

Threshold Conditions in SIR STD Models

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Abstract

We propose and analyze a heterogeneous, multigroup, susceptible-infective-recovery (SIR) sexually transmitted disease (STD) model where the desirability and acceptability in partnership formation are functions of the infected individuals. Then we investigate the dependent reproductive number (R_0) at the β_{ij} (the probability of disease transmission per contact between an infected partner in group j and a susceptible individual in group i), then we study the stability and unstability of the model in different states.

Mathematics Subject Classification: 92B

Keywords: Balance constraint; Reproductive number; Sensitivity; Transmission

1 Introduction

The effectiveness of improved sanitation, antibiotics, and vaccination programs created a confidence in the 1960s that infectious disease would soon be eliminated. Consequently, chronic disease such as cardiovascular disease and cancer received more attention in the United States and industrialized countries. But infectious disease have continued to be the major causes of suffering and mortality in developing countries.

Moreover, infectious disease agents adapt and evolve. So that new infectious disease have emerged and some existing diseases have reemerged [16]. Newly identified diseases include Lyme disease (1975), Legionnaire's disease (1976), toxic-shock syndrome (1978), hepatitis C (1989), hepatitis E (1990),

and hantavirus (1993). The human immunodeficiency virus (HIV), which is the etiological agent for acquired immunodeficiency syndrome (AIDS), emerged in 1981 and has become an important sexually transmitted disease throughout the world [5].

Antibiotic-resistant strains of tuberculosis, pneumonia, and gonorrhea have evolved. Malaria, dengue, and yellow fever have reemerged and are spreading into new regions as climate changes occur. Disease such as plague, cholera, and hemorrhagic fevers (Bolivian, Ebola, Lassa, Marburg, etc.) continue to erupt occasionally. Surprisingly, new infectious agents called prions have recently joined the previously known agents: viruses, bacteria, protozoa, and helminths (worms). Recent popular books have given us exciting accounts of the emergence and detections of new diseases [5]. It is clear that human or animal invasions of new ecosystems, global warming, environmental degradation, increased international travel, and changes in economic patterns will continue to provide opportunities for new and changes in economic patterns will continue to provide opportunities for new and existing infectious disease [17].

The emerging and reemerging diseases have led to a revived interest in infectious diseases. Mathematical models have become important tools in analyzing the spread and control of infectious diseases. The model formulation process clarifies assumptions, variables, and parameters; moreover, models provide conceptual results such as thresholds, basic reproduction numbers, contact numbers, and replacement numbers.

Mathematical models and computer simulations are useful experimental tools for building and testing theories, assessing quantitative conjectures, answering specific questions, determining sensitivities to changes in parameter values, and estimating key parameters from data. Epidemiology modeling can contribute to the design and analysis of epidemiological surveys, suggest crucial data that should be collected, identify trends, make general forecasts, and estimate the uncertainty in forecasts [6, 7, 5].

The spread of sexually transmitted disease (STD's) is complex. It depends on not only the transmission mechanism but also behavior of individuals involved in the transmission process. One of the determinants of the spread is the way that individuals select their sexual partners. In a mathematical model for the spread of STD's, it is important to understand and correctly account for the formation of their partnerships [11]. In modeling partnerships, the partnership formation must satisfy the balance constraints [1, 2, 3, 4, 11, 12, 13, 14]. There are mixing multigroup models where the balance constraints are automatically satisfied.

To investigate effects of behavior changes on the transmission dynamics a common approach is to use different sets of parameters and simulate the model for the whole course of the epidemic. Because of the complexity of the

transmission dynamics of STD's and difficulty of partnership formation do not change during the simulation [6].

A goal of this article is to better understand how models with dynamic partnership formation differ from the more traditional models where the number or desirability of partnership formation is constant. By making the partnership formation infection dependent, we can analyze how sensitive the transmission dynamics of the epidemic are to changes in sexual behaviors, and study sensitivity of model in different states.

2 Model Formation

Divide the susceptible, infected and recovered population into K groups, S_i , I_i and R_i , $i = 1, \dots, K$, and consider the simple transmission model system,

$$\begin{cases} dS_i/dt = \mu(S_i^0 - S_i) - \lambda_i S_i, \\ dI_i/dt = \lambda_i S_i - (\mu + \gamma_i) I_i, \\ dR_i/dt = \gamma_i I_i - \mu R_i, \end{cases} \quad i = 1, \dots, K, \quad (1)$$

where S_i is the susceptibles, I_i is infectives, R_i is recovered people, μ is the natural death rate, $1/\gamma_i$ is the average infectious period, and λ_i is the rate of infection. The formation of partnerships plays an essential role in determining the functional λ_i , which is one of the important factors in modeling STD's. We define a partnership to be sexual activity between two individuals where the infection can be transmitted. It depends on the desirability of these potential partners. We assume that people in each group behave the same when selecting a partner but that they have biases between groups. In other words, mixing within each group is assumed to be homogeneous, but there is heterogeneous mixing among the groups [10].

Let α_{ij} be the preference of people in group i to have a partner from j , that is, the fraction of people in group j with whom each individual in group i desires to form a partnership. This describes the desirability of group j to group i . It is also the acceptability of people in group i to have a partner from group j . If an individual from group i encounters an individual from group j , then the conditional probability that a partnership will form is

$$q_{ij} \equiv \alpha_{ij} \alpha_{ji}. \quad (2)$$

Define c_i to be the number of social contacts per unit time for a person in group i . The availability of partners from group j is the probability $c_j N_j / N$, where $N_k = S_k + I_k + R_k$ and $N = \sum_k c_k N_k$. Hence, an encounter of someone group i with another individual, the probability of a partnership forming between individuals from group i and group j is $q_{ij}(c_j N_j / N)$. We define β_{ij} to be the probability of disease transmission per contact between an infected partner in

group j and a susceptible individual in group i . The infection people rate of people in group i is

$$\lambda_i = c_i \sum_{j=1}^K q_{ij} \beta_{ij} (c_j I_j / N), \quad (3)$$

where we assume that I_j / N_j is the probability that a random contact from group j is with an infected individual [11, 10].

