DOI: 10.22481/intermaths.v2i2.9696
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Artigo | Article

INTERMATHS
ISSN 2675-8318
Vol. 2, N. 2, Jul - Dez 2021, p. 39 – 48

SIR model for propagation of COVID-19 in the Paraíba's State (Brazil)

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Modelo SIR para propagação da Covid-19 no Estado da Paraíba (Brasil)

Resumo

Este trabalho visa aplicar o modelo compartimental do tipo SIR (Susceptível - Infectado - Removido) na evolução do Covid-19 no Estado da Paraíba e na cidade de Campina Grande - PB. Para tanto, os parâmetros do modelo foram considerados variáveis ao longo da evolução no tempo, dentro de um intervalo adequado. O sistema de equações diferenciais foi resolvido numericamente usando o método de Euler. Os parâmetros foram obtidos ajustando-se o modelo aos dados de infectados fornecidos pela Secretaria de Saúde do Estado da Paraíba. De acordo com os resultados obtidos, o modelo descreve bem a população infectada. Houve redução no número efetivo de reprodução no Estado da Paraíba e na Cidade de Campina Grande nos períodos analisados. Ressalta-se que, compreender a dinâmica de transmissão da infecção e avaliação da eficácia das medidas de controle, é crucial para avaliar o potencial de ocorrência de transmissão sustentada em novas áreas. O modelo também pode ser aplicado para descrever a dinâmica da epidemia em outras regiões e países.

Palavras-chave: Modelagem matemática; Epidemiologia; Covid-19.

Abstract

This work aims to apply the SIR-type compartmental model (Susceptible - Infected - Removed) in the evolution of Covid-19 in Paraíba's State and Campina Grande City. For that, the parameters of the model were considered to be variable during time evolution, within an appropriate range. The system of differential equations was solved numerically using the Euler method. The parameters were obtained by adjusting the model to the infected data provided by the Paraíba Health Department. According to the results obtained, the model describes the infected population well. There was a reduction in the effective reproduction number in Paraíba and the town of Campina Grande. It is noteworthy that understanding the dynamics of infection transmission and evaluating the effectiveness of control measures is crucial to assess the potential for sustained transmission to occur in new areas. The model can also be applied to describe epidemic dynamics in other regions and countries.

Keywords: Mathematical modelling; Epidemiology; Covid-19.

MSC: 00A69; 00A71; 00A72.

Submetido em: 19 de outubro de 2021 – **Aceito em**: 17 de dezembro de 2021

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1 INTRODUCTION

Several reports in history highlight the epidemics of diseases that have had dramatic effects on the population. For example, the black plague of the 14th century, in Europe and Asia. Also known as bubonic plague, it was caused by a bacterium, which is transmitted to humans from fleas that infest mice and other rodents. The Spanish flu in 1918, caused by the influenza virus A H1N1 type, infected more than 500 million people and caused between 17 and 50 million deaths between 1918 and 1920 [1], [2]. At least a quarter of the entire population of the planet was infected. Swine flu in 2009, the first pandemic of the 21st century, was caused by an extremely violent variation of the H1N1 virus. It originated in Mexico in March/April 2009 and spread to over 75 countries in 3 months and reaching over 120 countries. Other diseases have also been reported, such as cholera, tuberculosis, smallpox, influenza, measles, and malaria, which have also caused many deaths [3], [4].

Covid-19 is a acute respiratory syndrome caused by the Sars-CoV-2 virus, possibly originated from bats [5]. The first official case was reported on December 12, 2019, in Wuhan City, Hubei Province of China [6]. In December 2019, an outbreak began to infect around 50 people in Wuhan and spread throughout the world, reaching several countries. On March 11, 2020, the World Health Organization (WHO) decrees that the world is experiencing a pandemic by the new coronavirus (Sars-CoV-2). In Brazil, the first reported case was on February 25, 2020, of a resident of the São Paulo City who was in Italy. In Paraíba's State, according to the State Health Department, the first confirmed case of Covid-19 was registered on March 18, 2020 [2]. As of August 15, 2021, were to over 207 million confirmed cases and 4,35 million deaths on the world.

