Capstone project: Stability Analysis of SEIS model with spatial variations

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Abstract

In this report we present an SEIS model for infectious diseases with latent period and no immune response for spatially heterogeneous environment. Spatial heterogeneity is designed by several metapopulations. It was shown that global dynamics of an epidemics completely depends on basic reproduction number R_0. By fixing the number of patches to two, we use next generation matrix method to obtain basic reproduction number and make further analysis on it. Migration rates of individuals are considered as one of the main factors that influence R_0. Moreover, some numerical simulations for the dynamics of the system with different initial conditions is presented.

Contents

1 Introduction

Epidemiology is a study of a behavior of infectious diseases. Mathematical modeling of epidemics predicts the pattern of an epidemics, thus plays an important role in describing and controlling the disease. It is widely used nowadays to provide epidemiologists with useful information for policy development. Epidemiological models were broadly studied by a number of authors since its first introduction in 1927 by Kermack and McKendrick (SIR model) [1]. Since then few more developed forms of a model were described and studied for various types of infectious diseases.

The general form of the model is SEIRS model, which divides population into 4 subgroups: S-susceptible, E-exposed, I-infected and R- recovered. There also exist some other models like SEI model, SIR model or SIS model, however all of them are particular cases of the general model. In this report we will focus on SEIS model, which was described for an infectious disease with latency period in the absence of immune system.

Moreover, most of the deterministic models do not consider migration of individuals. However, it is unrealistic to assume no migration of species because population and environment are spatially heterogeneous. Demographic and spatial parameters of a particular area can vary, because animals, birds, mosquitoes and any other species same as humans travel through the surface of the earth. Thus, it is important to include spatial structure to the epidemic model. Spatial structure can be described as continuous or discrete. Reaction-diffusion equation for continuous time space was discussed in a paper by Wu [2]. While we will focus on discrete space model which produces a coupled patch models, usually called metapopulation models. They consist of a system of ordinary differential equations describing the dynamics of each patch and the other patches by traveling [3].

The SEIS model for two metapopulations is considered in this study. We will analyze basic reproduction number to predict pattern of an epidemics. Also some graphs of simulations are provided.

2 SEIS model

The basic SEIS model can be shown by the system of ordinary differential equations as follows:

$$E' = \alpha SI - \beta E \tag{1}$$

$$I' = \beta E - \gamma I \tag{2}$$

$$S' = -\alpha SI + \gamma I \tag{3}$$

where S, E, and I represent the number of susceptible, exposed, and infected individuals, respectively. It is assumed that probability of getting one more exposed individual is proportional to the number of infected and susceptible individuals with the rate of α. Exposed individuals enter the infected compartment at the rate β, and the treatment rate is γ. However since there is no immune system effect all the recovered individuals join the susceptible compartment. Also, because epidemics outbreaks occur within a short time period in comparison with population growth time, it is usually assumed that population size is constant. Thus for total population size $N = S + E + I$, $N' = S' + E' + I' = 0$, which indicates no population growth. Figure 1 shows a progression diagram for the given model.

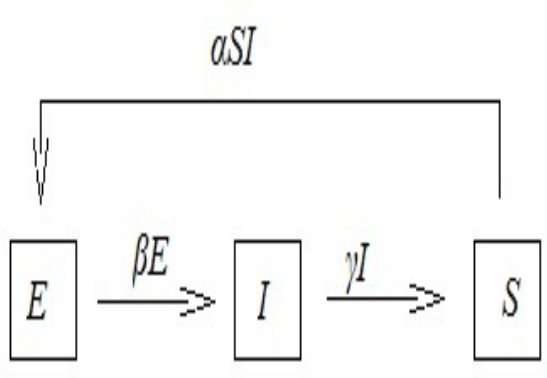


Figure 1: Progression of infection from susceptible (S) individuals through the exposed (E) and infected (I) compartments

These kind of epidemic models have a disease free (DFE) equilibrium state, at which the population remains in the absence of disease. Usually we consider treshold parameter called basic reproduction number R_0, such that if $R_0 < 1$, then DFE is locally assymptotically stable, and the disease cannot invade the population, but if $R_0 > 1$ then DFE is unstable and

invasion is always possible. In a simple words, basic reproduction number is an expected amount of succeptibles infected by one infective individual, so $R_0 > 1$ means one infected individual spreads the disease to more than one person, thus amount of infected individuals increases, and for $R_0 < 1$ each infected individuals produces less than one more infected individual and the amount of infected individuals slowly decreases. Basic reproduction number of a disease can be found by next generation matrix method, introduced by Watmough and van den Driessche [7], where R_0 is the spectral radius of the next generation matrix.

According to the method, we identify $\mathscr{F}_i$, $\mathscr{V}_i^+$ and $\mathscr{V}_i^-$ to be the rate of appearance of a new infections in compartment i, the rate of transfer of individuals into compartment i, and the rate of transfer of individuals out of compartment i respectively, where each of the functions are continuously differentiable,(at least twice) and $\mathscr{V}_i = \mathscr{V}_i^- - \mathscr{V}_i^+$. Moreover, we should notice that progression through E to I is not considered as a new infection, but as a progression of infected individual through different levels. Thus, from definitions of $\mathscr{F}_i$, $\mathscr{V}_i^+$ and $\mathscr{V}_i^-$ for equations (1)-(3) we get:

$$\mathscr{F} = \begin{pmatrix} \mathscr{F}_1 \\ \mathscr{F}_2 \\ \mathscr{F}_3 \end{pmatrix} = \begin{pmatrix} \alpha SI \\ 0 \\ 0 \end{pmatrix}, \mathscr{V}^+ = \begin{pmatrix} \mathscr{V}_1^+ \\ \mathscr{V}_2^+ \\ \mathscr{V}_3^+ \end{pmatrix} = \begin{pmatrix} 0 \\ \beta E \\ \gamma I \end{pmatrix}, V^- = \begin{pmatrix} \mathscr{V}_1^- \\ \mathscr{V}_2^- \\ \mathscr{V}_3^- \end{pmatrix} = \begin{pmatrix} \beta E \\ \gamma I \\ \alpha SI \end{pmatrix} \tag{4}$$

where each group of susceptible, exposed and infected represents each compartment, such that $i = 1$ is compartment of E, $i = 2$ corresponds to I, and consequently $i = 3$ to S.

