© REVISTA DE MATEMÁTICA: TEORÍA Y APLICACIONES 2023 **30**(1) : 89–111
CIMPA – UCR ISSN: 1409-2433 (PRINT), 2215-3373 (ONLINE)
DOI: https://doi.org/10.15517/rmta.v30i1.50566

MATHEMATICAL MODELS AND SIMULATIONS OF DIFFERENT SCENARIOS OF COVID-19 IN BRAZIL

MODELOS MATEMÁTICOS Y SIMULACIONES DE DIFERENTES ESCENARIOS DE COVID-19 EN BRASIL

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Received: 01/Apr/2022; Revised: 15/Nov/2022;
Accepted: 18/Oct/2022

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Abstract

In this paper, we develop successive mathematical models for describing the first and second waves of COVID-19 in Brazil, including the original strain, the two variants with the highest circulation (Gamma and Delta variants) and population vaccination. We started with a a simple initial model and using mathematical modelling techniques and the Heaviside step function, we improved it according to the necessities of describing the disease's behaviour, both considering the new variants or vaccination. In all cases, we performed computer simulations and compared the obtained curve with real data from the active cases, which reinforced the model's efficiency in describing the behaviour of the pandemic and highlighted the importance of population vaccination in describing the dynamics of the infections and reducing cases.

Keywords: COVID-19; mathematical modelling; SARS-CoV-2 variants; mathematical epidemiology; nonlinear systems of ODEs.

Resumen

En este artículo, desarrollamos modelos matemáticos sucesivos para describir la primera y la segunda ola de COVID-19 en Brasil, incluida la cepa original, las dos variantes de mayor circulación (variantes Gamma y Delta) y la vacunación de la población. Partimos de un modelo inicial simple y utilizando técnicas de modelado matemático y la función escalón de Heaviside, lo mejoramos según las necesidades de describir el comportamiento de la enfermedad, tanto considerando las nuevas variantes como la vacunación. En todos los casos, realizamos simulaciones informáticas y comparamos la curva obtenida con datos reales de los casos activos, lo que reforzó la eficiencia del modelo para describir el comportamiento de la pandemia y destacó la importancia de la vacunación de la población para describir la dinámica de los contagios y reducir los casos.

Palabras clave: COVID-19; modelación matemática; variantes de SARS-CoV-2; epidemiología natemática; sistemas no lineales de EDO.

Mathematics Subject Classification: 92C60

1 Introduction

In mid-December 2019, doctors in Wuhan, in the province of Hubei (China), had contact with patients presenting pneumonia symptoms of an unknown origin, besides severe respiratory effects. In early January, the first death from the new disease occurred in China and Chinese health authorities announced that the new virus could be transmitted between humans [7].

In February 2020, the mysterious disease was named COVID-19 (Corona Virus Disease) and the virus was named SARS-CoV-2 (for "Severe Acute Respiratory Syndrome - Coronavirus 2"). The number of deaths due to this new coronavirus surpassed 5 million individuals and reached several other countries [20]. Italy, south Korea and Iran experienced uncontrolled outbreaks of the disease. The first case in Brazil was registered on February 26, which was also the first in South America [12].

On March 11, 2020, the World Health Organization declared the outbreak as a pandemic and, since then, the world has followed an unimaginable increase in the number of cases and deaths and the disease has exposed society to very serious problems, such as saturation of health services, death without rituals and farewells, the collapse of the funerary system and the devastation of asylums. As a measure to control the pandemic, WHO indicated the massive use of masks, hygiene campaigns and the adoption of physical distancing rules between individuals and the use of lockdowns - some of which quite severe [1].

The peak of the first wave in Brazil occurred at the beginning of August [20] and the measure of restrictions and distancing were relaxed. Nevertheless, in mid-November 2020, an increase in the number of active cases of COVID-19 was again observed, causing a second wave of the disease, with a significantly greater amplitude than the first one. Among the possible causes of this second wave, we can list the change in behaviour of the population in face of the appearance of vaccines, generating a false feeling of safety in society and individuals that then caused a reduction in attention to the necessary safety measures; the *super spreader* events in Brazil, caused by the municipal elections; and the emergence of a new variant in the world, especially in Brazil.

In this work we, at first, developed a model that was able to describe the first wave of COVID-19 in Brazil and, again using modelling techniques, we improved this model in order to be able to describe the second wave, based on the information about the emergence of the new variant of the virus with its enhanced transmissibility in relation to the first variant and which is capable of more severely infecting individuals which had not shown symptoms when exposed to the first variant of the virus. In addition, we made another model including vaccination in Brazil and describing the two available vaccines at that moment, and both vaccines' capability of immunization. For all the models described above, we performed simulations and discussed the results.

2 Mathematical models and simulations

In this section, we initially present a modification of the model proposed by [11], with which it is possible to describe the behaviour of the first wave of COVID-19. We then introduce the first variant of SARS-CoV-2 detected in Brazil, the so-called Gamma variant, and for the description of the epidemiological situation, we present a compartmental diagram, the respective equations and the resulting simulation. Soon after, we included another variant, Delta, as well as the simulation of the scenario caused by this variant, together with the Gamma variant and the original strain. Finally, armed with data on vaccination in Brazil, we obtained a curve describing the evolution of the complete immunization of individuals and included this information in our model and presented a simulation of the current scenario in Brazil, with variants and with the advance of vaccination.

In all simulations, the starting point is January 1, 2020 (day 1), although the first case of COVID-19 in Brazil was diagnosed on February 27, 2020, in the city of São Paulo. The date was chosen to simplify the simulations and also because we are not sure that patient zero was really the first to be diagnosed, as the virus had already spread to several countries and there was a lack of tests to detect it. We use data from daily active cases published by [20] and numerically simulate the behaviour of COVID-19 for the years 2020 and 2021, according to the scenarios proposed in this work.

2.1 The original strain

In a previous work [11] we presented several models and simulations in order to describe the behaviour of the COVID-19 pandemic in Brazil. For these models, we selected the most complete model and we used it as a basis for this paper. It is identified as a SCEAIRD model. This model considers the following classes of individuals:

- $S(t)$: the susceptible;
- $C(t)$: the confined, i.e., individuals under a regime of social distancing;
- $E(t)$: the exposed, i.e., individuals who contracted the virus but are still unable to transmit it to others and do not manifest any kind of symptoms;
- $A(t)$: the asymptomatic, i.e., those who have and are able to transmit the virus but do not have relevant symptoms. The amount of these individuals was determined based on theoretical studies;

- $I(t)$: the infected individuals, i.e., those who have tested positive for the presence of COVID-19 and are therefore included in the statistical data;
- $R(t)$: the recovered individuals, i.e., those who have temporary immunity; and
- $D(t)$: indicating those whose death has been registered.

