

Epidemiological model for the construction of scenarios of the dissemination of COVID-19 in Codó-MA

Modelo epidemiológico para construção de cenários da disseminação da COVID-19 em Codó-MA

Modelo epidemiológico para la construcción de escenarios de la diseminación del COVID-19 en Codó-MA

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ABSTRACT

Background and objectives: due to the increase in the number of cases of the new coronavirus in the city of Codó-MA, there was a need to carry out a study on the spread of COVID-19 in the municipality in order to have a better knowledge and understanding of the problem. A study was carried out on the spread of COVID-19 in the city of Codó-MA, comparing the quantitative data on the number of cases in 2020 and 2021 between May and July and using the epidemiological model Susceptible-Infectious-Isolated-Recovered (SIQR). **Methods:** we collected daily data from the epidemiological bulletins made available by the Municipal Health Department of Codó (SEMUS-Codó), we chose the SIQR compartmental model to carry out the simulations, we assumed hypotheses and estimated the parameters in order to design the scenarios. We simulated scenarios such as social distancing of healthy individuals and social isolation of infected individuals. **Results:** in early 2020, cases increased more frequently than in early 2021, and approximately 20% of those infected were in social isolation. According to projections, more than 80% of cases of COVID-19 were not accounted for in Codó. In 2021, there was greater underreporting than in 2020, approximately 82% and 85%, respectively. **Conclusion:** from the results, the authors conclude that the social isolation of those infected is a more efficient method to contain an epidemic than the total blockade of the population and that the high number of underreported cases is because most of these cases are asymptomatic.

Keywords: COVID-19. Physical Distancing. Sub-Registration. Social Isolation. Morbidity.

RESUMO

Justificativa e objetivos: devido ao aumento do número de casos do novo coronavírus na cidade de Codó-MA, viu-se a necessidade para fazer um estudo sobre a propagação da COVID-19 no município para a ter melhor conhecimento e entendimento do problema. Foi realizado um estudo sobre a disseminação da COVID-19

na cidade de Codó-MA, sendo comparados os dados quantitativos dos números de casos nos anos de 2020 e 2021 entre os meses de maio e julho e utilizando o modelo epidemiológico Suscetíveis-Infeciosos-Isolados-Recuperados (SIQR). **Métodos:** coletamos os dados diários dos boletins epidemiológicos disponibilizados pela Secretaria Municipal de Saúde de Codó (SEMUS-Codó), escolhemos o modelo compartimental SIQR para a realização das simulações, supomos hipóteses e estimamos os parâmetros para podermos projetar os cenários. Simulamos cenários, tais como distanciamento social dos indivíduos sadios e isolamento social dos indivíduos infectados. **Resultados:** no início de 2020, os casos aumentaram com mais frequência do que no início de 2021, e aproximadamente 20% dos infectados estavam em isolamento social. De acordo com as projeções, mais de 80% dos casos de COVID-19 não foram contabilizados em Codó. Em 2021, houve maior subnotificação do que em 2020, aproximadamente 82% e 85%, respectivamente. **Conclusão:** a partir dos resultados, os autores concluem que o isolamento social dos infectados é um método mais eficiente para conter uma epidemia do que o bloqueio total da população e que o alto número de casos subnotificados são porque a maioria desses casos são assintomáticos.

Descritores: COVID-19. Distanciamento Físico. Sub-Registro. Isolamento Social. Morbidade.

RESUMEN

Antecedentes y objetivos debido al incremento en el número de casos del nuevo coronavirus en la ciudad de Codó-MA, surgió la necesidad de realizar un estudio sobre la propagación del COVID-19 en el municipio con el fin de tener un mejor conocimiento y comprensión de el problema. Se realizó un estudio sobre la propagación del COVID-19 en la ciudad de Codó-MA, comparando datos cuantitativos del número de casos en 2020 y 2021 entre mayo y julio y utilizando el modelo epidemiológico Susceptible-Infecioso-Aislado-Recuperado (SIQR). **Métodos:** recolectamos datos diarios de los boletines epidemiológicos que pone a disposición la Secretaría Municipal de Salud de Codó (SEMUS-Codó), elegimos el modelo compartimental SIQR para realizar las simulaciones, asumimos hipótesis y estimamos los parámetros para poder diseñar los escenarios. Simulamos escenarios como el distanciamiento social de personas sanas y el aislamiento social de personas infectadas. **Resultados:** a principios de 2020, los casos aumentaron con más frecuencia que a principios de 2021, y aproximadamente el 20% de los infectados se encontraban en aislamiento social. Según proyecciones, en Codó no se contabilizaron más del 80% de los casos de COVID-19. En 2021 hubo mayor subregistro que en 2020, aproximadamente 82% y 85%, respectivamente. **Conclusión:** de los resultados, los autores concluyen que el aislamiento social de los contagiados es un método más eficiente para contener una epidemia que el bloqueo total de la población y que el alto número de casos subregistrados se debe a que la mayoría de estos casos son asintomáticos.

