0 & 0 \\ \frac{1}{(\mu + \gamma)} & 0 & 0 \\ 0 & \frac{1}{(\mu + \gamma)} & 0 \\ 0 & 0 & \frac{1}{(\mu + \gamma)} \end{bmatrix}.$$

Therefore,

$$\lim_{x \rightarrow 0} FV^{-1} = \begin{bmatrix} \frac{\beta_1}{(\mu + \gamma)} & 0 & 0 \\ 0 & \frac{\beta_2}{(\mu + \gamma)} & 0 \\ 0 & 0 & \frac{\beta_3}{(\mu + \gamma)} \end{bmatrix}.$$

Hence, by the same argument in previous theorem,

$$\lim_{\substack{\tau_1 + \tau_2 \rightarrow 0 \\ \frac{w_0}{N} \rightarrow 0}} \mathcal{R}_0 = \rho(\lim_{x \rightarrow 0} FV^{-1}) = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}$$

which completes the proof. \square

Define $\mathcal{R}_0(\infty) = \frac{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} + \mathcal{R}_0^{(3)}}{3}$. The following theorem shows that there are two critical points in term of travel parameters for the disease spreads in case that there is an epidemic patch with $\mathcal{R}_0(\infty) < 1$.

Theorem 4.13. *For the model given by (4.27)-(4.35) with $\frac{w_0}{N}$ tends to zero, if $\mathcal{R}_0^{(i)} < 1$ and $\mathcal{R}_0^{(j)} > 1$ for some $i, j \in \{1, 2, 3\}$ and $i \neq j$ with $\mathcal{R}_0(\infty) < 1$, then there exist $\tau', \tau'' \in \mathbb{R}^+$ with $\tau' \geq \tau''$ such that*

- (i). $\mathcal{R}_0 < 1$ for $\tau_1 + \tau_2 > \tau'$
- (ii). $\mathcal{R}_0 > 1$ for $\tau_1 + \tau_2 < \tau''$.

Proof. Assume that $\mathcal{R}_0^{(i)} < 1$ and $\mathcal{R}_0^{(j)} > 1$ for some $i, j \in \{1, 2, 3\}$ and $i \neq j$ with

$$\mathcal{R}_0(\infty) = \frac{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} + \mathcal{R}_0^{(3)}}{3} < 1.$$

First, we consider an SIR epidemic model with three patches in which there is no travel between patches to derive \mathcal{R}_0 . By Theorem 4.10, we have

$$\mathcal{R}_0 = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}.$$

Therefore, if there is no travel between patches, then $\mathcal{R}_0 > 1$.

Next, we consider an SIR epidemic model with three patches in which there is a travel between patches with $\frac{w_0}{N}$ tends to zero. If there is a travel between patches but $\tau_1 + \tau_2$ tends to zero, then we have

$$\mathcal{R}_0 \rightarrow \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)} > 1$$

by Theorem 4.12. On the other hand, when $\tau_1 + \tau_2$ tends to infinity, we have

$$\mathcal{R}_0 \rightarrow \mathcal{R}_0(\infty) < 1$$

by Theorem 4.10. Hence, there exist $\tau', \tau'' \in \mathbb{R}^+$ with $\tau' \geq \tau''$ such that $\mathcal{R}_0 < 1$ for all $\tau_1 + \tau_2 > \tau'$ and $\mathcal{R}_0 > 1$ for all $\tau_1 + \tau_2 < \tau''$. \square

Finally, we derive the endemic equilibrium point of three patches model. Let $(\hat{S}_1, \hat{S}_2, \hat{S}_3, \hat{I}_1, \hat{I}_2, \hat{I}_3, \hat{R}_1, \hat{R}_2, \hat{R}_3)$ with $\hat{I}_i > 0$ for some $i \in \{1, 2, 3\}$ be an endemic equilibrium point of the model given by (4.27)-(4.35) and let $\hat{N}_i = \hat{S}_i + \hat{I}_i + \hat{R}_i$

be the total population number of patch i at an endemic state. Then we have $(\hat{N}_1, \hat{N}_2, \hat{N}_3)$ is an equilibrium point of the population model (2.10) with $n = 3$. By Theorem 4.6, $(\frac{N}{3}, \frac{N}{3}, \frac{N}{3})$ is a unique positive equilibrium point of the model (2.10) with $n = 3$. Thus

$$\hat{S}_i = \frac{N}{3} - \hat{I}_i - \hat{R}_i$$

for all $i \in \{1, 2, 3\}$. For deriving $\hat{I}_1, \hat{I}_2, \hat{I}_3, \hat{R}_1, \hat{R}_2$ and \hat{R}_3 , we can solve from the following system,

$$\frac{2\beta_1 \hat{S}_1 \hat{I}_1}{N} - \mu \hat{I}_1 - \gamma \hat{I}_1 + \frac{x}{d_{12}} \hat{I}_2 + \frac{x}{d_{13}} \hat{I}_3 - \frac{x}{d_{12}} \hat{I}_1 - \frac{x}{d_{13}} \hat{I}_1 = 0 \quad (4.58)$$

$$\frac{2\beta_2 \hat{S}_2 \hat{I}_2}{N} - \mu \hat{I}_2 - \gamma \hat{I}_2 + \frac{x}{d_{12}} \hat{I}_1 + \frac{x}{d_{23}} \hat{I}_3 - \frac{x}{d_{12}} \hat{I}_2 - \frac{x}{d_{23}} \hat{I}_2 = 0 \quad (4.59)$$

$$\frac{2\beta_3 \hat{S}_3 \hat{I}_3}{N} - \mu \hat{I}_3 - \gamma \hat{I}_3 + \frac{x}{d_{13}} \hat{I}_1 + \frac{x}{d_{23}} \hat{I}_1 - \frac{x}{d_{13}} \hat{I}_3 - \frac{x}{d_{23}} \hat{I}_3 = 0 \quad (4.60)$$

$$\gamma \hat{I}_1 - \mu \hat{R}_1 + \frac{x}{d_{12}} \hat{R}_2 + \frac{x}{d_{13}} \hat{R}_3 - \frac{x}{d_{12}} \hat{R}_1 - \frac{x}{d_{13}} \hat{R}_1 = 0 \quad (4.61)$$

$$\gamma \hat{I}_2 - \mu \hat{R}_2 + \frac{x}{d_{12}} \hat{R}_1 + \frac{x}{d_{23}} \hat{R}_3 - \frac{x}{d_{12}} \hat{R}_2 - \frac{x}{d_{23}} \hat{R}_2 = 0 \quad (4.62)$$

$$\gamma \hat{I}_3 - \mu \hat{R}_3 + \frac{x}{d_{13}} \hat{R}_1 + \frac{x}{d_{23}} \hat{R}_1 - \frac{x}{d_{13}} \hat{R}_3 - \frac{x}{d_{23}} \hat{R}_3 = 0 \quad (4.63)$$

with x is defined by (4.55). From (4.61)-(4.63), we have

$$(\mu d_{12} d_{13} + d_{13} x + d_{12} x) \hat{R}_1 = d_{12} d_{13} \gamma \hat{I}_1 + d_{13} x \hat{R}_2 + d_{12} x \hat{R}_3 \quad (4.64)$$

$$(\mu d_{12} d_{23} + d_{23} x + d_{12} x) \hat{R}_2 = d_{12} d_{23} \gamma \hat{I}_2 + d_{23} x \hat{R}_1 + d_{12} x \hat{R}_3 \quad (4.65)$$

$$(\mu d_{12} d_{23} + d_{23} x + d_{13} x) \hat{R}_3 = d_{13} d_{23} \gamma \hat{I}_3 + d_{23} x \hat{R}_1 + d_{13} x \hat{R}_2 \quad (4.66)$$

First, we let $D = d_{12} + d_{13} + d_{23}$. From (4.64) and (4.65), we have

$$(\mu d_{12} d_{13} + Dx) \hat{R}_1 = (\mu d_{12} d_{23} + Dx) \hat{R}_2 + d_{12} d_{13} \gamma \hat{I}_1 - d_{12} d_{23} \gamma \hat{I}_2. \quad (4.67)$$

From (4.65) and (4.66), we have

$$(\mu d_{12} d_{23} + Dx) \hat{R}_2 = (\mu d_{13} d_{23} + Dx) \hat{R}_3 + d_{12} d_{23} \gamma \hat{I}_2 - d_{13} d_{23} \gamma \hat{I}_3. \quad (4.68)$$

From (4.64) and (4.66), we have

$$(\mu d_{13} d_{23} + Dx) \hat{R}_3 = (\mu d_{12} d_{13} + Dx) \hat{R}_1 + d_{13} d_{23} \gamma \hat{I}_3 - d_{12} d_{13} \gamma \hat{I}_1. \quad (4.69)$$

Now, we can obtain \hat{R}_1, \hat{R}_2 and \hat{R}_3 in terms of \hat{I}_1, \hat{I}_2 and \hat{I}_3 by substituting some equation above into (4.64), (4.65) and (4.66). Finally, we can derive \hat{I}_1, \hat{I}_2 and \hat{I}_3 by substituting $\hat{S}_i = \frac{N}{3} - \hat{I}_i - \hat{R}_i$ and \hat{R}_i into equations (4.58)-(4.60) and solving this system. Hence, we can derive the endemic equilibrium point for this model.

Chapter 5

Numerical Simulations

In this chapter, we perform the numerical simulations to verify the theoretical hypotheses given in the previous chapter. Throughout this chapter, we set the demographic parameters and the recovery rate as follows. Setting the birth rate and natural death rate to be as $1/25550$ per day which corresponds to a life expectancy of 70 years and the recovery rate is about $1/7$ per day which corresponds to an average duration of infectiousness of 7 days. Therefore, $\mu = 0.000039$ per day and $\gamma = 0.142857$ per day. The travel parameters are treated as vary and effective contact rates in each patch will be given for each assumption.

5.1 Simulations of a model for two patches

We first consider the numerical simulations for two patches model which are satisfied with theory given in section 4.1. Throughout this section, the total population constant is assumed to be equal to 100,000 and let $d_{12} = 10$.

First, we will verify our theory by which the disease-free equilibrium is locally asymptotically stable. In order to show that the equilibrium point is locally asymptotically stable, initial conditions must be started sufficiently close to the equilibrium point.

Simulation 5.1. Consider an SIR epidemic model of two patches with initial conditions $S_1(0) = 49,980$, $S_2(0) = 50,016$, $I_1(0) = I_2(0) = 2$, and $R_1(0) = R_2(0) = 0$ and parameters are given by $w_0 = 2.0 \times 10^{-7}$, $\beta_1 = 0.13$, $\beta_2 = 0.09$, $\tau_1 = 1.5$ and $\tau_2 = 0.8$. So, $\mathcal{R}_0^{(1)} = 0.91$ and $\mathcal{R}_0^{(2)} = 0.63$. Therefore, $\mathcal{R}_0^{(i)} < 1$ for all $i = 1, 2$ and $\tau_2 < \tau_1$ which correspond to the conditions of Theorem 4.1. Thus, by the theoretical prediction of Theorem 4.1, the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ is locally asymptotically stable. The numerical results of this simulation given by Figure 5.1 show that the disease-free equilibrium is locally asymptotically stable since the solutions tend to the disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0)$ as time is increased. Note that pictures in the right column of Figure 5.1 show the solutions for long time. Hence, the theoretical prediction of Theorem 4.1 agree with the numerical results.

Next, we will verify Theorem 4.3 by giving the the following simulation.

Simulation 5.2. Consider an SIR epidemic model of two patches with initial conditions $S_1(0) = 39,990$, $S_2(0) = 60,006$, $I_1(0) = I_2(0) = 2$, and $R_1(0) = R_2(0) = 0$ and parameters are given by $w_0 = 1.67 \times 10^{-7}$, $\beta_1 = 0.13$, $\beta_2 = 0.09$, $\tau_1 = 1.5$ and $\tau_2 = 0.8$. So,

$$\mathcal{R}_0^{(1)} = 0.91 < 1 \text{ and } \mathcal{R}_0^{(2)} = 0.63 < 1.$$

By Theorem 4.3, we have $\mathcal{R}_0 < 1$. Moreover, the basic reproduction number can be derived directly. By computing the basic reproduction number given in section 4.1, we have $\mathcal{R}_0 = 0.78$. Thus, by both the theoretical prediction of Theorem 4.3 and the derived basic reproduction number, we have $\mathcal{R}_0 < 1$. That is, the disease cannot invade the population. The numerical results of this simulation is given by Figure 5.2. In particular, Figure 5.2(b) shows that there is no outbreak in both patches. Hence, both the theoretical prediction of Theorem 4.3 and the derived basic reproduction number agree with the numerical results. Note that Figure 5.2(a) shows the susceptible population number of patch 2 drops from the initial condition, it is not affected from infection but it is affected from the movement of susceptible individuals between patches or the natural death.

The two following simulations are satisfied with the prediction of Theorem 4.4.

Simulation 5.3. Consider an SIR epidemic model of two patches with the same initial conditions in Simulation 5.2 and parameters are given by $w_0 = 1.67 \times 10^{-7}$, $\beta_1 = 0.25$, $\beta_2 = 0.20$, $\tau_1 = 1.5$ and $\tau_2 = 0.8$. So,

$$\mathcal{R}_0^{(1)} = 1.75 > 1 \text{ and } \mathcal{R}_0^{(2)} = 1.40 > 1.$$

By Theorem 4.4, we have $\mathcal{R}_0 > 1$. Moreover, the basic reproduction number can be derived directly. By computing the basic reproduction number given in section 4.1, we have $\mathcal{R}_0 = 1.58$. Thus, by both the theoretical prediction of Theorem 4.4 and the derived basic reproduction number, we have $\mathcal{R}_0 > 1$. That is, the disease can invade a susceptible population. The numerical results of this simulation is given by Figure 5.3. In particular, Figure 5.3(b) shows that there is a large outbreak in both patches. Hence, both the theoretical prediction of Theorem 4.4 and the derived basic reproduction number agree with the numerical results. Moreover, by the right column of Figure 5.3, we see that the solution tends to the endemic equilibrium point.

Simulation 5.4. Consider an SIR epidemic model of two patches with the same initial conditions in Simulation 5.2 and the same parameters in Simulation 5.3 but travel parameters are given by $\tau_1 = 0.7$ and $\tau_2 = 0.3$. Then the derived basic reproduction number $\mathcal{R}_0 = 1.75$. The numerical results of this simulation is given by Figure 5.4. By the same argument in Simulation 5.3, we have both the theoretical prediction of Theorem 4.4 and the derived basic reproduction number agree with the numerical results. The RHS of Figure 5.4 shows that the solution tends to the point that the number of infectious individual is not equal to zero, an endemic point.

