ASSESSMENT OF THE MATHEMATICAL MODEL FOR INVESTIGATING COVID-19 PEAK AS A GLOBAL EPIDEMIC IN IRAN

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Abstract. Abstract. In this paper, we investigate the COVID-19 pandemic in Iran from a mathematical modeling perspective. By improving the well-known susceptible infected recovered (SIR) family of compartmental models and adding unreported cases obtain a local model for Iran. Since we only want infected cases, we have refused to add other classes which there are can be. We estimate the infected case by using the reported data of the first period of the outbreak and will apply the results to data of the provinces of Ardabil and Guilan which were available to us as well as published data from Iran. We show that, if some of the indexes are constant, the future infectious reported cases are predictable. Also, we show a good agreement between the reported data and the estimations given by the proposed model. We further demonstrate the importance of choosing this proposed model used to by finding the basic reproductive number. Also, we will estimate the probability distribution for the death rate. Our study can help the decision-making of public health.

1. Introduction

A novel coronavirus (nCoV), has been causing the deadliest pandemic since late 2019 and till now, 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 Wuhan, 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 [2], biological systems modeling [4, 13], signal processing [15] and control engineering [1]. Epidemiological mathematical models have been developed to help policy makers to take the right decisions.

There are five major types of models in literatures that can help us understand the transmissibility of the SARS-CoV-2 from its natural reservoirs to humans. In references [3, 5–8],

authors gave following models for Covid -19. But, finally by using reference [8], we believe that, the SIR model is the best mathematical model for prediction of pandemic Covid-19.

A first tentative mathematical model of this pandemic (see [5]), based on the Be-CoDiS model. For information of this model, see [6, 7].

Given the limitations of data access, we examine this model. Our objective is to develop a mathematical model, which recovers from data of reported cases, the number of unreported cases for the COVID-19 epidemic in Iran. For this epidemic, a modeling approach has been developed in [11], which did not consider unreported cases and did not consider in Iran. The purpose of the model is to predict forward in time the future number of cases in a time-line of the epidemic from early reported case data. Here, our goal is to apply this analysis for the COVID-19 epidemics in Iran and two provinces Ardabil and Guilan. In an early phase of the epidemic, the reported case data grows exponentially, which corresponds to a constant transmission rate. We assume that government measures and public awareness cause this early constant transmission rate to change to a time dependent exponentially decreasing rate. We identify the time dependent exponentially decreasing transmission rate from reported case data and project forward the time-line of the epidemic course.

Our model incorporates the following essential ingredients of COVID-19 epidemics: (1) the number of asymptomatic infectious individuals (with very mild or no symptoms), (2) the number of symptomatic reported infectious individuals (with severe symptoms) and (3) the number of symptomatic unreported infectious individuals (with mild symptoms).

We use data from worldometer website; https://www.worldometers.info/coronavirus/; Ardabil University of Medical Sciences and Guilan University of Medical Sciences.

2. The Model Description

Recently the researchers identified the behavioral effects of pandemic threat of Covid-19 which has not been described by any of the existing analytical models [9]. In this scenario an infected individual instead of being removed(recovery) contributes to the infection spreading upon the reinfection attempt. In this paper we used a new generalized SIR model, Susceptible-Infected(Reported and Unreported)- Susceptible- Reinfected (SIRUSI)to describe and predict the epidemics of Covid-19 in Iran and two provinces Ardabil and Guilan, . By this model we can find the daily number of unreported cases and we can estimate the number of symptomatic unreported infectious individuals too. The model variables and parameters is given by Table.1

We make the following assumptions for our modeling:
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 will not include these two factors in our model.
A diagram of an epidemic Model (Fig.1) for COvid-19 is considered as follows which it will be useful in the formulation of system of equations.

