Available online at http://sanad.iau.ir/journal/ijim/
Int. J. Industrial Mathematics (ISSN 2008-5621)
Vol.16, No.2, 2024 Article ID IJIM-1629, 17 pages
Research Article

Mathematical Modeling for Impact of Transportation in Covid-19, Report Case in Tehran, Iran

N. Eghbali* [1], M. Pourabd[2], S. A. Almasi [3], H. Taheri [1]

[1] Department of Mathematics, Faculty of Mathematical Sciences, University of Mohaghegh Ardabili, 56199-11367, Ardabil, Iran,

[2] Department of Mathematics, University of Mazandaran, 47415- 95447, Babolsar, Iran,

[3] Department of Civil Engineering, Imam Khomeini International University, Qazvin, Iran.

Submission Date: 2023/05/22, Revised Date: 2023/09/29, Date of Acceptance: 2024/08/28

Abstract

In this paper, we investigate a model for the COVID-19 coronavirus for Impact of transportation in Tehran. We introduce simple compartmental, Kermack-McKendrick-type epidemic models with homogeneously and heterogeneously-mixed populations, an endemic model for assessing the potential population-level impact of a hypothetical COVID-19 for Impact of transportation.

Keywords: Coronavirus pandemic globally, COVID-19 coronavirus, Mathematical modeling of infection disease, SEIRUS-model, Parameter identification, COVID-19 transmission dynamics in Iran, Two-patch mathematical model; Mobility data, Travel restrictions, social distancing, early diagnostic interventions.

* Corresponding author: Email: Eghbali287@gmail.com

1. Introduction

A novel coronavirus (nCoV), named as ‘‘2019-nCoV’’, is causing the deadliest pandemic in late 2019 and early 2020, defined as the coronavirus disease 2019 (COVID-19) by the World Health Organization (WHO). It is also known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The first cases occurred in early December, 2019, had been reported in China.

To date, many countries and regions have been locked-down and applied strict social distancing measures to stop the virus propagation. From a strategic and healthcare management perspective, the propagation pattern of the disease and the prediction of its spread over time is of great importance, to save lives and to minimize the social and economic consequences of the disease. Within the scientific community, the problem of interest has been studied in various communities including mathematical epidemiology [1], biological systems modeling [2-5], signal processing [6-8] and control engineering [9]. Epidemiological mathematical models have been developed to help policy makers to take the right decisions.

A first tentative mathematical model of this pandemic (see [10]), based on the Be-CoDiS model. For information of this model, see [11-15].

We explore the effectiveness of several additional strategies for the mitigation and suppression of Covid-19 spread in Iran, such as implementing Quarantine, social distancing and early diagnostic interventions.

The clinical spectrum of COVID-19 infection is broad, ranging from no symptoms to severe pneumonia. Approximately half of the COVID-19 patients (40–50) present in one study did not show any symptoms [16, 17]. Other patients developed fever, body aches, nausea, or diarrhea [18] typically 2 to 14 days after exposure to the virus. During the initial phase of COVID-19 in China (10–23 January 2020), only 14percent of total, to a community spread in China. Later, on 23 January, the Chinese government implemented a total lockdown of Wuhan City, which prevented further community spread [19-26].

In this study, we develop a model of COVID-19 transmission dynamics. We employed a mathematical model with five epidemiological compartments (susceptible, carried, infected, recovered, and unreported). It includes origin and destination data on various modes of transportation, including cars, buses and subways. The incubation and recovery rates were assumed to be the same in the two areas. Using the estimated model parameters, we carried out a patch-specific sensitivity analysis. Furthermore, we investigated the impacts of various intervention strategies on the patch-specific transmission dynamics, including limiting traveling between the two regions, implementing social distancing, and early diagnosis. This paper is organized as follows. In Section 2, we present a data description followed by a SEUR model with a mobility matrix and discuss the basic reproduction number. We have carried out parameter estimation and sensitivity analysis in Section 3. Numerical simulations under various mitigation scenarios have been investigated in Section 4. The paper concludes with a discussion of results and conclusions in Sections 5.

2. The Model Description

The model variables and parameter definitions represented are given as follows:

Variable Description

$S(t)$ Number of susceptible populations at time t

$E(t)$ Number of asymptomatic infectious at time t

$RI(t)$ Number of reported cases at time t i.e., symptomatic infectious with sever symptoms at time t

$UI(t)$ Number of unreported cases

$I(t) = RI(t) + UI(t)$

$R(t)$ Number of dead cases

Parameter Description

α Early detection and diagnostic rate per day.

γ Recavery rate.

B Transmission coefficient for the carrier subgroup.

p The proportion of undetected infectious individuals.

m_{12} The number of people traveling from patch 1 to patch 2 per day.

m_{21} The number of people traveling from patch 2 to patch 1 per day.

k Progression rate from S to I per day.

f Progression rate from E to I per day.

t_0 Time at which the epidemic started

$N_0 = N(t_0)$

$S_0 = S(t_0)$

$E_0 = E(t_0)$

$RI_0 = R(t_0)$

$UI_0 = U(t_0)$

We note that $R(t_0) = 0$.

