Epidemiology: Analysis And Construction Of A Mathematical And Computational Model In Complex Systems For The COVID-19 Pandemic

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Abstract. *The textbook mathematical model in epidemiology - SIS (Susceptible-Infected-Susceptible) provided the basis for proposing a new and improved model based on the observable behaviors of the current Covid-19 pandemic. The goal of this study was to analyze the behavior of the system and the influence of the LockDown factor on infected individuals. The model proposed here, called SIERDASHQ (Susceptible - Infected - Exposed - Recovered - Deceased - Asymptomatic - Symptomatic - Hospitalized - Quarantined), was simulated with values that expressed the situation of the pandemic at the national level, making it possible to compare data to the graphics produced by the program, which confirms the validity of the model.*

1. Introduction

Humanity has been concerned about widespread diseases, which can cause a large number of deaths. The problem is even greater when these diseases have a very high power of contamination and propagation, spreading very quickly in a short period of time. When a world-wide event occurs, we call it a pandemic, which due to COVID-19 is the state the world is currently in.

As the epidemic developed around the world, medical and world authorities realized the rapid spread of the disease and its potential danger for the collapse of health systems in affected countries. As a rule, the decisions taken by the authorities had a strong impact on the affected societies, especially in the productive sectors, causing harmful effects beyond the disease itself.

Due to COVID-19, studies began to be carried out with the aim of characterizing the type of epidemic, determining the causative factors and seeking ways to control it. A tool that helps this study is mathematical modeling, which consists of transforming real situations into mathematical models that, after being analyzed, provide results that can be interpreted and applied in reality [Mata 2021].

Epidemiological mathematical modeling is quite efficient in helping the decision-making process, the application of analytical models in the study of the development of epidemics can represent an important tool for decision-makers, allowing a balanced and informed analysis of the impact of the epidemic on health, on the

economy , among other areas of society [Deng et al. 2022]. For this reason, it is necessary to develop these models in order to provide a basis for correct decisions.

This paper aims to implement a complete deterministic model for the COVID-19 and analyze the impact that the lockdown has on the model population and on the spread of the disease. The following sections of the paper presents, respectively, the methodology used to implement the model, in sequence the results and analysis generated and acquired by the model implementation and the conclusions of the study.

2. Methodology

Mathematical modeling in Epidemiology is done through the study of equations that describe the interaction between the population and the environment, resulting in a detailed analysis of the disease. Based on this question, several other mathematical models in Epidemiology began to be studied, such as the compartmental models. They receive this name due to the fact that the population is divided into compartments (or classes), which indicate what state the individual is in [Sen 2021].

The model that was developed, in addition to having a large number of classes, has 19 relationships that occur between them, which makes it a very complex model and, due to this and our time, it is complex to describe all the relationships it performs. That's why a diagram that demonstrates the relationships was created, the classes are:

- Susceptible (x): Individuals who are capable of acquiring the virus;

- Exposed (y): Individuals who have had contact with the virus and can transmit it to susceptible individuals;

- Infected (z): Individuals who have contracted the disease and can transmit it to susceptible individuals;

- Asymptomatic (k): Individuals with the disease who did not show symptoms;

- Symptomatic (m): Individuals with the disease who presented symptoms;

- Hospitalized (p): Individuals who contracted the disease and required hospitalization;

- Quarantine (q): Individuals who spend a period of time in seclusion, which may or may not be contaminated;

- Recovered (u): Individuals who have returned to a healthy state and can no longer transmit the disease;

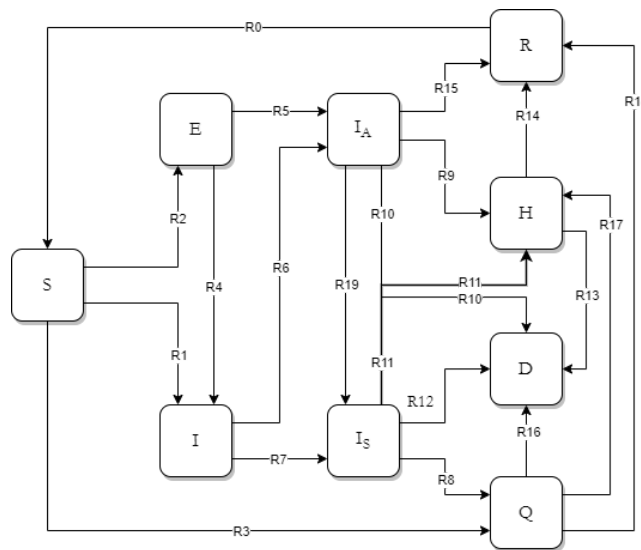- Deceased (o): Individuals who died due to the virus;

Figure 1. Model Diagram. S=Susceptible, I=Infected, E=Exposed, R=Recovered, D=Deceased, Ia=Asymptomatic, Is=Symptomatic, H=Hospitalized, Q=Quarantine.

