DEVELOPMENT OF A PROBABILISTIC MODEL FOR QUANTITATIVE RISK ASSESSMENT OF COVID-19 IN BRAZIL

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ABSTRACT

We have developed a probabilistic model to quantify the risks of COVID-19 explosion in Brazil, which is the epicenter of COVID-19 in Latin America. By explosion, we mean an excessive number of new infections that would overload the public health system. We made predictions from July 12th to October 10th, 2020 for various containment strategies, including business as usual, stay at home (SAH) for young and/or elderly, flight restrictions among regions, gradual resumption of business and the compulsory wearing of masks. They indicate that: if a SAH strategy was sustained, there would be a negligible risk of explosion and the public health system would not be overloaded. For the other containment strategies, the scenario that combines the gradual resumption of business with the mandatory wearing of masks would be the most effective, reducing risk to considerable category. Should this strategy is applied together with the investment in more Intensive Care Unit beds, risk could be reduced to negligible levels.

1 INTRODUCTION

Brazil is the epicenter of coronavirus disease (COVID-19) in Latin America and is the second hardest hit country, with almost 2,5 million confirmed cases and more than 88,000 deaths by end of July 2020 (worldometers, 2020). Indeed, infected people have been confirmed in all the 5 regions: North (N), Northeast (NE), Central-West (CW), Southeast (SE), and South (S). The lack of efficient risk management and poor risk communication to the public, linked to other environmental, socio-economic factors (e.g. high proportion of young population, who are more exposed, and thus virus spreads faster; high population density in urban centers and 'favelas'; economical pressure to come back to business to avoid massive unemployment and starvation) make the perspectives for Brazil even more worrisome. In this context, this work provides useful results for developing more efficient risk management and communication in Brazil.

Since late March, when reports about SARS-CoV-2 (hereinafter, the term virus without specification refers to SARS-CoV-2) transmission patterns in Brazil started to emerge, many containment strategies have been discussed and implemented to control its spread until a vaccine is developed, licensed and manufactured. These actions include social isolation (for the purposes of this work, this is equivalent to Stay At Home (SAH) measures), vertical isolation (when SAH is applied only to the elderly), restrictions on business/studies/social activities (hereinafter, the term business refers to all of these three types of activities), gradual resumption of business, national flights restrictions and wearing of face masks. This work simulates each of these strategies, keeping all other things the same (*Ceteris paribus*) in order to track their effectiveness.

To assist policymakers in making decisions, many mathematical models have been proposed to describe and predict the evolution of number of infections and deaths

in Brazil either at regional or national level (Canabarro et al., 2020; Coelho et al., 2020; Costa et al., 2020; Crokidakis, 2020; Mellan et al., 2020; Savi et al., 2020). However, at the best of authors' knowledge, all these models are deterministic, i.e. the model inputs and outputs are single-point estimates, usually expected values, without proper treatment about the uncertainty. This limits the application of these outcomes because actual values may greatly vary around the expected measures. Thus, deterministic predictions may lead to imprudent decisions and actions by managers and society, and thousands of deaths as a result. In fact, a recent study highlights the importance of acknowledging uncertainty as a main component of risk of COVID-19 pandemic (Aven & Bouder, 2020).

On the other hand, our model is probabilistic in nature. The great advantage of probabilistic over deterministic approaches is that results show not only what could happen, but how likely each outcome is. In this way, one can measure and communicate uncertainty in results. This is the main characteristic of our model.

There are a few probabilistic COVID-19 models to predict cases in Brazil (Crokidakis, 2020; Martinez et al., 2020; Sousa et al., 2020). Similarly to our model, they structure the population in stages and have parameters that govern the transition from one stage to another, e.g. the infection rate governs the transition from susceptible to infected individuals (note: this rate should not be confused with the reproduction number (R), i.e. a dimensionless value that describes the number of secondary cases one case would produce; for more details see (Delamater et al., 2019)). In comparison to these models, another feature that makes ours innovative is how we treat the infection rate. In the aforementioned models, this parameter is assumed to be constant over time and, then, the number of infected grows exponentially and is unlimited until the end of the forecast, which causes results to be overestimated. To simulate containment scenarios, they

(Crokidakis, 2020; Martinez et al., 2020; Sousa et al., 2020) manually alter the infection rate and generate predictions.

Conversely, the approach considered in this work is grounded on the concepts of population ecology (H Resit Akçakaya et al., 1999), in which the virus dynamics can be described not only in terms of the host parameters, but also of those inherent to the virus itself. We aggregate in the model the concept of Density-Dependence (DD), which is the modification in the influence of any factor that affects the population growth as the population density changes (H Resit Akçakaya et al., 1999). In this sense, the population density of exposed susceptible people (i.e. the carrying capacity of the virus) decreases over time as the virus spreads. This happens because the harder the virus finds susceptible people to infect, the lower the infection rate.

