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SARS-CoV-2 epidemic calculation in Italy by SEIR compartmental models

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Abstract

Purpose – After the identification of a novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at Wuhan, China, a pandemic was widely spread worldwide. In Italy, about 240,000 people were infected because of this virus including 34,721 deaths until the end of June 2020. To control this new pandemic, epidemiologists recommend the enforcement of serious mitigation measures like country lockdown, contact tracing or testing, social distancing and self-isolation.

Design/methodology/approach – This paper presents the most popular epidemic model of susceptible (S), exposed (E), infected (I) and recovered (R) collectively called SEIR to understand the virus spreading among the Italian population.

Findings – Developed SEIR model explains the infection growth across Italy and presents epidemic rates after and before country lockdown. The results demonstrated that follow-up of strict measures such that country lockdown along with high testing is making Italy practically a pandemic-free country.

Originality/value – These models largely help to estimate and understand how an infectious agent spreads in a particular country and how individual factors can affect the dynamics. Further studies like classical SEIR modeling can improve the quality of data and implementation of this modeling could represent a novelty of epidemic models.

Keywords SARS-CoV-2, SEIR modeling, Growth rates, Epidemic analysis, Italy population

Paper type Research paper

1. Introduction

Coronavirus is a big family of viruses that cause several health problems from normal fever to severe respiratory diseases [1]. These viruses have a direct impact on both human and animal bodies that tend to get a risk of mortality. Like Ebola in 2014 [2], animal coronaviruses can infect human beings by the consumption of wild animal meats. After the transmission to the first human subjects, the infection is quickly spread.

Current novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) disease is part of a group of viral diseases including SARS-CoV in 2003 [3] and the Middle East respiratory syndrome coronavirus in 2012 [4]. These viruses are mainly circulated by having physical contact with an infected person or absorption of air droplets if someone sneezes or coughs [5,6]. After the first case of SARS-CoV-2 was identified in Wuhan, China [5], the

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World Health Organization (WHO) announced a global health emergency because of its wide-spreading. Yet, there is no kind of evidence regarding its origination and development. Due to the high prevalence of nature, it expands all over the world, and currently above 190 nations are suffering due to this disease.

Medical scholars and biologists thought that the SAR-CoV-2 virus could spread by having contact with infected animals like bats or a nonhuman primate [7]. After this continuous happening of spillover events, the virus was spread through human body contacts, largely affecting a high number of people across the world [8]. This virus grows because of direct physical contact with infected people or droplets when infected individuals sneeze or cough. When patients are infected by SARS-CoV-2, unfortunately, they are not immediately vulnerable to any signs or symptoms. This period (between exposure to illness and having disease symptoms) is known as the incubation period, and a person can only spread this virus to others once after only they develop signs and symptoms of this disease [9]. Additionally, this epidemic is not spread through the food, and there is no evidence in spreading it by pets. WHO is suggesting the prevention methods of this epidemic through maintaining constant social distancing, self-isolation is recommended.

The majority of people infected by this pandemic are adults and old age individuals, and only 2.1% of global cases are found under 20 years of age [10]. The most common signs of this viral infection are fever, cough and breathing problems. At the same time, about 80% of infected patients are exposed to mild illness, 14% get severe sickness and 5% experience mortality. Initial reports underlined that people older than 60 years had a high risk of deaths [11,12]. Recent statistics indicate that nearly 10 million world population is infected including about 500,000 deaths [13]. Sixty percent of cases are identified from the European continent, followed by the USA with more than 2.5 million infected people. Except for a few countries, almost every European country was largely affected because of the present pandemic. After the virus entered Italy, it was spread at a rapid pace. In particular, the north Italian regions have been largely suffering because of a high number of cases [14]. Currently, Italy is reporting 240,000 cases including more than 34,500 deaths [15].

To understand virus transmissions in Italian residents, the individuals are assigned into four compartments susceptible, exposed, infectious or recovered (S, E, I, R) [16]. These compartmental models are helpful to project how the infectious disease progresses, predict an epidemic or help us to calculate the effects of possible interventions to control SARS-CoV-2 [17]. Several studies are established to understand the prediction of the present epidemic in Italy. The extended SIR (eSIR) has been applied to calculate the basic virus reproductive number in Italy and estimated it as 4.34 (95% CI, 3.04–6.00) [18]. The results of the modeling study demonstrated that serious social distancing measures coupled with widespread testing and contact tracing can help to mitigate the virus from the country [19]. Moreover, the intervention of SEIR modeling of the Italian epidemic helps to improve the reliability of virus predictions [20,21]. In addition to these studies, we conducted an independent study of total virus transmission in Italy and verified how pandemic has been varied between different stages of preventive measure conduction by SEIR compartmental modeling. The present SEIR model highlights an individual number of SEIR Italian populations to present a model significance by projections of SARS-CoV-2 growth.

