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A two-area epidemic model for the spread of COVID-19

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Abstract

In this paper, we model the spread of COVID-19 in a population of people travelling between two areas. New research implies that traveling of the asymptomatic infectious individuals, (i.e., infected individuals who have no symptoms of the disease and individuals with symptoms of the disease that are not detected by the healthcare system) can bring disease from one region to other regions even if the infectious individuals who are detected by the healthcare system, (i.e., confirmed cases), are inhibited from traveling among regions. We study the effect of travelling between two areas on the dynamics of COVID-19. Our model is formulated as a system of ordinary differential equations, with terms accounting for disease transmission, recovery, birth, death, and travel between two areas. We will give an explicit formula for calculating the basic reproduction number, $\mathcal{R}_0$, in the quarantine mode of two areas and explicit bounds on $\mathcal{R}_0$ for the case where the residents of both areas are in contact with each other. Our computations reveal the relationship between the basic reproduction number, a crucial quantity in epidemic control, and travel and return rates between areas. This suggests that it is essential to strengthen restrictions on passengers once infectious diseases appear.

Keywords: Mathematical Epidemiology, COVID-19, Epidemic Model, Two-Area
2020 MSC: 92D30, 92C60, 37N25, 34A34

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1 Introduction

Some components of infectious diseases can make their modelling complex, for example, spatial heterogeneity, which small household models can quantify. In [3], these stochastic models are briefly discussed. In [1], Arrigoni and Pugliese, by using continuous-time Markov chains, give a more general model for households. The use of partial differential equations is another approach to introduce spatial variation in epidemic models, [2]. Consider the specific disease COVID-19, which occurs through person-to-person contact in the tissues between two areas and spreads well through the transportation systems. The spread of transportation networks and the high speed of movement of people between different regions can cause the spread of disease from one region to another. In this situation, the travel of people between separate geographical regions plays a crucial role in the spread of the disease. Multi-area spatial models with ordinary differential equations are rooted in mathematical ecology, competing, and predator-prey metapopulations, [8, 9]. The problem with these models is the high number of equations; for example, a model with n areas and p compartments has pn^2 equations.

In mathematical epidemiology, several models have been used to separate geographical areas. In [10, 14] to study the global spread of influenza through the airline network, discrete-time difference equations are considered in a

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continuous state space. In [15], Sattenspiel and Dietz, by identifying the parameters related to measles transmission, investigated the spread of this disease by modelling travel between populations on the island of Dominica in the Caribbean Sea. They studied the behaviour of this model numerically. In [17], they studied the same model for travel between populations in the Canadian subarctic.

In this paper, we first formulate a mobility model for residents of two areas travelling between them. Note that the demographic model here is adapted from [15]. Our approach in this paper is geographic. However, it should be noted that there is an obvious connection to heterogeneous population modelling [17]. In the next step, we consider the time evolution of the COVID-19 disease in this model, by adapting the COVID-19 model presented and analyzed in [12]. We provide an exact derivation of the basic reproduction number $\mathcal{R}_0$ for each area in the quarantine mode of two areas and explicit bounds on $\mathcal{R}_0$ for the case where the residents of both areas are in contact with each other.

2 The mobility model

In [15], authors assume no birth or natural death of individuals; they assume only intercity travel. In this model, we assume birth and death occur at the same rate $d > 0$. In addition, we assume that birth occurs only in the area where people live, and their death occurs in any area.

Suppose we have two areas, so that the residents of Area 1 are the people who were born and naturally live there, and the travellers, who are the people not present in the area of their residence at the desired time. We use $N_{1,2}(t)$ for the number of residents of area 1 who are present in area 2. Letting N_i^r be the resident population of area i at time t for $i = 1, 2$, then the number of residents of areas 1 and 2 is respectively as follows,

$$N_1^r = \sum_{j=1}^{2} N_{1j}, \quad \text{and} \quad N_2^r = \sum_{j=1}^{2} N_{2j}. \tag{2.1}$$

Furthermore, let $N_i^p(t)$ denotes the population of individuals who are physically present in area i at time t for $i = 1, 2$, both residents and travelers.

$$N_1^p = \sum_{j=1}^{2} N_{j1}, \quad \text{and} \quad N_2^p = \sum_{j=1}^{2} N_{j2}. \tag{2.2}$$

As in [2], residents of area i ($i = 1, 2$), leave the site at a per capita rate $g_i \geq 0$ per unit time. A fraction $m_{ji} \geq 0$ of these outgoing individuals go to site j. Thus, if $g_i > 0$ then $\sum_{j=1}^{n} m_{ji} = 1$, with $m_{ii} = 0$ and $g_i m_{ji}$ is the travel rate from area i to area j for $i, j = 1, 2$. Residents of area i who are in area j return to i with a per capita rate of $r_{ij} \geq 0$, with $r_{ii} = 0$. Now, with the above assumptions and a large enough population, ordinary differential equations for population dynamics can be obtained.