Thus, our model includes two realistic features that the aforementioned approaches do not. First, for any containment scenario, as more people become infected, the susceptible population density decreases, and then does the infection rate. Secondly, to simulate different containment measures, we do not manually alter the respective infection rate, because we consider that containment strategies do not instantly reduce the infection rate since the start of the simulation. Instead, we consider that each containment strategy causes a reduction in the carrying capacity and, thus, accelerates the decrease in the infection rate over time. We perform this through Contest type DD modelling (H Resit Akçakaya et al., 1999), as we explain further.

A few more contributions are: (i) our model is structured by age groups (young and elderly) with different probabilities of fatality and/or infection, which allows to simulate specific containment strategies; (ii) it is a metapopulation model structured by 5 subpopulations, representing each Brazilian region, with different probabilities of fatality

and/or infection as well as different probabilities of dispersal between subpopulations; (iii) it is able to assess quantitatively the effectiveness of recent containment plans (e.g. (a) gradual resumption of economy; and (b) mass distribution and compulsory wearing of masks), no matter they are applied either in an isolated or integrated manner.

In this work, we use the well-known definition of risk as a measure of probability/frequency/likelihood and undesired consequences (CPR18E, 2005), PURPLE BOOK). More specifically, this work conducts a Quantitative Microbial Risk Assessment (QMRA), which is the formal process of estimating the probability of undesired consequences to humans due to exposure to one or more microbial pathogens (Duarte et al, 2019; Haas et al., 1999). The main objective of a QMRA is to predict relative risks for future scenarios and/or to evaluate the effectiveness of different containment measures.

Therefore, the aim of this paper is to develop an epidemiological probabilistic model for COVID-19 that overcomes the aforementioned drawbacks of other models and is tailored for a QMRA. To the best of our knowledge, this works conducts the first QMRA of COVID-19 in Brazil. We set out to answer the following questions in order to steer Brazilian policymakers on how to prioritize resources for designing containment scenarios:

- How many lives can we save and how many infections can we reduce until October 10th if we decide to implement a certain containment strategy?
- What is the probability of having a collapse in the Brazilian health system by October 10th for each containment scenario? Would a gradual economic

resumption plan be effective to reduce the risk of collapse? Is vertical isolation effective? What about Business as Usual (BAU) with the wearing of masks?

- Which regions are most at risk in the future? Which ones deserve the most effort to control the disease? What is the order of prioritization?
- What is the risk category for an integrated strategy where wearing of masks is mandatory for everyone out of home together with a gradual resumption of the economy? How many more Intensive Care Unit (ICUs) beds would it be necessary to invest, alongside with the integrated strategy, to reduce the risk to negligible levels?

The remainder of this work is structured as follows. First, we present the model structure and the assumptions, which is flexible in parameterization and can be used to simulate several containment scenarios. Next, we discuss the materials and methods to carry out a QMRA and explain how we consolidate and parameterize scenarios. Then, we present the model results for each scenario, compare them, answer the questions raised above, and discuss the advantages and limitations of the model. Finally, we draw some conclusions and propose suggestions for future works.

2 THE STRUCTURE OF OUR APPROACH AND ASSUMPTIONS

This section focuses on the structure of our approach, which concerns the arrangement of the equations and parameters that govern the models. In our model, we have a metapopulation (Brazil) divided into 5 subpopulations (regions) with potential for dispersal among them. Thus, we can predict the spatial structure of the infected population in Brazil over time. We subdivide Brazil into regions, instead of states, to keep the model and communication of risk simpler. A model that would represent dispersal among all the

26 states could become intractable, resulting in challenging risk communication to authorities as well as to the public.

Some models (Choi & Ki, 2020; Zhang et al., 2020) are tailored for estimating the reproduction number (R) of COVID-19, i.e. a dimensionless value that describes the number of secondary cases one case would produce. Thus, an outbreak is expected to continue if $R > 1$ and to end if $R < 1$. Although the R indicates, in a simple way, whether an outbreak will continue or not, estimating the R value is far from straightforward. According to (Delamater et al., 2019), the actual R value is affected by numerous biological, socio-behavioral, and environmental factors that govern pathogen transmission and, thus, is usually estimated by sophisticated mathematical models with many assumptions and sources of uncertainties, which are not communicated in the final R estimate. In the hand of experts, R can be a valuable concept. However, in the hand of policymakers and general public, who have not been trained in sophisticated mathematical techniques, it is easily misinterpreted and misapplied. Thus, we believe that a risk-based approach can better communicate predictions.

Our method allows for the quantification and categorization of the risk of explosion (i.e. the probability that the number of infected people surpasses a certain threshold within a short time interval, which would likely cause a collapse in the health system due to the lack of available IUCs. To understand the model's equations, one must first understand the definition of the risk of explosion and its categorization, as follows.

