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One Study of COVID-19 Spreading at The United States – Brazil – Colombia

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ABSTRACT. The present work concerns the COVID-19's spread over The United States, Brazil and Colombia. Although countries show differences in economic development, but similarities such as continental dimension or native social interaction, the spread of COVID-19 in them has some similarities. At the moment, the countries are living the disease with temporal delay. Thus, we used a database on WHO Coronavirus, Mathematical Modeling and Numerical Simulations to describe the most recent COVID-19 development patterns in these countries, which we saw.

Keywords: mathematical modeling, numerical analysis, COVID-19.

1 INTRODUCTION

The SARS-CoV-2 coronavirus pandemic causes the COVID-19 disease, for which we have no immune response or vaccine. The origin of COVID-19 is believed to have occurred in Wuhan, China, in late 2019. From China, the disease was rapidly transmitted globally by individuals who travelled to Europe and The United States.

On the America continent, the first cases of COVID-19 appeared in The United States. On January 21, 2020, the American Center for Disease Control and Prevention (CDC) confirmed the first case of COVID-19 in a 35-year-old man from Snohomish County, Washington, who returned from a trip to the region around Wuhan [24]. In February 2020, cases of COVID-19 were

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already emerging in several countries on the American continent. The coronavirus landed in Latin America on February 26, when Brazil confirmed a case in São Paulo, a 61-year-old man who returned from a trip to Italy [20]. The Colombia's first case of COVID-19 took place on March 6, 2020, a 19-year-old female who traveled to Milan, Italy [4]. Currently, COVID-19 has reached almost all countries on the American continent.

According to the World Health Organization (WHO), on July 31, 2020, The United States, Brazil and Colombia were the countries of the American continent with the highest numbers of daily infected cases [25]. By this date, 9.152.173 cases and 351.121 deaths by COVID-19 had already occurred in the American continent, comprising over 53.5% of the total number of reported cases in the world. The United States, Brazil and Colombia present 4.388.566, 2.552.265 and 276.055 cases with 150.054, 90.134 and 9.454 deaths, respectively, comprising over 48%, 28% and 3% of the total number of reported cases in the American continent [25].

The United States, Brazil and Colombia are in different moments in the epidemiological process, Colombia is in the exponential growth phase, Brazil is probably in the peak of the epidemic, while The United States is already experiencing a second wave of SARS-CoV-2 coronavirus infection. It is noteworthy that these three countries have very different Human Development Indexes (HDI) and territorial dimensions and, even so, they have in common high infection rates by the SARS-CoV-2 coronavirus.

The objective of this article is to carry out a mathematical study of the possible trends of the epidemic by COVID-19 in these three countries. This article was based on the data provided by the WHO [25] and the Susceptibles-Infectious-Recovered-Dead model, the SIRD model [6] [15].

The SIRD model is a classic compartmental model of the Kermack - McKendrick type [12] [13]. Compartmental models divide the population into several different compartments, for example, Susceptible population, Infectious population, Recovered population, Dead population, among others, and specify how individuals move through the compartments over time. Despite being a simple mathematical model, the SIRD is one of the most applied mathematical models to understand the current health crisis. Obviously, more realistic and complex models would better describe the dynamics of this epidemic, but data and information about COVID-19 are lacking to implement them. Reviews of epidemiological models can be found in [6] [15].

Regarding the adjustment of the parameters of the SIRD model for The United States, Brazil and Colombia, it appears that these parameters change frequently, depending on local political factors (closure of non-essential establishments, quarantine, movement restrictions...) [11], socio-economic factors (social and hygienic behaviors, lower per-capita income...) [8] [10], climatic factors (temperature, humidity, average wind speed, UV index...) [17], among others. In this context, it was decided to adjust the parameters of the SIRD model over time, based on data made available by WHO, using non-linear least squares methods [5] [14].

Regarding the numerical procedures to solve the SIRD model, first, the discretization of the ordinary differential equation system was performed using the Finite Difference Method. The resulting linear system of non-linear equations was solved iteratively by the Gauss-Seidel method until the convergence criterion was overcome. It was also found that all the matrices's coefficients of the iterative processes satisfy the Sassenfeld convergence criterion [7] [21] [22].

2 MATERIALS AND METHODS

2.1 Data Base

There are several data base source about COVID-19, e. g., Brazil's Coronavirus Panel [1], the National Institute of Health in Colombia [2], the Johns Hopkins Coronavirus Resource Center [3] and among other sources that exhibit the numbers of the infected, dead and more information as well.

But, to this work we used the WHO Coronavirus Disease (COVID-19) Dashboard [25] to keep integrity and uniformity of our numerical model.

From source WHO Coronavirus Dashboard we did not have the recovering data over time, so we used the assumption that says - the time for a person to be moved from the infected to the recovered compartmental can be about 14 days [16] [23]. Thus, we reconstructed the number of people in the compartments: Susceptible, Infected, Recovered and Dead.

In fact the coronavirus disease is not completely understanding at the moment, certainly there are additional parameters unknown that describing better the pattern it. So, we chose to take several data sets consolidated of the 14 days to do our simulations in order to get more realistic information. In this way, we got a simulations' clustering which permitted to understanding the fundamentals of the behavior coronavirus disease over the countries.

How already mentioned in the introduction section, the disease begins at The United States, Brazil and Colombia countries in a different times. The government actions (good or bad), civil liberties, and mass testing come interfering with the situation of COVID-19 in countries. All of these conducts imply at the number variations of the infected and dead people, what is transcribed at the WHO Coronavirus Disease (COVID-19) data base.