Table 1. The model variables and parameters description

| parameters and variables	Description
$S(t)$	Number of susceptible populations at time t
$I(t)$	Number of asymptomatic infectious at time t
$R(t)$	Number of reported infected cases at time t
$U(t)$	Number of unreported infected cases
t_0	Time at which the epidemic started
$S_0 = S(t_0)$	Number of susceptible at time t_0
$I_0 = I(t_0)$	Number of asymptomatic infectious at time t_0
$U_0 = U(t_0)$	Number of unreported cases at time t_0
τ	Contact transmission rate
$1/\nu$	Average time during which asymptomatic infectious are asymptomatic
$\nu_1 = f\nu$	Rate at which asymptomatic infectious become reported symptomatic
$\nu_2 = (1-f)\nu$	Rate at which asymptomatic infectious become unreported symptomatic
$1/\mu$	Average time symptomatic infectious have symptoms
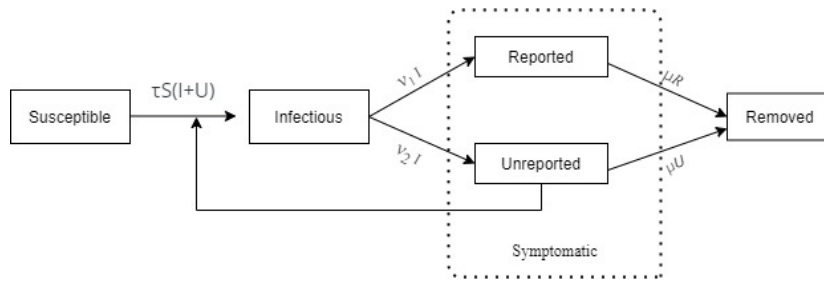
Figure 1. Modeling diagram for the transmission of Covid-19

On the basis of above stated assumptions and the flow diagram of COVID-19 showed in Figure.1, we formulated an dynamical system consisting of four first order differential equations shown as below:

$$(2.1) \qquad S'(t) = -\tau S(t)[I(t) + U(t)],$$

$$I'(t) = \tau S(t)[I(t) + U(t)] - \nu I(t),$$
$$R'(t) = \nu_1 I(t) - \mu R(t),$$
$$U'(t) = \nu_2 I(t) - \mu U(t).$$

Where the parameter f, the fraction of asymptomatic infections that become reported symptomatic infectious, this parameter plays an important role in our study is described in the next section. In short, we compare output data by solving the model and real data. Then we evaluate f such that this difference between real data and output data of the system should be minimal.

We consider these equations with initial conditions $S(t_0), I(t_0)$, $U(t_0)$ and $R(t_0) = 0$, Also we note that $R(t_0) = 0$. It should be noted that by due to the nature of this disease hardly anyone was immune at the beginning of the epidemic. It should be noted that by due to the nature of this disease hardly anyone was immune at the beginning of the epidemic, therefore, we assume that everyone in the understudy population is susceptible to infection.

3. Impact of unreported cases

In this section, we first estimate the starting time of the pandemic in Iran. For this study, we will use the data of Iran in the first 73 days of the registration of Covid-19 cases from 2/20/2020 to 5/2/2020.

The model cumulative number of Covid-19 cases at time t obtained by the following equation

$$(3.1) \qquad CR(t) = v_1 \int_{t_0}^{t} I(s)ds.$$

From the worldometer reports [16], we have obtained the reported cases per day. The cumulative data is depicted in Figure 2.
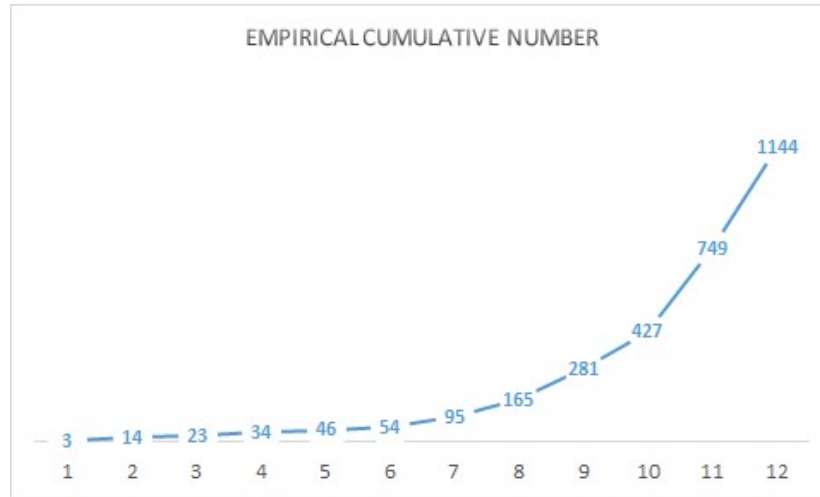

Figure 2. Empirical cumulative number of reported cases of Iran

Given the figure 2. the observed pattern of cumulative data appears to correspond to the exponential function behavior [3]. Therefore, we assume that $CR(t)$ as follows

$$(3.2) \qquad CR(t) = \chi_1 exp(\chi_2 t) - \chi_3.$$

We will evaluate χ_1, χ_2 and χ_3 by reported data cases in Iran. Note that time $t = 1$ will correspond to 20 February 2020. First we estimate the value of χ_2 numerically and then use a least square method and data to evaluate χ_1 and χ_3.