$$\begin{cases} \dfrac{dN_{11}}{dt} = d(N_1^r - N_{11}) + \sum_{j=1}^{2} r_{1j} N_{1j} - g_1 N_{11} = dN_{12} + r_{12} N_{12} - g_1 N_{11} \\[2ex] \dfrac{dN_{22}}{dt} = d(N_2^r - N_{22}) + \sum_{j=1}^{2} r_{2j} N_{2j} - g_2 N_{22} = dN_{21} + r_{21} N_{21} - g_2 N_{22}, \end{cases} \tag{2.3}$$

and,

$$\begin{cases} \dfrac{dN_{12}}{dt} = g_1 N_{11} - r_{12} N_{12} - dN_{12} \\[2ex] \dfrac{dN_{21}}{dt} = g_2 N_{22} - r_{21} N_{21} - dN_{21}. \end{cases} \tag{2.4}$$

From the combination of equations (2.3) and (2.4), the evolution of the resident population of area 1 is as follows,

$$\frac{dN_1^r}{dt} = \frac{d}{dt}(N_{11} + N_{12}) = 0, \tag{2.5}$$

and the change of people in area 1,

$$\frac{dN_1^p}{dt} = \frac{d}{dt}(N_{11} + N_{21}) = dN_{12} + r_{12} N_{12} - g_1 N_{11} + g_2 N_{22} - r_{21} N_{21} - dN_{21}. \tag{2.6}$$

Similarly, for area 2, the demographic changes are as follows,

$$\frac{dN_2^r}{dt} = \frac{d}{dt}(N_{22} + N_{21}) = 0, \tag{2.7}$$

and

$$\frac{dN_2^p}{dt} = dN_{21} + r_{12}N_{12} - g_2N_{22} + g_1N_{11} - r_{12}N_{12} - dN_{12}. \tag{2.8}$$

According to (2.5) and (2.7), the number of residents of areas 1 and 2 is a fixed quantity, but from (2.6) and (2.8), the number of individuals present in areas 1 and 2 are variable. Finally, the total population in the 2-area system is given by

$$N = \sum_{i=1}^{2} N_i^r = \sum_{i=1}^{2} N_i^p = \sum_{i=1}^{2}\sum_{i=1}^{2} N_{ij}, \tag{2.9}$$

N is constant because according to (2.5) and (2.7), the population of residents of both areas is constant. Equations (2.3) and (2.4) have initial values $N_{ij} \geq 0$ at $t = 0$ with fixed $N_i^r > 0$ for $i, j = 1, 2$ at $t = 0$, and called the linear mobility model. The model has the following unique equilibrium point because $d > 0$.

$$\hat{N}_{11} = \frac{(d + r_{12})(N_{11} + N_{12})}{d + r_{12} + g_1}, \qquad \hat{N}_{22} = \frac{(d + r_{21})(N_{21} + N_{22})}{d + r_{21} + g_2}, \tag{2.10}$$

and

$$\hat{N}_{12} = \frac{g_1(N_{11} + N_{12})}{d + r_{12} + g_1}, \qquad \hat{N}_{21} = \frac{g_2(N_{21} + N_{22})}{d + r_{21} + g_2}. \tag{2.11}$$

3 COVID-19 model

In each of these two areas, an epidemic model can be created. In nature, the most abundant species are viruses and parasites, because they reproduce quickly. This high-scale reproduction causes infectious diseases in humans or animals, so these species are important in the social, economic, and medical fields. One of these species is the coronavirus. According to the experience gained in China, using strict isolation measures can rapidly and significantly affect the dynamic of the epidemic, [6].

The beginning of working with mathematical models in epidemiology dates back to the 18th century. In [4], Bernnoli used a mathematical model to investigate the effectiveness of a technique against smallpox with the aim of influencing public health policies. Most of the models are compartmental models that divide the population into different classes, and these classes are transferred to each other with certain assumptions [5].

We use the model introduced in [12] by the author and its compartments, the class S for susceptible individuals; class A consists of two groups of individuals in the community, asymptomatic infectious individuals, i.e., infected individuals who have no symptoms of the disease and individuals with symptoms of the disease that are not detected by the healthcare system; the class D for infectious individuals who are detected by the healthcare system, i.e., confirmed cases; and the class of recovered individuals R.

Let S_{ij}, A_{ij}, and R_{ij} denote the number of susceptible, asymptomatic, and recovered individuals resident in area i who are present in area j at time t; thus, $N_{ij} = S_{ij} + A_{ij} + R_{ij} + D_j$ for all $i, j = 1, 2$.

In each area, there are seven equations. Since there are two areas, there is a total of 14 equations. The dynamics of the number of susceptibles, asymptomatics, confirmed cases, and recovered individuals originating from site i (with