According to the nomenclature already used, the new model was named SIERDASHQ (Susceptible - Infected - Exposed - Recovered - Deceased - Asymptomatic - Symptomatic - Hospitalized - Quarantine).

The constants corresponding to each transition rate are:

- R0: Recovered individuals who are susceptible to the virus again;
- R1: Susceptible individuals who are infected by the virus;
- R2: Susceptible individuals who are exposed to the virus;
- R3: Percent of lockdown;
- R4: Exposed individuals who have taken the test and are infected;
- R5: Contamination vectors who do not know they have the virus;
- R6: Infected individuals who are asymptomatic;
- R7: Infected individuals who are symptomatic;
- R8: Symptomatic individuals who are in quarantine;
- R9: Asymptomatic individuals who need to be hospitalized;
- R10: Asymptomatic individuals who have died;
- R11: Symptomatic individuals who need to be hospitalized;
- R12: Symptomatic individuals who have died;
- R13: Hospitalized individuals who have died;
- R14: Hospitalized individuals who have been discharged;
- R15: Asymptomatic individuals who have recovered;
- R16: Quarantined individuals who have died (not have been hospitalized);
- R17: Quarantined individuals who have been hospitalized;
- R18: Quarantined individuals who have recovered;
- R19: Asymptomatic individuals who become symptomatic;

From a deterministic perspective, the dynamics of the model represented in Fig. 1 are represented by the System of (differential) Equations on Figure 2.

$$\frac{dx}{dt} = \frac{1}{S2} \cdot \{(R0 \cdot x \cdot u) - [(R1 \cdot x \cdot z) + (R2 \cdot x \cdot y) + (R3 \cdot x \cdot q)]\}$$

$$\frac{dy}{dt} = \frac{1}{S2} \cdot \{(R2 \cdot x \cdot y) - [(R4 \cdot y \cdot z) + (R5 \cdot y \cdot k)]\}$$

$$\frac{dz}{dt} = \frac{1}{S2} \cdot \{[(R1 \cdot x \cdot z) + (R4 \cdot y \cdot z)] - [(R6 \cdot z \cdot k) + (R7 \cdot z \cdot m)]\}$$

$$\frac{dq}{dt} = \frac{1}{S2} \cdot \{[(R3 \cdot x \cdot q) + (R8 \cdot m \cdot q)] - [(R16 \cdot q \cdot o) + (R17 \cdot q \cdot p) + (R18 \cdot q \cdot u)]\}$$

$$\frac{dk}{dt} = \frac{1}{S2} \cdot \{[(R5 \cdot y \cdot k) + (R6 \cdot z \cdot k)] - [(R9 \cdot k \cdot p) + (R10 \cdot k \cdot o) + (R19 \cdot k \cdot m) + (R15 \cdot k \cdot u)]\}$$

$$\frac{dm}{dt} = \frac{1}{S2} \cdot \{[(R7 \cdot z \cdot m) + (R19 \cdot k \cdot m)] - [(R8 \cdot m \cdot q) + (R11 \cdot m \cdot p) + (R12 \cdot m \cdot o)]\}$$

$$\frac{do}{dt} = \frac{1}{S2} \cdot \{[(R10 \cdot k \cdot o) + (R12 \cdot m \cdot o) + (R13 \cdot o \cdot p) + (R16 \cdot q \cdot o)]\}$$

$$\frac{dp}{dt} = \frac{1}{S2} \cdot \{[(R9 \cdot k \cdot p) + (R11 \cdot m \cdot p) + (R17 \cdot p \cdot q)] - [(R13 \cdot o \cdot p) + (R14 \cdot p \cdot u)]\}$$

$$\frac{du}{dt} = \frac{1}{S2} \cdot \{[(R14 \cdot p \cdot u) + (R15 \cdot k \cdot u) + (R18 \cdot q \cdot u)] - (R0 \cdot u \cdot x)\}$$

Figure 2. Equations.