From data base, it can be seen that The United States is living a second wave contamination. Brazil, maybe, arrived at the infecting peak on the August month. Colombia, clearly, is going up at the infected number yet. So, we have a time delay of the COVID-19's spread in the countries. With these, we want to explain how disease spreading happens in the countries through numerical simulations. But with a cluster of simulations, not just a simulation alone.

2.2 Governing Equations

There are several mathematical modelling of the COVID-19 at the moment. But, to this work we considering the SIRD's model given by equations:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta}{N}SI & \frac{dI}{dt} &= \frac{\beta}{N}SI - (\gamma_R + \gamma_D)I \\ \frac{dR}{dt} &= \gamma_R I & \frac{dD}{dt} &= \gamma_D I \end{aligned} \tag{2.1}$$

where:

- t, S, I, R, D are time, susceptible, infected, recovered and death variables, respectively, N is an average population value;
- β is an infection rate, and γ_R and γ_D are recover and death rates, these parameters are calculated per day, with this it is possible to calculate the basic reproduction number $R_0 = \frac{\beta}{\gamma_R+\gamma_D}$.

At the initial time we have

$$S(0) = N \quad ; \quad I(0) = I_0 \quad ; \quad R(0) = R_0 \quad ; \quad D(0) = D_0, \tag{2.2}$$

and for end time, denoted by t_F, we admitted

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = \frac{dD}{dt} = 0. \tag{2.3}$$

The condition (2.3) was considered because at this moment the disease finished and the equations' steady state stays established.

2.3 SIRD's Numerical Modelling Proposal

The model (2.1) has 4 ordinary differential equations (ODE). Specifically, any ODE can be written as

$$\frac{d\Phi_l}{dt} = \Psi_l \text{ with } l = 1,\ldots,4 \tag{2.4}$$

so that

$$\begin{aligned}
\Phi_1 &= S \quad ; \quad \Psi_1 = -\tfrac{\beta}{N}SI \\
\Phi_2 &= I \quad ; \quad \Psi_2 = \tfrac{\beta}{N}SI - (\gamma_R + \gamma_D)I \\
\Phi_3 &= R \quad ; \quad \Psi_3 = \gamma_R I \\
\Phi_4 &= D \quad ; \quad \Psi_4 = \gamma_D I
\end{aligned}$$

therefore, all deductive numeric procedure at this work will be over equation (2.4).

The temporal discret grid considered is showed at the Figure (1). We denoted the time lapse like Δt, and the end time $t_F = (s-1)\Delta t$. The value k is a node that indicate the temporal position, or a time counter. Thus, $k = s$ means temporal nodes' total value.

From condition (2.2) we can write Φ_l^k like that

$$\begin{aligned}
\Phi_1(0) &= \Phi_1^1 = N \qquad \Phi_2(0) = \Phi_2^1 = I_0 \\
\Phi_3(0) &= \Phi_3^1 = 0 \qquad \Phi_4(0) = \Phi_4^1 = 0
\end{aligned} \tag{2.5}$$

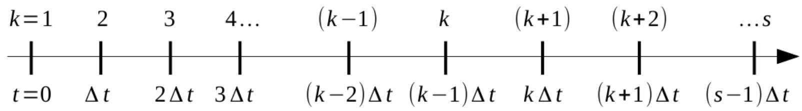

Figure 1: Temporal discret grid.

and the Neumann condition (2.3) we have too

$$\frac{d}{dt}\Phi_l(t_F) = \left.\frac{d\Phi_l}{dt}\right|^s = 0. \tag{2.6}$$

With respect to temporal derivative of the equations (2.4), they are approximated by forward second order finite difference in the node k

$$\left.\frac{d\Phi_l}{dt}\right|^k \simeq \frac{1}{2\Delta t}\left(-3\Phi_l^k + 4\Phi_l^{k+1} - \Phi_l^{k+2}\right) \tag{2.7}$$

similarly, the equations (2.6) are approximated by backward second order finite difference at the last node s

$$\left.\frac{d\Phi_l}{dt}\right|^s \simeq \frac{1}{2\Delta t}\left(3\Phi_l^s - 4\Phi_l^{s-1} + \Phi_l^{s-2}\right). \tag{2.8}$$

These approximations were used to obtain improved numerical results.

So, writing equation (2.4) to node k we can see

$$\left.\frac{d\Phi_l}{dt}\right|^k = \Psi_l^k \tag{2.9}$$

and inserting formula (2.7) at the last equation (2.9), what it leads to

$$\frac{1}{2\Delta t}\left(-3\Phi_l^k + 4\Phi_l^{k+1} - \Phi_l^{k+2}\right) = \Psi_l^k$$

or finally

$$-3\Phi_l^k + 4\Phi_l^{k+1} - \Phi_l^{k+2} = 2\Delta t \Psi_l^k. \tag{2.10}$$

The equality (2.10) is an our temporal difference equation, that describe the COVID-19 behaviour. We want to explain that the equation (2.10) is the temporal evolution for Φ_l. Numerically, from Figure (2), setting s we have to vary $k = 1,\dots,s-2$ to obtain the differences' equations at the points $k = 2,\dots,s-1$.

The first possible value is $s = 3$, so just a simple linear equation is found, and the Φ_l^2 is known at the time $t_F = \Delta t$.