Palabras clave: COVID-19. Distanciamiento Físico. Sub-Registro. Aislamiento Social. Morbosidad.

INTRODUCTION

Humanity has already gone through several epidemics, and at the end of 2019, in the city of Wuhan, China, a new viral infectious disease emerged that was designated by the World Health Organization (WHO) as COVID-19, caused by a virus called Severe coronavirus. Acute Respiratory Syndrome Coronavirus 2 of the Genus *Betacoronavirus* (SARS-CoV-2). In a short time, the virus spread around the world and, in early March 2020, it was already considered a pandemic.

Due to its rapid transmission, the first confirmed case in Brazil soon appeared, in São Paulo, on February 26, with a 61-year-old man who had a history of travel to Italy.¹ After confirmation of the first case, new cases appeared in all states of the country. The Ministry of Health recommended basic hygiene measures, such as washing the hands with soap and water and covering the mouth and nose when coughing or sneezing to avoid contamination. In Maranhão, the first case was confirmed on March 20 by the State Department of Health (SDH) in the city of São Luís. With the disease spreading throughout the territory, Codó soon had its first confirmed case on April 21, 2020, and since then, the numbers have only

increased in the city.²

Regarding the rapid spread of the virus, several studies have been carried out to understand how its spread occurs and, consequently, find measures that help to control and contain its transmission.³⁻⁷ One of the most used tools for this type of work are mathematical models, which have become important instruments in the analysis of the spread and control of infectious diseases. These models are strategies used to obtain some explanations and understanding of real situations, predicting important issues, such as changes caused by interventions in the spread of diseases.⁸⁻¹⁰

Many works were carried out with this same proposal; however, each city has its own population, cultural, social and economic reality. These factors contribute to the spread of a disease; Having said that, we sought to carry out a study of the city with our local reality that, since the first confirmed case of COVID-19, the numbers have grown rapidly. As it is a new, unknown disease and many cases are not serious, the population often does not take the necessary precautions. Therefore, there was a need to carry out a study on the spread of COVID-19 in the city of Codó to have better knowledge and understanding about the problems caused by the disease

and to alert the population so that everyone can take the necessary precautions, whether through vaccines or protective measures. It is also expected that this research will be able to provide data to the health agencies of the municipality and that, through this information, it will help the administrative authorities to adopt the best strategies for controlling and eradicating the virus.

This research aimed to carry out a study on the spread of COVID-19 in the city of Codó-MA and compare the quantitative number of cases in 2020 and 2021 between May and July using the epidemiological model Susceptible-Infectious-Isolated-Recovered (SIQR).

METHODS

The chosen study site was the city of Codó located in the east of the state of Maranhão, with an estimated population (2021) of around 123,368 inhabitants, according to the Brazilian Institute of Geography and Statistics (IBGE - *Instituto Brasileiro de Geografia e Estatística*).¹¹ The period in which cases began to appear more frequently was from May 2020, therefore, May to July 2020 and 2021 were chosen for comparisons to be made.

All data collected from the daily newsletters are in the public domain and were found on social networks such as Facebook® and Instagram®, through the official page of the Municipal Health Department of Codó (SEMUS-Codó - *Secretaria Municipal de Saúde de Codó*), which contains information on accumulated confirmed, suspected, recovered and dead cases since the beginning of the pandemic. With these data, we applied the SIQR epidemiological model to compare the main changes in case numbers that occurred over a one-year period.