Some modifications were introduced in the model proposed in [11]: exclusion of the parameter related to the percentage of individuals who abandoned the confinement and recovery and death rates of asymptomatic individuals, because we do not have enough information. With these changes, we have the following SCEAIRD model:

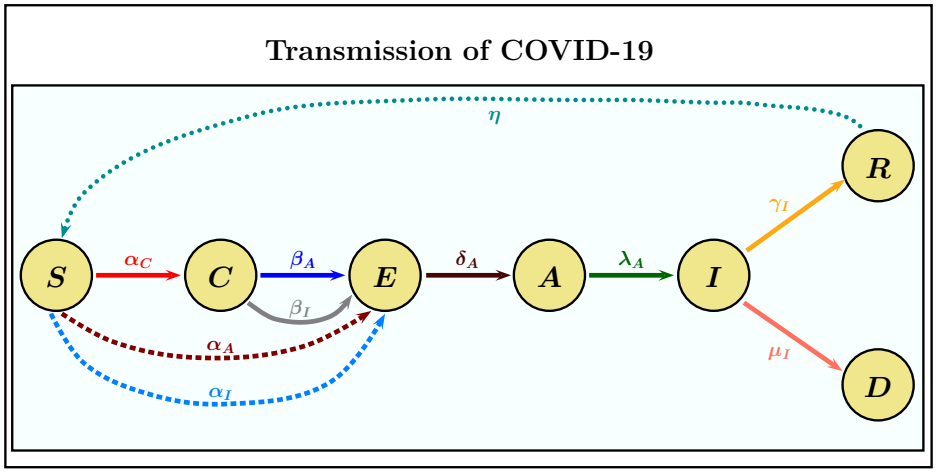

Figure 1: Relationship between individual classes to study the dynamics of COVID-19.

Based on the schematic model presented in Figure 1, we have the parameters needed to describe the dynamics:

- α_A: transmission coefficient of the virus from asymptomatic individuals to the susceptible ones, who contract the virus and become exposed individuals;
- α_I: transmission coefficient of the virus from symptomatic (infected) individuals to the susceptible ones, who contract the virus and become exposed individuals;
- α_C: rate of susceptible individuals who start the confinement regime;

- β_A: transmission coefficient of the virus from asymptomatic individuals to the confined ones, who contract the virus and become exposed;
- β_I: transmission coefficient of the virus from infected individuals to the confined ones, who contract the virus and become exposed;
- δ_A: rate of exposed individuals who become asymptomatic;
- λ_A: rate of asymptomatic individuals who tested positive to COVID-19;
- γ_I: recovery rate of infected individuals;
- μ_I: mortality rate of infected individuals; and
- η: rate of immunity loss.

Besides that, in this model we do not consider vital dynamics. So the population is distributed as

$$S(t) + C(t) + E(t) + A(t) + I(t) + R(t) + D(t) = N = \text{constant}.$$

Then, we can formulate the equations of SCEAIRD model as:

$$\begin{aligned}
\frac{\mathrm{d}S(t)}{\mathrm{d}t} &= -\alpha_C S(t) - \alpha_A S(t)A(t) - \alpha_I S(t)I(t) + \eta R(t), && (1)\\
\frac{\mathrm{d}C(t)}{\mathrm{d}t} &= \alpha_C S(t) - \beta_A C(t)A(t) - \beta_I C(t)I(t), && (2)\\
\frac{\mathrm{d}E(t)}{\mathrm{d}t} &= \alpha_A S(t)A(t) + \alpha_I S(t)I(t) + \beta_A C(t)A(t) + \beta_I C(t)I(t) \\
&\quad - \delta_A E(t), && (3)\\
\frac{\mathrm{d}A(t)}{\mathrm{d}t} &= \delta_A E(t) - \lambda_A A(t), && (4)\\
\frac{\mathrm{d}I(t)}{\mathrm{d}t} &= \lambda_A A(t) - \gamma_I I(t) - \mu_I I(t), && (5)\\
\frac{\mathrm{d}R(t)}{\mathrm{d}t} &= \gamma_I I(t) - \eta R(t), \quad \text{and} && (6)\\
\frac{\mathrm{d}D(t)}{\mathrm{d}t} &= \mu_I I(t). && (7)
\end{aligned}$$

For all the simulations, we used a fourth order Runge-Kutta numerical method to solve our system of ordinary differential equation in Wolfram Mathematica®. As a starting point, we consider the population of Brazil, which is about 214 million people [8], as totally susceptible, and we introduce one individual infected with the original strain and, in successive moments,

the model describes each of the new variants. For the other classes of individuals, the initial conditions are all equal to zero. Thus, for all simulations, we have the following fixed parameters: initial conditions $S(0) = \text{population of Brazil} = 213,911,805(\text{individuals})$, according to [8]; $I_i(0) = 1(\text{individuals})$; $C(0) = E_i(0) = A_i(0) = R_i(0) = D(0) = 0$, for $i = 1, 2, 3$ or without an index, that being the case; and with the value for the parameters: $\alpha_C = 0.4(\text{day}^{-1})$, according to [9]; $\gamma_{I_i} = 0.97(\text{day}^{-1})$ and $\mu_{I_i} = 0.03(\text{day}^{-1})$ according to [20], for $i = 1, 2, 3$ or without an index, if that is the case; and $\eta = 0.02(\text{day}^{-1})$.

Another important point to be considered is that the class of individuals we denote as "Infected" correspond to people who tested positive for COVID-19 and, therefore, are included in the database of detected cases. Individuals who have been exposed to the virus, who are asymptomatic, or who have symptoms but have not been tested are not categorized as "Infected" in our models. Consequently, we have found that both individuals from the Infected and Asymptomatic compartments are capable of transmitting the virus.

We carried out simulations of a number of active cases, using the system of ordinary differential equation, presented in equations (1)-(7), with the parameters common to all the simulations. The values for the parameters were: $\alpha_A = 3.27 \times 10^{-9}(\text{individuals}^{-1}\text{day}^{-1})$, $\alpha_I = 7.48 \times 10^{-9}$ $(\text{individuals}^{-1}\text{day}^{-1})$, $\beta_A = 1.54 \times 10^{-9}(\text{individuals}^{-1}\text{day}^{-1})$, $\beta_I = 2.80 \times 10^{-9}(\text{individuals}^{-1}\text{day}^{-1})$, $\delta_A = 0.6(\text{day}^{-1})$ and $\lambda_A = 0.6(\text{day}^{-1})$. The values were estimated in order to obtain coherent results so that the numerical solutions would be adjusted to the existing data provided in [20]. So, we obtained the graph presented in Figure 2.

Even after excluding some parameters of the SCEAIRD model proposed by [11], we obtained a curve that well describes the behaviour of the first wave of the pandemic. It is noteworthy that this curve was obtained using only the equations for the original strain and with the hypothesis of reinfection by the same strain of virus.