Simulation 5.3 and Simulation 5.4 have the same initial conditions and the same parameters except τ_1 and τ_2 . We focus on the numerical results for infectious population number of Simulation 5.3 and Simulation 5.4 given by Figure 5.3(b) and Figure 5.4(b), respectively. Then we see that an epidemic period and the most outbreak of each patch in Simulation 5.3 is different from Simulation 5.4. For example, the most outbreak in patch 2 of Simulation 5.3 occurs at about 110 day, while the most outbreak in patch 2 of Simulation 5.4 occurs at about 160 day. Hence, the changes of travel parameters τ_1 and τ_2 affect the outbreak duration of the disease.

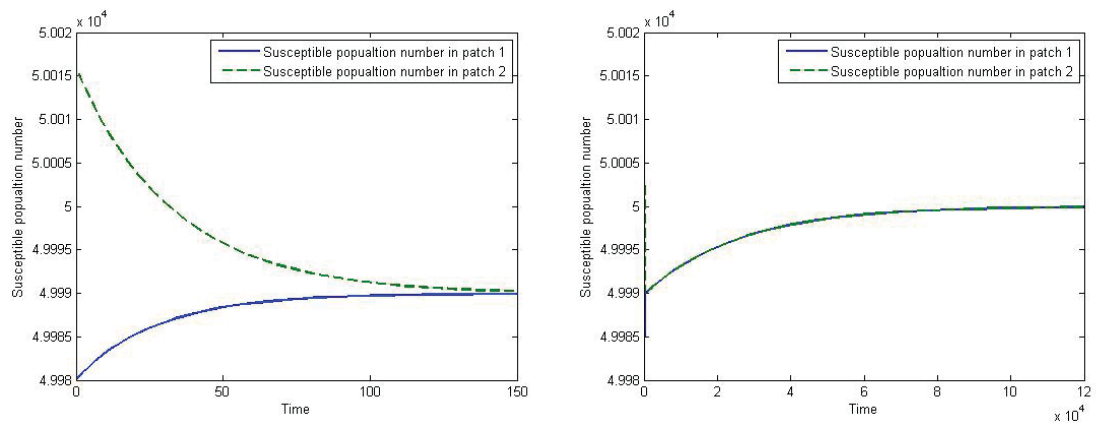
The three following simulations are in agreement with the theoretical conjectures of Theorem 4.5.

Simulation 5.5. Consider an SIR epidemic model of two patches with the same initial conditions in Simulation 5.2 and parameters are given by $w_0 = 1.67 \times 10^{-7}$, $\beta_1 = 0.15$, $\beta_2 = 0.10$, $\tau_1 = 1.5$ and $\tau_2 = 0.8$. So,

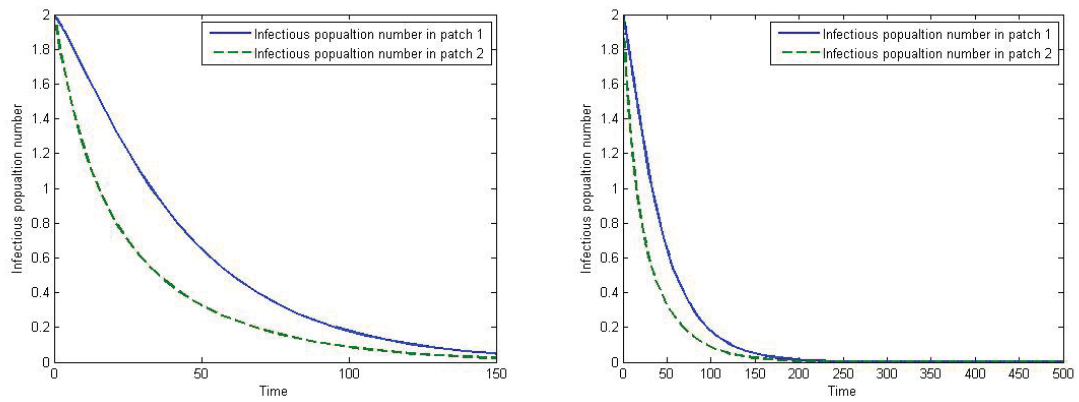
$$\mathcal{R}_0^{(1)} = 1.0497 > 1 \text{ and } \mathcal{R}_0^{(2)} = 0.6998 < 1.$$

Thus $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} = 1.7495 < 2$. By Theorem 4.5, we have $\mathcal{R}_0 < 1$ if $\epsilon < \epsilon^*$. By computing, we obtain $\epsilon = 0.63$ and $\epsilon^* = 0.95$. Therefore, $\mathcal{R}_0 < 1$ by Theorem 4.5. From the derived basic reproduction number given in section 4.1, we have $\mathcal{R}_0 = 0.8862$. By both theoretical methods, we have $\mathcal{R}_0 < 1$ which means that the disease cannot invade the population. The numerical results of this simulation is given by Figure 5.5 show that there is no outbreak in both patches. Hence, both theoretical methods agree with the numerical results.

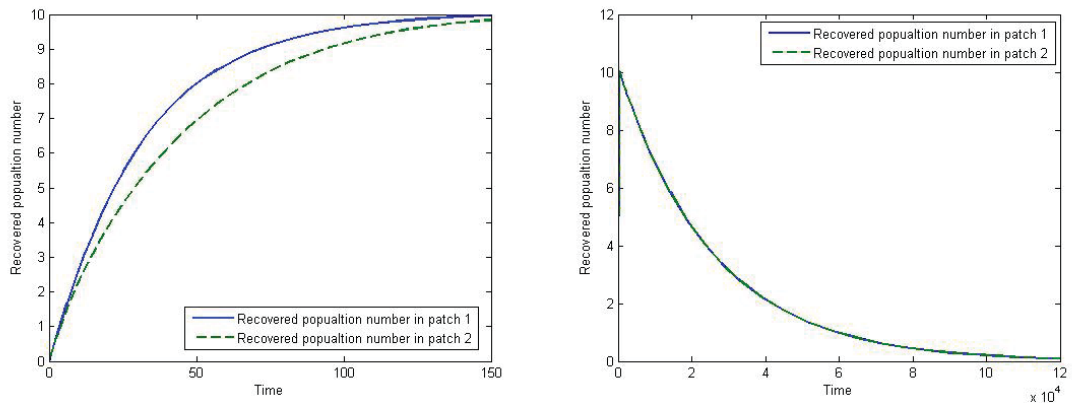
Simulation 5.6. Consider an SIR epidemic model of two patches with the same initial conditions in Simulation 5.2 and the same parameters in Simulation 5.5 but $\tau_1 = 1.0$ and $\tau_2 = 0.5$. Then $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} < 2$ but $\epsilon = 0.9997$ and $\epsilon^* = 0.9467$. Therefore, $\epsilon > \epsilon^*$. By Theorem 4.5, we have $\mathcal{R}_0 > 1$. From the derived basic reproduction number given in section 4.1, we have $\mathcal{R}_0 = 1.0494$. By both theoretical methods, we have $\mathcal{R}_0 > 1$ which means that the disease can invade a susceptible population. The numerical results of this simulation is given by Figure 5.6 show that there is an outbreak in patch 1. Hence, both theoretical methods agree with the numerical results.



(a) Susceptible population.

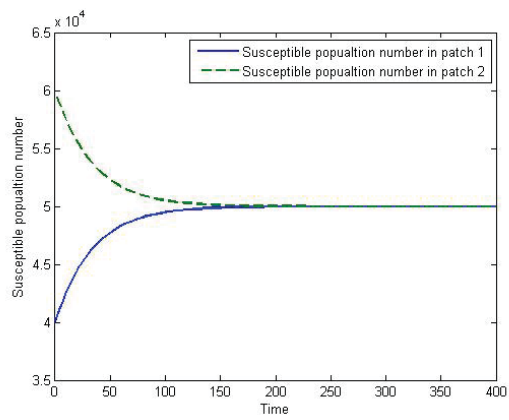


(b) Infectious population.

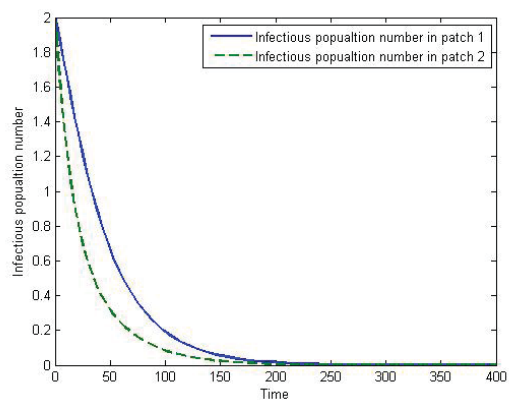


(c) Recovered population.

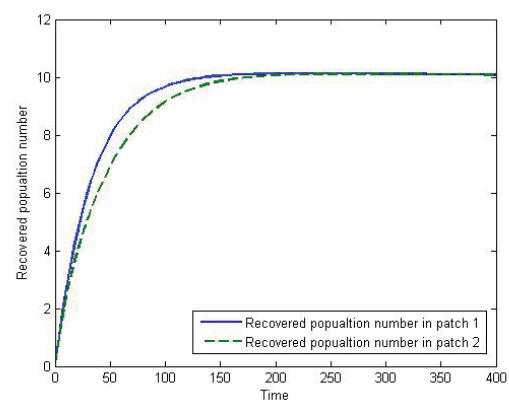
Figure 5.1: Numerical results of an SIR model with two patches for Simulation 5.1



(a) Susceptible population.

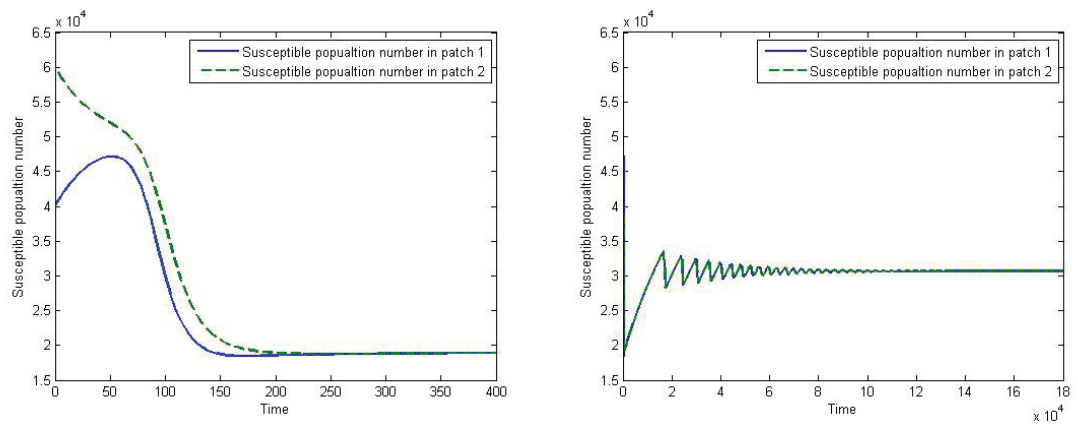


(b) Infectious population.

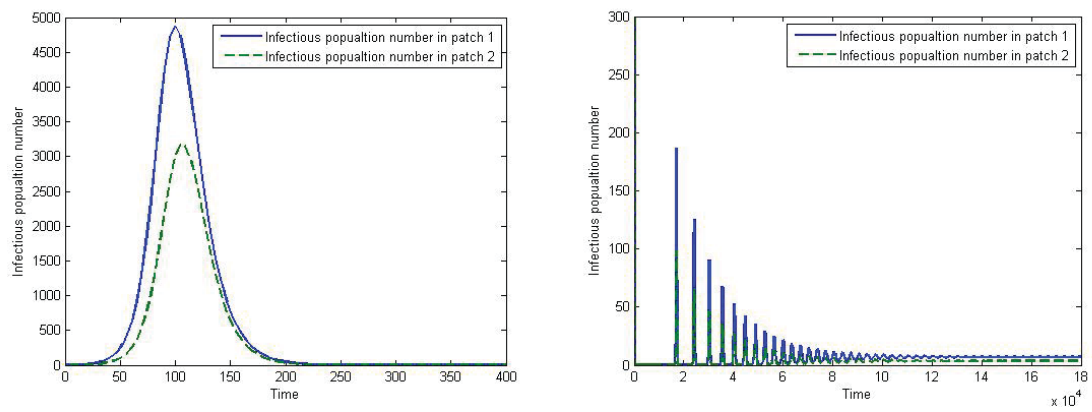


(c) Recovered population.

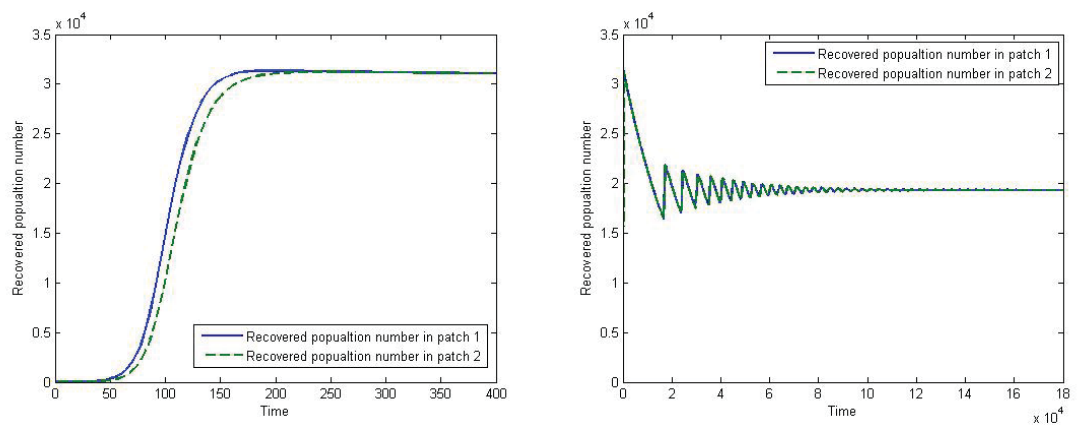
Figure 5.2: Numerical results of an SIR model with two patches for Simulation 5.2



(a) Susceptible population.

