Modelling the Covid-19 Disease in Colombia to define the likeliness of health system saturation - Feedback Systems

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***Abstract*—This project makes a Covid-19 model based on the SCIR epidemic model and uses differential equations to define the interaction between the states and basic data analysis to determine the parameters of this model base on the data gathered by esri Colombia. From this, the stability, observability, and controllability of the model is found prior to making a simulation to determine when the health care ICU capacity will be fulled.**

I. Introduction

Given the world pandemic humanity is going through and comparing the situation other countries are facing right now. It´s pertinent to be able to predict how the disease of the virus SARS-CoV-2 will spread in Colombia and determine whether the health system is prepared to face it or if there´s going to be a point where the health system will be saturated given the amount of patients requiring ICUs.

II. Modelling

In order to define if such a moment will be reached, a model can be made that simulates the behavior of the disease, considering how it spreads and how it affects the population in terms of severity.

To start, a model can be based on the SIR epidemic model [1][2]. It defines the population as being members of one of three sets: Susceptible, Infected, and Removed; it also, stipulates that a certain individual can change from a certain set to another according to a parameter. For example, someone can get infected according to a β chance of getting the virus. This model can be observed on figure 1.

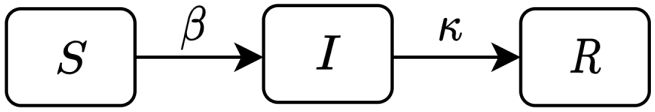

Fig. 1. Diagram of the SIR Epidemic model.

There are a couple things to consider regarding this model. For starters, this model doesn't fully show the severity of an individual in the infected set, and even worse it doesn't consider the asymptomatic case. Thus, a model more descriptive of the behavior for this virus is needed like the SCIR model [3]. Such expansion requires first to consider an intermediate set called Carriers, which contains all the individuals that are infected but present no symptoms and as such are more prone to infect susceptible individuals. Additionally, the set of infected needs to be broken into three severity set: Low, Moderate, and High-risk individuals. With this change, we can define low risk patients as those that are able to stay quarantined at home, presenting no risk to themselves and avoiding further infections, moderate risk patients as those that need medical care and due to that require quarantine in a hospital, and lastly the high risk represents those with complications on the level that loss of life is likely and as such need an ICU. With this model we can identify the health system capacity needed at any point in time while considering the infectious nature of asymptomatic cases and the time need for a patient to develop symptoms. The resulting model is the observed in the figure 2.

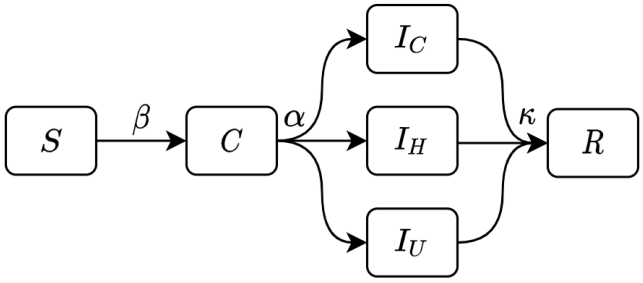

Fig. 2. Diagram of the SCIR Epidemic model considering severity of the infected cases.

Before proceeding it´s important to identify the flaws of this approach and particularly the model, be aware of it´s real capability and representation. Firstly, the model considers an evenly distributed population, this means that no matter the distance between any pair of individuals anyone has the same chance of getting infected considering the amount of carriers present. Secondly, it considers an scenario in which there are no deaths, births or any type of migration during the period of analysis. Thirdly, it doesn't take into account time; this one is particularly important because the virus also doesn't care about the time from the patient zero. Fourthly and regarding to the subject just discussed, since only the current amounts

in the sets are whats important to simulation of the model, this doesn't represent reality at all; given that a population with one infected person will act completely different to one that has half its population infected. Also, this models doesn't consider the case in which someone that recovered gets infected again; although there are cases in which someone got infected again or people that recovered getting tested positive, there isn't enough research on the subject and as such won't be considered. Lastly, this model considers only this disease affecting the population. All the cases described can be taken into account into a more complex model, but it's left for a further stage of this project.