Thus, the total population N can be written as the sum of the individuals of the above mentioned classes, that is:

$$N = x + y + z + k + p + q + m + o + u$$

The study of mathematical models has as main goal to analyze the rate of infection force and the basal reproducibility rate. The strength of infection is the rate at which the disease spreads, and determines the extent of transmission. It depends only on the number of infected individuals. The baseline reproducibility rate is the number of infections caused in susceptible individuals from a first infection and is related to the growth or decrease of the epidemic.

COVID-19 occurs through direct transmission through physical contact or proximity between healthy and infected individuals. This relationship is based on the Law of Mass Action, a principle studied in chemical kinetics that states that the rate of a reaction is directly proportional to the concentrations of the reactants, that is, as long as a particle moves, it has the same chance of meeting each other [Voit 2015].

The application of this Law to mathematical modeling is that, as transmission occurs with the encounter between susceptible and infected individuals, the variation of susceptible individuals is proportional to the number of infected individuals [Luiz 2012]. On the other hand, mathematics, which is very complex, needs to be solved and requires high precision in the results, therefore, the differential equations were solved by the 4th order Runge Kutta method.

The proposed simulation is the nearest approach from the experimental world than the other simulations presented by the literature. Due to its complexity in correlating the compartments of the individuals over the infection.

The values used by the constants in the model were collected from the reports of the Rio de Janeiro government [Secretaria de Estado de Saúde do Rio de Janeiro 2022].

A basis calculus was applied in the reports data to acquire a percentage for the rates. Then the model was adapted to become realistic and based on the reported values.

3. Results and discussion

Solving these differential equations, graphics that show the performance of this model were constructed. The model was simulated with values that expressed the situation of the pandemic at the national level, which generally represented the best for the study of LockDown, and then graphics were built that show the performance of this model, making it possible to compare data, which confirms the validity of the model. This validation was also carried out with less complex models, already published in national and international articles that simulate pandemic cases [Gomes 2020]. In addition, some validations of the model were built by a similarity comportament with other models and studies [Caccavo 2020].

The first analysis is the relationship between contaminated and infected. In Figure 3, there is a blue line, which represents the contaminated, in red the infected and in yellow the Deceased.
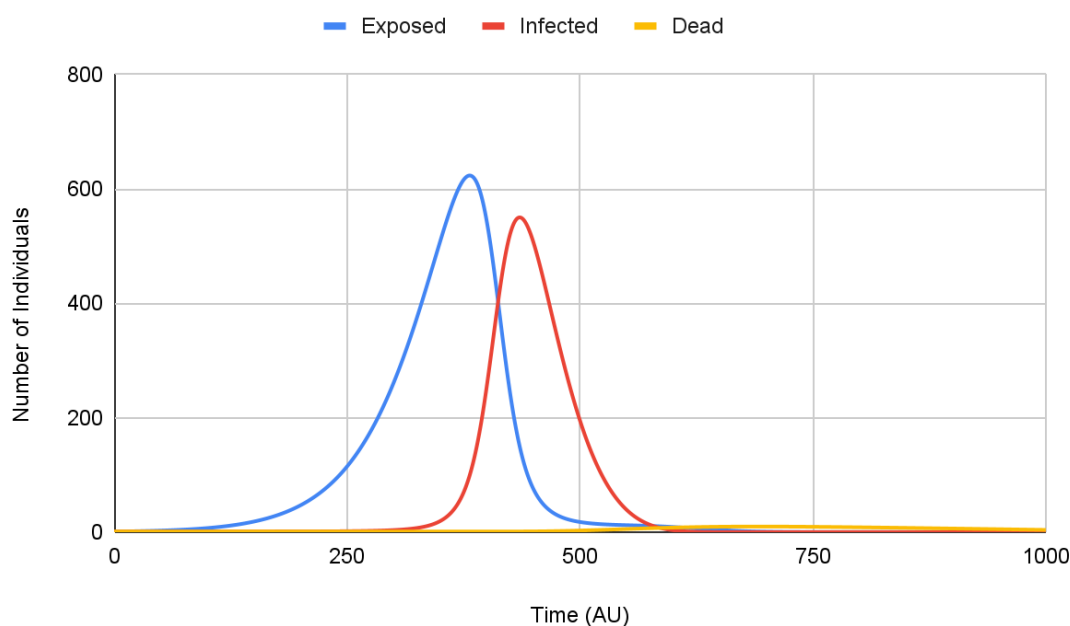

Figure 3. LockDown at a 10% rate.

An amount of 2000 inhabitants and a cycle of 700 iterations were applied to the model. Based on the statistical values, it can be seen that this result makes sense and is valid for the sample with which the simulation was performed (Figure 3).