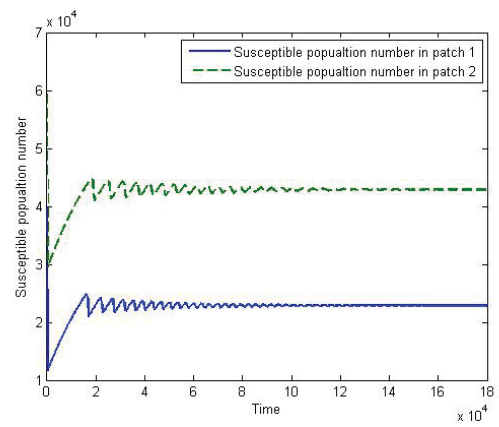
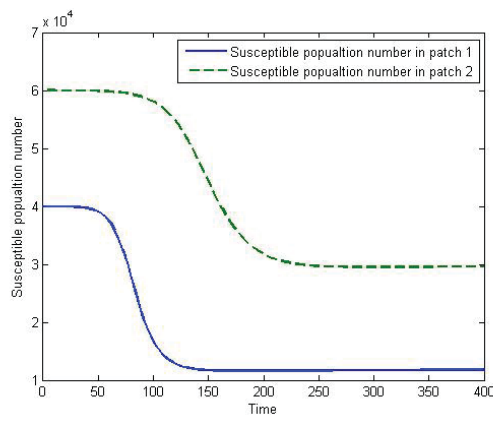


(b) Infectious population.

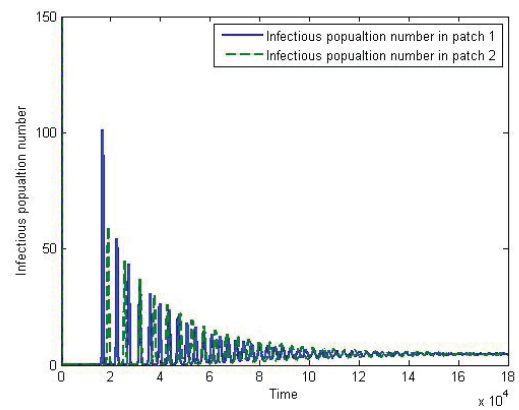
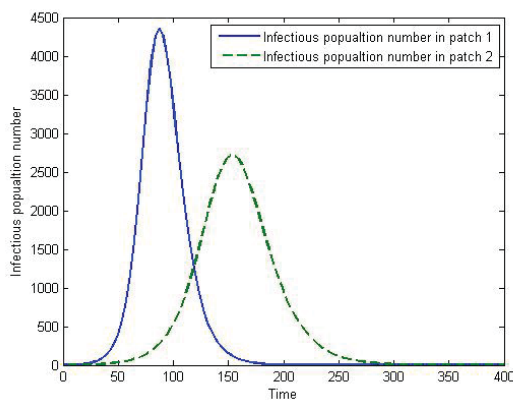


(c) Recovered population.

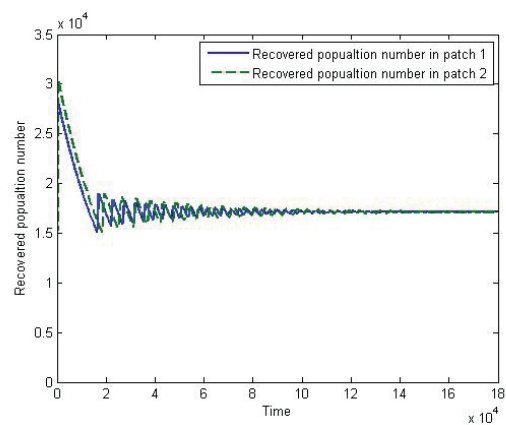
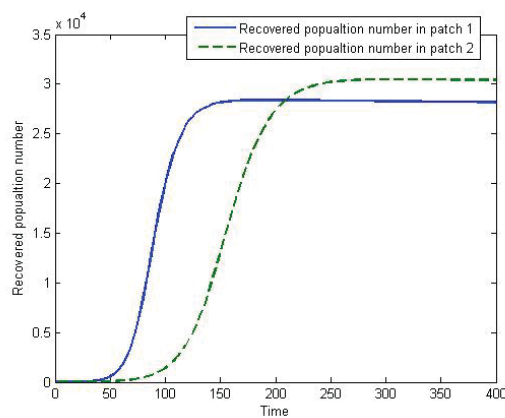
Figure 5.3: Numerical results of an SIR model with two patches for Simulation 5.3



(a) Susceptible population.

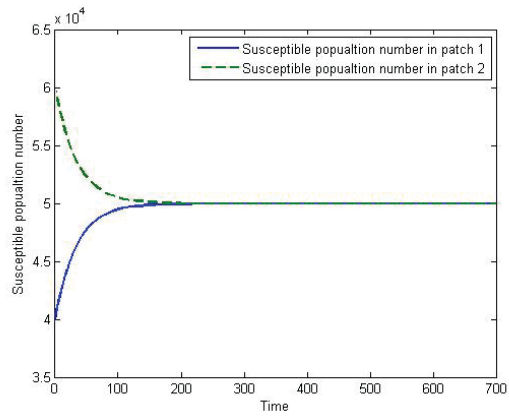


(b) Infectious population.

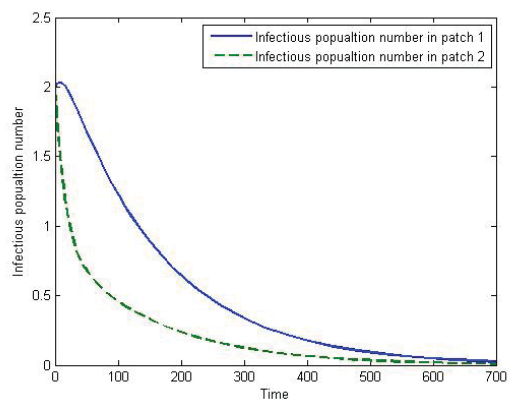


(c) Recovered population.

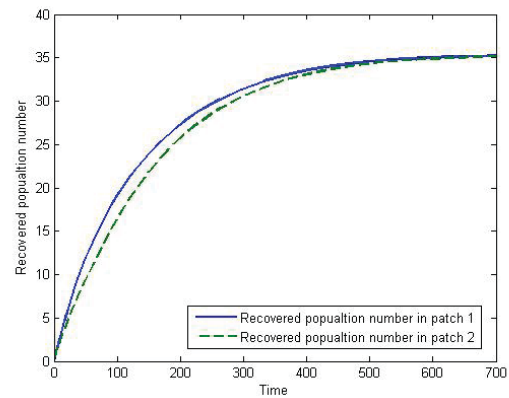
Figure 5.4: Numerical results of an SIR model with two patches for Simulation 5.4



(a) Susceptible population.

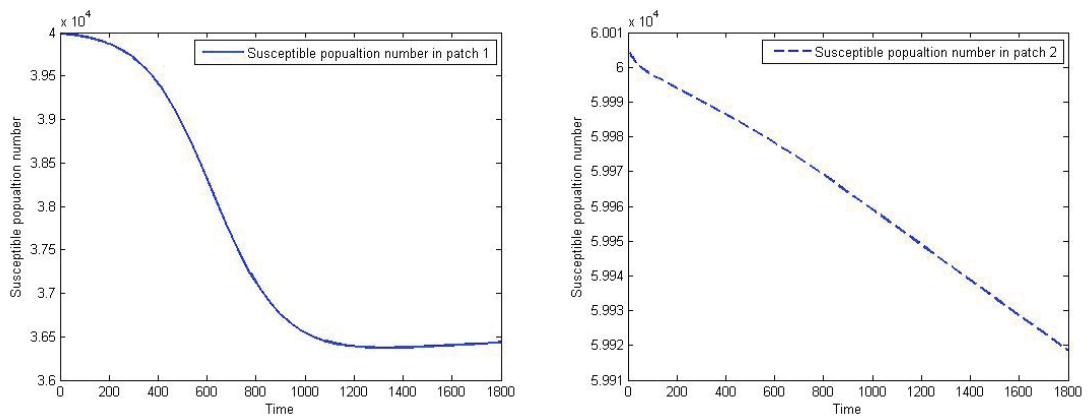


(b) Infectious population.

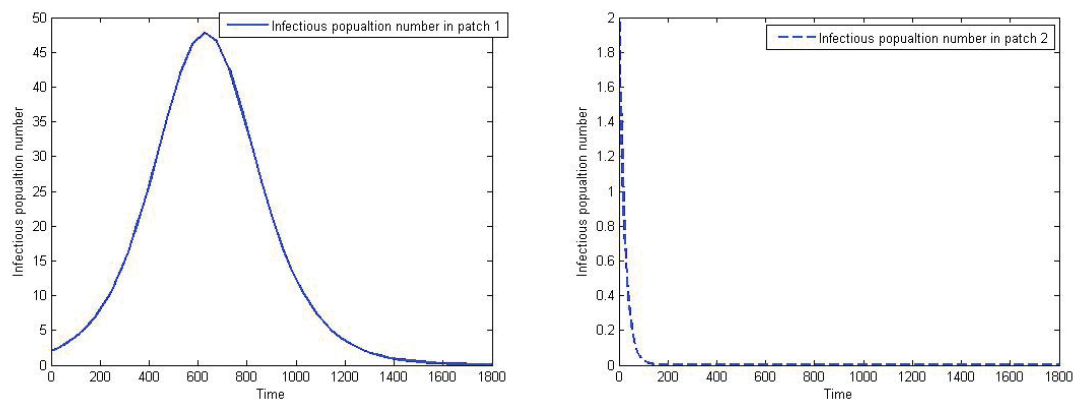


(c) Recovered population.

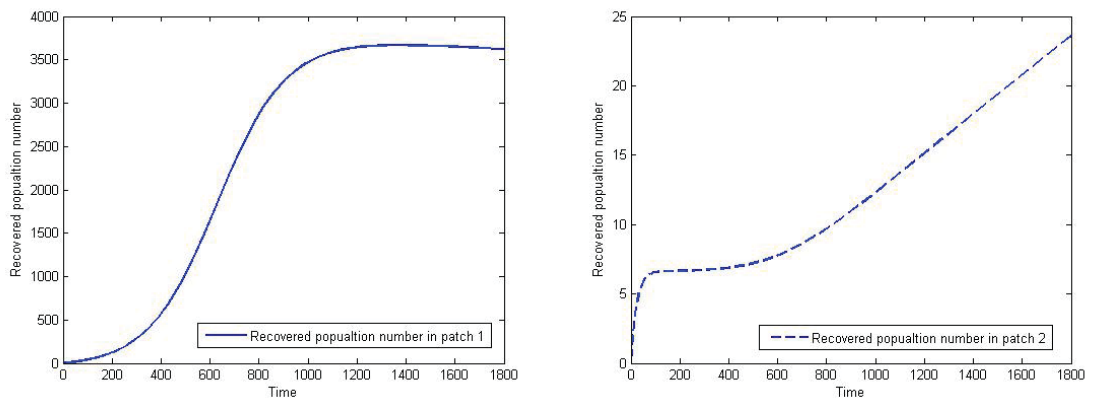
Figure 5.5: Numerical results of an SIR model with two patches for Simulation 5.5



(a) Susceptible population.



(b) Infectious population.



(c) Recovered population.

Figure 5.6: Numerical results of an SIR model with two patches for Simulation 5.6

5.2 Simulations of a model for three patches

In this section, we consider the numerical simulations for three patches model which are satisfied with theory given in section 4.2. Throughout this section, the total population constant is assumed to be equal to 150,000 and the distances between patches are set as follows; $D_{12} = 100$, $D_{13} = 200$ and $D_{23} = 300$ with $\theta = 1$.

The first simulation shows that the positive disease-free equilibrium is locally asymptotically stable which corresponds to the prediction of Theorem 4.6. We remark again that, for showing the equilibrium point is locally asymptotically stable, initial conditions must start near the equilibrium point.

Simulation 5.7. Consider an SIR epidemic model of two patches with initial conditions $S_1(0) = 50,008$, $S_2(0) = 49,988$, $S_3(0) = 49,998$, $I_1(0) = I_2(0) = I_3(0) = 2$, and $R_1(0) = R_2(0) = R_3(0) = 0$ and parameters are given by $w_0 = 2.0 \times 10^{-7}$, $\beta_1 = 0.12$, $\beta_2 = 0.08$, $\beta_3 = 0.06$, $\tau_1 = 1.5$ and $\tau_2 = 1.1$. So,

$$\mathcal{R}_0^{(1)} = 0.84, \mathcal{R}_0^{(2)} = 0.60 \text{ and } \mathcal{R}_0^{(3)} = 0.42$$

Therefore, $\mathcal{R}_0^{(i)} < 1$ for all $i = 1, 2, 3$ and $\tau_2 < \tau_1$ which correspond to the conditions of Theorem 4.8. Thus, by Theorem 4.8, we have the positive disease-free equilibrium is locally asymptotically stable. The numerical results of this simulation given by Figure 5.7 shows that the solution tends to the positive disease-free equilibrium $(\frac{N}{2}, \frac{N}{2}, \frac{N}{2}, 0, 0, 0, 0, 0, 0)$ as time is increased. Note that pictures in the right column of Figure 5.7 show the solution for long time. Hence, the theoretical prediction of Theorem 4.6 agrees with the numerical results.

The two following simulations are in agreement with the theoretical conjectures of Theorem 4.9.

Simulation 5.8. Consider an SIR epidemic model of two patches with initial conditions $S_1(0) = 30,008$, $S_2(0) = 49,988$, $S_3(0) = 69,998$, $I_1(0) = I_2(0) = I_3(0) = 2$, and $R_1(0) = R_2(0) = R_3(0) = 0$ and parameters are given by $w_0 = 1.43 \times 10^{-7}$, $\beta_1 = 0.13$, $\beta_2 = 0.11$, $\beta_3 = 0.09$, $\tau_1 = 1.5$ and $\tau_2 = 1.1$. So,

$$\mathcal{R}_0^{(1)} = 0.91, \mathcal{R}_0^{(2)} = 0.77 \text{ and } \mathcal{R}_0^{(3)} = 0.63$$

Therefore, $\mathcal{R}_0^{(i)} < 1$ for all $i = 1, 2, 3$. Applying Theorem 4.9, we have $\mathcal{R}_0 < 1$. From the basic reproduction number is derived in section 4.2, we obtain $\mathcal{R}_0 = 0.80$. Thus, by both the theoretical conjectures of Theorem 4.9 and the derived basic reproduction number, we have $\mathcal{R}_0 < 1$. That is, the disease cannot invade a population by theory. The numerical results of this simulation given by Figure 5.8. In particular, Figure 5.8(b) shows that there is no outbreak in all patch. Hence, both the theoretical conjectures of Theorem 4.9 and the derived basic reproduction number agree with the numerical results. Note that Figure 5.8(a) shows the susceptible population number in each patch increases or decreases from the initial conditions, it is not affected from infection but it is affected from the movement of susceptible individuals between patches or the natural death.