A. Dynamics

With the concept of the model clear, the interactions between sets can now be defined. For starters, restrictive conditions need to be defined in order for this model to stay real (not having a negative amount of population for example). First we define the infected set as the sum of all the subsets of infected, where: I_C is the amount of low risk infected patients, I_H is the amount of moderate risk infected patients, and I_S is the amount of high risk infected patients; having now something closer to the SCIR model, we can define the sum of all the sets: S representing the amount of susceptible individuals, C representing the amount of carrier individuals, I representing the amount of infected individuals, and representing the amount of removed individuals which includes everyone who either dies or recovers from the disease. This set must always be equal to the population N, in this scenario Colombia's population at $49'648.685$ according to the last estimate of the world bank [4].

$$I = I_C + I_H + I_U \tag{1}$$

$$N = S + C + I + R \tag{2}$$

Now the sets are redefined as a proportion of the total population that belongs to any given set and from this the differential equations that define the interactions can be defined.

$$s = S/N \quad (3) \qquad c = C/N \quad (4) \qquad i_c = I_C/N \quad (5)$$

$$i_h = I_H/N \quad (6) \qquad i_u = I_U/N \quad (7) \qquad r = R/N \quad (8)$$

Each differential equation is define from the parameters at the figure 2, with the addition of a parameter γ that represents the distribution between low, moderate, and high risk, for the transition between the carriers and infected and the transition between the carriers and the removed.

$$\frac{ds}{dt} = -\beta cs \tag{9}$$

$$\frac{dc}{dt} = \beta cs - \alpha c \tag{10}$$

$$\frac{di_c}{dt} = \gamma_1(\alpha c - \kappa i_c) \tag{11}$$

$$\frac{di_h}{dt} = \gamma_2(\alpha c - \kappa i_h) \tag{12}$$

$$\frac{di_u}{dt} = \gamma_3(\alpha c - \kappa i_u) \tag{13}$$

$$\frac{dr}{dt} = \kappa(\gamma_1 i_c + \gamma_2 i_h + \gamma_3 i_u) \tag{14}$$

B. Parameters

With the differential equations defined, it is needed to define each parameter. In a real scenario this parameters change from time to time and depend on many variables, for this project each one needs to be defined as a constant and extracted from real data in order to have a closer representation of reality. We define each parameters as:

- β: Transmission rate.
- α: Infection rate of carriers. This means the rate at which individuals that were infected but hadn't developed symptoms or weren't diagnosed, start developing symptoms or test positive and enter quarantine as a result.
- γ_1: Proportion of low risk infected, can stay at home.
- γ_2: Proportion of medium risk infected, need hospital care.
- γ_3: Proportion of high risk infected, need ICU.
- κ: Removing rate.

Also since gamma is a distribution, it needs to hold that:

$$\gamma_1 + \gamma_2 + \gamma_3 = 1 \tag{15}$$

Now to find the value each parameter is found using Euler's method [5], where each time interval is considered as one day, taking into account that it is how often the database has been updated. Therefore, each parameter is defined as a value depending on a relation between a day n and the next day $n+1$.

$$\beta = \frac{1}{c_n} - \frac{s_{n+1}}{s_n c_n} \tag{16}$$

$$\alpha = \beta s_n - \frac{c_{n+1}}{c_n} + 1 \tag{17}$$

$$\kappa = \frac{r_{n+1} - r_n}{\gamma_1 i_{c_n} + \gamma_2 i_{h_n} + \gamma_3 i_{u_n}} \tag{18}$$

The gammas can be extracted directly from the data by finding the distribution of new daily infected between the levels of severity.