The model used was the SIQR epidemiological model. The SIQR model is an extension of the SIR model, and divides the population into four compartments that indicate the situation of each individual in relation to the development of the disease in each unit of time (t), namely: (S) individuals susceptible to being contaminated; (I) individuals who have been infected and can transmit the disease to susceptible individuals; (Q) individuals who acquired the disease and are isolated, i.e., they were diagnosed and are receiving treatment away from interaction with other people; and (R) individuals who have received treatment and are recovered. Therefore, the total population of the region under study can be written, which is represented by the constant N as the sum of all the compartments mentioned above,^{2,4,7,11} namely:

$$N(t) = S(t) + I(t) + Q(t) + R(t) \quad (1)$$

The SIQR model is represented by a set of systems of ordinary differential equations:

$$\frac{dS}{dt} = -\alpha SI - \mu S \quad (2)$$

$$\frac{dI}{dt} = (1 - \phi_1)(1 - \eta)\alpha SI - (\gamma + \mu)I \quad (3)$$

$$\frac{dQ}{dt} = (1 - \phi_1)\eta\alpha SI - (\rho + \mu)Q \quad (4)$$

$$\frac{dR}{dt} = \phi_1(1 - \eta) + \phi_2\eta\alpha SI + \rho Q + \gamma I - \mu R \quad (5)$$

Therefore, α is the transmission rate; γ is the out-of-hospital recovery rate; μ is natural mortality rate; η is the rate of isolation of infectious individuals; ρ is recovery rate of individuals in quarantine; ϕ_{-1} is the mortality rate of non-isolated individuals; ϕ_{-2} is the mortality rate of isolated individuals. We denote that each equation represents the entry and exit of individuals from one compartment to another. As individuals enter a given compartment, the number increases, when they leave, the number decreases.

Assumptions about model

To carry out the simulations, some hypotheses were formulated about the model above and parameter estimates.

- We consider that not all people are equally likely to be infected;
- Susceptibility is the same for everyone, but for practical simulation purposes, we only consider a percentage of the susceptible population;
- To simulate mortality curves, assume that a rate of infected individuals will eventually die from the disease;
- The incubation period varies after exposure to the virus from 2 to 14 days;¹²
- We consider that people who test positive quickly have been isolated and are not likely to contaminate other individuals;
- We believe that, after recovery, individuals are immune to the disease, although there are cases of reinfection;

Parameter estimates

Based on the data collected and the hypotheses formulated, the parameter values were estimated to carry out the projections. Taking into account that the municipality of Codó is not very populous, there are about 123,368 inhabitants and a demographic density of 27.06 inhab./km², according to IBGE estimates.¹¹ It was considered that, when the virus reached its peak of contamination, it did not reach the entire population of Codó, due to its low demographic density. Therefore, we assume that not all population was susceptible. We consider that only 90% of the population was susceptible to being contaminated by COVID-19, i.e., 111,031 inhabitants.

After an individual is tested positive, they are quickly isolated and has no chance of contaminating other people, however there are indications that they can infect other individuals during this period.¹³ Some studies point out that many cases are not notified, reaching 80% or more underreporting.¹²⁻¹⁴ Therefore, we assume that the number of COVID-19 cases is much higher than the numbers confirmed by SEMUS-Codó and that only 20% of cases were legitimately registered; therefore, it was assumed that the rate of isolation of infectious individuals was $\eta = 0.20$.

The fatality rate is the rate that calculates the proportion of the risk of death in the diagnosed infected population. In this work, the fatality rate provided by SEMUS-Codó in the months indicated for the study was used, which has an average of 3.94%. The mortality rate is the proportion of deaths in relation to all cases of infection, diagnosed or not. According to Bitar's study, the ϕ_{-1} mortality rate is 3.4%.¹³ Therefore, to calculate the mortality rate of a fraction of isolated infected individuals, we use the following formula, according to the isolation rate of infected people η and the mortality rate of COVID-19:

$$\phi_2 = \frac{(0.0394 \cdot 0.20 + \phi_1 \cdot (\eta - 0.20))}{\eta} \quad (6)$$

