Highlights

Analysis of the COVID-19 outbreak in Espírito Santo-Brazil, utilising SIRD model and governmental data

Guilherme Guimarães Fernandes Viana, Thieres Carlini Rego, Frederico Damasceno Bortoloti

- Upload of the Espírito Santo state official COVID-19 governmental panel dataset into the COVID-19 Data Hub;
- Simulation of the Espírito Santo's pandemic scenario with a SIRD model adjusting its parameters to match the government policies and decrees on social-isolation;
- Comparison between models using Brazilian standard parameters provided by the Covid-19 Data Hub and Espírito Santo's specific adjusted parameters.

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Guilherme Guimarães Fernandes Viana[a], Thieres Carlini Rego[a], Frederico Damasceno Bortoloti[a]

[a] *Department of Production Engineering, Federal University of Espírito Santo, Av. Fernando Ferrari, 514, Goiabeiras, Vitória, 29075-910, Espírito Santo Brazil*

Abstract

In this paper, we apply the use of the SIRD model to create an analysis of the governmental COVID-19 data of the Espírito Santo state in Brazil. By using the public data on the pandemic, provided by the local and federal government, and setting the social isolation parameters of the simulation to match the non-pharmaceutical and social distancing decisions made by the government, we aim to understand better the reality that took place, by generating graphs and analysis within the SIRD model. Having a deeper knowledge of the pandemic and its toll on the state will allow the discussion of governmental decisions related to social isolation and the effects of a more precise social distancing parameters in the model.

Keywords: SIRD model, COVID-19, Epidemic simulation, Data analysis, Social distancing

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1. Introduction

The year of 2020 challenged the whole world to face an unpredictable and unwary disease. SARS-COV-2 was responsible for an unforeseen pandemic, a scenario that made both scientific and government spheres to look for solutions as they were already dealing with it [1]. One year later, we have a much better understanding about the infection and its spread. There are several vaccines developed by different labs and researchers, and it is expected that the population will be immune by mid-2022 [2]. The scenario that took place in Brazil was bad compared to the world, many states had high lethality rates due to the large number of people in vulnerable situations [3].

The pandemic and its implications seem to be something entirely new but, looking through history, humanity has dealt with many large-scale infectious diseases. The Plague, Cholera and Influenza are major examples of this reality. Quarantine is nothing new to the human race, it is new only in scale to the globalised modern society [4].

Throughout 2020, several questions were asked about which were the riskiest moments to get exposed and what decisions regarding the limitation of travel [5] were most effective controlling the infection. Therefore, when researching the COVID-19 data of the studied state, it became clear that there were plenty of gaps to comprehend before blindly accepting the stagnant situation. The whole medical environment went through changes on how to approach suspected cases and how to deal with ICU capacity, while documents and guidelines were constantly being made to help during all these months [6]. It is reasonable to conclude that the society in general had no clear solution on how to display data and define the optimal steps to deal with the SARS-COV-2 and its implications during the first months of the pandemic.

Nevertheless, it was shown to be very important to study COVID-19 in all aspects, from social distancing and non-pharmaceutical measures to symptoms patterns. Being able to predict curves of infection, understand how each government policy affected the number of cases and modelling the next steps of immunisation became key in dealing with this danger [7]. Modelling is a very important approach to predict the outcome while managing possible decisions and understanding the rates, and it became crucial to minimise deaths when handling isolation, vaccination and distribution of medical facilities. Therefore, it was a very logical subject to study, since the coronavirus is a current topic and there is plenty of data being provided from the whole world.

One of the most used models to predict and understand infectious diseases epidemics is the SIR model [8] and its variations. It stands for Susceptible, Infected and Recovered [9]. Other epidemics modelling methods can be used to study disease spread, such as the Susceptible-Infected-Susceptible (SIS) [10], the Bayesian approach [11], auto regressive integrated moving average (ARIMA) [12] [13] and Random Forest time series [13]. In the COVID-19 context, a systematic review observed that compartmental models, such as SIR and its variations, have been the most used ones when compared to statistical, AI-based, Bayesian, hybrid, agents-based and Network models [14].

Because of the geographic location of our university, academic research on a state level is encouraged, so the state selected for the research is the state of Espírito Santo, in the southeast region of Brazil. The state has approximately forty-six thousand square kilometres with a resident population around four million [15], a small but wealthy state inside the Brazilian reality.

The state of Espírito Santo is an educated state with above Brazilian average HDI [15], and its proximity to major Brazilian states, such and Rio de Janeiro, Minas Gerais and Bahia, makes it even more relevant. The state of Espírito Santo has been one of the most transparent in Brazil in terms of numbers and disease data [16]. It has also one of the highest index of human development nationally [15], which allowed it to have better options when dealing with ICU cases, mobilising medical staff and secluding COVID-19-only hospitals. Since early March-2020, there is a governmental official online panel updated daily with information regarding suspected and confirmed cases all across 78 cities within the state. It is provided by the government and has a handful visual representation of the spread evolution and population statistics, as well as a CSV file for download containing a quick description of each notified case that has ever been reported to the health system [17].

Each government or data source has its own parameters and measuring devices, which means when comparing raw data between different countries, it will not be automatically comparable. For example, the Italian panel [18] differs in many ways to the one provided by the World Health Organization [19], therefore there is discrepancy between how and what you can research and present.

When compared to other data sources of the world, the Espírito Santo's panel lacks several information that are commonly seen in global databases, but the existence of this panel enabled the application of SIR model, further conclusions about government decisions and how the infection was dealt within the state.

The SIR model is a model that employs the usage of algebraic and statistical theorems to draw epidemic evolution curves. The model framework exploits several equations to define parameters for the model [20]. These parameters indicate key points to the understanding of the pandemic, varying by type of study and availability of each data. Consequently, not all parameters are used in all situations because, for example, some assume the existence of a vaccine, which is something not available in some cases.

In the beginning of 2020, a library using Python programming language was written by worldwide researchers, making more accessible to others the study of the COVID-19 spread trough SIR models. The library was named CovsirPhy GitHub repository [21].

This Python library for COVID-19 enables scenario analysis for data-informed decisions. The main data source proposed for this project is a unified database of COVID-19 numbers from all over the world, called COVID-19 Data Hub [22]. The hub contains the COVID-19 standard variables, government policies trackers [23] and other features for better data visualisation and applicability. Designed for academic and practical purposes, containing information in all three administration levels, it generates error logs to spot mismatches in the official data and inform authorities. All sources are properly documented, along with their citations. The data regarding the Brazilian social-distancing policies in this database has put some restrains in its applicability, since some of the parameters used are not specified by province/state, but for Brazil as a whole.

Understanding curves about immunisation and how rates of infection changed throughout time will expand the scope of analysis, granting glimpses of solutions for the current COVID-19 pandemic and for future epidemics.

2. Objectives

The objective is to apply the SIRD model to Espírito Santo's COVID-19 data to understand and provide explanations regarding the use of COVID-19 data and the non-pharmaceutical governmental social distancing policies during the outbreak. Firstly, clarifying how data was collected and exposed by the Espírito Santo government, then answering questions regarding the understanding of dispersion and infection rate graphs.

Data modelling is the main focus of research. The application of a SIRD model to understand the reality that took place generating results and predictions is the main goal. But we also point out how data is provided by the government and medical facilities, such as what to do in order to generate and study this data in a most productive way.

Analysing the government official decisions, regarding social distancing and non-pharmaceutical measures, by correlating them to the rates of infection (α), recovery (β) and lethality (γ) to fit in the SIRD model we hope to identify its effectiveness. Therefore, by the end of the research, the time frame of how these rates evolved will be provided.

Another objective is the implementation of the state of Espírito Santo COVID-19 Panel data into the COVID-19 Data Hub. By making this data available worldwide we hope to stimulate and help researches and studies. With the results of this research, we hope to add valuable information regarding coronavirus to the public.

This article is organised as follows. In Section 3, the bases of the SIR model, some of its variations, parameters and equations are presented followed by exposures of the government policies and decrees that took place in the state discussed in this study in Section 4. A literature review of correlated studies is in Section 5, allowing the discussions of some of the possible methods used by researches to model the outbreak. The GitHub CovsirPhy library used for the simulations is presented in Section 6. At the Data Section 7, further explanation about the variables and the source is given. The methods Section 8 clarifies the process used to model the data. In the Result Section 9 the graphs, parameters and comparisons are exposed. Conclusions and future possible works are discussed in Section 10, allowing the expansion of the scope on the topic and opening the possibility for new suggested researches.

3. SIR model and its variations

Since the beginning of the 2020 pandemic, many specialists in diverse areas have been accompanying the spread both in local and global realities. Regarding the Brazilian reality, studies were done in different states such as São Paulo [24] and Rio de Janeiro [25]. A technical note [26] made by by Federal University of Espírito Santo (UFES) members and other collaborators, that provided predictions for the Covid-19 cases, deaths and spread with data from Espírito Santo was developed in the early studies of the pandemic. Local level applications of compartmental models provided guidelines to this research. The capacity to model computer programs and convert raw data into contributions for the comprehension of the COVID-19 outbreak allowed prominent advances in the research of the virus, its unfolding consequences and counter measures effectiveness [27].