2.2 The Gamma variant

One of the hypotheses proposed to explain the amplitude of the second wave of COVID-19 is the fact that symptomatic individuals have a lower average age than those who had symptoms in the first wave of the disease. This can be attributed to the fact that individuals who were asymptomatic to the first variant of the virus, when in contact with the second variant, manifest symptoms, which, in most cases, are severe [3, 16]. Using previously obtained and this new information, a model was obtained to describe the dynamics of COVID-19 including the Gamma variant, as presented in Figure 3.

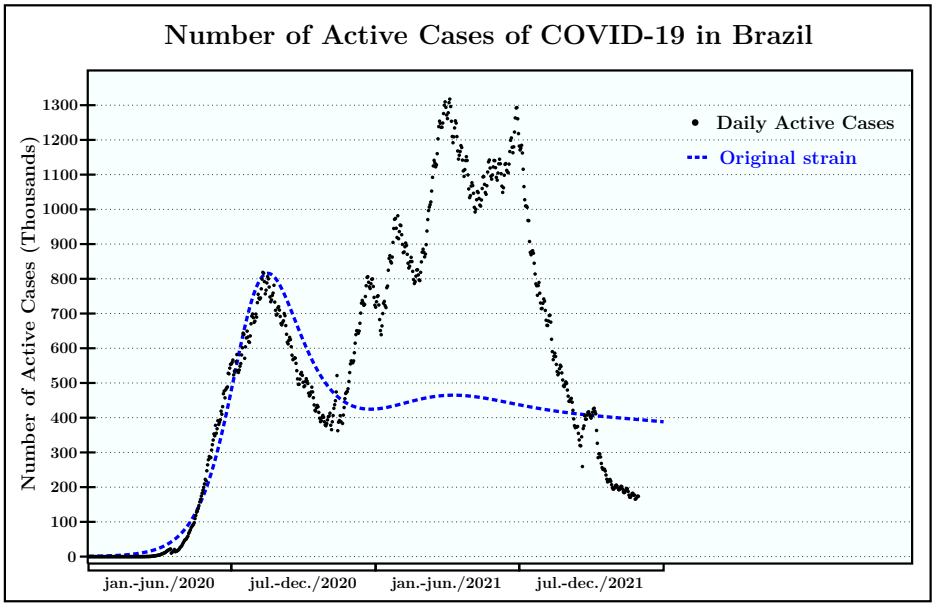

Figure 2: Number of active cases of COVID-19 obtained from [20] and the simulation using the SCEAIRD model.

Based on the schematic model presented in Figure 3, we have the new parameters useful to describe the dynamics:

- α_{A_1}: transmission coefficient of the virus of the first variant from asymptomatic individuals to the susceptible ones, who contract the virus and become exposed individuals to this variant;

- α_{I_1}: transmission coefficient of the virus of the first variant from symptomatic (infected) individuals to the susceptible ones, who contract the virus and become exposed individuals to this variant;

- α_{A_2}: transmission coefficient of the virus of the second variant from asymptomatic individuals to the susceptible ones, who contract the virus and become exposed individuals to this variant;

- α_{I_2}: transmission coefficient of the virus of the second variant from symptomatic (infected) individuals to the susceptible ones, who contract the virus and become exposed individuals to this variant;

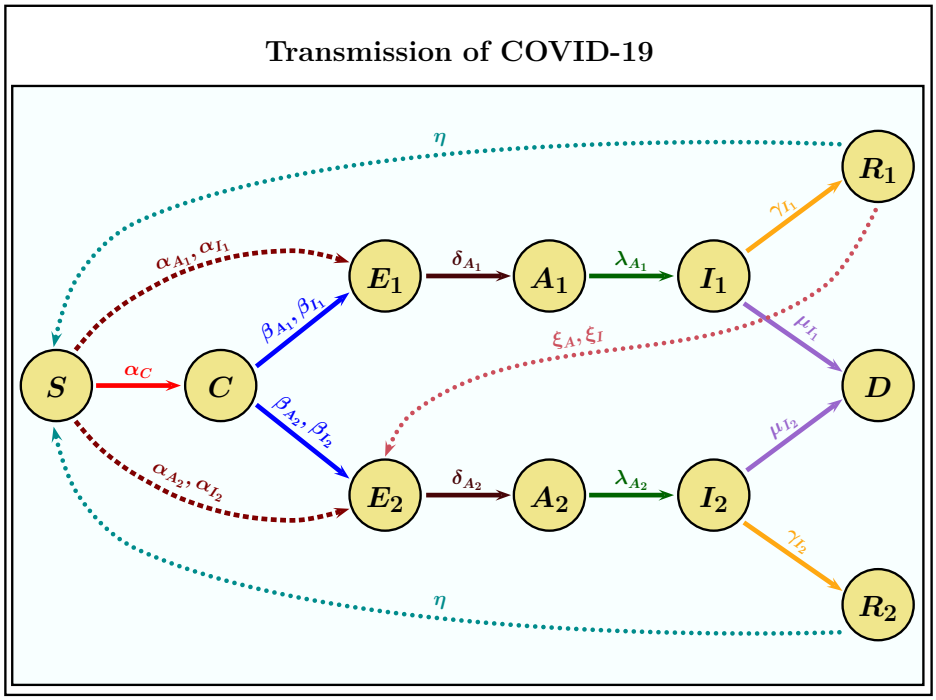

Figure 3: Relationship between individual classes to study the dynamics of COVID-19, with the possibility of reinfection with a different variant.

- β_{A_1}: transmission coefficient of the virus of the first variant from asymptomatic individuals to the confined ones, who contract the virus and become exposed individuals to this variant;
- β_{I_1}: transmission coefficient of the virus of the first variant from infected individuals to the confined ones, who contract the virus and become exposed individuals to this variant;
- β_{A_2}: transmission coefficient of the virus of the second variant from asymptomatic individuals to the confined ones, who contract the virus and become exposed individuals to this variant;
- β_{I_2}: transmission coefficient of the virus of the second variant from infected individuals to the confined ones, who contract the virus and become exposed individuals to this variant;
- $\delta_{A_1} = \delta_{A_2}$: rate of exposed individuals who become asymptomatic, regardless of which variant of the virus;

- $\lambda_{A_1} = \lambda_{A_2}$: rate of asymptomatic individuals who tested positive to COVID-19, regardless of which variant of the virus;
- $\gamma_{I_1} = \gamma_{I_2}$: recovery rate of infected individuals, regardless of which variant of the virus;
- μ_{I_1}: mortality rate of infected individuals, caused by the first variant;
- μ_{I_2}: mortality rate of infected individuals, caused by the second variant;
- ξ_A: rate of individuals who were asymptomatic for the first variant, had temporarily immunity and now become exposed to the second variant of the virus; and
- ξ_I: rate of individuals who were infected for the first variant, had temporarily immunity and now become exposed to the second variant of the virus.