As the infection rate of isolated people undergoing hospital treatment is already estimated, we estimate the recovery rate of individuals in hospital isolation or at home and, for that, we use the non-hospital recovery rate γ , which refers to a portion of the population who is not quarantined and who recovers on his own without medical treatments. We used the following formula:

$$\rho = \frac{1}{(1 - \eta) \cdot (3.5/0.20) + \frac{1}{\gamma}} \quad (7)$$

Regarding the natural mortality rate μ , as we do not have precise data for the city of Codó, we used the mortality rate for the state of Maranhão which, according to IBGE data, is equivalent to 0.00563%.¹⁵

One of the most important parameters in an epidemic is R_{-0} the average number of people that an infectious individual can infect during the period of disease infectivity, i.e., the time in which the infected can transmit the disease to the susceptible. if $R_{-0} < 1$, the disease will not be able to spread on a large scale and will not reach the population; however, if $R_{-0} > 1$, infected individuals infect more than one person on average and high contagion can occur among the population.¹⁶ In this work, we used a value based on data made available by SEMUS-Codó, i.e., $R_{-0} = 3.1$.

The infection rate of α -susceptible individuals was assumed, through this rate we will know the number of healthy people who are contaminated in a time interval and the speed with which they pass from compartment (S) to class (I). Therefore, the following formula was used:

$$\alpha = \frac{\zeta R_0 \gamma}{N} \quad (8)$$

In order to know the number of healthy people who withdrew from interaction with society, we assume that a percentage of the population q strictly adhered to the recommendation to stay at home and the rest went about their lives normally. For this, we use the average number of people per family, according to IBGE, it has an

average of 3.5 people per family.¹⁵

We consider that in each family all members adhered to the recommendation of social distancing, except for one, who continues to interact with people far from home anyway. For the part of the population that complies with strict distancing, we assume a basic reproduction number of 0.99 and for members who remain in contact with the society, we assume a basic reproduction number $(0.99 + R_{-0})/2$. We saw that α is sensitized by ζ , so the parameter ζ is defined as:

$$\zeta = \frac{\left(\frac{2.5q}{3.5} \cdot 0.99 + \frac{q}{7} \cdot (0.99 + R_0) + (1 - q) \cdot R_0\right)}{R_0} \quad (9)$$

It is important to emphasize that there is a difference between social isolation and social distancing: social isolation is carried out by those people who tested positive and were removed from interaction with society; social distancing is carried out by uninfected people who have decided not to interact with the population, i.e., they have stayed away from society on their own.¹¹

Parameter analysis is the key piece for epidemiological modeling, because, through them, we discover the errors and uncertainties of collected data. According to table 1, we have a summary of all estimated parameters of the SIQR model.

Table 1. Estimated values for the parameters.

Parameters	Values	Meaning
N	111,031	Population susceptible to contagion
η	0.20	Isolation rate of infectious individuals
γ	1/14	Non-hospital recovery rate
μ	0.00563%	Natural mortality rate
ϕ_{-1}	3.4%	Mortality rate of non-isolated individuals
ϕ_{-2}	Equation (6)	Mortality rate of isolated individuals
R_{-0}	3.1	Amount that an infectious can infect other people
q	0.1 < 0.8	Percentage of isolation of the healthy population
ρ	Equation (7)	Recovery rate of individuals in isolation
A	Equation (8)	Infection rate of susceptible individuals
ζ	Equation (9)	Parameter sensitized by q

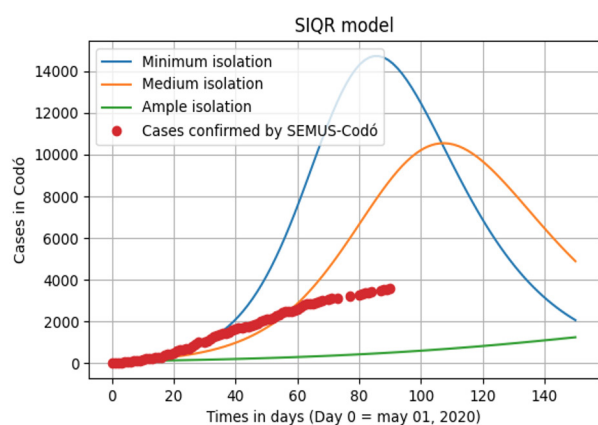
Different scenarios were used for the infected population and for the healthy population. We consider that a percentage of the infected population was isolated, namely: 20% is minimum isolation, which is the minimum number of infected people who can be confined; 40% is medium isolation, it is the mean isolation of the infected population who are away from social interaction; 80% is ample isolation, it is the highest value of infected people who can be removed from society.