The first task is to understand how and when SIR model can be used and how precise it can be. The model has a wide range of features and variables [20] that can be used depending on the goal of the research and the available data. Even in the simplest form, SIR model is known for generating results and predictions that represent reality [28].

For the basic SIR model, there are some main concepts necessary to understand the algorithm (Tab. 1).

Table 1: Main definitions of the SIR model.

Main Variables in SIR model	**Definition**	**Description**
S(t)	Susceptible	Individuals that have never been infected and are able to catch the disease
I(t)	Infected	Individuals that are infected (confirmed cases)
R(t)	Removed	Individuals that had the disease and either deceased or recovered (assumed to be immune)
N	Population	Total number of individuals
R_0	Basic Reproductive Number	Average number of individuals infected by one case in a totally susceptible population in absence of interventions aimed at controlling the infection
α	Transmission rate	The rate in which the transmissions happen
β	Recovery rate	The rate in which infected individuals recover from the disease

SIR stands for susceptible (S), infected (I) and removed (R). The susceptible population (S) is the number of individuals susceptible to be infected at a defined time, once these individuals are infected with the disease they are considered infected (I), this number consider both asymptomatic and symptomatic infected individuals [9]. Once the individual recovers and no longer has the disease or he deceases from it, he is considered removed (R), the individuals that recovered are assumed to be immune for life [20]. The assumption that the recovered individuals are immune for life is a limitations of the base model considering that Covid-19, such as other diseases, is capable of reinfecting a recovered person. The method uses the transmission rate (α) and recovery rate (β), both vary accordingly to the disease selected. Mitigation strategies affect the transmission rate (α) [29].

The SIR model belongs to the class of compartmental models because the population under study is being divided into compartments (S, I, and R) and with assumptions about the nature and time rate of transfer of individuals from one compartment to another [30], as shown in Fig. 1.

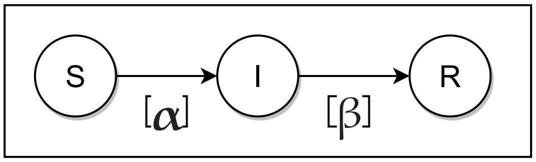

Figure 1: SIR schematic, susceptible (S), infected (I) and removed (R)

The variables in the model correlate, and some assumptions are necessary in order to achieve results. One important assumption in the basic model is that the population is fixed [20], and the relations can be expressed by the following equations that govern the model.

$$S + I + R = N \tag{1}$$

$$\frac{dS}{dt} = -\alpha SI \tag{2}$$

$$\frac{dI}{dt} = \alpha SI - \beta I \tag{3}$$

$$\frac{dR}{dt} = \beta I \tag{4}$$

where S, I, R and N are from Tab. 1 and the Eq. 2, 3 and 4 are differential equations. In the SIR model, these equations set the ratio that individuals are transitioning from one group to another at a defined time (t) in terms of its parameters (α) and (β). This relation can be seen in Fig. 2 as a graph, plotting the integration of each compartment differential equation over time, given initial conditions and the parameters, where it is possible to forecast an infectious disease spread.

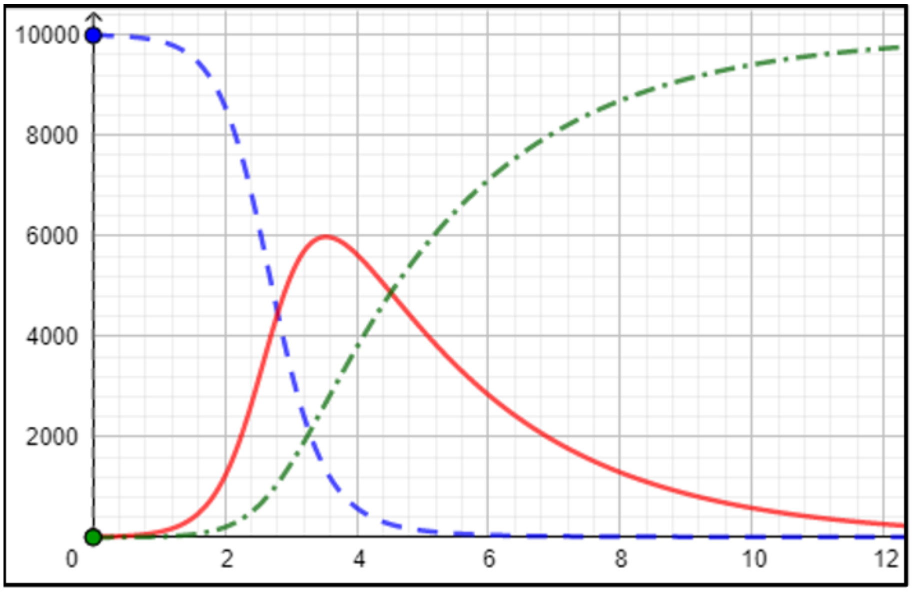

Figure 2: Plot for the basic SIR (susceptible, infected, and recovered) model. Model parameters are α, the transmission rate ($\alpha = 3$), and β, the recovery rate ($\beta = 0.4$).

The Basic Reproductive Number (R_0) is an infectious disease parameter. The parameter represents the average number of people infected by one case in a completely susceptible population. Based in conditions where there are no safety measures taking place, such as social distancing, mandatory mask use and others safety courses of action [20]. This numeric value allows to understand how infectious is the disease and its growing pace in case of an outbreak. Once R_0 gets close to the 1 threshold, the chances of an epidemic or an endemic spread rise [31].

There are variations in the SIR method to be considered depending on the data available and reality of the decease. Some of the most used ones are SIR-D [32, 33] and SEIR [34]. The existence of a vaccine and herd immunity are also variables that can alter the basis model [20]:

- SIRD
  - (R) stands only for the recovered individuals
  - The (D) category, defined by the number of deaths, is included in the model
  - The lethality rate (γ) is added as a parameter

- SIR with birth and death
  - Assumes all deaths are natural
  - The constant rate of birth and death (M) is considered
- SIR with constant Vaccination at Birth
  - Assumes that a portion (p) of population is vaccinated at birth
- SIR with Saturated Susceptible population
  - Birth and death are not constants
  - Assumes that susceptible individuals are born at a rate M(S,I,R)
- SEIR
  - The (E) category, defined by the number of exposed individuals
- SIR with Delay
  - Assumes that once a individual from the susceptible population (S) is infected he only becomes a part of the infected population (I) after a certain span of time
- SIR with Quarantine (SIQR)
  - Assumes that some individuals are under quarantine, therefore altering the values of the infection rate parameters

There are several options of possible examinations by altering the data provided when applying the SIR model. But before discovering which satisfactory conclusions we could achieve, we needed to understand how data was collected, and how the parameters of isolation and risk exposure were counted. Infection happens based on how much the susceptible population is at risk of getting contaminated [20]. The SIR approach was used in the early stages of the pandemic in Brazil, it was shown that the proportion of asymptomatic individuals affects the amplitude of the peak of symptomatic infected, suggesting that it is important to test the population [35].

4. Public policies and social isolation

Social isolation can be viewed as the percentage of available time people are getting at risk, measured by days of work, study and others activities per week. Its impact on a pandemic outbreak cannot be overlooked and control strategies must be put in place as quickly as possible in order to control the transmission rate [36]. It is also defined, by how the rate of infection is changing, likely provoked by usage of masks, hand sanitisers and other safety measures. The different SIR models take into account those variables as inputs, and use them to refine and predict the number of infected, deceased, healthy individuals and others numbers depending on which SIR is being used [9].

The non-pharmaceutical policies established by the government, such as restrictions to entertainment or commercial opening hours, affect deeply the rate of infection (α) and, therefore, the predictions generated by simulations models [37], so it is key to understand the impact of this measures. With these measures impact identified and correlated to the time they were imposed, conclusions can be made about timing in civil measures and how effective they were. In the beginning of the pandemic the government actions were made by official decrees and ordinances until the risk map system was implemented, as seen on Table 2. All the government's official decrees, ordinances and law projects related to the pandemic were available at the official coronavirus panel [17].

To implement the risk map the state was divided into smaller counties and, by using a Threat × Vulnerability matrix, they were to be classified weekly. The Threat axis is based in the number of cases per one million individuals and the Vulnerability axis is based in the percentage of occupied ICU beds. Based on this matrix the counties are classified as low risk, moderate risk, high risk and extreme risk; symbolised by, green, yellow, red and dark red respectively. Therefore, starting from April 19, 2020, the government releases a weekly update of the state risk map 3, in which each county is painted in the colour representing the outbreak reality at that point in time.