Nevertheless, with help the Figure (2) again, if $s > 3$ we will have to solve l systems of the $(s-2)$ difference equations to compute Φ_l^{s-1} (labeled to star symbol) to $t_F = (s-2)\Delta t$. It remembering

Figure 2: Computational temporal grid until s.

which at the square symbol the initial condition (2.5) is assumed and the triangle symbol the Neumann condition (2.6) is used as well. Particularly, the system mentioned is the kind of

$$\begin{bmatrix} 4 & -1 & & & & & & \\ -3 & 4 & -1 & & & & & \\ & -3 & 4 & -1 & & & & \\ & & \ddots & \ddots & \ddots & & & \\ & & & \ddots & \ddots & \ddots & & \\ & & & & \ddots & \ddots & \ddots & \\ & & & & & \ddots & \ddots & \ddots \\ & & & & & \ddots & \ddots & \ddots \\ & & & & & -3 & 4 & -1 \\ & & & & & 1 & -1 & 1 \end{bmatrix} \begin{bmatrix} \Phi_l^2 \\ \Phi_l^3 \\ \Phi_l^4 \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \Phi_l^{s-2} \\ \Phi_l^{s-1} \end{bmatrix} = \begin{bmatrix} 2\Delta t \Psi_l^1 + 3\Phi_l^1 \\ 2\Delta t \Psi_l^2 \\ 2\Delta t \Psi_l^3 \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ \vdots \\ 2\Delta t \Psi_l^{s-3} \\ 3/4\Delta t \Psi_l^{s-2} \end{bmatrix}. \quad (2.11)$$

Note that the system (2.11) is not a linear system. The terms

$$\Psi_l^2 = \Psi_l^2\left(\Phi_l^2\right) \quad \ldots \quad \Psi_l^{s-2} = \Psi_l^{s-2}\left(\Phi_l^{s-2}\right); \quad l = 1,\ldots,4$$

are known if the $\Phi_l^2,\ldots,\Phi_l^{s-2}$ values were explicit. But they are unknown! Thus, we use a iterative strategy to solve the system (2.11) how presented in [9].

Without loss of generality, if $s = 4$ the system (2.11) becomes

$$\begin{bmatrix} 4 & -1 \\ -1 & 1 \end{bmatrix} \begin{bmatrix} \Phi_l^2 \\ \Phi_l^3 \end{bmatrix} = \begin{bmatrix} 2\Delta t \Psi_l^1 + 3\Phi_l^1 \\ 3/4\Delta t \Psi_l^2 \end{bmatrix}$$

whose the iterative process associated can be like

$$\begin{bmatrix} 4 & -1 \\ -1 & 1 \end{bmatrix} \begin{bmatrix} {}^{IT+1}\Phi_l^2 \\ {}^{IT+1}\Phi_l^3 \end{bmatrix} = \begin{bmatrix} 2\Delta t \Psi_l^1 + 3\Phi_l^1 \\ 3/4\Delta t \ {}^{IT}\Psi_l^2 \end{bmatrix} \quad (2.12)$$

where $IT = 0,1,\ldots,IT_{MAX}$, and IT_{MAX} means iteration maximum number. Particularly, we have a linear system to each specific IT. Furthermore, we choose the Gauss-Seidel method to solve (2.12) because the convergence is guaranteed. it is easy to see that the Sassenfeld criterium is verified. The stopped criteria value of the Gauss-Seidel method used in this work was 10^{-7}.

When $IT = 0$ the system (2.12) becomes

$$\begin{bmatrix} 4 & -1 \\ -1 & 1 \end{bmatrix} \begin{bmatrix} {}^{1}\Phi_l^2 \\ {}^{1}\Phi_l^3 \end{bmatrix} = \begin{bmatrix} 2\Delta t \Psi_l^1 + 3\Phi_l^1 \\ 3/4\Delta t \ {}^{0}\Psi_l^2 \end{bmatrix} \quad (2.13)$$

so that:

- Φ_l^1 is known (initial condition);
- $\Psi_l^1 = \Psi_l^1 \left(\Phi_l^1\right)$ is known, of course;
- ${}^0\Psi_l^2 = \Psi_l^1$ is admitted how our prediction hypothesis.

Thus, we have the linear system's solution ${}^1\Phi_l = \left[{}^1\Phi_l^2 \;\; {}^1\Phi_l^3\right]^T$ by means of Gauss-Seidel method. Now, if $IT = 1$ we find

$$\left[\begin{array}{rr} 4 & -1 \\ -1 & 1 \end{array}\right] \left[\begin{array}{c} {}^2\Phi_l^2 \\ {}^2\Phi_l^3 \end{array}\right] = \left[\begin{array}{l} 2\Delta t \Psi_l^1 + 3\Phi_l^1 \\ 3/4\Delta t \;\; {}^1\Psi_l^2 \end{array}\right] \tag{2.14}$$

so that ${}^1\Psi_l^2 = \Psi_l\left({}^1\Phi_l\right)$ is our prediction hypothesis again. It solving (2.14), we get ${}^2\Phi_l = \left[{}^2\Phi_l^2 \;\; {}^2\Phi_l^3\right]^T$.

After this, if the ${}^2\Phi_2$ is less than one (which means an end to the spread of covid-19) we accept the ${}^2\Phi_l \equiv \Phi_l$ as numerical solution of the SIRD's (2.4) at the time $t = 2\Delta t$. Otherwise, we set $s = 5$ and do the all process again to a new time $t = 3\Delta t$, and so on.