The following assumptions would help in the derivation of the model:

1) There is no emigration from the total population and there is no immigration into the population. In fact, the current model is only suitable for countries or territories with a relevant number of people infected by COVID-19, where the local spread is very important.

2) Since there is no clear scientific evidence of the effect of the humidity and the temperature on SARS-CoV-2, we have not included these two factors in our model.

A diagram of an epidemic Model for COvid-19 is considered as follows of our model and will be useful in the formulation of model equations.

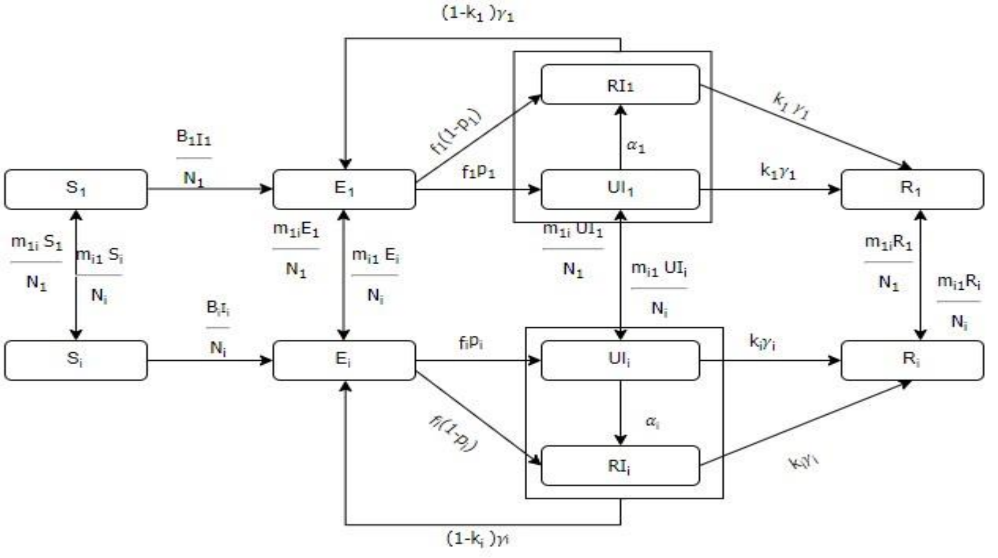

Figure 1: Model of Covid-19

Based on assumptions and definitions of variables and parameters mentioned above, the following system of ordinary equations is obtained.

The mobility matrix is defined by $M = (m_{ij})_{2\times 2}$, as proposed in [4, 15]. The mobility matrix captures the movement of individuals between patch 1 and patch 2 and we set m_{ij} to be the number of people traveling from a patch i to a patch j per unit time (day) and m_{ji} to be the number of people traveling from a patch j to a patch i per unit time (day). In this study, we assumed that the number of traveling between two patches is symmetric $(m_{ij} = m_{ji})$. It is also assumed that the traveling occurs instantaneously, so no infection is transmitted during the traveling process. It should be noted that the number of people quarantined per day is not available in any of the regions. Therefore, we do not consider the amount of quarantined people in this system of equations. It is also assumed that the person will go to the hospital after the contamination, from which as people reported infected are named as indicated by RU and a group not reporting their illness are indicated by UI, this group may self-quarantine at home or with a coefficient of m migrate to another area. In any case, it is assumed that he will migrate after recovery.

In this proposed model, people are susceptible to disease after recovery with a factor of $(1-k)\gamma$.

$$S'_i(t) = -\frac{B_i I_i}{N_i} S_i - m_{ij}\frac{S_i}{N_i} + m_{ji}\frac{S_j}{N_j}, \qquad (2.1)$$
$$E'_i(t) = \frac{B_i I_i}{N_i} S_i - f_i E_i + m_{ji}\frac{E_j}{N_j} - m_{ij}\frac{E_i}{N_i} + (1-k_i)\gamma_i I_i,$$
$$UI'_i(t) = f_i p_i E_i - \alpha_i UI_i - \gamma_i UI_i + m_{ji}\frac{UI_j}{N_j} - m_{ij}\frac{UI_i}{N_i},$$
$$RI'_i(t) = f_i(1-p_i)E_i + \alpha_i UI_i - \gamma_i RI_i,$$

$$R'_i(t) = k_i\gamma_i UI_i + k_i\gamma_i RI_i + m_{ji}\frac{R_j}{N_j} - m_{ij}\frac{R_i}{N_i},$$

together with $N = S + E + RI + UI + R$.

We consider these equations with initial conditions $S(t_0), E(t_0), UI(t_0)$, $RI(t_0)$, $R(t_0)$ and $N(t_0) = 0$.

3. Analysis of the Model

The equilibrium of system (2.1) is obtained by setting the right-hand side of the equations to be equal to zero. The disease-free equilibrium E_0 is given by

$$(\frac{m_{ji}S_jN_i}{m_{ij}N_j}, \frac{m_{ji}E_jN_i}{(f_iN_i + m_{ij})N_j}, \frac{(f_ip_iE_iN_j + m_{ji}UI_j)N_i}{(\alpha_iN_i + \gamma_iN_i + mij)N_j}, \frac{f_i(1-p_i)E_i + \alpha_iUI_i}{\gamma_i}, \frac{(k_i\gamma_iN_jI_i + m_{ji}R_j)N_i}{m_{ij}N_j}).$$

Since the basic reproduction number is obtained by evaluating at the disease equilibrium under the assumption of the initial stage (i.e., $S_i(t) = N_i(t)$), so we have the following theorem.

