Journal of Population Therapeutics & Clinical Pharmacology

RESEARCH ARTICLE
DOI: 10.47750/jptcp.2023.30.11.001

Generalized SIRD epidemiological model for Covid-19 in Tolima-Colombia

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Submitted: 24 March 2023; Accepted: 10 April 2023; Published: 01 May 2023

ABSTRACT

This article presents an application of the generalized SIRD model from the fractional calculation approach with the Caputo derivative as a prediction tool. In addition, the infection, recovery and mortality rates are optimized, obtaining a better fit in the predictions to the real data. Finally, the graphs obtained using the Python programming language and their respective com- parative analysis are presented.

Keywords: *COVID19, SIRD*

INTRODUCTION

The severe acute respiratory syndrome coronavirus 2 (SARSCoV-2) caused by the disease caused by coronavirus 2019 (COVID-19), has resulted in a pan- demic that has generated crises in all social areas [1]. Some of the clinical diseases caused by covid-19 infection are acute respiratory distress syndrome, cytokine release syndrome (CRS), multiorgan failure, and death. Direct viral damage and uncontrolled inflammation have been suggested to be contribut- ing factors in the severity of COVID-19 illness [2]. The COVID-19 pandemic has emphasized the critical role of an effective host immune response in controlling a virus infection and has demonstrated the devastating effect of immune dysregulation. Understanding the nature of the immune response to SARS-CoV-2 pathogenesis is key to developing effective treatments for COVID-19. Interdisciplinary work, such as medicine and mathematics in this case, plays a crucial role in mitigating contagion and treatment, gener- ating tools for anticipating and controlling present and future epidemics [3]. Regarding the mathematical modeling of the coronavirus disease COVID-19, it has been shown to be very useful for governments when defining appropri- ate policies [4]. Fractional calculus and fractional differential equations have recently been applied in numerous areas of mathematics, physics, engineer- ing, medicine, bioengineering, and other applied sciences [5]. Dynamic systems are generally modeled deterministically given their ad- vantages in risk reduction, reduction of time and expenses, in addition to their sensitivity analysis [6]-[12]. The SIRD (Susceptible-Infected-Recovered-Deceased) epidemiological model is a commonly used model in pandemic prediction.

This model is determined by the rates of change in the dynamic groups mentioned above. these rates of change are represented by derivatives or rate of change over time for each group. In 1946, a generalization of this notion of rate of change called fractional derivative appears, where its order is not only integer, but any real number can be considered in its domain. Some advantages to consider the generalization of this classic SIRD model to a fractional model lies in the fact that its study is not done locally in time but rather the history of the dynamic system is considered, a process known as the memory effect [13]-[15]. In this paper, a fractional model is presented by using Caputo's fractional derivatives where the fractional order of differentiation ν can be used to describe different strains and genomes of the coronavirus which can vary with mutations. As a result, some numerical and graphical results are presented using the Caputo fractional derivative dis- cretization described in [16] that describe the development of the pandemic applying the SIRD model for the department of Tolima, Colombia.

SIRD Model

The SIRD epidemiological model, noted by its acronym in English (Susceptible- Infected-Recovered-Deceased), considered one of the simplest mathematical models that allows describing how pandemics evolve, presents a dynamic in a group of the population that is considered susceptible to suffering from the disease. illness. A simple scheme that explains the behavior of the individ- uals in the possible groups (Suceptible - Infected - Recovered - Deceased) is shown in the following graph, where a susceptible individual can continue as susceptible in a period of time (day) or pass to be infected and where in a new period of time to recover or die.