The risk classifications made the counter-measures automatic. The government defined a different set of actions for each of the levels, each week a new map was released and, if the region changed from a lower risk to a higher one, new social distancing rules would be added. This also affected the data by allowing each region to have different transmission rates and social distancing parameters. The main set of measures of each level are:

Table 2: Espírito Santo main decrees and ordinances prior to risk map

Date	Description
2 March 2020	Brazil Federal Government declares National Public Health Emergency Status (ESPIN)
13 March 2020	(Decreto 4593-R) Definition of possible governmental measures
17 March 2020	Presential Public Schools Classes suspended (210 days with extensions) Concerts, movie theaters, night clubs and similar events suspended (210 days with extensions)
19 March 2020	(Decreto 4604-R) Public non-essential services and electives surgical procedures procedures suspended (120 days)
20 March 2020	(Decreto 4605-R) Lockdown (15 days)
02 April 2020	(Decreto 0446-S) Espírito Santo government declare Public Health Emergency Status
03 April 2020	(Portaria SESA 058-R) safety measures recommendations for the commercial and service sectors
06 April 2020	(Portaria SESA 062-R) safety measures recommendations for the industrial sector
11 April 2020	(Decreto 4626-R) Commercial and services sectors suspended (49 days with extensions)
19 April 2020	(Portaria SESA 068-R) implementations of the risk map for the state
30 April 2020	(Decreto 4644-R) 30 days extension of Decreto 4626-R

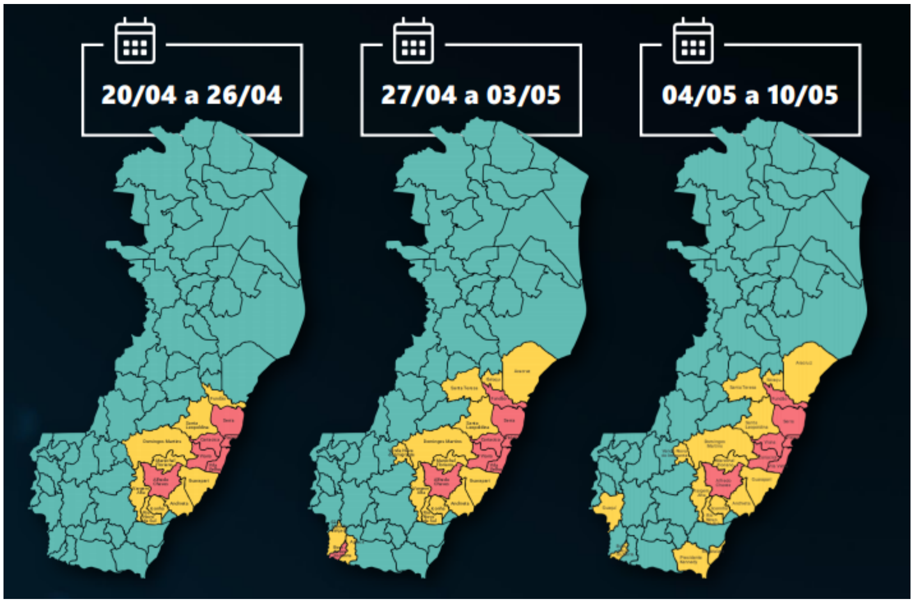

Figure 3: Risk Maps of Espírito Santo from April 20, 2020 to May 4, 2020, showing municipalities with low risk (green), moderate risk (yellow) and high risk (red), with no extreme risk (dark red) yet.

- Low Risk (green regions)
  - Only one client allowed per 10 meters square in small commercial facilities
  - Only once client allowed per 14 meters square in shopping malls and big galleries
  - implementations of sanitary barrier between regions and in the main roads
- Moderated Risk (yellow regions)
  - Only one client allowed per 10 meters square in small commercial facilities
  - Only once client allowed per 14 meters square in shopping malls and big galleries
  - Big galleries and shopping malls can only open during one shift
  - implementations of sanitary barrier between regions, in the main roads and intercity bus stations

- High Risk (regions red)
  - Public non-essential services suspended
  - Only essential services are allowed to function normally
  - Commercial facilities can only function in the delivery or drive-through systems
  - Big galleries and shopping malls must be closed
  - Public transportation workers that are sixty years old or more must be reallocated
  - Public transportation that run an AC system are taken out of circulation
  - implementations of sanitary barrier between regions, in the main roads and intercity bus stations
- Extreme Risk (dark red regions)
  - Public non-essential services suspended
  - Essential services must be closed by 8 pm
  - Commercial facilities can only function in the delivery system
  - Big galleries and shopping malls must be closed
  - Public transportation workers that are sixty years old or more must be reallocated
  - Public transportation that run an AC system are taken out of circulation
  - Public transportation is shut down during weekends
  - implementations of sanitary barrier between regions, in the main roads and intercity bus stations

The details regarding the peculiarities of the data, its origin and how this social distances measures can affect the SIR model will be better explained in future sections of this article.

5. Related works

Studies made prior to this one, and its results, encouraged deeply our research. Academics in different countries around the world have put effort studying this outbreak in order to understand the pandemic [7], identifying possible counter measures [29] and look for possible solutions for the future to come, since it is now clear that humanity is susceptible to this scenario. Some studies have used the basic SIR model and its variations in country level [38] and province/state level [24] [25] to look for reliable predictions. By making use of mathematics tools some studies aimed to better simulate reality. When using SIR to forecast the maximum number of active cases and peak time of the COVID-19 outbreak, a Logistic growth curve model was used for better accuracy in short-term projection while a Time Interrupted Regression model evaluated the impact of lockdown and other interventions [39].

Other studies used a Bayesian Susceptible-Infect-Removed model to specify transmissions rates and spatial association including neighbouring county transmissions [40]. A hybrid SIR-Bayesian model [41] was also used to simulate Brazilian reality, the fused model had the goal to take in account the under-reported cases. Other studies had a different proposed solution to the same problem of unaccounted cases in Brazil [42, 43]. During the course of the pandemic, it was identified that the Brazilian data had intrinsic problems: the country is to big, many states did not have a reliable counting of cases and there was a big delay in the reports. Researches proposed models [44] to forecast the pandemic by taking account the notifications delay in the reports of data aiming to fill this gap in the available information. The state of Espírito Santo has small land area and its panel [17] was implemented early, therefore these structural problems in the data were not taken in account in this research.

Many varieties of studies were conducted in order to analyse the pandemic outbreak, a systematic and critical review of studies encompassing more than 80 countries and 240 articles [14] observed that, out of the main possible approaches, the compartmental models, that include SIR and its variations, are the most used for COVID-19 simulation/forecasting and that most of the studies published had a focus on data from Asian, followed by Europe.

Additionally, some researches made use of machine learning to achieve their objectives. Researchers used Machine Learning and variations of the SIR model the forecast scenarios and then compare them [9], another approach was to use a combination of both to propose a model for smart health care and the well-being of the citizens, aiming to predict if the virus will spread in the population or die out in the long run [45]. The use of a hybrid model between SIR, adaptive network-based fuzzy inference system (ANFIS) and multi-layered perceptron-imperialist competitive algorithm (MLP-ICA) was proposed to predict time series of infected individuals and mortality rate [46]. To this day there is still not a consensus on a optimal model.

The base model that suits the best the propose of this research and the available data is the SIR model for epidemics. Other models may not be able to proper represent the reality, as said by Odagaki [47] "COVID-19 has unusual characteristics: (1) transmission of the virus by presymptomatic patients and existence of asymptomatic infectious patients, and (3) patients, symptomatic or asymptomatic, can be identified by polymerase chain reaction (PCR) test. Because of these characteristics, the number of infected cannot be obtained directly, the number of daily-confirmed new cases and its time dependence are the only essential data. Therefore, COVID-19 showing these characteristics may not be represented properly by the SIR and the SEIR models which assume that the number of patients is known and do not treat quarantined patients as a compartment."

A study was made with the Brazilian data, including the Espírito Santo one, using a SEIRD mathematical model the analyse some states [48]. The research concluded that the Espírito Santo state would not have problems regarding ICU demand, but that was not the case in reality [17]. Therefore, we believed that using another variation of the SIR model and take the government measures into account could provide an improvement over this previous result.

The SIQR model allows to adjust quarantine data and parameters [49], in this way it is possible to calibrate the model with the details of the social distancing, such as school closures, lockdowns and other non-pharmaceutical measures, in each specific case. The SIQR has been successfully applied to model the COVID-19 pandemic in in other countries, such as Japan [38], Italy [50] and in the state of Rio de Janeiro - Brazil [25]. Although both states - Rio de Janeiro and Espírito Santo - are neighbours and share some similarities, the governmental decisions regarding the pandemic outbreak were done at state level, therefore the parameters for each state are not the same.

By analysing the previous researches, the variations of the SIR method and the available data, we chose the SIRD mode. The SIRF model was an option, but the characteristics of the available data for the state much favours SIRD, since the SIRF method takes into account the post deceased confirmed cases and its parameters.

The model schematics and variables differ from the basic one presented earlier, the schematic can be seen on Fig. 4 and the variables are defined in Fig. 3.

Table 3: Main definitions of the SIRD model.