If it is possible to understand how a disease spreads in a given population, then government officials will be better equipped to fight it through social distancing, quarantine of those who had contact with infected people or vaccination. For that, a part of the knowledge that is used is called Mathematical Epidemiology. This study area emerged shortly after the Spanish flu pandemic, from the works carried out between 1927 and 1933 by two Scottish researchers, Anderson McKendrick and William Kermack [7], [8], [9], who developed the compartmental models that divide the population between susceptible, infected, and recovered/removed to describe the dynamics of virus transmission [1], [3].

In this sense, mathematical models are useful tools, since they can project scenarios of the impact of the disease in each city, region, and country. Based on both available data on infected people, deaths, and occupation of beds, as well as on predictions about the evolution of the disease and the intensity of social isolation, it is possible to determine the moment and the correct way to relax the isolation measures and start opening of the economy. Estimation of changes in transmission over time can provide information into the epidemiological situation and help identify whether outbreak control measures are having a measurable effect. Such analysis can inform predictions about future growth, help estimate risk to other counties, and guide the design of alternative interventions.

Projections of the Covid-19 epidemic in Brazil and several countries, based on the SIR-type models and its variations they are reported in the literature and are used to estimate how fast the virus is propagating [1], [2], [10], [12], [13]. A number that plays an important role in understanding epidemiological behaviour is the basic reproduction number ($\mathcal{R}_0$) measures the ease with which the virus is transmitted, that is, how many people an infected individual can infect in the contagious period. The condition $\mathcal{R}_0 < 1$ is a sufficient condition for the pandemic to be extinguished. In Franco and Dutra [2] the disease infection rate (α) and the basic reproduction number ($\mathcal{R}_0$) were obtained. The $\mathcal{R}_0$ value for Brazil was estimated at 3.7 in the analyzed period February 25, 2020 to March 23, 2020. The $\mathcal{R}_0$ value for Paraíba's State was estimated at 2.23 in the analysed period March 28, 2020 to May 3, 2020. In Souza *et al.* [13] the $\mathcal{R}_0$ value for Brazil was estimated at 3.1 according to data available at the Covid-19 data during the first 3 months of the epidemic.

In Shi *et al.* [14] reports that the spread of Covid-19 was effectively controlled in Wanzhou (China) by breaking the transmission chain through social distancing, extensive contact tracing, mass testing and strict quarantine of close contacts. The authors reported a reduction of basic reproduction number ($\mathcal{R}_0$) as a consequence of rigorous propagation control measures.

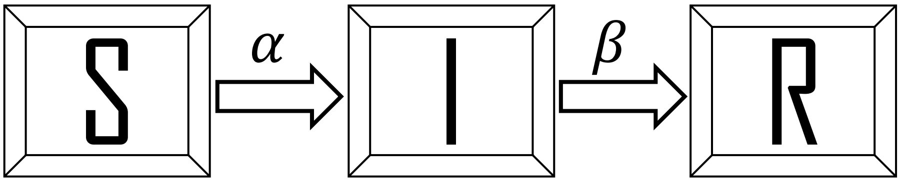
The effective reproduction number $\mathcal{R}(t)$ indicates average number of people that an infected individual will infect after containment measures are taken or a part of the population becomes immune. For some time t after thebeginning of the contamination of the disease, it will stop spreading when $\mathcal{R}(t) < 1$. In Batista and Silva [15] they adapted SIR model considering the effects of birth and mortality to model the dissemination dynamics of Covid-19 in Brazil, as well as in the Paraíba's State and the Campina Grande City, Brazil. The model was validated with the comparison with official data of the numbers of confirmed cases, recoveries, and deaths. It was possible to obtain the temporal variation of the contagion rate, which reflects the greater or lesser adherence to social isolation by the populations involved.