Besides that, in this model we do not consider any variation in the total population, which remains constant. The population is, therefore, distributed as

$$\begin{aligned} &S(t) + C(t) + E_1(t) + A_1(t) + I_1(t) + R_1(t) \\ &\quad + E_2(t) + A_2(t) + I_2(t) + R_2(t) + D(t) = N. \end{aligned}$$

However, as the second variant of SARS-CoV-2 appeared in Brazil in November, we have that the equations referring to this variant only contribute to the model from that date onwards. To solve this problem, we formulated the system of equations using the Heaviside step function - $H(x)$. So, considering the start of circulation of the new variant at a time τ, we have the following set of equations:

$$\begin{aligned} \frac{\mathrm{d}S(t)}{\mathrm{d}t} &= \eta[R_1(t) + R_2(t)] - S(t)[\alpha_C + \alpha_{A_1} A_1(t) + \alpha_{I_1} I_1(t) \\ &\quad + \alpha_{A_2} A_2(t) + \alpha_{I_2} I_2(t)], \qquad (8) \\ \frac{\mathrm{d}C(t)}{\mathrm{d}t} &= \alpha_C S(t) - C(t)[\beta_{A_1} A_1(t) + \beta_{I_1} I_1(t) \\ &\quad + \beta_{A_2} A_2(t) + \beta_{I_2} I_2(t)], \qquad (9) \\ \frac{\mathrm{d}E_1(t)}{\mathrm{d}t} &= S(t)[\alpha_{A_1} A_1(t) + \alpha_{I_1} I_1(t)] + C(t)[\beta_{A_1} A_1(t) + \beta_{I_1} I_1(t)] \\ &\quad - \delta_{A_1} E_1(t), \qquad (10) \\ \frac{\mathrm{d}A_1(t)}{\mathrm{d}t} &= \delta_{A_1} E_1(t) - \lambda_{A_1} A_1(t), \qquad (11) \end{aligned}$$

$$\frac{\mathrm{d}I_1(t)}{\mathrm{d}t} = \lambda_{A_1}A_1(t) - \gamma_{I_1}I_1(t) - \mu_{I_1}I_1(t), \tag{12}$$

$$\frac{\mathrm{d}R_1(t)}{\mathrm{d}t} = \gamma_{I_1}I_1(t) - \eta R_1(t) - \xi_A R_1(t)A_2(t) - \xi_I R_1(t)I_2(t), \tag{13}$$

$$\begin{aligned}\frac{\mathrm{d}E_2(t)}{\mathrm{d}t} &= H(t-\tau)\{S(t)[\alpha_{A_2}A_2(t) + \alpha_{I_2}I_2(t)] \\ &\quad + C(t)[\beta_{A_2}A_2(t) + \beta_{I_2}I_2(t)]\} \\ &\quad + \{R_1(t)[\xi_A A_2(t) + \xi_I I_2(t)] - \delta_{A_2}E_2(t)\},\end{aligned} \tag{14}$$

$$\frac{\mathrm{d}A_2(t)}{\mathrm{d}t} = H(t-\tau)[\delta_{A_2}E_2(t) - \lambda_{A_2}A_2(t)], \tag{15}$$

$$\frac{\mathrm{d}I_2(t)}{\mathrm{d}t} = H(t-\tau)[\lambda_{A_2}A_2(t) - \gamma_{I_2}I_2(t) - \mu_{I_2}I_2(t)], \tag{16}$$

$$\frac{\mathrm{d}R_2(t)}{\mathrm{d}t} = H(t-\tau)[\gamma_{I_2}I_2(t) - \eta R_2(t)], \quad \text{and} \tag{17}$$

$$\frac{\mathrm{d}D(t)}{\mathrm{d}t} = \mu_{I_1}I_1(t) + \mu_{I_2}H(t-\tau)I_2(t). \tag{18}$$

According to [4], the variant Gamma, which was observed in Brazil and Japan only after November of 2020, is between 1.4 and 2.2 times more transmissible than the original coronavirus strain.

We performed simulations of a number of active cases, using the system of ordinary differential equations presented in equations (8)-(18), with the initial conditions and parameters described before and the value for the new parameters: $\alpha_{A_1} = \alpha_A$, $\alpha_{I_1} = \alpha_I$, $\beta_{A_1} = \beta_A$, $\beta_{I_1} = \beta_I$, $\delta_{A_1} = \delta_{A_2} = 0.6(\mathrm{day}^{-1})$, $\lambda_{A_1} = \lambda_{A_2} = 0.6(\mathrm{day}^{-1})$, $\alpha_{A_2} = 2\alpha_{A_1}$, $\alpha_{I_2} = 2\alpha_{I_1}$, $\beta_{A_2} = 1.05\beta_{A_1}$, $\beta_{I_2} = 1.05\beta_{I_1}$, $\xi_A = 9.35 \times 10^{-10}(\mathrm{individuals}^{-1}\mathrm{day}^{-1})$ and $\xi_I = 1.87 \times 10^{-9}(\mathrm{individuals}^{-1}\mathrm{day}^{-1})$, were estimated in order to obtain coherent values so that the obtained approximate solutions were adequately adjusted to the existing data provided in [20]; and $\tau = 320(\mathrm{day})$. In this manner, we obtained the graph presented in Figure 4.

In Figure 4, we can see that the curve obtained when we include the Gamma variant seems to describe the behaviour of the first and second waves, including the circulation of this new variant as the main responsible for the greater amplitude of the second wave, when compared with the first one. If there was not the emergence of a new variant, in this case Delta, as well as the start of the vaccination program, we would have a decrease in cases, but the number of active cases would not go to zero, because we have the chance of reinfection both by the original strain and by the Gamma variant. Cases including the Delta variant and vaccination will be studied in Sections 2.3 and 2.4.