2. Materials and methods

2.1 Dataset description

In the last weeks of December 2019, the first coronavirus case was identified, and the WHO has officially declared it as a global pandemic on March 11, 2020 [22]. In this study, we considered only the Italy SARS-CoV-2 epidemic data to design the SEIR model. The total Italian population of 60.5 million people is considered a suspicious type. Initially, two Chinese tourists were confirmed on January 31, 2020 and after a week an Italian citizen returning from

Wuhan confirmed to be positive. Thereafter cluster of 16 cases was detected from the Lombardy region from February 21, 2020 [23,24].

Many infectious diseases have a latent phase such as the period between the people is infected but not yet infectious and this delay is called the incubation period. The WHO confirmed the incubation for SARS-CoV-2 is of a maximum of 14 days [25]. This delay between getting an infection and the contagious state included within the SIR model by adding exposed population E, and keeps infected individuals moving from S to E and from E to I compartments before transfer into the infectious state. The recovered (R) population depends upon the disease length.

As mentioned, recent numbers highlighting those 239,706 individuals that were infected including 34,678 deaths reported on the study date (June 26, 2020). These numbers confirm a 14% mortality rate (i.e. 14 members have died among 100 infected cases). As mentioned, the disease infection rate largely depends on the mortality rate and the number of susceptible people exposed to the SARS-CoV-2 disease. Based on evidence, assumptions are made such that total population (N) = 60,461,826; initial exposed $E_0 = 10$; primary infected (I_0) = 3 and recovered (R) = 0.

2.2 GLM and poisson regression

The logistic regression model is a part of broad category models called generalized linear models (GLMs). The GLMs include also Poisson regression (PR), linear regression, ANOVA, etc. In this study, PR models were employed to manage epidemic count. These models are helping to analyze count and rate data to evaluate the effect of explanatory variables (x-values) on a particular response (y-value). A PR model is a GLM, where the output count value follows the Poisson distribution and assumes a log of predicted values, which can be modeled into a linear form by unknown parameters. Mathematically, the PR model presented as

$$\log(y) = \alpha + \beta_1 x_1 + \beta_2 x_2 + \ \ldots + \ \beta_n x_n$$

Where y: response variable, α & β : numeric coefficients, and x: explanatory variable.

In this epidemic data, variance denotes virus spread, and mean presents the average of daily register cases. In PR, mean and variance related as $\mathrm{Var}(X) = \sigma^2 E(X)$; Where $E(X)$ is mean and σ^2 is the dispersion parameter. When the dispersion parameter (σ^2), $\mathrm{Var}(X) = E(X)$ condition occurs, the hold Poisson model has completely fit for a particular dataset.

R statistical software version 3.6.2 was used to conduct data analysis and model development because *R* has a broad range of statistical packages for epidemic analysis [26]. Library “COVID-19 analytics” was employed to export the world statistical data and the *glm ()* command is used to model GLMs.

2.3 Overview of SEIR model

The SEIR epidemic model simulates the time variations of an epidemic phenomenon and helps to have a mathematical understanding of infectious disease spreading. It presents relationships among people with disease contraction, present infected and those who have been recovered or of death at a given time in a population. Traditionally, it models both dynamic and mutual interaction of individuals between four different compartments (i.e. S, E, I and R). Susceptible population (S) is potentially subjected to infection. The compartmental SEIR model is presented in Figure 1.

In a preliminary analysis, virus spread follows the transitions of the form $S \rightarrow E \rightarrow I \rightarrow R$. Susceptible population can contract the virus and become exposed, ultimately infected and then recovered. By introducing a new transition $S \rightarrow E$, the infection probability rate is the same as before (i.e. all susceptible can be exposed immediately). The infectious individuals can spread disease, each person exposes β (beta) new cases per day, and γ (gamma) represents recovery rates. The new transition probability E to I is one as every exposed individual turn into infected, the population E and the rate have new parameter δ (delta). These parameters can vary among suspects and infectious comportments since it depends on people's interaction. If the person has been contacted with someone who was infected with SARS-CoV 2 is defined $\frac{dS}{dt} \leq 0$, and if the person recovered or death is defined as $\frac{dR}{dt} \geq 0$

Collectively the variables, which used to derive model equations is defined

N: total population and $N = S(t) + E(t) + I(t) + R(t)$; where $S(t)$: number of people susceptible on day t, $E(t)$: number of people exposed on day t, $I(t)$: number of people infected on day t and $R(t)$: number of people recovered on day t

β: expected amount of people an infected person infects per day; $\beta = \frac{D}{S}$; $0 < \beta < 1$.