2.1 Risk of explosion and categorization

Risk categorization has been used in various fields of QRA to make risk communication easier (e.g. industrial QRA (CPR18E, 2005), ecological QRA (IUCN, 2001), microbial QRA for water safety management (WHO, 2016), microbial QRA of

schistosomiasis (Duarte et al., 2014). It transforms quantitative risk into qualitative risk categories. This is especially helpful for risk communication to the general public and politicians, who are mostly unfamiliar with quantitative risk language. Thus, we here propose four risk categories and the correct understanding of these is paramount to a correct interpretation of the results:

- CRITICAL RISK (CR): >50% probability of explosion within 21 days.
- HIGH RISK (HI): >20% probability of explosion within 28 days.
- CONSIDERABLE RISK (CO): >10% probability of explosion within 90 days.
- NEGLIGIBLE RISK (NE): <10% probability of explosion within 90 days.

The method for reaching the above categories is as follows. Quantitative risk has three dimensions: probability, undesired consequence, and time (Duarte et al., 2019; IUCN, 2001), and then we established bounds for these three dimensions in order to form a risk category. In our case, the undesired consequence for all categories is the explosion of the disease (many infected people in a short time period) in such a way that the health system is unable to serve all critical cases.

Brazil has only 16.3 IUC beds per 100,000 population (e.g. Germany has 33.9 per 100,000), and this is the main bottleneck in public hospital capacity for the treatment of COVID-19 (Beatriz Rache et al., 2020). Our model gives predictions in terms of infected people, $I(t)$, and not in number of critical cases in need of ICU beds. The available number of ICUs is 34,318 (Min. da Saude, 2020), and the proportion of infected people that

develop critical conditions, and then need ICU, is 2% (worldometers, 2020). Thus, it follows that:

$ICU\ capacity = 34{,}318 = (number\ of\ infected\ at\ time\ t) \times 2\%$. And, then, the explosion threshold is crossed when:

$$number\ of\ infected\ at\ time\ t \geq \frac{34{,}318}{0.02} = 1{,}715{,}900.$$

By means of Monte Carlo simulation, we generate 10,000 predictions for each day, *t*, from July 12th 2020. From that sample of results, for each *t*, we calculate the frequency per time-step that the prediction crosses the explosion threshold, which yields an estimate of the probability of explosion at *t*.

With respect to the time dimension, assuming that critical cases need around 21 to 28 days to be discharged (based on the opinion of an infectious disease doctor at the Santa Lúcia Hospital in Brazil (Hospital Santa Lucia, 2020), we then define 21, 28, 90 and 90 days for CR, HI, CO and NE respectively. Regarding the probability dimension, the bounds are the same as those in the red list categories of the International Union for the Conservation of Nature (IUCN) (IUCN, 2001) (i.e. >50%, >20%, >10% and <10%, respectively for CR, HI, CO and NE).

Note that the proposed categories do not consider the probability of massive deaths as is common in industrial QRA. Our categories seek indicating the risk of overloading the health system, which is associated not only with deaths, but also with high numbers of sick people and substantial socio-economic costs. Conversely, risk categories based on deaths could neglect very infectious diseases with low rates of death, although the health system would be overloaded. Thus, we preferred to consolidate our undesired consequence in terms of infections, as these categories can serve as a proxy for

QMRA of future pandemics and these will not neglect infectious diseases with low fatality rates.

2.2 The model

Our model also allows for fast simulation and generation of results for varying scenarios regarding different containment measures, thus assessing their effectiveness in terms of reducing number of infections, deaths and, then, risk. Yet, the model is composed of submodels that represent regions, and thus it is possible to identify the subpopulations, where SARS-CoV-2 might persist, and hence this help decide which areas should be prioritized.

We separate each subpopulation into three states: Susceptible; Infected; and Recovered. When Susceptible individuals get Infected, they may either become Recovered or die (represented by the “Deaths Counter” box) in Figure 1, which shows a simplified diagram of our model. After recovery, we assumed that a person cannot get Infected again, although it is still unknown if a Recovered person gains immunity. Studies have showed that after an infection, a small production of antibodies can suffice to almost certainly guarantee immunity to the disease, however, immunity may dramatically fall 90

days since recovery (Long et al., 2020; Robbiani et al., 2020). We assumed that recovered people will stay immune over the 90 days forecasted period.