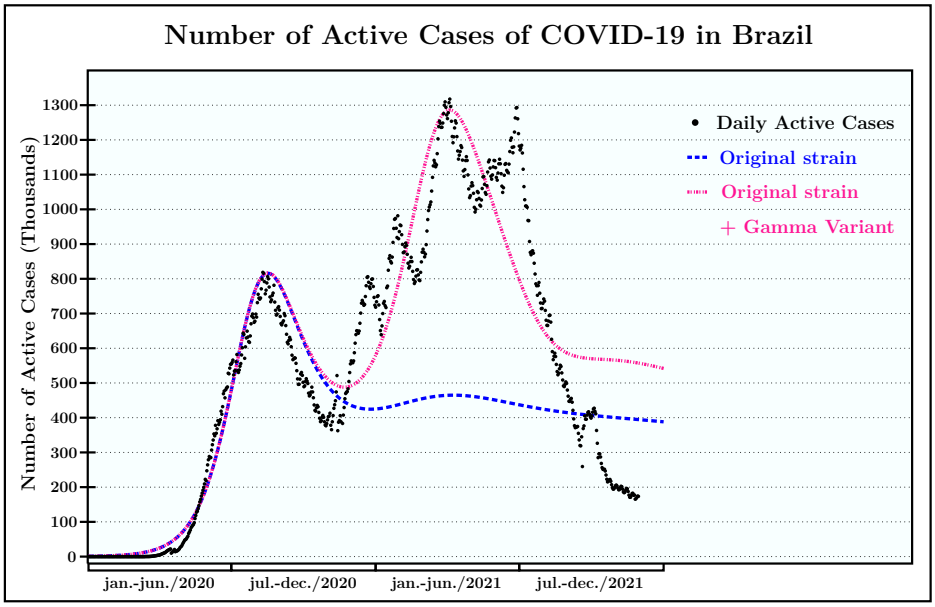

Figure 4: Number of active cases of COVID-19 obtained from [20] and the simulation using the SCEAIRD model with the Gamma variant.

2.3 The Delta variant

To date, we do not have information in the literature on epidemiological data on the dynamics of the Delta variant of SARS-CoV-2. Thus, we used some data obtained from internet portals and estimated other parameters, in order to better adjust the curve for the Infected population.

The Delta variant (B.1.617.2) was first detected in India in December 2020 and spread to several countries, including Brazil, from April 2021 [5]. Where the Delta variant was identified, it was also found that it spreads rapidly among humans [17]. It is a highly transmissible variant, it has the potential to increase disease severity, and may be less affected by the efficacy of vaccines [2]. However, results show that people infected with the Delta variant are less likely to transmit the virus if they are fully immunized compared to people who have not been immunized [6].

Thus, we consider the proposed scheme in Figure 3 and add the following classes of individuals:

- $E_3(t)$: individuals exposed to the Delta variant;
- $A_3(t)$: individuals who contracted the Delta variant but do not manifest symptoms;

- $I_3(t)$: individuals infected with the Delta variant and who tested positive for COVID-19; and
- $R_3(t)$ individuals who acquired resistance, this being temporary.

Furthermore, we consider that the individual who was asymptomatic to the original strain of the virus and the Gamma variant, upon coming into contact with the Delta variant, may manifest symptoms, which are generally more severe than those seen when there is infection by the original strain or by the Gamma variant. The new diagram with the relationship between individuals is shown in Figure 5.

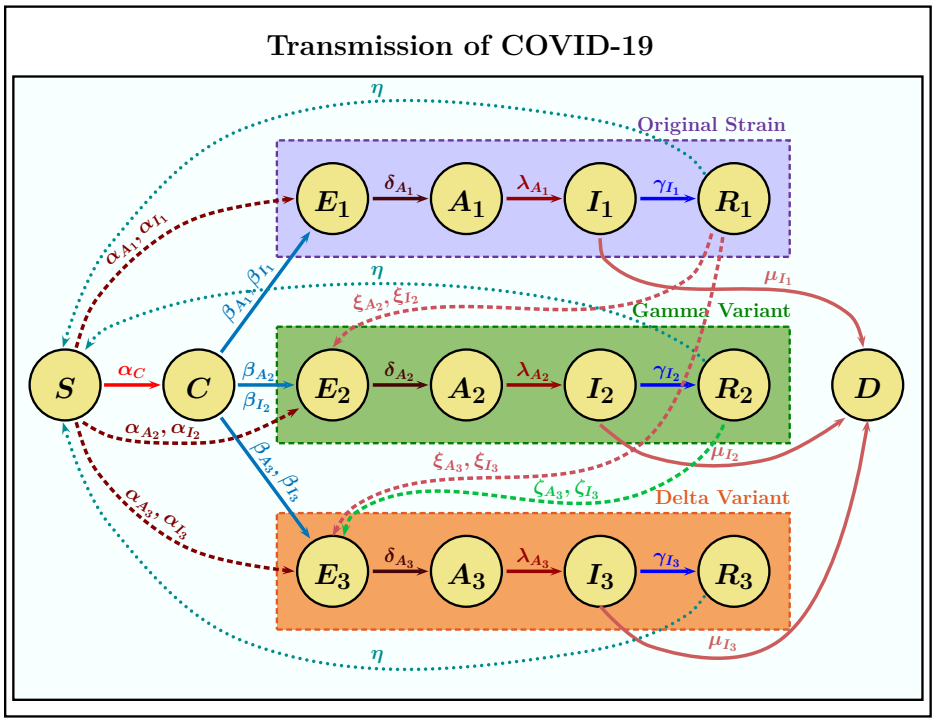

Figure 5: Relationships between the classes of individuals proposed for the study of the dynamics of COVID-19 with the inclusion of individuals infected with the Delta variant.

Based on the schematic model shown in Figure 5, we have the following additional parameters to describe the dynamics:

- α_{A_3}: Delta variant virus transmission coefficient from asymptomatic to susceptible individuals who contract the virus and become individuals exposed to this variant;

- α_{I_1}: transmission coefficient of the Delta variant virus from symptomatic (infected) to susceptible individuals, who contract the virus and become individuals exposed to this variant;

- β_{A_3}: transmission coefficient of the Delta variant virus from asymptomatic individuals to those confined, who contract the virus and become individuals exposed to this variant;

- β_{I_3}: transmission coefficient of the Delta variant virus from infected individuals to confined individuals, who contract the virus and become individuals exposed to this variant;

- $\delta_{A_3} = \delta_{A_1}$: rate of exposed individuals who become asymptomatic, regardless of which virus variant;

- $\lambda_{A_3} = \lambda_{A_1}$: rate of asymptomatic individuals testing positive for COVID-19, regardless of which virus variant;

- $\gamma_{I_3} = \gamma_{I_1}$: recovery rate of infected individuals, regardless of which virus variant;

- μ_{I_3}: mortality rate of infected individuals, caused by the Delta variant;

- ξ_{A_3}: rate of individuals who were asymptomatic for the original strain, had temporary immunity and are now exposed to the Delta variant;

- ξ_{I_3}: rate of individuals who were infected by the original strain, had temporary immunity and are now exposed to the Delta variant;

- ζ_{A_3}: rate of individuals who were asymptomatic for the Gamma variant, had temporary immunity and are now exposed to the Delta variant; and

- ξ_{I_3}: rate of individuals who were infected with the Gamma variant, had temporary immunity and are now exposed to the Delta variant.