3 Features of the model

3.1 Balance constraints

A major advantage of the selective mixing model is that the balance constraints are automatically satisfied because if we let the number of contacts per unit time of people in group i with people in group j be T_{ij} , then it follows form

$$T_{ij} = q_{ij} (c_j N_j / \sum_k c_k N_k) c_i N_i = q_{ji} (c_i N_i / \sum_k c_k N_k) c_j N_j = T_{ji} \quad (4)$$

that the balance constraint is always satisfied [8, 9, 10, 11, 12, 13]. Using the advantages of the selective mixing model, we further assume that the desirability and acceptability depend on the fraction of infected individuals in the populations. This assumption characterizes possible behavior changes of sexually active individuals. More specifically, we assume that the desirability of people in group i having a partner in group j or acceptability of people in group j people in group i , q_{ij} , is a decreasing function of the fraction of infected individuals in group j [10]. Then, the mutually acceptable rates for partnership formation can be expressed as

$$q_{ij} = q_{ji} = \alpha_{ij} (I_j / N_j) \alpha_{ji} (I_i / N_i), \quad (5)$$

and the infection rate are

$$\lambda_i = c_i \sum_{j=1}^K \beta_{ij} \alpha_{ij} (I_j / N_j) \alpha_{ji} (I_i / N_i) (c_j I_j / \sum_k c_k N_k). \quad (6)$$

3.2 The number of partners

The number of sexual partners per individual in many multi-group models is assumed to be c_i . However, if the mixing is biased, the number of partners will vary in time depending on the combination of desirability, acceptability, and availability. From Section 2 and [11], the number of partners per person in group i is

$$n_i = c_i \left(\sum_{j=1}^K q_{ij} (c_j N_j / \sum_k c_k N_k) \right), \quad (7)$$

3.3 Example

Consider a two group model governed by

$$\begin{cases} dS_i/dt = \mu(S_i^0 - S_i) - \lambda_i S_i, \\ dI_i/dt = \lambda_i S_i - (\mu + \gamma_i) I_i, \\ dR_i/dt = \gamma_i I_i - \mu R_i, \end{cases} \quad i = 1, 2, \quad (8)$$

with

$$\lambda_i = c_i \sum_{j=1}^2 q_{ij} \beta_{ij} (c_j I_j / N) \quad (9)$$

and

$$n_i = c_i \left(\sum_{j=1}^2 q_{ij} (c_j N_j / \sum_k c_k N_k) \right), \quad (10)$$

Now, we use the following model parameters,

$S_1^0 = 450$, $S_2^0 = 200$, $S_1(0) = 450$, $S_2(0) = 200$, $I_1(0) = 50$, $I_2(0) = 350$, $R_1(0) = 0$, $R_2(0) = 0$, $\alpha_{11} = 0.7$, $\alpha_{12} = 0.8$, $\alpha_{21} = 0.6$, $\alpha_{22} = 0.4$, $\mu = 0.05$, $\gamma_1 = 0.1$, $\gamma_2 = 0.05$, $c_1 = 10$, $c_2 = 5$.

The dynamics of the susceptibles, infecteds and recovereds for different β_{ij} 's are shown in Fig.1, Fig.2, Fig.3, Fig.4, Fig.5 and Fig.6.

4 The Disease-Free Equilibrium

Since R_i does not effect S_i or I_i in system (8), consider the equivalent system

$$\begin{cases} dS_i/dt = \mu(S_i^0 - S_i) - \lambda_i S_i, \\ dI_i/dt = \lambda_i S_i - (\mu + \gamma_i) I_i, \end{cases} \quad i = 1, 2. \quad (11)$$

Consider the case where is no infection, i.e. $I \equiv 0$. Then (11) reduces to

$$dS_i/dt = \mu(S_i^0 - S_i). \quad (12)$$

Setting $dS_i/dt = 0$ here shows an equilibrium of (8) at $E_0 = (S_i^0, 0)$. This is the disease-free equilibrium. Thus, in the absence of infectives the susceptibles have an equilibrium value of S_i^0 . Now investigating the stability of this equilibrium will derive the so-called reproductive number, R_0 .

4.1 The Reproductive Number, R_0

The Jacobian matrix (1) at $I_i = 0$ has the following form of

$$J^0 = \begin{pmatrix} c_1 \beta_{11} q_{11} (S_1^0 / N^0) - \delta_1 & c_1 \beta_{12} q_{12} (S_1^0 / N^0) & \cdots & c_1 \beta_{1K} q_{1K} (S_1^0 / N^0) \\ c_2 \beta_{21} q_{21} (S_2^0 / N^0) & c_2 \beta_{22} q_{22} (S_2^0 / N^0) - \delta_2 & \cdots & c_2 \beta_{2K} q_{2K} (S_2^0 / N^0) \\ \vdots & \vdots & \ddots & \vdots \\ c_K \beta_{K1} q_{K1} (S_K^0 / N^0) & c_K \beta_{K2} q_{K2} (S_K^0 / N^0) & \cdots & c_K \beta_{KK} q_{KK} (S_K^0 / N^0) - \delta_K \end{pmatrix}, \quad (13)$$

with $\delta_i \equiv \mu + \gamma_i$ and $N^0 = \sum_{j=1}^2 c_j S_j^0$. Stability of this Jacobian matrix J^0 gives threshold conditions for the epidemic. In general, it is difficult to derive an explicit formula of the reproductive number and usually the eigenvalues of (13) must be determined numerically. We have investigated this problem analytically for the two-group model (8), where the classification of groups may be social, economic, ethnic, or geographic by locating the eigenvalues of the Jacobian matrix at the infection-free equilibrium. The Jacobian matrix of (8) at $I_i = 0$ has the form of

$$J^0 = \begin{pmatrix} c_1 \beta_{11} q_{11} (S_1^0 / N^0) - \delta_1 & c_1 \beta_{12} q_{12} (S_1^0 / N^0) \\ c_2 \beta_{21} q_{21} (S_2^0 / N^0) & c_2 \beta_{22} q_{22} (S_2^0 / N^0) - \delta_2 \end{pmatrix}. \quad (14)$$

We simplify the notation by defining $e_{ij} = c_i q_{ij} (S_i^0 / N^0)$. Then

$$J^0 = \begin{pmatrix} e_{11} \beta_{11} - \delta_1 & e_{12} \beta_{12} \\ e_{21} \beta_{21} & e_{22} \beta_{22} - \delta_2 \end{pmatrix}. \quad (15)$$