Theorem 3.1 There is a unique disease-free equilibrium E_0 for the model represented by system (2.1).

Proof. This theorem is proved by substituting E_0 into system (2.1). The results show that all the derivatives are equal to zero.

To establish the linear stability of E_0, we use the next generation operator approach on system (2.1) to compute the basic reproduction number R_0. This is determined using the approach by Van den Driessche and Watmough [16]. For the notation of the matrices F and V, we have

$$\begin{bmatrix} f_1 + \frac{m_{12}}{N_1} & -(1-k_1)\gamma_1 & -m_{21}N_2 & 0 \\ -f_1 & \gamma_1 + \frac{m_{12}}{N_1} & 0 & -\frac{m_{21}}{N_2} \\ -\frac{m_{12}}{N_1} & 0 & f_2 + \frac{m_{21}}{N_2} & -(1-k_2)\gamma_2 \\ 0 & -\frac{m_{12}}{N_1} & -f_2 & \gamma_2 + \frac{m_{21}}{N_2} \end{bmatrix}$$

Evaluating F at the disease-free equilibrium, we obtain

$$\begin{bmatrix} 0 & \beta_1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

and, thus

$$\mathrm{F}V^{-1} = \frac{1}{|V|}\begin{bmatrix} \beta_1\nu_{12} & \beta_1\nu_{22} & 0 & \beta_1\nu_{42} \\ 0 & 0 & 0 & 0 \\ 0 & \beta_2\nu_{24} & \beta_2\nu_{34} & \beta_2\nu_{44} \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The eigenvalues for the matrix FV^{-1} are given by

$$\mathrm{F}V^{-1} = \begin{vmatrix} x - \frac{\beta_1 v_{12}}{|V|} & -\frac{\beta_1 v_{22}}{|V|} & 0 & -\frac{\beta_1 v_{42}}{|V|} \\ 0 & x & 0 & 0 \\ 0 & -\frac{\beta_2 v_{24}}{|V|} & x - \frac{\beta_2 v_{34}}{|V|} & -\frac{\beta_2 v_{44}}{|V|} \\ 0 & 0 & 0 & x \end{vmatrix}$$

So

$$x = 0$$

$$x = \frac{\beta_1 v_{12}}{|V|}$$

$$x = \frac{\beta_2 v_{34}}{|V|}.$$

The spectral radius is given by

$$r(FV^{-1}) = \frac{\beta_1 v_{12}}{|V|}$$

or

$$r(FV^{-1}) = \frac{\beta_2 v_{34}}{|V|}$$

which gives the effective reproduction number as

$$R_e = \frac{\beta_1 v_{12}}{|V|}$$

or

$$R_e = \frac{\beta_2 v_{34}}{|V|}.$$

4. Local Stability of the Disease-Free Equilibrium

The Jacobian matrix for the system is given by

$$\mathrm{J}= \begin{bmatrix} -B_i - m' + m'' & 0 & 0 & 0 & 0 \\ B_i & -f_i + m'' - m' & (1-k_i)\gamma_i & (1-k_i)\gamma_i & 0 \\ 0 & f_i p_i & -\alpha_i - \gamma_i + m'' - m' & 0 & 0 \\ 0 & f_i(1-p_i) & \alpha_i & -\gamma_i & 0 \\ 0 & 0 & k_i\gamma_i & k_i\gamma_i & m'' - m' \end{bmatrix}$$

which $m' = \frac{m_{ij}}{N_i}$ and $m'' = \frac{m_{ji}}{N_j}$.

The disease-free equilibrium point E_0 is discussed by examining the above Jacobian matrix at the steady point E_0. Now, at the disease-free equilibrium, the Jacobian matrix is given by

$$J_{E_0}= \begin{bmatrix} -B_i - m' + m'' & 0 & 0 & 0 & 0 \\ B_i & -f_i + m'' - m' & (1-k_i)\gamma_i & (1-k_i)\gamma_i & 0 \\ 0 & f_i p_i & -\gamma_i + m'' - m' & 0 & 0 \\ 0 & f_i(1-p_i) & 0 & -\gamma_i & 0 \\ 0 & 0 & k_i\gamma_i & k_i\gamma_i & m'' - m' \end{bmatrix}$$

For stability of the disease-free equilibrium, it is required that the $trace(J_{E_0}) < 0$ and the $det(J_{E_0}) > 0$. Thus, from the Jacobian matrix, it is clearly seen that

$$trace(J_{E_0}) < 0.$$

The determinant of the Jacobian matrix is also given by

$$det(J_{E_0}) = (B_i + m' - m'')(f_i + m' - m'')(\gamma_i + m' - m'')^2 > 0.$$

Therefore, the disease-free equilibrium is locally asymptotically stable. This is established by the fact that the $trace(J_{E_0}) < 0$ and the $det(J_{E_0}) > 0$.