Simulation 5.9. Consider an SIR epidemic model of two patches with the same initial conditions in Simulation 5.8 and parameters are given by $w_0 = 1.43 \times 10^{-7}$, $\beta_1 = 0.15$, $\beta_2 = 0.17$, $\beta_3 = 0.19$, $\tau_1 = 1.5$ and $\tau_2 = 1.1$. So,

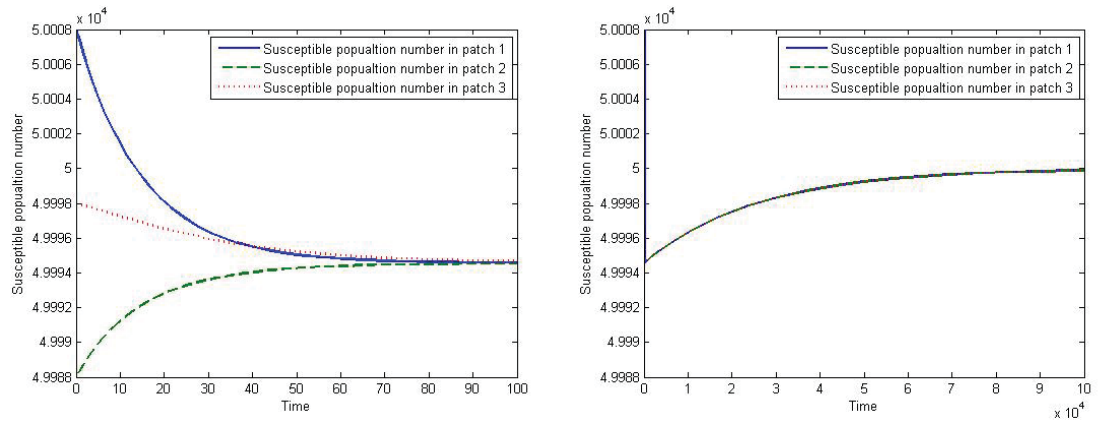
$$\mathcal{R}_0^{(1)} = 1.05, \mathcal{R}_0^{(2)} = 1.19 \text{ and } \mathcal{R}_0^{(3)} = 1.33$$

Therefore, $\mathcal{R}_0^{(i)} > 1$ for all $i = 1, 2, 3$. Applying Theorem 4.9, we have $\mathcal{R}_0 > 1$. From the basic reproduction number is derived in section 4.2, we obtain $\mathcal{R}_0 = 1.21$. Thus, by both the theoretical conjectures of Theorem 4.9 and the derived basic reproduction number, we have $\mathcal{R}_0 > 1$. That is, the disease can invade a susceptible population by theory. The numerical results of this simulation given by Figure 5.9 show that there is a large outbreak in all patch. Hence, both the theoretical conjectures of Theorem 4.9 and the derived basic reproduction number agree with the numerical results. We remark that the solution tends to the epidemic equilibrium point.

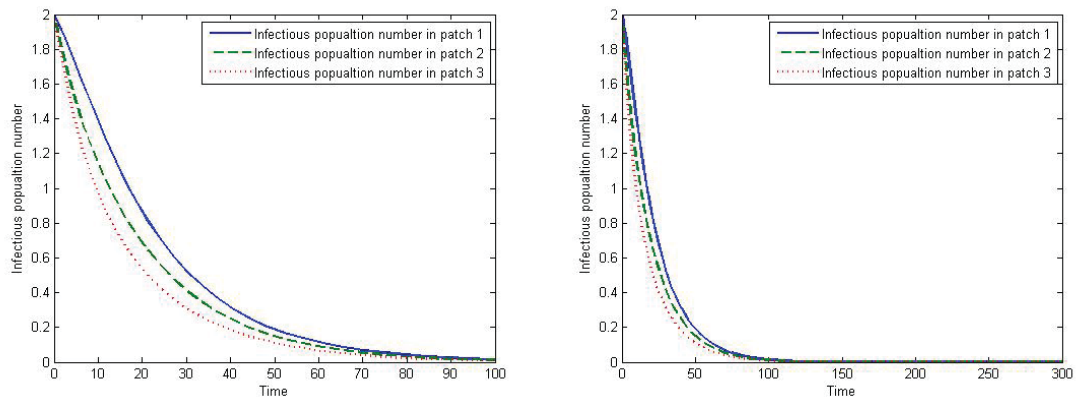
Simulation 5.10. Consider an SIR epidemic model of two patches with the same initial conditions in Simulation 5.8 and the same parameters in Simulation 5.9 but $\tau_2 = 0.8$. Then the derived basic reproduction number $\mathcal{R}_0 = 1.17$. The numerical results of this simulation given by Figure 5.10. By the same argument in Simulation 5.9, we have both the theoretical prediction of Theorem 4.9 and the derived basic reproduction number agree with the numerical results.

Next, we compare the results of the two simulations above. Note that this comparison is similar to the comparison of two patches simulations

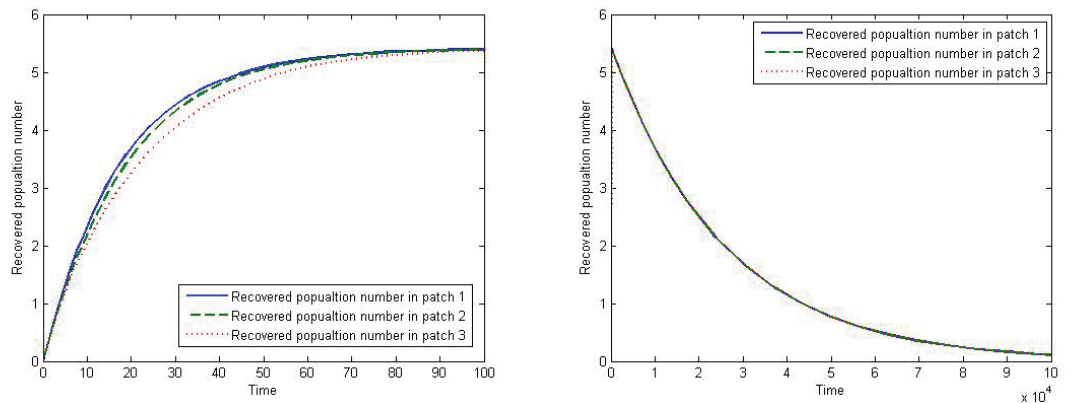
Simulation 5.9 and Simulation 5.10 have the same initial conditions and the same parameters except τ_2 . We focus on the numerical results for infectious population number of Simulation 5.9 and Simulation 5.10 given by Figure 5.9(b) and Figure 5.10(b), respectively. Then we see that an epidemic period and the most outbreak of each patch in Simulation 5.9 is different from Simulation 5.10. For example, the most outbreak in patch 3 of Simulation 5.9 occurs at about 250 day, while the most outbreak in patch 3 of Simulation 5.10 occurs at about 180 day. Hence, the changes of travel parameter τ_2 affect the outbreak duration of the disease.



(a) Susceptible population.

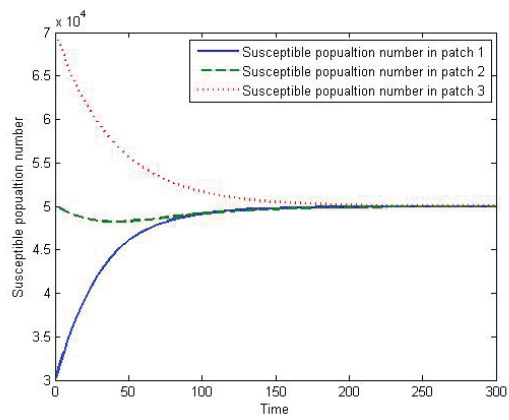


(b) Infectious population.

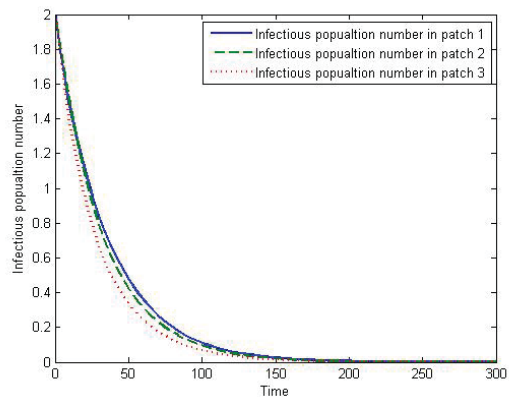


(c) Recovered population.

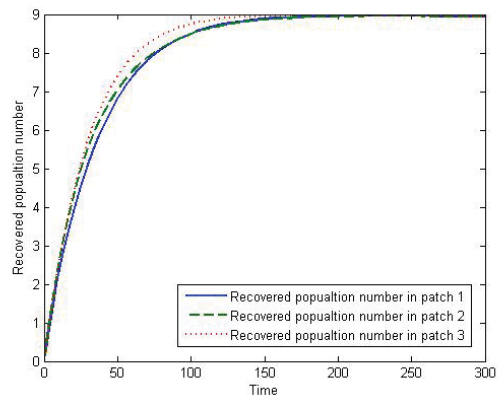
Figure 5.7: Numerical results of an SIR model with three patches for Simulation 5.7



(a) Susceptible population.

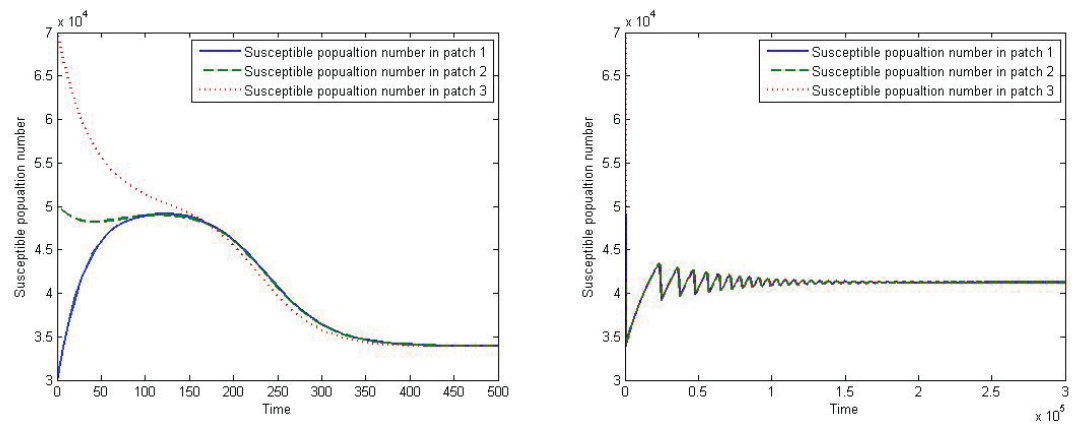


(b) Infectious population.

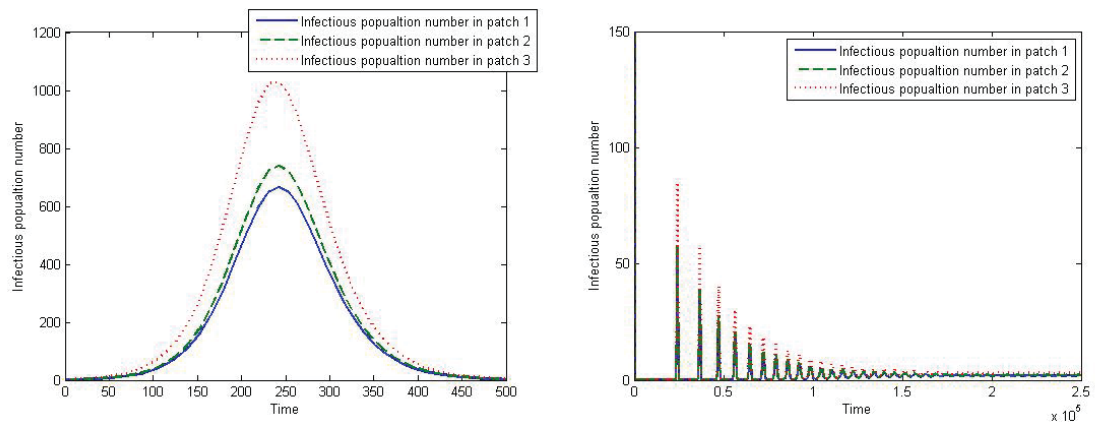


(c) Recovered population.

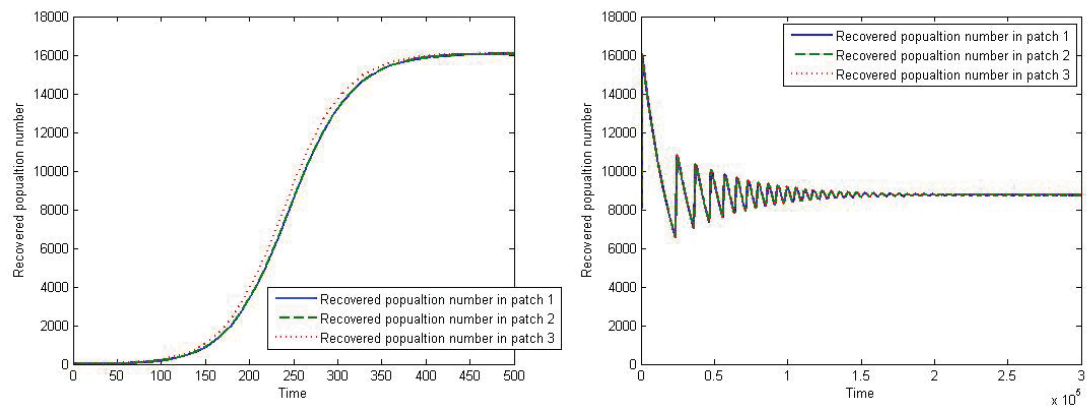
Figure 5.8: Numerical results of an SIR model with three patches for Simulation 5.8



(a) Susceptible population.