An important factor that we can take away from this graphic (Figure 3) is that it was formed with a LockDown of 10% for susceptible individuals. Now analyzing the simulation with 20% LockDown (Figure 4).
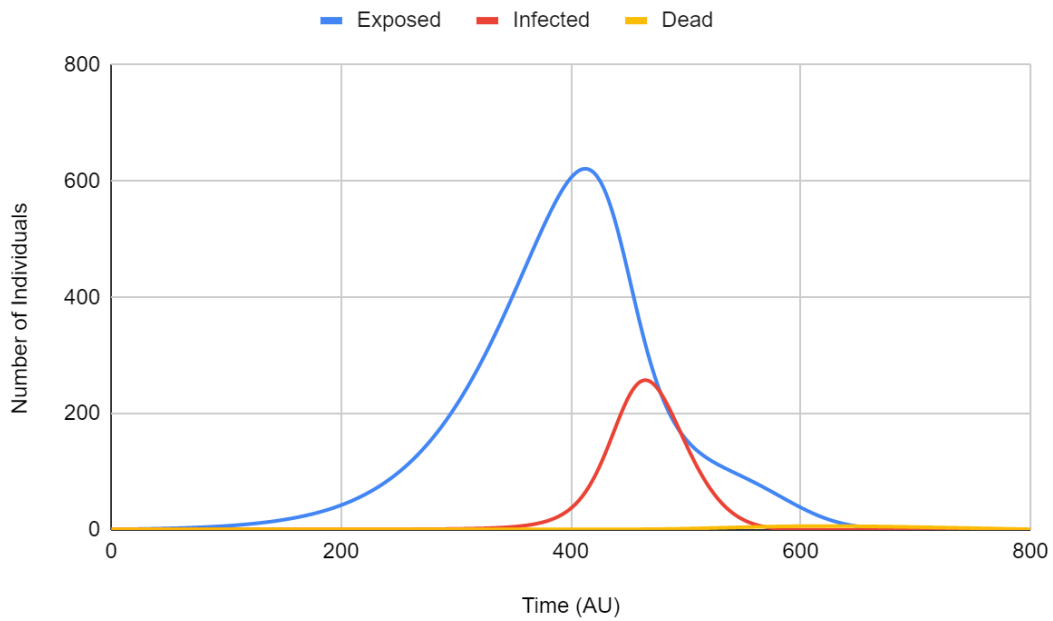
Figure 4. LockDown at a 20% rate.

The red line shows the fall of the infected and the blue line represents the exposed. The blue line remains with the same amplitude but with a delay, that is, it took more cycles to reach. The exposure factor is not contaminated and therefore its value is not greatly affected by LockDown (Figure 4).

It is still possible to compare the variation of the LockDown factor in relation to the number of infected individuals, which makes clear its influence on the pandemic and that its presence in the dynamics is a fundamental tool for the control of the infected.
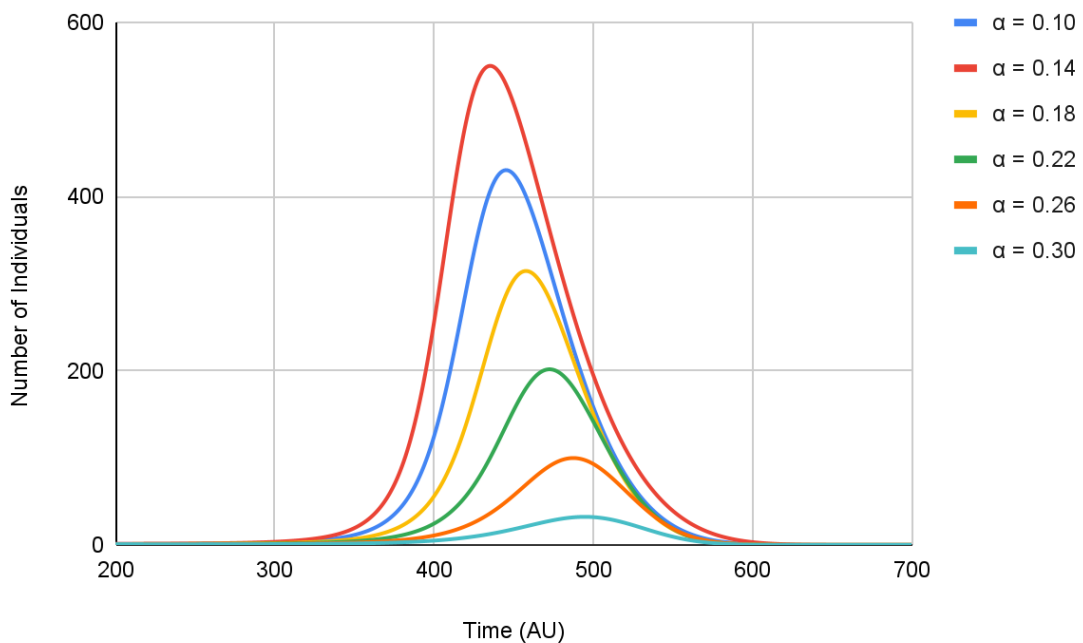

Figure 5. LockDown Factor Variation.