δ: the rate of exposed individuals turns into infectious cases.

γ: the proportion of infected recovering per day ($\gamma = 1/D$); where D is the number of days an infected person can spread the disease.

R_0: the total number of people an infected person infects ($R_0 = \beta/\gamma$).

From the above transitions, the model SEIR model equations can be derived as

$$\frac{dS}{dt} = -\beta I \frac{S}{N}$$

$$\frac{dE}{dt} = \beta I \frac{S}{N} - \delta E$$

$$\frac{dI}{dt} = \delta E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

We set up the "R" function to be dependent on the input of initial values of S, R, E and I for time (t) in days.

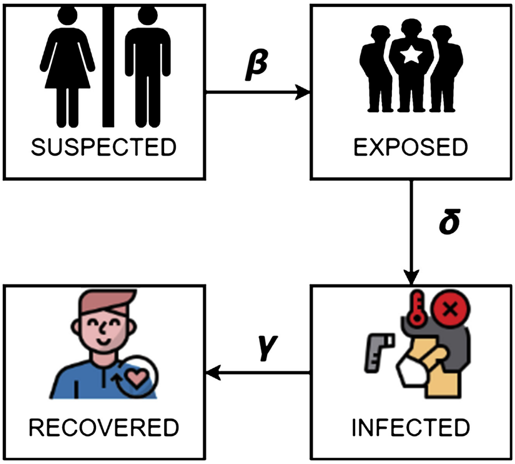

Figure 1.
The compartmental SEIR model

3. Results

3.1 Dataset outcomes

The epidemic curve presents time-series data of infected patients during an epidemic over a specific time. The variations in basic reproduction rates (R_0) across Italy by monthly distribution is depicted in Figure 2. The epidemic curves (both log and linear) in terms of registered cases are presented in Figure 3. The decrease of infectious growth after imposing serious mitigation measures such as country lockdown, social distancing and self-isolation can be observed. Similarly, the basic reproduction rate had varied over a distinct time to reflect the effects of preventive actions.

At the initial phase of the outbreak, the reproduction number (R_0) has been observed between 1.6 and 2.3 (95% CI) and results in a substantial virus outbreak all over the nation. On the eighth

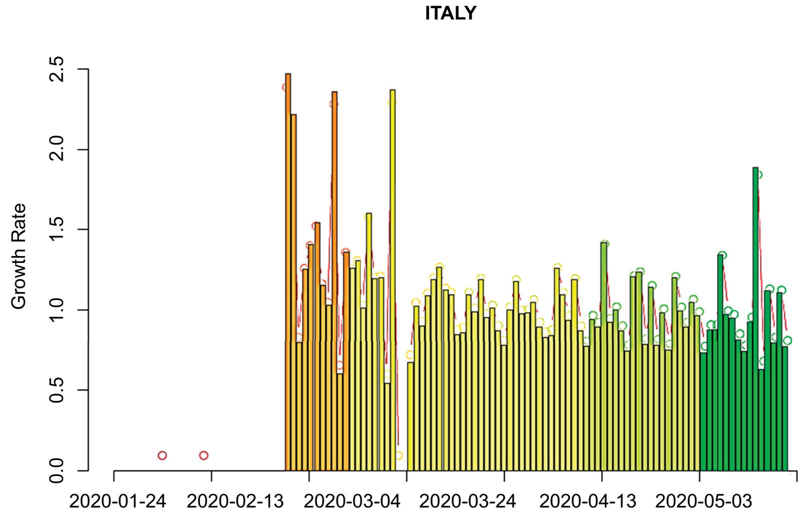

Figure 2.
Monthly distribution of basic reproduction number (R_0) (*Red: growth rate before lockdown; Yellow: after first weeks of lockdown; Green: substantial reduction of infection rate for one month)