Main Variables in SIRD model	**Definition**	**Description**
S(t)	Susceptible	Individuals that have never been infected and are able to catch the disease
I(t)	Infected	Individuals that are infected (confirmed cases)
R(t)	Recovered	Individuals that had the disease and recovered (assumed to be immune)
D(t)	Fatal	Fatal cases (confirmed deaths)
N	Population	Total number of individuals
R_0	Basic Reproductive Number	Average number of individuals infected by one case in a totally susceptible population in absence of interventions aimed at controlling the infection
α	Transmission rate	The rate in which the transmissions happen
β	Recovery rate	The rate in which infected individuals recover from the disease
γ	Lethality rate	The rate in which infected individuals decease

The population (N) is assumed to be fixed and the equations that rule the model are

$$S + I + R + D = N \tag{5}$$

$$\frac{dS}{dt} = -\alpha SI \tag{6}$$

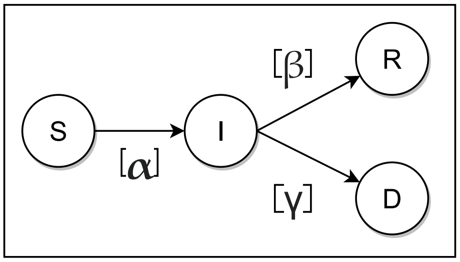

Figure 4: SIRD schematic, susceptible (S), infected (I), recovered (R) and deaths (D)

$$\frac{dI}{dt} = \alpha SI - (\beta + \gamma)I \tag{7}$$

$$\frac{dR}{dt} = \beta I \tag{8}$$

$$\frac{dD}{dt} = \gamma I \tag{9}$$

where S, I, R, D and N are from Tab. 3 and the Eq. 6, 7, 8 and 9 are differential equations.

6. CovsirPhy library

CovsirPhy is a Python library for COVID-19 data analysis with phase-dependent SIR-derived ODE (ordinary differential equation) models, maintained by contributors all over the world [21]. Developers make the library available for download on a GitHub repository [1], and all the necessary datasets by country are retrieved from public databases.

The library contains are able to simulate the following SIR variations:

- SIR
- SIRD
- SIRF
- SIRF with exposed/waiting cases

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[1] `https://github.com/lisphilar/covid19-sir`

- SIR-F with vaccination
- SIR-F with re-infection

The CovsirPhy code, used for modelling in this article, extracts isolation parameters from the "Oxford COVID-19 Government Response Tracker (*OxCGRT*) [23]. It is a School founded in 2010 that aims to provide governments, and public policy-making with better knowledge and information about the world. A department from the University of Oxford (UK) that ranges science from computing and medicines to social science.

Throughout the pandemic, this School has been tracking government decisions and social measures from about 70 countries, and making it available for studies and comparisons. Therefore, having the social isolation parameters being drawn from this database was an ideal choice to correctly model the COVID-19 data. These predefined values were considerable reliable and useful for the CovsirPhy package, making it possible to calculate the final index.

The final index that is used inside the CovsirPhy package, extracted from the Oxford hub, is the stringency index. It focuses on the availability of transportation and social activities, relying on the population to follow the current social measures [51].

The stringency index (I) is calculated using 8 containment and closure policy indicators (C1-C8) and one health system policies indicator (H1) [23]. Each one of the indicators refers to a specific situation regarding the social distance policies and governmental actions as seen on Tab.4. Other indexes were developed to measure government decisions regarding containment, economic support and health policies; such as the economic support index, legacy stringency index, containment and health index and government response index [23].

The value of the stringency index (I) is the average of these nine subindices

$$I = \frac{1}{9}\sum_{j=1}^{9} I_j \tag{10}$$

where I is the stringency index, and I_j is a sub-index j pertaining to an individual policy indicators from Tab. 4.

Table 4: Stringency Index indicators

Main ID	**Description**	**Values**
C1	Closings of schools and universities	0- no measures 1- recommend closing or all schools open with alterations resulting in significant differences compared to non-Covid-19 operations 2- require closing (only some levels or categories) 3- require closing all levels
C2	Closings of workplaces	0- no measures 1- recommend closing 2- require closing for some sectors 3- require closing for all-but-essential workplaces
C3	Cancelling public events	0- no measures 1- recommend cancelling 2- require cancelling
C4	Limits on gatherings	0- no restrictions 1- restrictions on very large gatherings (above 1000 people) 2- restrictions on gatherings between 101-1000 people 3- restrictions on gatherings between 11-100 people 4- restrictions on gatherings of 10 people or less)

C5	Closing of public transport	0- no measures 1- recommend closing (or significantly reduce volume/route/means of transport available) 2- require closing
C6	Confinement	0- no measures 1- recommend not leaving house 2- require not leaving house with exceptions for daily exercise, grocery shopping, and 'essential' trips 3- require not leaving house with minimal exceptions
C7	Restrictions on internal movement between cities/regions	0- no measures 1- recommend not to travel between regions/cities 2- internal movement restrictions in place
C8	Record restrictions on international travel	0- no restrictions 1- screening arrivals 2- quarantine arrivals from some or all regions 3- ban arrivals from some regions
H1	Record presence of public info campaigns	0- no Covid-19 public information campaign 1- public officials urging caution about Covid-19 2- coordinated public information campaign

The stringency index is divided by type of activity (study, work, entertainment, commercial, etc) and public measures to contain the spread. It is a key component of this modelling, since it can estimate and alter how isolated the population was in numerical ways. With that, it is possible to closely predict how infection and recovery rates were changing during the months of COVID-19 dealing, since the acceleration of the spread can be seen on a daily basis.

The main source of jhu data (total number by day of confirmed, recovered and fatal cases) of the CovsirPhy package is the COVID-19 Data Hub [22]. From this hub, the algorithm is able to collect number of confirmed, recovered, fatal and tested individuals daily for any region of the world, that was previously uploaded.

In the case of Brazil the state and federal governments have the responsibility on the COVID-19 counter measures, although the most of the decisions were made in state level. Each state government made different decisions on the restrains and quarantine of the population. Originally there was no synchronised official data for the state of Espírito Santo in the Data Hub, so the upload of the official state panel [17] to their data sources was necessary. As soon as the line list obtained from our local government got connected to the COVID-19 Data Hub [22], the CovsirPhy library can download the Espírito Santo numbers as the base source of data to run the model.

Once the data of Espírito Santo, previously uploaded in the COVID-19 Data Hub [22], is downloaded by the CovsirPhy library for usage, its isolation parameters and stringency index are automatically set equally to the Brazilian ones in the Hub. This peculiarity compromises the proper simulation of the model since each state inside Brazil had different social isolation measures and, therefore, must have different parameters as well. To solve this situation, the values of isolation parameters are adjusted so to match the values that represent the non-pharmaceutical measures applied inside Espírito Santo. This adjustment allows a recalculation of the stringency index and it was done following the official policies and decrees that were submitted during the pandemic. This situation will also permit the comparison between the scenario of the state with national parameters with the adjusted one, allowing to analyse how the social distancing measures of the state applied on the Brazilian average.

The aim of adjusting the isolation quantitative variables that compose the stringency index is to proper understand the effects of the government policies and decrees in the numbers. This can be seen due to the fact that these variables, through the stringency index (I), change the rates α, β and γ. This change in the rates is the key tho separate the spread in phases, therefore, allowing the analysis and illustration of each time frame during the COVID-19 outbreak, and the comparison between them.

The CovsirPhy package has multiple classes and subpackages to handle COVID-19 SIR model, with many options of study and different models for analysis. At Methods, Section 8, we discuss how we transformed our data and how these numbers were extracted from *OxCGRT* [23]and Datahub.io [21].

7. Data

In the context of the Brazilian outbreak and reliable data for the Espírito Santo state, the most precise data was the one from the governmental panel [17], therefore it was the one used in this study.

The panel of Espírito Santo was developed by making it accessible online the information that the medical facilities were already gathering before the panel was created [17]. It has a bottom-up methodology, which means it is a more automatic process for the hospitals and clinics to provide the data, although it is not the optimal approach in order to correctly collect and study the data.

To be able to apply this data properly it was necessary to upload it in the worldwide data hub [22]. By doing so the data can be used in the CovsirPhy library, not only for this research but for anyone that seeks it.

The Panel of Espírito Santo [17] was uploaded to the main database, allowing anyone who accesses the hub to study how numbers and the scenario evolved in the reality reported. Making the data available allowed the proper use of all functions inside the library with the Espírito Santo's numbers, which was key to the study

In order to properly seek the right data and correctly propose conclusions by using the Espírito Santo's data in a way viable to the SIRD model, it was necessary to analyse other countries data [52] and compare it to the local one [17]. Parallel to the comparison its was necessary to identify the variables [53] to develop a deeper understanding on non-pharmaceutical measures to slow the disease outbreak. By doing so it was possible to identify topics and variables inside the model that suited the best the research with the available material.

Based on this reality, the model needed adaptations and merge of official information in order to provide the accurate data necessary. When uploaded to the Data Hub, the state data is automatically associated with the social distancing indicators, previously shown on Tab. 4, set for Brazil in the hub.

To make the simulation more accurate, the indicators $C1$ to $C8$ and $H1$, that are not bound by country level measures, were altered to match the social distancing data provided by the government weekly through the risk map, Fig. 3, and the official decrees, Tab. 2. All the decrees, risk maps and official information on the pandemic policies were made available by the government in the official COVID-19 panel [17].

The time frame of our data begins in March 22, 2020, before the first confirmed case in the State in March. 5 2020, and goes until the April 28, 2021. The data were used as they were, and no gaps were filled with any interpolated values in order to complete the time series.