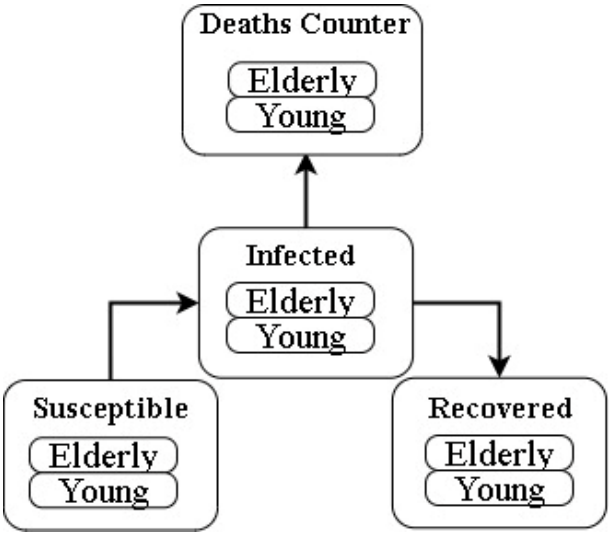

Figure 1. Simplified schematic representation of Covid-19 dynamics in human population.

Let $N_s^i(t)$ denote the number of people in state s in region i at time t. The structure of each subpopulation is: young susceptible $(s = 1)$, young infected $(s = 2)$, young recovered $(s = 3)$, elderly susceptible $(s = 4)$, elderly infected $(s = 5)$ and elderly recovered $(s = 6)$. Therefore, the model projects the number of infected people $(I^i(t) = N_2^i(t) + N_5^i(t))$ for each region i for a period of time of 90 days, from July 12th, 2020 to October 10th, 2020.

In ecology, resources are often limited in a habitat. For instance, plants in a garden compete with each other for soil nutrients, fishes in a lake compete for food. Analogously, in our model SARS-CoV-2 in Brazil compete for exposed susceptible people to infect, survive and reproduce. The more infected people, the less susceptible ones and the less resources available for SARS-CoV-2. To model the infection rate as a function of the number of infected at time t, we use the Contest type of DD that occurs when the resources are shared unequally and randomly amongst the individuals, leading to survival

and reproduction of some at the expense of others (H R Akçakaya & Root, 2013). In other words, the rationale for that assumption is that, the lower the size of susceptible population exposed to the virus, the lower the infection rates. In this situation, there would be less resources allowing the virus to spread as it starts to compete for susceptible bodies to continue reproduction, until a point where the host population reaches herd immunity, making the spread of disease from person to person very unlikely.

We assume that competition among viruses is unequal (Contest type) because susceptible hosts (resources) are divided unfairly among viruses, as viruses that are in exposed/unprotected hosts are more likely to find other susceptible ones than those that are in unexposed/protected hosts (e.g. staying at home, wearing face masks). This is modeled through the following equation:

$$\beta^i(t) = \frac{\beta^i_{max} \cdot \mathrm{K_k} \cdot S^i}{\beta^i_{max} \cdot I^i(t) - I^i(t) + \mathrm{K_k} \cdot S^i} \qquad \text{(Equation 1)}$$

where β^i_{max} is the maximum infection rate observed in region i, $\mathrm{K_k}$ is the scenario-specific exposure index; and S^i is the region-specific susceptible population. $\beta^i(t)$ in turn determines the stage-specific infection rates $a_{22}(t)$, $a_{55}(t)$, $a_{25}(t)$ and $a_{52}(t)$ (see Table 2).

DD approach is based on ecological modelling (H R Akçakaya & Root, 2013). For example, other models that use Contest type for DD are: European mudminnow in the Australia Floodplain, Trout cod in Southeast Australia, Sand-lizard in Central

Sweden, Helmeted honeyeater in Australia and Florida key deer (H Resit Akçakaya et al., 2004).

The following model represents one replication that specifically predicts the population for each region from a time step t to $t+1$ (the variables of the model are described in Table 1):

$$\begin{bmatrix} N_1^i(t+1) \\ N_2^i(t+1) \\ N_3^i(t+1) \\ N_4^i(t+1) \\ N_5^i(t+1) \\ N_6^i(t+1) \end{bmatrix} = \begin{bmatrix} a_{11} & 0 & 0 & 0 & 0 & 0 \\ 0 & a_{22}^i(t) & 0 & 0 & a_{25}^i(t) & 0 \\ 0 & a_{32} & a_{33} & 0 & 0 & 0 \\ 0 & 0 & 0 & a_{44} & 0 & 0 \\ 0 & a_{52}^i(t) & 0 & 0 & a_{55}^i(t) & 0 \\ 0 & 0 & 0 & 0 & a_{65} & a_{66} \end{bmatrix} \times \begin{bmatrix} N_1^i(t) \\ N_2^i(t) \\ N_3^i(t) \\ N_4^i(t) \\ N_5^i(t) \\ N_6^i(t) \end{bmatrix} - \begin{bmatrix} 0 \\ \alpha_2 * N_2^i(t) \\ 0 \\ 0 \\ \alpha_5 * N_5^i(t) \\ 0 \end{bmatrix}$$

where a_{su} is the transition rate from state u to state s, and a_{uu} is the permanence rate in state u ($u, s \in [1,6]$). For instance, a_{32} is the transition rate from state 2 (young infected) to 3 (young recovered), i.e. the recovery rate for young, while a_{11} is the permanence rate in state 1 (young susceptible); α_2 and α_5 are the mortality of infected young and elderly individuals respectively.