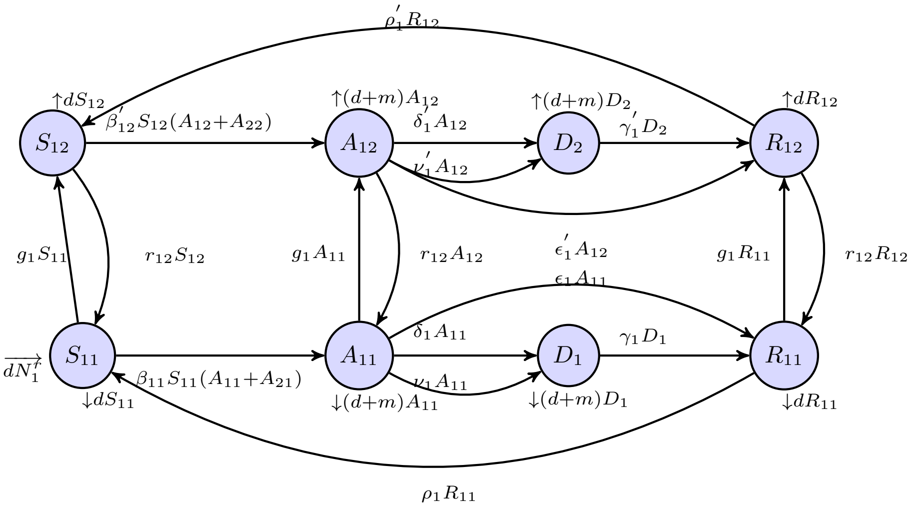

Figure 1: The flowchart of the model 3.1

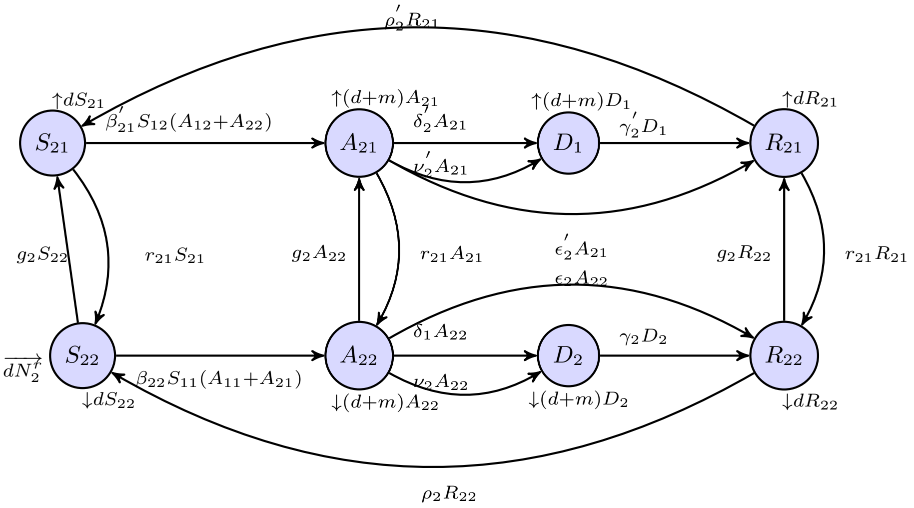

Figure 2: The flowchart of the model 3.2

$= 1, 2)$ are given by the following system.

$$
\begin{cases}
\dfrac{dS_{11}}{dt} = d(N_1^r - S_{11}) + r_{12}S_{12} - g_1 S_{11} - \beta_{11}S_{11}(A_{11} + A_{21}) + \rho_1 R_{11}, \\
\dfrac{dA_{11}}{dt} = r_{12}A_{12} - g_1 A_{11} + \beta_{11}S_{11}(A_{11} + A_{21}) - (\delta_1 + \nu_1 + \epsilon_1)A_{11} - (d + m)A_{11}, \\
\dfrac{dR_{11}}{dt} = r_{12}R_{12} - g_1 R_{11} + \gamma_1 D_1 - (d + \rho_1)R_{11} + \epsilon_1 A_{11}, \\
\dfrac{dS_{22}}{dt} = d(N_2^r - S_{22}) + r_{21}S_{21} - g_2 S_{21} - \beta_{22}S_{221}(A_{22} + A_{12}) + \rho_2 R_{22}, \\
\dfrac{dA_{22}}{dt} = r_{21}A_{21} - g_2 A_{22} + \beta_{22}S_{22}(A_{22} + A_{12}) - (\delta_2 + \nu_2 + \epsilon_2)A_{22} - (d + m)A_{22}, \\
\dfrac{dR_{22}}{dt} = r_{21}R_{21} - g_2 R_{22} + \gamma_2 D_2 - (d + \rho_2)R_{22} + \epsilon_2 A_{22}, \\
\dfrac{dD_1}{dt} = (\delta_1 + \nu_1)A_{11} + (\delta_2^{'} + \nu_2^{'})A_{21} - (\gamma_2^{'} + \gamma_1 + d + m)D_1,
\end{cases}
\tag{3.1}
$$

and for $j \neq i$,

$$\begin{cases} \dfrac{dS_{12}}{dt} = g_1 S_{11} - r_{12}S_{12} - \beta'_{12}S_{12}(A_{12}+A_{22}) + \rho'_1 R_{12} - dS_{12}, \\ \dfrac{dA_{12}}{dt} = g_1 A_{11} - r_{12}A_{12} + \beta'_{12}S_{12}(A_{12}+A_{22}) - (\delta'_1+\nu'_1+\epsilon'_1)A_{12} - (d+m)A_{12}, \\ \dfrac{dR_{12}}{dt} = g_1 R_{11} - r_{12}R_{12} + \gamma'_1 D_2 - (d+\rho'_1)R_{12} + \epsilon'_1 A_{12}, \\ \dfrac{dS_{21}}{dt} = g_2 S_{22} - r_{21}S_{21} - \beta'_{21}S_{21}(A_{21}+A_{11}) + \rho'_2 R_{21} - dS_{21}, \\ \dfrac{dA_{21}}{dt} = g_2 A_{22} - r_{21}A_{21} + \beta'_{21}S_{21}(A_{21}+A_{11}) - (\delta'_2+\nu'_2+\epsilon'_2)A_{21} - (d+m)A_{21}, \\ \dfrac{dR_{21}}{dt} = g_2 R_{22} - r_{21}R_{21} + \gamma'_2 D_1 - (d+\rho'_2)R_{21} + \epsilon'_2 A_{21}, \\ \dfrac{dD_2}{dt} = (\delta_2+\nu_2)A_{22} + (\delta'_1+\nu'_1)A_{12} - (\gamma'_1+\gamma_2+d+m)D_2. \end{cases} \tag{3.2}$$