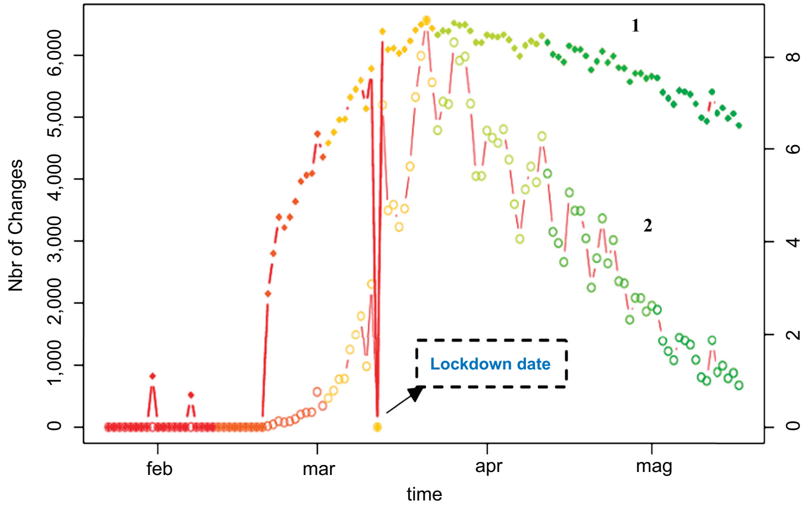

Figure 3.
Epidemic curves (1: Log scale curve and 2: Regular scale curve)

day after the commencement of lockdown, the infection rate has dropped significantly from 2.3 to 0.7–1.1 (95% CI). This value continues to decline until the first week of May. A sudden hike ($R_0 = 1.8$) was observed in mid-May and it might be caused because asymptomatic individuals are avoided screening and focused only on symptomatic individuals. The partial lockdown ongoing yet in Italy and recent growth touches the least R_0 value of 0.5.

3.2 Epidemic analysis by GLMs

To fit GLM to count the number of registered cases, we fit the model using Poisson error coefficients. Poisson error distribution and logarithm as link functions are specified to prepare predicted values to be positive. The dataset consists of the Italian population diagnosed SARS-CoV-2 positive within days from an initial virus outbreak. The GLM-Poisson GR value equals nearly one, and the Poisson model is completely for the given Italian epidemic data. The plot diagram of the monthly wise distribution of infected cases is presented in supplementary materials.

Figure 4 represents a GLM-Poisson model of registered cases from Italy. The model exponential coefficient is a multiplicative factor of 0.037, which means each additional month of country lockdown 96.3% (1−0.037*100%) decreases in the expected number of infected people.

3.3 SEIR epidemic model outcomes

To develop the SEIR model of the SARS-CoV-2 epidemic in Italy, we estimated model parameters of data from February 20 (Day 1) to May 10 (Day 80) to explain how the national lockdown (commenced from March 9, 2020) decreased virus spread to explain epidemic spread. There is an ongoing number of case growth before lockdown and the number of case changes is hovering around 5,000. In mid-March, the country announced mitigation measures to control the infection. From there onward, there is constant decay in growth rate and several infected cases. Therefore, after imposing the country lockdown there was a constant

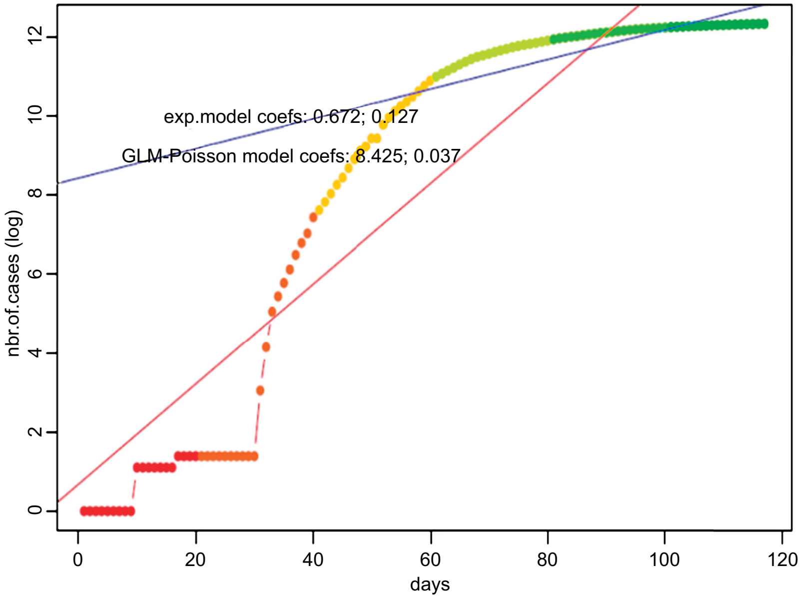

Figure 4.
GLM-Poisson model of total cases per population

stabilization that has been observed for two months. The comparison of the global epidemic versus Italy epidemic is well depicted in Figure 5.