Furthermore, in this model we do not consider the vital dynamics. So the population is distributed as

$$\begin{aligned} &S(t) + C(t) + E_1(t) + A_1(t) + I_1(t) + R_1(t) + E_2(t) \\ &\quad + A_2(t) + I_2(t) + R_2(t) + E_3(t) + A_3(t) + I_3(t) + R_3(t) + D(t) = N. \end{aligned}$$

However, as the Delta variant of SARS-CoV-2 appeared in Brazil in May 2021, similarly to what we did when the Gamma variant was introduced, we again use the Heaviside step function - $H(x)$, considering the start of circulation of the Gamma variant at one time as τ_2 and of the Delta variant as τ_3. So, we have the following set of equations:

$$\begin{aligned}
\frac{\mathrm{d}S(t)}{\mathrm{d}t} &= \eta[R_1(t)+R_2(t)+R_3(t)] - S(t)[\alpha_C + \alpha_{A_1}A_1(t) + \alpha_{I_1}I_1(t) \\
&\quad + \alpha_{A_2}A_2(t) + \alpha_{I_2}I_2(t) + \alpha_{A_3}A_3(t) + \alpha_{I_3}I_3(t)], \qquad (19)\\
\frac{\mathrm{d}C(t)}{\mathrm{d}t} &= \alpha_C S(t) - C(t)[\beta_{A_1}A_1(t) + \beta_{I_1}I_1(t) + \beta_{A_2}A_2(t) + \beta_{I_2}I_2(t) \\
&\quad + \beta_{A_3}A_3(t) + \beta_{I_3}I_3(t)], \qquad (20)\\
\frac{\mathrm{d}E_1(t)}{\mathrm{d}t} &= S(t)[\alpha_{A_1}A_1(t) + \alpha_{I_1}I_1(t)] + C(t)[\beta_{A_1}A_1(t) + \beta_{I_1}I_1(t)] \\
&\quad - \delta_{A_1}E_1(t), \qquad (21)\\
\frac{\mathrm{d}A_1(t)}{\mathrm{d}t} &= \delta_{A_1}E_1(t) - \lambda_{A_1}A_1(t), \qquad (22)\\
\frac{\mathrm{d}I_1(t)}{\mathrm{d}t} &= \lambda_{A_1}A_1(t) - \gamma_{I_1}I_1(t) - \mu_{I_1}I_1(t), \qquad (23)\\
\frac{\mathrm{d}R_1(t)}{\mathrm{d}t} &= \gamma_{I_1}I_1(t) - [\xi_{A_2}A_2(t) + \xi_{I_2}I_2(t) + \xi_{A_3}A_3(t) + \xi_{I_3}I_3(t)]R_1(t), \\
&\quad - \eta R_1(t), \qquad (24)\\
\frac{\mathrm{d}E_2(t)}{\mathrm{d}t} &= H(t-\tau_2)\{S(t)[\alpha_{A_2}A_2(t) + \alpha_{I_2}I_2(t)] \\
&\quad + C(t)[\beta_{A_2}A_2(t) + \beta_{I_2}I_2(t)] + R_1(t)[\xi_{A_2}A_2(t) + \xi_{I_2}I_2(t)] \\
&\quad - \delta_{A_2}E_2(t)\}, \qquad (25)\\
\frac{\mathrm{d}A_2(t)}{\mathrm{d}t} &= H(t-\tau_2)[\delta_{A_2}E_2(t) - \lambda_{A_2}A_2(t)], \qquad (26)\\
\frac{\mathrm{d}I_2(t)}{\mathrm{d}t} &= H(t-\tau_2)[\lambda_{A_2}A_2(t) - \gamma_{I_2}I_2(t) - \mu_{I_2}I_2(t)], \qquad (27)\\
\frac{\mathrm{d}R_2(t)}{\mathrm{d}t} &= H(t-\tau_2)\{\gamma_{I_2}I_2(t) - \eta R_2(t) - [\zeta_{A_3}A_3 + \zeta_{I_3}I_3]R_2(t)\}, \qquad (28)\\
\frac{\mathrm{d}E_3(t)}{\mathrm{d}t} &= H(t-\tau_3)\{S(t)[\alpha_{A_3}A_3(t) + \alpha_{I_3}I_3(t)] \\
&\quad + C(t)[\beta_{A_3}A_3(t) + \beta_{I_3}I_3(t)] + [\xi_{A_3}A_3(t) + \xi_{I_3}I_3(t)]R_1(t) \\
&\quad - \delta_{A_3}E_3(t) + [\zeta_{A_3}A_3 + \zeta_{I_3}I_3]R_2(t)\}, \qquad (29)\\
\frac{\mathrm{d}A_3(t)}{\mathrm{d}t} &= H(t-\tau_3)[\delta_{A_3}E_3(t) - \lambda_{A_3}A_3(t)], \qquad (30)\\
\frac{\mathrm{d}I_3(t)}{\mathrm{d}t} &= H(t-\tau_3)[\lambda_{A_3}A_3(t) - \gamma_{I_3}I_3(t) - \mu_{I_3}I_3(t)], \qquad (31)
\end{aligned}$$

$$\frac{\mathrm{d}R_3(t)}{\mathrm{d}t} = H(t-\tau_3)[\gamma_{I_3} I_3(t) - \eta R_3(t)], \quad \text{and} \tag{32}$$

$$\frac{\mathrm{d}D(t)}{\mathrm{d}t} = \mu_{I_1} I_1(t) + H(t-\tau_2)\mu_{I_2} I_2(t) + H(t-\tau_3)\mu_{I_3} I_3(t). \tag{33}$$

We performed a simulation of the number of active cases, using this ordinary differential equations system, presented in the equations (19)-(33), with the conditions and parameters described before, and we have the value of the new parameters: $\alpha_{A_3} = 2.3\alpha_{A_1}$, $\alpha_{I_3} = 2.5\alpha_{I_1}$, $\beta_{A_3} = 1.08\beta_{A_1}$, $\beta_{I_1} = 1.1\beta_{I_1}$, $\delta_{A_3} = \delta_{A_1}$, $\lambda_{A_3} = \lambda_{A_1}$, $\xi_{A_2} = 9.35 \times 10^{-10}$ $(\text{individuals}^{-1}\text{day}^{-1})$, $\xi_{I_2} = 1.87\times10^{-9}$ $(\text{individuals}^{-1}\text{day}^{-1})$, $\xi_{A_3} = 4.67\times 10^{-10}$ $(\text{individuals}^{-1}\text{day}^{-1})$, $\xi_{I_3} = 9.35 \times 10^{-10}(\text{individuals}^{-1}\text{day}^{-1})$, $\zeta_{A_3} = \xi_{A_3}$, $\zeta_{I_3} = 1.40 \times 10^{-9}(\text{individuals}^{-1}\text{day}^{-1})$, which were estimated in order to obtain coherent values so that the obtained approximate solution did manage to describe the data provided in [20]; and $\tau_2 = 320(\text{day})$ and $\tau_3 = 516(\text{day})$. Thus, we obtained the graph shown in Figure 6.