$$\chi_1 = 3.7831, \chi_2 = 0.4768, \chi_3 = 0.2344$$

As shown In the figure 3. by placing the obtained parameters χ_1, χ_2 and χ_3 in equation (3.2), the dots corresponds to $t \rightarrow CR(t)$ are fitted from the confirmed infected cases correspond on real data.
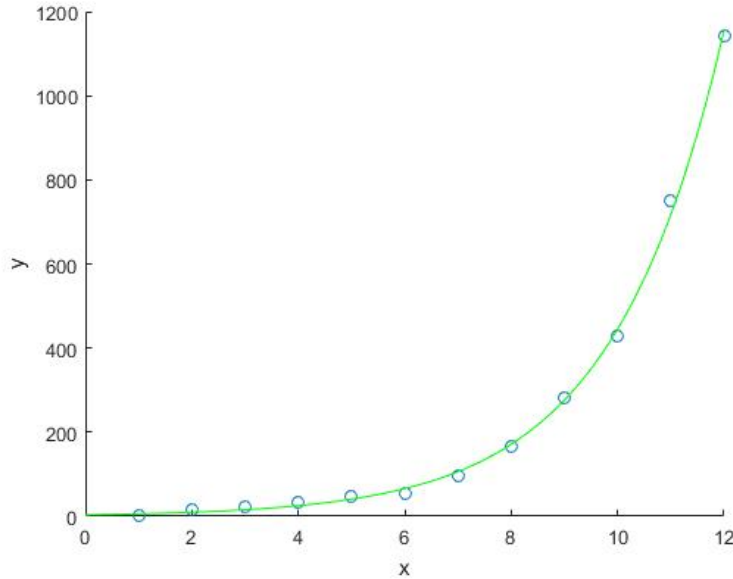
Figure 3. Confirmed cases

Also note that we can obtain starting time of this pandemic with putting $CR(t_0) = 0$:

$$t_0 = \frac{1}{\chi_2}(ln(\chi_3) - ln(\chi_1)) = -5.8324.$$

Now with this amount of $t_0 = -5.8324$, we estimated that the starting time of this pandemic is February 13.

By solving the system (2.1) as like the method used of [9]If the cumulative number of reported infections obey of(3.1) then, we have

$$(3.3) \qquad\qquad I_0 = \frac{\chi_3 \chi_2}{f v},$$

$$(3.4) \qquad\qquad U_0 = \frac{(1 - f)v}{\mu + \chi_2} I_0$$

and

$$(3.5) \qquad\qquad \tau_0 = \frac{\chi_2 + v}{S_0} \frac{\mu + \chi_2}{v_2 + \mu + \chi_2}.$$

During the above phase of pandemic $\tau(t) = \tau_0$ is constant. When strong government measures such as quarantine and public closings are implemented, the second phase begins. The actual effects of these measures are complex, and we use an exponential decrease for a time-dependent decreasing transmission rate $\tau(t)$ in the second phase to incorporate these effects. The formula for $\tau(t)$ during the second phase is

$$(3.6) \qquad\qquad \tau(t) = \tau_0, \quad 0 \leq t \leq N,$$

$$\tau(t) = \tau_0 exp(-\mu(t - N)), \quad N < t.$$

The date N and the value of μ are chosen, so that the cumulative reported cases in the numerical simulation of the epidemic aligns with the cumulative reported case data after day

N, when the public measures take effect. In this way, we are able to project forward the time-path of the epidemic after the government imposed public restrictions take effect.

Again by applying the method in [9] we can compute the basic reproductive number R_0:

$$(3.7) \qquad R_0 = \frac{\chi_2 + \nu}{\nu} \frac{\mu + \chi_2}{(1-f)\nu + \mu + \chi_2} (1 + \frac{(1-f)\nu}{\mu}).$$