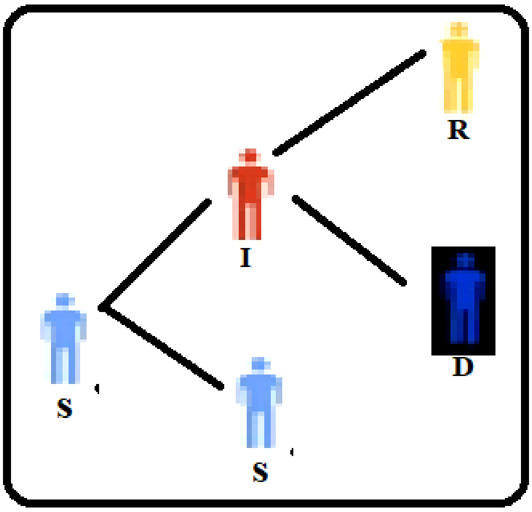

FIGURE 1: Dynamic S-I-R-D (Own elaboration)

The SIRD model in its assumptions considers that the speed with which the pandemic is passing allows births and deaths caused by another type of disease or event to be neglected. If a healthy individual is infected, he will become infectious immediately and it is also considered that when this individual recovers, he acquires immunity. Here it should be noted that considerations specific to the disease such as recovery time, mortality, pop- ulation characteristics such as sex, age, territorial location, etc. Herein lies the importance of the interdisciplinary work mentioned above with the aim of creating tools that contribute to predicting the behavior of a pandemic and allow making the right decisions for its control.

Mathematics in the SIRD model

This section presents the mathematical representation of the SIRD model in terms of rates of change or derivatives. As can be seen in

Figure 1, the number of infected individuals is subtracted from the group of susceptible individuals for each unit of time, which will be considered in days. The group of infected is divided into two new classes that make up the groups of recovered and deceased. These classes are cumulative, that is, the newly recovered and deceased are added to the total present on the previous day, respectively. Therefore, using the daily exchange rates in each group, the SIRD model can be represented by the following system of equations:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\sigma IS}{N} \\ \frac{dI}{dt} &= \frac{\sigma IS}{N} - (\mu + \delta)I \\ \frac{dR}{dt} &= \delta I \\ \frac{dD}{dt} &= \mu I \end{aligned} \qquad (2.1)$$

under the conditions N = S + I + R + D, S0 = S(0),I0 = I(0) > 0 yR(0) = 0. The parameters to be taken into account in the SIRD model are the following:

N Study population

d Duration of the virus in the human body

β Transmissibility index (infected contacts)

b Probability that a person will recover

m Probability that a person dies

p Probability of contagion (Rate of contagion between contacts) Where:

$$\begin{aligned} \sigma &= \beta p \\ \delta &= \frac{b}{d} \\ \mu &= \frac{m}{d} \end{aligned} \qquad (2.2)$$

which we will call the parameters of the model. An important result is that the shape of the graphs for the Susceptible-Infected-Recovered-Deceased groups depends on the values of these parameters, therefore the sanitary control measures taken by the government can be quantified, that is, the interest is focused in establishing measures to control the parameters in order to flatten the curve, which means that the peak takes longer to arrive, in addition to not being so high that collapses occur in the care clinics and vital economic activities can continue . Some of the strategies that have been implemented by the different governments to control the parameters and therefore the control of infections are: The contagion rate that an infected individual has in a susceptible population is called the basic reproductive rate and is denoted as R0, that is, R0 represents the number of individuals that an infected individual is capable of infecting while infectious.

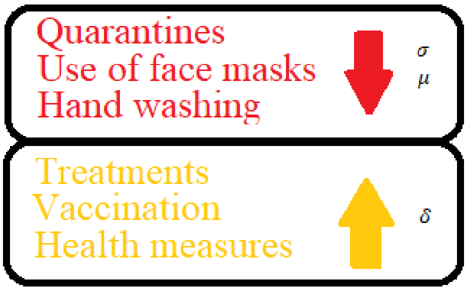

FIGURE 2: Control of parameters (Own elaboration)

$$R_0 = \frac{\beta}{\gamma} S \qquad (2.3)$$

this rate is extremely important since if its value is greater than 1, the infec- tion will grow exponentially.