The numerical process finishes if we get the ${}^m\Phi_2 < 1$ to some $0 < m < IT_{MAX}$. Finally, we have some gains with strategy provided here:

- the governing equations system (2.4) is solved by a convergent methodology to any time;
- our implicit methodology does not need a severe restriction on the Δt value.

The implicit method together with Gauss-Seidel and Lax's law guarantee it. Besides, the t_F time is discovered in the computational run's time. To performance all simulation we developed a *Fortran 90* code that solve the SIRD's governing equations from auxiliary conditions.

2.4 Parameters' Optimization

The parameters' optimization in the SIRD (2.1) is done as in [18, 19], that is, solving a nonlinear least square problem. We define the vector function $\mathsf{u}(t) = (S(t), I(t), R(t), D(t))$, the vectors of parameters $\mathsf{q} = (\beta, \gamma_R, \gamma_D)$ and the known data y at times $t_1, \ldots t_n$. Given a function $F(\mathsf{u}, \mathsf{q})$, we estimate the parameters q by solving the following nonlinear least square problem

$$\begin{cases} \underset{\mathsf{q}}{min} \dfrac{1}{2} ||F(\mathsf{u}, \mathsf{q}) - \mathsf{y}||_2^2 \\ \mathsf{q} \geq 0 \end{cases} . \tag{2.15}$$

3 DISCUSSION AND CONCLUDING REMARKS

In this section we introduce our analyse of the COVID-19 and simulations as well. The reader will see here that the country's richness, its continental dimension or native social interaction are not avoid the Sars-CoV-2 infection. By other hand, it is good to explain we used normalized measures, that allow us to compare the disease spread at the countries. We setting N population values like 328.200.000, 211.000.000, 49.650.000 to The United States (USA), Brazil (BRA) and Colombia (COL), respectively. Thus the SIRD's model variables kept at the $[0,1]$ window. Also, the times counting begins in $t = 0$ which corresponds to 2020-01-20 (USA), 2020-02-26 (BRA) and 2020-03-06 (COL). We remember that our simulations were done with data taken every 14 days to each country. That it led to label the simulations like $S_1, \ldots, S_6$.

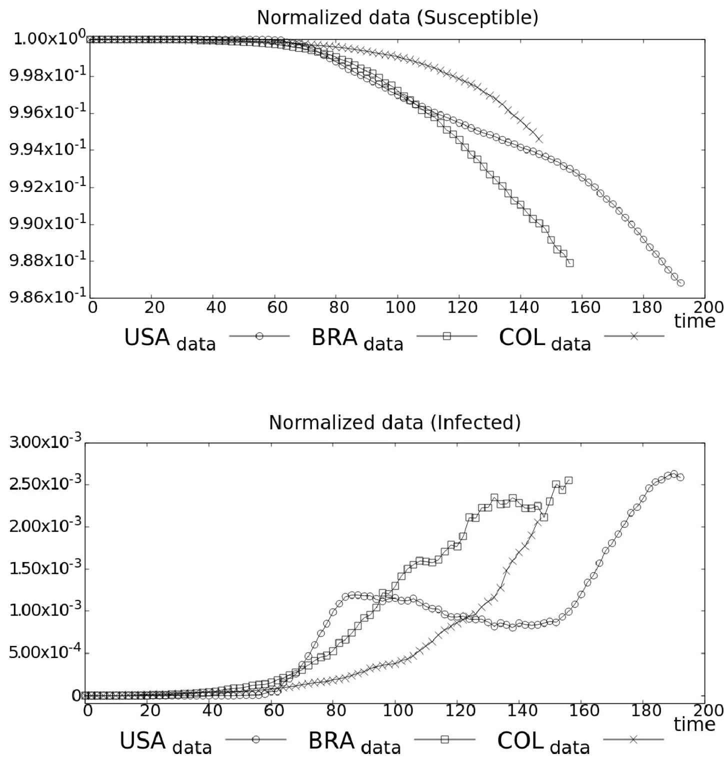

Figure 3: Susceptible (top), and infected (bottom) normalized data

The Figures (3)-(4) show the data for susceptible, infected, recovered and dead in the time. We preferred to display them this shape to see the COVID-19 rises at the countries. For latin countries, the infected number came going up, but it looks like the Brazil already reached the peak. The american population is living a second wave and walks to second peak, probably. Additionally, the recover and dead people increase. But with a recover number much higher than the death.

The Figure (5) shows the susceptible decrease dynamic of The United States, and our simulations. We started simulations at the date 2020-05-04. From Figure (6) it is possible to see a changing of the disease's drop behavior near of $t = 139$ (date 2020-06-07) by our simulations. Here, in the neighborhood of the date, it seems that there is an inflection point. This is more evident, if we

