JOURNAL OF MECHANICS OF CONTINUA AND MATHEMATICAL SCIENCES
www.journalimcms.org

ISSN (Online) : 2454 -7190 Vol.-16, No.-2, February (2021) pp 1-8 ISSN (Print) 0973-8975

MODIFIED SIRD MODEL OF EPIDEMIC DISEASE DYNAMICS: A CASE STUDY OF THE COVID-19 CORONAVIRUS

Asish Mitra

Associate Professor, Dept. of Physical & Material Sciences,
College of Engineering and Management, Kolaghat, KTPP Township,
Midnapur (East), WB, India

Email: mitra_asish@yahoo.com

https://doi.org/10.26782/jmcms.2021.02.00001

(Received: December 19, 2020; Accepted: January 30, 2021)

Abstract

The present study shows that a simple epidemiological model can reproduce the real data accurately. It demonstrates indisputably that the dynamics of the COVID-19 outbreak can be explained by the modified version of the compartmental epidemiological framework Susceptible-Infected-Recovered-Dead (SIRD) model. The parameters of this model can be standardized using prior knowledge. However, out of several time-series data available on several websites, only the number of dead individuals (D(t)) can be regarded as a more reliable representation of the course of the epidemic. Therefore it is wise to convert all the equations of the SIRD Model into a single one in terms of D(t). This modified SIRD model is now able to give reliable forecasts and conveys relevant information compared to more complex models.

Keywords: COVID-19, Epidemic Disease, Modified SIRD Model, Parameter Estimation.

I. Introduction

A model is an element that takes after a framework or article in specific perspectives, however is simpler to work with when contrasted with the first framework. A mathematical model uses the language of arithmetic to convey a more refined and accurate depiction of the structure. The aim of utilizing models are 1) better comprehension of frameworks, 2) reproduction of a framework's conduct, 3) expectation of its future conduct, and at last 4) framework control. Nonetheless, we need to recollect two things for this situation: i) Models are not special and various models can coincide for a single framework, ii) A model is just a replica of the real-world case and all models have their domain of applications, outside of which, they are invalid. Models for epidemic diseases gauge things, for example, the size of the initial pool of the susceptible individuals, the disease progression, the total number infected, the span of the outbreak, the peak incidence and to appraise different epidemiological parameters, for example, the reproductive number.

Since the remarkable work published in 1927 by W. O. Kermack and A. G. McKendrick [XX], the epidemiological models are taken to capture the essential features of the course of an epidemic. According to the study of Daley and Gani [V], the epidemiological models have three main aims: (i) to recognize better the mechanism by which diseases spread, (ii) to anticipate the future course of the pandemic, and (iii) to suggest strategies which permit us to control the spread of the sickness. However, to achieve these three goals, first of all, our model must be able to describe the real data from the past [V].

Modeling pandemic with compartmental models of Kermack and McKendrick (for an introduction see [XI, XV, X]) has been one of the most active problems in recent times [XVII, I, III, IV, VI, XIII, VII].

According to Kermack and McKendrick's compartmental models, an individual in an overall population has a spot with one of the M compartments and the number of people in various compartments keeps on changing with time. If we address each stage during a pandemic with a compartment and monitor the number of people in every compartment then we can easily model the dynamics of the epidemic. Identifying the compartments as the nodes of a graph, the communication between different compartments, represented by a set of rate equations, can be viewed as the edges of the graph. Some of the nodes may have multiple edges and some of the edges could be bi-directional also [examples: Figs. 1, 2]. The primary test of demonstrating a pandemic like Covid-19 isn't the shortage of numerical models however it is of the solid information for the compartments being thought of.

The entire modeling framework will be justifiable if the associated parameters are physically interpretable and hence predictions from it match the real-world data.

II. Mathematical Models & Materials

As per the simplest epidemiological model, denoted as the SIR model of Kermack and McKendrick (1927), which is the acronym of Susceptible, Infected and Recovered individuals, the entire population is comprising of susceptible, infective and recovered individuals, with the functions S(t), I(t) and R(t) at time t (measured, for example, in days). In this model, the possible transitions between the compartments are as follows: susceptible individuals may become infected, and infected individuals may recover. There is for example no chance for recovered individuals to become susceptible or infected again. A compartmental

Fig. 1. The Basic SIR Model

model for the propagation of disease is shown in Fig. 1, and is equivalent to the following set of differential equations [II]:

$$\frac{dS}{dt} = -\beta \frac{SI}{S_0} \quad (1)$$

$$\frac{dI}{dt} = \beta \frac{SI}{S_0} - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

where S_0 is the size of the initial pool of the susceptible individuals, β the infection rate (β>0) and γ the removal rate of infectives (γ> 0). The mean duration of infectiousness and the average period of infectivity is represented by 1/β and 1/ γ (see [VIII, XII]), respectively. The above system of equations is now fully specified by the infection and removal rates β and γ and by a set of initial conditions. Usually, one takes R(0) = 0 since no one has yet had the chance to recover or die. We consider the initial moment t = 0 when I_0 = 1 if the epidemic is set off by a single infected individual. The numerical computation will give us the number of susceptible, infected and recovered individuals as a function of time.