Generalized SIRD

Although several complex models for the transmission dynamics of COVID- 19 have recently been proposed. In our study we use a relatively simple and more popular model used in the field of mathematical epidemiology. The SIRD model consists of three mutually distinct categories. First are those people who could potentially contract the disease S(t), second are those who currently have the disease and can infect others I(t) (infectious), then R(t) means recovered where this is the group of people who have already con- tracted the disease and have now recovered from the disease and finally D(t) which represents the group of individuals who have died from the disease. With all the mathematical models, we have to make several assumptions to simplify real-world phenomena because things are too complicated to express everything in a set of simple equations, so the first assumption we make here is that the epidemic is big enough. short, so it doesn't last long enough for us to assume that the total population remains constant. The second assumption in the model relates to how the disease is transmitted, and we assume that the rate of increase in infectiousness is proportional to the con- tact between the susceptible and the infectious, and we further assume that this occurs at a constant rate. Finally, our third assumption is related to the rate of elimination and this is the category R(t), so there is a constant rate that could be a mortality rate or a recovery rate. The SIRD model with the Caputo derivative is given by

$$\begin{aligned} \frac{{}_{*}D^{\gamma}_{a+}S}{dt} &= -\frac{\sigma I S}{N} \\ \frac{{}_{*}D^{\gamma}_{a+}I}{dt} &= \frac{\sigma I S}{N} - (\mu + \delta) I \\ \frac{{}_{*}D^{\gamma}_{a+}R}{dt} &= \delta I \\ \frac{{}_{*}D^{\gamma}_{a+}D}{dt} &= \mu I \end{aligned} \tag{3.1}$$

where N = S + I + R + D is the total population. The initial conditions attached to the equations are S0 = S(0),I0 = I(0) > 0 yR(0) = 0.

Discretization of the generalized SIRD model

For the partition in the study time in days given by

$$P = \{a = t_0, t_1, \ldots, t_k, \ldots, t_N = b\}$$

from day a to day b [a, b], the caputo derivative is discretely approximated by:

$$_{h}({}_{*}D^{\gamma}_{a+}\varphi)_{Re}\, t_k) = \frac{h^{-\gamma}}{\Gamma(1-\gamma)} \sum_{j=0}^{k-1} Ca_{a,j,k}\varphi(t_j) \tag{3.2}$$

where

$$Ca_{a,j,k} = [k-j]^{-\gamma} - [k-j-1]^{-\gamma}. \tag{3.3}$$

Substituting in the generalized SIRD model we obtain the system of equations for the variables S, I, R y D:

$$\begin{aligned} \frac{h^{-\gamma}}{\Gamma(1-\gamma)} \sum_{j=0}^{k-1} Ca_{j,k} S_j &= -\frac{\sigma I_k S_k}{S_k + I_k + R_k + D_k} \\ \frac{h^{-\gamma}}{\Gamma(1-\gamma)} \sum_{j=0}^{k-1} Ca_{j,k} I_j &= \frac{\sigma I_k S_k}{S_k + I_k + R_k + D_k} - (\mu + \delta) I_k \\ \frac{h^{-\gamma}}{\Gamma(1-\gamma)} \sum_{j=0}^{k-1} Ca_{j,k} R_j &= \delta I_k \\ \frac{h^{-\gamma}}{\Gamma(1-\gamma)} \sum_{j=0}^{k-1} Ca_{j,k} D_j &= \mu I_k \end{aligned} \tag{3.4}$$

This system of equations is solved using the Python programming language using real data for the department of Tolima, Colombia obtained from the database of the National Institute of Health (INS) Colombia https://www.ins.gov.co/Noticias/paginas/coronavirus.aspx.

Parameter parameter optimization

The different mitigation strategies imposed by the government to control the pandemic generate variation in the behavior of the parameters, such as a quarantine, a de-escalation and again a strict quarantine, the use or non-mandatory use of masks. This causes the parameters to fluctuate over time. Therefore, it is necessary to adjust these parameters by partitioning the time and recalculating them in each subpartition. In the classic SIRD model it is necessary to enter the value of the rates σ, μ and δ, however, given that we know the historical data and the memory effect of the Caputo fractional derivative, these can be optimized. parameters minimizing the error in the approximation estimates. For this, the squared error between the data generated in the solution of the system of equations and the known real data is minimized, which we will denote St, st, It, it, Rt, rt and Dt, dt respectively. Thus, the function that represents the squared error is expressed as:

$$EC(\sigma, \mu, \delta, \gamma) = \sum_{k=1} (S_k - s_k)^2 + (I_k - i_k)^2 + (R_k - r_k)^2 + (D_k - d_k)^2 \ . \qquad (3.5)$$

This equation must be minimized since it represents the distance between the data obtained through the estimation and the actual historical data.