For social distancing, we used the same values, 20%, 40%, and 80%, for minimum, medium, and ample distancing, respectively. However, in this other scenario, these values are for healthy people who decided to stay at home, not having contact with society.

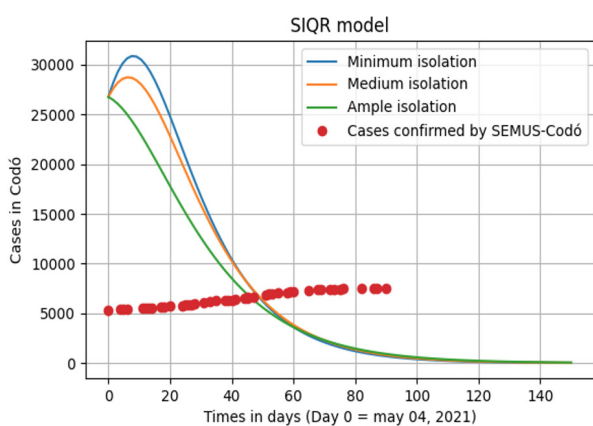
RESULTS

For the following projections, we consider different scenarios for the healthy population in social distancing, over a 150-day time frame. We estimated the basic reproduction number $R_{-0}=3.1$ and the mean time of the infectious period in 14 days. In this simulation, we did not change the value of η , and only the value of q changed, as we can see in figure 1.

- In the first situation, we consider η equal to 0.20, i.e., 20% of the infected population was in social isolation and q equal to 0.20, i.e., 20% of the healthy population was in social distancing;
- In the second situation, we did not change the value of η , we kept it at 0.20 as previously mentioned and we considered q equal to 0.40, in other words, 40% of the healthy population was in distancing;
- In the third situation, we kept the value of η equal to 20% and assumed that q is 0.80, in other words, suppose that 80% of the healthy population was in distance.



(A)



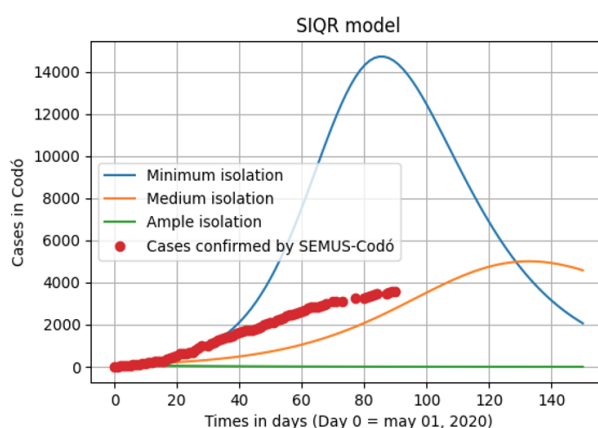
(B)

Figure 1. (A) Social distancing of healthy individuals vs number of infected individuals in 2020 over a period of 150 days. (B) Social distancing of healthy individuals vs number of infected individuals in 2021 in the period of 150 days.

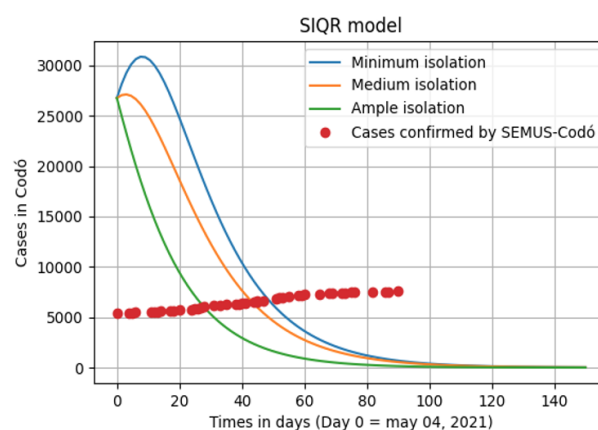
Source: author.

In the following simulation, we reversed roles, keeping the rate of the healthy population in social distancing q at 0.20 and using other values for infectious individuals in isolation η . We maintained the basic reproduction number $R_{-0}=3.1$ and the average time of the infectious period at 14 days, as shown in figure 2.