The mobility scheme in Figures 1 and 2 describes the inward and outward commuting individuals who travel between areas in the multiarea system. The parameters are defined in Table 1.

Equations (3.1) and (3.2) for all $i, j = 1, 2$ describe the evolution of the number of susceptible, asymptomatic, confirmed cases, and recovered individuals according to the assumptions of the mobility model.

Proposition 3.1. The nonnegative orthant $\mathbb{R}^8_{\geq 0}$ is positively invariant under the flow of (3.1) and (3.2), and for all $t > 0$ and $i, j = 1, 2$, $S_{ii} > 0$, and $S_{ij} > 0$ provided that $g_i m_{ji} > 0$. Furthermore, solutions of (3.1) and (3.2) are bounded.

Proof . All solutions of the system are smooth. And if all components of the solution of the system have nonnegative initial conditions, and any of the compartments are zero at time $t = t_i \geq 0$, then the derivatives are nonnegative. For example, if $S_{11}(t_1) = 0$ and $X(t_1) \geq 0$ for all other components of the solution, we get

$$\frac{dS_{11}(t_1)}{dt} = dN^r_1 + r_{12}S_{12}(t_1) + \rho_1 R_{11}(t_1) \geq 0,$$

which implies $S_{11}(t_1^+) \geq 0$, and hence $S_{11}(t)$ is nonnegative for all times $t \geq 0$. By similar arguments, we can prove that all compartments are nonnegative at all times $t \geq 0$.

From (3.1), for $i = 1, 2$ if $S_{ii} = 0$ at $t = 0$, then

$$\frac{dS_{ii}}{dt} = dN^r_i + r_{ij}S_{ij} + \rho_i R_{ii} > 0, \quad i, j = 1, 2, \quad i \neq j,$$

and thus $S_{ii} > 0$ for $t > 0$. Similarly, from (3.2) we have

$$\frac{dS_{ij}}{dt} = g_i S_{ii} + \rho'_i R_{ij} > 0 \;\; i, j = 1, 2, \quad i \neq j.$$

Thus for $t > 0$, $S_{ij} > 0$ for $i \neq j$. Furthermore the positive invariance of $\mathbb{R}^8_{\geq 0}$ and the constant population property implies boundedness of the solutions. □

Theorem 3.1. Suppose that systems (3.1) and (3.2) are at equilibrium and that a given area 1 is at the DFE. Then, area 2 is at the DFE.

Proof . According to the assumption, suppose that area 1 is at DFE, i.e., $A_{11} = 0$ and $A_{21} = 0$. Consider The second equation of (3.1),

$$\frac{dA_{11}}{dt} = r_{12}A_{12}.$$

As area 1 is at the DFE, so $\dfrac{dA_{11}}{dt} = 0$, and thus, since $r_{12} > 0$, it follows that $A_{12} = 0$. Now we consider the second equation of (3.2), so we have

$$\frac{dA_{12}}{dt} = \beta'_{12}S_{12}A_{22}.$$

Since $\beta_{12}^{'} > 0$, Proposition 3.1 implies $S_{12} > 0$ for $t > 0$, hence $A_{22} = 0$, and area 2 is at the DFE. □

According to the above theorem, area 1 is at the DFE if

$$S_{11} = \hat{N}_{11}, \quad A_{11} = 0, \quad D_1 = 0, \quad R_{11} = 0, \quad S_{21} = \hat{N}_{21}, \quad A_{21} = 0, \quad R_{21} = 0.$$

So, the DFE equilibrium point in area 1 is as follows.

$$DFE^1 = (\hat{N}_{11}, 0, 0, 0, \hat{N}_{21}, 0, 0) \in \mathbb{R}_+^7.$$

Similarly, the DFE equilibrium point in area 2 is given below:

$$DFE^2 = (\hat{N}_{22}, 0, 0, 0, \hat{N}_{12}, 0, 0) \in \mathbb{R}_+^7.$$

Theorem 3.2. Suppose systems (3.1) and (3.2) are at equilibrium, and COVID-19 is endemic in area 1. Then the disease is endemic in area 2.