In this research, to proper simulate the SIRD algorithm with the data available, parameters such as immunity prior to the pandemic, vaccination at birth or any other vaccine related parameter were not used, since there was no vaccine for the virus while most of the data was collected and, even after the development of the vaccine, the State did not have a reasonable number of vaccinated people.

Inside CovsirPhy package, the main procedure downloads the data and use it for modelling by extracting the variables from both COVID-19 Data Hub [14] and Oxford Government Tracker [23]. By doing that, it generates an CSV (comma-separated values) file called $covid19dh.csv$. It contains these variables, ranked by day and province from the whole world, since beginning of January 2020 until today. The file has the following information:

- Observation Date
- Tests
- Confirmed
- Deaths
- Population
- ISO3
- Province/State
- Country/Region
- Covid policy trackers ($C1 - C8$ and $H1$)

- Stringency index (I)

In the first part, the raw data, is extracted from the COVID-19 Data Hub and, as the Espírito Santo's Government panel was implemented, it is synchronised with current confirmed numbers. The second part defines how isolated each province was at that particular day. Therefore, the CovsirPhy package is able to calculate the stringency index necessary for the modelling.

As mentioned before, the isolation parameters encountered in this database had the same values for both Espírito Santo and Brazil. Knowing that this was inconsistent with reality, the parameters had to be recalculated in order to correctly continue the analyses. By following the index guide provided and comparing with government decisions, a CSV file with different isolation parameters for Espírito Santo was manually created.

That decision is very useful in order to compare different approaches on isolation and how reliable is the quarantine reality for the whole country. The method to use the altered variables was to replace the generated $covid19dh.csv$ file with a fixed one, and disallow the CovsirPhy to update the downloaded database.

Splitting and distributing the data within the time frame is key to correctly model and explain scenarios. These partitions are called phases, and they are pre-established by the algorithm in order to calculate different rates for each reality. Therefore, months that do not have similar restrictions are placed in different phases and have different rates.

Moreover, phases can also be defined by the user, allowing the library to proper estimate rates when isolation really occurred inside the state. Having a fewer quantity of time frames permits better comparisons, as it is more concrete to see which isolation measure impacted best. On the other hand, a broader quantity of phases permits better analysis of how the rates were slightly changing through time.

8. Methods

The tool chosen to model the Espírito Santo's reality was the CovsirPhy package. The utilisation of this library is briefed here, as the Python source code can be obtained inside our GitHub. The aim is to explain how data was transformed inside the code and which results were gathered through the process. For the purpose of replication and broader understanding of this article, a GitHub [2] repository containing all necessary CSV and Python source files was created, including all graphs and tables generated in the process. For the experiments, we used Python version 3.8.9 and CovsirPhy package version 2.18.0, both updated 28th of April, 2021.

Before any usage of the data the upload of the COVID-19 panel of Espírito Santo was made into the COVID-19 Data Hub.

8.1. Scenario 1: Brazil's generic isolation parameters

The first scenario is carried out with the existing Brazilian generic isolation parameters directed downloaded from the Data Hub, and its complete process is shown in Fig 5. Our time frame is from 22nd March 2020 to 28th April 2021.

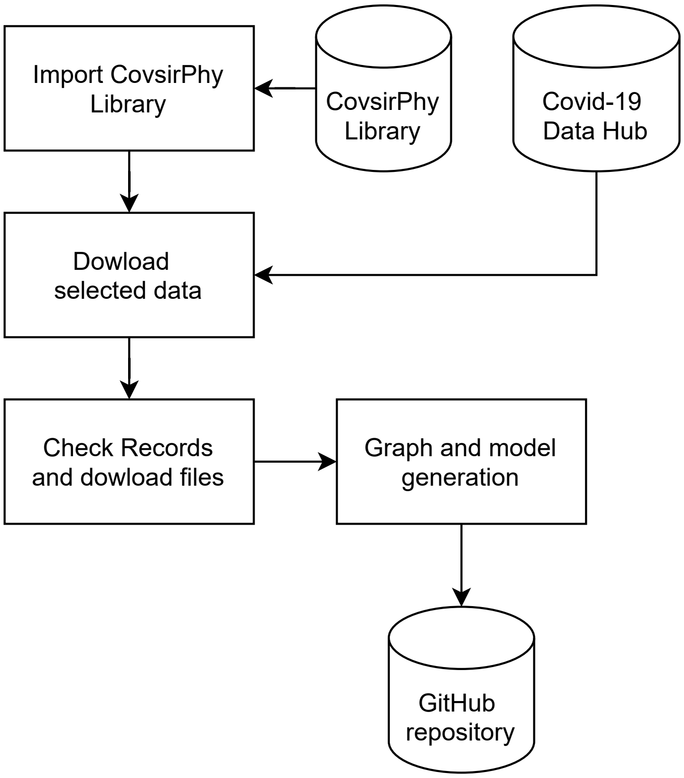

Figure 5: Schematic of the first scenario.

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[2] https://github.com/guilhermegfv/CovsirPhy-bra-es

Initially, the algorithm downloads the data from the Data Hub. The Hub extracts information about confirmed cases from the Panel ES [17] and the isolation parameters from the Oxford source [23]. The libraries required to run the CovsirPhy are updated and all requirements declared inside its Kaggle code-book are satisfied.

The Python code loads data for country and province set to Brazil and Espírito Santo. An instance is created called $es_scenario$ that will carry out the data necessary for the modelling. All the required graphs are generated, as well as tables with the correspondent values.

The first graph that is generated is the S-R trend. It is the first signal of how phases were defined for the execution. The code produces an automatic separation of the phases - resulting in 32 time frames - which can be later manually altered. The parameters (α, β and γ) are calculated for each phase based on the data and on variation of the stringency index by interactions of the algorithm. No time out for the estimating was set, as we seek the optimal results.

A table with all parameter values is downloaded for comparison. The basic reproductive number R_0 for each phase is calculated and, by utilising the parameters for the last phase, the model is able to predict future scenarios. For this article, the simulations continued for 60 days starting from 28 April, 2021. Lastly, a table with the isolation values used for the modelling is downloaded.

In this first scenario, we used the standard isolation values downloaded from the Oxford Government Tracker. It mimics the values set for all Brazil. There are the 9 parameters of isolation (C1-C8, H1) and the calculated stringency index.

8.2. Scenario 2: Espírito Santo's specific isolation parameters

The second scenario schematic is shown in Fig. 6. For this scenario, the stringency index (I) changes due to the adjusting of the parameters that compose it ($C1 - C8$ and $H1$). We altered the $covid19dh.csv$ file with these values adjusted to better suit Espírito Santo's reality. The aim is that, by providing the proper numeric quantification of how isolated the state was, the rates and our conclusions will be more accurate.

The CSV file contains columns for each parameter and the stringency index all ranked by day, making it 402 days of analysis and 402 lines of data. This way each day of the time frame can have different values for the parameters and for the stringency index, consequently. All the adjusting done for the second scenario was based on official data and information provided by the government via the COVID-19 panel.

The argument `update_interval` of *cs.DataLoader* is set to prevent download of new data.

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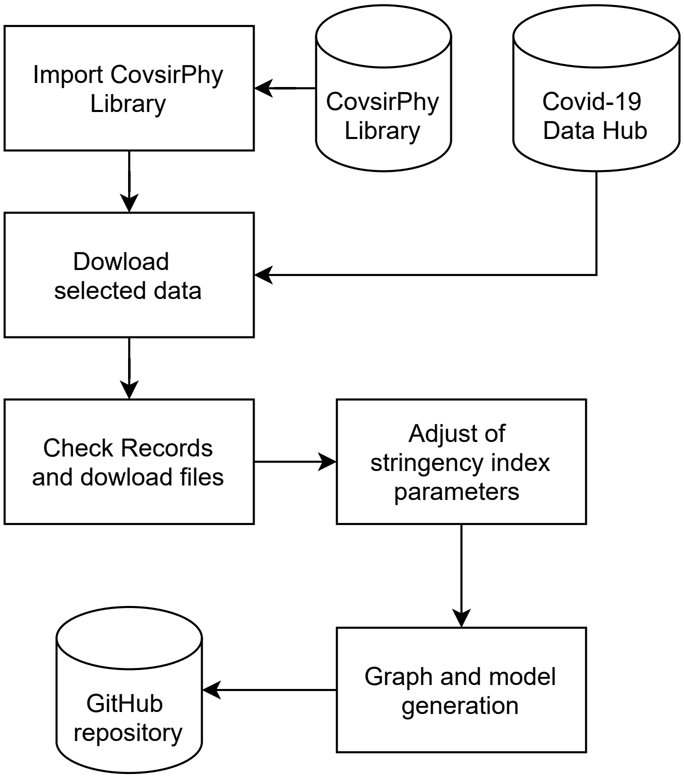

Figure 6: Schematic of the second scenario, where the altering in the index stringency parameters was made.