We focus in this work on the Covid-19 data in Paraíba's State, where the pandemic accounted counts $31,712$ confirmed cases according to government data on June 17, 2020. On December 02, 2020, the Covid-19 outbreak in Paraíba's State accounted for $146,528$ confirmed cases and $3,316$ deaths as reported on [16]. Like this, the objective of this work is to describe the evolution of the Covid-19 epidemic in Paraíba's State and the Campina Grande City through the SIR-type model, where the disease infection rate α and the recovery rate β are considered dynamically and are obtained by adjusting the model to the data of infected individuals during the first 3 months of the epidemic. The effective reproduction number $\mathcal{R}(t)$ was obtained, which allowed to predict epidemic evolution in region and evaluate the effect of containment measures.

2 THE MODEL

The SIR model developed by A. Kermack and W. McKendrick [7], [8], [9] starts from the assumption that an individual goes through stages (or compartments) of susceptibility (S), infection (I), and removed (R) because he recovered and acquired permanent immunity throughout life; or ended up dying. Considering a homogeneous and constant population N (population size), $N = S(t) + I(t) + R(t)$, the dynamics of the SIR model occurs as follows: when there is contact between susceptible and infected individuals, it results in removing a fraction of the susceptible population, at an (αIS) rate, to the infected compartment. At the same time, the infected population has a recovery rate (β). Therefore, a fraction of the population is removed from the infected compartment to the removed compartment at a rate (βI). The removed compartment is made up of individuals who died or were healed. Cured people develop immunity, so they are not put back in the susceptible compartment. The incubation period is relatively short. The model does not take into account asymptomatic individuals and susceptible that have been exposed to infective individuals. We ignore births, deaths from other factors, or migratory effects. Figure 1 shows the representation of the SIR-type model.

Figure 1: Representation of the SIR-type model



The system of non-linear differential equations that describes the Covid-19 epidemic temporal evolution is given by [3], [17], [18]:

$$\begin{cases} \dfrac{dS}{dt} = -\alpha \dfrac{IS}{N} \\[2ex] \dfrac{dI}{dt} = \alpha \dfrac{IS}{N} - \beta I \\[2ex] \dfrac{dR}{dt} = \beta I \end{cases} \tag{1}$$

where α is the disease infection rate and β is the disease recovery rate.

Consider a constant population with total population N and the initial conditions: $I(0) = I_0$, $S(0) = S_0$ and $R(0) = 0$. The disease will be controlled when $\frac{dI}{dt} \leq 0$. From the second system equation (1), this condition is equivalent to:

$$\alpha\frac{I_0 S_0}{N} - \beta I_0 \leq 0 \Longrightarrow \frac{\alpha S_0}{\beta N} \leq 1. \tag{2}$$

Considering that, at the outset of the epidemic we have, $S_0/N \approx 1$ [6], the basic number of reproduction ($\mathcal{R}_0 = \alpha S_0/\beta N = \alpha/\beta$) is the average number of people that an infected individual will infect in the absence of combat measures. Therefore, when $\mathcal{R}_0 > 1$, the infected population grows exponentially. However, when $\mathcal{R}_0 < 1$, the disease is contained.

In our investigation we modify the SIR equations so as to have dynamic updates of α and β during time evolution. Throughout the simulations, we run α within interval [0.08, 0.51] and β within [0.08, 0.12]. Thus, at any time after the beginning of the contamination of the disease, it is contained when $\mathcal{R}(t) = \frac{\alpha S(t)}{\beta N} \leq 1$. For a constant population, $S(t) \leq S_0$ e $S(t) = N - I(t) - R(t)$. While the number of infected $I(t)$ and removed $R(t)$ is relatively small when compared to the value of N, it is reasonable to consider $S(t) \approx N$ [6] in numerical simulation. The evolution of the the epidemic and effect of social isolation measures were evaluated by the effective reproduction number $\mathcal{R}(t) = \frac{\alpha}{\beta}$ and the critical condition is still approximately $\mathcal{R}(t) = 1$.