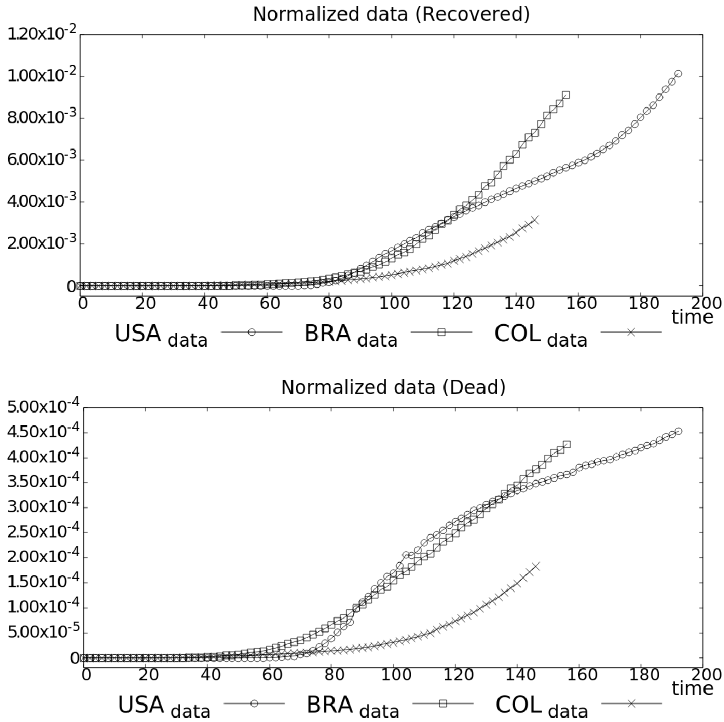

Figure 4: Recovered (top), and dead (bottom) normalized data

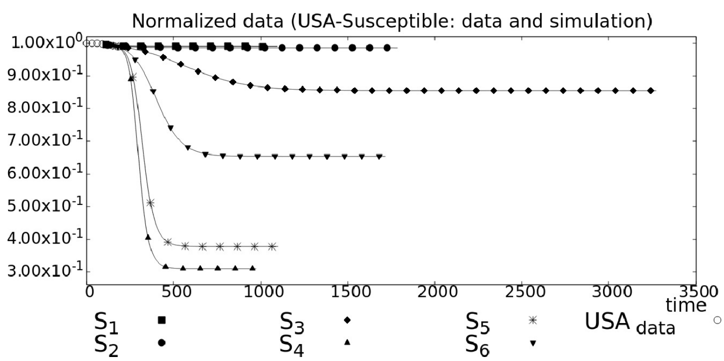

Figure 5: USA-Susceptible reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and simulations $S_1, \ldots, S_6$.

look at the Figures (7-8) as well. We emphasize that the date 2020-06-07 corresponds to a 14 days after the George Floyd's assassinate (2020-05-25) at the Minneapolis-US. Maybe, the inflection point could be correlated to not social distancing of the USA people manifestation about the assassinate. Which could to evidence the start of the second wave of Sars-CoV-2 infection.

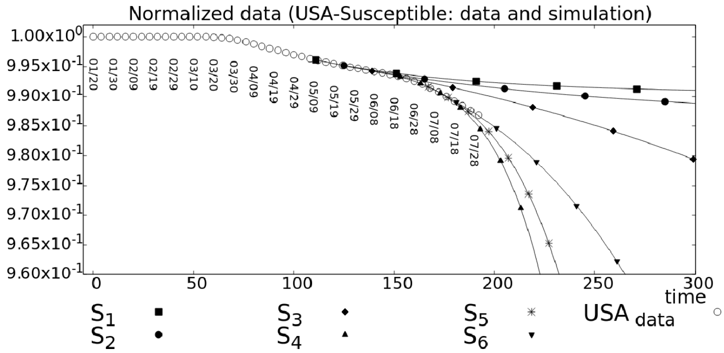

Figure 6: The zoom of the Figure (5).

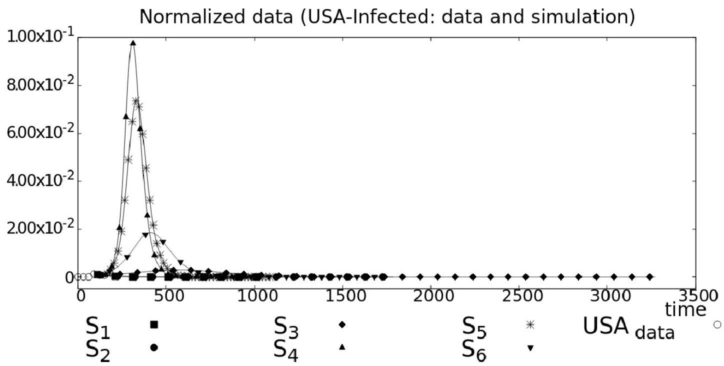

Figure 7: USA-Infected reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and simulations $S_1, \ldots, S_6$.

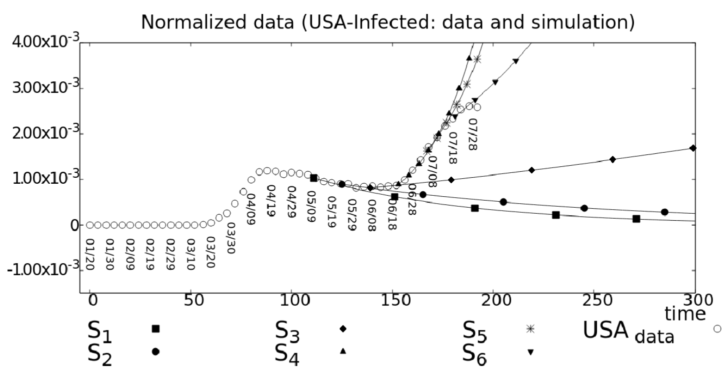

Figure 8: The zoom of the Figure (7).

