A mathematical model for analyzing the behavior of COVID-19 in Dominican Republic

Abstract

In this paper a mathematical model is constructed and theoretically examined to analyze the transmission mechanism of COVID-19 in the Dominican Republic. The mathematical model is represented by 8 states, called $SEP_aI_ATRI_SV$. The main mathematical properties of the model have been proved, such as the non-negativity of the solutions, as well as the existence and uniqueness of the solution. In addition, the equilibrium points were determined as well as the control number R_c and the basic reproduction number, R_0. Finally, the sensitivity analysis and numerical simulations of the model were performed.

Keywords: mathematical model, control number.

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1 Introduction

Historically speaking, since humanity began to live together in more or less numerous communities, epidemics appeared. In this sense, Thucydides, (see (21)), a historian of ancient Greece, tells the story of the epidemic that hit the city of Athens, back in 430-426 BC. He uses known terms, such as symptoms, progression and number of deaths. Etymologically speaking, the word epidemic comes from the Greek words, *epi*, above, *demos*, people, and *logos*, which means study. Without leaving classical Greece, the wise and physician Hippocrates is considered the father of epidemiology. He managed to establish the relationship between a disease and its environment, as well as indicate the factors that influence the spread of a disease over time (refer to (12)).

Nowadays, the existence of a serious outbreak of respiratory disease in Wuhan, China was reported in December 2019. The cause of the outbreak was due to the presence of a new coronavirus,

which, according to the WHO Declaration on the Wuhan Pneumonia Cluster (see (23)), was identified and isolated from a single patient in early January and subsequently verified in 16 additional patients. The virus is believed to have a zoonotic origin, since in the Huanan market, live animals and seafood are sold. Also, according to (8), comparisons made with the genetic sequences of this virus and bat coronaviruses show a 96 percent similarity.

On the other hand, according to (19), in Santo Domingo, Dominican Republic, on March 1, 2020, the Ministry of Public Health confirmed the first case of coronavirus disease 2019 (COVID-19). The patient was a male, 62 years old, of Italian nationality, who entered the country on February 22, 2020, from Pesaro, Marche Region in Italy, where a coronavirus outbreak had been ongoing since January 2020, and by that time had already affected 888 people in Italy.

The patient was treated at a health center at his lodging location in La Altagracia province, from where he was transferred to the Dr. Ramón de Lara Military Hospital. Based on the patient's travel history and symptoms, health professionals suspected that it was this new coronavirus. A clinical sample was collected and sent to the Dr. Defilló National Public Health Laboratory, where tests confirmed the diagnosis.

2 Model flowchart and parameter estimation

In this section we propose a mathematical model that attempts to reproduce the evolution of COVID-19 in the Dominican Republic. For this, we will assume that the epidemic begins with a certain number of infected people ($I(0) = I_0$), who have not yet recovered or died (i.e.: $R_0 = 0$), which defines the initial number of susceptible people as $S_0 = D - I_0$.

Let's explain in a little detail the choice of the parameters that appear in Tables 1 and 2. We consider that the total population in Dominican Republic (DR) is $N \approx 11117874$. We must emphasize that all the parameters are calculated for the case of the situation in DR.

To calculate the rate of people who go from susceptible to exposed, $c_S(t)$, we take into account the proportion of people in the population classified as susceptible, D that gives a total quantity of $D \times N = 8961006$. From this value we subtract the population over 65 years of age, which, according to (22), was 666952 people. This is justified because in the DR, people of this age were very well cared for from COVID-19. Consequently, we have

$$8961006 - 666952 = 8294054,$$

and then, in percentage terms with respect to N we have that $c_S(t) = 0.7460$.

To estimate the proportion of susceptible individuals get isolated, z, the proportion of people in the population who qualify as susceptible, D, was taken into account and multiplied by the number of people who do so. For the case of Dominican Republic (DR), a good approximation would be one thousand per million. That is,

$$z = D \times \frac{1000}{1000000} = 0.00081.$$

Taking into account that in the DR, almost all susceptible people are exposed, it was assumed that z and the rate of exposed people who decide to isolate themselves, m, are similar. Then $z \approx m \approx 0.0008$.

In RD we can assume that the entire vaccinated population was exposed. So, the rate of people going from vaccinated to exposed is $q_V(t) = \alpha = 0.6522$.

To calculate the rate of people not infected due to vaccination, κ, the information provided by (13) and (14) was taken into account. In this sense, the proportion of vaccinated people in the population, α, and the effectiveness of the vaccine were multiplied. In the case of the DR, the AstraZeneca vaccine was applied, which, according to (22), is 76 percent. Then

$$\kappa = 0.6522 \times 0.76 = 0.4957.$$

As for the rate of people who go from exposed to asymptomatic infected, y, the proportion of people in the population who qualify as susceptible, D, and the effective contact rate, $\tilde{\mathrm{n}}$, were multiplied. Then

$$\tau = D \times \tilde{\mathrm{n}} = 0.1780 \times 0.8060 = 0.1435.$$

Let us note that the value reached is practically equal to that obtained in (7), which placed it at 0.1429.

The rate n of isolated people who decide to expose themselves in DR is technically equal to the rate of people who go from susceptible to exposed, $c_S(t)$. Thus, $n \approx c_S(t) \approx 0.7458$.

On the other hand, to estimate the rate of people who go from asymptomatic infected to symptomatic infected, $\bar{\omega}$, it was taken into account the proportion of asymptomatic infected people who die from the infection, φ_A, based on which we have that

$$\bar{\omega} = 1 - \varphi_A = 1 - 0.8602 = 0.1398.$$

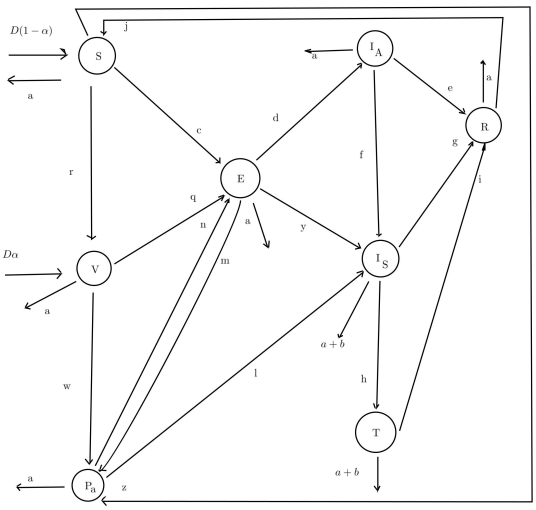

Figure 1: Model flowchart.

To estimate the rate of people who go from symptomatic infected to recovered, $g = \upsilon e$, the indications of (9) regarding the rate of recovered people who become susceptible again were considered. Again, for the case of DR, these two parameters are similar, consequently

$$j \approx g \approx 0.9921.$$

As regards the proportion of people who go from isolated to symptomatic infected, l, it was obtained by multiplying the rate of exposed people who decide to isolate themselves, m, and the effective contact rate, $\tilde{\mathrm{n}}$. Thus

$$l = m \times \tilde{\mathrm{n}} = 0.0008 \times 0.1780 = 0.00014.$$

Regarding the proportion of vaccinated people who isolate themselves, w, taking into account the opinion of some of the staff of the Department of Public Health, it was estimated that it was 2% of the total number of vaccinated people.