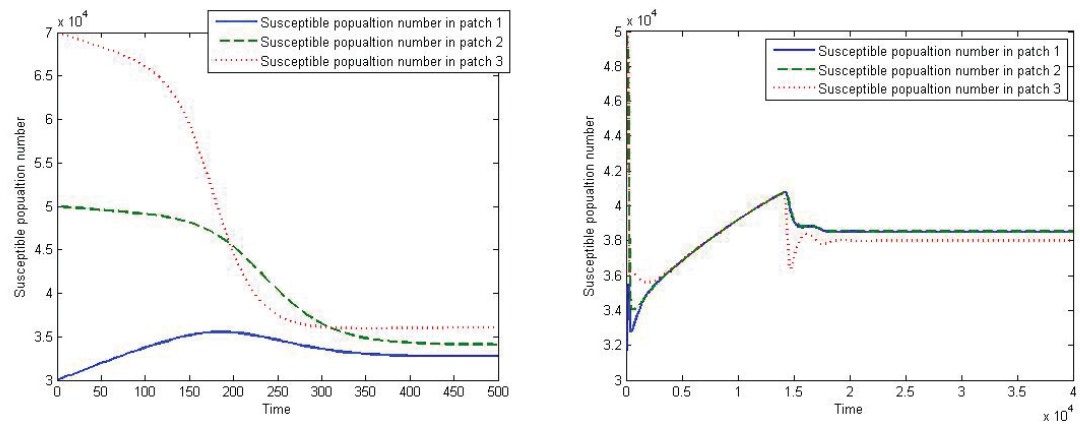


(b) Infectious population.

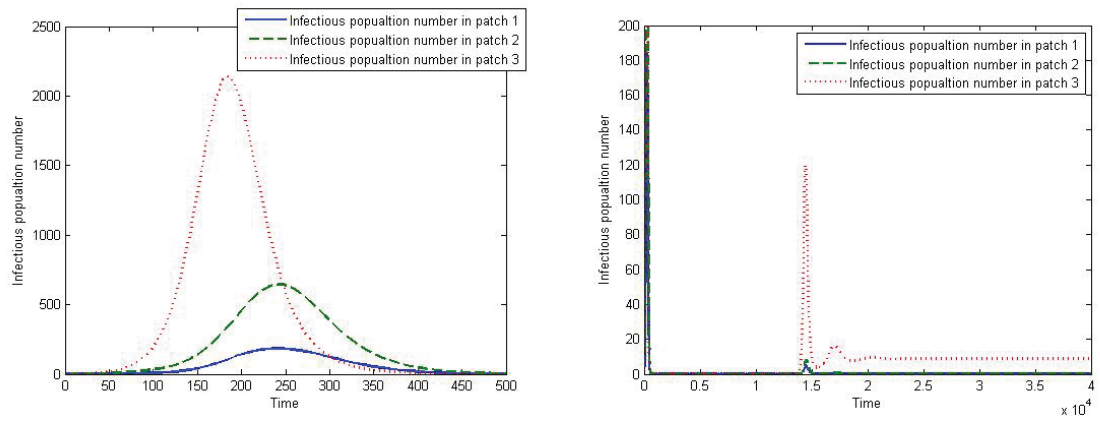


(c) Recovered population.

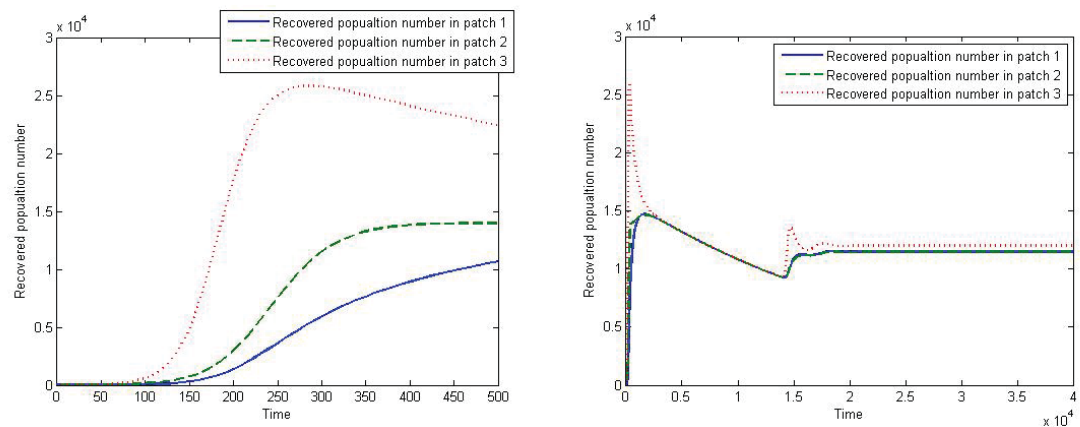
Figure 5.9: Numerical results of an SIR model with three patches for Simulation 5.9



(a) Susceptible population.



(b) Infectious population.



(c) Recovered population.

Figure 5.10: Numerical results of an SIR model with three patches for Simulation 5.10

The following figure shows the behavior of the basic reproduction number with respect to $\tau_1 + \tau_2$ for an SIR epidemic model of three patches with $w_0 = 1.43 \times 10^{-7}$, $\beta_1 = 0.08$, $\beta_1 = 0.11$ and $\beta_1 = 0.17$. So, the basic reproduction numbers of each patch in isolation are as follows,

$$\mathcal{R}_0^{(1)} = 0.5598 < 1, \mathcal{R}_0^{(2)} = 0.7698 < 1 \text{ and } \mathcal{R}_0^{(3)} = 1.1897 > 1$$

Therefore,

$$\mathcal{R}(\infty) = \frac{\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} + \mathcal{R}_0^{(3)}}{3} = 0.8398 < 1$$

which corresponds to the conditions of Theorem 4.13. Thus, by the conjectures of Theorem 4.13, there are τ' and τ'' such that

- (i). $\mathcal{R}_0 < 1$ for $\tau_1 + \tau_2 > \tau'$
- (ii). $\mathcal{R}_0 > 1$ for $\tau_1 + \tau_2 < \tau''$.

Next, we look the graph of the basic reproduction number with respect to $\tau_1 + \tau_2$ given by Figure 5.11. We see that

- (i). $\mathcal{R}_0 < 1$ for $\tau_1 + \tau_2 > 2.171$
- (ii). $\mathcal{R}_0 > 1$ for $\tau_1 + \tau_2 < 2.171$.

Therefore, the conjectures of Theorem 4.13 agree with the numerical results where $\tau' = \tau'' = 2.171$.

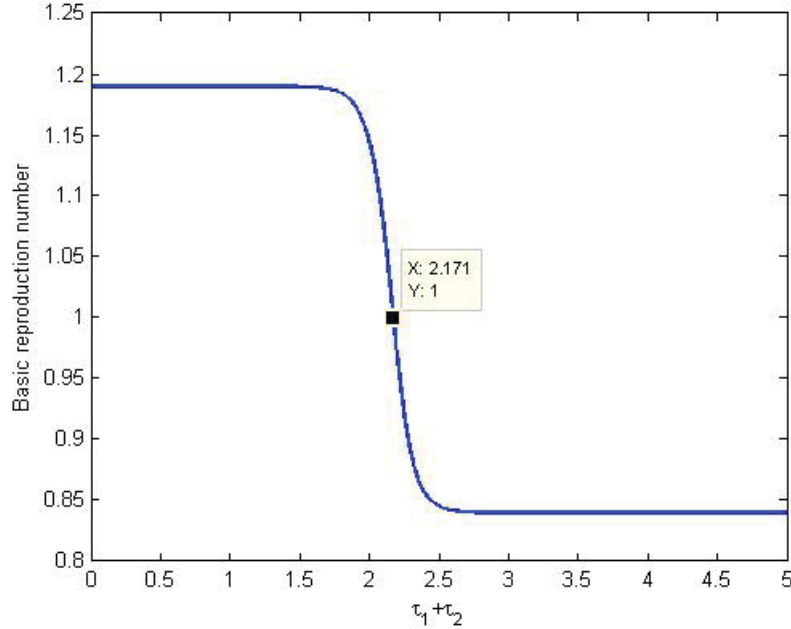


Figure 5.11: The basic reproduction number with respect to $\tau_1 + \tau_2$ for an SIR epidemic model of three patches with parameter values are given in the text.

Moreover, we see that $\mathcal{R}_0 \rightarrow 1.1897 = \max_{1 \leq i \leq 3} \mathcal{R}_0^{(i)}$ as $\tau_1 + \tau_2 \rightarrow 0$ and $\mathcal{R}_0 \rightarrow 0.8398 = \mathcal{R}(\infty)$ as $\tau_1 + \tau_2 \rightarrow \infty$ which correspond to the conjecture of Theorem 4.12 and Theorem 4.10, respectively.

Chapter 6

Conclusion

For both two patches and three patches model, we derived the disease-free equilibrium point and showed that the positive disease-free equilibrium point is unique. The population number in each patch at a disease state is in balance by gravity movement. Moreover, the extinction of a population has occurred in some patch when $\tau_2 > \tau_1$. On the other hand, when $\tau_2 < \tau_1$, there exist individuals in all patch. We can give an illustration as follows. By stability analysis, we have

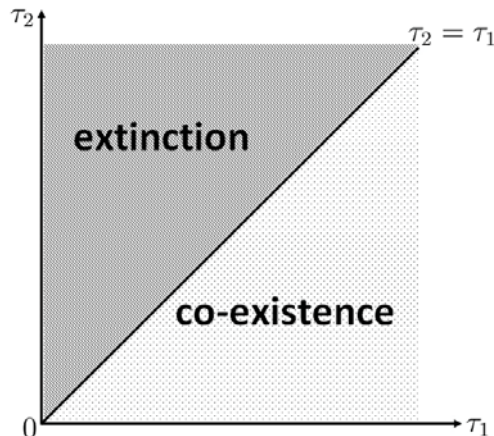


Figure 6.1: The area for the extinction and co-existence of a population.

shown that the positive disease-free equilibrium point is locally asymptotically stable if the basic reproduction numbers of each patch in isolation are less than one and $\tau_2 < \tau_1$ which are the sufficient conditions but not necessary conditions. The basic reproduction number of both models are derived by the next generation method. The basic reproduction number of two patches model can be obtained explicitly while the basic reproduction number of three patches model can be obtained implicitly or numerically due to the complexity.

In two-patch model, we established Lemma 4.2 to obtain the conditions for which the spectral radius of a next generation matrix is less than one. We applied this lemma to Theorem 4.3, Theorem 4.4 and Theorem 4.5. From Theorem 4.3 and Theorem 4.4, if the basic reproduction number of all patches in isolation are less than one, then $\mathcal{R}_0 < 1$. On the other hand, if the basic reproduction

number of all patches in isolation are greater than one, then $\mathcal{R}_0 > 1$. It implies that the global epidemic threshold have dominated by the transmission in each patch if they are all below or above the local threshold regardless of the effect of travel although there are travels between patches, that is, the disease spread is independent on travel parameters τ_1 and τ_2 . An interesting case occurs when the model that have an epidemic patch and a nonepidemic patch under which there is no travel between patches. This case is shown by Theorem 4.5 under the condition $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} < 2$. This theorem gives a threshold of the disease spread depending on the parameter ϵ which is the term of travel parameters τ_1 and τ_2 . Thus, the disease spread depends on travel parameters τ_1 and τ_2 in an interesting case. Note that for an interesting case under the condition $\mathcal{R}_0^{(1)} + \mathcal{R}_0^{(2)} > 2$, we have shown that $\mathcal{R}_0 > 1$ by remark after Theorem 4.5. We give an illustration of the area for which $\mathcal{R}_0 < 1$ or $\mathcal{R}_0 > 1$ by applying our theorems as follows.

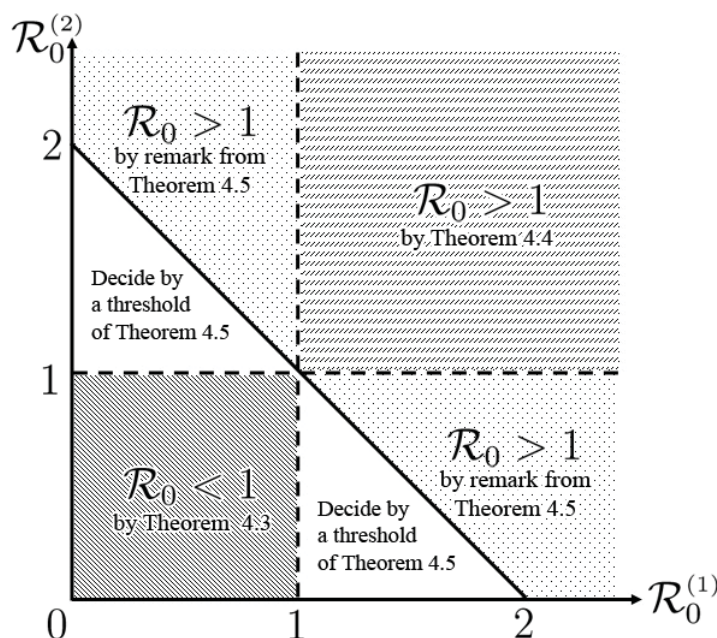


Figure 6.2: The area for which $\mathcal{R}_0 < 1$ or $\mathcal{R}_0 > 1$ by the conjectures of Theorem 4.3, Theorem 4.4 and Theorem 4.5.

In three-patch model, we established theorem showing that for a population model, there exists a unique positive equilibrium point which is independent from distance. It implies that there exists a unique positive disease-free equilibrium. According to Theorem 4.9, we obtained the bound of the basic reproduction number, the upper bound of \mathcal{R}_0 is the maximum of the basic reproduction numbers of each patch in isolation and the lower bound of \mathcal{R}_0 is the minimum of the basic reproduction numbers of each patch in isolation. It implies that if the basic reproduction number of all patches in isolation are less than one, then $\mathcal{R}_0 < 1$. On the other hand, if the basic reproduction number of all patches in isolation are greater than one, then $\mathcal{R}_0 > 1$. It is similar to two-patch model that the global epidemic threshold have dominated by the transmission in each patch if they are

all below or above the local threshold regardless of the effect of travel although there are travels between patches. We considered the model with the several conditions such as $\tau_1 + \tau_2$ tends to infinity, there is no travel between patches and $\tau_1 + \tau_2$ tends to zero with $\frac{w_0}{N}$ tends to zero given by Theorem 4.10, Theorem 4.11 and Theorem 4.12, respectively. By the result of Theorem 4.10, Theorem 4.11 and Theorem 4.12, we established Theorem 4.13 showing the existence for a threshold given by $\tau_1 + \tau_2$ under $\mathcal{R}(\infty) < 1$ in an interesting case that have an epidemic patch and a nonepidemic patch under which there is no travel between patches. That is, travel parameters τ_1 and τ_2 affect the global epidemic threshold in an interesting case. We give an illustration of the area for which $\mathcal{R}_0 < 1$ or $\mathcal{R}_0 > 1$ by the conjectures of Theorem 4.13 as follows.