Some transition rates (i.e. a_{11}, a_{22}, $a_{32}, a_{33}, a_{44}, a_{65}, a_{65}$) are random variables that follow PDFs with parameters that are constant over time; therefore, a value is randomly selected from the associated PDF for an iteration and kept constant for the entire 90 time-step period. On the other hand, the stage-specific infection rates (i.e. $a_{22}(t), a_{25}(t), a_{52}(t), a_{55}(t)$) are nonparametrical stochastic processes because they are random and dependent both on the interaction among individuals and on the susceptible

population exposed to the infection. Therefore, their PDFs change over time and a value is randomly selected from the associated PDF at *t*.

Next, we update the $N_s^i(t+1)$ estimates in order to account for the dispersal of individuals by adding the number of entries and subtracting the number of exits for each subpopulation:

$$\begin{bmatrix} N^{EU}(t+1) \\ N^{NA}(t+1) \\ N^{LA}(t+1) \\ N^{AS}(t+1) \\ N^{AF}(t+1) \\ N^{OC}(t+1) \end{bmatrix} = \begin{bmatrix} N'^{EU}(t+1) \\ N'^{NA}(t+1) \\ N'^{LA}(t+1) \\ N'^{AS}(t+1) \\ N'^{AF}(t+1) \\ N'^{OC}(t+1) \end{bmatrix} + [M]_{6x6} \begin{bmatrix} N'^{EU}(t+1) \\ N'^{NA}(t+1) \\ N'^{LA}(t+1) \\ N'^{AS}(t+1) \\ N'^{AF}(t+1) \\ N'^{OC}(t+1) \end{bmatrix} - [M]_{6x6}^{T} \begin{bmatrix} N'^{EU}(t+1) \\ N'^{NA}(t+1) \\ N'^{LA}(t+1) \\ N'^{AS}(t+1) \\ N'^{AF}(t+1) \\ N'^{OC}(t+1) \end{bmatrix},$$

where $[M]_{6x6}$ is a matrix comprising the dispersal rates (m_{ij}) of individuals from region j to region i. The dispersal rates, alongside with other parameters, are shown in Table 2 and the rationale for estimating them are presented in section 4.3 (Parameterizing the model and initial conditions).

Table 1. Definition of the model variables.

Variable	Symbol	Description
Number of infected individuals in region *i* at time *t*	$I^i(t)$	Assessment endpoint described as minimum, average and maximum values, with a 95% confidence interval
Region-specific infection rate	$\beta(t)^i$	Number of expected new cases of infection caused by one infected person in each region *i* per week (see Equation 1)
Region-specific standard deviation of the frequency of infection	σ^i	Standard deviation of the infection rate

Variable	Symbol	Description
Scenario-specific exposure index	K_k	Portion of the susceptible population actually exposed to the virus in each scenario *k*
Region-specific susceptible population	S^i	Number of individuals that are not infected with COVID-19 per region and may become infected
Region-specific fatality rate	α_2^i, α_5^i	Expected proportion of individuals that die because of the infection per region, daily, for young ($s = 2$) and elderly ($s = 5$)

Table 2. Definition of the model parameters.

Parameter	Symbol	Assumptions (Data Source or Rationale)	μ	σ
Age-specific exposure	c_{su}	The probability of the virus being transmitted among young is higher than among elderly (transmission from state *u* to state *s*) (More details on Exposure assessment section).	$\begin{cases} c_{22} = 1 \\ c_{25} = c_{52} = 0.5 \\ c_{55} = 0.25 \end{cases}$	
Time to recover	T_{rec}	Most individuals take two weeks to recover (LAN et al., 2020).	14 days	
Permanence rate in the susceptible stage	$\begin{cases} a_{11} \\ a_{44} \end{cases}$	The proportion of infected is very little, so there is a slight decrease in the susceptible population as more people get infected (educated guess).	0.99	0.01
Stage-specific infection rates	$\begin{cases} a_{22}^i(t) \\ a_{55}^i(t) \\ a_{52}^i(t) \end{cases}$	Directly proportional to the infection rate and corrected by the age-specific exposure. More details on Frequency assessment section (Note that $(a_{52}^i(t) = a_{25}^i(t))$	$\begin{cases} c_{22}(\beta^i - 1) + 1 \\ c_{55}(\beta^i - 1) + 1 \\ c_{25}(\beta^i - 1) + 1 \end{cases}$	$\begin{cases} c_{22}\sigma^i \\ c_{55}\sigma^i \\ c_{25}\sigma^i \end{cases}$
Recovery rate	$\begin{cases} a_{32} \\ a_{65} \end{cases}$	More details on Frequency assessment section; $\omega_{rec} = 1/T_{rec}$ (LAN et al., 2020).	$\begin{cases} \omega_{rec}(1 - \alpha_2) \\ \omega_{rec}(1 - \alpha_5) \end{cases}$;	
Permanence rate in the recovered stage	$\begin{cases} a_{33} \\ a_{66} \end{cases}$	The probability of a recovered individual being re-infected is zero (LAN et al., 2020).	1.0	
Dispersal rate of individuals among regions	m_{ij}	More details on Parameterizing the model and Initial conditions section	$0.3 \cdot \exp(-D_{ij}^{0.8})$	
Threshold for explosion	I_{exp}	Explosion threshold (new infections since the initial time-step)(MIN. DA SAUDE, 2020; WORLDOMETERS, 2020)	1,715,900	