The large eigenvalue of J^0 ,

$$\lambda = (1/2)((a_{11} + a_{22}) + \sqrt{(a_{11} + a_{22})^2 - 4(a_{11}a_{22} - e_{12}\beta_{12}e_{21}\beta_{21})}), \quad (16)$$

with $a_{ii} = e_{ii}\beta_{ii} - \delta_i$, is real. If $\lambda < 0$, the zero solution of (8) is stable, and if $\lambda > 0$, it is unstable. Now, if define the reproductive number by

$$R_0 = (1/\delta_1 + \delta_2)(e_{11}\beta_{11} + e_{22}\beta_{22} + \sqrt{\sigma_1^2 - 4\sigma_2}), \quad (17)$$

with $\sigma_1 = e_{11}\beta_{11} + e_{22}\beta_{22} - \delta_1 - \delta_2$, and $\sigma_2 = (e_{11}\beta_{11} - \delta_1)(e_{22}\beta_{22} - \delta_2) - e_{12}\beta_{12}e_{21}\beta_{21}$. Then, if $R_0 > 1$ the epidemic spreads in the population and if $R_0 < 1$ the epidemic dies out.

4.2 Sensitivity studies

Consider the two group where the probability of disease transmission people in group 2, (β_{21}, β_{22}) , and the average probability of disease transmission people in group 1, $a \equiv \beta_{11} + \beta_{12}$ are fixed. We now use $\beta \equiv \beta_{12}$, $0 \leq \beta \leq a$, as a parameter to study the effects of the relative probability of transmission people in group 2 on the reproductive number. A large β implies that the probability of disease transmission per contact between an infected partner in group 2 and a susceptible individuals in group 1 is more than the probability of disease transmission per contact between an infected partner in group 1 and a susceptible individuals in own group. In terms of β ,

$$R_0(\beta) = (1/(2\mu - \gamma_1 - \gamma_2))(e_{11}(a - \beta) + e_{22}\beta_{22} + \sqrt{\sigma_1^2 - 4(\sigma_2)}), \quad (18)$$

with $\sigma_1 = e_{11}(a - \beta) + e_{22}\beta_{22} - \delta_1 - \delta_2$, and $\sigma_2 = (e_{11}(a - \beta) - \delta_1)(e_{22}\beta_{22} - \delta_2) - e_{12}\beta e_{21}\beta_{21}$. By analyzing R_0 as a function of β , we have the following result.

4.2.1 Example

For two group model (8) with parameters, $S_1^0 = 200, S_2^0 = 400, \alpha_{11} = 0.7, \alpha_{12} = 0.8, \alpha_{21} = 0.6, \alpha_{22} = 0.4, \beta_{21} = 0.1, \beta_{22} = 0.2, \mu = 0.05, \gamma_1 = 0.1, \gamma_2 = 0.05, c_1 = 10, c_2 = 5, a = 1,$ we let β_{22} increase from 0 to 0.8, we have Fig.7. The dynamics of the susceptibles, infecteds and recovered for different β 's are shown in Fig.8.

5 Generalization to a continuum

Let x be a continuous state vector of characteristics of individuals in the population (such age, geographical positions, or behavioral traits) defined in a set X [11]. Let $S(t, x), I(t, x)$ and $R(t, x)$ be continuous densities of the susceptible, infecteds and recovered respectively and $N_k(t, x) = S(t, x) + I(t, x) + R(t, x).$

Assume that the desirability of an individual of state x to form partnership with an individual of state y is described by $\alpha(x, y), x, y \in X.$ Then the acceptability of an individual of state y to an individuals of state x is $\alpha(y, x).$

Define $c(x)$ to be the number of social contacts per unit time for a person in state $x.$ The availability of individuals with state y in the population is $c(x)N_k(t, x)/N(t)$ where $N(t) = \int_{x \in X} c(x)N_k(t, x)dx$ is the total population.

The infection rate of a susceptible individual of state x infected from an infected individual of state y at time t can be expressed by

$$\lambda(t, x) = (c(x)/N(t)) \int_{y \in X} c(y)\beta(x, y)\alpha(x, y)\alpha(y, x)I(t, y)dy, \tag{19}$$

where $\beta(x, y)$ is the transmission rate of the disease from an infected individual of state y to a susceptible individual of state $x,$ and the number partners of an individuals of state x per unit time is

$$n(t, x) = (c(x)/N(t)) \int_{y \in X} c(y)\alpha(x, y)\alpha(y, x)N_k(t, y)dy. \tag{20}$$

The probability of a partnership forming $q(x, y) \equiv \alpha(x, y)\alpha(y, x)$ is symmetric and the balance constraints are automatically satisfied.

The dynamics of the epidemic is governed by the following system,

$$\begin{cases} \partial S(t, x)/\partial t = \mu(S^0(x) - S(t, x)) - \lambda(t, x)S(t, x), \\ \partial I(t, x)/\partial t = \lambda(t, x)S(t, x) - (\mu - \gamma(x))I(t, x), \\ \partial R(t, x)/\partial t = \gamma(x)I(t, x) - \mu R(t, x), \end{cases} \tag{21}$$

with $\lambda(t, x)$ as in (9).