9. Results

The SIRD mode focus on evaluating how the groups of population, susceptible (S), infected (I), recovered (R) and deaths (D), evolved through time. At day 0, the whole population can be considered as Susceptible, ignoring immunity variables, such as birth immunity and vaccination. The main graph of S-R trend allows us to understand toll of the disease on the total population by exposing the daily raw numbers, the results for the first and second run are shown respectively in Fig.7 and Fig.8.

The graph shows the detection of 31 phases for the first scenario and 32 for the second, the curve of susceptible-recovery translates how infection and recovery was happening. The faster the number of susceptible people are decreasing, the more infectious the spread currently is. Therefore, by analysing any given point in the curve, we can understand the direction of the pandemic through the tangent of that same given point. The more vertical the tangent values of the selected time, the faster the infection is happening. This graph is similar for both runs, it is natural due to the fact that the raw numbers for the variables are the same, the main change is the variation in the numbers and length of phases. The library automatically defines phases based in the parameters through time.

The plotted epidemic curves are in Fig. 9 for the first and Fig. 10 for the second run. These graphs estimate 60 days of spread with the current parameters of isolation - rates detected at last phase - and then plot values of confirmed, infected and fatal cases for this time frame. Therefore, by persisting the same quarantine restrictions that are being applied at 28th April 2021, the pandemic is bound to reduce its spread.

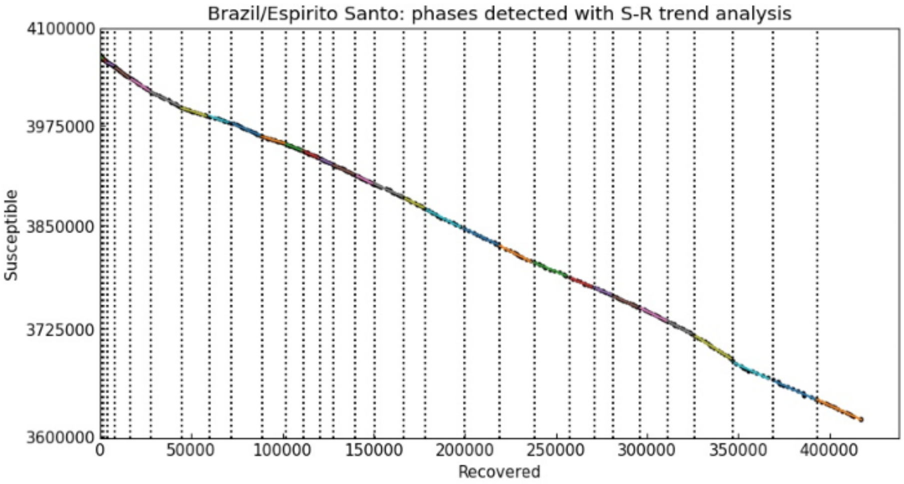

Figure 7: Susceptible-Recovered Trend with defined phases - Scenario 1

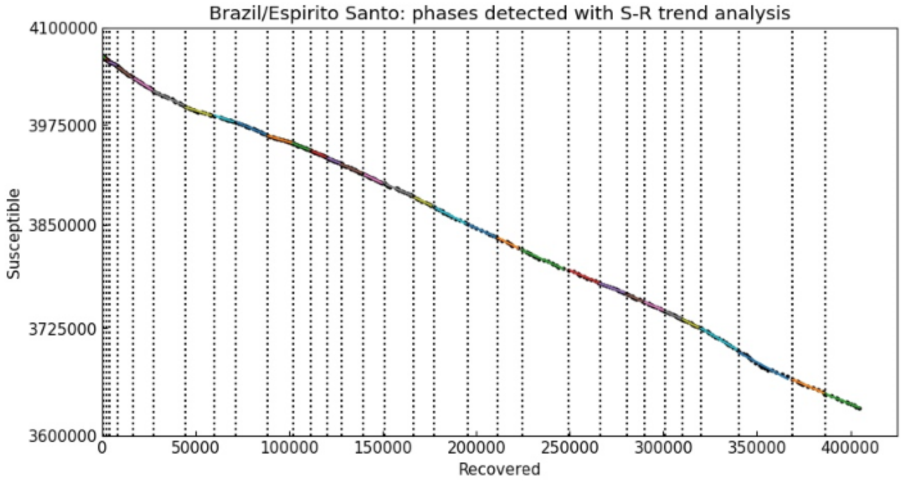

Figure 8: Susceptible-Recovered Trend with defined phases - Scenario 2

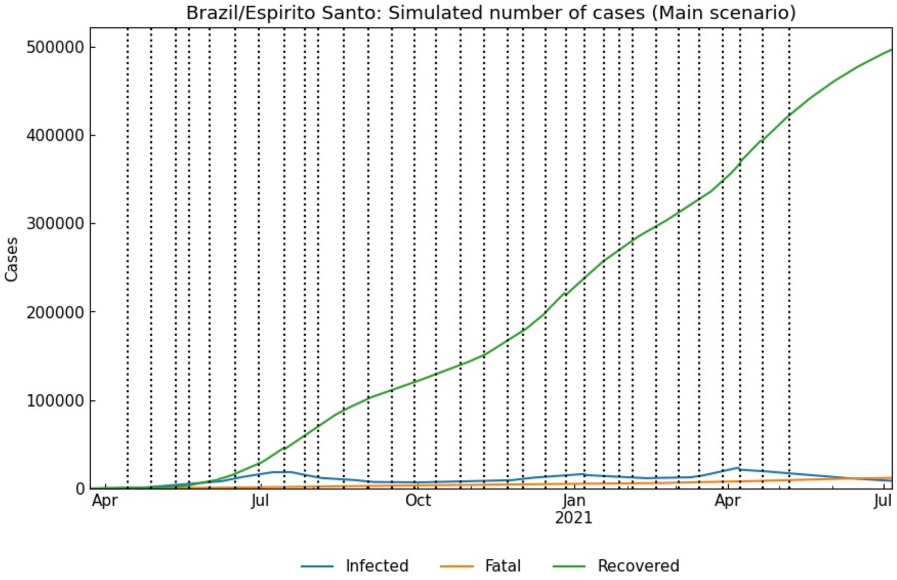

Figure 9: Epidemic curves for generic isolation parameters

To better compare both scenarios a comparison graph for the prediction of confirmed cases was plotted, as seen in Fig. 11. The prediction is made based on the last identified phase of each model. This variation makes reassures how the set of parameters alter the model, therefore proving that the correct use of parameters increase the accuracy of the model.

By quantifying the interactions between the phases, the model provides numerical values for the rates (α, β and γ) that govern the movement of the individuals from one population to another. This result is displayed as a CSV file, following the library default settings, and as a graph. This graph is a key point of the method, as shown in Fig.12 for the Scenario 1 and Fig.13 for the Scenario 2, the rates in each phase are the link to the understanding of the government policies, as these policies are the origin of the parameters fluctuation.

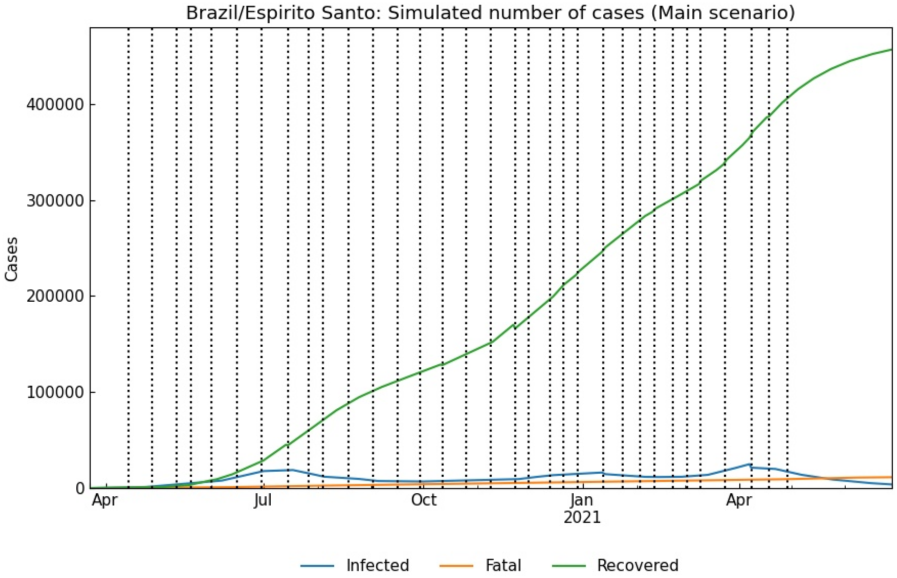

Figure 10: Epidemic curves for specific isolation parameters

To better analyse how the rates of infection (α) and lethality (γ) correlate, an amplified graph of the rates in the specific isolation parameters scenario is generated and shown on Fig. 14.

This closer look exposes the accelerated evolution of the infection rate in the first weeks of the pandemic due to the few policies put in place at that time. The infection rate starts high until May. 2020, then the effects of the quarantine that started in the previous weeks is noticeable. By October rules of social restrictions were reduced due to the continuously falls of the lethality rate in the previously months. Following this loose on the restrictions, we face the growth of α and γ. This correlation reaffirms the impact of the social distancing, and, therefore, the importance of the stringency index, in the reality of the outbreak.