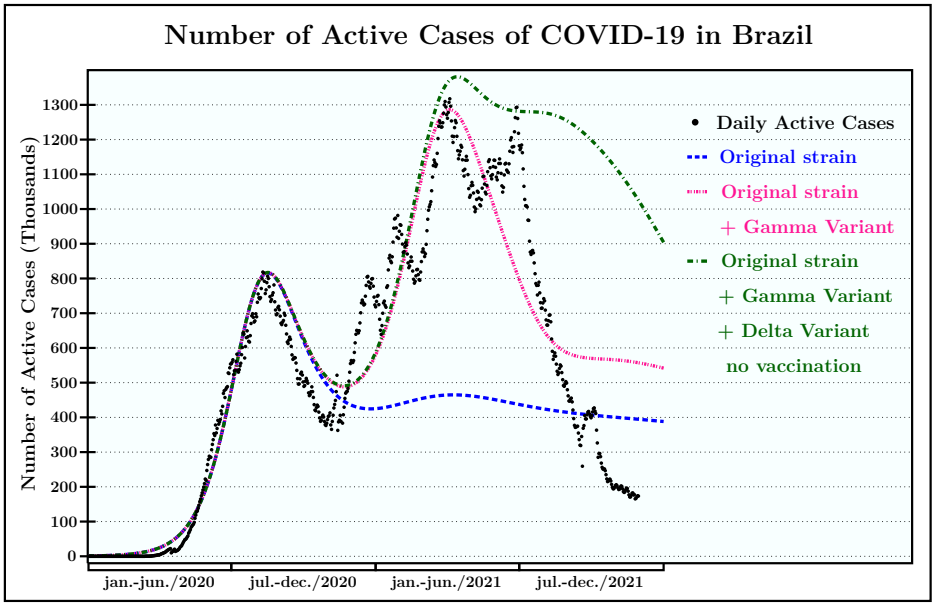

Figure 6: Number of active cases of COVID-19 obtained from [20] and the simulation using the SCEAIRD model with the Gamma and Delta variants, without vaccination.

Observing the graph in Figure 6, we have the curve obtained when we add the Delta variant to the model previously containing both the original strain and the Gamma variant, we have a curve that describes the first and second waves,

but which, after the peak of the second wave, results in a number of active cases greater than the actual data [20]. This would be the scenario observed in Brazil if the vaccination program had not started in January, but it was mitigated by the inclusion of vaccination, as presented in the Section 2.4.

2.4 Modelling including vaccination

In Brazil, the National Vaccination Campaign against COVID-19 started on January 18, 2021, and four vaccines are currently available in Brazil: CoronaVac®, developed by the Chinese laboratory Sinovac Life Science Co. Ltd. in partnership with the Butantan Institute [10]; AZD1222® or ChAdOx1-S nCoV-19®, developed by the University of Oxford in partnership with the AstraZeneca laboratory and the Oswaldo Cruz Foundation (Fiocruz) [18]; Comirnaty®, produced by the pharmaceutical company Pfizer, in partnership with the company BioNTech [15]; and Janssen Ad26.COV2.S®, produced by the American pharmaceutical Johnson & Johnson [19]. Each of these vaccines has a different vaccine schedule and effectiveness.

Until today, over 165,000,000 people have received at least one dose and 128,481,994 have received the second dose or the only single dose [14]. The graph presented in Figure 7 provides us with information about the immunization behaviour as a function of time.

As the vaccination data are very dynamic and we observed a step in the number of people with full immunization on May 25, which corresponds to day 115 of the simulations, we considered the data from that day onwards for adjustment via the method of least squares. It is worth noting that this leap is due to the beginning of the application of the second dose of the AZD1222® vaccine, according to the vaccine schedule proposed in the manufacturer's package insert. The graph with the number of people who received the second dose of vaccines and the curve obtained by the least squares method is shown in Figure 8.

As described in the package inserts of the vaccines used, immunization takes place, on average, 2 weeks both after the application of the second dose or after the single dose. Thus, we used day 400 as the initial day of immunization and included immunization in the model as a reduction in the flow into the infected compartment, either from the original strain or from the Gamma and Delta variants, with this subtraction given by the following equation:

$$\psi(t) = H(t-400)e\frac{\phi(t)}{N}, \tag{34}$$

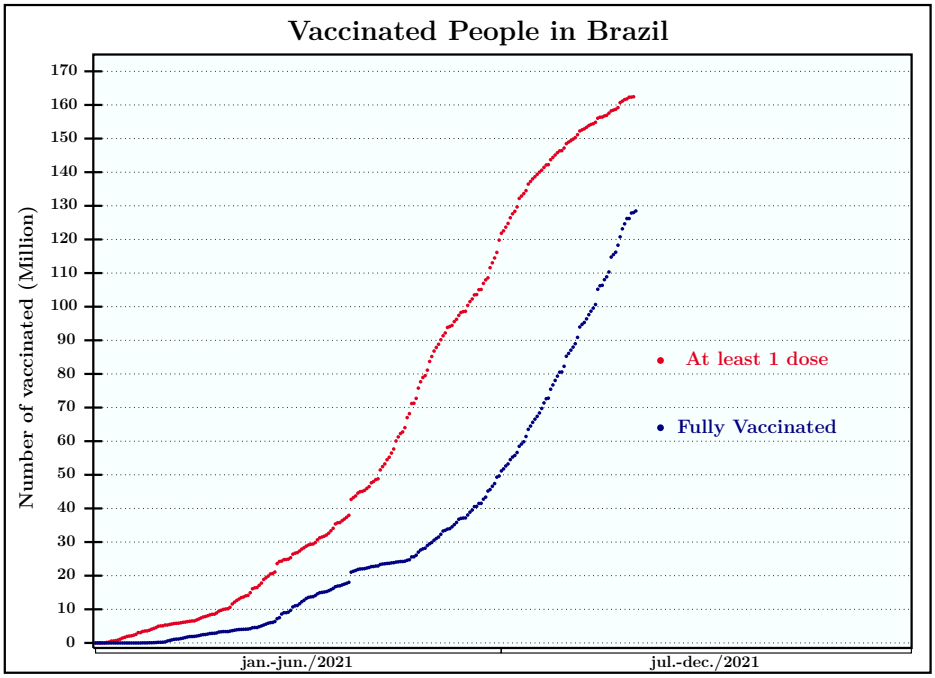

Figure 7: Number of people with at least one dose and with full immunization. Source: [14].

where $H(t)$ is the Heaviside step function, e is the average vaccine efficacy rate, $\phi(t)$ is the function that describes the complete immunization curve, obtained using the least squares method method, and N is the total population of Brazil.