5. Numerical Simulation

We illustrate the analytical results of the model by carrying out numerical simulation of the models using a set of estimated parameter values obtained from literature. The system is simulated using ODE solvers coded in MATLAB programming language. Simulation of the covid-19 under treatment intervention and vaccination interventions combined is carried out to investigate the impact of the key parameters on the spread of Covid-19 and how their influence can be controlled. The population of Tehran by region to be used for S values in the equation is as follows:

Table 1: population of Tehran by region

$Area$	1	2	3	4	5	6	7
$Population$	493889	692579	330004	917261	856565	250753	312002
$Area$	8	9	10	11	12	13	14
$Population$	425044	174115	326885	308176	240909	253054	489101
$Area$	15	16	17	18	19	20	21
$Population$	659468	267678	278254	419249	255533	367600	186319
$Area$	22						
$Population$	175398						

The total population of Tehran province is 8,679,936.

According to the graph 2, the largest population is present in regions 4 and 5.

The available data is related to the number of trips of the population from regions 4 and 5 to other regions. By referring to the detailed map of Tehran regions, it can be seen that regions 4 and 5 are far from each other.

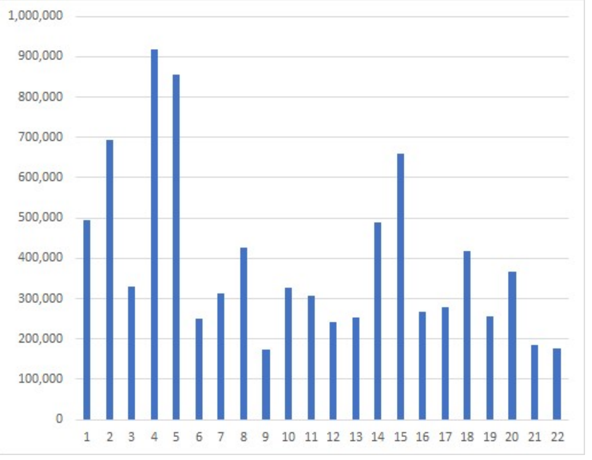

Figure 2: Population by region

Table 2: The number of people traveling from high-risk areas 4 and 5 to other areas

Areas	*first day*	*secand day*	*third da*	*forth da*	*fifth day*	*sixth da*	*seventh d*
1	325478	342751	327941	329741	332457	172541	62471
2	482147	491547	473214	482415	471541	215471	85142
3	215471	225471	217458	208471	211451	121247	45127
4	75412	82413	77415	71452	76541	25847	13541
5	62458	69741	65214	68941	58741	28641	14521
6	550145	621547	590514	541258	587146	261471	57961
7	201451	220145	215412	216321	219541	121451	25641
8	295214	310412	305412	296324	291654	155412	45214
9	125471	131541	135412	125471	128791	65841	12541
10	221458	225412	215474	215641	203415	171451	26541
11	210154	215412	206541	209741	208471	126547	21654
12	156471	165487	162458	148751	156541	63251	8215
13	154154	175416	156147	148745	149871	73651	10584
14	352145	368541	354125	342157	351547	141578	45714
15	442514	475142	421547	429847	445821	154781	65412
16	179841	185461	181457	178415	171541	62541	12654
17	187541	205414	188654	187415	191451	25471	6541
18	251474	292874	277451	266451	282541	71541	25654
19	178451	182541	162451	175415	136415	45871	18791
20	245874	255874	251457	226541	219541	62417	22541
21	120245	125478	123458	118954	119654	42365	11547
22	120541	123654	118541	119654	112961	54126	16594

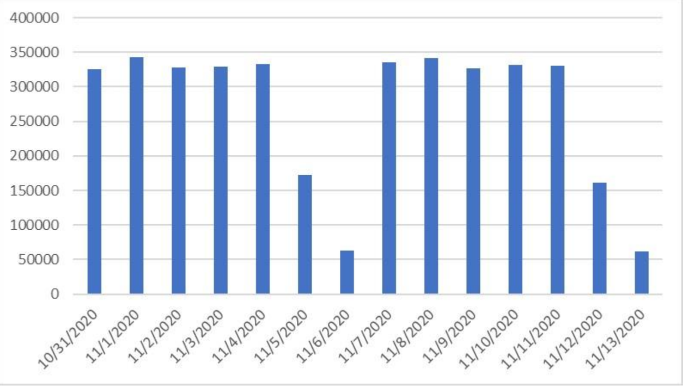

Figure 3: Migration from high-risk zones 4 and 5 to zone 1 per day

As you can see in the diagram of table 4, on non-holiday days, the average number of people who commute between these regions 4 and 5 and region 1 is very close to each other, so the average value can be used to estimate the number of infected cases and this issue can be extended to the rest of the region as well. In table 3, the average values for m_{ij} can be seen.