The system of differential equations was solved numerically using Euler's recursive method. Also implemented within the computational code the method developed by Santos, Almeida and Moura [12], to obtain the effective reproduction number $\mathcal{R}(t) = \alpha/\beta$. The equations are solved for a wide range of α and β values and the ones corresponding to those solutions closest to real data are kept. Official data on infected individuals were obtained from repository the Paraíba Health Department and available of [16].

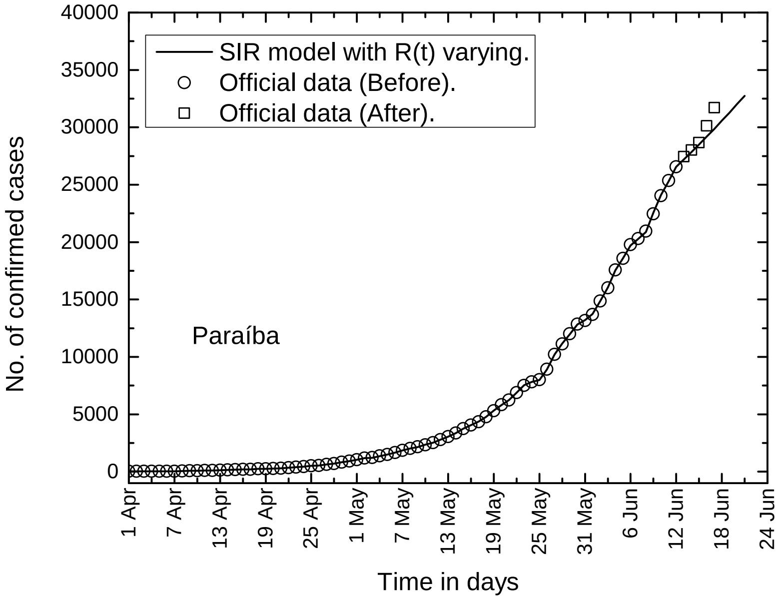
3 RESULTS AND DISCUSSIONS

To reduce the spread of a disease caused by an infectious agent, we must reduce the infection rate α through the adoption of protection and hygiene measures, in addition to restrictive measures such as distancing and social isolation. Allied to these measures, we must increase the disease recovery rate β, and this can be done through the use of medication and vaccination of the population. As at the beginning of the Covid-19 epidemic, we did not have medicines and vaccines, we based ourselves on scenarios reported in the literature, considering different periods in which infected individuals remain in circulation, being able to transmit the virus to susceptible people, due to social distance measures. Thus, throughout the simulation, we consider the α in the range [0.08, 0.51] and the β in the range [0.08, 0.12].

Figure 2 shows the comparison of the confirmed cases in Paraíba's State with the data provided by the SIR model considering a wide range of α and β during the period from April 01, 2020, to June 12, 2020. The initial parameters used are $S(0) = 4,010,000$ (estimated population of the Paraíba's State by the Brazilian Institute of Geography and Statistics (IBGE)),

$R(0) = 1$, and $I(0) = 21$, with 21 being the number of confirmed cases in Paraíba's State in April 01, 2020. that it is reasonable to assume $S(t)/N \approx 1$ at the beginning of the epidemic given that the number of recovered and deceased people as of April 01 should be, at most, of the same order as the number of infected people, which is negligible in respect to the total population. The simulated data based on the SIR model, are very close to the official data provided by the State Health Department, which indicates that the model describes well the number of infected for the analyzed period.

Figure 2: Comparison between confirmed cases and data obtained with the SIR model in Paraíba's State.



Using α and β best values obtained as of June 12 performing a 5-day average from June 8 to 12, an extrapolation (prediction) with the model for a period of eight days was considered. Official data were obtained after the prediction. It was observed that the official cases on June 17, 2020, in Paraíba's State were $31,712$ and the projection of the model was $29,883$ infected, which corresponds to a relative error of 5.7%.