Since it is natural for the system to have a non-negative initial conditions, our functions $\mathscr{F}, \mathscr{V}^+$ and $\mathscr{V}^-$ should satisfy following axioms:

A(1) *Since each function represents direct transfer of individuals, they are all non-negative.* In other worlds, if $E, I, S \geq 0$ then $\mathscr{F}, \mathscr{V}^+, \mathscr{V}^- \geq 0$, which is true from equations (1)-(3).

A(2) *If the compartment is empty, then there can be no transfer of individuals out of compartment.* Thus, if $E, I, S = 0$ then, $\mathscr{V}^- = 0$. It is also true, according to our definition of $\mathscr{V}^-$ in (4).

A(3) *Incidence of infection for uninfected compartment is zero.* In our example we have only one uninfected compartment - S, which corresponds to $i = 3$. Thus, $\mathscr{F}_3 = 0$.

A(4) *If the population is free of disease, then the population will remain free of disease. That is, there is no immigration of infectives to the system by outside.* This can be written as, if $E = I = 0$ (compartments 1 and 2), then $\mathscr{F}_i = 0$ and $\mathscr{V}_i^+ = 0$, for $i = 1, 2$. This is also true for given model.

A(5) *If $\mathscr{F}$ is set to zero, then all the eigenvalues of Jacobian matrix evaluated at DFE have negative real parts.*

An equilibrium solution with $E = I = 0$ has the form $x_0 = (0, 0, S_0)^t$. If we rewrite equations (1)-(3) as vector valued function $\mathscr{G} = [E', I', S']^t$ then the Jacobian matrix evaluated at x_0 will be:

$J = \left[\frac{d\mathscr{G}}{dE} \quad \frac{d\mathscr{G}}{dI} \quad \frac{d\mathscr{G}}{dS}\right] = \begin{bmatrix} -\beta & \alpha S_0 & 0 \\ \beta & -\gamma & 0 \\ 0 & \gamma - \alpha S_0 & 0 \end{bmatrix}$

with eigenvalues: $\lambda_{1,2} = \frac{-(\gamma+\beta) \pm \sqrt{(\gamma+\beta)^2 - 4\beta(\gamma - \alpha S_0)(\gamma+\beta)}}{2}$. Since $\gamma + \beta > \sqrt{(\gamma+\beta)^2 - 4\beta(\gamma - \alpha S_0)(\gamma+\beta)}$

and α, β, γ's are all positive, our eigenvalues have negative real parts. Thus, our model satisfies all of axioms and we can apply next generation matrix method.

According to [7] next generation matrix has a form of FV^{-1}, where F and V are defined as follows:

$$F = \left[\frac{d\mathscr{F}}{dE}(x_0) \quad \frac{d\mathscr{F}}{dI}(x_0)\right], V = \left[\frac{d\mathscr{V}}{dE}(x_0) \quad \frac{d\mathscr{V}}{dI}(x_0)\right] \tag{5}$$

From equations (1)-(3) we have

$F = \begin{bmatrix} 0 & \alpha \\ 0 & 0 \end{bmatrix}$ and $V = \begin{bmatrix} \beta & 0 \\ -\beta & \gamma \end{bmatrix}$

This gives us $R_0 = \frac{\alpha}{\gamma}$. It is clear that $R_0 < 1$ and DFE is asymptotically stable if $\alpha < \gamma$ and $R_0 > 1$ and DFE is unstable for $\alpha > \gamma$. This means that disease dies out in a closed system if rate of getting infected is less than recovery rate.

3 SEIS with spatial heterogeneity

As we have stated before, the model will include spatial effects on a population. For this purposes Lloyd and May [4], in their research, divide the population into connected subpopulations: such that S_i, E_i, and I_i indicates number of susceptible, exposed and infective in patch i and the total population of patch i is $N_i = S_i + E_i + I_i$. In their model infective individuals of one patch can infect susceptible individuals of another patch, however the model does not consider an explicit movement of individuals between patches. Sattenspiel and Dietz [5] have shown a metapopulation epidemic model where an explicit movement of individuals is included, and each sub-group is labelled according to their patch of origin as well as a patch of residency at a given time. Arino and van den Driessche also used a similar techniques to formulate SIS model [6]. In this paper we will use the

notation from [6]. To formulate a model including geographical mobility, let us denote S_{ij} to indicate the number of susceptible individuals from patch i staying at patch j at the moment, I_{ij} and E_{ij} will be defined according to the same logic. Residents of patch i leaves their patch of origin at the per capita rate of $g_i \geq 0$ per unit time, with a fraction $m_{ij} \geq 0$ going to a particular patch j. Consequently $g_i m_{ij}$ is the travel rate from patch i to patch j. It logically follows from the definition that $m_{ii} = 0$ and $\sum_{j=1}^{n} m_{ij} = 1$. Also residents of patch i return their home at per capita rate of $r_{ij} \geq 0$ with $r_{ii} = 0$. It is natural to assume that $g_i m_{ij} > 0$ if and only if $r_{ij} > 0$ [3].