Table 3: Continued table

Areas	8th day	9th day	10th day	11th day	12th day	13th day	14th day
1	335478	341521	326541	331547	329874	161457	61254
2	475412	495784	471654	479851	473651	206541	76321
3	215641	224514	218412	2105414	212654	115472	41521
4	74512	84512	79841	73651	75621	26351	12541
5	63514	68754	63254	67841	59841	27854	13254
6	562154	635214	583254	574516	596541	226541	52147
7	205414	221054	214547	215474	221547	120365	26541
8	298541	312541	309841	299847	285414	142351	41236
9	127854	129651	132541	124987	127841	63514	16541
10	225414	228541	216541	210654	209541	155624	23651
11	206541	211654	202541	207841	210361	121654	19874
12	152641	161547	165841	152147	152457	58623	7846
13	158741	159874	152641	149741	151247	68751	11547
14	346581	262451	351247	345871	349874	124154	41265
15	458741	462541	459412	445871	443251	145214	61541
16	180321	189541	182547	186251	175412	57981	11651
17	189541	198254	189541	185412	192541	26584	7541
18	255641	271541	278415	265412	278951	75412	27261
19	181451	183541	178541	171541	163251	49874	25412
20	249874	254874	248751	229841	225461	58951	18741
21	116541	122365	121457	115241	119654	39541	12541
22	116541	119841	121541	117451	119651	51241	15471

Table 4: The average values of the number of trips m_{ij} on non-holiday days from areas 4 and 5 to other areas of Tehran

$Area$	1	2	3	6	7
$The\ average\ values\ of\ the\ number\ of\ tr$	332332.9	479721.6	216008.4	584228.9	215090.6
$Area$	8	9	10	11	12
$The\ average\ values\ of\ the\ number\ of\ tr$	300520	128956	217209.1	208925.7	157434.1
$Area$	13	14	15	16	17
$The\ average\ values\ of\ the\ number\ of\ tr$	155657.7	342453.9	448468.7	181078.7	191576.4
$Area$	18	19	20	21	22
$The\ average\ values\ of\ the\ number\ of\ tr$	272075.1	171359.8	240808.8	120304.7	119037.6

Here according to the studies done [13] suppose that $\gamma_i = \frac{1}{14}$ and $f_i = \frac{1}{7}$. It is also assumed that γ_i and f_i are equal for $i = 1,2,\ldots,22$.

We make the same assumption for the rest of the parameters. The value of p_i can be also be used from [23]. The value of k_i is also used in [24], which can be estimated using the available data. We can estimate the B_i value of the transfer rate.

To estimate the parameters using this model, we need the number of infected cases in each region, see Table 5.

Table 5: The number of reported infected people under treatment in Tehran city

$first\ day$	$second\ day$	$third\ day$	$forth\ day$	$fifth\ day$
2020/10/31	2020/11/1	2020/11/2	2020/11/3	2020/11/4
325	332	331	336	337
$sixth\ day$	$seventh\ day$	$eighth\ day$	$nineth\ day$	$tenth\ day$
2020/11/5	2020/11/6	2020/11/7	2020/11/8	2020/11/9
336	341	342	345	349
$eleventh\ day$	$twelveth\ day$	$thierteenth\ da$	$fourteenth\ day$	
2020/11/10	2020/11/11	2020/11/12	2020/11/13	
354	361	359	364	

The number of diseases for Tehran province is in table 4 and can be modified by a single model. So, we can write this model as in the bellowing form. Also, we estimate parameters in this model.

$$S'(t) = -\frac{BI}{N}S, \qquad (5.1)$$
$$E'(t) = \frac{BI}{N}S - fE + (1-k)\gamma I,$$
$$UI'(t) = fpE - \gamma UI,$$
$$RI'(t) = f(1-p)E - \gamma RI,$$
$$R(t) = k\gamma UI + k\gamma RI.$$

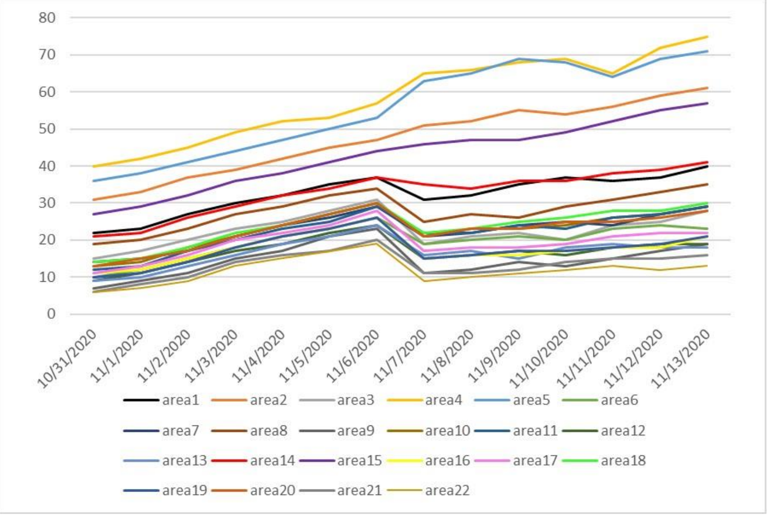

Figure 4: The number of infected cases in Tehran by region from 2020/10/31 to 2020/11/13