2.3 QMRA methodology

The model presented was used to conduct a QMRA for COVID-19 by following the same general steps proposed by (Duarte et al., 2019): (i) characterize the problem; (ii) describe the scenarios (SCNs); (iii) parameterize the model and initial conditions; (iv) assess frequency; (v) assess exposure; and (vi) quantify and categorize the risks. Each of these steps generates a specific result of the QMRA and, then, the Results section is structured in this order. This methodology has already been applied to run a QMRA for schistosomiasis disease (Duarte et al., 2014).

RAMAS Metapop v.6.0 software (Akçakaya and Root, 2013) was adopted for running the simulations with 10,000 replications. This software is not itself a model, but a computational tool for constructing a metapopulation approach and running probabilistic simulation via the Monte Carlo method. We share all the model files in RAMAS format (Siqueira et al., 2020) .

3 RESULTS

3.1 Characterizing the problem

We aim at assessing quantitatively the risks of SARS-CoV-2 in order to provide health managers in Brazil with useful information about the dynamics of the disease under several control strategies. To ensure that the results of this study would meet managers' needs, we chose as assessment endpoints: (i) the number of infected people; (ii) and the number of deaths. Moreover, we provide results as PDFs for those endpoints over time, with an average value and a confidence interval (CI).

This QMRA is intended to be conservative in the sense that it does not underestimate risks. Then, whenever different sources provided different parameters

estimates for the PDF that governs a transition rate, a_{su}, then we considered the most conservative ones. More specifically, the outputs of this QMRA are as follows: (i) prediction of the infected subpopulation over time for each region and, then, for Brazil (metapopulation) over 90 days; (ii) prediction of the cumulative number of deaths in Brazil over 90 days; (iii) risk curves of explosion; (iv) time to explosion; (v) risk categorization; and a (vi) comparison of these results for all scenarios defined in the next section.

Data regarding the number of infected people for each day, from Mar 28th 2020 to Jun 2nd 2020, for each FU, was gathered from the public database managed by the (Min. da Saude, 2020) BHM, and then grouped into regions. The processed data (grouped by regions) are available in Appendix, Table A1.

3.2 Description of scenarios

It is quite intricate to predict/assess all the potential events (e.g. meteorological and environmental conditions, numerous control strategies, various novel medical tools, changes in hygiene and cleaning culture, transportation restrictions in all modes, and events like virus mutation) that might occur in the future and influence SARS-CoV-2 transmission. Thus, our model does not aim to be precisely predictive, only descriptive.

In this context, we defined five SCNs in Table 3. SCN-1 is the benchmark, while SCN-0, SCN-2, SCN-3, SCN-4 and SCN-5 represent the isolated application of each of the most common containment strategies under discussion. This allows us to track which strategies are the most effective in terms of reducing infections, deaths and risk of explosion when compared to SCN-1. Lastly, SCN-6 is the integrated strategy SCN-3+SCN-4.

Table 3. Description of scenarios

Scenario	Description
SCN-0 (stay at home)	Similar to what had been done from March 28th to June 21st, i.e.: business restricted to only the essential (e.g., grocery stores, drugstores), social isolation and flight restrictions; wearing of masks: mandatory for everyone out of home, but there are great levels of indiscretion by population, since there are no penalties well defined by law and police oversight is almost nil.
SCN-1 (business as usual)	Business as usual (as before COVID-19); no flight restriction; *Ceteris paribus* SCN-1 SCN-0.
SCN-2 (flight restriction)	100% national touristic flights canceled; *Ceteris paribus* SCN-1.
SCN-3 (gradual resumption of business)	Gradual resumption of non-essential business in 5 steps (30%, 47.5%, 65%, 82.5% and finally 100% of the business as usual), during the next 15, 30, 45, 60 and 75 days respectively); *Ceteris paribus* SCN-1.
SCN-4 (mandatory wearing of masks)	Mandatory wearing of surgical masks (Leung et al., 2020), with penalties well defined by federal law and intensive police oversight; *Ceteris paribus* SCN-1.
SCN-5 (vertical isolation)	Only the young in the business as usual, while the elderlies stay at home; *Ceteris paribus* SCN-1.
SCN-6 (integrated strategy)	SCN-3 and SCN-4 applied together.