The rates of lethality (γ) peaks in the end of May, when the quarantine had just reached the length of ten weeks. This effect is due to the low capacity of the health system, that led to a overcrowding of ICU beds. The low availability of respiratory equipment and little testing also played a hole in the development of this scenario. After the peak, the lethality lowered until November. During the first months of 2021 the public and governmental perception was that the situation was under control, but, following the

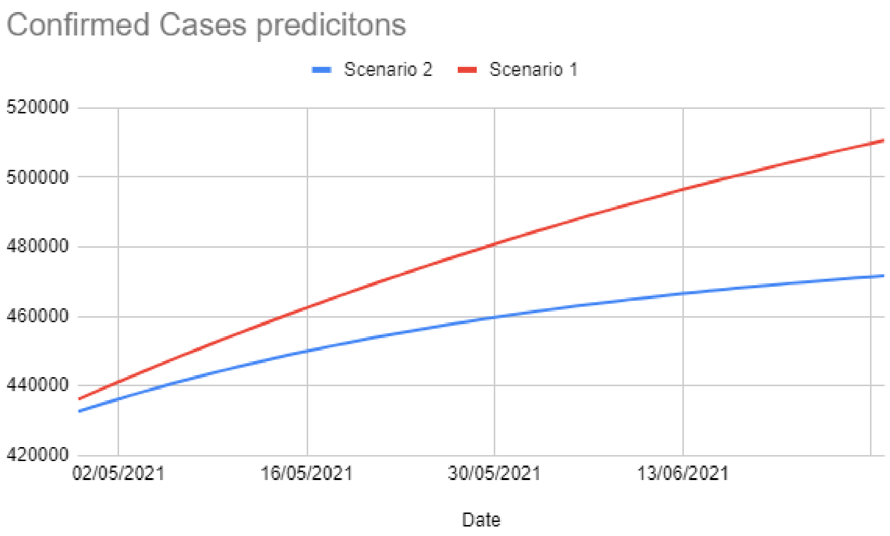

Figure 11: Confirmed cases predictions comparison between scenario 1 and 2

national holiday of Carnival (15, 16 and 17 of February, 2021), the infection rate started a new upraising that led to another ICU availability crisis, even though the infection rate reached only seventy per cent of what it was in May, 2020 [17]. This new near-collapse lead to a new increase of the lethality rate.

The recovery rate (β) evolves continuously until December,2020, it has peaks during the end of May and August during this stretch, reaching its highest values in December and November. In the end of December, 2020, there is a decrease in the parameter, reaching a very low value in late March, 2021. This observation leads, once more, to the understanding that loosening the social distancing measures in the beginning of 2021 was a hasty decision.

The basic reproductive number (R_0) varies from phase to phase as seen in Fig. 15 for the first run and Fig.16 for the second one. For a proper variation analysis of (R_0) in the second run a zoomed version of the original graph, shown on Fig.17 was plotted.

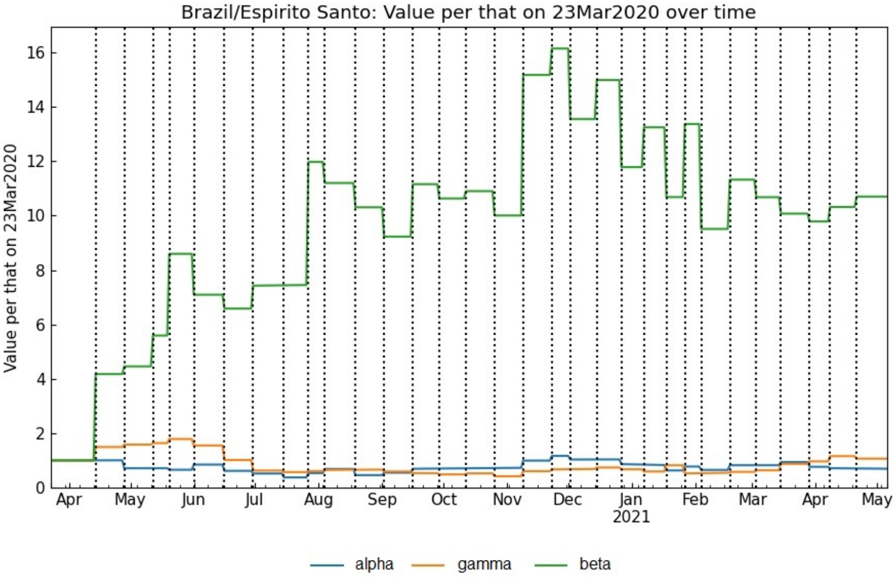

Figure 12: Rates of infection α, recovery β and lethality γ through time - Scenario 1

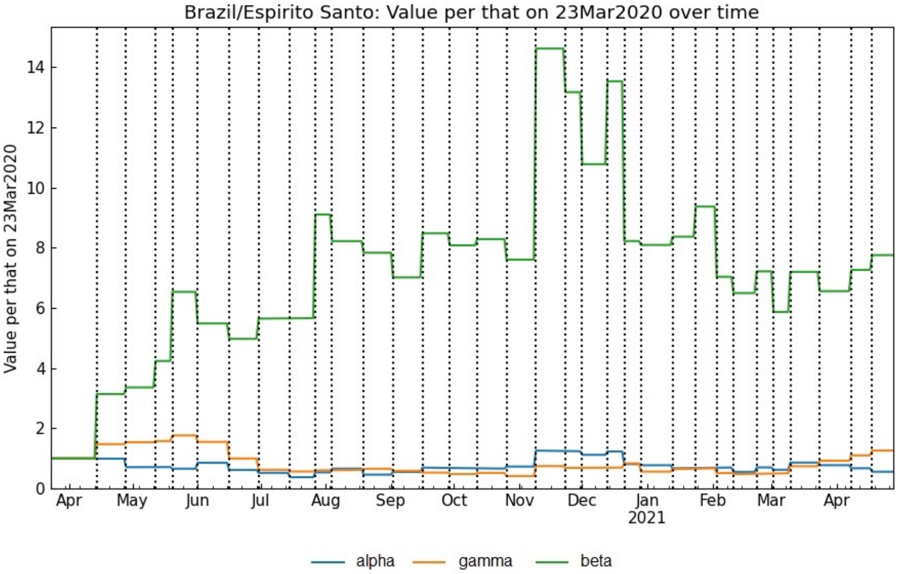

Figure 13: Rates of infection α, recovery β and lethality γ through time - Scenario 2

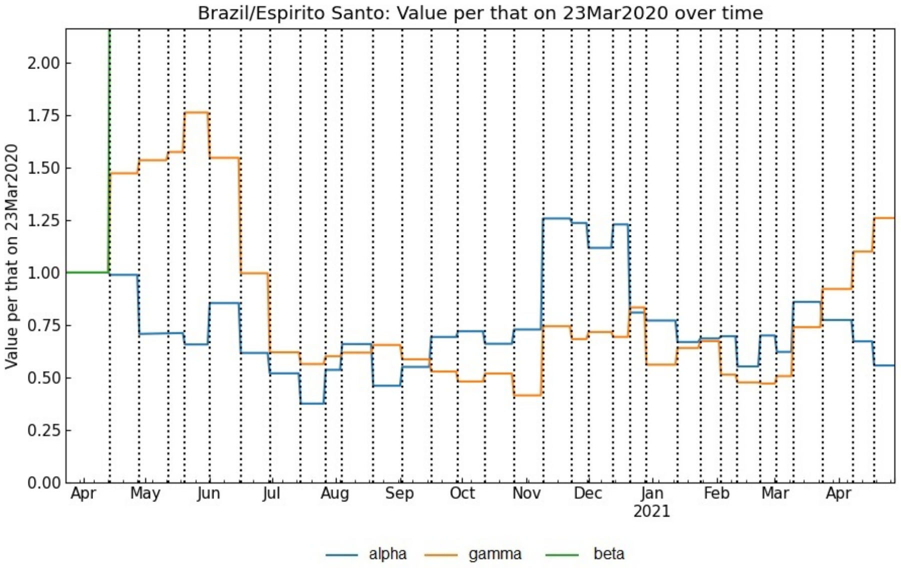

Figure 14: Rates of infection α, recovery β and lethality γ through time for Scenario 2, zoomed in for better analysis

The basic reproductive number value during a phase represents how contagious the disease was at that stretch. The high value is due the increase in the number of infected people in the beginning of the outbreak, once this number stabilises and the situation is more under control, (R_0) stabilises as well, but does not stop oscillating. The effects of the quarantine are visible with the big decrease between July and August. After the loose on the restrictions in the beginning of 2021, R_0 rises until the social distancing policies begin to harden again.

A complete graph for scenario 2 is plotted to better analyse the development of the variables. The graph is seen in Fig. 18. The number of susceptible and recovered individuals is plotted on the right y axis and the infected and fatal ones in the left y axis, this is done in order to proper visualise the graph since the values of S and R are greatly bigger than the others. It is clear when looking at the development of the infected numbers that the disease spreads in waves, this waves are created by the variations on social isolation and counter measures. The late apex of the infected number can be explained by the arrival of new variations of the virus in the state in mid March, 2021.