- $q = 0.20$, i.e., with this value, we consider that 20% of the healthy population is isolated and η equal to 0.20, i.e., 20% of the infected population was in social isolation;
- $q = 0.20$, again 20% of the healthy population is isolated and η equal to 0.40, therefore, 40% of the infected population was in isolation;
- $q = 0.20$, we kept the same value for the healthy population and η equal to 0.80, in other words, suppose that 80% of the infected population was isolated.



(C)

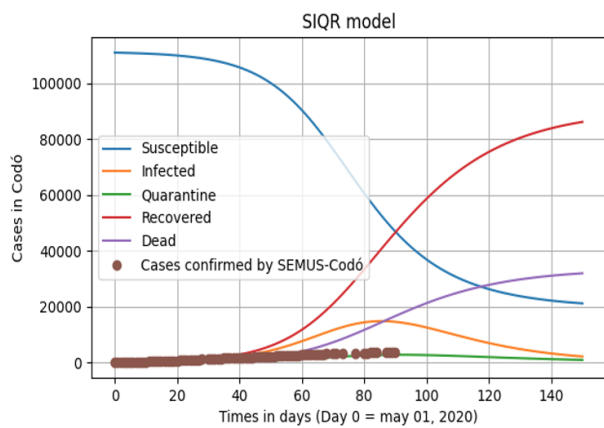


(D)

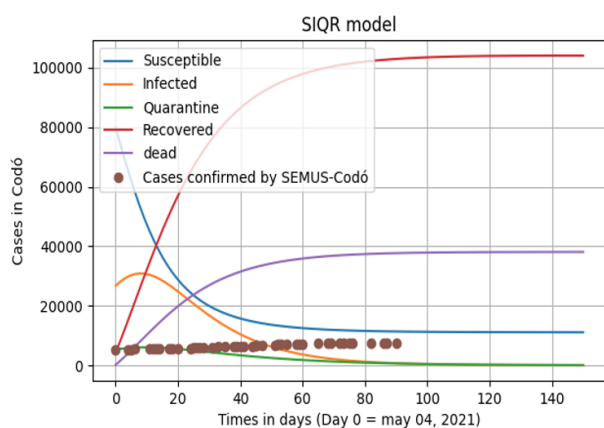
Figure 2. (C) Isolation of infected individuals vs healthy population in 2020 over a period of 150 days. (D) Isolation of infected individuals vs healthy population in 2021 within 150 days.

Source: author.

In Figure 3, we used all compartments in a 150-day scenario where 20% of the q healthy population was socially distancing and 20% of the infectious were isolated.



(E)



(F)

Figure 3. (E) Scenario involving all compartments of the SIQR model in the year 2020. (F) Scenario involving all compartments of the SIQR model in 2021.

Source: author.

DISCUSSION

According to projections, in figure 1(A),(B), approximately 20% of the healthy population in the period from May to July 2020 and 2021 were socially distancing and less than 20% of the infected population were socially isolated. In figure 2(C) and (D), both values are considered very low.¹³ The ideal value for social isolation of the population would be 80%, however this percentage is impossible, because people need to leave home to work and survive, especially in the city of Codó, where there is a high poverty rate, since people social isolation measures affect the less financially favored classes more.

When we use social isolation at 20%, the virus reached its contamination peak around day 80, with approximately 15,400 cases. In figure 2(C), on that same date, the number of cases confirmed by SEMUS-Codó was 3,277, therefore, we can say that there were more or less 18,677 cases of COVID-19. The numbers confirmed by the secretariat represent 18% of the total amount, i.e., 82% of the cases of the new coronavirus were not accounted for

on that date. There are many unreported cases because of the huge group of asymptomatic infected people.^{12-14,17}

In an epidemic forecasting study in Shanghai, the rate of asymptomatic infections was very high, at around 90%.¹⁸ Based on these works and projections, we can suggest that the factors that contributed to high underreporting were the large number of asymptomatic cases and the lack of rapid tests. Generally, rapid tests are mostly applied to symptomatic individuals, disregarding the huge potential for asymptomatic infected people, since the numbers of infected and unconfirmed cases grow faster than the number of confirmed cases.^{12,17}

When we use 40% for healthy population in social distancing, as in figure 1(A), COVID-19 cases peaked with more than 10,000 cases, and when we put 40% for infectious population in isolation, the case numbers reached its peak with approximately 5,000 cases, as we can see in figure 2(C), with a large decrease in cases.