To solve the system (2.1) it is necessary that the parameters μ ,ν, N, f and s_0 be determined. Note that s_0 is considered as the total population. Also we assume $1/\nu$ means that the average period of infectiousness of both unreported symptomatic infectious individuals and reported symptomatic infectious individuals is 14 days. We assume $1/\mu$, which means that the average period of infectiousness of asymptomatic infectious individuals is 7 days. These values can be modified as further epidemiological information becomes known. Here the parameter N considered 5 days before the peak day. Note that the results are not very sensitive to value of N and can be considered 5 to 15 days before the peak day. As mentioned earlier the important parameter is f, so we principally aim to gain the correct value of parameter f. To do this, we solve the system for different value of f. The results obtained from the system (2.1) for every value f are compared the principle reported data from [?]who), the correct value f is choosing by observe more consistency between them. One of the best criterion is the Akaike information criterion (AIC) as follows

$$(3.8) \qquad AIC = n \ln \frac{SSE}{n} + 2k$$

where n is the number of data points in the data set, k is the number of parameters fitted plus one and SSE is the least-squares error. We should notice, the importance to determine the correct value of the parameter f is that by recognizing the f, the unreported cases are estimated, also we consider the same amount to continuing the analysis. We assume $f = 0.1$ to $f = 0.9$, which means that 10% to 90% of symptomatic infectious cases reported. In fact, the actual value of f is unknown. For the numerical simulation, the system (2.1) was numerically solved with the Runge-Kutta-Fehlberg method. The data obtained from the Akaike test (3.8) for the reported infected cases of Iran are given in the table 2.

Table 2. Akaike Information Criterion (AIC)for Iran reported cases

f	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
AIC	1083.9	1083.8	1083.3	1080.9	1069.8	1008.2	1102.5	1399.8	1641.4

To better compare the results and understand the importance of the value of parameter f, In what follows, we plotted the graph of $t \to R(t)$ for different f's, as shown in figure 4 by changing the value of f the number of infected individuals is obtained by system (2.1) is changed.
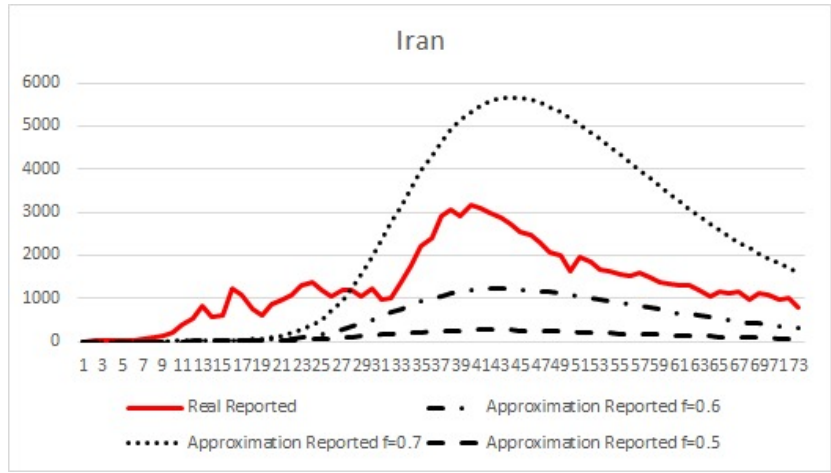
Figure 4. The values R(reported infected cases) of this diagram obtained from the solving of system (2.1) in Iran for f = 0.5, f=0.6 and f=0.7. We compare them with real reported cases.

The lowest values of AIC are related to $f = 0.6$ as shown in table 2 but this value can just estimate the reported data, because the disease is epidemic and even one person causes a significant change in the number of infected, so for predicting the infected future individuals, we should consider the parameter f more than the minimum value, So by attention figure 4 for prediction, we accept $f = 0.7$.

Reproductive Number R_0 is 7.9671. In other words, the expected number of disease cases (secondary infection) produced by the infected individual in Iran was 7.9.

Finally, we are ready to find the unreported cases. With $f = 0.7$ we can get an estimation of the daily unreported cases in the first outbreak period. We plot the graph of $t \rightarrow U(t)$ for $f = 0.7$ where shown in figure 5 .
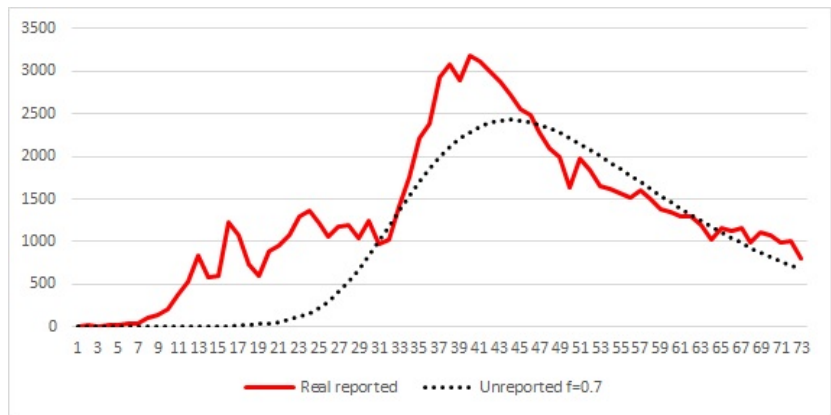

Figure 5. Comparison between unreported infected cases and real reported cases in Iran.