Taking to account all the factors that we have already stated, we came up with the following model:

Within the patch

$$E'_{ii} = \sum_{k=1}^{n} r_{ik} E_{ik} - g_i E_{ii} + \sum_{k=1}^{n} \alpha S_{ii} I_{ki} - \beta E_{ii}, \tag{6}$$

$$I'_{ii} = \sum_{k=1}^{n} r_{ik} I_{ik} - g_i I_{ii} + \beta E_{ii} - \gamma I_{ii}, \tag{7}$$

$$S'_{ii} = \sum_{k=1}^{n} r_{ik} S_{ik} - g_i S_{ii} - \sum_{k=1}^{n} \alpha S_{ii} I_{ki} + \gamma I_{ii}. \tag{8}$$

Between patches

$$E'_{ij} = g_i m_{ji} E_{ii} - \sum_{k=1}^{n} r_{ik} E_{ik} + \sum_{k=1}^{n} \alpha S_{ij} I_{kj} - \beta E_{ij}, \tag{9}$$

$$I'_{ij} = g_i m_{ji} I_{ii} - \sum_{k=1}^{n} r_{ik} I_{ik} + \beta E_{ij} - \gamma I_{ij}, \tag{10}$$

$$S'_{ij} = g_i m_{ji} S_{ii} - \sum_{k=1}^{n} r_{ik} S_{ik} - \sum_{k=1}^{n} \alpha S_{ij} I_{kj} + \gamma I_{ij}. \tag{11}$$

Now for the sake of our research and in order to simplify our calculations, we fix the number of patches to be 2, and get the following system of differential

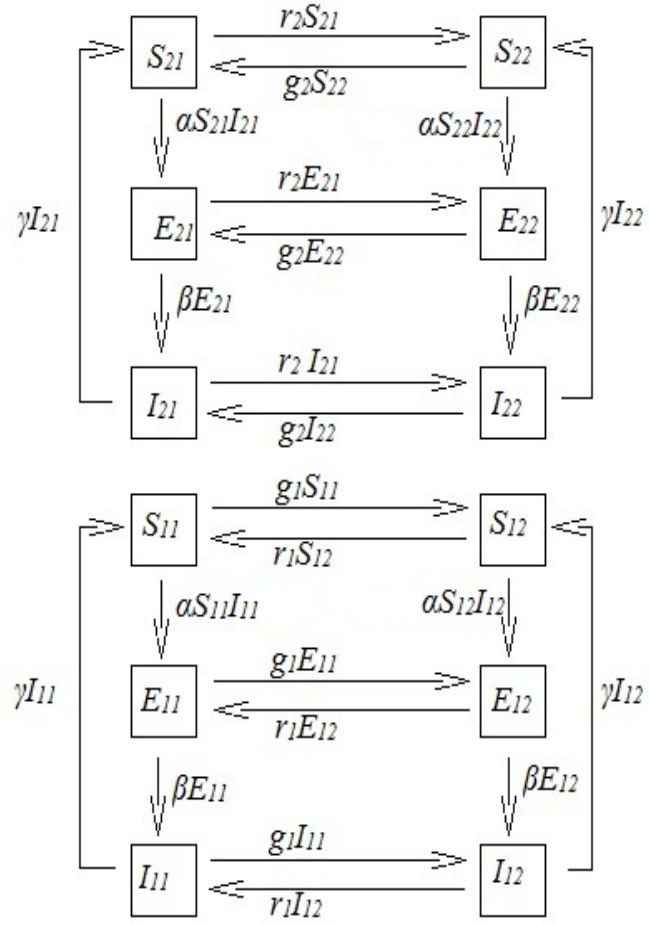


Figure 2: Progression of infection from susceptible (S) individuals through the exposed (E) and infected (I) compartments for the treatment model with spatial heterogeneity

equations:

$$E'_{11} = r_{12}E_{12} - g_1E_{11} + \alpha S_{11}(I_{11} + I_{21}) - \beta E_{11}, \tag{12}$$
$$E'_{12} = g_1E_{11} - r_{12}E_{12} + \alpha S_{12}(I_{12} + I_{22}) - \beta E_{12}, \tag{13}$$
$$E'_{21} = g_2E_{22} - r_{21}E_{21} + \alpha S_{21}(I_{11} + I_{21}) - \beta E_{21}, \tag{14}$$
$$E'_{22} = r_{21}E_{21} - g_2E_{22} + \alpha S_{22}(I_{12} + I_{22}) - \beta E_{22}, \tag{15}$$
$$I'_{11} = r_{12}I_{12} - g_1I_{11} + \beta E_{11} - \gamma I_{11}, \tag{16}$$
$$I'_{12} = g_1I_{11} - r_{12}I_{12} + \beta E_{12} - \gamma I_{12}, \tag{17}$$
$$I'_{21} = g_2I_{22} - r_{21}I_{21} + \beta E_{21} - \gamma I_{21}. \tag{18}$$
$$I'_{22} = r_{21}I_{21} - g_2I_{22} + \beta E_{22} - \gamma I_{22}, \tag{19}$$
$$S'_{11} = r_{12}S_{12} - g_1S_{11} - \alpha S_{11}(I_{11} + I_{21}) + \gamma I_{11}, \tag{20}$$
$$S'_{12} = g_1S_{11} - r_{12}S_{12} - \alpha S_{12}(I_{12} + I_{22}) + \gamma I_{12}, \tag{21}$$
$$S'_{21} = g_2S_{22} - r_{21}S_{21} - \alpha S_{21}(I_{11} + I_{21}) + \gamma I_{21}, \tag{22}$$
$$S'_{22} = r_{21}S_{21} - g_2S_{22} - \alpha S_{22}(I_{12} + I_{22}) + \gamma I_{22} \tag{23}$$

If we sum up all equations we will see that $N' = 0$, which means there is no population increase.