The remaining parameters were taken as they appeared in their respective citations.

Table 1: Estimated parameters with their sources.

Parameters	Description	Value	Source
r	Proportion of susceptible persons vaccinated	0.5514	(10)
j	Rate of recovered people who become susceptible again	0.9915	(9)
α	Proportion of vaccinated people in the population	0.6522	(13)
$(1-\alpha)$	Proporción de personas no vacunadas	0.3478	(13)
$c_S(t)$	Rate of people going from susceptible to exposed	0.7460	Estimado
$\tilde{\text{n}}$	Effective contact rate	0.1780	(16)
q_A	Probability of becoming infected after being in contact with an asymptomatic infected person $I_A(t)$	0.8683	(7)
q_T	Probability of becoming infected after being in contact with a person under treatment $T(t)$	0.0063	(17)
q_S	Probability of becoming infected after being in contact with a symptomatic person $I_S(t)$	0.0065	(17)
D	Proportion of susceptible people	0.8060	(15)
z	Proportion of susceptible people who get isolated	0.00081	Estimate
$q_V(t)$	Rate of people going from vaccinated to exposed	0.6522	Estimate
κ	Rate of people not infected due to being vaccinated	0.4957	Estimate from (13), (14)
τ	Rate of people who go from exposed to asymptomatic infected	0.1435	Estimate
m	Rate of exposed people who decide to isolate themselves	0.0008	Estimate
n	Rate of isolated people who decide to expose themselves	0.7458	Estimate
Π	Rate of people going from exposed to symptomatic infected	0.0565	(17)
$(1-\Pi)$	Proportion of exposed people who have become infected, without presenting symptoms	0.9435	(17)

Table 2: Estimated parameters with their sources (continuation of Table 1).

a	Natural death rate	0.00607	(11)
b	Death rate from infection	0.019	(18)
$\bar{\omega}$	Rate of people going from asymptomatic infected to symptomatic infected	0.1398	Estimate
e	Proportion of symptomatic infected people who have recovered naturally	0.050	(5)
$(1-e)$	Proportion of symptomatic infected people who have not recovered naturally and undergo medical treatment	0.950	Estimate from (5)
θ	Proportion of asymptomatic infected people who have healed naturally	0.1398	(7)
$(1-\theta)$	Proportion of asymptomatic infected people who did not heal naturally and presented symptoms	0.8602	Estimate from (7)
υ	Rate of people leaving from symptomatic infected to recovered	0.9921	Estimate
$1-\upsilon$	Rate of people who do not go from asymptomatic infected to recovered, and go to treatment	0.0079	Estimate
i	Recovery rate of people undergoing treatment	0.9924	(17)
y	Rate of people who go from exposed to asymptomatic infected	0.1435	Estimate
w	Proportion of vaccinated people who get isolated	0.02	Estimate
l	Proportion of people who go from isolated to symptomatic infected	0.00014	Estimate

3 Formulation of the model

For this model we will assume that the population is homogeneous, that is, people have the same probability of contact with each other. Also, the total population $N(t)$ according to their health status, is composed of:

- $S(t)$: Susceptible. These are people who are not infected with the disease, but who have a complete probability of becoming infected with COVID-19. The rate of people who go from susceptible to exposed is given by

$$c_S = \tilde{\mathrm{n}} \frac{q_A I_A(t) + q_S(t) I_S(t) + q_T T(t)}{N}, \tag{3.1}$$

  where $\tilde{\mathrm{n}}$ is the effective contact rate, q_A, q_S, q_T is the probability of becoming infected after being in contact with an asymptomatic, symptomatic and treated infected person respectively.

- $E(t)$: Exposed. These can be infected without symptoms or with symptoms, at a rate of $d = \tau(1 - \Pi)$ and $y = \Pi\tau$ respectively. Here Π is the rate of people who go from exposed to symptomatic infected and τ is the rate of people who go from exposed to asymptomatic infected.

- $I_A(t)$: Asymptomatic Infected. Under this condition, people can recover at a rate e or turn into symptomatic infected. The rate of people turning from asymptomatic infected to symptomatic infected is $f = \varpi(1 - \theta)$, where θ is the proportion of asymptomatic infected who have healed naturally and ϖ is the rate of people turning from asymptomatic infected to symptomatic infected.

- $I_S(t)$: Symptomatic Infected. At this point, people are either recovering or moving on to treatment, where $g = \upsilon e$ and $h = \upsilon(1 - e)$ are their respective rates.

- $R(t)$: Recovered. Since the infection is recurrent, recovered patients have a rate j of going from recovered to susceptible again.

- $T(t)$: Under treatment, whether in hospitals or elsewhere. Here people have a rate i of becoming recovered or a rate $a + b$ of dying from natural causes or from infection respectively.

- $P_a(t)$: People in isolation. Under this condition, people have a rate n of being exposed or a rate l of presenting the symptoms of infection.

- $V(t)$: Vaccinated. Since the vaccine is not completely effective, it is estimated that vaccinated people can go on to be exposed and contract the disease. The rate of people who go from vaccinated to exposed is

$$q_V(t) = (1 - \kappa)c_S, \tag{3.2}$$

  where κ is the rate of people who are not infected because they are vaccinated.

Consequently the total population $N(t)$ is

$$S(t) + E(t) + I_A(t) + I_S(t) + R(t) + T(t) + P_a(t) + V(t) = N(t). \tag{3.3}$$

On the other hand, we assume that after having close contacts with symptomatic, asymptomatic and treated people, susceptible people become exposed to infection. In that sense, we conjecture that the transmission rate of infection from asymptomatic people to susceptible people is lower than that of symptomatic and treated people.

Considering that the disease is still ongoing, we add 2 vital dynamics referring to those who died from natural causes a and those who died from infection, b. The other parameters of this model are described in Table 1 and Table 2.

From the flowchart in Figure 1, we derive the following system of nonlinear ordinary differential equations:

$$
\begin{aligned}
\frac{dS}{dt} &= (1-\alpha)D + jR(t) - (z+r+a+c_S)S(t),\\
\frac{dE}{dt} &= c_S S(t) + q_V V(t) + nP_a(t) - (m+a+d+y)E(t),\\
\frac{dI_A}{dt} &= dE(t) - (f+a+e)I_A(t),\\
\frac{dI_S}{dt} &= fI_A(t) + yE(t) + lP_a(t) - (g+a+b)I_S(t),\\
\frac{dR}{dt} &= eI_A(t) + gI_s(t) + iT(t) - (a+j)R(t),\\
\frac{dT}{dt} &= hI_S(t) - (i+a+b)T(t),\\
\frac{dP_a}{dt} &= wV(t) + mE(t) + kS(t) - (a+n+l)P_a(t),\\
\frac{dV}{dt} &= \alpha D + rS(t) - (q_V + a + w)V(t),
\end{aligned}
$$

with the following initial conditions:

$$
\begin{aligned}
S(0) &> 0,\\
E(0) &\geq 0,\\
I_A(0) &\geq 0,\\
I_S(0) &\geq 0,\\
R(0) &\geq 0,\\
T(0) &\geq 0,\\
P_a(0) &\geq 0,\\
V(0) &\geq 0,\\
N(0) &> 0.
\end{aligned}
\tag{3.4}
$$