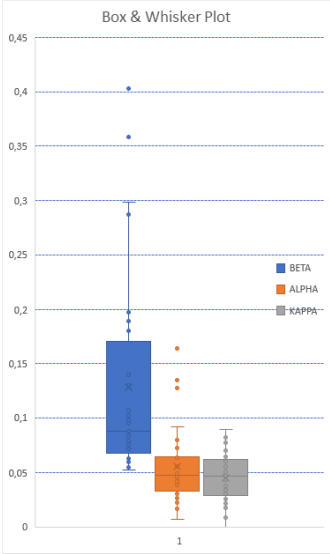

Fig. 3. Box and Whiskers plot of the parameters β, α, and κ.

C. Data

The data used to define the parameters was extracted from the database of esri Colombia [6], an entity in charge of keeping track of every single case of Covid-19, and that means all of those that have been tested and identified whether they presented symptoms previously or not. This data was processed to extract from it the data relevant to this model [7].

There are some considerations to be taken into account here regarding how the data was handled. First, all asymptomatic cases are considered to have started 14 days prior to the diagnosis, this in order to consider those individuals as carriers as early as WHO considers it able currently [8], but it's important to consider that this cases could have been infected in more o less days than considered. Second, esri changes the state of deceased cases and leaves no trace of the severity of the patients the days before; although it can be assumed that a patient that dies was in a high risk situation, there can also be a case which presented soft symptoms and had quick complications, this cases didn't occupy an ICU during their time infected. Finally, to calculate the parameters the first 14 days and the most recent 14 days were ignored; this is because the data at the start is not consistent with the parameters since it considers people as discrete values it means that from one day to another if only one gets infected it can count as a double increase per day of the infection given that we don't have that many cases, and we ignore the most recent days since there may be some unidentified asymptomatic cases that could affect the data.

Now each parameter was calculated by each time intervals using the equations 16, 17, and 18. From this ones a time graph plotting how the parameters change overtime and a distribution of these can be made and can be seen in figures 3 and 4.

There are some important aspects to consider here given that this parameters will be what influences the most the model. Beta changes wildly over time and can be influenced by how people react to the spread of the disease (ex. washing

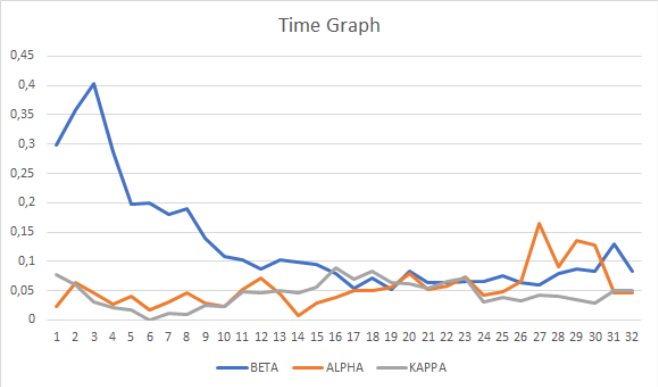

Fig. 4. Graph for the parameters β, α, and κ over time units.

hands, social distancing, face masks, etc.), therefore beta can represent the interactions that lead to transmission and hence can be used as the input of the system. Alpha is supposed to represent how fast someone goes from getting infected to having symptoms of being diagnosed, but from the data it only represents how fast someone can get diagnosed and as such is heavily influenced by the ability of the labs to process samples and can be affected by a machine breaking or lack of personnel. Kappa is simpler, since a person once diagnosed it is easily know if they have recovered or have died and consequently is the one that shows the least amount of variance. For this parameter we consider it's median as a base constant to simulate the system, in order to avoid extremes. Having as a result:

- $\beta = 0.0878610407$
- $\alpha = 0.0474115920$
- $\kappa = 0.0467383215$

For the gammas a different approach was made. All the days were considered starting from the first diagnosis, and a distributions between new diagnoses and their severity was calculated for each day. Over the distributions obtained, a mean was calculated and a portion of the variance was considered in order satisfy the equation 15. The result was the values for each gamma as:

- $\gamma_1 = 0.9238$
- $\gamma_2 = 0.0509$
- $\gamma_3 = 0.0253$

D. Health Capacity

There are many ways to consider health care capacity. For this project the following will be considered: the capacity is completely available at the start of the simulation, there are no other disease or cases that requires of such capacity, top ICU will be define as a capacity since lower risk levels have alternatives in treatment while ICU is critical and requires a lot of medical personnel and complex and costly equipment. Given the date that this project is being made, the Colombia's Health Ministry has already done something to increase the amount of ICU available in four phases [9]. From this report and with the considerations taken we have four scenarios of ICU available:

- Phase One: 5.300 Units
- Phase Two: 7.800 Units
- Phase Three: 10.300 Units
- Phase Four: 12.476 Units

While constructing and adapting to standard this amount of ICUs takes time, for this project only the when, if it does happen, such capacity would be reached by the high-risk patients.

E. Feedback Systems

Taking into account the equations 9 and 10, we can represent the same diagram from figure 2 as a feedback system. For this we now don't define each element as a set but as a given value that gets affected by each time unit. In this case we model susceptible, carrier, and high-risk infected since those are the ones that have a feedback loop and are relevant to the question aimed to answer. In this scenario we consider S, C, and I_U as states of the system with the same dynamics from the equation stated with output the amount of people currently in need of an ICU.

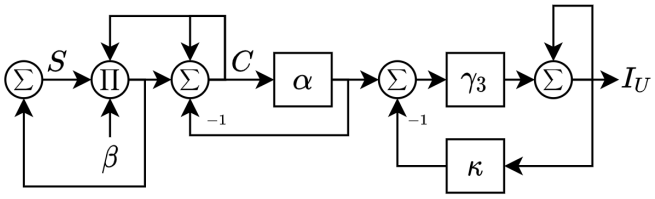

Fig. 5. Diagram of the SCIR Epidemic model considering severity of the infected cases set as a feedback system.

Our inputs can consist of all the rates of change, but since it was defined that κ has an approximate constant behaviour and from the data and γ_3 is just a distribution and therefore is mostly set and won't be affected by external factors; mainly due to the severity of the illness depending solely on an individuals health. Therefore, we assume β and α as possible inputs, mostly due to these being rates that are greatly affected by a population's behaviour.

Although α can also be modelled as an input, in this stage of the project only β will be considered due to it's quite direct impact. Still, α is an extremely important rate, as it was stated before α is supposed to represent the rate of symptoms or diagnosis, but clearly it's dependent on the ability of the system to identify and diagnose such individuals fast. In a perfect system such rate would be high enough that no carriers would be allowed to infect others and in a terrible system no one would be identified and a lot of people would die without the system realizing there was ever a virus. Thus α is an extremely important variable to study and further analyze in later stages of this project.

1) Stability: Taking into consideration the equations that represent the dynamics of the system, it can be simplified to the following cases:

1) $0 = -\beta cs \rightarrow c = 0 \vee s = 0$
2) $0 = (\beta s - \alpha)c \rightarrow c = 0 \vee s = \frac{\alpha}{\beta}$
3) $c = \frac{\kappa i_c}{\alpha}$
4) $c = \frac{\kappa i_h}{\alpha}$
5) $c = \frac{\kappa i_u}{\alpha}$
6) $0 = \gamma_1 i_c + \gamma_1 i_h + \gamma_1 i_u \rightarrow i_c = 0 \wedge i_h = 0 \wedge i_u = 0$

Given case 6 and from cases 3, 4, and 5 it can be concluded that $c = 0$. Therefore, s and r can be any number as long as they satisfy equation 2, hence there are N stability points.