Same as we did it before, our $\mathscr{F}, \mathscr{V}^+, \mathscr{V}^-$ functions are respectively:

$$\begin{pmatrix} \alpha S_{11}(I_{11} + I_{21}) \\ \alpha S_{12}(I_{12} + I_{22}) \\ \alpha S_{21}(I_{11} + I_{21}) \\ \alpha S_{22}(I_{12} + I_{22}) \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} r_{12}E_{12} \\ g_1E_{11} \\ g_2E_{22} \\ r_{21}E_{21} \\ r_{12}I_{12} + \beta E_{11} \\ g_1I_{11} + \beta E_{12} \\ g_2I_{22} + \beta E_{21} \\ r_{21}I_{21} + \beta E_{22} \\ r_{12}S_{12} + \gamma I_{11} \\ g_1S_{11} + \gamma I_{12} \\ g_2S_{22} + \gamma I_{21} \\ r_{21}S_{21} + \gamma I_{22} \end{pmatrix}, \begin{pmatrix} g_1E_{11} + \beta E_{11} \\ r_{12}E_{12} + \beta E_{12} \\ r_{21}E_{21} + \beta E_{21} \\ g_2E_{22} + \beta E_{22} \\ g_1I_{11} + \gamma I_{11} \\ r_{12}I_{12} + \gamma I_{12} \\ r_{21}I_{21} + \gamma I_{21} \\ g_2I_{22} + \gamma I_{22} \\ g_1S_{11} + \alpha S_{11}(I_{21} + I_{11}) \\ r_{12}S_{12} + \alpha S_{12}(I_{12} + I_{22}) \\ r_{21}S_{21} + \alpha S_{21}(I_{11} + I_{21}) \\ g_2S_{22} + \alpha S_{22}(I_{22} + I_{12}) \end{pmatrix}.$$

Infected compartments E_{ij} and I_{ij} gives $m = 8$, and equilibrium solution with $E_{ij} = I_{ij} = 0$ has a form $x_0 = (0, 0, 0, 0, 0, 0, 0, 0, S_1, \frac{g_1S_1}{r_{12}}, \frac{g_2S_2}{r_{21}}, S_2)^t$, where S_1 and S_2 are positive solutions of $r_{12}S_{12} = g_1S_{11}$ and $r_{21}S_{21} = g_2S_{22}$ respectively. We assume $S_1 = S_{11}$ and $S_2 = S_{22}$ and from the statements above we can derive S_{12} and S_{21}.

Before proceeding to constructing next generation matrix, we should check whether axioms A(1)-A(5) still hold: all the functions are non-negative for positive S_{ij}, E_{ij} and I_{ij}; for $S_{ij} = I_{ij} = E_{ij} = 0$, $\mathscr{V}_i^- = 0$; $\mathscr{F}_i = 0$ for

$i > 8$; and for $E_{ij} = I_{ij} = 0$, $\mathscr{F}_i = \mathscr{V}_i^+ = 0$ for $i = 1, ..., 8$. Thus, our system satisfies A(1)-A(4). Next, we construct a Jacobian matrix of a system evaluated at DFE to check for A(5). We will not write all the eigenvalues of the system, because some of them are too long and complicated, the most simplest ones are $\lambda_1 = -g_1 - r_{12}$ and $\lambda_2 = -g_2 - r_{21}$. Tacking to account that g_i's and r_{ij}'s are all positive, we conclude that eigenvalues has negative real parts, which satisfies axiom A(5). Since all the axioms hold, we can move to the construction of next generation matrix and finding basic reproduction number. In order to simplify our calculations, without loss of generality, let us assume $S_1 = S_2 = 1$ is a DFE. Thus, our F and V matrix, defined in the same manner as in equation (5) are:

$$F = \begin{bmatrix} 0 & 0 & 0 & 0 & \alpha & 0 & \alpha & 0 \\ 0 & 0 & 0 & 0 & 0 & \alpha g_1/r_{12} & 0 & \alpha g_1/r_{12} \\ 0 & 0 & 0 & 0 & \alpha g_2/r_{21} & 0 & \alpha g_2/r_{21} & 0 \\ 0 & 0 & 0 & 0 & 0 & \alpha & 0 & \alpha \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \tag{24}$$

$$V = \begin{bmatrix} g_1 + \beta & -r_{12} & 0 & 0 & 0 & 0 & 0 & 0 \\ -g_1 & r_{12} + \beta & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & r_{21} + \beta & -g_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & -r_{21} & g_2 + \beta & 0 & 0 & 0 & 0 \\ -\beta & 0 & 0 & 0 & g_1 + \gamma & -r_{12} & 0 & 0 \\ 0 & -\beta & 0 & 0 & -g_1 & r_{12} + \gamma & 0 & 0 \\ 0 & 0 & -\beta & 0 & 0 & 0 & r_{21} + \gamma & -g_2 \\ 0 & 0 & 0 & -\beta & 0 & 0 & -r_{21} & g_2 + \gamma \end{bmatrix} \tag{25}$$

The largest eigenvalue of a matrix FV^{-1} will be the basic reproduction number.

3.1 Equal travel rates

Since we have two square matrices of size 8 and 7 parameters, it will be too complicated to analyze basic reproduction number. That is why, let us start with a slightly simplified case, with 5 parameters.In order to do so,

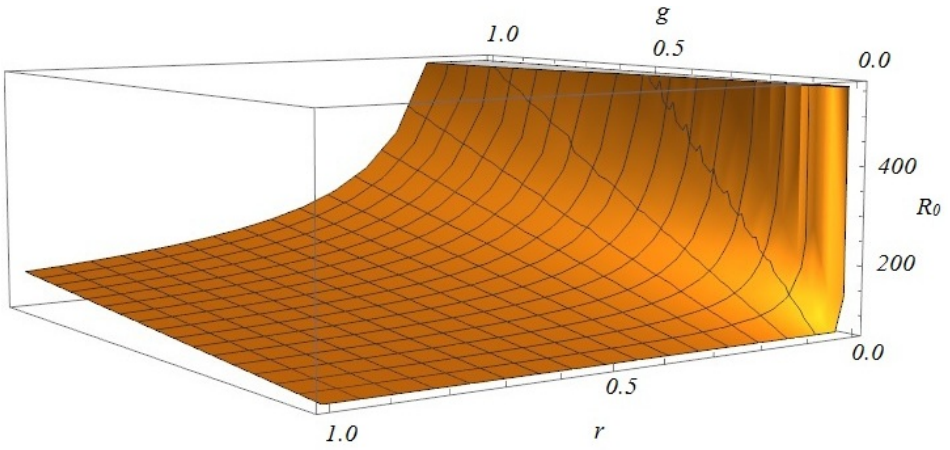


Figure 3: Basic reproduction number as a function travel rates with $\alpha = 0.7$ $\gamma = 0.01$