RESULTS

In Colombia, as throughout the world, COVID-19 affected social and eco- nomic practices, in addition to the number of deaths that have been gener- ated as a result of the disease. The country faced a public health challenge of mitigating infections and at the same time achieving economic reactiva- tion. Predictive mathematical models provide a great observational tool for decision making. On March 6, 2020, the first case of COVID-19 in Colombia was confirmed. Due to the health emergency, the country began preven- tion with the mandatory use of masks, mandatory quarantines, extensive implementation of tests, acquisition of hospital care units, etc. Next, the behavior of COVID-19 can be observed with real data for the department of Tolima-Colombia for the groups of susceptible, infected, recovered and de- ceased people, filtered from the database provided by the National Institute of Health in Colombia (INS). The data range for the study is located between the period of time (03-17-2020) taken as the initial day until (10-20-2022) as the final day. https://www.ins.gov.co/Noticias/paginas/coronavirus.aspx.The need for measures in the search to flatten the curve of infection is applied the mandatory use of masks and escalated or progressive confinements as a strategy to flatten the curve of infected and not collapse the care units. These measures vary the contagion rate β. Lack of lockdowns are also presented, where the contagion rate rises again and therefore the presence of peaks in the infected graph is observed. This variability in the contagion rate creates the need to recalculate the parameter β in the dates of confinements or quar- antines to be used in the SIRD model. Another important measure that is taken into account is the inclusion of vaccination, presenting a variability of increase in the recovery rate γ. The variability of the parameters through-

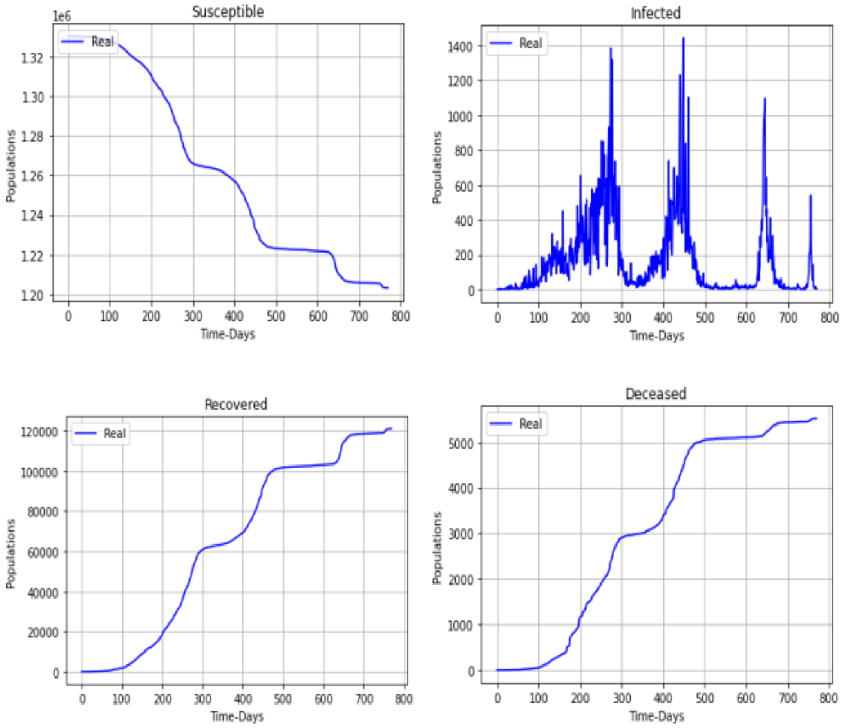

FIGURE 4: Real data for the department of Tolima - Colombia (Own elabora- tion)

out the process creates the need to recalculate these parameters and to be able to identify the changes in the models. The information provided by the INS (National Institute of Health-Colombia) was taken from the real data of Susceptible, infected, recovered and deceased people in the department of Cundinamarca between March 17, 2020 and October 20, 2022. Group- ing the previous results For the numerical approximations of the fractional SIRD model with the Caputo derivative, the following graphical results are obtained using the Python programming language.