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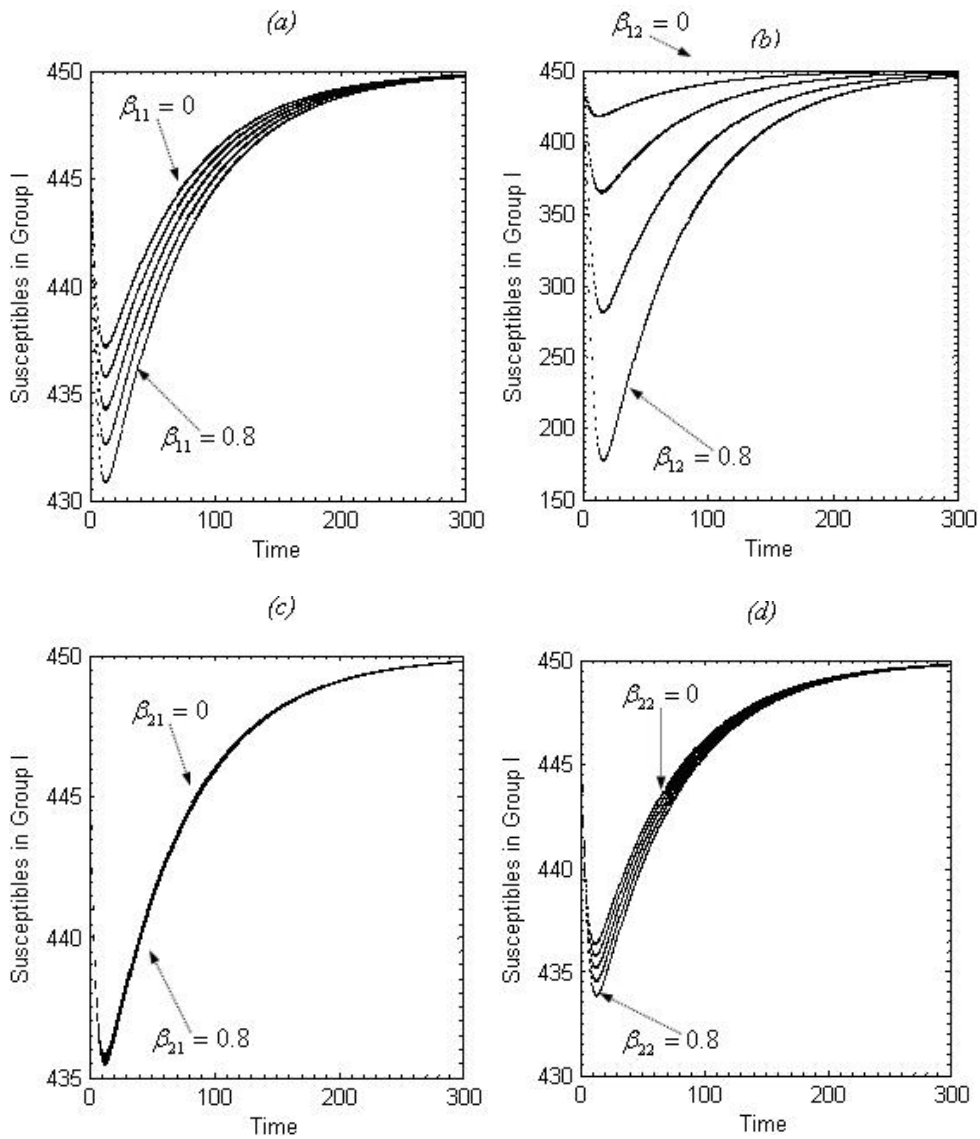


Figure 1: (a) : $0 \leq \beta_{11} \leq 0.8$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (b) : $\beta_{11} = 0.2$, $0 \leq \beta_{12} \leq 0.8$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (c) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $0 \leq \beta_{21} \leq 0.8$, $\beta_{22} = 0.2$, (d) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $0 \leq \beta_{22} \leq 0.8$.

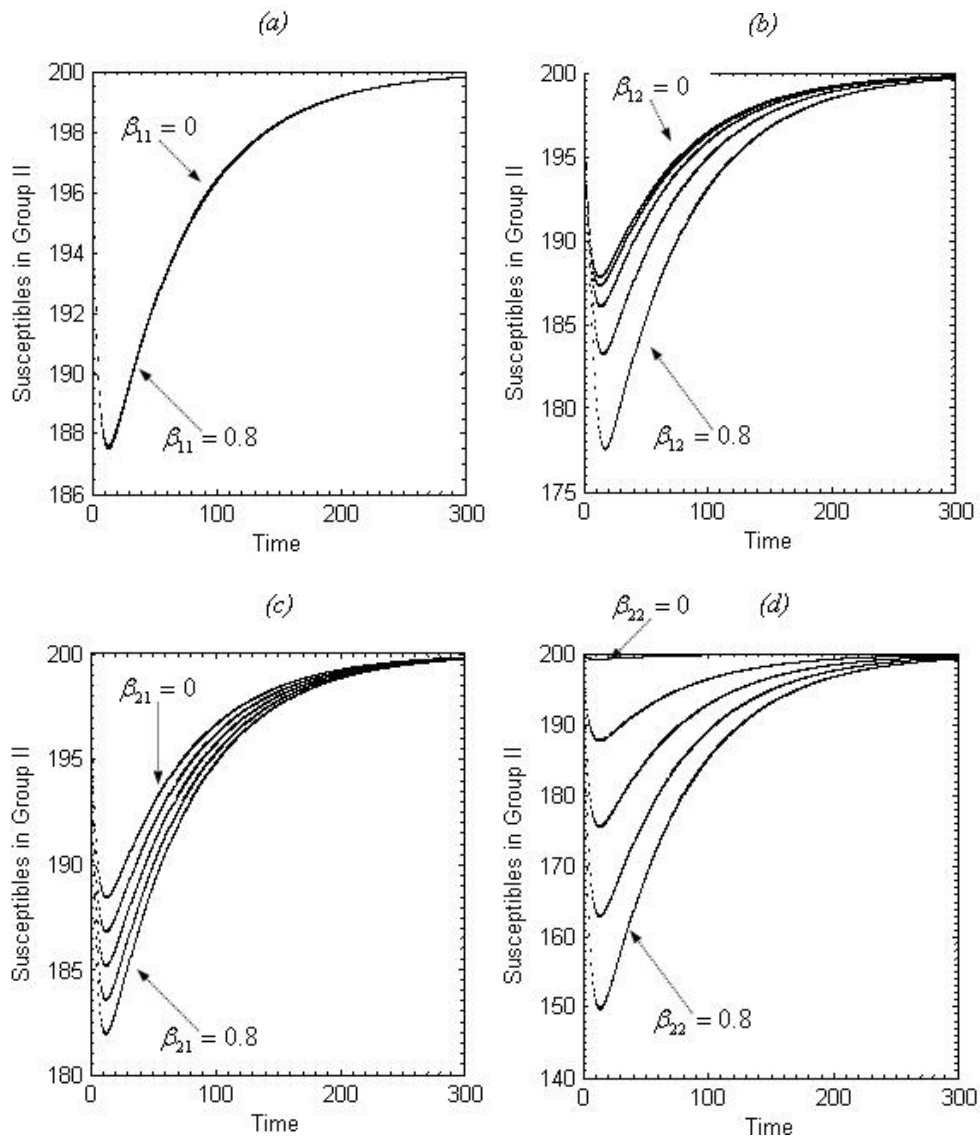


Figure 2: (a) : $0 \leq \beta_{11} \leq 0.8$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (b) : $\beta_{11} = 0.2$, $0 \leq \beta_{12} \leq 0.8$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (c) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $0 \leq \beta_{21} \leq 0.8$, $\beta_{22} = 0.2$, (d) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $0 \leq \beta_{22} \leq 0.8$.