Proof . The endemicity of the disease in area 1, means that for some $q \in \{1, 2\}$, $A_{q1} > 0$. To continue the proof, we must show that if the disease is endemic in area 1, we have $A_{11} > 0$. If $q \neq 1$, and $A_{11} = 0$. Since the system is at equilibrium, from (3.1),

$$0 = \frac{dA_{11}}{dt} = r_{12}A_{12} + \beta_{11}S_{11}A_{21}.$$

Since for $t > 0$, $\beta_{11}S_{11} > 0$, we have $A_{21} = 0$, which contradicts $A_{21} > 0$. Hence, $A_{11} > 0$ if the disease is endemic in area 1. Now consider the second equation of (3.2) and assume $A_{12} = 0$. Since the system is at equilibrium, we have

$$0 = \frac{dA_{12}}{dt} = g_1 A_{11} + \beta_{12}^{'} S_{12} A_{22},$$

this implies that $A_{11} = 0$, which is a contradiction. Thus $A_{12} > 0$ and $A_{22} > 0$. Hence, the disease is endemic in area 2. □

4 The Basic Reproduction Number

The basic reproduction number, R_0, is a crucial quantity in epidemic models. There are several methods for computation of R_0, see [11]. We use the next-generation matrix method. We apply this method for the evaluation of the basic reproduction of the model.

First, note that if area 1 is isolated from area 2, i.e. $r_{12} = g_1 = g_2 = r_{21} = 0$, the equilibrium points in the mobility model in area 1 are $\hat{N}_{11} = N_1^r$ and $\hat{N}_{21} = 0$. Also, when area 1 is isolated due to the refusal of travel between the two areas, the population of residents and the physical population will equalize. According to these assumptions, we will calculate the Basic Reproduction Number in area 1. We use the next-generation matrix [7] and the method of [18]. By ordering the infectious variables as

$$A_{11}, D_1, A_{21},$$

we form the $\mathcal{F}$ and $\mathcal{V}$ matrices as follows.

$$\mathcal{F} = \begin{bmatrix} \beta_{11}S_{11}(A_{11} + A_{21}) \\ (\delta_1 + \nu_1)A_{11} + (\delta_2^{'} + \nu_2^{'})A_{21} \\ \beta_{21}^{'}S_{21}(A_{21} + A_{21}) \end{bmatrix}, \quad \text{and} \quad \mathcal{V} = \begin{bmatrix} (\delta_1 + \nu_1 + \epsilon_1)A_{11} + (d + m)A_{11} \\ (\gamma_2^{'} + \gamma_1 + d + m)D_1 \\ (\delta_2^{'} + \nu_2^{'} + \epsilon_2^{'})A_{21} + (d + m)A_{21} \end{bmatrix}.$$

By linearizing the $\mathcal{F}$ and $\mathcal{V}$ at the DFE point, we have

$$F_1 = \begin{bmatrix} \beta_{11}N_1^r & 0 & \beta_{11}N_1^r \\ (\delta_1 + \nu_1) & 0 & (\delta_2^{'} + \nu_2^{'}) \\ 0 & 0 & 0 \end{bmatrix}, \quad \text{and} \quad V_1 = \begin{bmatrix} \delta_1 + \nu_1 + \epsilon_1 + d + m & 0 & 0 \\ 0 & \gamma_2^{'} + \gamma_1 + d + m & 0 \\ 0 & 0 & \delta_2^{'} + \nu_2^{'} + \epsilon_2^{'} + d + m \end{bmatrix}.$$

Since V_1^{-1} is diagonal, by [18], the basic reproduction number for the system (3.1) is

$$\mathcal{R}_0 = \rho(F_1 V_1^{-1}),$$

where $\rho(.)$ is the spectral radius; hence the basic reproduction number of area 1 is as follows

$$\mathcal{R}_0^1 = \frac{\beta_{11} N_1^r}{\delta_1 + \nu_1 + \epsilon_1 + d + m}, \tag{4.1}$$

Similarly, the basic reproduction number of area 2 when, $r_{12} = g_1 = g_2 = r_{21} = 0$, i.e., area 1 is isolated from area 2, is as follows,

$$\mathcal{R}_0^2 = \frac{\beta_{22} N_2^r}{\delta_2 + \nu_2 + \epsilon_2 + d + m}. \tag{4.2}$$

The DFE is locally asymptotically stable in area $i, i = 1, 2$, if $\mathcal{R}_0^i < 1$, and unstable if $\mathcal{R}_0^i > 1$. We summarize this result in the following theorem.

Theorem 4.1. Let $\mathcal{R}_0^i$ be defined in (4.1) and (4.2). If $\mathcal{R}_0^i < 1$, then the DFE of area i, is locally asymptotically stable. If $\mathcal{R}_0^i > 1$, then the DFE is unstable.

Suppose the systems (3.1) and (3.2) are at DFE. The DFE point in this model in both areas is as follows,

$$DFE = (\hat{N_{11}}, \hat{N_{12}}, \hat{N_{21}}, \hat{N_{22}}, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0) \in \mathbb{R}_+^{14}.$$