It can be seen that, with a LockDown factor above 30%, the number of infected individuals would be so close to zero that the probability of not having a pandemic is high (Figure 5).

In Figure 6 there is a panoramic view of the system. In this simulation, the value of symptomatic was higher than asymptomatic, but it depends on the values used, and these values change from country to country, region to region.
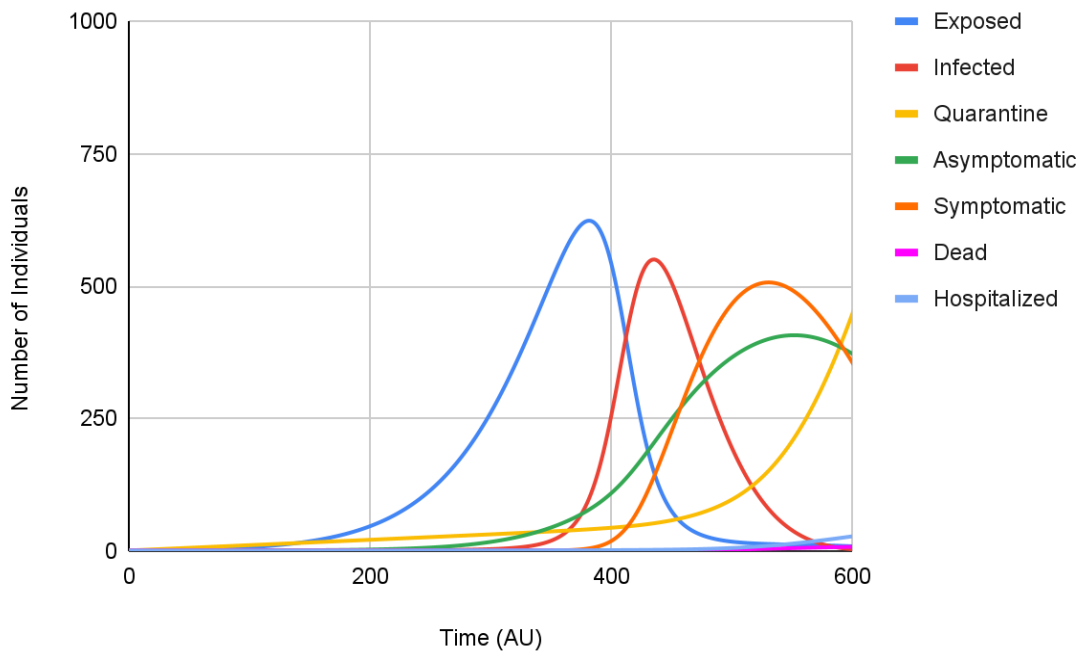

Figure 6. Full system.

The results present the infection dynamics of an epidemic disease, the influence of a Lock-Down in the same dynamic and a short parametric analysis and evaluation about the Lock-Donw appliance on the model and its influence over the infecteds.

4. Conclusions

With the current model, it was possible to understand more clearly the epidemiological dynamics, which is fundamental for the next step of the research, where we will seek to further complement the system, with economic issues. More than that, this system makes it possible to simulate and compare different situations, which is extremely important to understand the impacts of actions and to help in the decision-making process during the pandemic of COVID-19. It is worth remembering that this model is unique and not described in the literature, which made its implementation essential.

The study results show how important Lock-Down is, even in a small population as modeled. Also an overview about the COVID-19 dynamics and the concepts in symptomatic and asymptomatic individuals implementation. The parametric evaluation represents the possibility in the Lock-Down appliance to delay or reduce the infection and disease spread.

The pandemic dynamics is not a simple implementation and requires a long study due to the complexity and high spread. Also a pure deterministic model is not enough to represent the randomness of infection disease over a human population. For that motive a stochastic research is necessary. Even though, a deterministic model can help in understanding the pandemic dynamics and decision taking.

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