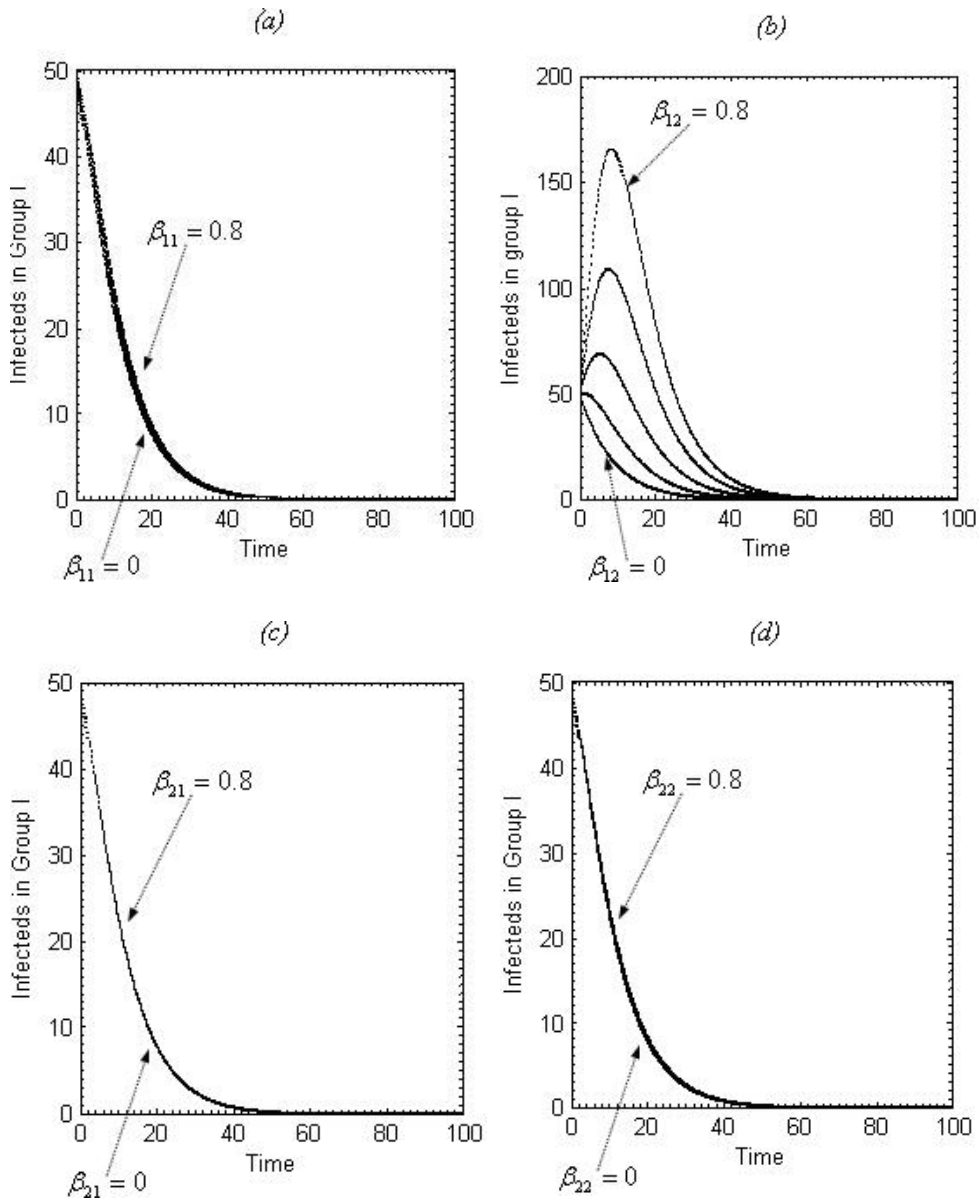


Figure 3: (a) : $0 \leq \beta_{11} \leq 0.8$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (b) : $\beta_{11} = 0.2$, $0 \leq \beta_{12} \leq 0.8$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (c) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $0 \leq \beta_{21} \leq 0.8$, $\beta_{22} = 0.2$, (d) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $0 \leq \beta_{22} \leq 0.8$.