lets assume that $g_1 = g_2 = g$ and $r_{12} = r_{21} = r$, such that rates of return and transfer are equal for both cities. Tacking it into account, we construct next generation matrix, and it gives us

$$R_0 = \frac{\alpha(g+r)}{\gamma r}. \tag{26}$$

We can consider R_0 as a function of g and r. Taking to account $\alpha > 0$ and $\gamma > 0$ we find partial derivatives with respect to each variable and get:

$$\frac{dR_0}{dg} = \frac{\alpha}{\gamma r} > 0, \tag{27}$$

$$\frac{dR_0}{dr} = -\frac{\alpha g}{\gamma r^2} < 0. \tag{28}$$

Thus, R_0 is increasing with respect to g and decreasing with respect to r, which also can be seen from the Figure 3, 4. Also,

$$\lim_{r\to 1}\lim_{g\to 1}\frac{\alpha(g+r)}{\gamma r} = \frac{2\alpha}{\gamma} \tag{29}$$

From the graphs we also can see that as g and r goes to 1, R_0 approaches to $\frac{2\alpha}{\gamma}$. For Figure 3, R_0 goes to 140 and for Figure 4 it approaches to 0.3428

Thus, $R_0 < 1$ for $2\alpha < \gamma$ and $R_0 > 1$ for $2\alpha > \gamma$. We can assume that infection dies out if recovering rate of infected individuals is more than twice larger that rate of getting infected.

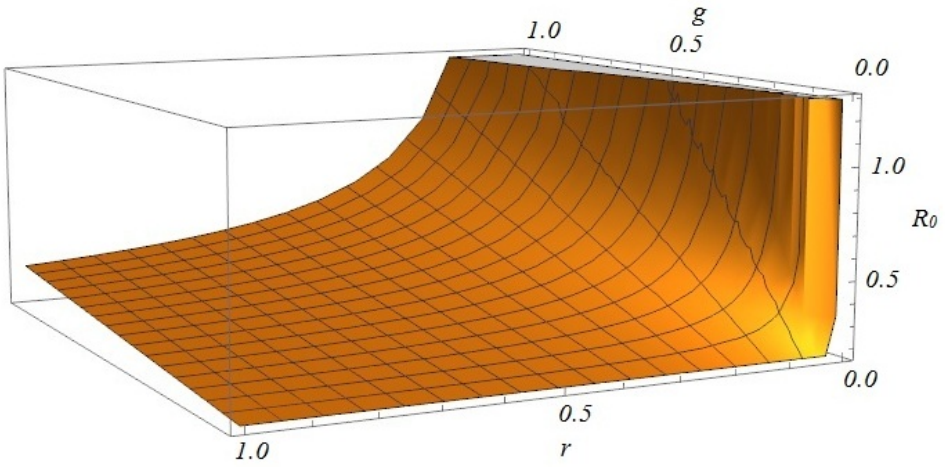


Figure 4: Basic reproduction number as a function of travel rates with $\alpha = 0.12$ $\gamma = 0.7$

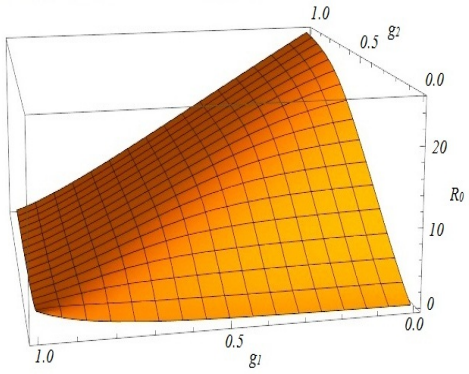
3.2 Unequal travel rates

Although it is much simpler to analyze R_0 for equal travel rates, it is not quite realistic. In a real life we don't have two almost identical cities with equal travel rates among each other. It is more common to have one big city and a province or suburb, so that rate of moving into one is much higher than to another. That is why it is important to consider unequal travel rates case. For this reason we will go back to our original situation with 7 parameters. Using software we can find an exact value of R_0. However as you can see from equation (30), is too complicated to analyze. Thus, we will only try to represent it graphically using mathematical software.

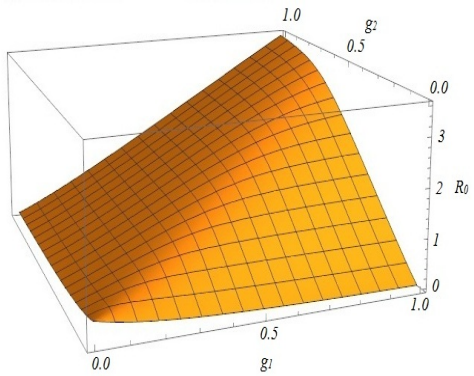
$$R_0 = \frac{\alpha(\beta^2\gamma^2 r_{12}g_2 + ... + \sqrt{(-\beta^2\gamma^2 r_{12}g_2 - ...)^2 - 4(\beta^4\gamma^4 r_{12}^2 g_2 r_{21} + ...)})}{2\gamma r_{12}r_{21}(\beta + r_{12} + g_1)(\gamma + r_{12} + g_1)(\beta + g_2 + r_{21})(\gamma + g_2 + r_{21})} \tag{30}$$

Since, we do not have a control over parameters α, β and γ, we will consider them as numbers. However, we have a control over travel rates: g_1, g_2, r_{12} and r_{21}, and since there are 4 parameters, we cannot present it graphically simultaneously. Thus we will fix some of them and do numerical simulations. Since we have noticed from previous examples that R_0 usually depends on a ratio of $\frac{\alpha}{\gamma}$, we will consider few cases with them. All of the values of α and γ were chosen randomly, such that it satisfies conditions written below.