3.3 Parameterizing the model and Initial Conditions

Table 1 and Table 2 summarized the variables, parameters and initial conditions of the model. The daily infection rate and fatality rate per age class can be estimated from data made available by the BHM (Min. da Saude, 2020); the mean incubation and transmission period (Lauer et al., 2020); the time taken to recover (Lauer et al., 2020); and the proportion of the young and elderly infected (IBGE, 2020).

However, there is still a lack of scientific information, due to the unprecedented characteristic of the disease. Thus, we estimated two parameters of the model via conservative educated opinion of the authors: the permanence rate in state 2 (young susceptible); and the permanence rate in state 4 (elderly susceptible) (see Table 2 for the rationale and assumptions regarding these parameters).

Some parameters were estimated using a mean value and others a mean and standard deviation (SD) (μ and σ columns in Table 2 respectively). To make the latter stochastic, we consider that they follow a Normal distribution. One can make good use of a Gaussian approach in the vital rates of biological models because there is a reasonable reason for random values not to be too far away from average, i.e. there are biological limitations preventing very large deviations and natural forces from equilibrium that bring vital rates back to their average values. For probabilistic simulation, RAMAS converts the parameters of a Normal distribution into the corresponding Lognormal counterpart, which avoids bias resulting from truncation because all parameters are greater than zero.

We model the migration rates among regions as a function of the distance between them, i.e. the migration rate between regions *i* and *j* is defined as:

$$m_{ij} = a \cdot \exp\left(\frac{-D_{ij}^{c}}{b}\right) \qquad \text{(Equation 2)}$$

where a, b, c are constants, and D_{ij} is the distance between *i* and *j*. This implies that, the farther two regions are, the lower the migration rates between them. Note that the results of the function are symmetrical, i.e. $m_{ij} = m_{ji}$. This parameter will mainly influence the scenarios where flights are restricted (SCN-0 and SCN-2) and it is expected that such restrictions will reduce the final number of infected population. However, we consider the beneficial effect of such restrictions from a macro point-of-view only, that is, an infected person in region *i* will not carry the virus to a region *j*. We do not

consider the beneficial effect that flight restrictions would cause in reducing the transmission inside airplanes and airports (micro point of view), where we would need to understand the dynamics of the transmission inside crowded and closed places, something that is out of the scope of this paper.

Although the current proportion of infected individuals is very low (around 1%), we estimate the initial number of susceptible individuals by subtracting the number of infected individuals for each region and age group from the total population.

3.4 Frequency assessment

When exposed to infected individuals, a susceptible individual may get infected, in accordance with an infection rate. The daily infection rate, β^i, can be estimated by processing the data on the daily number of confirmed cases in each state provided by BHM (Min. da Saude, 2020); see Table A1 (Appendix). To that end, we grouped states into regions, and calculated the infection rate in each region by dividing the number of accumulated infections in $t + 1$ by the number of infections in t. From this sample of values, we computed the mean (μ) and SD (σ) in each region and checked if there were outliers outside a 99.7% CI ($\mu \mp 3\sigma$). If there were outliers, we calculated μ and σ and checked for outliers again. We repeated this process for each region until there were no more outliers in the sample. From the final sample of each region, we estimated the mean, SD, and maximum (β^i_{max}) values of β^i (see Table 4).

Table 4. Daily infection rate (mean and standard deviation) for each region.

	Infection rate		
Subpopulation	Mean	Maximum	SD
North	1.0634	1.1575	0.0400
Northeast	1.0656	1.1772	0.0404
Central-west	1.0580	1.1151	0.0200
Southeast	1.0452	1.1117	0.0235
South	1.0446	1.1056	0.0215

After an individual gets infected, (s)he may either die or recover. We estimated the fatality rate (α^i) (i.e. the rate at which infected individuals may die) per day, dividing the number of accumulated deaths by the number of accumulated infections at a time *t*. Similarly to the infection rate, we calculated the mean and SD of the fatality rate in each region and removed the outliers. To distinguish the fatality rates of young (α_2^i) and elderly (α_5^i), it was assumed that 71.4% of the deaths occurred to elderlies, and 29.6%, to young (Poder360, 2020). It can be expressed as: $\alpha_2^i = 0.296 \cdot \alpha^i$; $\alpha_5^i = 0.714 \cdot \alpha^i$.