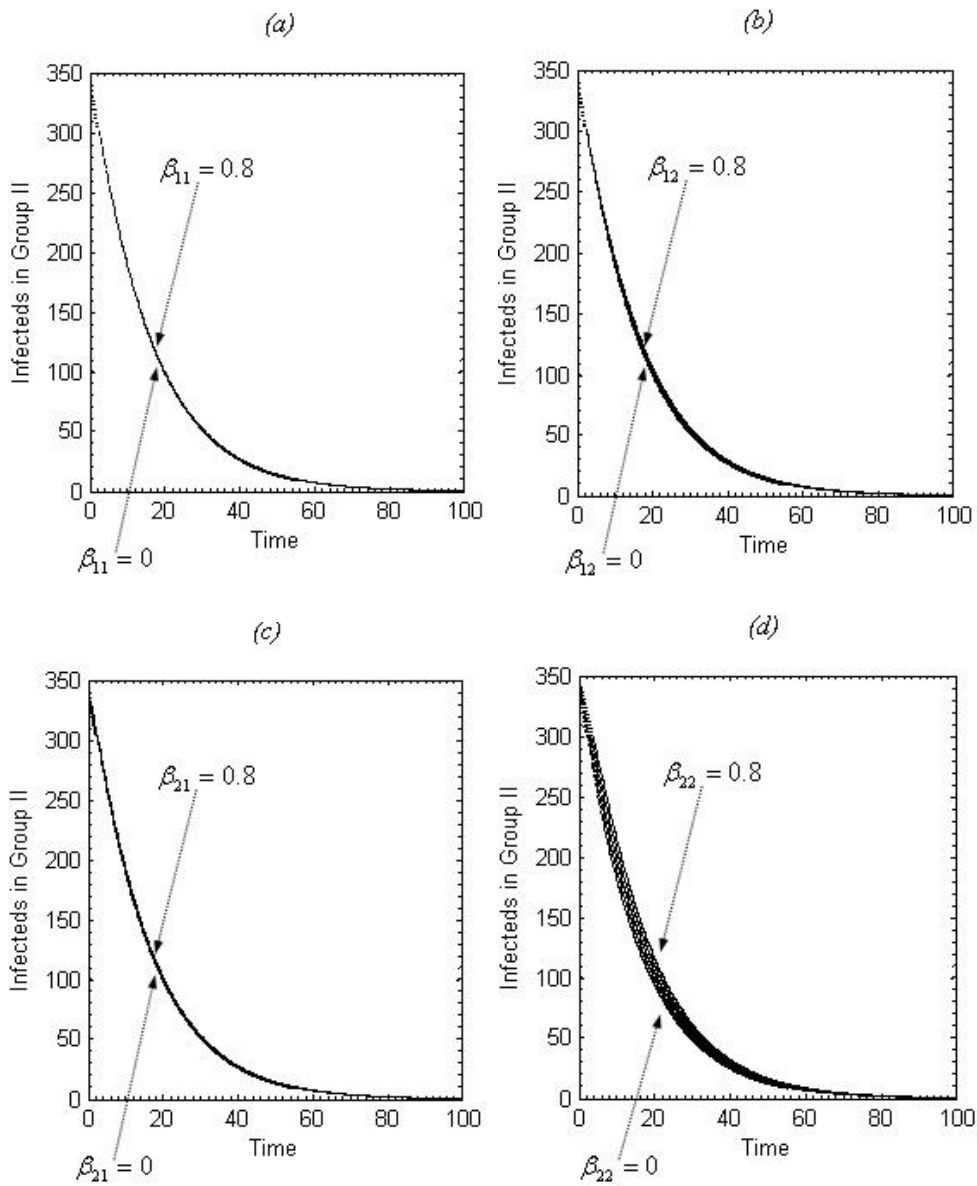


Figure 4: (a) : $0 \leq \beta_{11} \leq 0.8$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (b) : $\beta_{11} = 0.2$, $0 \leq \beta_{12} \leq 0.8$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (c) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $0 \leq \beta_{21} \leq 0.8$, $\beta_{22} = 0.2$, (d) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $0 \leq \beta_{22} \leq 0.8$.

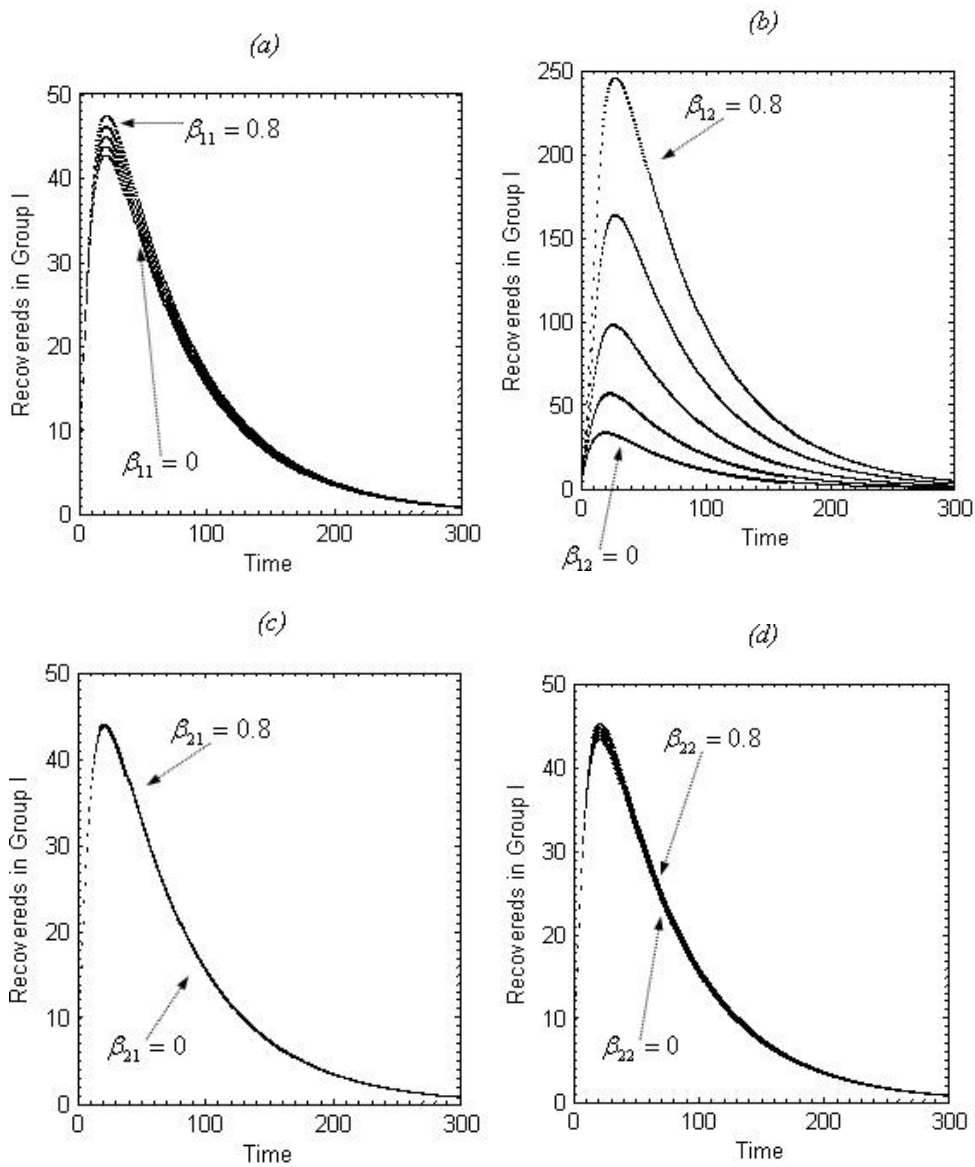


Figure 5: (a) : $0 \leq \beta_{11} \leq 0.8$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (b) : $\beta_{11} = 0.2$, $0 \leq \beta_{12} \leq 0.8$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (c) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $0 \leq \beta_{21} \leq 0.8$, $\beta_{22} = 0.2$, (d) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $0 \leq \beta_{22} \leq 0.8$.