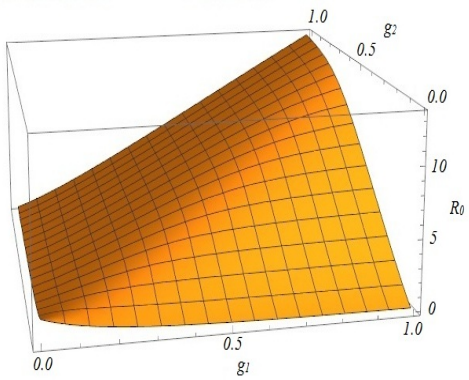
	α	γ
$\alpha > \gamma$	$\alpha = 0.65$	$\gamma = 0.21$
$\alpha < \gamma$	$\alpha = 0.3$	$\gamma = 0.7$
$2\alpha > \gamma$	$\alpha = 0.47$	$\gamma = 0.39$
$2\alpha < \gamma$	$\alpha = 0.19$	$\gamma = 0.81$



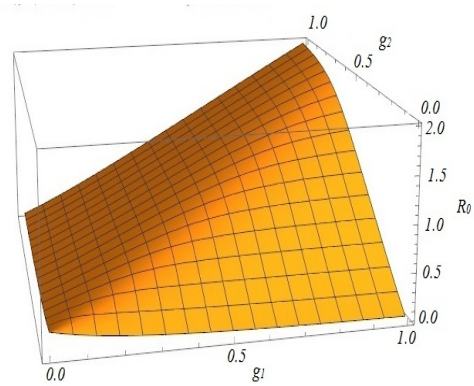
(a) $\alpha > \gamma$



(b) $\alpha < \gamma$



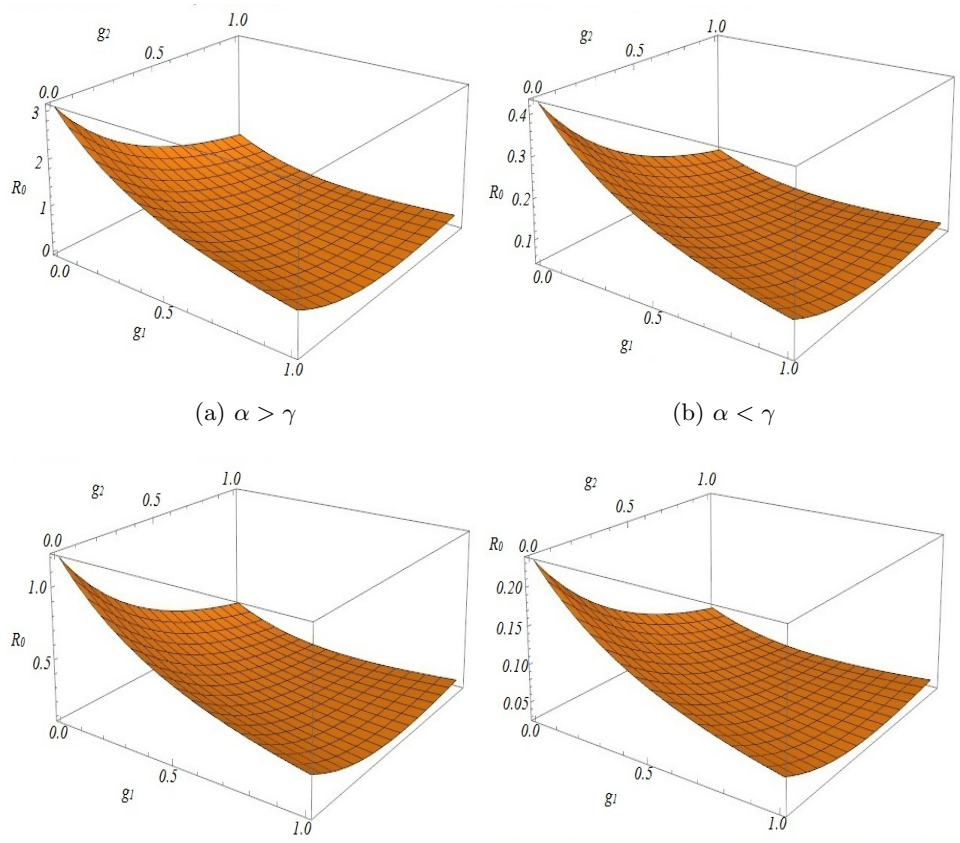
(c) $2\alpha > \gamma$



(d) $2\alpha < \gamma$

Figure 5: R_0 as a function of g_1 and g_2 for fixed r_{ij}'s, α, β and γ

For the Figure 5 we fix $r_{12} = 0.104$, $r_{21} = 0.07$ and $\beta = 0.37$. It is clear from the graph that R_0 is increasing function with respect to g_i's, however we can observe the changes on a scale of R_0 depending on each case. Figure 6 represents the same function R_0 as Figure 5, but this time we chose $r_{12} = 0.8$ and $r_{21} = 0.73$. All other parameters are the same. If we compare two figures, it is clear that for a larger r_{ij}'s the values of R_0 considerably decreases. In