The Figure (8) shows the inverse tendency over infected people. The COVID-19 changes from deceleration to acceleration status. For we this is a characteristic of a new infection wave. The

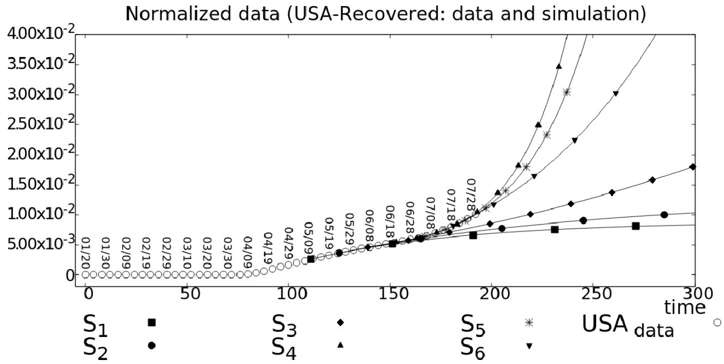

Figure 9: USA-Recovered reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and our simulations $S_1, \ldots, S_6$.

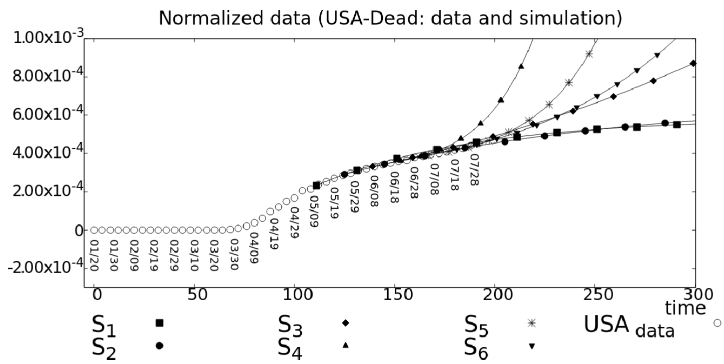

Figure 10: USA-Dead reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and our simulations $S_1, \ldots, S_6$.

simulations predicts a new peak arising at the country, which can be seen at the Figure (7) by means of S_4, S_5, S_6. However, it is seen that the peak is being attenuating at the country.

Beyond of that, The United States have indicated a value climb at the recover and death's compartments. But, we emphasized the recovered number's magnitude is higher than the death number, see the Figures (9) and (10). Particularly, by our last simulations, it can be seen a damping of the accumulated numbers as well.

For Brazil, the Figure (11) shows the susceptibles' decelerating dynamic, and our simulations too. The our simulations started in the date 2020-05-12 because the COVID-19 cases became more manifest. Different of The United States, by means of our predictions, Brazil and Colombia do not live a second infection wave so far. Colombia, whose simulations started in the date 2020-05-14, presents the same pattern of Brazil's susceptible, see the Figure (13). However, the Colombia's Covid-19 disease is more accelerated than Brazil, it's further evident in the last days, see the Figure (12) and Figure (14).

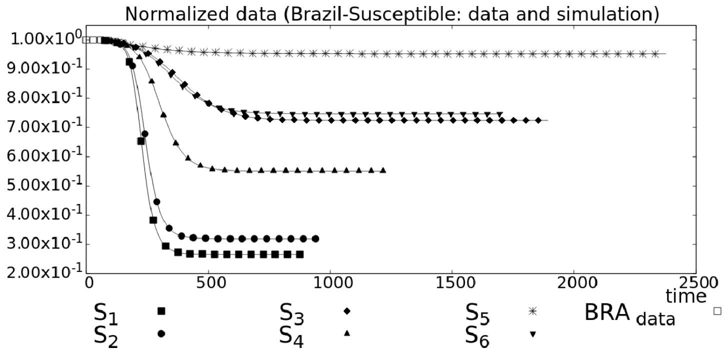

Figure 11: Brazil-Susceptible reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and simulations $S_1, \ldots, S_6$.

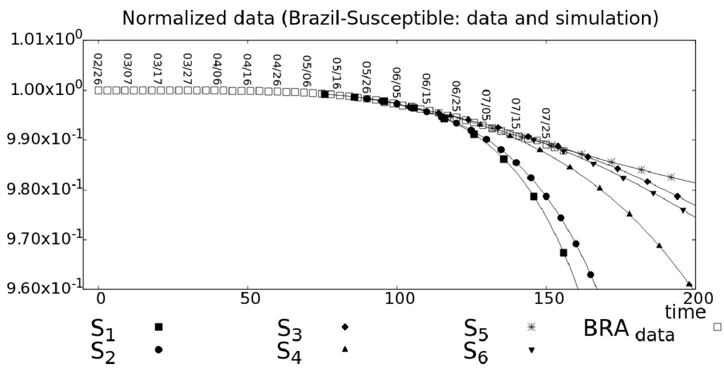

Figure 12: The zoom of the Figure (11).

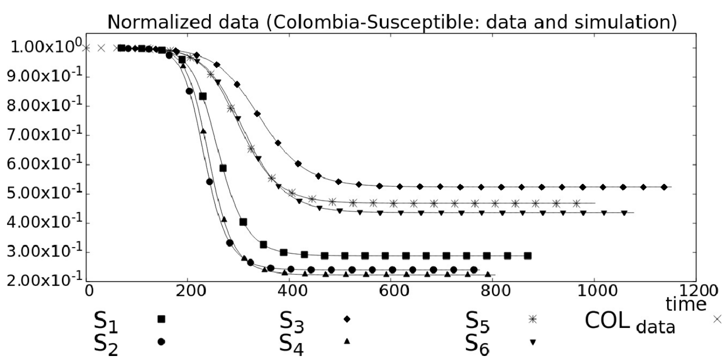

Figure 13: Colombia-Susceptible reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and simulations $S_1, \ldots, S_6$.