In this case, we check the local stability of DFE in both areas, again using the next-generation method. We arranged the infected areas as follows,

$$A_{11},\ A_{12}\ , A_{21}\ , A_{22}\ , D_1\ , D_2.$$

We form the $\mathcal{F}$ and $\mathcal{V}$ matrices as follows,

$$\mathcal{F} = \begin{bmatrix} \beta_{11} S_{11}(A_{11} + A_{21}) \\ \beta^{'}_{12} S_{12}(A_{12} + A_{22}) \\ \beta^{'}_{21} S_{21}(A_{21} + A_{11}) \\ \beta_{22} S_{22}(A_{22} + A_{12}) \\ (\delta_1 + \nu_1)A_{11} + (\delta^{'}_2 + \nu^{'}_2)A_{21} \\ (\delta_2 + \nu_2)A_{22} + (\delta^{'}_1 + \nu^{'}_1)A_{12} \end{bmatrix}, \quad \text{and} \quad \mathcal{V} = \begin{bmatrix} -r_{12}A_{12} + g_1 A_{11} + (\delta_1 + \nu_1 + \epsilon_1)A_{11} + (d+m)A_{11} \\ -g_1 A_{11} + r_{12}A_{12} + (\delta^{'}_1 + \nu^{'}_1 + \epsilon^{'}_1)A_{12} + (d+m)A_{12} \\ -g_2 A_{22} + r_{21}A_{21} + (\delta^{'}_2 + \nu^{'}_2 + \epsilon^{'}_2)A_{21} + (d+m)A_{21} \\ -r_{21}A_{21} + g_2 A_{22} + (\delta_2 + \nu_2 + \epsilon_2)A_{22} + (d+m)A_{22} \\ (\gamma^{'}_2 + \gamma_1 + d + m)D_1 \\ (\gamma^{'}_1 + \gamma_2 + d + m)D_2 \end{bmatrix}.$$

By linearizing the $\mathcal{F}$ and $\mathcal{V}$ at the DFE point, we have

$$F = \begin{bmatrix} F_{11} & F_{11} & 0 \\ F_{21} & F_{21} & 0 \\ F_{31} & F_{32} & 0 \end{bmatrix},$$

in which $F_{11} = \begin{bmatrix} \beta_{11}\hat{N}_{11} & 0 \\ 0 & \beta^{'}_{12}\hat{N}_{12} \end{bmatrix}$, $F_{21} = \begin{bmatrix} \beta^{'}_{21}\hat{N}_{21} & 0 \\ 0 & \beta_{22}\hat{N}_{22} \end{bmatrix}$,
$F_{31} = \begin{bmatrix} (\delta_1 + \nu_1) & 0 \\ 0 & (\delta^{'}_1 + \nu^{'}_1) \end{bmatrix}$ and $F_{32} = \begin{bmatrix} (\delta^{'}_2 + \nu^{'}_2) & 0 \\ 0 & (\delta_2 + \nu_2) \end{bmatrix}$.

Matrix V is a block diagonal matrix with three blocks in the form of $V = diag(V_1, V_2, V_3)$. Where

$$V_1 = \begin{bmatrix} g_1 + (\delta_1 + \nu_1 + \epsilon_1) + (d+m) & -r_{12} \\ -g_1 & r_{12} + (\delta^{'}_1 + \nu^{'}_1 + \epsilon^{'}_1) + (d+m) \end{bmatrix},$$

$$V_2 = \begin{bmatrix} r_{21} + (\delta^{'}_2 + \nu^{'}_2 + \epsilon^{'}_2) + (d+m) & -g_2 \\ -r_{21} & g_2 + (\delta_2 + \nu_2 + \epsilon_2) + (d+m) \end{bmatrix},$$

and

$$V_3 = \begin{bmatrix} \gamma^{'}_2 + \gamma_1 + d + m & 0 \\ 0 & \gamma^{'}_1 + \gamma_2 + d + m \end{bmatrix}.$$

Furthermore, V^{-1} is block diagonal and

$$FV^{-1} = \begin{bmatrix} F_{11}V_1^{-1} & F_{11}V_2^{-1} & 0_{2\times 2} \\ F_{21}V_1^{-1} & F_{21}V_2^{-1} & 0_{2\times 2} \\ F_{31}V_1^{-1} & F_{32}V_2^{-1} & 0_{2\times 2} \end{bmatrix}. \tag{4.3}$$

Theorem 4.2. We have:

$$\min\{c_i : i = 1, ..., 4\} \leq \mathcal{R}_0 \leq \max\{c_i : i = 1, ..., 4\}, \tag{4.4}$$

in which:

$$c_1 = \beta_{11}\hat{N}_{11}v_{11}^{-1}(1) + \beta_{12}^{'}\hat{N}_{12}v_{21}^{-1}(1) + \beta_{21}^{'}\hat{N}_{21}v_{11}^{-1}(1) + \beta_{22}\hat{N}_{22}v_{21}^{-1}(1)$$

$$c_2 = \beta_{11}\hat{N}_{11}v_{12}^{-1}(1) + \beta_{12}^{'}\hat{N}_{12}v_{22}^{-1}(1) + \beta_{21}^{'}\hat{N}_{21}v_{12}^{-1}(1) + \beta_{22}\hat{N}_{22}v_{22}^{-1}(1)$$

$$c_3 = \beta_{11}\hat{N}_{11}v_{11}^{-1}(2) + \beta_{12}^{'}\hat{N}_{12}v_{21}^{-1}(2) + \beta_{21}^{'}\hat{N}_{21}v_{11}^{-1}(2) + \beta_{22}\hat{N}_{22}v_{21}^{-1}(2)$$

$$c_4 = \beta_{11}\hat{N}_{11}v_{12}^{-1}(2) + \beta_{12}^{'}\hat{N}_{12}v_{22}^{-1}(2) + \beta_{21}^{'}\hat{N}_{21}v_{12}^{-1}(2) + \beta_{22}\hat{N}_{22}v_{22}^{-1}(2).$$