Already in ample isolation, when 80% of the infectious population is isolated, the numbers do not leave zero. In the previous simulation, we saw that when the distanced healthy population is 80%, cases reach just over 1,500. Thus, we observe that, with an increase in the infectious population in isolation, η directly leads to a lower growth of the compartment of infectious individuals (I) capable of spreading the disease and that the quarantine measure is more effective than the total blockade of the population.

Numerical results of quarantined individuals have a great influence on the transmission of COVID-19 infection. In this way, the minimization of transmission is related to the application of a quarantine policy.¹⁹ The number of infected individuals can be reduced through mass testing, but the implementation of strict and immediate quarantine leads to reductions of about 90% in the total number of cases.¹⁷

It was observed that the numbers of cases of COVID-19 are much higher than those confirmed by SEMUS-Codó. Until May 11, 2021, the number of confirmed cases was 5,466. According to the simulations in Figure 2 (D), on the same date, the underreported cases were approximately 32,000. Adding this value, we have approximately 37,466, i.e., they were almost 7 times greater than those recorded by SEMUS-Codó. The 5466 represent approximately 15%, and the 32,000 underreported represent 85% of cases.

It can be seen that there was a large number of underreporting, and this can be explained because the rapid tests are mostly applied to symptomatic individuals. A study of unreported case estimation indicates that testing only symptomatic patients may overlook more than 50% of COVID-19 patients, who play an important role in transmitting the virus. It also suggests a scenario where placing only confirmed cases in quarantine is not able to prevent the spread of the virus due to the fact that there are a large number of undiagnosed cases. And the number of infected individuals can be reduced through mass testing.¹⁷

With all compartments of the SIQR model, Figure 3(E), initially, there are many susceptible people, becau-

se, as the number of infected increases, the number of susceptible agents will decrease and, consequently, the number of recovered ones will increase.¹⁹ We have seen that the number of underreported cases grows faster than the number of confirmed and isolated q individuals. This imbalance has been observed worldwide, with many undocumented cases of infection.^{12-14,17}

As shown in figure 3(F), as of day 80, the entire population has already recovered and there are no more infectious agents to contaminate the susceptible, which also decreased significantly. As the percentage of circulation approaches zero, representing almost complete blockage, the number of cases tends to zero and stabilizes at a constant final value. In other words, the quarantine of those infected, symptomatic or not, contributes to the reduction of basic reproduction, reducing the rate of contamination.⁴

The predictions were very close to reality and were in line with the cases confirmed by SEMUS-Codó. In 2021, there was less spread than in 2020. Initially, cases increased very quickly and the government imposed protective measures such as social distancing, wearing masks and hand hygiene to contain the spread of the virus.

Between the months of May and July 2020 and 2021, we had no information regarding any case of the COVID-19 variant. The first dose of the vaccine started on January 21, 2021, and by the end of July 2021, only 14% of the population had taken the second dose. However, as the contamination peak had already occurred, the use of vaccine did not interfere with the simulations' value.

Based on the simulations, we concluded that increasing the amount of rapid testing in the entire population, with or without symptoms and stricter quarantine measures, would decrease a large amount of COVID-19 case numbers. However, the lack of resources is a challenging task for low-income countries or regions, resulting in a much smaller number of confirmed patients. Depending on the scenario, mass testing and strict quarantine measures could drastically reduce the total number of cases by 90% to 95%.¹⁷

The results found here may suffer interference from external agents, such as public managers, climatic and cultural, economic factors, etc. Please note that this is a 2020 and 2021 survey and results may be out of date. It would be interesting if future studies studied long-term sequels caused by COVID-19. We believe that the results of our study can provide guidance for coping with COVID-19 in the municipality.