Figure 6 presents the SEIR model of individual compartments of SARS-CoV-2 case distribution. The individual compartments four-population category is presented in the supplementary materials. The number of susceptible individuals to this virus remains low for the first week. When these people meet infected people, then it triggers to expose signs or symptoms of the disease, they are brought into the infectious compartment. However, as the infection continues, there is a sharp drop in the susceptible compartment toward the end of the 80 days. There is little or no change in the number of susceptible people following a decrease in the number of infected individuals. Indeed, every infected case has closed by either recovery or death.

The number of infected individuals increased from the first 35 to 48 days, but the maximum number of infections was observed on Day 40. However, after Day 48 the infection rate decreased as a result of getting the outbreak in control. It is because of the continuous enforcement of lockdown measures in the country and outbreak awareness. The recovery rate started rising from the Day 36 of the outbreak, continued to keep up the pace until Day 56 of the outbreak, and then remained constant as the infectious rate was decreasing. This shows a major success rate of analyzing the outbreak and getting in control of the SARS-CoV-2 epidemic spread.

4. Discussion

On February 25, 2020, the health ministry of the Italian government declared a serious outbreak of the SARS-CoV-2 epidemic following with lab confirmation of suspected cases from the Lombardy region. This outbreak appears as a spillover from a constant outbreak in Milan and other cities since March 2020 [27]. To control this pandemic on March 9, 2020, the national government strictly imposed a country lockdown including the closure of malls, sports events and schools.