The above formulation of the SIR model is free from any demographic realization (natural births, deaths, migrations), this guarantees the entire population under study is completely closed. This is reasonable for some acute diseases (influenza, measles etc.) where the disease generation time is faster than that of the demographic process.

One of the genuine disadvantages of the SIR model is that individuals who recover and who die are is treated similarly - there are no different compartments for the dead and recovered individuals. This drawback can be addressed by separating the compartments for the dead and recovered population as is done in the SIRD model

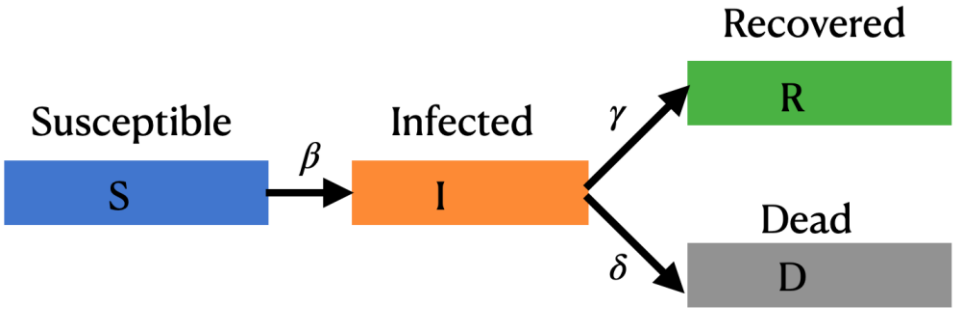

Fig. 2. SIRD Model

[Fig. 2]. The following set of equations describes the disease dynamics ([I, XIX]):

$$\frac{dS}{dt} = -\beta \frac{SI}{S_0} \quad (4)$$

$$\frac{dI}{dt} = \beta \frac{SI}{S_0} - (\gamma + d)I \quad (5)$$

$$\frac{dR}{dt} = \gamma I \quad (6)$$

$$\frac{dD}{dt} = dI \quad (7)$$

The particular model is now fully specified by three rates and by a set of initial conditions S_0, I_0, R_0 and D_0. These are nonlinear first-order ordinary differential equations. Accordingly, numerical methods are applied for the solution of this set, considering them as initial value problems.

The compartmental models predict that how the population in different compartments changes with time. In the SIR model, the population in S and R compartments can only diminish and increase respectively, however, in the I compartment it can increase as well as decrease. At the beginning of the epidemic, almost everybody is in the S compartment with a very small fraction in I and nobody in the R compartment. Toward the finish of the pandemic, everybody is in the R compartment with nobody in S or I compartment. The same happens for the SIRD model also where the decrease in I compartment happens due to recovery (R) and deaths (D).

In the SIRD model, a new transmission coefficient has been introduced which is the death rate or mortality rate, d. In this model, d/γ indicates the number of deaths to the number of infected people and hence it is named as fatality rate [XVIII]. In the websites, the time series data are available for confirmed case C(t), recovered case R(t) and dead case D(t). The time series I(t) for the population in compartment I can be acquired by taking away R and D from C: I(t) = C(t) - R(t) - D(t). One of the advantages of the SIRD model is that it has three transmission coefficients and we have the data for three-time series I(t); R(t) and D(t) available so it is possible to compute the time dependency of all the three coefficients as well as the reproduction number R.

One important disadvantage of this model is that does not consider the characteristic latency of this disease, biologically the incubation of the SARS-CoV-2 [XVI]. However, as previously mentioned, SIRD considered this subpopulation as part of the Susceptible, and this setting is reasonable because there isn't a report of the exposed population, making this model useful for the particular available data.

Usually, one takes $R_0 = D_0 = 0$ since none has yet had the chance to recover or die. The initial value of infected individuals, I_0, defines the system of equations fully, as then $S_0 = N - 1_0$. We consider the initial moment t = 0 when $I_0 = 1$ if the epidemic is set off by a single infected individual. With these initial values, most of the authors solved these equations. But there is a big question regarding the choice of S_0. It is chosen as S_0 = total population – initial infection. But this choice is somewhat arbitrary, as the true value of S_0 can be estimated only a posteriori.