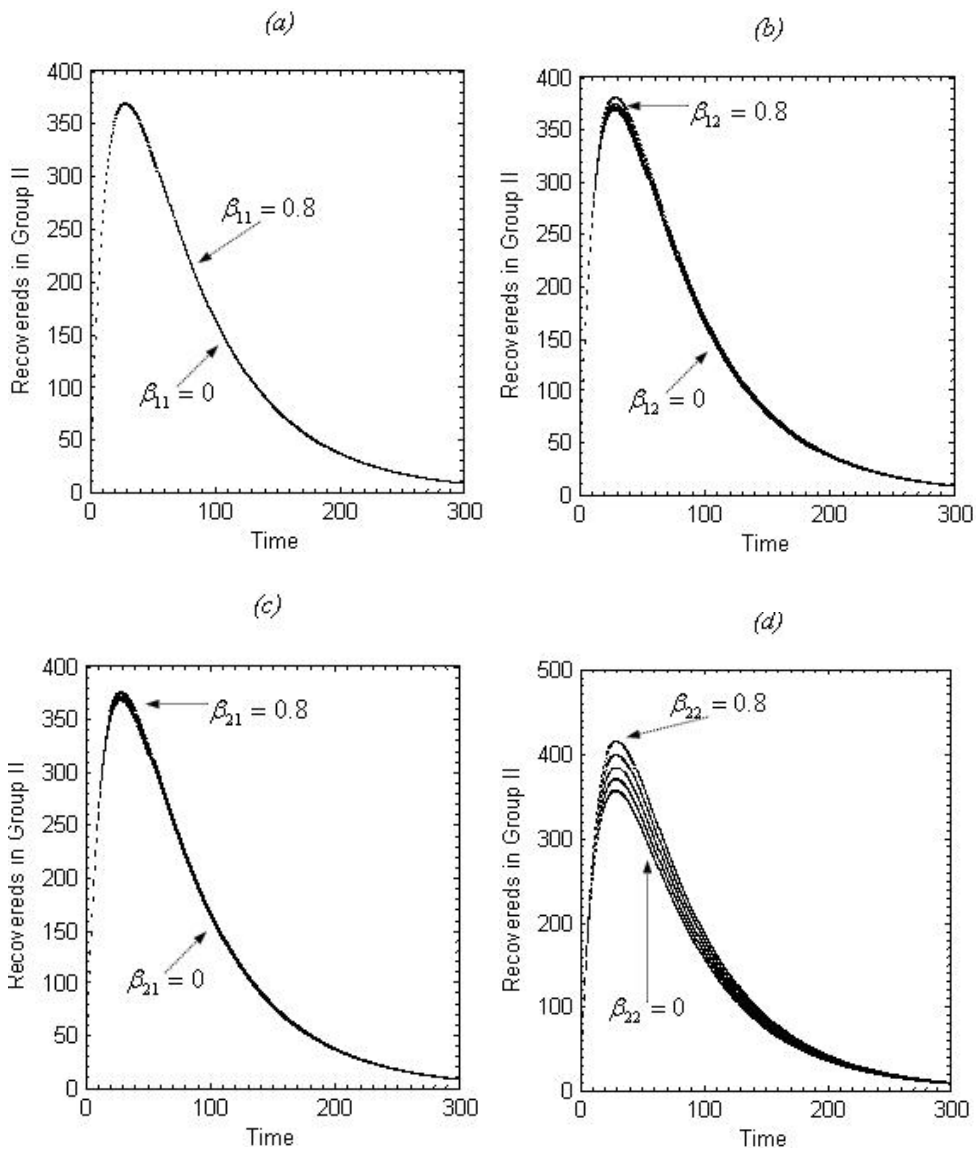


Figure 6: (a) : $0 \leq \beta_{11} \leq 0.8$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (b) : $\beta_{11} = 0.2$, $0 \leq \beta_{12} \leq 0.8$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, (c) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $0 \leq \beta_{21} \leq 0.8$, $\beta_{22} = 0.2$, (d) : $\beta_{11} = 0.2$, $\beta_{12} = 0.1$, $\beta_{21} = 0.1$, $0 \leq \beta_{22} \leq 0.8$.