2) Observability: Given that the model is not linear, first it must be linearized near an equilibrium point. Getting further ahead to the results, the simulation gives a minimum value of $12'210.705$ for the susceptibility which means $37'437.980$ in the removed set according to the equation 2 and for it to be one of the equilibrium points defined in section II-E1. Now to get the matrix A in order to determine stability, the dynamics are partially derived and evaluated around the equilibrium point defined.

$$Eq = \begin{bmatrix} \frac{2442141}{9929737} \\ 0 \\ 0 \\ 0 \\ 0 \\ \frac{7487596}{9929737} \end{bmatrix} \tag{19}$$

$$\frac{\partial \dot{s}}{\partial s} = -\beta c \quad (20) \qquad \frac{\partial \dot{s}}{\partial c} = -\beta s \quad (21)$$

$$\frac{\partial \dot{c}}{\partial s} = \beta c \quad (22) \qquad \frac{\partial \dot{c}}{\partial c} = \beta s - \alpha \quad (23)$$

$$\frac{\partial \dot{i_c}}{\partial c} = \gamma_1 \alpha \quad (24) \qquad \frac{\partial \dot{i_c}}{\partial i_c} = -\kappa\gamma_1 \quad (25)$$

$$\frac{\partial \dot{i_h}}{\partial c} = \gamma_2 \alpha \quad (26) \qquad \frac{\partial \dot{i_h}}{\partial i_h} = -\kappa\gamma_2 \quad (27)$$

$$\frac{\partial \dot{i_u}}{\partial c} = \gamma_3 \alpha \quad (28) \qquad \frac{\partial \dot{i_u}}{\partial i_u} = -\kappa\gamma_3 \quad (29)$$

$$\frac{\partial \dot{r}}{\partial i_c} = \kappa\gamma_1 \quad (30) \qquad \frac{\partial \dot{r}}{\partial i_h} = \kappa\gamma_2 \quad (31) \qquad \frac{\partial \dot{r}}{\partial i_u} = \kappa\gamma_3 \quad (32)$$

With these equations and the equilibrium point, we define the matrix A, considering the first element of the equilibrium point as s_e

$$A = \begin{bmatrix} 0 & -\beta s_e & 0 & 0 & 0 & 0 \\ 0 & \beta s_e - \alpha & 0 & 0 & 0 & 0 \\ 0 & \gamma_1 \alpha & -\kappa\gamma_1 & 0 & 0 & 0 \\ 0 & 0 & \gamma_2 \alpha & -\kappa\gamma_2 & 0 & 0 \\ 0 & 0 & 0 & \gamma_3 \alpha & -\kappa\gamma_3 & 0 \end{bmatrix} \tag{33}$$

Additionally, considering the output must answer the problem, then the system should consider the infected patients with high-risk as an output, and as such the matrix C is defined.

$$C = \begin{bmatrix} 0 & 0 & 0 & 0 & 1 & 0 \end{bmatrix} \tag{34}$$

Withe the matrices defined, the observability can be define. For ease, it is calculated using the next script in Python.

```
Wo = obsv(A, C)
print("Wo = ", Wo)
print("Det(Wo) = ", np.linalg.det(Wo))
```

The result of this operation states that the determinant for the observability matrix is equal to zero, therefore this system is not observable. This makes sense given that part of the system is completely unreachable to the data. Even if the output considered all the infected and removed individuals, those that can be accounted for, the susceptible and carriers can not be identified by any means from this data, mainly because from the data an individual can only be identified as a carrier after they've been diagnosed an thus they are no longer carriers; besides the susceptible depends on the amount of carriers, so the problem persists. it can be easily concluded that the system in fact is not observable.

3) Controllability: For controlability, the same matrix A is used with the vector B that defines which states are affected by the input, considering as our input the transmission rate β. A similar snippet of code is as in observability used to determine whether the system is controllable.

$$B = \begin{bmatrix} -1 \\ 1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \tag{35}$$

```
Wc = ctrb(A, B)
print("Wc = ", Wc)
print("Det(Wc) = ", np.linalg.det(Wc))
```

This code results in the determinant for the controllabilirty matrix to be equal to $5.31 * 10^{-44}$ and more important than the specific number it states that the system is in fact controllable. This result makes sense in the terms that in fact controlling only the transmission rate, the system can reach stability and this is done by two ways: either all the population gets infected and eventually everyone has recovered or died, or the disease is quickly controlled by controlling the transmission rate of the virus by social distancing, quarantine, and other recommended measures and making the amount of carriers increase slower, as close to a zero rate as possible, than the time it takes them to get infected.