The basic reproduction number, R_0, is an important index for quantifying the transmission of pathogens. It is defined as the average number of people infected by

an individual over the disease infectivity period in a totally susceptible population and reveals the transmissibility of the outbreak at the initial phase. For the SIRD model, it is given by $R_0=\beta/(\gamma+ d)$ [I].

Out of several time-series data available on several websites, only D(t) can be regarded as a reliable representation of the epidemic course. Therefore we convert all the above-mentioned equations into a single one in terms of D(t).

From eqs (4) and (7), we get

$$\frac{dS}{dD} = \frac{\frac{dS}{dt}}{\frac{dD}{dt}} = \frac{-\beta\frac{SI}{S_0}}{dI} = -\frac{\beta S}{dS_0}$$

$$\frac{dS}{S} = -\frac{\beta dD}{dS_0}$$

$$\int_{S_0}^{S}\frac{dS}{S} = -\frac{\beta}{dS_0}\int_{D_0}^{D} dD$$

$$ln\frac{S}{S_0} = -\frac{\beta}{dS_0}(D - D_0) = -\frac{\beta D}{dS_0} \quad \text{(initial condition D (0)=0)}$$

$$S(t) = S_0 e^{-\frac{\beta D}{dS_0}} \tag{8}$$

Similarly, from eqs (6) and (7), we can write

$$\frac{dR}{dD} = \frac{\frac{dR}{dt}}{\frac{dD}{dt}} = \frac{\gamma I}{dI} = \frac{\gamma}{d}$$

$$\int_{R_0}^{R} dR = \frac{\gamma}{d}\int_{D_0}^{D} dD = \frac{\gamma}{d}(D - D_0)$$

$$R(t) = \frac{\gamma}{d}D \tag{9}$$

Eq (7) can be rewritten as

$$I(t) = \frac{\dot{D}}{d} \tag{10}$$

Now total population

$$S(t) + I(t) + R(t) + D(t) = S(0) + I(0) + R(0) + D(0) = S_0 + I_0 \cong S_0$$

As R(0) = D(0) = 0 and I_0 is negligible compared to S_0. Putting the values S, I and R from eqs (8), (10), (9) respectively, in the above equation, we get

$$S_0 e^{-\frac{\beta D}{dS_0}} + \frac{\dot{D}}{d} + \frac{\gamma}{d} D + D = S_0$$

$$dS_0 e^{-\frac{\beta D}{dS_0}} + \dot{D} + \gamma D + dD = dS_0$$

$$dS_0 e^{-\frac{\beta D}{dS_0}} + \dot{D} + (\gamma + d)D = dS_0$$

$$\dot{D} = dS_0 \left(1 - e^{-\frac{\beta D}{dS_0}}\right) - (\gamma + d)D \qquad (11)$$

The above single eq (11) is equivalent to the full set of equations (4 to 7) of the SIRD model. This modified SIRD model is more competent as the time series of deaths D(t) is regarded as the authentic representation of the epidemic's course.

Database

In the present study, epidemiological data were collected from the website [IX]. It gives the number of dead individuals day-wise for various countries.

III. Calibration & Parameter Estimation of the Model with the Data

The data for D is centered on rolling averages performed over a window of 4 days. The data for $\dot{D}$ are centered rolling averages performed over a window of 4 days. Then it is plotted in the (D, $\dot{D}$) plane. Built-in function nlinfit [XIX] based on Gauss-Newton's algorithm is used to find the least square fitting with the eq (11). It gives the best fit values of the parameters β, γ, d and S_0. Data are taken for several countries and the above numerical computation is made. Results for those countries are shown in Table 1.

Table 1. Best fit values of the parameters β, γ, d, S_0, and R_0.

Country	β, day^{-1}	γ, day^{-1}	d, day^{-1}	S_0	R_0
US	0.2718	0.0133	0.000177	15005000	20.133
Spain	0.3865	0.0413	0.001312	1010000	9.073
Austria	0.3009	0.0740	0.001020	55000	4.012
Belgium	0.3140	0.0714	0.003685	205000	4.181
Denmark	0.3120	0.0336	0.002400	9500	8.667
UK	0.2846	0.0312	0.001141	1305000	8.811
Iran	0.2675	0.0227	0.000174	1205000	11.682
Portugal	0.2576	0.0372	0.000800	70500	6.779

IV. Limitations:

Models have their limitations. It is difficult to construct a completely precise model: there exist some elements about the disease that is unknown or even unknowable. As such, the present study has few limitations (besides those mentioned in the Mathematical Model

section). In the present analysis, the following factors, having a significant role in the disease dynamics, have not been considered: the incubation period of the disease dynamics, the health profile, age-distribution and genetic makeup of the population, the heterogeneous contact transmission network, the nature of the diseases/virus, availability of medical infrastructure, social mixing, personal hygiene, geographical location etc. The current study is based on a mathematical modeling perspective.