As we expect at the beginning of the epidemic, can see that we have many unreported cases of infections.

4. Modeling predictions for Iran

In this section, we use the technique developed in previous sections for determining f and then we find the unreported cases. It is noticed that, for each one of the provinces Ardabil and Guilan the value of f is changed and the unreported cases are dependent on the first outbreak period from 2/15/2020 until 3/25/2020.

Province Guilan:

Table 3. Guilan Reported (2/15/2020 - 2/26/2020)

15th	16th	17th	18th	19th	20th	21th	22th	23th	24th	25th	26th
3	7	7	5	10	25	25	28	40	42	39	34

By using the data of Table 3 the parameters of χ_1, χ_2, χ_3 and t_0 are obtained as following:

$$\chi_1 = 42.0853, \chi_2 = 0.1720, \chi_3 = 55.0536 , t_0 = 1.5617 \ R_0 = 3.4990$$

Table 4. Guilan (AIC)

f	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
AIC	382.5	381.2	379.6	377.8	375.9	373.9	371.7	369.4	366.8

The lowest values of AIC are related to $f = 0.9$ as shown in table 4, also the value of AIC for $f = 0.8$ is near of $f = 0.9$. It seems in the province of Guilan the reported infected cases are more real than in Iran's reported cases. In fact, due to the smaller geographical area, the news is spread quickly, which leads to the rapid growth of awareness and faster recognition of the Covid -19 virus by susceptible people. Also maybe the multiplicity of medical centers in Guilan province be another reason for this issue. This theory is just an interpretation of the data obtained by the system 2.1, which must be examined by statistical researchers in order to make a final statement. With $f = 0.9$ we can get an estimation of the daily unreported cases in the first outbreak period, the results are shown in figure6.
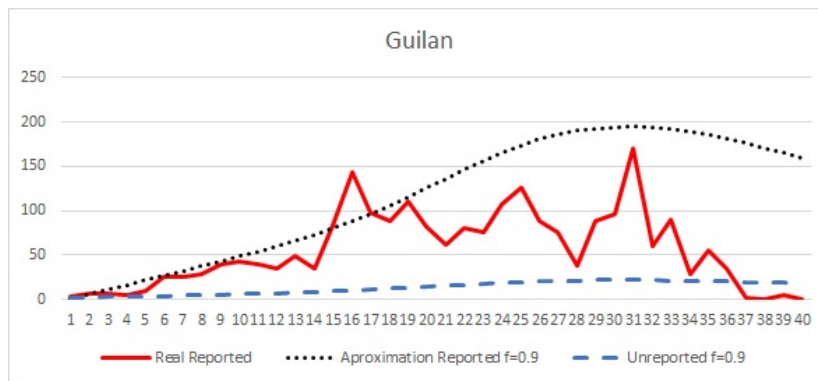

Figure 6. Diagram of Unreported and Reported Infected Cases from Solving of System 2.1 and Real Reported Cases for f=0.9 in Guilan

Ardabil province is located in a cold region in northwestern Iran and has been selected due to its geographical location and adaptation of people to the Influenza and cold, also Because

some of the symptoms of flu, COVID-19, and other respiratory illnesses are similar. The virus first appeared time on 20 Feb in Ardabil. As previously described, for obtaining the suitable value of f, need the number of reported cases. The relevant data set used between $2/20/2020$ until $5/15/2020$ are given in table5
Province Ardabil:

Table 5. Ardabil Reported $(2/20/2020 - 3/4/2020)$

$20th$	$21th$	$22th$	$23th$	$24th$	$25th$	$26th$	$27th$	$28th$	$29th$	$1th$	$2th$	$3th$	$4th$
1	1	4	11	8	13	16	32	7	29	46	10	47	21

The parameters χ_i, $i = 1, 2, 3$, t_0 and the reproduction number R_0 are obtained as follows, $\chi_1 = 49.0853, \chi_2 = 0.1336, \chi_3 = 65.5267$, $t_0 = 2.6822$ $R_0 = 2.9380$
Using the values obtained for the parameters, the system 2.1 is solved for the value $f = 0.1$ until $f = 0.9$. The data obtained from the Akaike test (3.8) for the reported infected cases of Ardabil are given in the table 6.