To estimate the parameters of the system of equations (5.1) using the data in table 4, we use the least squares method. It is necessary to mention that the total number of infected cases reported in 22 regions in Tehran is more than hospitalized cases, as shown in figure 5:

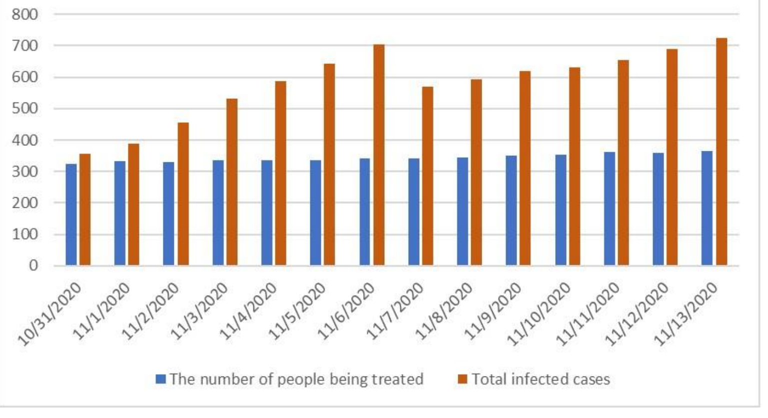

Figure 5: Comparison of the number of people under treatment and infected cases in Tehran since 2020/10/31 to 2020/11/13

In this paper, it is very important to pay attention to the difference between dates of figure 5. Also, the type of quarantine and the number of people in quarantine are not available, so it is not possible to be sure that all infected people reported have quarantined themselves at home, but we are sure that the hospitalized people are in hospital quarantine and there is no possibility of spreading the disease from them to others. In order to better estimate the parameters, according to the modeling of the problem with the system of equations (2.1) with the assumption that the unreported people have the possibility of spreading the disease to others, we will consider the reported people who are not hospitalized as unreported people.

Using the data of table 4, the parameters of the equations (5.1) will be as described in table 6.

Table 6: Parameters of differential equations (5.1) (single regional model of Tehran province)

$parameter\quad name$	γ	f	$B(Estimated)$	$p(Estimated)$	$k(Estimated)$
$value$	$\frac{1}{14}$	$\frac{1}{7}$	0.241	0.9	0.09

Using the estimated parameters, it can be seen that the reported infected cases are very close to the estimated dates obtained from the system of equations of Tehran's single-zone model for polluted cases.

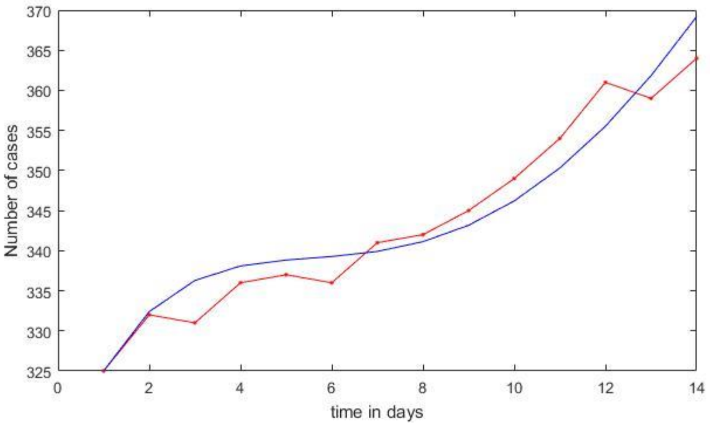

Figure 6: Comparison of the reported infected cases of Tehran city and the estimated infected cases from the equation (5.1)

Note that, the initial values are considered as follows, it should be noted that E_0 is the number of employed people in Tehran, which according to the reports of the Iranian Statistics Center, the 0.3 of the population of Tehran are employed. Also, the number of unreported infected people is twice the number of reported infected people.

$$S_0 = 9423703,$$
$$E_0 = 0.3S_0,$$
$$RI_0 = 325,$$
$$UI_0 = 700.$$

The number of infected cases in area 4 and 5 can be seen in Table 7.

Table 7: The number of infected cases in area 4 and 5 of 2020/10/31 to 2020/11/13

	$first\quad day$	$second\quad day$	$third\quad day$	$forth\quad day$	$fifth\quad day$
$area\quad 4$	40	42	45	49	52
$area\quad 5$	36	38	41	44	47
	$sixth\quad day$	$seventh\quad day$	$eighth\quad day$	$nineth\quad day$	$tenth\quad day$
$area\quad 4$	53	57	65	66	68

$area \quad 5$	50	53	63	65	69
	$eleventh \quad day$	$twelveth \quad day$	$thierteenth \quad day$	$fourteenth \quad day$	
$area \quad 4$	69	65	72	75	
$area \quad 5$	68	64	69	71	
sum	76	80	86	93	99
sum	103	110	128	131	137
sum	137	129	141	146	

Infected cases of area 1 and 2 of 2020/10/31 to 2020/11/13 are as following table 8:

Table 8: Infected cases of area 1 and 2 of 2020/10/31 to 2020/11/13

	$first \quad day$	$second \quad day$	$third \quad day$	$forth \quad day$	$fifth \quad day$
$area \quad 1$	22	23	27	30	32
$area \quad 2$	31	33	37	39	42
	$sixth \quad day$	$seventh \quad day$	$eighth \quad day$	$ninth \quad day$	$tenth \quad day$
$area \quad 1$	35	37	31	32	35
$area \quad 2$	45	47	51	52	55
	$eleventh \quad day$	$twelfth \quad day$	$thirteenth \quad day$	$fortheenth \quad day$	
$area \quad 1$	37	36	37	40	
$area \quad 2$	54	56	59	61	

Using the parameters of table 5, we solve the system of equations (2.1) for regions 4 and 5 to region 1 and vice versa. The only remaining and unknown parameter in this system is parameter α, which we estimate using the least squares method and data from tables 6, 7 and table 3. As expected, this value is very small and has a value equal to $\alpha = 71e - 8$.

The results for the estimated contaminated cases and the actual data are shown in Figure 7.

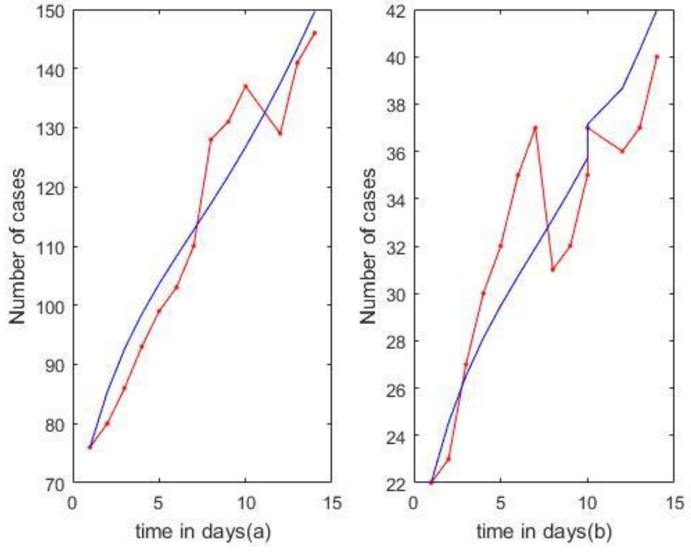

Figure 7: a) The blue line is the estimated data for regions 4 and 5 and the red line is the actual data b) The blue line is the estimated data for region 1 and the red line is the actual data

Also, using these parameters, the system has been solved for region 2, and the results can be seen in Figure 8.

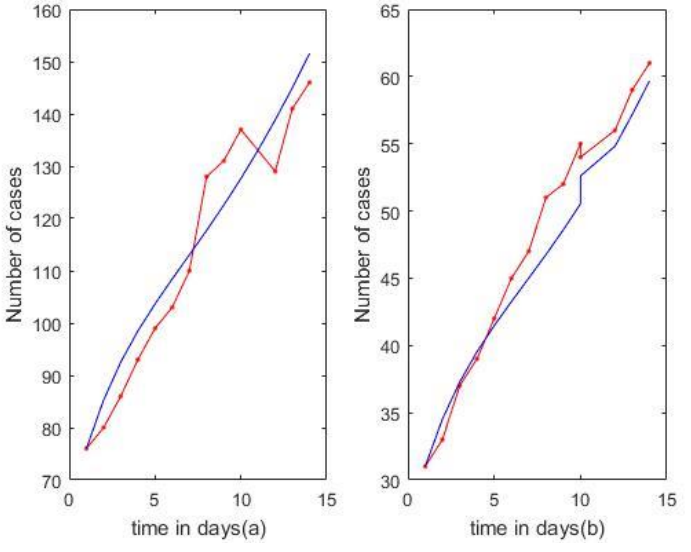

Figure 8: a) The blue line is the estimated infected cases of regions 4 and 5 and the red line is the actual infected cases b) The blue line is the estimation of infected cases of region 2 and the red line is the actual infected cases

This work can be done for all regions and the impact of traveling from regions 4 and 5 to other regions on Corona days should be investigated.

References

[1] Brauer F. and Castillo-Chavez C. (2012), "Mathematical Models in Population Biology and Epidemiology", Springer.

[2] Chen T. M., Rui J., Wang Q. P., Zhao Z. Y., Cui J. A. and Yin L. (2020), "A mathematical model for simulating the phase-based transmissibility of a novel coronavirus", Infectious Diseases of Poverty, Vol. 9 No. 1, pp. 1-8, Doi: org/10.1186/s40249-020-00640-3.

[3] Haefner J. (2005), "Modeling Biological Systems: Principles and Applications", Springer.

[4] Hyman J. M. and Laforce T. (2003), "Modeling the Spread of Influenza Among Cities, In Biomathematical Modeling Applications in Homeland Security", SIAM: Philadelphia, PA, USA.

[5] Vries G. de, Hillen T., Lewis M., Schõnfisch B. and Muller J. (2006), "A Course in Mathematical Biology: Quantitative Modeling with Mathematical and Computational Methods", ser. Monographs on Mathematical Modeling and Computation, Society for Industrial and Applied Mathematics.