Colombia do not rich the disease peak, yet. This can be seen through of the Figure (16). The COVID-19's spread come increasing and its peak is still far away.

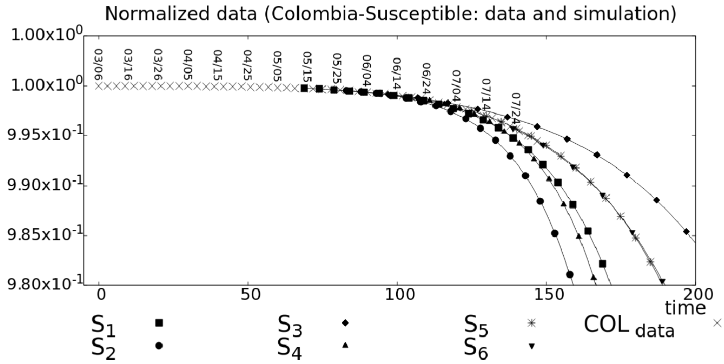

Figure 14: The zoom of the Figure (13).

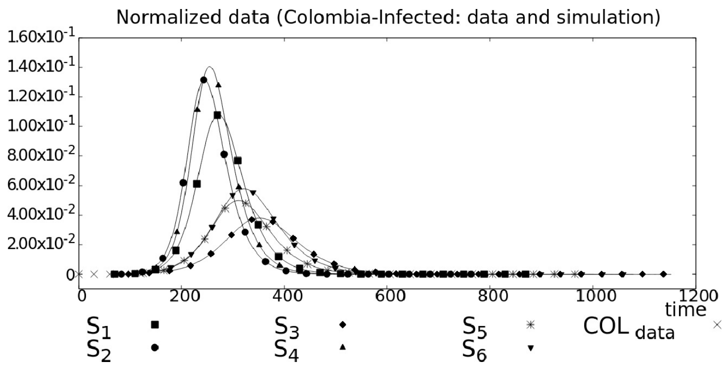

Figure 15: Colombia-Infected reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and simulations $S_1,\dots,S_6$.

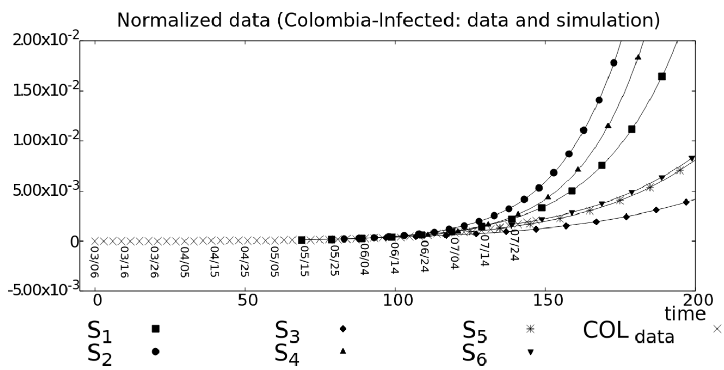

Figure 16: The zoom of the Figure (15).

Nevertheless, to Brazil it is possible to infer the disease peak and plateau happen between August and September in the present year, see the Figure (18). We assume it because at the months May and June the COVID-19 became decelerating.

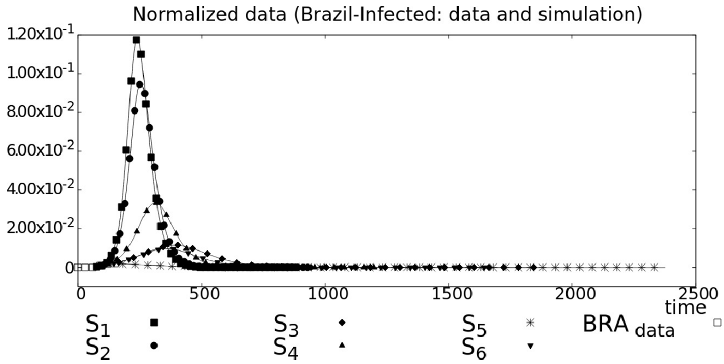

Figure 17: Brazil-Infected reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and simulations $S_1, \ldots, S_6$.

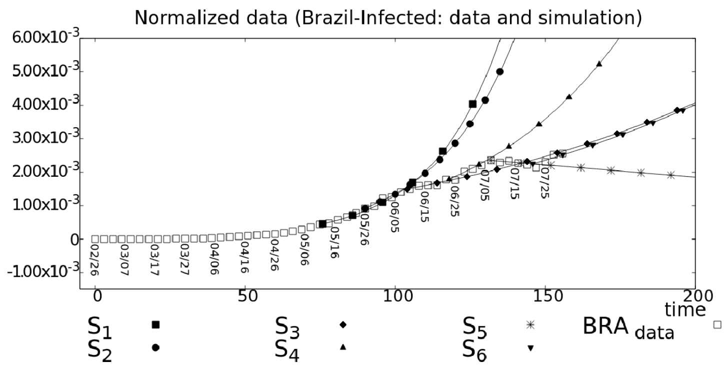

Figure 18: The zoom of the Figure (17).