The CoronaVac® vaccine has an average efficiency of 51%, two weeks after the application of the second dose [10]; the vaccine AZD1222 (ChAdOx1-S nCoV-19)® has an efficacy of 76%, 21 days after the application of the second dose [18]; Comirnaty® has 95% efficacy in two weeks after the application of the second dose [15]; and Janssen Ad26.COV2.S®, has an efficiency of 67% after 14 days of single dose application [19].

According to [13], until October, 365017390 vaccine doses were delivered by the Ministry of Health, with distribution, according to each manufacturer, as follows: 28.5 % of CoronaVac®; 35.6 % of AZD1222 (ChAdOx1-S nCoV-19)®; 34.6 % of Comirnaty®; and 1.3 % of Janssen Ad26.COV2.S®. Thus, using this information and data on vaccine efficacy, we conclude that the weighted mean average vaccination efficacy rate in Brazil is $e = 75.3\%$.

Using this information about the vaccination scheme and the proposed modelling for the dynamics of COVID-19, with the original strain and the variants,

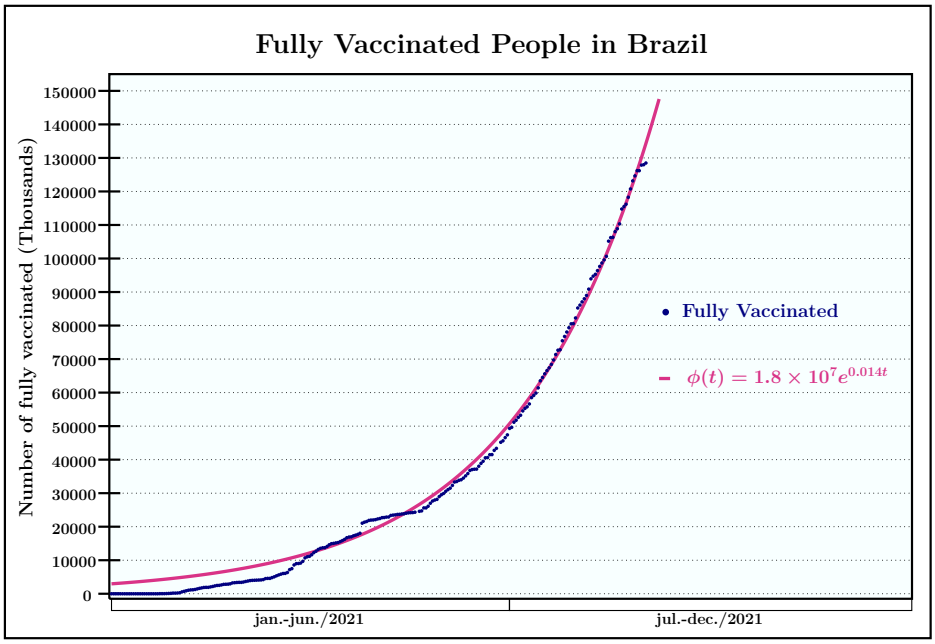

Figure 8: Number of people with full immunization and the adjusted curve. Source: [14].

and using the reduction in the flow of infected given by the equation 34, we performed a simulation of this pandemic scenario, which is presented in the comparative graph in Figure 9.

According to the graph in Figure 9, we can see that the curve obtained when we use the proposed function for vaccination, approximately describes the behaviour of the real data. Furthermore, this curve, when compared to the curve obtained when we added the Delta variant, shows a greater decrease in cases, approaching the actual behaviour of the pandemic. This result is extremely important, because it reinforces the importance of vaccination in controlling the disease.

Although it describes quite well the behaviour of the curve of active cases, the graph obtained with the simulation including vaccination shows a decrease in cases, unlike what occurs in real data from [20]. This difference is due, among other factors, to the evolutive dynamics of COVID-19 in the population, in face of the increased vaccination, resulting in more flexible security measures and social distancing, which leads to the occurrence of new cases, even in previously

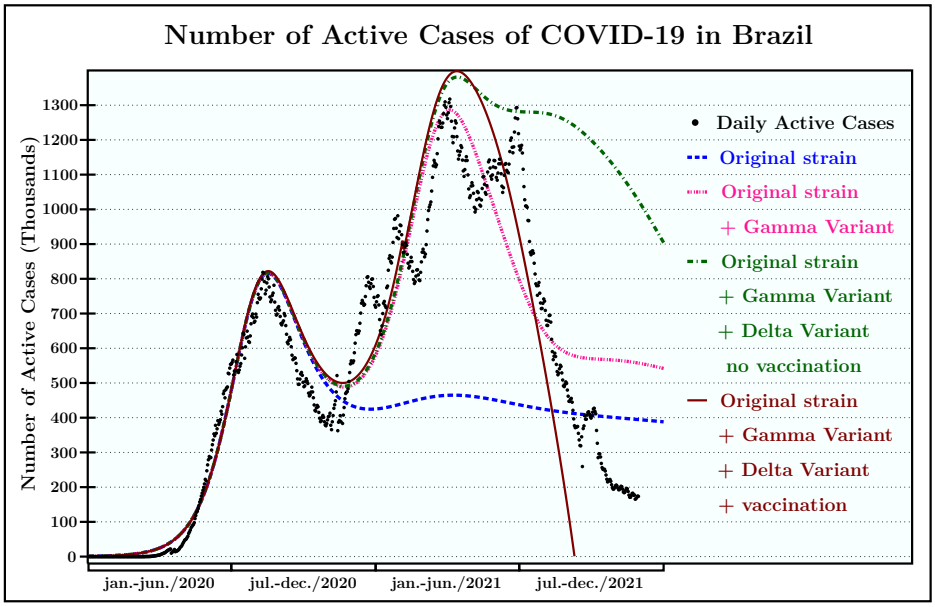

Figure 9: Number of active cases of COVID-19 obtained from [20] and the simulation using the SCEAIRD model with the Gamma and Delta variants, including vaccination.

infected individuals. Another possible consideration for this aspect is that of the function used to simulate the complete immunization is simply an exponential; with more data, one could be able to obtain other curves for when the vaccination programme modifies its tendency.

3 Conclusions

In this paper, using behavioural assumptions together with systems of ordinary differential equations, we present efficient epidemiological models for describing the COVID-19 pandemic in Brazil, describing the pandemic contagion waves and their amplitudes as qualitatively confirmed by the graphs obtained through numerical simulations. The technique proposed for the inclusion of new variants, through the addition of compartments for the use of the Heaviside step function, can be easily used to simulate new scenarios if new variants appear and also if there is a change in the form of immunization of the population. However, the proposed models do not consider vital dynamics, since the simulations are for a period of two years, and do not consider the population's behavioural changes, which results in a small difference between the curves obtained and the real data.

Acknowledgements

The authors would like to thank to IMECC - Unicamp for support in the development of this work.

Financial support

M. Lima thanks CAPES (Grantee 88887.369830/2019-00) for financial support.

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