[6] Wu J. T., Leung K. and Leung G. M. (2020), "Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study", The Lancet, Vol. 395 No. 10225, pp. 689-697, Doi: org/10.1016/S0140-6736(20)30260-9.

[7] Yang W., Karspeck A. and Shaman J. (2014), "Comparison of filtering methods for the modeling and retrospective forecasting of influenza epidemics", PLOS Computational Biology, Vol. 10 No. 4, Doi: org/10.1371/journal.pcbi.1003583.

[8] Worldometer website: https://www.worldometers.info/coronavirus/country/iran/

[9] Azar A. (2020), "Control Applications for Biomedical Engineering Systems", Elsevier Science.

[10] Ivorra B. and Ramos A. M. (2020), "Application of the Be-CoDis mathematical model to forecast the international spread of the 2019 Wuhan coronavirus outbreak", Technical Report, 9 February 2020, pp. 1–13, DOI: 10.13140/RG.2.2.31460.94081.

[11] Ivorra B. and Ramos A. M. (2020), "Validation of the forecasts for the international spread of the oronavirus disease 2019 (COVID-19) done with the Be-CoDis mathematical model", Technical Report, 28 February 2020, pp. 1–7, DOI: 10.13140/RG.2.2.34877.00485.

[12] Ivorra B., Ramos A. M. and Ngom D. (2015), "Be-CoDiS: A mathematical model to predict the risk of human diseases spread between countries-validation and application to the 2014-2015 Ebola Virus Disease epidemic", Bulletin of Mathematical Biology, Vol. 77 No. 9, (pp. 1668–1704, DOI: 10.1007/s11538-015-0100-x.

[13] Kim B. N., Kim E., Lee S. and Oh C. (2020), "Mathematical Model of COVID-19 Transmission Dynamics in South Korea: The Impacts of Travel Restrictions", Social Distancing, and Early Detection, Processes, Vol. 8, DOI: 10.3390/pr8101304.

[14] Lancaster P. (1969), "Theory of Matrices", Academic Press, New York, NY, USA.

[15] Lee J. M., Choi D., Cho G. and Kim Y. (2012), "The effect of public health interventions on the spread of influenza among cities", J. Theor. Biol., Vol. 293, pp. 131–142.

[16] Van den Driessche, P. and Watmough, J. (2002), "Reproduction numbers and sub-threshold endemic equilibrium for compartmental models of disease transmission", Math. Biosci., Vol. 180, pp. 29-48.

[17] Verity R., Okell L. C., Dorigatti I., Winskill P., Whittaker C., Imai N., Cuomo-Dannenburg G., Thompson H., Walker P. Fu, H. et al. (2020), "Estimates of the severity of COVID-19 disease", medRxiv.

[18] Center for Disease Control (CDC). Available online: https://www.cdc.gov/coronavirus/2019-ncov/ symptoms-testing/symptoms.html (accessed on 27 May 2020).

[19] Li R., Pei S., Chen B., Song Y., Zhang T., Yang W. and Shaman J. (2020), "Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2) ", Science, Vol. 6490, pp. 489–493.

[20] Lin Q., Zhao S., Gao D., Lou Y., Yang S., Musa S. S., ... and He D. (2020), "A conceptual model for the outbreak of Coronavirus disease 2019 (COVID-19) in Wuhan, China with individual reaction and governmental action", International Journal of Infectious Diseases, Vol. 93, pp. 211-216, Doi: org/10.1016/j.ijid.2020.02.058.

[21] Liu Z., Magal P., Seydi O. and Webb G. (2020), "Understanding unreported cases in the COVID-19 epidemic outbreak in Wuhan, China, and the importance of major public health interventions", Biology, Vol. 9 No. 3, Doi: org/10.3390/biology9030050.

[22] Rohatgi V. K. and Saleh A. M. (2015), "An Introduction to Probability and Statistics", John Wiley and Sons.

[23] Taheri H., Eghbali N., Pourabd M. and Zhu H. (2022), "Assessment of the Mathematical Model for Investigation Covid-19 Peak as a Global Epidemic in Iran", Mathematical Analysis & Convex Optimization, Vol.3 No.2, pp. 129-142.

[24] Taheri H., Eghbali N. and Pourabd M. (2025), "The Investigation of Variant Vaccination Models in Iran", Int. J. Nonlinear Anal. Appl., Vol. 16 No. 2, pp. 177–191, http://dx.doi.org/10.22075/ijnaa.2023.31446.4631.

[25] Tang B., Wang X., Li Q., Bragazzi N. L., Tang S., Xiao Y. and Wu J. (2020), "Estimation of the transmission risk of 2019-nCov and its implication for public health interventions", J. Clin. Med., Vol. 9 No. 2, Doi: 10.3390/jcm9020462.

[26] Tang B., Bragazzi N. L., Li Q., Tang S., Xiao Y. and Wu J. (2020), "An updated estimation of the risk of transmission of the novel coronavirus (2019-nCov) ", Infectious Disease Modelling, Vol. 5 pp. 248- 255, Doi: org/10.1016/j.idm.2020.02.001.