This two scenarios both eventually reach stability but under quite different removed scenarios. Therefore it would be interesting in another stage of the project to have a more detailed model that determines the difference in removed by splitting it between recovered and dead, this way a controller can be made which tries to control the transmission rate given the amount of diagnosed or dead and from this make simulations of different approaches to actually handling the disease.

III. Implementation

With the model, it's states, dynamics, and parameters defined, the next process is to program the simulation. Python is used to achieve this with the NumPy library for the mathematical operations and matplotlib for the plots. The code is straight forward in which it simply defines the model as a function dependent on the current state and the iterates for an interval of time and saves the values of each state for each iteration.

```
import numpy as np
import matplotlib.pyplot as plt

# Colombia's Population
N = 49648685

# Parameter Definition
b = 0.0878610407
a = 0.0474115920
g1 = 0.9238
g2 = 0.0509
g3 = 0.0253
k = 0.0467383215

# States definition by wholes
# and by proportion
S = N - 2; C = 2; IC = 0
IH = 0; IU = 0; R = 0

s = S/N; c = C/N; ic = IC/N
ih = IH/N; iu = IU/N; r = R/N

# Definition of the model
def covid_19(x):
    return -b*x[0]*x[1],                \
            b*x[0]*x[1]-a*x[1],         \
            g1*(a*x[1]-k*x[2]),         \
            g2*(a*x[1]-k*x[3]),         \
            g3*(a*x[1]-k*x[4]),         \
            k*(g1*x[2]+g2*x[3]+g3*x[4])

# Time Units definition
T = 1000
t = np.linspace(0, T, T + 1)

# Variable initialization for simulation
X = np.zeros((T + 1, 6))
X[0, :] = [s, c, ic, ih, iu, r]

for i in range(T):
    dX = covid_19(X[i,:])
    X[i + 1,:] = X[i] + dX
```

From this we can graph the model during T time units. It's important to acknowledge that the time units considered during the simulation because the real world data works more closely to difference equations because people gradually get infected but always the amount of infected is an integer, but in this scenario the simulation runs by time unit and a portion of

the population gets infected. This means that it would appear as if an individual is a fraction infected and as such may be in the susceptible and carrier sets at the same time. To correct this the simulation runs more iterations for a single day and is later adjusted in the plot.

IV. Results

From the simulation it is obtained the figure 6 in which it can be observed how the population changes from set to set as time moves and that it reaches: a minimum of $12'210.705$ people that didn't get infected, maximum of $6'393.558$ carriers, maximum of $5'872.019$ low-risk infected, maximum of $1'422.209$ moderate-risk infected, maximum of 796.145 high-risk infected, and $36'458.013$ being the amount of people that recovered or died by the end of the simulation. Given how the system is only stable when all the sets except susceptible and removed contain zero individuals, with more iterations and simulation over a longer period of time it may give a higher number of removed and lower of susceptible, but it's clear that the curve is softening by the time the simulation ends, so it isn't needed.

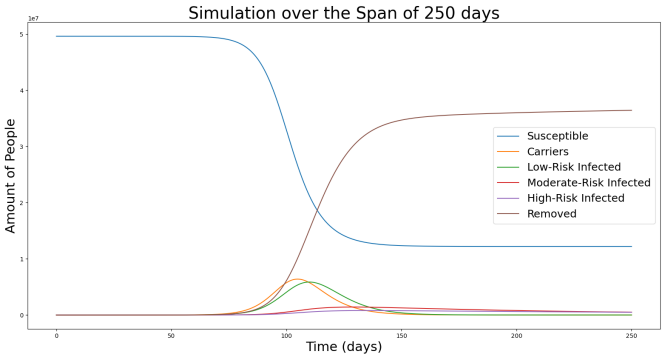

Fig. 6. Plot of the simulation for the model for Covid - 19 defined.