Estimated data vs actual data

In this case, each graph in figure 9 for the susceptible, infected, recovered and deceased group respectively was obtained by programming the system of equations described in equations 3.4 using the Python program against the real data of the pandemic in the department of Cundinamarca-Colombia. For the analysis of our adjustment to the real data with the simulated results of the SIRD model, the determination coefficient was also used, find- ing $R^2 = 0.999339142$ for the susceptible group where we understand that 99.93% of the real data is explained by S (Susceptible) in the model. Similarly, a $R^2 = 0.6394$, $R^2 = 0.999730139$was obtained and$R^2 = 0.999197157$, for an explanation of the real data of 63.94%, 99.97% and 99.91% through the variables I (Infected), R (Recovered) and D (Deceased) in the system of equations (3.4) respectively. As mentioned before, the usefulness of this result lies in the possible use in decision making in the prediction of possible mitigation scenarios for future situations, not only of public health but also in those where the SIRD model hypotheses are applicable. This result can also be used in any region where there is previous information on the evolution of the pandemic in the three classes described as susceptible-infected-recovered-deceased. Similarly, the model parameters were recalculated according to the variability observed in the data.

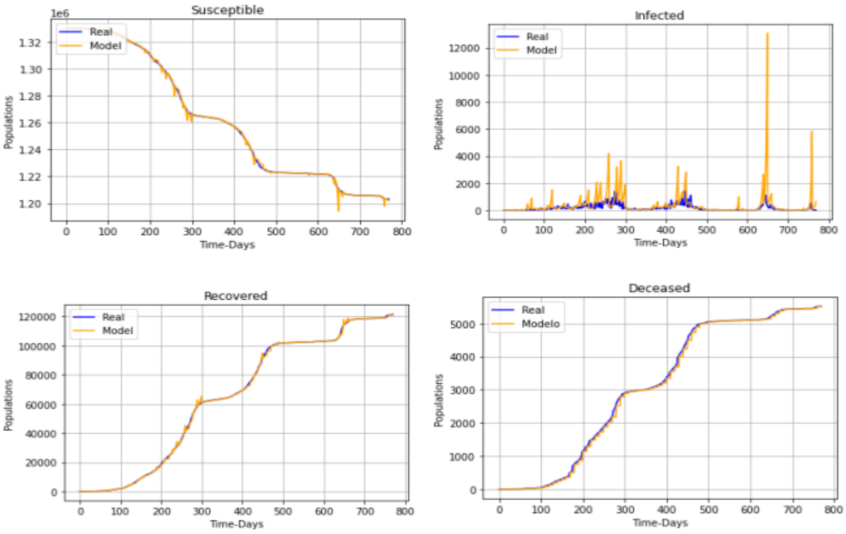

FIGURE 5: Simulated data vs real data for the department of Tolima - Colom- bia (Own elaboration)

CONCLUSIONS

We finally conclude the importance of developing accurate tools that al- low satisfactory predictions that illuminate decision-making in the control of other diseases, pandemics or dynamics that have the same assumptions. Also to establish the adjustment of the parameters generating subpartitions that can effectively identify the changes in said parameters in this case for a generalization of the SIRD model, that is to say diseases or pandemic phe- nomena where the susceptible, recovered, infected or dead can be established using the memory of the disease and where the intervening parameters can be adjusted by identifying their variability with least squares and with time partitions using fractional calculation and numerical analysis. The results obtained given the explanation through the coefficient of determination is a guarantee of a good prediction that allows the entities in charge to optimize all kinds of resources and also provide tools to knowledge. The existence of different fractional derivatives also allows new studies in search of improving both the predictions and the computational work and the analysis of sensi- tivity and stability in the solutions that allow improvements to these results obtained.