By making $k_1 = (z+r+a+c_S), k_2 = (m+a+d+y), k_3 = (f+a+e), k_4 = (g+a+b), k_5 = (a+j), k_6 = (i+a+b), k_7 = (a+n+l), k_8 = (q_V+a+w)$, the system of equations that defines the model 3.4, is transformed into the following system of nonlinear ordinary differential equations:

$$
\begin{aligned}
\frac{dS}{dt} &= (1-\alpha)D + jR(t) - k_1 S(t),\\
\frac{dE}{dt} &= c_S S(t) + q_V V(t) + nP_a(t) - k_2 E(t),\\
\frac{dI_A}{dt} &= dE(t) - k_3 I_A(t),\\
\frac{dI_S}{dt} &= fI_A(t) + yE(t) + lP_a(t) - k_4 I_S(t),\\
\frac{dR}{dt} &= eI_A(t) + gI_s(t) + iT(t) - k_5 R(t),\\
\frac{dT}{dt} &= hI_S(t) - k_6 T(t),\\
\frac{dP_a}{dt} &= wV(t) + mE(t) + zS(t) - k_7 P_a(t),\\
\frac{dV}{dt} &= \alpha D + rS(t) - k_8 V(t).
\end{aligned}
\tag{3.5}
$$

4 Qualitative analysis of the model

In this section, some properties of the model defined in the system of equations (3.5) are analyzed, specifically the feasible region or boundedness of the solution, the positivity of the solution, the equilibria and their stability.

Theorem 1. *(Positivity of the solution.) With the notation introduced in the previous section, let us define the set*

$$\Lambda(t) = \{S(t),\, E(t),\, I_A(t),\, I_S(t),\, T(t), V(t),\, P_a(t),\, R(t) \in \mathbb{R}^8 : \\ S > 0,\, E \geq 0,\, I_A \geq 0,\, I_S \geq 0,\, R \geq 0,\, T \geq 0,\, P_a \geq 0,\, V \geq 0\}. \tag{4.1}$$

Then the set of fixed points of the system (3.5) $\{S,\, E,\, I_A,\, I_S,\, R,\, T,\, P_a,\, V\}$ *are all positive, for all* $t \geq 0$.

Solution 4.1. Without loss of generality, let us take the first equation of the system of differential equations (3.5). We have

$$\frac{dS}{dt} = (1-\alpha)D + jR(t) - k_1 S(t),$$

and then

$$\frac{dS}{dt} \geq -k_1 S(t). \tag{4.2}$$

By integrating (4.2) we deduce

$$\int \frac{dS}{S} = \int -k_1 dt,$$

and consequently

$$S(t) \geq e^{C_1} e^{-k_1 t}. \tag{4.3}$$

Taking into account the initial condition $S(0) = S_0$ and equation (4.2)), we have $S(t) \geq S_0\, e^{-k_1 t}$, with $S_0 = e^{C_1}$.

In a similar way, with the rest of equations of the system (3.5) we have

$$E(t) \geq E_0\, e^{-k_2 t},\; I_A(t) \geq (I_A)_0\, e^{-k_3 t},\; I_S(t) \geq (I_S)_0\, e^{-k_4 t},$$
$$T(t) \geq T_0\, e^{-k_5 t},\; V(t) \geq V_0\, e^{-k_6 t},\; P_a(t) \geq (P_a)_0\, e^{-k_7 t},\; R(t) \geq R_0\, e^{-k_8 t},$$

which completes the proof. In that sense, all solutions of the model (3.5), for $t \geq 0$, are all positive.

Theorem 2. *(Feasible region for the solution of the model.) The region* $\Psi = \{S,\, E,\, I_A,\, I_S,\, R,\, T,\, P_a,\, V \in \mathbb{R}^8 : N \leq \frac{D}{a}\}$ *is positively invariant under the flow given by equations (3.4), which means that the solution of the system is well defined epidemiologically and mathematically.*

Solution 4.2. From (3.3)), we have

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI_A}{dt} + \frac{dI_S}{dt} + \frac{dR}{dt} + \frac{dT}{dt} + \frac{dP_a}{dt} + \frac{dV}{dt}. \tag{4.4}$$

Now we simplify each variable and parameter of the model (3.4), that is

$$\begin{aligned}
D(1-\alpha) + D\,\alpha &= D, \qquad (4.5)\\
-(z+r+a+c_S)\,S + c_S S + rS + z\,S &= -a\,S,\\
-(m+a+d+y)\,E + d\,E + y\,E + m\,E &= -a\,E,\\
-(f+a+e)\,I_A + f I_A &= -a\,I_A - e\,I_A,\\
-(g+a+b)\,I_S + h\,I_S &= -a\,I_S - (g+b-h)\,I_S,\\
-(i+a+b)\,T &= = a\,T - (i+b)\,T,\\
-(q_V+a+w)\,V + q_V\,V + w\,V &= -a\,V,\\
-(a+n+l)\,P_a + n\,P_a + l\,P_a &= -a\,P_a,\\
-(a+j)\,R + j\,R &= -a\,R.
\end{aligned}$$

Replacing the results of (4.5) in the equation (4.4), we have

$$\frac{dN}{dt} = D - a(S + E + I_A + I_S + R + T + P_a + V) - e\, I_A - (g + b - h)\, I_S - (i + b)\, T.$$

In this way,

$$\frac{dN}{dt} = D - a\, N - [e\, I_A + (g + b - h)\, I_S + (i + b)\, T] \leq D - a\, N.$$

Let us assume that $N(t)$ is constant in a time t, then

$$0 \leq D - a\, N \Leftrightarrow N(t) \leq \frac{D}{a}.$$

Therefore, each solution of the equations in model (3.4) with the initial conditions (3.4) remains in

$$\Psi = \{S,\, E,\, I_A,\, I_S,\, R,\, T,\, P_a,\, V \in \mathbb{R}^8 : N \leq \frac{D}{a}\}$$

for all $t \geq 0$.

So, the set Ψ is the feasible region of the solutions of the model (3.4).

Our next target is to prove that the model (3.5) has a unique solutions. To do this, we will first prove the following theorem.

Theorem 3. *Let* $\mathfrak{N}_1(t, S)$, $\mathfrak{N}_2(t, E)$, $\mathfrak{N}_3(t, I_A)$, $\mathfrak{N}_4(t, I_S)$, $\mathfrak{N}_5(t, T)$, $\mathfrak{N}_6(t, V)$, $\mathfrak{N}_7(t, P_a)$, *y* $\mathfrak{N}_8(t, R)$ *be the kernels of the functions in the model* (3.5)*, then these kernels satisfy the Lipschitz conditions. In addition, if*

$$0 \leq k_1, k_2, k_3, k_4, k_5, k_6, k_7, k_8 < 1, \tag{4.6}$$

these kernels are contractions.