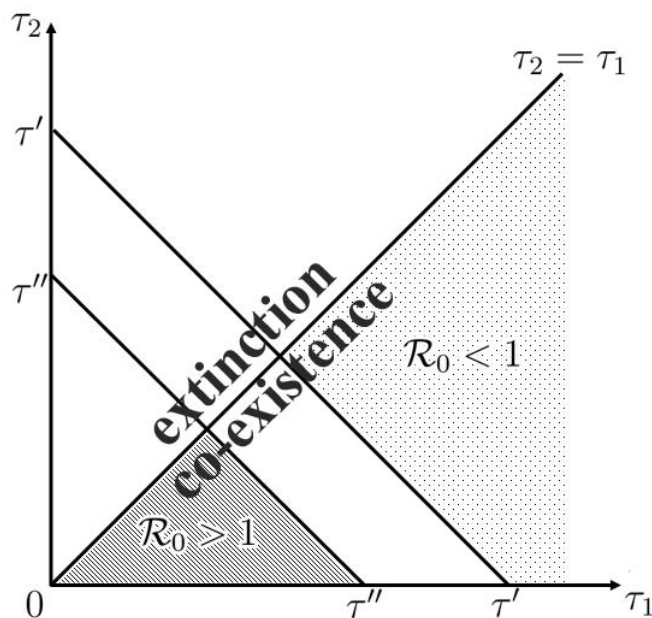


Figure 6.3: The area for which $\mathcal{R}_0 < 1$ or $\mathcal{R}_0 > 1$ by the conjectures of Theorem 4.13.

According to a simulation given by Figure 5.11, we see that $\tau' = \tau''$. Thus two critical points in Theorem 4.13 may be equal. Therefore, if $\tau' = \tau''$, then it is nothing to analyze. On the other hand, if $\tau' \neq \tau''$, then we have a gap between τ' and τ'' that does not find out how the global epidemic threshold occurs.

Observe that, in both models, if the basic reproduction numbers of each patch in isolation are less than one, then the disease-free equilibrium point is locally asymptotically stable and $\mathcal{R}_0 < 1$ which are compatible that an epidemic dies out. The numerical simulations shown are in agreement with theory. In particular, by comparing of the numerical results, we see that the changes of travel parameters τ_1 and τ_2 affect the outbreak duration of the disease.

In the special case for three patches model in which all distance between patches tends to infinity or θ tends to infinity, population travels tends to zero. Then the basic reproduction number for this case tends to the basic reproduction number in case there is no travel between patches which is shown by Theorem

4.11. That is, the basic reproduction number of this special case tends to the maximum of the basic reproduction numbers of each patch in isolation.

Finally, the future work arising from these studies is fitting the data of the real incidence of disease to the model of two patches and three patches for indicating the disease spread. The extension from this research is analyzing the model with $n > 3$, focusing on the change of distance between patches to the disease spread or formulating the model with a gravity law in which the total population is not constant. It remains how the global epidemic threshold occurs when $\mathcal{R}(\infty) > 1$ in Theorem 4.13.



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Appendix A

Details of the Proof

In this appendix, we will give the details for deriving the Jacobian matrix of both two patches and three patches. The detail for finding the inverse matrix of V for three patches will be given.

A.1 Jacobian matrix for an epidemic model of two patches

In order to find the Jacobian matrix for the model given by (4.1)-(4.6), we first replace some variables in equations (4.1) and (4.2) as follows.

- (i). Replace a variable $S_2(t)$ with $N - N_1(t) - I_2(t) - R_2(t)$ in equation (4.1).
- (ii). Replace a variable $N_2(t)$ with $N - N_1(t)$ in equation (4.1).
- (iii). Replace a variable $S_1(t)$ with $N - N_2(t) - I_1(t) - R_1(t)$ in equation (4.2).
- (iv). Replace a variable $N_1(t)$ with $N - N_2(t)$ in equation (4.2).

Note that N is the total population constant with $N = N_1(t) + N_2(t)$. Then the Jacobian matrix for (4.1)-(4.6) at a point $(S_1^*, S_2^*, I_1^*, I_2^*, R_1^*, R_2^*)$ is given by

$$J = [a_{ij}]_{6 \times 6}$$

where the entries a_{ij} are given as follows

$$\begin{aligned} a_{11} = & \mu - \mu - \left(\frac{N_1^* \beta_1 I_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) + \frac{w_0}{d_{12}} \left[N_1^{*\tau_2} (N - N_1^*)^{\tau_1 - 1} (-1) \right. \\ & + (N - N_1^* - I_2^* - R_2^*) \left(N_1^{*\tau_2} (\tau_1 - 1) (N - N_1^*)^{\tau_1 - 2} (-1) \right. \\ & \left. \left. + (N - N_1^*)^{\tau_1 - 1} \tau_2 N_1^{*\tau_2 - 1} \right) \right] - \frac{w_0}{d_{12}} \left[(N - N_1^*)^{\tau_2} N_1^{*\tau_1 - 1} \right. \\ & \left. + S_1^* \left((N - N_1^*)^{\tau_2} (\tau_1 - 1) N_1^{*\tau_1 - 2} + N_1^{*\tau_1 - 1} \tau_2 (N - N_1^*)^{\tau_2 - 1} (-1) \right) \right] \\ a_{21} = & 0 \end{aligned}$$

$$\begin{aligned}
a_{31} &= \left(\frac{N_1^* \beta_1 I_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \\
a_{41} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
a_{51} &= \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* \\
a_{61} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
a_{12} &= 0 \\
a_{22} &= \mu - \mu - \left(\frac{N_2^* \beta_2 I_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) + \frac{w_0}{d_{12}} \left[N_2^{*\tau_2} (N - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad + (N - N_2^* - I_1^* - R_1^*) \left(N_2^{*\tau_2} (\tau_1 - 1) (N - N_2^*)^{\tau_1-2} (-1) \right. \\
&\quad \left. \left. + (N - N_2^*)^{\tau_1-1} \tau_2 N_2^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{12}} \left[(N - N_2^*)^{\tau_2} N_2^{*\tau_1-1} \right. \\
&\quad \left. + S_2^* \left((N - N_2^*)^{\tau_2} (\tau_1 - 1) N_2^{*\tau_1-2} + N_2^{*\tau_1-1} \tau_2 (N - N_2^*)^{\tau_2-1} (-1) \right) \right] \\
a_{32} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
a_{42} &= \left(\frac{N_2^* \beta_2 I_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \\
a_{52} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
a_{62} &= \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* \\
a_{13} &= \mu - \left(\frac{N_1^* \beta_1 S_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) + \frac{w_0}{d_{12}} \left[N_1^{*\tau_2} (N - N_1^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - I_2^* - R_2^*) \left(N_1^{*\tau_2} (\tau_1 - 1) (N - N_1^*)^{\tau_1-2} (-1) + (N - N_1^*)^{\tau_1-1} \tau_2 N_1^{*\tau_2-1} \right) \right] \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_1^*)^{\tau_2} (\tau_1 - 1) N_1^{*\tau_1-2} S_1^* + N_1^{*\tau_1-1} S_1^* \tau_2 (N - N_1^*)^{\tau_2-1} (-1) \right] \\
a_{23} &= \frac{w_0}{d_{12}} N_2^{*\tau_2} (N - N_2^*)^{\tau_1-1} (-1) \\
a_{33} &= \left(\frac{N_1^* \beta_1 S_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) - \mu - \gamma + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
&\quad - \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) \\
a_{43} &= \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
a_{53} &= \gamma + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* \\
a_{63} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^*
\end{aligned}$$

$$\begin{aligned}
a_{14} &= \frac{w_0}{d_{12}} N_1^{*\tau_2} (N - N_1^*)^{\tau_1-1} (-1) \\
a_{24} &= \mu - \left(\frac{N_2^* \beta_2 S_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) + \frac{w_0}{d_{12}} \left[N_2^{*\tau_2} (N - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - I_1^* - R_1^*) \left(N_2^{*\tau_2} (\tau_1 - 1) (N - N_2^*)^{\tau_1-2} (-1) + (N - N_2^*)^{\tau_1-1} \tau_2 N_2^{*\tau_2-1} \right) \right] \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_2^*)^{\tau_2} (\tau_1 - 1) N_2^{*\tau_1-2} S_2^* + N_2^{*\tau_1-1} S_2^* \tau_2 (N - N_2^*)^{\tau_2-1} (-1) \right] \\
a_{34} &= \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
a_{44} &= \left(\frac{N_2^* \beta_2 S_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) - \mu - \gamma + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
&\quad - \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) \\
a_{54} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
a_{64} &= \gamma + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* \\
a_{15} &= \mu + \frac{\beta_1 S_1^* I_1^*}{N_1^{*2}} + \frac{w_0}{d_{12}} \left[N_1^{*\tau_2} (N - N_1^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - I_2^* - R_2^*) \left(N_1^{*\tau_2} (\tau_1 - 1) (N - N_1^*)^{\tau_1-2} (-1) + (N - N_1^*)^{\tau_1-1} \tau_2 N_1^{*\tau_2-1} \right) \right] \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_1^*)^{\tau_2} (\tau_1 - 1) N_1^{*\tau_1-2} S_1^* + N_1^{*\tau_1-1} S_1^* \tau_2 (N - N_1^*)^{\tau_2-1} (-1) \right] \\
a_{25} &= \frac{w_0}{d_{12}} N_2^{*\tau_2} (N - N_2^*)^{\tau_1-1} (-1) \\
a_{35} &= -\frac{\beta_1 S_1^* I_1^*}{N_1^{*2}} + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \\
a_{45} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
a_{55} &= -\mu + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* - \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* \right) \\
a_{65} &= \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* \right) - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
a_{16} &= \frac{w_0}{d_{12}} N_1^{*\tau_2} (N - N_1^*)^{\tau_1-1} (-1) \\
a_{26} &= \mu + \frac{\beta_2 S_2^* I_2^*}{N_2^{*2}} + \frac{w_0}{d_{12}} \left[N_2^{*\tau_2} (N - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - I_1^* - R_1^*) \left(N_2^{*\tau_2} (\tau_1 - 1) (N - N_2^*)^{\tau_1-2} (-1) + (N - N_2^*)^{\tau_1-1} \tau_2 N_2^{*\tau_2-1} \right) \right] \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_2^*)^{\tau_2} (\tau_1 - 1) N_2^{*\tau_1-2} S_2^* + N_2^{*\tau_1-1} S_2^* \tau_2 (N - N_2^*)^{\tau_2-1} (-1) \right]
\end{aligned}$$

$$\begin{aligned}
a_{36} &= \frac{w_0}{d_{12}}(\tau_1 - 1)N_1^{*\tau_2}N_2^{*\tau_1-2}I_2^* - \frac{w_0}{d_{12}}\tau_2N_2^{*\tau_2-1}N_1^{*\tau_1-1}I_1^* \\
a_{46} &= -\frac{\beta_2S_2^*I_2^*}{N_2^{*2}} + \frac{w_0}{d_{12}}\tau_2N_2^{*\tau_2-1}N_1^{*\tau_1-1}I_1^* - \frac{w_0}{d_{12}}(\tau_1 - 1)N_1^{*\tau_2}N_2^{*\tau_1-2}I_2^* \\
a_{56} &= \frac{w_0}{d_{12}}\left(N_1^{*\tau_2}N_2^{*\tau_1-1} + (\tau_1 - 1)N_1^{*\tau_2}N_2^{*\tau_1-2}R_2^*\right) - \frac{w_0}{d_{12}}\tau_2N_2^{*\tau_2-1}N_1^{*\tau_1-1}R_1^* \\
a_{66} &= -\mu + \frac{w_0}{d_{12}}\tau_2N_2^{*\tau_2-1}N_1^{*\tau_1-1}R_1^* - \frac{w_0}{d_{12}}\left(N_1^{*\tau_2}N_2^{*\tau_1-1} + (\tau_1 - 1)N_1^{*\tau_2}N_2^{*\tau_1-2}R_2^*\right)
\end{aligned}$$

with $N_i^* = S_i^* + I_i^* + R_i^*$ for all $i = 1, 2$.

A.2 Jacobian matrix for an epidemic model of three patches

In order to find the Jacobian matrix for the model given by (4.27)-(4.35), we first replace some variables in equations (4.27), (4.28) and (4.29) as follows.

- (i). Replace a variable $S_3(t)$ with $N - N_1(t) - N_2(t) - I_3(t) - R_3(t)$ in Eq.(4.27).
- (ii). Replace a variable $N_3(t)$ with $N - N_1(t) - N_2(t)$ in Eq.(4.21).
- (iii). Replace a variable $S_1(t)$ with $N - N_2(t) - N_3(t) - I_1(t) - R_1(t)$ in Eq.(4.28).
- (iv). Replace a variable $N_1(t)$ with $N - N_2(t) - N_3(t)$ in Eq.(4.22).
- (v). Replace a variable $S_2(t)$ with $N - N_1(t) - N_3(t) - I_2(t) - R_2(t)$ in Eq.(4.29).
- (vi). Replace a variable $N_2(t)$ with $N - N_1(t) - N_3(t)$ in Eq.(4.23).