Figure 3 shows the moving averages of the values of $\mathcal{R}(t)$, obtained every five days in Paraíba's State. The moving average value of $\mathcal{R}(t)$ at the beginning (April 2, 2020) is 3.0, following a downward trend to 1.6, at the end of the analyzed period.

Figure 3: $\mathcal{R}(t)$ (5-day average) starting April 2, 2020 for the Paraíba's State.

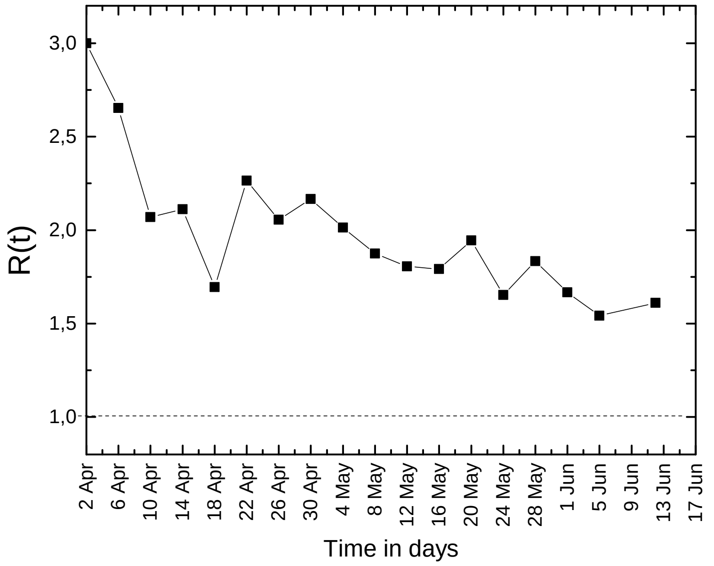


Figure 4 shows the evolution in time of the confirmed cases and the data provided by the SIR model obtained, considering a wide range of α and β, for Campina Grande City. The period considered was from April 18, 2020 to June 12, 2020 and the initial parameters used are $S(0) = 409,000$ (estimated population by IBGE), $R(0) = 1$, and $I(0) = 12$. It is noticed that the model fitted well to the official data for the analyzed period. After June 12th an extrapolation (prediction) of the model was made for a period of eight days. It was observed that the official cases on June 17, 2020, in Campina Grande City were $4,783$ and the model projection was $4,597$, which corresponds to a relative error of 3.9%.

Figure 4: Comparison between confirmed cases and data obtained with the SIR model for Campina Grande City.