In order to answer what was asked, the high-risk patients can be plotted alongside horizontal lines marking the four caps of the ICU available and can be observed in figure 7. The plot needs to be set with the Y - Axis logarithmic because otherwise the horizontal lines are not discernible. From the resulting simulation it can be obtained the exact time unit for the simulation where such caps are reached. This caps are reached:

- Phase 1: Day 72.25 of the simulation
- Phase 2: Day 74.75 of the simulation
- Phase 3: Day 76.5 of the simulation
- Phase 4: Day 77.75 of the simulation

Which taken into account an starting point of February 27, the same day the data starts, those dates would be:

- Phase 1: May 9, 2020 at 06:00
- Phase 2: May 11, 2020 at 18:00
- Phase 3: May 13, 2020 at 12:00
- Phase 4: May 14, 2020 at 18:00

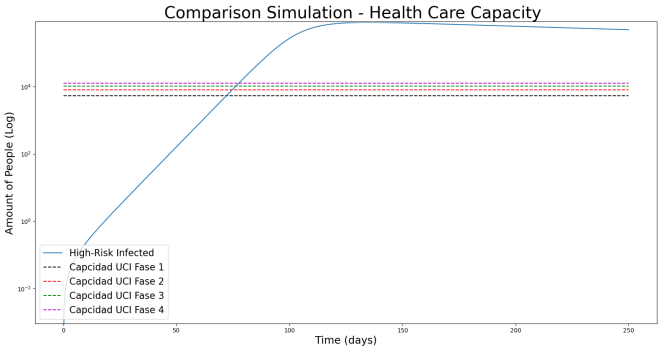

Fig. 7. Plot of the simulation for the model for Covid - 19 of high-risk patients with the four health care caps.

Lastly, the model can be compared to the real data by plotting only the time corresponding to real data. This can be seen in the figure 8, and evidently they are not that similar. Although the numbers "fit" a little, they are quite different. This is due to multiple aspects like: the real β and α being functions over time instead of constants, the model representing a non changing population behaviour while in the real data aspects like the quarantine are evident, and the simulation taking into account all the population while the real data only those who have been identified.

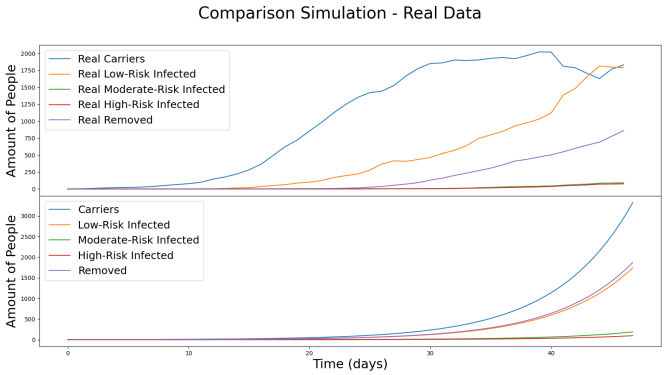

Fig. 8. Plot of the simulation for the model for Covid - 19 comparing it with the real data.

V. Conclusions & Observations

Even though the model and according simulation partially satisfactory, the discrepancies between the model and the real data only show how much more work it needs before it being able to fully represent such complex contexts and systems like an epidemic in a country. There were many obstacles in this process, from processing correctly all the data to defining accurately a model that was detailed enough to answer the question but not too complex that it wouldn't be able to be defined from the data available; on such note it's important to also emphasise on the idea of different approaches when it comes to processing the data, because it can show the "hidden" parameters that can better represent any given model. Consequently, there are some proposals to further develop this project in order to have a more accurate model that can also make broader predictions, not only regarding the health care system ICU capacity, and even give the ability to experiment

with scenarios and see how it affects the situation short, medium, and long term.