REFERENCES

1. JE Jr Peacock, DM Herrington, SL Edelstein, AL Seals, ID Plumb, S Saydah, WH Lagarde, MS Runyon, PD Maguire, A Correa, WS Wein- traub, TF Wierzba, JW Sanders. Survey of Adherence with COVID-19 Prevention Behaviors During the 2020 Thanksgiving and Winter Hol- idays Among Members of the COVID-19 Community Research Part- nership.. J Community Health 47, 71-78 (2022).
2. Wang Y, Perlman S. COVID-19: Inflammatory Profile. Annu Rev Med. 2022 Jan 27;73:65-80. doi: 10.1146/annurev-med-042220-012417. Epub 2021 Aug 26. PMID: 34437814.
3. S Momtazmanesh, A Saghazadeh, JCA Becerra, K Aramesh, FJ Barba, F Bella, A Blakney, M Capaccioli, R Castagna, U Crisanti, T Davtyan, T Dorigo, J Ealy, M Farokhnia, G Grancini, M Gupta, A Harbi, W Krysztofiak, A Kulasinghe, CM Lam, A Leemans, B Lighthill, V Limongelli, P Lopreiato, L Luongo, CR Maboloc, R Malekzadeh, OC Gomes, M Milosevic, J Nouwen, D Ortega-S´anchez, J Pawelek, S Pra- manik, S Ramakrishna, O Renn, S Sanseviero, D Sauter, M Schreiber, FW Sellke, MA Shahbazi, N Shelkovaya, WH Slater, D Snoeck, S Szta- jer, LQ Uddin, L Veramendi-Espinoza, R Vinuesa, WC Willett, D Wu, K Z˙ yniewicz, N Rezaei. International Scientific Collaboration Is Needed to Bridge Science to Society: USERN2020 Consensus Statement.. SN Compr Clin Med 3, 1699-1703 (2021).
4. S Batabyal, A Batabyal. Public healthcare system capacity during COVID-19: A computational case study of SARS-CoV-2.. Health Sci Rep 4, e305 (2021).
5. G´omez Plata, A. R., & Capelas de Oliveira, E. (2019). Introducci´on al c´alculo fraccional. Editorial Neogranadina.
6. S Majee, S Adak, S Jana, M Mandal, TK Kar. Complex dynamics of a fractional-order SIR system in the context of COVID-19.. J Appl Math Comput, 1-24 (2022).
7. Swati, Nilam. Fractional order SIR epidemic model with Beddington- De Angelis incidence and Holling type II treatment rate for COVID-19.. J Appl Math Comput, 1-25 (2022).
8. FT Akyildiz, FS Alshammari. Complex mathematical SIR model for spreading of COVID-19 virus with Mittag-Leffler kernel.. Adv Differ Equ 2021, 319 (2021).
9. Y Chen, F Liu, Q Yu, T Li. Review of fractional epidemic models.. Appl Math Model 97, 281-307 (2021).
10. RT Alqahtani. Mathematical model of SIR epidemic system (COVID- 19) with fractional derivative: stability and numerical analysis.. Adv Differ Equ 2021, 2 (2021).
11. A Taghvaei, TT Georgiou, L Norton, A Tannenbaum. Fractional SIR Epidemiological Models.. medRxiv (2020)
12. F Nda¨ırou, I Area, JJ Nieto, CJ Silva, DFM Torres. Fractional model of COVID-19 applied to Galicia, Spain and Portugal.. Chaos Solitons Fractals 144, 110652 (2021).
13. H Mohammadi, S Rezapour, A Jajarmi. On the fractional SIRD math- ematical model and control for the transmission of COVID-19: The first and the second waves of the disease in Iran and Japan.. ISA Trans 124, 103-114 (2022).
14. KS Nisar, S Ahmad, A Ullah, K Shah, H Alrabaiah, M Arfan. Math- ematical analysis of SIRD model of COVID-19 with Caputo fractional derivative based on real data.. Results Phys 21, 103772 (2021).
15. H Jahanshahi, JM Munoz-Pacheco, S Bekiros, ND Alotaibi. A fractional-order SIRD model with time-dependent memory indexes for encompassing the multi-fractional characteristics of the COVID-19.. Chaos Solitons Fractals 143, 110632 (2021).
16. D. Baleanu, K. Diethelm, E. Scalas, J. Trujillo, Fractional Calcu- lus: Models And Numerical Methods Second Edition. World Scientific Publish- ing Company, ISBN 9789813140059, 2016.