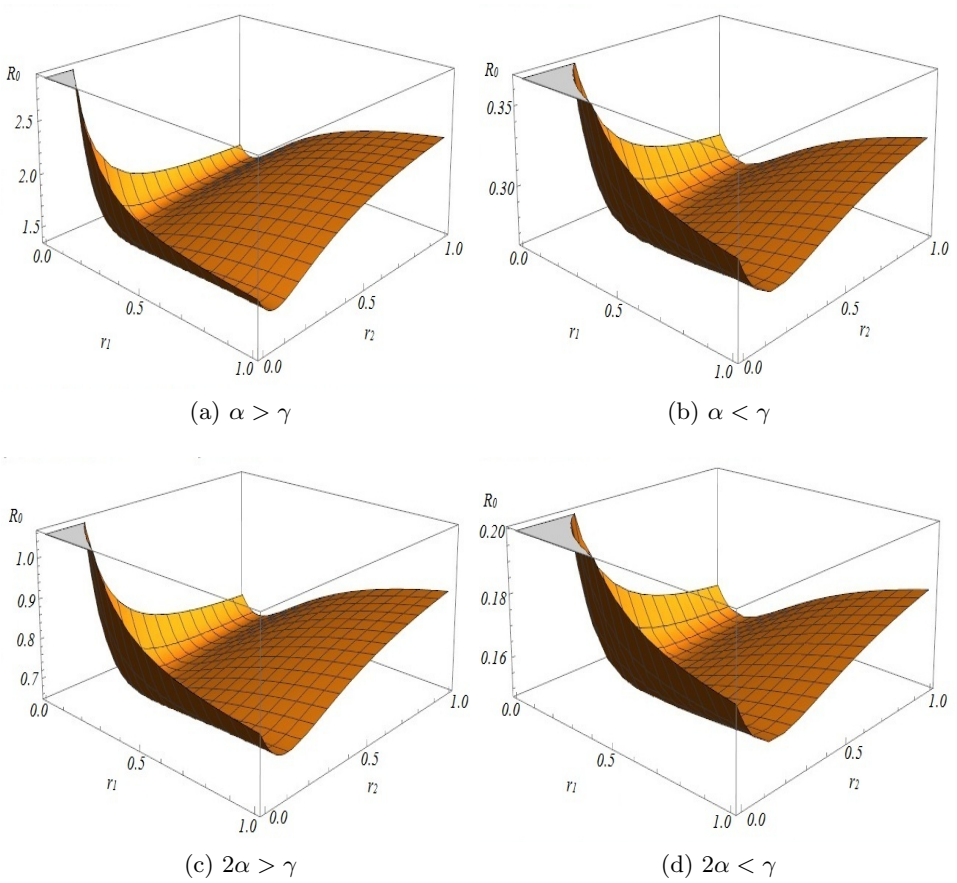


(a) $\alpha > \gamma$ (b) $\alpha < \gamma$

(c) $2\alpha > \gamma$ (d) $2\alpha < \gamma$

Figure 6: R_0 as a function of g_1 and g_2 for fixed r_{ij}'s, α, β and γ

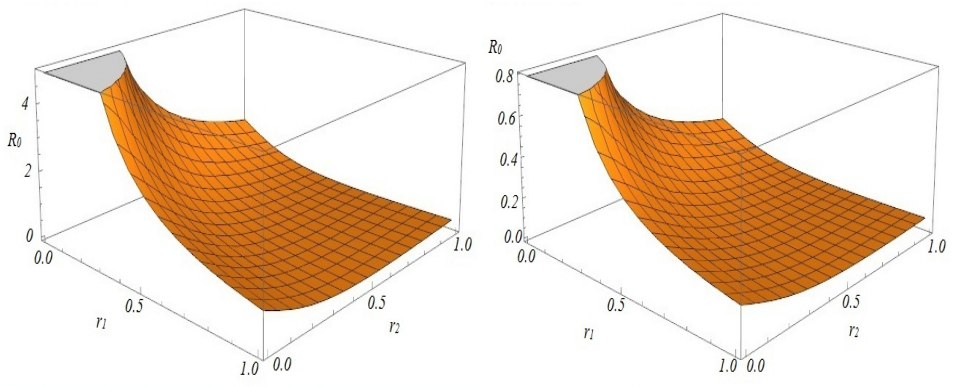
Figure 7 we fix $g_1 = 0.12$ and $g_2 = 0.09$, for the other parameters we use the same values as before, except for r_{ij}'s which are now variables. Here we see the same situation as we have discussed before, R_0 increases as g_i's increase and less than one for $\alpha < \gamma$ or $2\alpha < \gamma$. Figure 8 also supports our hypothesis, since for $g_1 = 0.64$ and $g_2 = 0.71$, which are greater than assigned values from previous case, the range of basic reproduction number is also larger.



(a) $\alpha > \gamma$ (b) $\alpha < \gamma$

(c) $2\alpha > \gamma$ (d) $2\alpha < \gamma$

Figure 7: R_0 as a function of r_{12} and r_{21} for fixed g_i's, α, β and γ



(a) $\alpha > \gamma$ (b) $\alpha < \gamma$

(c) $2\alpha > \gamma$ (d) $2\alpha < \gamma$

Figure 8: R_0 as a function of r_{12} and r_{21} for fixed g_i's, α, β and γ

3.3 Generalization

In order to make the results simple, in the two previous subsections we used a slightly simplified version of DFE state. Now, let us go back to original DFE, which is $x_0 = (0, 0, 0, 0, 0, 0, 0, 0, S_1, \frac{g_1 S_1}{r_{12}}, \frac{g_2 S_2}{r_{21}}, S_2)^t$. This time we will not fix S_1 and S_2 to be equal 1. Instead, we will consider the general case, when $S_{11} = m$ and $S_{22} = n$ where m, n are real numbers, and accordingly rewrite S_{12} and S_{21}. This change will lead to slight modifications in F matrix, consequently our reproduction number will change. For the general case,

$$R_0 = \frac{\alpha(\beta^2\gamma^2 g_2 n r_{12} + .. + \sqrt{(-\beta^2\gamma^2 g_2 n r_{12} + ..)^2 - 4(\beta^4\gamma^4 g_1 g_2 m n r_{12} r_{21} + ..)})}{2\gamma r_{12}(\beta + g_1 + r_{12})(\gamma + g_1 + r_{12}) r_{21}(\beta + g_2 + r_{21})(\gamma + g_2 + r_{21})} \tag{31}$$