Note that N is the total population constant with $N = N_1(t) + N_2(t) + N_3(t)$. Then the Jacobian matrix for (4.27)-(4.35) at a point $(S_1^*, S_2^*, S_3^*, I_1^*, I_2^*, I_3^*, R_1^*, R_2^*, R_3^*)$ is given by

$$G = [b_{ij}]_{9 \times 9}$$

where the entries b_{ij} are given as follows

$$\begin{aligned}
b_{11} &= \mu - \mu - \left(\frac{N_1^*\beta_1I_1^* - \beta_1S_1^*I_1^*}{N_1^{*2}}\right) \\
&+ \frac{w_0}{d_{12}}\tau_2N_1^{*\tau_2-1}N_2^{*\tau_1-1}S_2^* + \frac{w_0}{d_{13}}\left[N_1^{*\tau_2}(N - N_1^* - N_2^*)^{\tau_1-1}(-1)\right. \\
&+ (N - N_1^* - N_2^* - I_3^* - R_3^*)\left(N_1^{*\tau_2}(\tau_1 - 1)(N - N_1^* - N_2^*)^{\tau_1-2}(-1)\right. \\
&+ \left.(N - N_1^* - N_2^*)^{\tau_1-1}\tau_2N_1^{*\tau_2-1}\right) \left. - \frac{w_0}{d_{12}}\left(N_2^{*\tau_2}N_1^{*\tau_1-1} + (\tau_1 - 1)N_2^{*\tau_2}N_1^{*\tau_1-2}S_1^*\right)\right. \\
&- \frac{w_0}{d_{13}}\left[(N - N_1^* - N_2^*)^{\tau_2}N_1^{*\tau_1-1} + S_1^*\left((N - N_1^* - N_2^*)^{\tau_2}(\tau_1 - 1)N_1^{*\tau_1-2}\right.\right. \\
&\left.\left.+ N_1^{*\tau_1-1}\tau_2(N - N_1^* - N_2^*)^{\tau_2-1}(-1)\right)\right]
\end{aligned}$$

$$b_{21} = 0$$

$$\begin{aligned}
b_{31} &= \frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} S_1^* \right) + \frac{w_0}{d_{23}} N_3^{*\tau_2} \left[(N - N_1^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_3^* - I_2^* - R_2^*) (\tau_1 - 1) (N - N_1^* - N_3^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} S_3^* - \frac{w_0}{d_{23}} \tau_2 (N - N_1^* - N_3^*)^{\tau_2-1} (-1) N_3^{*\tau_1-1} S_3^* \\
b_{41} &= \left(\frac{N_1^* \beta_1 I_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* \\
b_{51} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
b_{61} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
b_{71} &= \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} R_1^* \\
b_{81} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
b_{91} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
b_{12} &= \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} S_2^* \right) + \frac{w_0}{d_{13}} N_1^{*\tau_2} \left[(N - N_1^* - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_2^* - I_3^* - R_3^*) (\tau_1 - 1) (N - N_1^* - N_2^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} S_1^* - \frac{w_0}{d_{13}} \tau_2 (N - N_1^* - N_2^*)^{\tau_2-1} (-1) N_1^{*\tau_1-1} S_1^* \\
b_{22} &= \mu - \mu - \left(\frac{N_2^* \beta_2 I_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) \\
&\quad + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} S_3^* + \frac{w_0}{d_{12}} \left[N_2^{*\tau_2} (N - N_2^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - N_3^* - I_1^* - R_1^*) \left(N_2^{*\tau_2} (\tau_1 - 1) (N - N_2^* - N_3^*)^{\tau_1-2} (-1) \right) \right. \\
&\quad \left. + (N - N_2^* - N_3^*)^{\tau_1-1} \tau_2 N_2^{*\tau_2-1} \right] - \frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} S_2^* \right) \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_2^* - N_3^*)^{\tau_2} N_2^{*\tau_1-1} + S_2^* \left((N - N_2^* - N_3^*)^{\tau_2} (\tau_1 - 1) N_2^{*\tau_1-2} \right. \right. \\
&\quad \left. \left. + N_2^{*\tau_1-1} \tau_2 (N - N_2^* - N_3^*)^{\tau_2-1} (-1) \right) \right] \\
b_{32} &= 0 \\
b_{42} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^*
\end{aligned}$$

$$\begin{aligned}
b_{52} &= \left(\frac{N_2^* \beta_2 I_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* \\
b_{62} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
b_{72} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
b_{82} &= \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} R_2^* \\
b_{92} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
b_{13} &= 0 \\
b_{23} &= \frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} S_3^* \right) + \frac{w_0}{d_{12}} N_2^{*\tau_2} \left[(N - N_2^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - N_3^* - I_1^* - R_1^*) (\tau_1 - 1) (N - N_2^* - N_3^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} S_2^* - \frac{w_0}{d_{12}} \tau_2 (N - N_2^* - N_3^*)^{\tau_2-1} (-1) N_2^{*\tau_1-1} S_2^* \\
b_{33} &= \mu - \mu - \left(\frac{N_3^* \beta_3 I_3^* - \beta_3 S_3^* I_3^*}{N_3^{*2}} \right) \\
&\quad + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} S_1^* + \frac{w_0}{d_{23}} \left[N_3^{*\tau_2} (N - N_1^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_3^* - I_2^* - R_2^*) \left(N_3^{*\tau_2} (\tau_1 - 1) (N - N_1^* - N_3^*)^{\tau_1-2} (-1) \right) \right. \\
&\quad \left. + (N - N_1^* - N_3^*)^{\tau_1-1} \tau_2 N_3^{*\tau_2-1} \right] - \frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} S_3^* \right) \\
&\quad - \frac{w_0}{d_{23}} \left[(N - N_1^* - N_3^*)^{\tau_2} N_3^{*\tau_1-1} + S_3^* \left((N - N_1^* - N_3^*)^{\tau_2} (\tau_1 - 1) N_3^{*\tau_1-2} \right. \right. \\
&\quad \left. \left. + N_3^{*\tau_1-1} \tau_2 (N - N_1^* - N_3^*)^{\tau_2-1} (-1) \right) \right] \\
b_{43} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
b_{53} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
b_{63} &= \left(\frac{N_3^* \beta_3 I_3^* - \beta_3 S_3^* I_3^*}{N_3^{*2}} \right) + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
&\quad - \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* \\
b_{73} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} R_3^* - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
b_{83} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} R_3^* - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} R_2^*
\end{aligned}$$

$$\begin{aligned}
b_{93} &= \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
&\quad - \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} R_3^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} R_3^* \\
b_{14} &= \mu - \left(\frac{N_1^* \beta_1 S_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) \\
&\quad + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} S_2^* + \frac{w_0}{d_{13}} \left[N_1^{*\tau_2} (N - N_1^* - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad + (N - N_1^* - N_2^* - I_3^* - R_3^*) \left(N_1^{*\tau_2} (\tau_1 - 1) (N - N_1^* - N_2^*)^{\tau_1-2} (-1) \right. \\
&\quad \left. \left. + (N - N_1^* - N_2^*)^{\tau_1-1} \tau_2 N_1^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} S_1^* \\
&\quad - \frac{w_0}{d_{13}} \left[(N - N_1^* - N_2^*)^{\tau_2} (\tau_1 - 1) N_1^{*\tau_1-2} S_1^* + N_1^{*\tau_1-1} S_1^* \tau_2 (N - N_1^* - N_2^*)^{\tau_2-1} (-1) \right] \\
b_{24} &= \frac{w_0}{d_{12}} N_2^{*\tau_2} (N - N_2^* - N_3^*)^{\tau_1-1} (-1) \\
b_{34} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} S_1^* + \frac{w_0}{d_{23}} N_3^{*\tau_2} \left[(N - N_1^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_3^* - I_2^* - R_2^*) (\tau_1 - 1) (N - N_1^* - N_3^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} S_3^* - \frac{w_0}{d_{23}} \tau_2 (N - N_1^* - N_3^*)^{\tau_2-1} (-1) N_3^{*\tau_1-1} S_3^* \\
b_{44} &= \left(\frac{N_1^* \beta_1 S_1^* - \beta_1 S_1^* I_1^*}{N_1^{*2}} \right) - \mu - \gamma \\
&\quad + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* - \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) \\
&\quad + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* - \frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) \\
b_{54} &= \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
b_{64} &= \frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* \right) - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
b_{74} &= \gamma + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} R_1^* \\
b_{84} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
b_{94} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} R_1^* - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
b_{15} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} S_2^* + \frac{w_0}{d_{13}} N_1^{*\tau_2} \left[(N - N_1^* - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_2^* - I_3^* - R_3^*) (\tau_1 - 1) (N - N_1^* - N_2^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} S_1^* - \frac{w_0}{d_{13}} \tau_2 (N - N_1^* - N_2^*)^{\tau_2-1} (-1) N_1^{*\tau_1-1} S_1^*
\end{aligned}$$

$$\begin{aligned}
b_{25} &= \mu - \left(\frac{N_2^* \beta_2 S_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) \\
&\quad + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} S_3^* + \frac{w_0}{d_{12}} \left[N_2^{*\tau_2} (N - N_2^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad + (N - N_2^* - N_3^* - I_1^* - R_1^*) \left(N_2^{*\tau_2} (\tau_1 - 1) (N - N_2^* - N_3^*)^{\tau_1-2} (-1) \right. \\
&\quad \left. \left. + (N - N_2^* - N_3^*)^{\tau_1-1} \tau_2 N_2^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} S_2^* \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_2^* - N_3^*)^{\tau_2} (\tau_1 - 1) N_2^{*\tau_1-2} S_2^* + N_2^{*\tau_1-1} S_2^* \tau_2 (N - N_2^* - N_3^*)^{\tau_2-1} (-1) \right] \\
b_{35} &= \frac{w_0}{d_{23}} N_3^{*\tau_2} (N - N_1^* - N_3^*)^{\tau_1-1} (-1) \\
b_{45} &= \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
b_{55} &= \left(\frac{N_2^* \beta_2 S_2^* - \beta_2 S_2^* I_2^*}{N_2^{*2}} \right) - \mu - \gamma \\
&\quad + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* - \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) \\
&\quad + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* - \frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) \\
b_{65} &= \frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* \right) - \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
b_{75} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
b_{85} &= \gamma + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} R_2^* \\
b_{95} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} R_2^* - \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
b_{16} &= \frac{w_0}{d_{13}} N_1^{*\tau_2} (N - N_1^* - N_2^*)^{\tau_1-1} (-1) \\
b_{26} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} S_3^* + \frac{w_0}{d_{12}} N_2^{*\tau_2} \left[(N - N_2^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - N_3^* - I_1^* - R_1^*) (\tau_1 - 1) (N - N_2^* - N_3^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} S_2^* - \frac{w_0}{d_{12}} \tau_2 (N - N_2^* - N_3^*)^{\tau_2-1} (-1) N_2^{*\tau_1-1} S_2^* \\
b_{36} &= \mu - \left(\frac{N_3^* \beta_3 S_3^* - \beta_3 S_3^* I_3^*}{N_3^{*2}} \right) \\
&\quad + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} S_1^* + \frac{w_0}{d_{23}} \left[N_3^{*\tau_2} (N - N_1^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad + (N - N_1^* - N_3^* - I_2^* - R_2^*) \left(N_3^{*\tau_2} (\tau_1 - 1) (N - N_1^* - N_3^*)^{\tau_1-2} (-1) \right. \\
&\quad \left. \left. + (N - N_1^* - N_3^*)^{\tau_1-1} \tau_2 N_3^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} S_3^* \\
&\quad - \frac{w_0}{d_{23}} \left[(N - N_1^* - N_3^*)^{\tau_2} (\tau_1 - 1) N_3^{*\tau_1-2} S_3^* + N_3^{*\tau_1-1} S_3^* \tau_2 (N - N_1^* - N_3^*)^{\tau_2-1} (-1) \right]
\end{aligned}$$

$$\begin{aligned}
b_{46} &= \frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
b_{56} &= \frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
b_{66} &= \left(\frac{N_3^* \beta_3 S_3^* - \beta_3 S_3^* I_3^*}{N_3^{*2}} \right) - \mu - \gamma \\
&\quad + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* - \frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) \\
&\quad + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* - \frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* \right) \\
b_{76} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} R_3^* - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
b_{86} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} R_3^* - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
b_{96} &= \gamma + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
&\quad - \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} R_3^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} R_3^* \\
b_{17} &= \mu + \frac{\beta_1 S_1^* I_1^*}{N_1^{*2}} + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} S_2^* + \frac{w_0}{d_{13}} \left[N_1^{*\tau_2} (N - N_1^* - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad + (N - N_1^* - N_2^* - I_3^* - R_3^*) \left(N_1^{*\tau_2} (\tau_1 - 1) (N - N_1^* - N_2^*)^{\tau_1-2} (-1) \right. \\
&\quad \left. \left. + (N - N_1^* - N_2^*)^{\tau_1-1} \tau_2 N_1^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} S_1^* \\
&\quad - \frac{w_0}{d_{13}} \left[(N - N_1^* - N_2^*)^{\tau_2} (\tau_1 - 1) N_1^{*\tau_1-2} S_1^* + N_1^{*\tau_1-1} S_1^* \tau_2 (N - N_1^* - N_2^*)^{\tau_2-1} (-1) \right] \\
b_{27} &= \frac{w_0}{d_{12}} N_2^{*\tau_2} (N - N_2^* - N_3^*)^{\tau_1-1} (-1) \\
b_{37} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} S_1^* + \frac{w_0}{d_{23}} N_3^{*\tau_2} \left[(N - N_1^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_3^* - I_2^* - R_2^*) (\tau_1 - 1) (N - N_1^* - N_3^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} S_3^* - \frac{w_0}{d_{23}} \tau_2 (N - N_1^* - N_3^*)^{\tau_2-1} (-1) N_3^{*\tau_1-1} S_3^* \\
b_{47} &= -\frac{\beta_1 S_1^* I_1^*}{N_1^{*2}} + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* \\
b_{57} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
b_{67} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} I_1^* - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
b_{77} &= -\mu + \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* - \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* \right) \\
&\quad + \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* - \frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} R_1^* \right)
\end{aligned}$$