Solution 4.3. Let S_1 y S_2, E_1 y E_2, I_{A_1} y I_{A_2}, I_{S_1} y I_{S_2}, T_1 y T_2, V_1 y V_2, P_{a1} and P_{a2}, R_1 y R_2 be functions for their respective kernels.

$$\begin{aligned}
||\mathfrak{N}_1(t, S_1) - \mathfrak{N}_1(t, S_2)|| &= ||D(1-\alpha) + jR - k_1 S_1 - [D(1-\alpha) + jR - k_2 S_2]|| \\
&\leq k_1\, ||S_1 - S_2||, \\
||\mathfrak{N}_2(t, E_1) - \mathfrak{N}_2(t, E_2)|| &= ||c_S S + q_V V + nP_a - k_2 E_1 - [c_S S + q_V V + nP_a - k_2 E_2]|| \\
&\leq k_2\, ||E_1 - E_2||, \\
||\mathfrak{N}_3(t, I_{A_1}) - \mathfrak{N}_3(t, I_{A_2})|| &= ||dE - k_3 I_{A_1} - [dE - k_3 I_{A_2}]|| \leq k_3\, ||I_{A_1} - I_{A_2}||, \\
||\mathfrak{N}_4(t, I_{S_1}) - \mathfrak{N}_4(t, I_{S_2})|| &= ||fI_A + yE + lP_a - k_4 I_{S_1} - [fI_A + yE + lP_a - k_4 I_{S_2}]|| \\
&\leq k_4\, ||I_{S_1} - I_{S_2}||, \\
||\mathfrak{N}_5(t, T_1) - \mathfrak{N}_5(t, T_2)|| &= ||hI_S - k_5 T_1 - [hI_S - k_5 T_2]|| \leq k_5\, ||T_1 - T_2||, \\
||\mathfrak{N}_6(t, V_1) - \mathfrak{N}_6(t, V_2)|| &= ||D\alpha + rS - k_6 V_1 - [D\alpha + rS - k_6 V_2]|| \leq k_6\, ||V_1 - V_2||, \\
||\mathfrak{N}_7(t, P_{a_1}) - \mathfrak{N}_7(t, P_{a_2})|| &= ||wV + mE + zS - k_7 P_{a_1} - [wV + mE + zS - k_7 P_{a_2}]|| \\
&\leq k_7\, ||P_{a_1} - P_{a_2}||, \\
||\mathfrak{N}_8(t, R_1) - \mathfrak{N}_8(t, R_2)|| &= ||eI_A + gI_S + iT - k_8 R_1 - [eI_A + gI_S + iT - k_8 R_1 - R_2]|| \\
&\leq k_8\, ||R_1 - R_2||.
\end{aligned}$$

Then, the Lipschitz conditions are satisfied under the assumption (4.6). In addition, $k_1, k_2, k_3, k_4, k_5, k_6, k_7$ and k_8 are contractions for their respective kernels.

We will now prove the uniqueness of solution theorem.

Theorem 4. *The system of equations given by the model* (3.5) *has a unique solution.*

Solution 4.4. Integrating on both sides of the equations of the model (3.5), we obtain the following Volterra-type integral equations:

$$\begin{aligned}
S(t) - S(0) &= \int_0^t [D\,(1-\alpha) + jR(t) - k_1 S(t)]\, d\varphi, \qquad (4.7)\\
E(t) - E(0) &= \int_0^t [c_S S(t) + q_V V(t) + nP_a(t) - k_2 E(t)]\, d\varphi,\\
I_A(t) - I_A(0) &= \int_0^t [d\,E(t) - k_3 I_A(t)]\, d\varphi,\\
I_S(t) - I_S(0) &= \int_0^t [fI_A(t) + yE(t) + lP_a(t) - k_4 I_S(t)]\, d\varphi,\\
R(t) - R(0) &= \int_0^t [eI_A(t) + gI_S(t) + iT(t) - K_5 R(t)]\, d\varphi,\\
T(t) - T(0) &= \int_0^t [hI_S(t) - k_6 T(t)]\, d\varphi,\\
P_a(t) - P_a(0) &= \int_0^t [wV(t) + mE(t) + zS(t) = k_7 P_a(t)]\, d\varphi,\\
V(t) - V(0) &= \int_0^t [\alpha\, D + rS(t) - k_8 V(t)]\, d\varphi.
\end{aligned}$$

Now, by taking into account the kernels $\mathfrak{N}_1$, $\mathfrak{N}_2$, $\mathfrak{N}_3$, $\mathfrak{N}_4$, $\mathfrak{N}_5$, $\mathfrak{N}_6$, $\mathfrak{N}_7$, and $\mathfrak{N}_8$, we can rewrite the system (4.7) in the following way:

$$\begin{aligned}
S(t) &= S(0) + \int_0^t \mathfrak{N}_1(\varphi, S)\, d\varphi, \qquad (4.8)\\
E(t) &= E(0) + \int_0^t \mathfrak{N}_2(\varphi, E)\, d\varphi,\\
I_A(t) &= I_A(0) + \int_0^t \mathfrak{N}_3(\varphi, I_A)\, d\varphi,\\
I_S(t) &= I_S(0) + \int_0^t \mathfrak{N}_4(\varphi, I_S)\, d\varphi,\\
R(t) &= R(0) + \int_0^t \mathfrak{N}_5(\varphi, R)\, d\varphi,\\
T(t) &= T(0) + \int_0^t \mathfrak{N}_6(\varphi, T)\, d\varphi,\\
P_a(t) &= P_a(0) + \int_0^t \mathfrak{N}_7(\varphi, P_a)\, d\varphi,\\
V(t) &= V(0) + \int_0^t \mathfrak{N}_8(\varphi, V)\, d\varphi.
\end{aligned}$$

Now, let us suppose there is another solution. Let $S_1(t)$, $E_1(t)$, $I_{1_A}(t)$, $I_{1_S}(t)$, $R_1(t)$, $T_1(t)$, P_{1_a}, $V_1(t)$

be these solutions. We can rewrite (4.8) in the following way

$$\begin{aligned}
S(t) - S_1(t) &= \int_0^t [\mathfrak{N}_1(\varphi, S) - \mathfrak{N}_1(\varphi, S_1)]\, d\varphi, \\
E(t) - E_1(t) &= \int_0^t [\mathfrak{N}_2(\varphi, E) - \mathfrak{N}_2(\varphi, E_1)]\, d\varphi, \\
I_A(t) - I_{1_A}(t) &= \int_0^t [\mathfrak{N}_3(\varphi, I_A) - \mathfrak{N}_3(\varphi, I_{1_A})]\, d\varphi, \\
I_S(t) - I_{1_S}(t) &= \int_0^t [\mathfrak{N}_4(\varphi, I_S) - \mathfrak{N}_4(\varphi, I_{1_S})]\, d\varphi, \\
R(t) - R_1(t) &= \int_0^t [\mathfrak{N}_5(\varphi, R) - \mathfrak{N}_5(\varphi, R_1)]\, d\varphi, \\
T(t) - T_1(t) &= \int_0^t [\mathfrak{N}_6(\varphi, T) - \mathfrak{N}_6(\varphi, T_1)]\, d\varphi, \\
P_a(t) - P_{1_a}(t) &= \int_0^t [\mathfrak{N}_7(\varphi, P_a) - \mathfrak{N}_7(\varphi, P_{1_a})]\, d\varphi, \\
V(t) - V_1(t) &= \int_0^t [\mathfrak{N}_8(\varphi, V) - \mathfrak{N}_8(\varphi, V_1)]\, d\varphi.
\end{aligned} \tag{4.9}$$