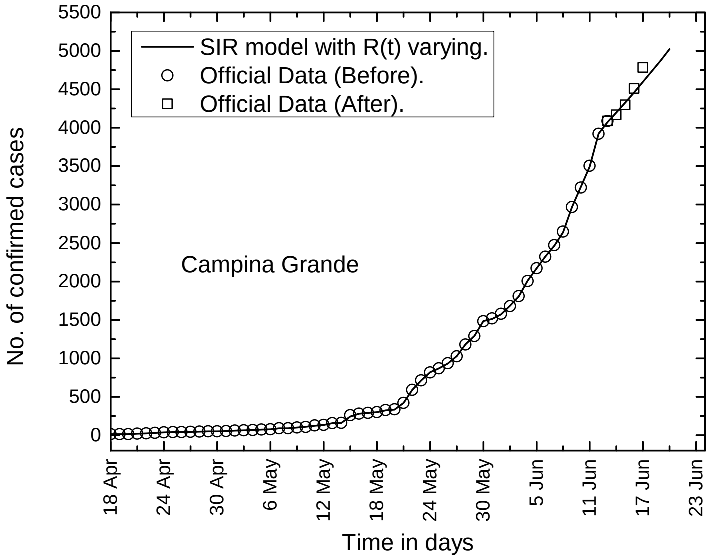
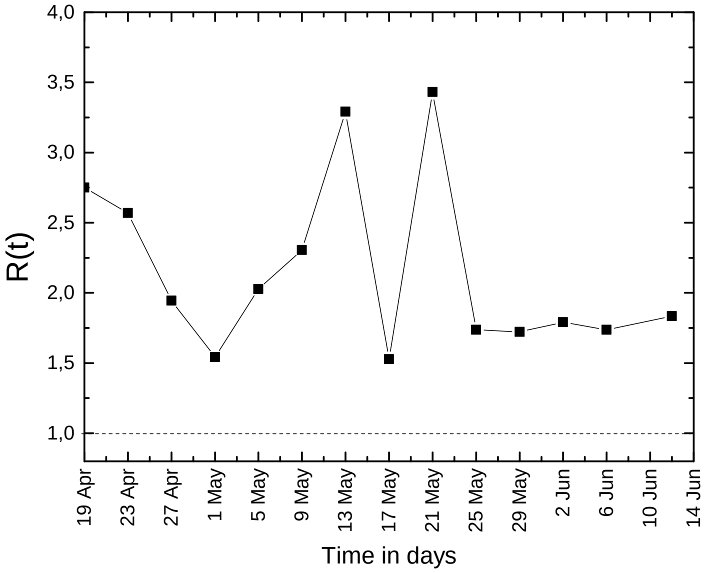


Figure 5 shows the moving averages of the values of $\mathcal{R}(t)$, obtained every five days for Campina Grande City. The moving average value of $\mathcal{R}(t)$ at the beginning (April 19, 2020) was 2.75 and decreased to 1.83 at the end of the analyzed period. It is noticed that the worst scenario happened on May 21, 2020, where $\mathcal{R}(t)$ reached a value of 3.4, indicating a drop in the social isolation index.

Figure 5: $\mathcal{R}(t)$ (5-day average) starting April 19, 2020 for Campina Grande City.



4 CONCLUSIONS

Using the SIR-type compartmental simple model, it was possible to obtain the effective reproduction number $\mathcal{R}(t)$ and to analyze the evolution of the Covid-19 epidemic in Paraíba's State and Campina Grande City. It is observed that in Paraíba's State the effective reproduction number $\mathcal{R}(t)$ followed a downward trend during the analyzed period. In Campina Grande City it is noticed that the worst scenario happened on May 21, 2020, where one can infer that there was relaxation of the measures of social isolation, since in this period there was no vaccine and/or effective treatments.

It should be noted that measures of social isolation, quarantine, use of personal protective equipment, and personal/collective hygiene habits are important to reduce the infection rate α, and consequently the $\mathcal{R}$ to a value less than 1, which characterizes the control of the epidemic. By fitted the parameters it was possible to conclude that the SIR Model describes well the data of infected individuals in Paraíba's State and Campina Grande City for the analyzed periods. It was also possible to make good predictions for short periods with a relative percentage error of less than 10%. The predictions for longer times may not be as accurate and the number of people infected with Covid-19 may be much higher than the reported cases, due to the underreporting that may occur.

Finally, knowing the dynamics of infection of the disease through mathematical models SIR-type helps to design different scenarios for different regions (cities, states, countries) and allows to help a possible gradual easing in isolation measures, and, preventing a collapse in the public and private health system. More complex models include other categories of individuals in the population, such as the SIRD (susceptible, Infected, Recovered, Deceased) model, which divides removed people into Recovered and Deceased. With this, other parameters are included, such as recovery and mortality rates. The SIR model can be modified considering the total non-constant population. In this case, recruitment in the susceptible class is considered, due to births and immigration, in addition to mortality due to other factors. A variation of the SIR model that makes the modelling closer to reality consists of the SEIR type model that incorporates compartment E (Exposed) that represents the state of latency (incubation period), individuals in that state have the infectious agent in their body, however, the symptoms have not yet started.

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