Table 6. Ardabil (AIC)

f	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
AIC	661.5	627.8	594.7	574.7	583.4	616.6	657.5	696.9	732.7

As shown in Table 6, the minimum value of AIC corresponds to $f = 0.4$, the unreported cases are estimated for this value of f and compared with approximated reported cases and real reported ones. The results are shown in figure 7.
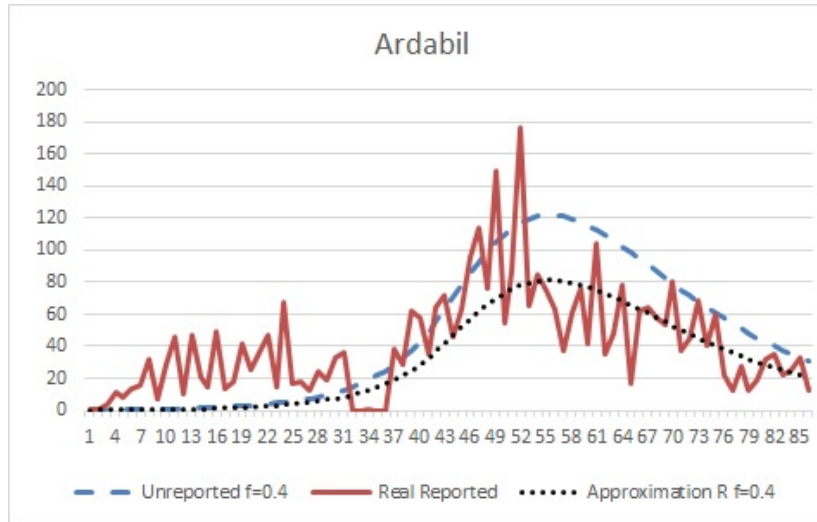

Figure 7. Diagram of Unreported and Reported Infected Cases from Solving of System 2.1 and Real Reported Cases for f=0.4

Assuming no change in health conditions and instructions, the parameters do not change in different outbreak periods in any province. In fact, this assumption can be made at the

beginning of each peak of the disease after the outbreak. So we can obtain predictions of the number of infected cases by using data from the first few days of the Pandemic. For instance, we consider a new wave of outbreaks in Iran(with data for 12 days, i.e. from October 18 to October 30, 2020, see Table 7). Note that in order to demonstrate the ability to predict the number of infected individuals using the proposed model 2.1, it does not matter which peak we consider, only the conditions must be constant during the period. Set $f = 0.7$ according to the contents described before. By solving the system 2.1, prediction the number of infected cases will be estimated, the results are given in Figure 8. Here the time $t = 1$ will corresponds to 18 October 2020.

Table 7. Iran Reported (10/18/2020 - 10/29/2020)

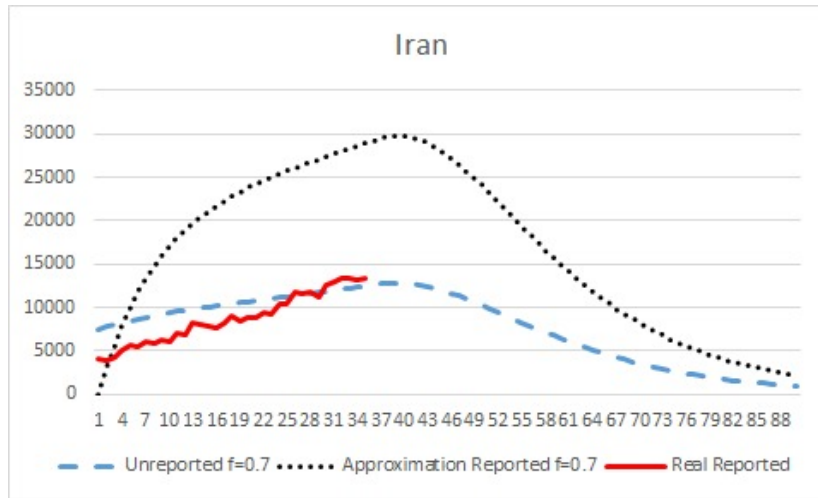| 18th	19th	20th	21th	22th	23th	24th	25th	26th	27th	28th	29th
3890	4251	5039	5616	5471	6134	5814	6191	5960	6968	6824	8293