Proof . The matrix 4.3 is 6×6, and we can not compute the exact value of the spectral radius of it, i.e., $\mathcal{R}_0 = \rho(FV^{-1})$. The last two columns show that 0 is an eigne value with algebraic multiplicity two. The other eigenvalues are those of the following 4×4 matrix:

$$\begin{bmatrix} F_{11}V_1^{-1} & F_{11}V_2^{-1} \\ F_{21}V_1^{-1} & F_{21}V_2^{-1} \end{bmatrix}. \tag{4.5}$$

We can compute upper and lower bounds for this quantity. For this purpose, we use the Ferobenius theorem, which states that in a nonnegative matrix, the spectral radius lies between the minimum and maximum of all column sums (row sums) of the matrix, see [13]. The column sums of the nonnegative matrix FV^{-1} are c_i's, $i = 1, .., 4$. Hence, by using the Ferobenius theorem, we obtain 4.4 as bounds for the basic reproduction number of the system. □

Theorem 4.3. We have:

$$\min\{r_i : i = 1, ..., 4\} \leq \mathcal{R}_0 \leq \max\{r_i : i = 1, ..., 4\}, \tag{4.6}$$

in which:

$$\begin{aligned}
r_1 =& \beta_{11}\hat{N}_{11}v_{11}^{-1}(1) + \beta_{11}\hat{N}_{11}v_{12}^{-1}(1) + \beta_{11}\hat{N}_{11}v_{11}^{-1}(2) + \beta_{11}\hat{N}_{11}v_{12}^{-1}(2) \\
r_2 =& \beta_{12}^{'}\hat{N}_{12}v_{21}^{-1}(1) + \beta_{12}^{'}\hat{N}_{12}v_{22}^{-1}(1) + \beta_{12}^{'}\hat{N}_{12}v_{21}^{-1}(2) + \beta_{12}^{'}\hat{N}_{12}v_{22}^{-1}(2) \\
r_3 =& \beta_{21}^{'}\hat{N}_{21}v_{11}^{-1}(1) + \beta_{21}^{'}\hat{N}_{21}v_{12}^{-1}(1) + \beta_{21}^{'}\hat{N}_{21}v_{11}^{-1}(2) + \beta_{21}^{'}\hat{N}_{21}v_{12}^{-1}(2) \\
r_4 =& \beta_{22}\hat{N}_{22}v_{21}^{-1}(1) + \beta_{22}\hat{N}_{22}v_{22}^{-1}(1) + \beta_{22}\hat{N}_{22}v_{21}^{-1}(2) + \beta_{22}\hat{N}_{22}v_{22}^{-1}(2).
\end{aligned}$$

Proof . Now we use the column version of the Ferobenius theorem. Row sums of FV^{-1} are r_i's, $i = 1, ..., 4$. And by using the Ferobenius theorem, we obtain 4.6 as bounds for the basic reproduction number of the system. □

Theorem 4.4. Suppose that $\beta_{ii} = \beta_{ij}^{'} = \beta_i$ for all $i, j = 1, 2$ and $i \neq j$ and $\mathcal{R}_0^1 \leq \mathcal{R}_0^2$. Also, suppose that parameters δ, ν and ϵ are equivalent in two areas. Then $\mathcal{R}_0^1 \leq \mathcal{R}_0 \leq \mathcal{R}_0^2$.

Proof . We consider the following two blocks of matrix F

$$F_{11} = \begin{bmatrix} \beta_1\hat{N}_{11} & 0 \\ 0 & \beta_1\hat{N}_{12} \end{bmatrix} \text{ and } F_{21} = \begin{bmatrix} \beta_2\hat{N}_{21} & 0 \\ 0 & \beta_2\hat{N}_{22} \end{bmatrix}.$$

Therefore, for each $i, j = 1, 2$, $F_{ij} = F_{i1}$ and block matrix FV^{-1} is equivalent to $F_{i1}V_{jj}^{-1}$. Since F_{11} and F_{21} are diagonals, their multiplication by V_{11}^{-1} is equal to the multiplication of row l of V_{11}^{-1} by $\beta_l\hat{N}_{il}$ for $l = 1, 2$ and $i = 1, 2$. Thus, we consider the first column of $F_{i1}V_{11}^{-1}$ for $i = 1, 2$ and assume that $[\mathbb{1}^T F_{i1}V_{11}^{-1}]_1$ is the sum of the entries in the first column of $F_{i1}V_{11}^{-1}$ with condition $\mathbb{1}^T = (1, 1, \cdots, 1)$. So

$$[\mathbb{1}^T F_{i1}V_{11}^{-1}]_1 = \beta_1\hat{N}_{11}v_{11}^{-1}(1) + \beta_2\hat{N}_{12}v_{21}^{-1}(1) + \beta_1\hat{N}_{21}v_{11}^{-1}(1) + \beta_2\hat{N}_{22}v_{21}^{-1}(1). \tag{4.7}$$