V. Conclusion:

In the present study, compartmental epidemiological framework SIR and SIRD models are explained. In the websites, the time series data are available for confirmed case C(t), Recovered case R(t) and dead case D(t). The time series I(t) for the population in compartment I can be obtained by subtracting R and D from C: I(t) = C(t) - R(t) - D(t). However, the number of dead individuals (D(t)) can be regarded as a more reliable representation of the epidemic's course. Therefore, all the equations of the SIRD Model involving S(t), I(t), R(t) and D(t) are then converted into a single one in terms of D(t), which is a modified SIRD model. The current analysis shows explicitly the widespread behaviour of the COVID-19 in the (D, $\dot{D}$) plane. The vital communication of the present examination is: basic models ought not to be excused from the earlier for more intricate and as far as anyone knows more precise plans, which certainly expound and yet depend essentially on large parameters that it is difficult to fix unequivocally.

Transparency Declaration:

The author declares no conflicts of interest.

References

I. Anastassopoulou et al. Data-based analysis, modelling and forecasting of the covid-19 out-break. PLOS ONE, 2020. doi:10.1371/journal.pone.0230405.

II. Asish Mitra, Covid-19 in India and SIR Model, J. Mech.Cont. & Math. Sci., 15, 1-8, 2020.

III. Castilho et al. Assessing the efficiency of different control strategies for the coronavirus (covid-19) epidemic. ArXiv e-prints, 2020, 2004.03539.

IV. Chen et al. A time-dependent sir model for covid-19 with undetectable infected persons. ArXiv e-prints, 2020, 2003.00122.

V. D. J. Daley and J. Gani. Epidemic Modelling: An Introduction. Cambridge University Press, 2001.

VI. Duccio Fanelli and Francesco Piazza. Analysis and forecast of covid-19 spreading in China, Italy and France. Chaos, Solitons and Fractals, 134:109761, 2020, 2003.06031. doi:10.1016/j.chaos.2020.109761.

VII. Goncalo Oliveira. Refined compartmental models, asymptomatic carriers and covid-19. ArXiv e-prints, 2020, 2004.14780. doi:10.1101/2020.04.14.20065128.

VIII. Herbert W. Hethcote. The mathematics of infectious diseases. SIAM Review, 42(4):599-653, 2000.

IX. https://data.humdata.org/dataset/novel-coronavirus-2019-ncov-cases.

X. Julie Blackwood and Lauren M. Childs. An introduction to compartmental modeling for the budding infectious disease modeler. Letters in Biomathematics, 5:1:195-221, 2018. doi:10.1080/23737867.2018.1509026.

XI. Keeling Matt J. and Pejman Rohani. Modeling Infectious Diseases in Humans and Animals. Princeton University Press, 2008.

XII. Lipsitch et al. Transmission dynamics and control of severe acute respiratory syndrome.Science, 300(5627):1966-1970, 2003. doi:10.1126/science.1086616.

XIII. Loli et al. Preliminary analysis of covid-19 spread in Italy with an adaptive SEIRD model. ArXiv e-prints, 2020, 2003.09909.

XIV. Md. Zaidur Rahman, Md. Abul Kalam Azad, Md. Nazmul Hasan, : MATHEMATICAL MODEL FOR THE SPREAD OF EPIDEMICS, J. Mech.Cont. & Math. Sci., Vol.-6, No.-2, January (2012) Pages 843-858.

XV. Michael Y Li. An Introduction to Mathematical Modeling of Infectious Diseases. Springer International Publishing, 2018.

XVI. Natalie M Linton et all. Incubation period and other epidemiological characteristics of 2019 novel coronavirus infections with right truncation: a statistical analysis of publicly available case data. Journal of clinical medicine, 9(2):538, 2020.

XVII. Prem et al. The effect of control strategies to reduce social mixing on outcomes of the covid-19 epidemic in Wuhan, China: a modelling study. The Lancet, 5:261-270, 2020. doi:10.1016/S2468-2667(20)30073-6.

XVIII. S. Gupta, R. Shankar Estimating the number of COVID-19 infections in Indian hot-spots using fatality data, arXiv:2004.04025 [q-bio.PE]

XIX. Solving applied mathematical problems with MATLAB / Dingyu Xue, Chapman & Hall/CRC.

XX. Villaverde. Estimating and simulating a SIRD model of covid-19 for many countries, states, and cities. https://cepr.org/active/publications/discussion_papers/dp.php?dpno=14711, 2020.

XXI. W. O. Kermack and A. G. McKendrick. A contribution to the mathematical theory of epidemics. Proc. R. Soc. Lond. A, 115(772):700–721, 1927.