Figure 8. Prediction of Unreported and Reported Infected Cases for f=0.7

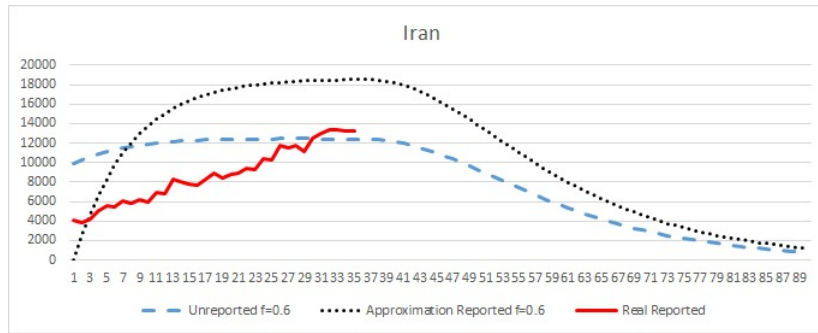Note that in this case R_0 is 1.6426. If we accept $f = 0.6$, the prediction is given by figure 9:

Figure 9. Prediction of Unreported and Reported Infected Cases for f=0.6

Also, in this case, we have $R_0 = 1.6568$ which is more than the previous (in case $f = 0.7$).

In the last of this section, we investigate the probability distribution of death rates for reported cases and hospitalized cases. The average death rate among reported cases in Iran, in the first period of the outbreak (from 2/20/2020 to 5/2/2020) is 0.071942. Cauchy distribution [10] with parameters $\sigma = 0.01137$ and $\mu = 0.06462$ is fitted to Iran's data. The P-value ([10]) for a Kolmogorov-Smirnov test [10] with the null hypothesis for the data distribution is Cauchy i. e. $p = 0.51995$ and for the Chi-Squared test [10] is $p = 0.82768$, see figure 10.
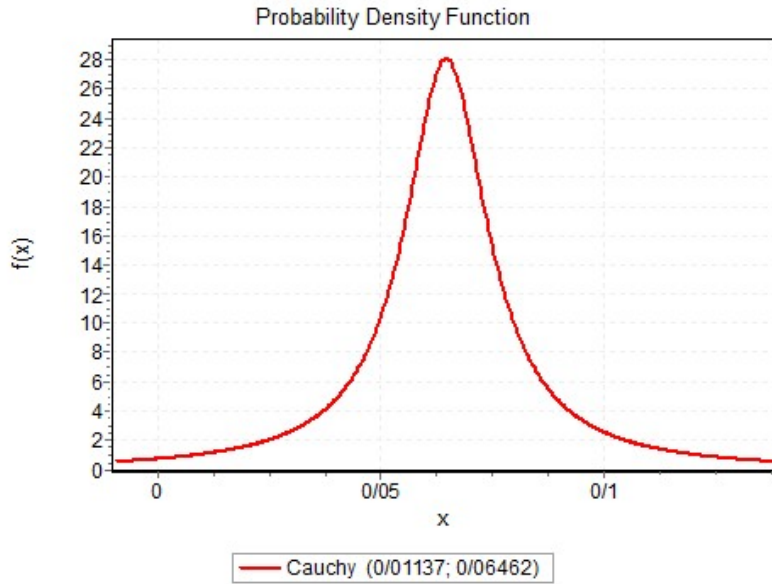

$$\text{Figure 10. } f(x) = \frac{1}{\pi\sigma(1 + (\frac{x - \mu}{\sigma})^2)}$$

The average death rate among hospitalized cases in Guilan province, in the first period of the outbreak (2/15/2020 until 3/25/2020) is 0.189389.

Gamma distribution [10] with parameters $\alpha = 1.5485$ and $\beta = 0.20282$ is fitted to Guilan's data. The P-value for a Kolmogorov-Smirnov test with the null hypothesis for the data distribution is Gamma, i. e. $p = 0.93522$ and for the Chi-Squared test is $p = 0.96459$, see figure11.