Let us take norms in (4.9) to obtain

$$\begin{aligned}
||S(t) - S_1(t)|| &\leq \int_0^t ||\mathfrak{N}_1(\varphi, S) - \mathfrak{N}_1(\varphi, S_1)||\, d\varphi, \\
||E(t) - E_1(t)|| &\leq \int_0^t ||\mathfrak{N}_2(\varphi, E) - \mathfrak{N}_2(\varphi, E_1)||\, d\varphi, \\
||I_A(t) - I_{1_A}(t)|| &\leq \int_0^t ||\mathfrak{N}_3(\varphi, I_A) - \mathfrak{N}_3(\varphi, I_{1_A})||\, d\varphi, \\
||I_S(t) - I_{1_S}(t)|| &\leq \int_0^t ||\mathfrak{N}_4(\varphi, I_S) - \mathfrak{N}_4(\varphi, I_{1_S})||\, d\varphi, \\
||R(t) - R_1(t)|| &\leq \int_0^t ||\mathfrak{N}_5(\varphi, R) - \mathfrak{N}_5(\varphi, R_1)||\, d\varphi, \\
||T(t) - T_1(t)|| &\leq \int_0^t ||\mathfrak{N}_6(\varphi, T) - \mathfrak{N}_6(\varphi, T_1)||\, d\varphi, \\
||P_a(t) - P_{1_a}(t)|| &\leq \int_0^t ||\mathfrak{N}_7(\varphi, P_a) - \mathfrak{N}_7(\varphi, P_{1_a})||\, d\varphi, \\
||V(t) - V_1(t)|| &\leq \int_0^t ||\mathfrak{N}_8(\varphi, V) - \mathfrak{N}_8(\varphi, V_1)||\, d\varphi.
\end{aligned} \tag{4.10}$$

Taking into account that the Lipschitz condition is satisfied for the kernels in (4.10), we have

$$\begin{aligned}
||S(t) - S_1(t)|| &\leq k_1\, t\, ||S(t) - S_1(t)||, \\
||E(t) - E_1(t)|| &\leq k_2\, t\, ||E(t) - E_1(t)||, \\
||I_A(t) - I_{1_A}(t)|| &\leq k_3\, t\, ||I_A(t) - I_{1_A}(t)||, \\
||I_S(t) - I_{1_S}(t)|| &\leq k_4\, t\, ||I_S(t) - I_{1_S}(t)||, \\
||R(t) - R_1(t)|| &\leq k_5\, t\, ||R(t) - R_1(t)||, \\
||T(t) - T_1(t)|| &\leq k_6\, t\, ||T(t) - T_1(t)||, \\
||P_a(t) - P_{1_a}(t)|| &\leq k_7\, t\, ||P_a(t) - P_{1_a}(t)||, \\
||V(t) - V_1(t)|| &\leq k_8\, t\, ||V(t) - V_1(t)||.
\end{aligned} \tag{4.11}$$

Consequently,

$$\begin{aligned}
||S(t) - S_1(t)||\,(1 - k_1\, t) &\leq 0, \\
||E(t) - E_1(t)||\,(1 - k_2\, t) &\leq 0, \\
||I_A(t) - I_{1_A}(t)||\,(1 - k_3\, t) &\leq 0, \\
||I_S(t) - I_{1_S}(t)||\,(1 - k_4\, t) &\leq 0, \\
||R(t) - R_1(t)||\,(1 - k_5\, t) &\leq 0, \\
||T(t) - T_1(t)||\,(1 - k_6\, t) &\leq 0, \\
||P_a(t) - P_{1_a}(t)||\,(1 - k_7\, t) &\leq 0, \\
||V(t) - V_1(t)||\,(1 - k_8\, t) &\leq 0.
\end{aligned} \tag{4.12}$$

Then, since all contractive constants are non-negative and less than 1 (see (4.6)):

$$\begin{aligned}
||S(t) - S_1(t)|| &= 0 \Rightarrow S(t) = S_1(t), \\
||E(t) - E_1(t)|| &= 0 \Rightarrow E(t) = E_1(t), \\
||I_A(t) - I_{1_A}(t)|| &= 0 \Rightarrow I_A(t) = I_{1_A}(t), \\
||I_S(t) - I_{1_S}(t)|| &= 0 \Rightarrow I_S(t) = I_{1_S}(t), \\
||R(t) - R_1(t)|| &= 0 \Rightarrow R(t) = R_1(t), \\
||T(t) - T_1(t)|| &= 0 \Rightarrow T(t) = T_1(t), \\
||P_a(t) - P_{1_a}(t)|| &= 0 \Rightarrow P_a(t) = P_{1_a}(t), \\
||V(t) - V_1(t)|| &= 0 \Rightarrow V(t) = V_1(t).
\end{aligned}$$

Therefore, the model (3.5) has a unique solution.

4.1 Free equilibrium points and reproduction number

To calculate the free equilibrium points of the model (3.5), we set the right-hand side of the equations of this model equal to zero. In addition, we take $I_A = I_S = R = T = 0$. Next we solve the rest of equations of (3.5). In this way

$$D\,(1 - \alpha) = k_1\, S^*, \tag{4.13}$$

$$c_s\, S^* + q_v\, V^* + n\, P_a^* = k_2\, E^*, \tag{4.14}$$

$$D\,\alpha + r\, S^* = k_6\, V^*, \tag{4.15}$$

$$w\, V^* + z\, S^* = k_7\, P_a^*. \tag{4.16}$$

So, from (4.13)), we have

$$D\,(1-\alpha) = k_1\,S^* \Leftrightarrow S^* = \frac{D\,(1-\alpha)}{k_1}. \tag{4.17}$$

Substituting (4.17) in (4.15), we obtain

$$D\,\alpha + r\left[\frac{D\,(1-\alpha)}{k_1}\right] = k_6\,V^* \Rightarrow V^* = \frac{k_1\,D\,\alpha + r\,D\,(1-\alpha)}{k_1 k_6}. \tag{4.18}$$

Now we substitute (4.18) and (4.17) in (4.16) to obtain

$$\frac{w\left[\frac{k_1\,D\,\alpha + r\,D\,(1-\alpha)}{k_1 k_6}\right] + z\left[\frac{D\,(1-\alpha)}{k_1}\right]}{k_7} \Rightarrow P_a^* = \frac{w\,[k_1 D\,\alpha + r\,D\,(1-\alpha)] + z\,[D(1-\alpha)\,k_6]}{k_1 k_6 k_7}. \tag{4.19}$$

Finally, another substitution, in this case (4.17), (4.18) and (4.19) in (4.14), allow us to obtain

$$\begin{aligned} E^* &= \frac{c_s k_6 k_7 [D\,(1-\alpha)] + q_v\,k_7 [k_1\,D\,\alpha + r\,D\,(1-\alpha)] +}{k_1 k_2 k_6 k_7} \\ &+ \frac{n\,[w\,[k_1 D\,\alpha + r\,D\,(1-\alpha)] + z\,[D(1-\alpha)\,k_6]]}{k_1 k_2 k_6 k_7}. \end{aligned}$$