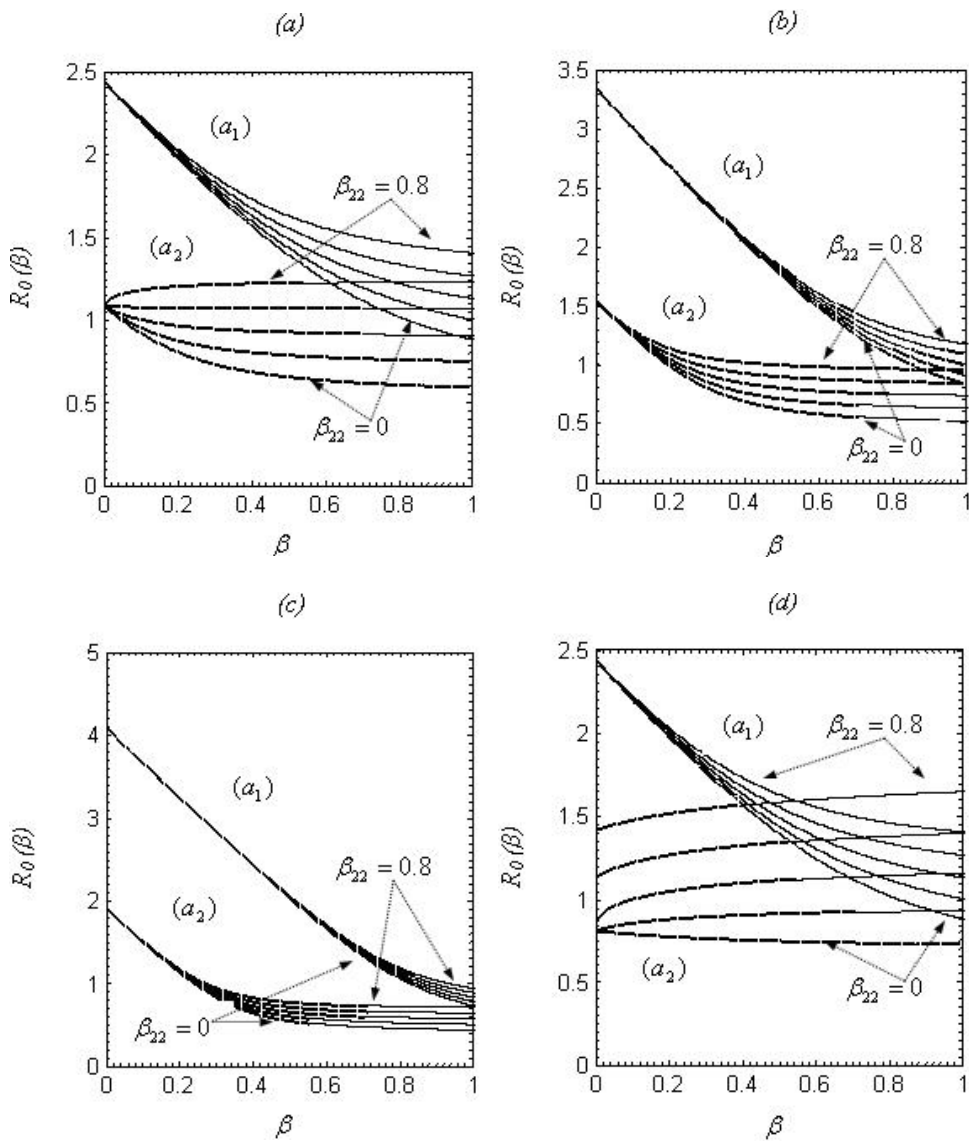


Figure 7: (a): $(S_1^0 = 200, S_2^0 = 400, c_1 = 10, c_2 = 5, (a_1) : a = 1/2, (a_2) : a = 1)$, (b): $(S_1^0 = 400, S_2^0 = 400, c_1 = 10, c_2 = 5, (a_1) : a = 1/2, (a_2) : a = 1)$, (c): $(S_1^0 = 400, S_2^0 = 200, c_1 = 10, c_2 = 5, (a_1) : a = 1/2, (a_2) : a = 1)$, (d): $(S_1^0 = 200, S_2^0 = 400, a = 1, (a_1) : c_1 = 10, c_2 = 5, (a_2) : c_1 = 5, c_2 = 10)$.

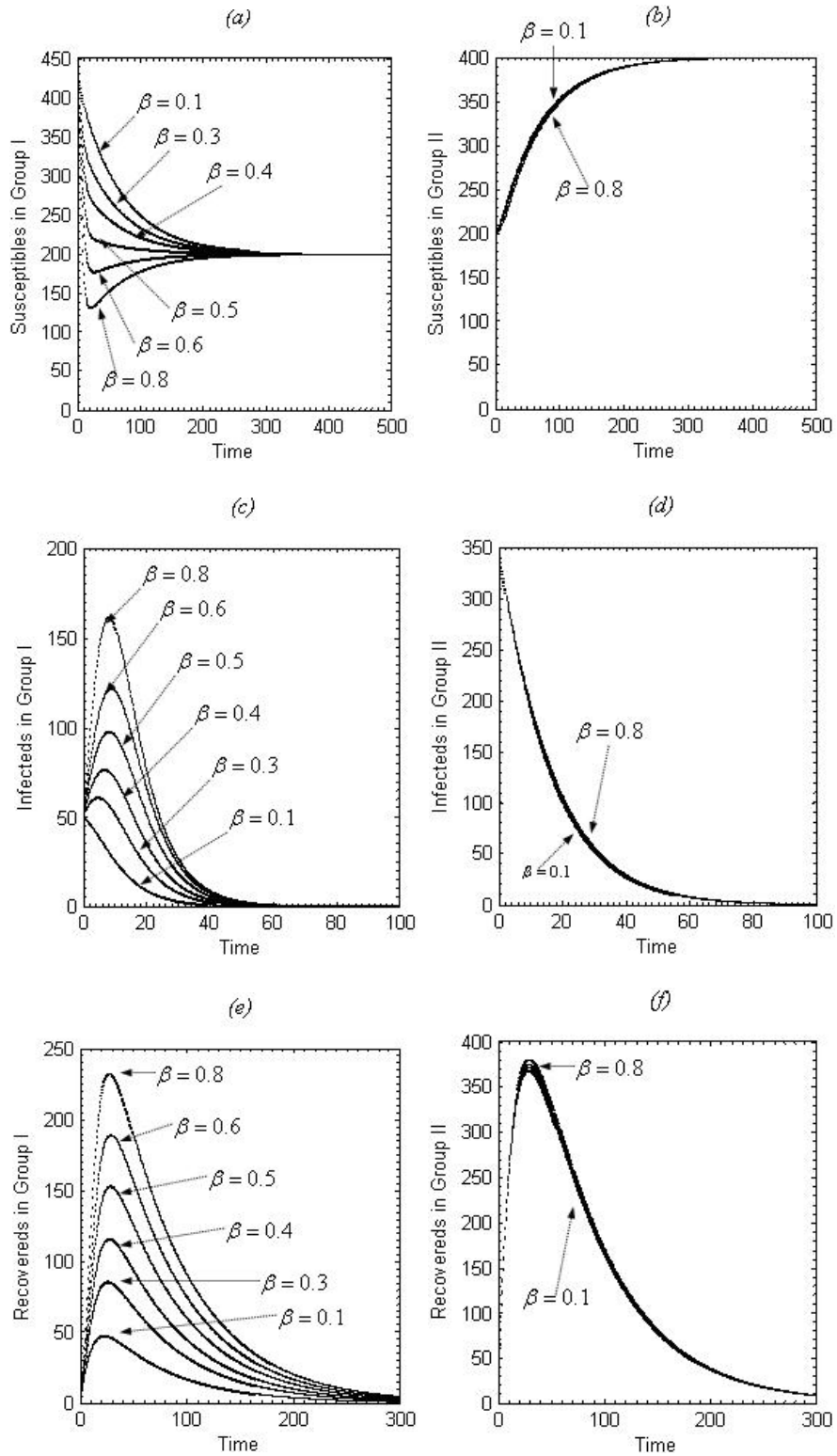


Figure 8: $S_1^0 = 200$, $S_2^0 = 400$, $\alpha_{11} = 0.7$, $\alpha_{12} = 0.8$, $\alpha_{21} = 0.6$, $\alpha_{22} = 0.4$, $\beta_{21} = 0.1$, $\beta_{22} = 0.2$, $\mu = 0.05$, $\gamma_1 = 0.1$, $\gamma_2 = 0.05$, $c_1 = 10$, $c_2 = 5$, $a = 1$.