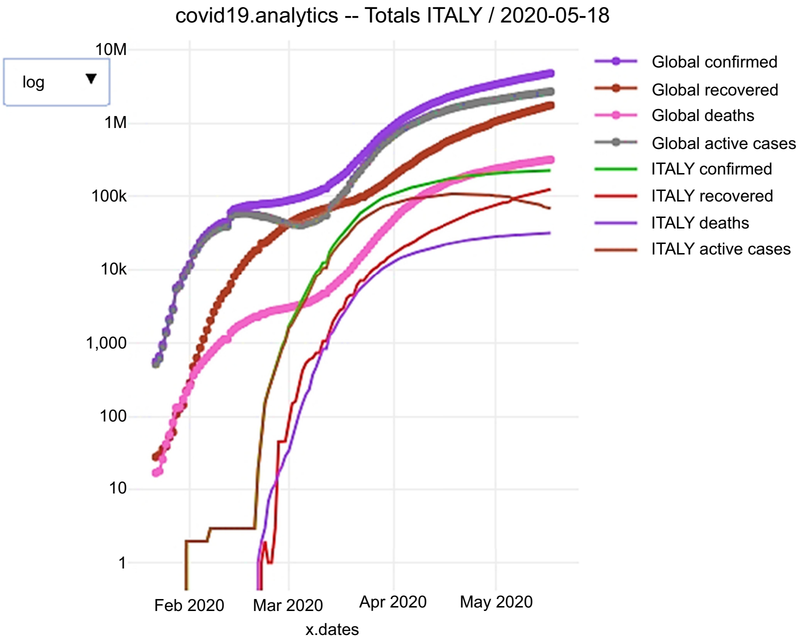

Figure 5.
Comparison of global epidemic vs Italy epidemic

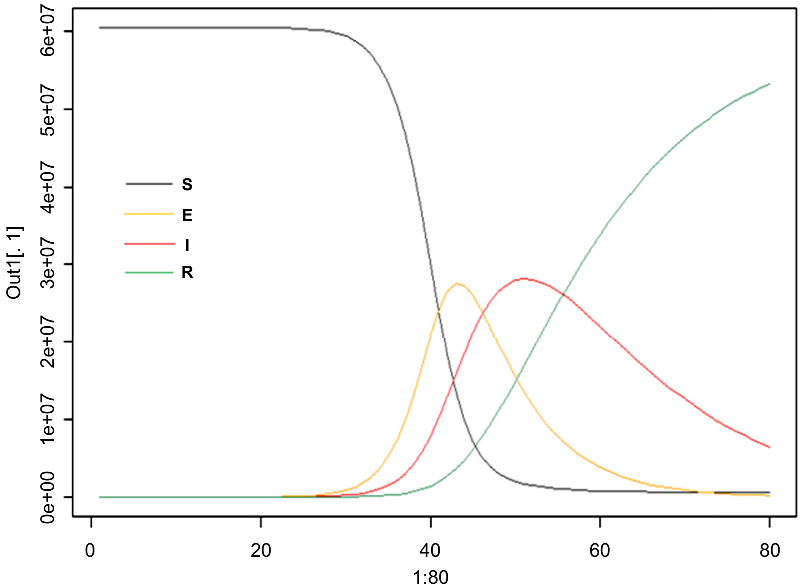

Figure 6.
SEIR model outcome

In this study, we presented an SEIR mathematical model within the context of the virus spread among the Italian population. These data-driven models are from time to time highly useful to understand epidemic trends in the specific region [28,29]. Moreover, computer programs like *R* statistics are often used to calculate reproduction numbers and analyze the dynamics of preventive measures of an infectious disease. Due to this most epidemiologists have extensively used these models for disease forecasting when a novel epidemic like SAR-CoV-2 occurs [23]. These models can transform the way of epidemic origination and spread. We demonstrated four different compartmental groups related to SARS-CoV-2 and performed the trend analysis among them.

SEIR models can be used where human bodies can directly infect each other. A patient who recovered from disease is also modeled to have a solid immunity after the illness exposure. Consider an epidemic that occurs on a time scale that is much shorter than that of the population, in other words, regard the population as having a constant size and ignore births and deaths then we have the following system of nonlinear ordinary differential equations. The SEIR model is adopted to understand the spread of SARS-CoV-2, the transmission behavior, the incidence of recovery rates, and ultimately to help the government and policymakers. To describe the SEIR model, we used the model on the initial outbreak data of the Lombardy region, Italy, as it is where the epidemic has started.

We considered the 80-day period to identify the SARS-CoV-2 population of Italy and individually evaluated the epidemic growth of four model groups (Refer to Figure 6). For the susceptible group from the day the virus originated to the first two weeks, there is the observation of the ideal trend in case registration. Thereafter there is a constant decrease in this group for three weeks, which is the follow-up with the constant trend. On the other hand, there is a steady rise in infected cases in the third and fourth weeks. After this period, the Italian government-imposed mitigation measures across the country. If we observe from Figure 6, the population infected by the virus tended to decrement after Day 48. Thereafter the situation comes under control, and people are hardly infected. When infected cases are reduced, the recovery population is simultaneously increased. From the third week, there was an ongoing trend of recovered cases.

The controlling actions presented contemplate a significant increase in recovery percentage and decrement in infected patients. About 96% of decrement in infected patients over an additional month of country lockdown (Refer Figure 4). This percentage indicates the drastic differences in two compartments (exposed and infected) observed and high gain in the decrement of infected toll. The projected drop in the number of infections shown in Figure 6 is very sensitive to the recent data used because these data are the ones responsible for changes in epidemic trends. To hold an epidemic with the same condition, the government measures should not be lifted until the virus completely eradicates from the country or else infections might rise again. The improvements can be possible with the complete integration of time-delay coordinates of SEIR models.

5. Conclusion

In this study, data-driven modeling of SARS-CoV-2 Italy epidemic trends was designed through the SEIR model. The nonlinear differential equation was formulated and solved mathematically using R-statistical software. According to this model, we highlighted the necessity of imposing country lockdown to control epidemic growth rates. The estimated value of R_0 before lockdown measured 2.3 ± 0.16, while R_0 is estimated to be 0.8 in the worst-case scenario of this epidemic. These measures could vary according to determinants such as individual behavior, viral evolution, healthcare infrastructure and patient immunity levels.

However, the model presented has significantly predicted the possible epidemic outcomes and it has some limitations. At present, we do not have sufficient information about recovery patient conductions after discharge. Therefore, we assumed that the model does not allow the passage from the recovered compartment to the susceptible compartment. The model considers the assumptions of the exposed category may neither possess little infection ability nor differentiate the symptomatic cases from asymptomatic ones. The consequent epidemic prediction did not consider the second phase lockdown established on May 4. It cannot be excluded that a less stringent lockdown can cause the second epidemic outbreak in the country. SEIR model calculations help in understanding the dynamics and characteristics of SARS-CoV-2 disease. These models largely help to estimate and understand how an infectious agent spreads in a particular country and how individual factors can affect the dynamics. Further studies like classical SEIR modeling can improve the quality of data and implementation of this modeling could represent a novelty of epidemic models.

Supplementary material

The code and compartmental SEIR diagrams can be archived from: https://github.com/nalinichintalapudi/SEIR-model.git.

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