We also have by assumption, $\mathcal{R}_0^1 \leq \mathcal{R}_0^2 \Rightarrow \beta_1(\hat{N}_{11} + \hat{N}_{12}) \leq \beta_2(\hat{N}_{22} + \hat{N}_{21})$. By applying the above inequality in equation 4.7, we have

$$\beta_1(\hat{N}_{11} + \hat{N}_{12})(v_{11}^{-1}(1) + v_{21}^{-1}(1)) \leq [\mathbb{1}^T F_{i1}V_{11}^{-1}]_1 \leq \beta_2(\hat{N}_{22} + \hat{N}_{21})(v_{11}^{-1}(1) + v_{21}^{-1}(1)).$$

Table 1: Description of Parameters of the models 3.1 and 3.2

Notation	Description of Parameter
S_{ii} $(i=1,2)$	Susceptible individuals residents of area i who are present in area i
S_{ij} $(i=1,2),\ i\neq j$	Susceptible individuals residents of area i who are present in area j
A_{ii} $(i=1,2)$	Asymptomatic individuals residents of area i who are present in area i
A_{ij} $(i=1,2),\ i\neq j$	Asymptomatic individuals residents of area i who are present in area j
D_1	Identified individuals residents in area 1 and area 2 who are present in area 1
D_2	Identified individuals residents in area 1 and area 2 who are present in area 2
R_{ii} $(i=1,2)$	Recovered individuals residents of area i who are present in area i
R_{ij} $(i=1,2),\ i\neq j$	Recovered individuals residents of area i who are present in area j
d	Natural death and birth rate
m	Infectious death rate
r_{ij} $(i=1,2)\ i\neq j$	Return rate from area i to area j
g_i $(i=1,2)$	Travel rate from area i to area j $(j\neq i)$
β_{ii} $(i=1,2)$	Transmission rate from susceptible to Asymptomatic individuals residents of area i who are present in area i
$\beta_{ij}^{'}$ $(i=1,2),\ i\neq j$	Transmission rate from susceptible to Asymptomatic individuals residents of area i who are present in area j
δ_{ii} $(i=1,2)$	The rate of identification of Infected individuals residents of area i who are present in area i by the government
$\delta_{ij}^{'}$ $(i=1,2),\ i\neq j$	The rate of identification of Infected individuals residents of area i who are present in area j by the government
ν_{ii} $(i=1,2)$	Referral rate of Infected individuals residents of area i who are present in area i to identification centers
$\nu_{ij}^{'}$ $(i=1,2),\ i\neq j$	Referral rate of Infected individuals residents of area i who are present in area j to identification centers
γ_i $(i=1,2)$	Transmission rate from Identification center i to recover individuals residents of area i who are present in area i
$\gamma_i^{'}$ $(i=1,2)$	Transmission rate from Identification center j $(j\neq i)$ to recover individuals residents of area i who are present in area j $(j\neq i)$ to identification centers
ϵ_i $(i=1,2)$	Transmission rate from Asymptomatic to recover individuals residents of area i who are present in area i
$\epsilon_i^{'}$ $(i=1,2)$	Transmission rate from Asymptomatic to recover individuals residents of area i who are present in area j $(j\neq i)$
ρ_i $(i=1,2)$	Transmission rate from recovered to susceptible individuals residents of area i who are present in area i
$\rho_i^{'}$ $(i=1,2)$	Transmission rate from recovered to susceptible individuals residents of area i who are present in area j $(j\neq i)$

Each diagonal block V_{ii} for $i=1,2$ of V has a column sum $(\delta+\nu+\epsilon)+(d+m)$ (assuming the parameters are equivalent in the two areas), i.e., $\mathbb{1}^T V=(\delta+\nu+\epsilon)+(d+m)\mathbb{1}^T$. Hence $\mathbb{1}^T V^{-1}=\frac{1}{(\delta+\nu+\epsilon)+(d+m)}\mathbb{1}^T$. Therefore,

$$\mathcal{R}_0^1=\frac{\beta_1 N_1^r}{(\delta+\nu+\epsilon)+(d+m)}\leq\ [\mathbb{1}^T F_{i1}V_{11}^{-1}]_1\leq\ \frac{\beta_2 N_2^r}{(\delta+\nu+\epsilon)+(d+m)}=\mathcal{R}_0^2.$$

By a similar argument, it can be shown that this inequality is true for every column of FV^{-1}. □

Theorem 4.5. If $\mathcal{R}_0<1$, then the DFE of (3.1) and (3.2) is locally asymptotically stable. If $\mathcal{R}_0>1$, then the DFE of (3.1) and (3.2) is unstable.

5 Discussion

The SAR epidemic model formulated in (3.1) and (3.2) describes the movement between the two areas. The mobility (travel) component of the system in equations (2.3) and (2.4) has a single stable equilibrium, as shown in (2.10) to (2.11), which represents the DFE equilibrium of model (3.1) and (3.2). If the system is at an equilibrium and area i is at the DFE (or endemic) equilibrium, or for $i=1,2$, then area $j\neq i$, is also at the DFE (or endemic) equilibrium.

With the beginning of a COVID-19 outbreak in one of the areas (or both areas), the number of infected in both areas can be determined as a function of time by numerically solving systems (3.1) and (3.2). The basic reproduction number $\mathcal{R}_0$ is derived. Our computations reveal the relationship between the basic reproduction number, a crucial quantity in epidemic control, and travel and return rates between areas. This suggests that it is essential to strengthen restrictions on passengers once we know infectious diseases have appeared.

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