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REFERENCES

1. Ministério da Saúde (BR). Acha que está com sintomas da COVID-19?. https://www.coronavirus.ms.gov.br/?page_id=29.
2. G1. Governo confirma o primeiro caso do novo coronavírus no Maranhão. <https://g1.globo.com/ma/maranhao/noticia/2020/03/20/governo-confirma-o-primeiro-caso-do-novo-coronavirus-no-maranhao.ghtml>.
3. Camilo MJ, Moura DFC, Salles RM. Modelagem matemática para epidemia de COVID-19 no Brasil. *Rev Mil de Ciência e Tecn.* 2020; 2(37):1-12. <http://ebrevistas.eb.mil.br/CT/article/view/6772>.
4. Gomes SCP, Monteiro IO, Rocha CR. Modelagem dinâmica da COVID-19 com aplicação a algumas cidades brasileiras. *Revista Thema.* 2020; 18:1-25. <https://periodicos.ifsul.edu.br/index.php/thema/article/view/1793>.
5. Ma J, Dushoff J, Bolker B. et al. Estimating Initial Epidemic Growth Rates. *Bull Math Biol.* 2013; 76:245-260. doi: 10.1007/s11538-013-9918-2
6. Floquet S, Leite TN, Câmara RCP. et al. A matemática no combate à epidemia: estudo sobre a COVID-19 na região do vale do São Francisco. *REVASF.* 2021; 24(11):100-146. Disponível em: <https://www.periodicos.univasf.edu.br/index.php/revasf/article/view/1561>.
7. Huppert A, Katriel G. Mathematical modeling, and prediction in infectious disease epidemiology. *CMI.* 2013; 11(19):999-1005. doi: 10.1111/1469-0691.12308
8. Bertone AMA, Bassanezi RC, Jafelice RSM. Modelagem Matemática. Uberlândia, MG:UFU, 2014. <https://repositorio.ufu.br/handle/123456789/25315>.
9. Rocha DIC. Modelos matemáticos aplicados à epidemiologia. Porto. Dissertação [Mestrado em Métodos Quantitativos em Economia e Gestão] - Faculdade de Economia da Universidade do Porto; 2012. doi: 10216/63680
10. Khan MA, Atangana A. Modeling the dynamics of novel coronavirus (2019 nCov) with fractional derivative. *Alex Eng J.* 2020; 4(59):2379-2389. doi: 10.1016/j.aej.2020.02.033.
9. IBGE. Cidades e Estados. <https://www.ibge.gov.br/cidades-e-estados/ma/codo.html>.
10. Li XP, Ullah S, Zahir H. et al. Modeling the dynamics of coronavirus with super-spreader class: A fractal-fractional approach. *Results Phys.* 2022; 34:105179. doi: 10.1016/j.rinp.2022.105179.
11. Bitar S, Steinmetz WA. Scenarios for the Spread of COVID-19 in Manaus, Northern Brazil. *An Acad Bras Ciênc* 2020; 92(4):1-12. doi: 10.1590/0001-37652020200615
12. Li R, Pei S, Chen B. et al. Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV-2). *Science.* 2020; 6490(368):489-493. doi: 10.1126/science.abb322
13. IBGE. Síntese de indicadores sociais uma análise das condições de vida da população brasileira. <https://necat.ufsc.br/sintese-de-indicadores-sociais-ibge/>.

14. Driessche PVD, Watmough J. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math Biosci.* 2021; 2(180):29-48. doi: 10.1016/S0025-5564(02)00108-6
15. Zhan C, Shao L, Zhang X. et al. Estimating unconfirmed COVID-19 infection cases and multiple waves of pandemic progression with consideration of testing capacity and non-pharmaceutical interventions: A dynamic spreading model. *Inf. Sci.* 2022; 607:418-439. doi: 10.1016/j.ins.2022.05.093
16. Ma Y, Xu S, An Q. et al. Coronavirus disease 2019 epidemic prediction in Shanghai under the "dynamic zero-COVID policy" using time-dependent SEAIQR model. *J Biosaf Biosecur.* 2022; 2(4):105-113. doi: 10.1016/j.jobb.2022.06.002
17. Adnan, Ali A, Rahman M. Investigation of time-fractional SIQR Covid-19 mathematical model with fractal-fractional Mittag-Leffler kernel. *Alex Eng J.* 2022, 10(61):7771-7779. doi: 10.1016/j.aej.2022.01.030

AUTHORS' CONTRIBUTIONS

Antonia Lisboa dos Santos contributed to the planning, conception, design of the article, interpretation of data and revision of the article.

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