If we assume that initially there are no people exposed because they are isolated, then $E = I_A = I_S = T = R = 0$. So, we would have a free equilibrium point, given by

$$E^* = \{S^*, 0, 0, 0, 0, V^*, P_a^*, 0\}. \tag{4.20}$$

In addition, if $\alpha = 1$, then we obtain a free equilibrium point in which every susceptible person is vaccinated, with at least one dose. Under this scenario it follows that

$$S^* = 0,\, V^* = \frac{D}{k_6},\, P_a^* = \frac{w\,D}{k_6 k_7},$$

and then

$$E^*_{\alpha=1} = \{0, 0, 0, 0, 0, V^*, P_a^*, 0\}. \tag{4.21}$$

The equilibrium free point corresponds to people who have not received any dose of the vaccine. Then

$$S^* = \frac{D}{k_1},\, V^* = \frac{r\,D}{k_1\,k_6},\, P_a^* = \frac{D\,(w\,r + z k_6)}{k_1\,k_6\,k_7},$$

and consequently,

$$E^*_{\alpha=0} = \{S^*, 0, 0, 0, 0, V^*, P_a^*, 0\}. \tag{4.22}$$

Following (2), we find that $\mathfrak{R}_0$ is the basic reproduction number of secondary cases produced by a primary infection during the infectious period in a fully susceptible population. The control quantity, $\mathfrak{R}_c$, is used to represent the same quantity for a system that incorporates vaccination as an intervention strategy. These quantities are widely used by public health organizations as an indicator of the severity of a particular epidemic, allowing to establish whether the considered infection will be endemic on not. These numbers can be calculated by constructing two matrices: the rate of appearance of new infections, $\mathbb{F}$, and the rate of transfer of individuals by all other means, Λ. Thus, $\mathfrak{R}_c$, is defined, according to (1) as the spectral radius of the matrix $\mathbb{F}\,\Lambda^{-1}$ that is, as the dominant eigenvalue of

$$\mathfrak{R}_c = \mathbb{F}\,\Lambda^{-1}. \tag{4.23}$$

For the given matrix Λ the related Jacobian matrix related to E, I_A, I_S, T, is constructed, whereas for the matrix $\mathbb{F}$, the rate of people who go from susceptible to exposed is used, c_s, together with the

rate of people going from vaccinated to exposed, q_v. Therefore: $\Lambda = \begin{pmatrix} -k_2 & 0 & 0 & 0 \\ (1-\Pi)\,\tau & -k_3 & 0 & 0 \\ \Pi\,\tau & \varpi(1-\theta) & -k_4 & 0 \\ 0 & 0 & \upsilon(1-e) & -k_5 \end{pmatrix}$

and then

$$\Lambda^{-1} = \begin{pmatrix} -\frac{1}{k_2} & 0 & 0 & 0 \\ \frac{(1-\Pi)\,\tau}{k_2\,k_3} & -\frac{1}{k_3} & 0 & 0 \\ \frac{\tau\,[\varpi\,(1-\Pi)(1-\theta)+\Pi\,k_3]}{k_2\,k_3\,k_4\,k_5} & \frac{\varpi\,(1-\theta)}{k_3\,k_4} & -\frac{1}{k_4} & 0 \\ \frac{\upsilon\,\tau\,(1-e)\,[\varpi\,(1-\Pi)(1-\theta)+\Pi\,k_3]}{k_2\,k_3\,k_4\,k_5} & \frac{\varpi\,\upsilon\,[(1-e)\,(1-\theta)]}{k_3\,k_4\,k_5} & \frac{\upsilon\,(1-e)}{k_4\,k_5} & -\frac{1}{k_5} \end{pmatrix}. \tag{4.24}$$

On the other hand, $\mathbb{F} = c_s + q_v$ and, as a consequence.

$$\mathbb{F} = \begin{pmatrix} c_s + q_v \\ 0 \\ 0 \\ 0 \end{pmatrix}. \tag{4.25}$$

Taking into account (3.1) and (3.2), we have

$$\begin{aligned} c_s + q_v &= \tilde{\mathrm{n}}\left(\frac{q_A + q_S + q_T}{N}\right) S + \tilde{\mathrm{n}}\,(1-k)\left(\frac{q_A + q_S + q_T}{N}\right) V \\ &= \frac{\tilde{\mathrm{n}}\,(q_A + q_S + q_T)\,[S + (1-k)\,V]}{N}. \end{aligned}$$

Considering now the free points, the matrix (4.25) is transformed in

$$\mathbb{F} = \begin{pmatrix} 0 & \frac{\tilde{\mathrm{n}}\,q_A\,[S^* + (1-k)\,V^*]}{N^*} & \frac{\tilde{\mathrm{n}}\,q_S\,[S^* + (1-k)\,V^*]}{N^*} & \frac{\tilde{\mathrm{n}}\,q_T\,[S^* + (1-k)\,V^*]}{N^*} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}. \tag{4.26}$$

Now, we make

$$\Upsilon = \tilde{\mathrm{n}}\left[\frac{S^* + (1-k)\,V^*}{N^*}\right]$$

and the matrix (4.26) is transformed in

$$\mathbb{F} = \begin{pmatrix} 0 & q_A\Upsilon & q_S\Upsilon & q_T\Upsilon \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}. \tag{4.27}$$

As $\mathfrak{R}_{\mathfrak{c}}$ is the largest eigenvalue of $F\,\Lambda^{-1}$, we have

$$\begin{aligned} \mathfrak{R}_{\mathfrak{c}} = {} & q_A\,\Upsilon\,\frac{(1-\Pi)\,\tau}{k_2 k_3} + q_S\,\Upsilon\,\tau\frac{[\varpi\,(1-\Pi)(1-\theta)+\Pi k_3]}{k_2 k_3 k_4} \\ & + q_T\,\Upsilon\,\upsilon\tau\,(1-e)\,\frac{[\varpi\,(1-\Pi)(1-\theta)+\Pi k_3]}{k_2 k_3 k_4 k_5}, \end{aligned}$$

and then

$$\mathfrak{R}_{\mathfrak{c}} = \Upsilon\,\tau\left[\frac{q_A\,(1-\Pi)k_4 k_5 + [\varpi k_5\,(1-\Pi)(1-\theta) + \Pi k_3\,(q_S\,k_5 + q_T\,(1-e)\,\upsilon)]}{k_2 k_3 k_4 k_5}\right]. \tag{4.28}$$

Let us note

$$\begin{aligned} \Upsilon = \frac{\tilde{\mathrm{n}}\,[S^* + (1-k)\,V^*]}{N^*} &= \frac{\tilde{\mathrm{n}}\,[\frac{D\,(1-\alpha)}{k_1} + (1-k)\,\frac{D[k_1\,\alpha + r\,(1-\alpha)]}{k_1\,k_6}]}{\frac{D}{a}} \\ &= \tilde{\mathrm{n}}\,a\left[\frac{k_6\,(1-\alpha) + (1-k)\,[k_1\,\alpha + r\,(1-\alpha)]}{k_1\,k_6}\right]. \end{aligned}$$

Therefore

$$\begin{aligned}\mathfrak{R}_c &= \left[\frac{q_A\,(1-\Pi)k_4\,k_5+[(\varpi\,(1-\Pi)(1-\theta)+\Pi k_3)\,(q_S\,k_5+q_T\,(1-e)\,\upsilon)]}{k_2k_3k_4k_5}\right]\\ &\times \left[\frac{k_6\,(1-\alpha)+(1-k)\,[k_1\,\alpha+r\,(1-\alpha)]}{k_1\,k_6}\right]\tau\,\tilde{\mathrm{n}}\,a. \end{aligned} \tag{4.29}$$