$$\begin{aligned}
b_{87} &= \frac{w_0}{d_{12}} \left(N_2^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_1^{*\tau_1-2} R_1^* \right) - \frac{w_0}{d_{12}} \tau_2 N_1^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
b_{97} &= \frac{w_0}{d_{13}} \left(N_3^{*\tau_2} N_1^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_1^{*\tau_1-2} R_1^* \right) - \frac{w_0}{d_{13}} \tau_2 N_1^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
b_{18} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} S_2^* + \frac{w_0}{d_{13}} N_1^{*\tau_2} \left[(N - N_1^* - N_2^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_1^* - N_2^* - I_3^* - R_3^*) (\tau_1 - 1) (N - N_1^* - N_2^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} S_1^* - \frac{w_0}{d_{13}} \tau_2 (N - N_1^* - N_2^*)^{\tau_2-1} (-1) N_1^{*\tau_1-1} S_1^* \\
b_{28} &= \mu + \frac{\beta_2 S_2^* I_2^*}{N_2^{*2}} + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} S_3^* + \frac{w_0}{d_{12}} \left[N_2^{*\tau_2} (N - N_2^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - N_3^* - I_1^* - R_1^*) \left(N_2^{*\tau_2} (\tau_1 - 1) (N - N_2^* - N_3^*)^{\tau_1-2} (-1) \right. \right. \\
&\quad \left. \left. + (N - N_2^* - N_3^*)^{\tau_1-1} \tau_2 N_2^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} S_2^* \\
&\quad - \frac{w_0}{d_{12}} \left[(N - N_2^* - N_3^*)^{\tau_2} (\tau_1 - 1) N_2^{*\tau_1-2} S_2^* + N_2^{*\tau_1-1} S_2^* \tau_2 (N - N_2^* - N_3^*)^{\tau_2-1} (-1) \right] \\
b_{38} &= \frac{w_0}{d_{23}} N_3^{*\tau_2} (N - N_1^* - N_3^*)^{\tau_1-1} (-1) \\
b_{48} &= \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
b_{58} &= -\frac{\beta_2 S_2^* I_2^*}{N_2^{*2}} + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
&\quad - \frac{w_0}{d_{12}} (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* \\
b_{68} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} I_2^* - \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} I_3^* \\
b_{78} &= \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* \right) - \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
b_{88} &= -\mu + \frac{w_0}{d_{12}} \tau_2 N_2^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* - \frac{w_0}{d_{12}} \left(N_1^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_2^{*\tau_1-2} R_2^* \right) \\
&\quad + \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* - \frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} R_2^* \right) \\
b_{98} &= \frac{w_0}{d_{23}} \left(N_3^{*\tau_2} N_2^{*\tau_1-1} + (\tau_1 - 1) N_3^{*\tau_2} N_2^{*\tau_1-2} R_2^* \right) - \frac{w_0}{d_{23}} \tau_2 N_2^{*\tau_2-1} N_3^{*\tau_1-1} R_3^* \\
b_{19} &= \frac{w_0}{d_{13}} N_1^{*\tau_2} (N - N_1^* - N_2^*)^{\tau_1-1} (-1) \\
b_{29} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} S_3^* + \frac{w_0}{d_{12}} N_2^{*\tau_2} \left[(N - N_2^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad \left. + (N - N_2^* - N_3^* - I_1^* - R_1^*) (\tau_1 - 1) (N - N_2^* - N_3^*)^{\tau_1-2} (-1) \right] \\
&\quad - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} S_2^* - \frac{w_0}{d_{12}} \tau_2 (N - N_2^* - N_3^*)^{\tau_2-1} (-1) N_2^{*\tau_1-1} S_2^*
\end{aligned}$$

$$\begin{aligned}
b_{39} &= \mu + \frac{\beta_3 S_3^* I_3^*}{N_3^{*2}} + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} S_1^* + \frac{w_0}{d_{23}} \left[N_3^{*\tau_2} (N - N_1^* - N_3^*)^{\tau_1-1} (-1) \right. \\
&\quad + (N - N_1^* - N_3^* - I_2^* - R_2^*) \left(N_3^{*\tau_2} (\tau_1 - 1) (N - N_1^* - N_3^*)^{\tau_1-2} (-1) \right. \\
&\quad \left. \left. + (N - N_1^* - N_3^*)^{\tau_1-1} \tau_2 N_3^{*\tau_2-1} \right) \right] - \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} S_3^* \\
&\quad - \frac{w_0}{d_{23}} \left[(N - N_1^* - N_3^*)^{\tau_2} (\tau_1 - 1) N_3^{*\tau_1-2} S_3^* + N_3^{*\tau_1-1} S_3^* \tau_2 (N - N_1^* - N_3^*)^{\tau_2-1} (-1) \right] \\
b_{49} &= \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* \\
b_{59} &= \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
b_{69} &= -\frac{\beta_3 S_3^* I_3^*}{N_3^{*2}} + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} I_1^* + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} I_2^* \\
&\quad - \frac{w_0}{d_{13}} (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} I_3^* - \frac{w_0}{d_{23}} (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} I_3^* \\
b_{79} &= \frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} R_3^* \right) - \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* \\
b_{89} &= \frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} R_3^* \right) - \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* \\
b_{99} &= -\mu + \frac{w_0}{d_{13}} \tau_2 N_3^{*\tau_2-1} N_1^{*\tau_1-1} R_1^* - \frac{w_0}{d_{13}} \left(N_1^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_1^{*\tau_2} N_3^{*\tau_1-2} R_3^* \right) \\
&\quad + \frac{w_0}{d_{23}} \tau_2 N_3^{*\tau_2-1} N_2^{*\tau_1-1} R_2^* - \frac{w_0}{d_{23}} \left(N_2^{*\tau_2} N_3^{*\tau_1-1} + (\tau_1 - 1) N_2^{*\tau_2} N_3^{*\tau_1-2} R_3^* \right)
\end{aligned}$$

with $N_i^* = S_i^* + I_i^* + R_i^*$ for all $i = 1, 2, 3$.

A.3 Matrix inverse of V for three patches

Recall the matrix V given in section 4.2,

$$V = \begin{bmatrix} \mu + \gamma + \frac{x}{d_{12}} + \frac{x}{d_{13}} & -\frac{x}{d_{12}} & -\frac{x}{d_{13}} \\ -\frac{x}{d_{12}} & \mu + \gamma + \frac{x}{d_{12}} + \frac{x}{d_{23}} & -\frac{x}{d_{23}} \\ -\frac{x}{d_{13}} & -\frac{x}{d_{23}} & \mu + \gamma + \frac{x}{d_{13}} + \frac{x}{d_{23}} \end{bmatrix}$$

with $x = w_0 \left(\frac{N}{3} \right)^{\tau_1 + \tau_2 - 1}$. Consider the determinant of the matrix V and its inverse as follows.

$$\begin{aligned}
V^{-1} &= \frac{1}{\det V} \begin{bmatrix} \left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right)\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{23}^2} & -\left(-\frac{x}{d_{12}}\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{13}d_{23}}\right) & \frac{x^2}{d_{12}d_{23}} + \frac{x}{d_{13}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right) \\ -\left(-\frac{x}{d_{12}}\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{13}d_{23}}\right) & \left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right)\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{13}^2} & -\left(-\frac{x}{d_{23}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right) - \frac{x^2}{d_{12}d_{13}}\right) \\ \frac{x^2}{d_{12}d_{23}} + \frac{x}{d_{13}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right) & -\left(-\frac{x}{d_{23}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right) - \frac{x^2}{d_{12}d_{13}}\right) & \left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right)\left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{12}^2} \end{bmatrix}^T \\
&= \frac{1}{\det V} \begin{bmatrix} \left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right)\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{23}^2} & \frac{x^2}{d_{13}d_{23}} + \frac{x}{d_{12}}\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) & \frac{x^2}{d_{12}d_{23}} + \frac{x}{d_{13}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right) \\ \frac{x^2}{d_{13}d_{23}} + \frac{x}{d_{12}}\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) & \left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right)\left(e + \frac{x}{d_{13}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{13}^2} & \frac{x^2}{d_{12}d_{13}} + \frac{x}{d_{23}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right) \\ \frac{x^2}{d_{12}d_{23}} + \frac{x}{d_{13}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right) & \frac{x^2}{d_{12}d_{13}} + \frac{x}{d_{23}}\left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right) & \left(e + \frac{x}{d_{12}} + \frac{x}{d_{13}}\right)\left(e + \frac{x}{d_{12}} + \frac{x}{d_{23}}\right) - \frac{x^2}{d_{12}^2} \end{bmatrix}
\end{aligned}$$

where $e = \mu + \gamma$ and A^T denotes the transpose of a matrix A . We can simplify this matrix as the inverse matrix of V given by equation (4.56).

Appendix B

Theoretical Background

In this appendix, we collect some theoretical background which is used in this research.

B.1 Spectral radius and matrix norm

Let A be a square matrix. The *characteristic equation* in variable λ of A is defined by $\det(A - \lambda I) = 0$ where I is the identity matrix. The solutions λ of the characteristic equation are called *eigenvalues*.

Definition B.1. Let A be a square matrix with its eigenvalues $\lambda_1, \dots, \lambda_n$. Then the *spectral radius* of A denoted by $\rho(A)$ is defined as $\rho(A) = \max_{i=1, \dots, n} |\lambda_i|$.

Theorem B.2. (see [34], p.24) *If A is a square matrix and $A = [a_{ij}]_{n \times n}$ with $a_{ij} \geq 0$ for all $i, j \in \{1, \dots, n\}$, then*

$$\min_{1 \leq i \leq n} s_i \leq \rho(A) \leq \max_{1 \leq i \leq n} s_i$$

where s_i denotes the sum of entries of i -th column of A .

Definition B.3. A function $\|\cdot\| : \mathbb{R}^{m \times n} \rightarrow \mathbb{R}$ is called a *matrix norm* on $\mathbb{R}^{m \times n}$ if

- (i). $\|A\| \geq 0$ for all matrices $A \in \mathbb{R}^{m \times n}$ and $\|A\| = 0$ if and only if $A = 0$
- (ii). $\|\alpha A\| = |\alpha| \|A\|$ for all $\alpha \in \mathbb{R}$ and for all matrices $A \in \mathbb{R}^{m \times n}$
- (iii). $\|A + B\| \leq \|A\| + \|B\|$ for all matrices A and B in $\mathbb{R}^{m \times n}$.

Theorem B.4. (see [35], p.114) *Let $\|\cdot\|$ be a matrix norm. Then*

$$\rho(A) = \lim_{k \rightarrow \infty} \|A^k\|^{\frac{1}{k}}$$

for every a square matrix A .

Theorem B.5. (see [36], p.11) *Every matrix norm is a continuous function of all elements of a matrix.*

B.2 Stability and Routh-Hurwitz criterion

Consider the autonomous system

$$\frac{dx_i}{dt} = f_i(x_1, \dots, x_n), \quad i = 1, \dots, n \quad (\text{B.1})$$

where $x_i \in \mathbb{R}^n$ and f_i is a continuous function for all i .

Definition B.6. A point $x^* \in \mathbb{R}^n$ is called an *equilibrium point* of the autonomous system (B.1) if $f_i(x^*) = 0$ for all $i = 1, \dots, n$.

Definition B.7. Let $x^* \in \mathbb{R}^n$ be an equilibrium point of the autonomous system (B.1). Then x^* is said to be

- (i). *stable* if for each number $\epsilon > 0$, there exists a number $\delta = \delta(\epsilon) > 0$ such that if $\phi(t)$ is any solution of (B.1) having $\|\phi(t_0) - x^*\| < \delta$, then solution $\phi(t)$ exists for all $t \geq t_0$ and $\|\phi(t) - x^*\| < \epsilon$ for all $t \geq t_0$
- (ii). *locally asymptotically stable* if it is stable and for every $t_0 \geq 0$, there exists a $\delta_0 > 0$ such that $\lim_{t \rightarrow \infty} \phi(t) = x^*$ whenever $\|\phi(t_0) - x^*\| < \delta_0$ where $\phi(t)$ is the solution of (B.1).
- (iii). *unstable* if it is not stable.

where $\|y\|$ denotes the Euclidean norm of a vector y .

Definition B.8. Let

$$F(X) = \begin{bmatrix} F_1(X) \\ \vdots \\ F_n(X) \end{bmatrix}$$

where $X = (x_1, \dots, x_n) \in \mathbb{R}^n$ and F_i is continuous function for all i . The *Jacobian matrix* of F at X_0 is defined as

$$J = \begin{bmatrix} \frac{\partial F_1}{\partial x_1} & \cdots & \frac{\partial F_1}{\partial x_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial F_n}{\partial x_1} & \cdots & \frac{\partial F_n}{\partial x_n} \end{bmatrix}_{X=X_0}$$

where $X_0 = (x_1^0, \dots, x_n^0) \in \mathbb{R}^n$.

Theorem B.9. (see [37], p.474) Let $x^* \in \mathbb{R}^n$ be the equilibrium point of (B.1) and J^* be the Jacobian matrix of (B.1) at x^* . Then the equilibrium point x^* is locally asymptotically stable if all eigenvalues of J^* have negative real parts and unstable if at least one eigenvalue of J^* has positive real part.

Theorem B.10. Routh-Hurwitz Criterion (see [38], p.150) *Given the polynomial*

$$P(\lambda) = \lambda^n + a_1\lambda^{n-1} + \dots + a_{n-1}\lambda + a_n$$

where the coefficients a_i are real constants for all $i = 1, \dots, n$. Define the n Hurwitz matrices using the coefficients a_i of the characteristic polynomial:

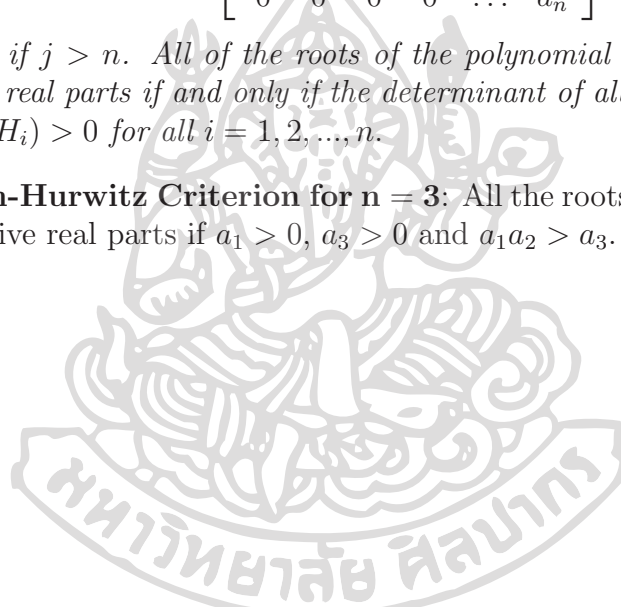
$$H_1 = [a_1], \quad H_2 = \begin{bmatrix} a_1 & 1 \\ a_3 & a_2 \end{bmatrix}, \quad H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{bmatrix}$$

and

$$H_n = \begin{bmatrix} a_1 & 1 & 0 & 0 & \dots & 0 \\ a_3 & a_2 & a_1 & 1 & \dots & 0 \\ a_5 & a_4 & a_3 & a_2 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & \dots & a_n \end{bmatrix}$$

where $a_j = 0$ if $j > n$. All of the roots of the polynomial $P(\lambda)$ are negatives or have negative real parts if and only if the determinant of all Hurwitz matrices are positive: $\det(H_i) > 0$ for all $i = 1, 2, \dots, n$.

Routh-Hurwitz Criterion for $n = 3$: All the roots of $P(\lambda)$ are negatives or have negative real parts if $a_1 > 0$, $a_3 > 0$ and $a_1 a_2 > a_3$.



Biography

Name	Mr. Sompon Puangsun
Address	69 Moo 7 Tambol Wang Chan, Amphur Kaeng Krachan, Petchaburi, 76170
Institution Attended	
2010	Bachelor of Science (Mathematics), Silpakorn University
2013	Master of Science (Mathematics), Silpakorn University