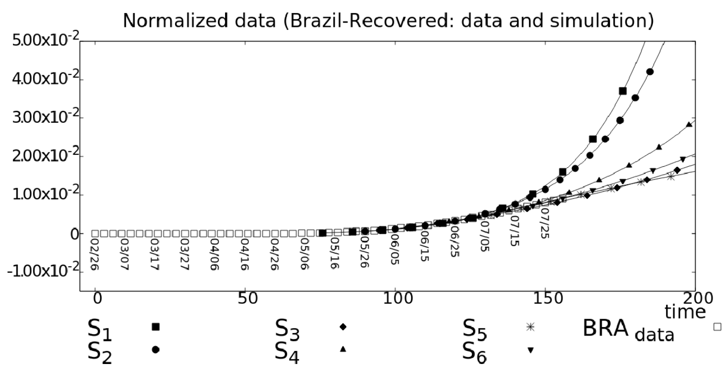

Figure 19: Brazil-Recovered reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and our simulations $S_1, \ldots, S_6$.

Analogous to The United States, the recovered and death Brazilians numbers have increased at the values, Figures (19)-(20) but with different magnitudes between them as well. This pattern happens to Colombia as well, see the Figures (21)-(22).

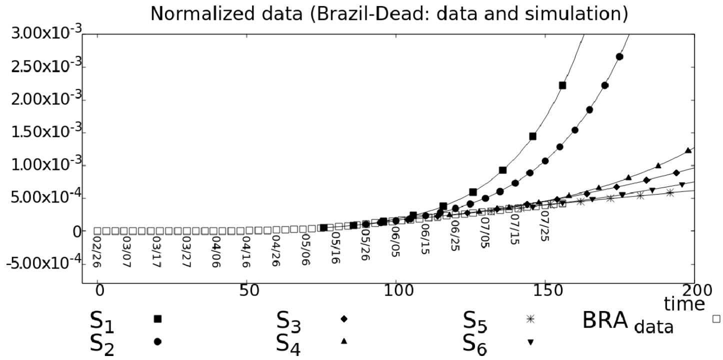

Figure 20: Brazil-Dead reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and our simulations $S_1, \dots, S_6$.

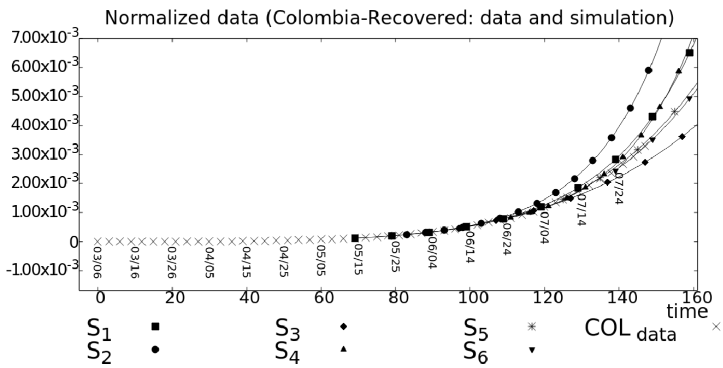

Figure 21: Colombia-Recovered reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and our simulations $S_1, \dots, S_6$.

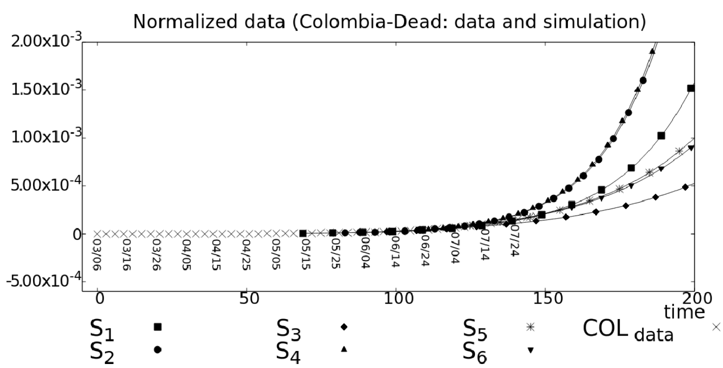

Figure 22: Colombia-Dead reconstructed data from WHO Coronavirus Disease (COVID-19) Dashboard [25] and our simulations $S_1, \dots, S_6$.

Table 1: R_0 data table on July.

country	date	β	γ_R	γ_D	R_0
USA	07/05	0.09131	0.05733	0.00089	1.56
	07/12	0.08919	0.06327	0.00094	1.38
	07/19	0.08036	0.06456	0.00100	1.22
Brazil	07/07	0.07805	0.07836	0.00215	0.96
	07/14	0.07242	0.07928	0.00226	0.88
	07/21	0.09547	0.08086	0.00227	1.14
Colombia	07/02	0.08825	0.06218	0.06218	0.70
	07/09	0.09908	0.06589	0.06589	0.75
	07/16	0.10950	0.05251	0.05251	1.04
	07/23	0.08730	0.05634	0.05634	0.77

We calculated the basic reproduction number R_0 for the last simulations on July. The Table (1) presents the values calculated by means of the model (2.15). Particularly, we split the data sets consolidated of the 14 days to see a better accuracy about disease's spreading. The United States is fighting with disease, its R_0 comes decreasing. The Brazil's R_0 came dropping but it changed. If it persists, it's possible increasing infection again. The Colombia's R_0 is oscillating and all care are necessary at the currenty time.

Finally, we emphasize that the COVID-19's dynamic of the Brazil and Colombia are the same, but as delay. Of course the next days are crucials, the countries cannot relax your fight actions against COVID-19. The our simulations predict that there are some control over COVID-19 disease in theses countries, yet. Clearly, we do not know the specific proceedings which provide it. But if they relax, the countries could have a second wave infection similar to the one the United States is currently experiencing. These patterns evidencing that the economic development, the continental dimension and the native social interaction does not retard the COVID-19 spreading.

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