By making $\alpha=\kappa=r=0$ in (4.29), we deduce the following expression for $\mathfrak{R}_0$:

$$\mathfrak{R}_0=\left[\frac{q_A\,(1-\Pi)k_4\,k_5+[(\varpi\,(1-\Pi)(1-\theta)+\Pi k_3)\,(q_S\,k_5+q_T\,(1-e)\,\upsilon)]}{k_2k_3k_4k_5}\right]\left[\frac{\tau\,\tilde{\mathrm{n}}\,a}{k_1}\right]. \tag{4.30}$$

Rewriting the equation (4.29) in terms of $\mathfrak{R}_0$ we have

$$\mathfrak{R}_c=\left[\frac{k_6\,(1-\alpha)+(1-k)\,[k_1\,\alpha+r\,(1-\alpha)]}{k_6}\right]\mathfrak{R}_0 \tag{4.31}$$

Again, if $\alpha=0$, we will be in the situation where no one is vaccinated. Then the corresponding effective reproduction control number is given by

$$\mathfrak{R}_c=\left[1+\frac{(1-\kappa)\,r}{k_6}\right]\mathfrak{R}_0. \tag{4.32}$$

If $\alpha=r=0$, then $\mathfrak{R}_{\mathfrak{c}}=\mathfrak{R}_{\mathfrak{o}}$.

In addition, if $\alpha=1$, everybody will have at least the first vaccine. Therefore, the corresponding effective reproduction control number will be

$$\mathfrak{R}_c=\left[\frac{(1-\kappa)\,k_1}{k_6}\right]\mathfrak{R}_{\mathfrak{o}}. \tag{4.33}$$

On the other hand, if $\alpha=\kappa=1$, as before, we have $\mathfrak{R}_{\mathfrak{c}}=\mathfrak{R}_{\mathfrak{o}}$.

Given the above scenarios, it can be said that if $\mathfrak{R}_c>1$ the pandemia of COVID-19 could remain in our daily lives, while if $\mathfrak{R}_c<1$, the infection will disappear.

4.2 Sensitivity analysis of the model

Here we see the sensitivity analysis of the model, which is used to relate the parameters that influence $\mathfrak{R}_{\mathfrak{c}}$ and $\mathfrak{R}_{\mathfrak{o}}$. A sensitivity analysis is recommended to understand the factors responsible for the transmission and prevalence of contagious diseases. In this sense, it is important to verify under which conditions the parameters of a model allow us to have $\mathfrak{R}_{\mathfrak{c}}<1$ and $\mathfrak{R}_{\mathfrak{o}}<1$.

In (4), we found that for this analysis, the following formula is used:

$$\mathcal{S}(x)=\frac{x}{\mathfrak{R}_{\mathfrak{c}}}\times\frac{\partial\,\mathfrak{R}_{\mathfrak{c}}}{\partial x}.$$

In the Table 3 we present the sensitivity indices of $\mathfrak{R}_{\mathfrak{c}}$ with respect to different parameters of the model.

The graphical analysis of the sensitivity for $\mathfrak{R}_{\mathfrak{c}}$ with respect to the parameters in model (3.5) is shown in Figure 3. The areas of the rectangles shown in this figure does not appear in a proper scale. They just indicate an intuitive idea of each sensitivity. The values of the sensitivity indices of each variable appear above or below each rectangle, depending if the corresponding value is positive or negative.

As shown in Table 3, the parameters r, q_A, q_S, q_T, φ, θ and τ are positive, which shows that as their values increase, they have a great impact on the spread of the disease, and as they decrease, the disease also decreases or disappears from the population. Let us note that the largest positive indices correspond to the parameters τ and q_A.

On the other hand, the parameters α, κ and e present negative sensitivity indices, which implies that they reduce the disease in the population as their value increase. For this case, we observe that the smallest negative indices are κ and α. Therefore, the recommendation derived from this study is to minimize parameters with positive indices and maximize parameters with negative indices.

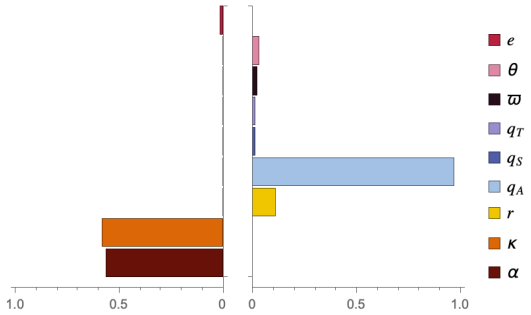

Figure 2: Sensivity indices for $\mathfrak{R}_c$ with respect to to the parameters introduced in model (3.5).

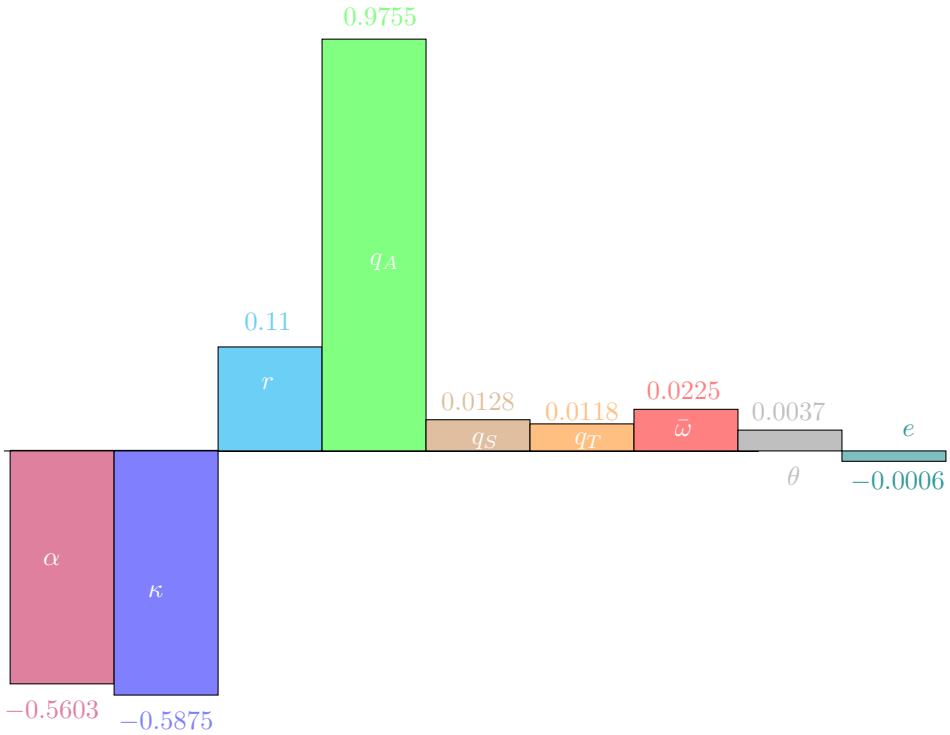

Figure 3: Sensivity indices for $\mathfrak{R}_c$ with respect to to the parameters introduced in model (3.5).

Table 3: Sensitivity indices of $\mathfrak{R}_{\mathfrak{c}}$ with respect to the model parameters adjusted to the Dominican Republic.