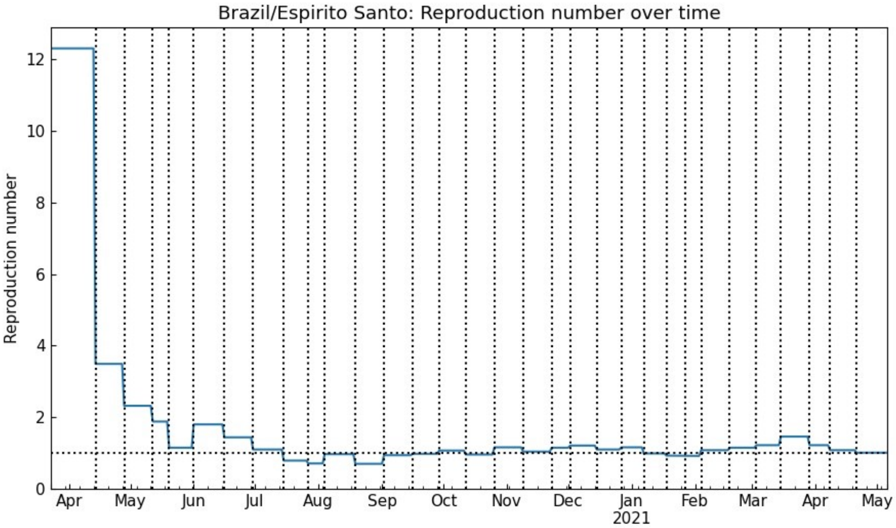

Figure 15: Basic Reproductive Number (R_0) for each phase through time in the first scenario

10. Conclusion and Future work

The objective is to understand and provide explanations regarding the use of Espírito Santo's COVID- 19 data and the non-pharmaceutical governmental social distancing policies during the outbreak. The use of a SIRD model, through the CovsirPhy library, allowed the simulation of the outbreak scenario and, by adjusting the parameters of the stringency index (I) within the model, more precise results were exposed. For this larger objective to be achieved the upload of the states COVID-19 panel was previously made. This achieved milestone enabled not only this research, but any other study that permeate Espírito Santos data on the pandemic.

With the presented results it was possible to link the government non-pharmaceutical official measures with the rates of infection (α), recovery (β) and lethality (γ). Although is hard to observe a specific link between one given measure and the change of the rates, given the complexity of the disease and the overwhelming variables, the effects of a group of measures, such as a full lockdown quarantine contemplating many of them at the same time, are clearly observable. It is clear now that these big measures have deep impact in the spread of the disease and its tool on the population. Granting all this, this research did not take in account the social and economic impacts of this

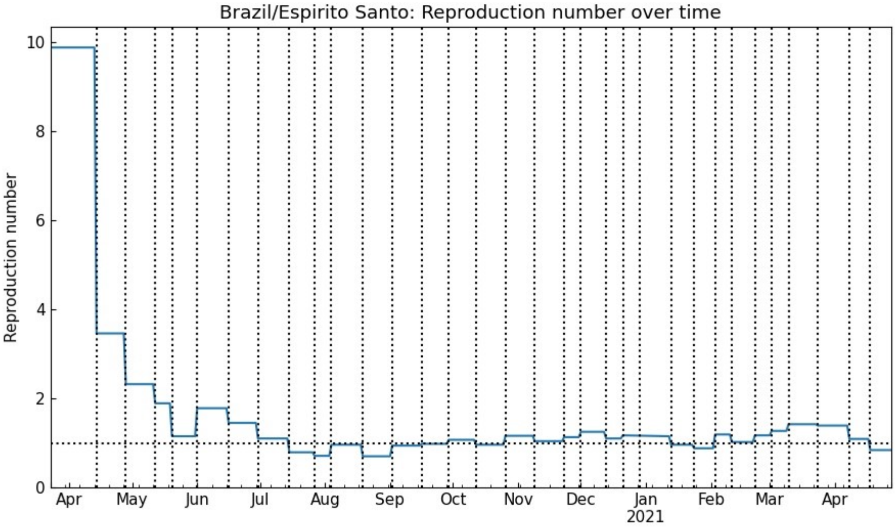

Figure 16: Basic Reproductive Number (R_0) for each phase through time in the second scenario

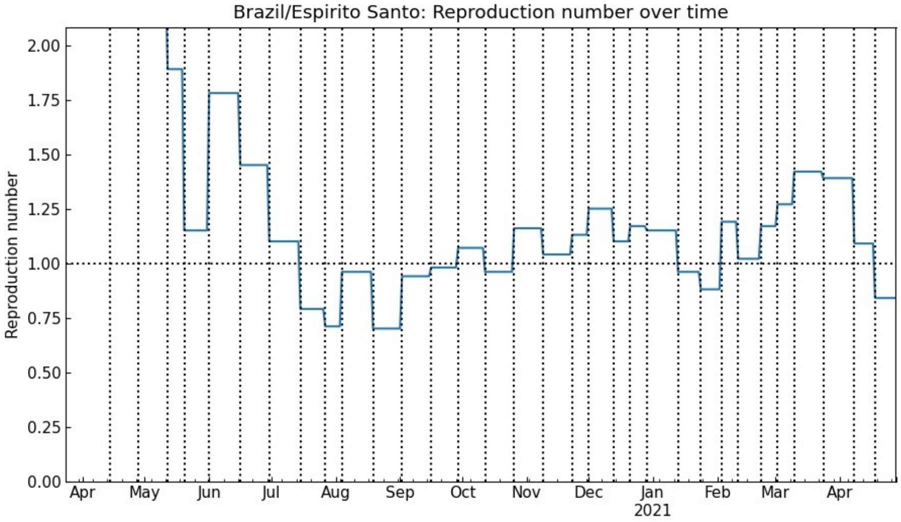

Figure 17: Basic Reproductive Number (R_0) for each phase through time in the second scenario, zoomed version

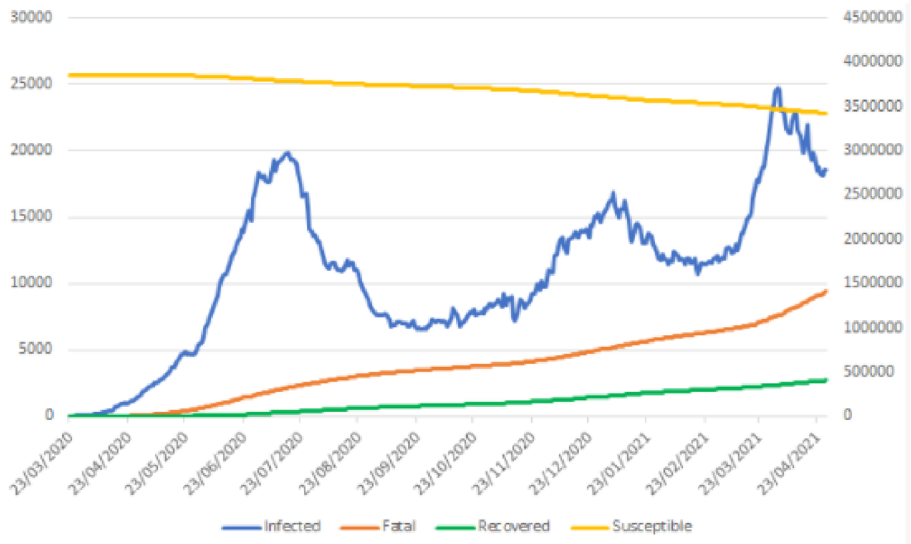

Figure 18: Complete graph for the scenario 2, with Recovered and Susceptible on the right y axis and Infected and Fatal on the left y axis.

measures.

Facing the comparison of the simulations having the same data source, however variations in its parameters for social-distancing, it becomes clear that, due to the fact that most of the counter measures to combat the pandemic are decisions of the state governments, Brazil has a big population, vast national territory and other geographical reasons, it is complex to define social-distancing parameters that represent the reality for the whole country as one. To dismember Brazil in states and using specific parameters when dealing with its COVID-19 data enables more precise results, therefore more accurate predictions.

During the development of this research new possible applications of this methodology appeared in the horizon. Replicating the process in a variety of states and then comparing the results would bring new light to the knowledge of which non-pharmaceutical decisions are more effective in the Brazilian context. It would also allow to compare the governments of different states under, not only raw numbers and public perception, but more detailed data. Unfortunately, the spectrum only reached the Espírito Santo state, although enhanced the visibility and transparency of the Brazilian data academically.

Looking at the results a distinct variable may have influenced the parameters of the outbreak. The available ICU bed at a given point in time might interfere deeply in the lethality rate (γ), not only on that given point in time, but also in the following weeks. With this given possibility, studies containing ICU beds availability, and how it affected the number of deaths, can bring a profounder comprehension of the pandemic.

Despite the fact that reinfection by COVID-19 is still not fully studied, it has been a clear fact that it happens. we believe that the development of a research making use of a SIR based model that is able to analyse and simulate data with this reinfection parameter would rise the accuracy of the predictions. The fact that the Brazilians not always complied with the governmental measures taking place also are not taking in account, the rates in which the population respected and followed the government restrictions and guidelines can be explored in future works.

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