The average death rate among hospitalized cases in Ardabil in the first period of the outbreak (from 2/20/2020 to 5/15/2020) is 0.114413. Rayleigh distribution [10] with parameter $\sigma = 0.09129$ is fitted to Ardabil's data in the first period of the outbreak (2/20/2020 until 5/15/2020). The P-value for a Chi-Squared test with the null hypothesis for the data distribution is Rayleigh, i. e. $p = 0.87997$, see figure 12.
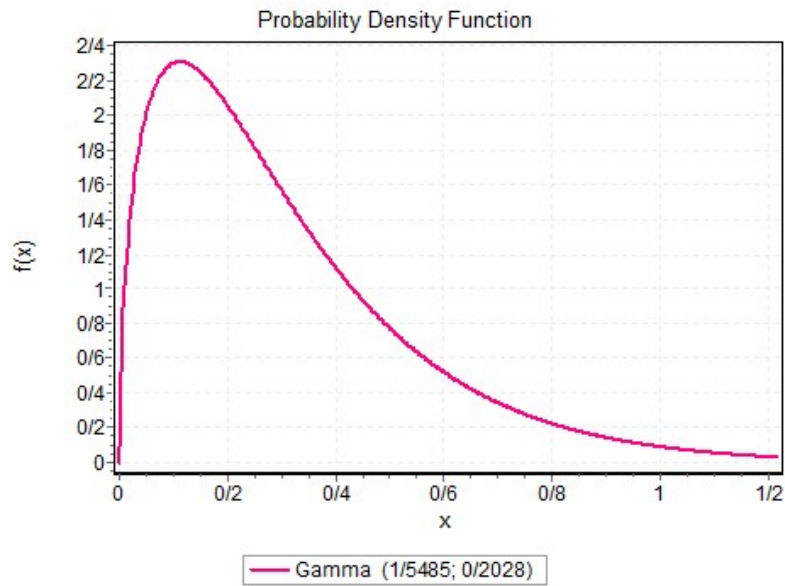
Figure 11. $f(x) = \dfrac{1}{\Gamma(\alpha)\beta^\alpha} x^{\alpha-1} e^{-\frac{x}{\beta}}, \quad \Gamma(\alpha) = \int_0^\infty t^{\alpha-1} e^{-t} dt$
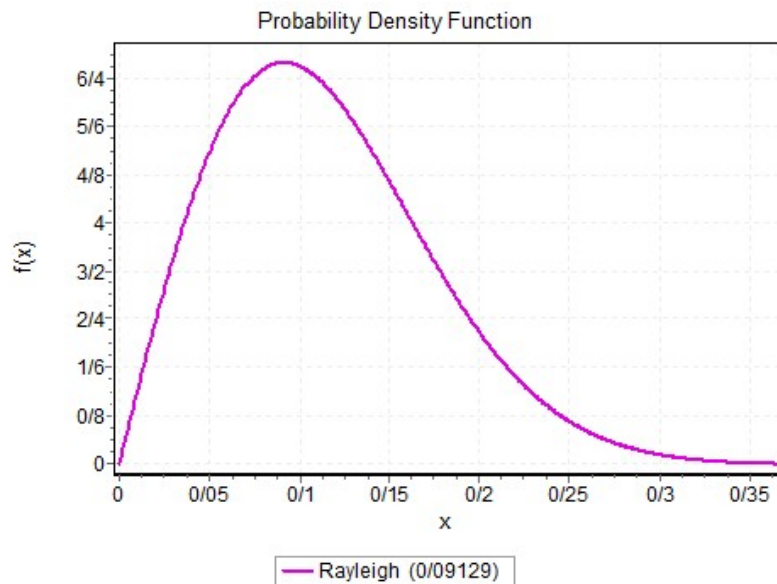
Figure 12. $f(x) = \dfrac{2}{\sigma^2} x e^{-\frac{x^2}{\sigma^2}}$

5. Conclusion and discussions

In this study, we use the generalized SIR model to study and predict the epidemic Covid-19 in Iran and two provinces Ardabil and Guilan(for reasons for choosing these two provinces can be found in the text). Also, in estimating the proportion of patients who are reported to be symptomatic, we introduced the proper AIC method, and then, we investigated the daily number of unreported infected cases in the first period of the outbreak. The results for Iran and Ardabil showed that there were almost unreported cases as the same number as the reported one, unlike Gilan, where reported cases of infection are almost acceptable. This estimation can be made for any period of a disease outbreak. The next achievement of this study is that The reported daily cases and unreported daily cases are predicted for the coming 90 days since 18 October 2020 by having just the number of patients per day in the first few days of every outbreak is the next achievement of this study.

Also, We found that the distribution of death rates in Iran, Guilan and Ardabil are respectively, Cauchy, Gamma, and Rayleigh. This result can help public health administration and medical researchers to determine the percentage of patients who die after treatment changes.

6. Acknowledgement

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