- For starters, β and α need to be better defined. In order to do this there are two approaches: define these parameters as an specific function and calculate it's future values during the simulation or make an ML model that can predict parameters with the data at each moment. The difference between the approaches consists on how much should time be involved; defining a function consists on postulating a time-dependent function that makes an accurate relation between time units and parameters values; on the other hand, an ML model can ignore the time, because it is really unimportant for the behaviour, and considers only the data at any time and predicts the parameters based on the states of the system at that time, not the time per se.
- Besides defining accurately the parameters, α can be adapted to have a variable ξ that accurately represents the rate of symptoms and in such scenario α could be modified to alter the delay of the system in response to the outbreak and get closer to the value of ξ. With this, there is a parameter α truly defines the time needed for someone to develop symptoms and a parameter ξ that represents the current capability of diagnosing those with symptoms and those without. The difficulty trying to implement this would lie on the data, since there is only data for what has been identified.
- Some tuning can be made to the parameters that haven't been mentioned, by the time this stage of the project has been delivered there will be more data available thus better estimations can be made.
- Make a distinction on the removed set between the ones who have dies and the ones who have recovered. That way more and better conclusions can be made, as well as being able to try situations.
- Making the parameters more dependent on the system's current state. For example, people can react if a sudden increase in infected appears and take more precautions affecting this way the transmission parameter. This in order to be able to have more dynamic simulations in which there can be events involved like a sudden introduction of a vaccine, a concert, etc.
- Expanding the interactions between sets and each set with itself, for example taking into account low-risk infected individuals that have been diagnosed but feel "good enough" and the go out and infect people or the death to recovered ratio increasing once the ICU capacity has been capped, if there aren't any emergency beds available people that need care won't have.
- Defining a controller which directly affects how the population is "reacting" to the state of the virus. This in order to simulate different scenarios and approaches to handling the virus and being able to analyze the distribution of the population at the end of the simulation

Those are some ideas that could greatly improve this model and it's ability to predict how the current situation will develop.

REFERENCES

[1] Mathematical Association of America. "The SIR Model for Spread of Disease - The Differential Equation Model." MAA.org. https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model (retrieved Apr. 19, 2020)

[2] M. J. Keeling, L. Danon, Mathematical modelling of infectious diseases, British Medical Bulletin, Volume 92, Issue 1, December 2009, Pages 33–42, https://doi.org/10.1093/bmb/ldp038

[3] K. Veeren, "An SCIR Model of Meningococcal Meningitis," M.S thesis, Dept. Mathematics, Virginia Commonwealth Univ., Richmond, VA, USA, 2008.

[4] *Population, total - Colombia*, The World Bank, 2018. [Online]. Available: https://data.worldbank.org/indicator/SP.POP.TOTL?locations=CO

[5] Mathematical Association of America. "The SIR Model for Spread of Disease - Euler's Method for Systems." MAA.org. https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-eulers-method-for-systems (retrieved Apr. 19, 2020)

[6] *Casos positivos de COVID-19 en Colombia*, Instituto Nacional de Salud, Ministerio de Salud, Gobierno Nacional de Colombia, Apr. 2020. [Online]. Available: https://www.datos.gov.co/Salud-y-Protecci-n-Social/Casos-positivos-de-COVID-19-en-Colombia/gt2j-8ykr/data

[7] *Covid-19-Colombia-Daily-Case-Proccessed*, David Contreras work based ont the data from Instituto Nacional de Salud, Ministerio de Salud, Gobierno Nacional de Colombia, Apr. 2020. [Online]. Available: https://github.com/DavidContrerasFranco/Covid-19-Colombia-Daily-Case-Proccessed/blob/master/Casos_positivos_de_COVID-19_en_Colombia_27042020.xlsx

[8] World Health Organization, "Coronavirus disease 2019 (COVID-19)," WHO, Geneva, Switzerland, Situation Report – 90, Accessed: Apr. 19, 2020. [Online]. Available: https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200419-sitrep-90-covid-19.pdf?sfvrsn=551d47fd_4

[9] Ministerio de Salud. (2020, Apr. 3). *Press Release No. 123 - 2020, Expansión hospitalaria, una estrategia para atención de la covid-19*. [Online]. Available: https://www.minsalud.gov.co/Paginas/Expansion-hospitalaria-una-estrategia-para-atencion-de-la-covid-19-.aspx