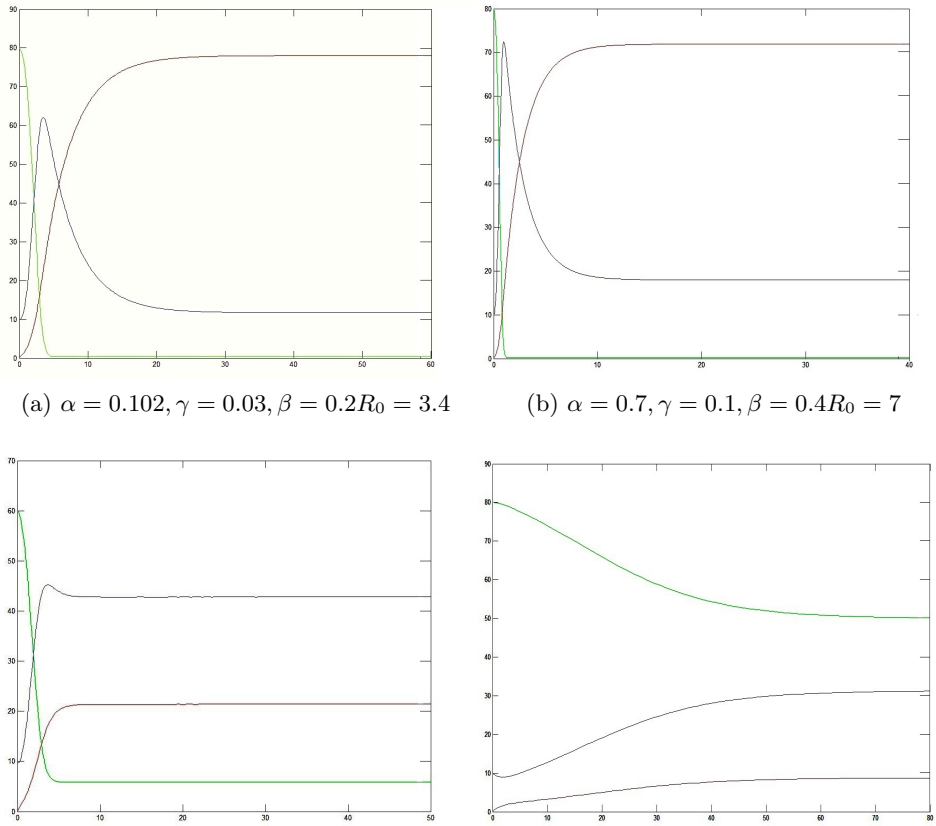
We will not do any mathematical operations on it, since it is too long and complicated. However, if we carefully look at the expression of R_0 at equation (31) we first see that it looks quite similar to the value in equation (30), except for existence of m and n which were ones, in above case. This allows us to assume that it will behave in the same manner. Secondly, as you can see, our newly introduced parameters m and n appear only on numerator, which means that R_0 is proportional to m and n. This statement seems logical, since it is natural that the risk of getting infected is higher in large population areas.

4 Numerical simulations

In this report, we considered an SEIS model with spatial heterogeneity. Now we present some numerical simulations to the behavior of the whole system for different values of parameters. We let $S = \sum_{i=1}^{n}\sum_{j=1}^{n} S_{ij}$, $E = \sum_{i=1}^{n}\sum_{j=1}^{n} E_{ij}$ and $I = \sum_{i=1}^{n}\sum_{j=1}^{n} I_{ij}$, then use Matlab software to plot the graph of differential equations. In Figure 7 green line indicates $S(t)$, blue $E(t)$ and red $I(t)$.

5 Example of a disease

SEIS model describes a disease with dormant periods and absence of immune effect, like tuberculosis, H1N1 influenza or syphilis. Although, sometimes they have lethal results, in case of early detection of a disease successful



(a) $\alpha = 0.102, \gamma = 0.03, \beta = 0.2 R_0 = 3.4$

(b) $\alpha = 0.7, \gamma = 0.1, \beta = 0.4 R_0 = 7$

(c) $\alpha = 0.12, \gamma = 0.7, \beta = 0.35 R_0 = 0.171$

(d) $\alpha = 0.01, \gamma = 0.5, \beta = 0.14 R_0 = 0.02$

Figure 9: The behavior of each compartment S, E, and I as a function of time, for indicated parameters.

treatment can be made. However, even after the recovering an individual can still be susceptible to the disease, thus they usually analyzed by SEIS model. One of the most recent H1N1 influenza outbreaks happened in 2009. It affected many countries all around the world, and caused some serious results and even death. A study by Haghdoost and Baneshi [8] presents the data for influenza outbreak in Iran. In their paper, they also found that the force of infection (in our study denoted by αSI) has a high impact on basic reproduction number. According to their data, an estimated R_0 at the first month was 1.21, however it kept increasing and become 1.28 and 1.32 for the second and third months respectively. Also according to the data, the force of infection increases over time, which is natural since the number of infected individuals increases.

6 Conclusion

In this report we have examined SEIS model with spatial heterogeneity for epidemic diseases like TB and influenza. This topic was already considered in several other papers. However, all of them either consider SEIS model for spatially homogeneous population or, describe spatial heterogeneity for a different models (SIR, SIS). In this report we combine both, spatial heterogeneity and SEIS model. The next generation matrix method introduced by van den Driessche and Watmough [7] was used for finding the basic reproduction number. The basic reproduction number is necessary for describing the dynamics of the system around DFE. Relations of R_0 to infection rates (α, γ) and travel rates (g_i, r_{ij}) was given. It is shown above that R_0 approaches to $\frac{\alpha}{\gamma}$ for spatially homogeneous case and to $\frac{2\alpha}{\gamma}$ for equal travel rates case. Also, it was shown graphically that R_0 increases as travel rate from a compartment increases and decreases as return rates increases. The results of our study allow us to assume that for a spatially heterogeneous population, the best policy to overcome epidemics is to set $r_{ij} = 1$ and $g_i = 0$. In this case $R_0 = \frac{\alpha}{\gamma}$, and this is the lowest possible value of basic reproduction number, according to the model. This way of fixing parameters represents the case without movement, when the citizens are captivated in their original compartments. This results coincides with common governmental practice of isolating infectious regions.

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Zhuldyzay Baki

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