Parameters	Sensitivity indices of the parameters
$\mathcal{S}(\alpha)$	$\frac{\alpha[(1-\kappa)(k_1-r)-k_6]}{(1-\kappa)[r(1-\alpha)+\alpha k_1]+(1-\alpha)k_6} = -0.5603 < 0$
$\mathcal{S}(\kappa)$	$\frac{\kappa[-r(1-\alpha)-\alpha k_1]}{(1-\kappa)[r(1-\alpha)+\alpha k_1]+(1-\alpha)k_6} = -0.5875 < 0$
$\mathcal{S}(r)$	$\frac{r(1-\alpha)(1-\kappa)}{(1-\kappa)[r(1-\alpha)+\alpha k_1]+(1-\alpha)k_6} = 0.11 > 0$
$\mathcal{S}(q_A)$	$\frac{(1-\pi)k_4k_5q_A}{(1-\pi)k_4k_5q_A+[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S+(1-e)\upsilon q_T]} = 0.9755 > 0$
$\mathcal{S}(q_S)$	$\frac{[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S]}{(1-\pi)k_4k_5q_A+[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S+(1-e)\upsilon q_T]} = 0.0128 > 0$
$\mathcal{S}(q_T)$	$\frac{\upsilon q_T(1-e)[(1-\pi)\varpi(1-\theta)+\pi k_3]}{(1-\pi)k_4k_5q_A+[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S+(1-e)\upsilon q_T]} = 0.0118 > 0$
$\mathcal{S}(\varpi)$	$\frac{(1-\pi)\varpi(1-\theta)[k_5q_S+(1-e)\upsilon q_T]}{(1-\pi)k_4k_5q_A+[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S+(1-e)\upsilon q_T]} = 0.0225 > 0$
$\mathcal{S}(\theta)$	$\frac{(1-\pi)\varpi\theta[k_5q_S+(1-e)\upsilon q_T]}{(1-\pi)k_4k_5q_A+[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S+(1-e)\upsilon q_T]} = 0.0037 > 0$
$\mathcal{S}(e)$	$-\frac{e\upsilon q_T[(1-\pi)\varpi(1-\theta)+\pi k_3]}{(1-\pi)k_4k_5q_A+[(1-\pi)\varpi(1-\theta)+\pi k_3][k_5q_S+(1-e)\upsilon q_T]} = -0.0006 < 0$
$\mathcal{S}(\tau)$	$\mathcal{S}(\tau) = \frac{\tau}{\mathfrak{R}_{\mathfrak{c}}} \times \frac{\partial \mathfrak{R}_{\mathfrak{c}}}{\partial \tau} = 1 > 0$

5 Numerical simulations of the model

The numerical simulations are based on the model introduced in (3.4):

$$\begin{aligned}
\frac{dS}{dt} &= (1-\alpha)D + jR(t) - (z+r+a+c_S(t))S(t),\\
\frac{dE}{dt} &= c_S(t)S(t) + q_V(t)V(t) + nP_a(t) - (m+a+d+y)E(t),\\
\frac{dI_A}{dt} &= dE(t) - (f+a+e)I_A(t),\\
\frac{dI_S}{dt} &= fI_A(t) + yE(t) + lP_a(t) - (g+a+b)I_S(t),\\
\frac{dR}{dt} &= eI_A(t) + gI_s(t) + iT(t) - (a+j)R(t),\\
\frac{dT}{dt} &= hI_S(t) - (i+a+b)T(t),\\
\frac{dP_a}{dt} &= wV(t) + mE(t) + kS(t) - (a+n+l)P_a(t),\\
\frac{dV}{dt} &= \alpha D + rS(t) - (q_V(t)+a+w)V(t),
\end{aligned}$$

where $c_S(t)$ y $q_V(t)$ are defined in (3.1) and (3.2) respectively

$$c_S(t) = \tilde{\mathrm{n}}\frac{q_AI_A(t) + q_SI_S(t) + q_TT(t)}{N}, \quad q_V(t) = (1-\kappa)c_S(t).$$

These are the parameters we have taken:

$$r = 0.554; j = 0.9915; \alpha = 0.6522; \tilde{\mathrm{n}} = 0.1780; qA = 0.8683; qT = 0.0063; qS = 0.0065;$$

$$d = 0.8060; z = 0.00081; \kappa = 0.4957; \tau = 0.1435; m = 0.0008; n = 0.7458; \Pi = 0.0565;$$

$$a = 0.00607; b = 0.019; \bar{\omega} = 0.1398; e = 0.05; \theta = 0.1398; v = 0.079; i = 0.9924;$$

$$y = 0.1435; \omega = 0.02; l = 0.0014; D = 0.8060; N = 11,117,874;$$

$$f = \bar{\omega}(1-\theta) = 0.120256; g = ve = 0.00395; h = v(1-e) = 0.07505.$$

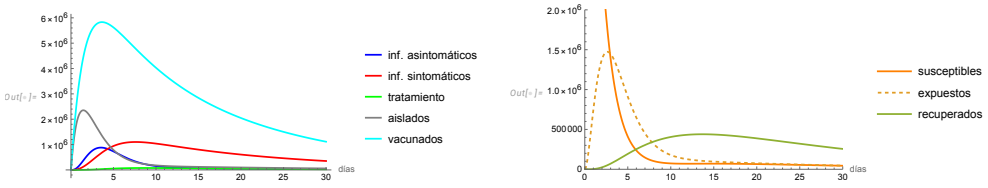

Figure 4: Evolution of some populations according the model (3.4).

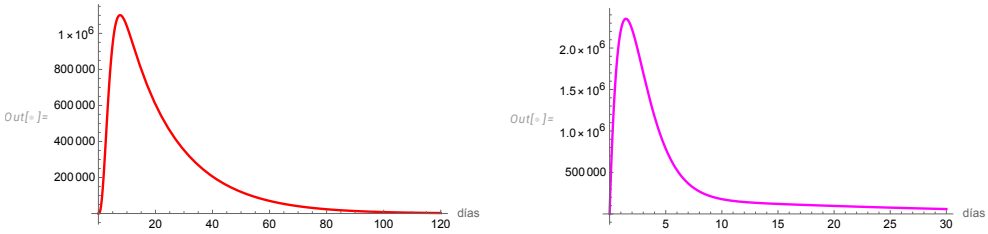

Figure 5: In the graph on the left, the evolution of symptomatic infected people according to the model. On the right, a graph of people in isolation.

6 Conclusion

We have built a mathematical model to predict the behavior of COVID-19 in the Dominican Republic. In this way, we performed a detailed mathematical analysis of this model, which allowed us to determine both the control number, $\mathfrak{R}_c$ and the basic reproduction number, $\mathfrak{R}_o$. In addition, theorems on the existence and uniqueness of solutions for the model, as well as their non-negativity, were demonstrated.

Regarding the sensitivity of the system with respect to the parameters, it was shown that the highest positive rates correspond to the rate of people who go from exposed to asymptomatic infected, τ and the probability of becoming infected after being in contact with an asymptomatic infected person, q_A. Likewise, the parameters with the lowest negative rates refer to the rate of people not infected because they are vaccinated, κ and the proportion of vaccinated people in the population α. Finally, the health authorities of the Dominican Republic were recommended to minimize the parameters with positive rates and maximize the parameters with negative rates.

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