The recovery rates (a_{32}, a_{65}) (i.e. the daily transition rate from infected to recovered) can be estimated based on the incubation and transmission period of those who develop symptoms. A study suggested that transmission of SARS-CoV-2 also occurs during the incubation period (Mellan et al., 2020). Thus, we considered the recovery time as the sum of incubation and transmission intervals. According to (Lauer et al., 2020), under conservative assumptions, recovery lasts 14 days. Thus, after 2 weeks, it is highly unlikely that an infected individual would still be in the transmission period. This is also

in accordance with, and well supported by, the recommendation of the U.S. Centers for Disease Control and Prevention for the period of active monitoring of infected people (14 days = 2 weeks) (WhiteHouse, 2020). Thus, we estimated the mean recovery rate as $\alpha_{32}^{i} = \left(\frac{1}{14\ days}\right) * (1 - \alpha_{2}^{i})$, for the young individuals (note that the same can be done for the elderly, by using α_{65}^{i} and α_{5}^{i}).

3.5 Exposure assessment

Human exposure to SARS-CoV-2 mostly occurs when people go out of home for business. Since March 28th (G1, 2020) until June 21st (AgenciaBrasil, 2020) all the Brazilian states had only the essential business running and most people have stayed at home; we call this as SAH strategy (SCN-0). Obviously, this strategy is not sufficient to reduce exposure to zero, mainly because the essential business have been still working and/or because part of the population did not take the strategy seriously. Thus, from Mar 28th to Jun 21st, the exposed susceptible population has been reduced to some percentage (greater than zero) of the total susceptible population due to this SAH strategy. Henceforward, when we say that there is K_k of exposure index in a scenario *k*, it means that K_k of the susceptible population is exposed to the virus. In the BAU scenario (SCN-1), the exposure was set to be 100% because it is our benchmark ($K_1 = 100\%$).

To determine this percentage for SCN-0, we proceeded as follows. First, we have almost every parameter needed to simulate SCN-0, except for the exposure index (i.e. portion of the susceptible population exposed to the virus).

The SCN-0 model was calibrated through trial-and-error problem-solving. The simulation was repeated over various attempts until the real values of infected people were all within the predicted 99.3% confidence interval (i.e. the region bounded by the

boxplots in Fig 2A). In this way, we obtained a $K_0 = 12.5\%$ in a SAH scenario. Note that the registered deaths are also within the boundaries of the simulated results (Fig. 2B).

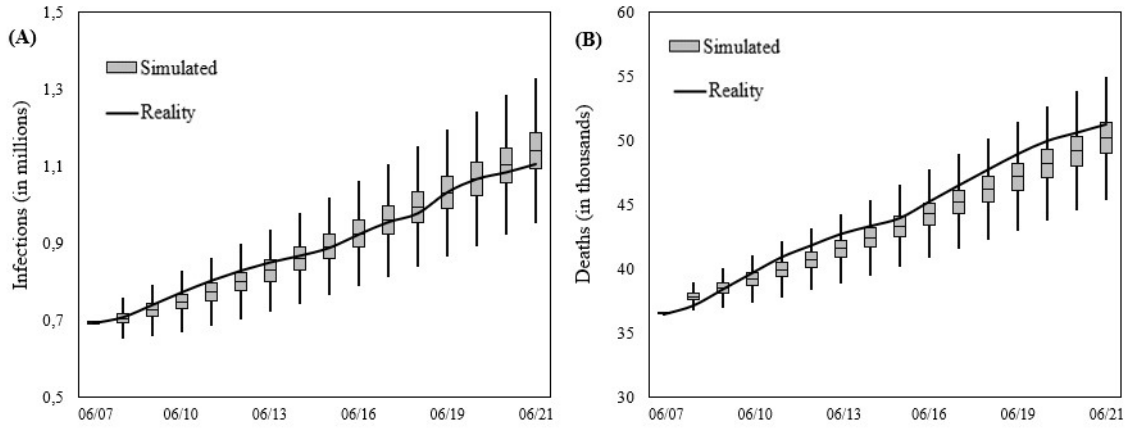

Figure 2. Calibration procedure of the model for a SAH scenario for the period June 7-21 for infections (A) and deaths (B). The line represents the registered values and the boxplots contain the simulation results.

SCN-2 considers BAU as in SCN-1 and, thus, $K_2 = K_1 = 100\%$. For SCN-3, which represents a gradual return to BAU, we considered that initially, $K_3 = 12.5\%$, and then this percentage increases by 17.5% every 15 days, until reaching the BAU scenario, $K_3 = 100\%$.

Finally, SCN-4 considers wearing of masks by all the population during business time. The exposure index was based on a study that evaluated the effectiveness of Surgical Face Masks (SFM) in reducing the detection of coronaviruses, influenza viruses and rhinoviruses in exhaled breath and coughs of children and adults with acute respiratory illness (Leung et al., 2020). The results showed that SFMs could prevent transmission of these viruses from symptomatic individuals. They estimated the efficacy of SFMs in reducing respiratory virus frequency of detection and viral shedding in respiratory droplets (aerodynamic diameter > 5 μm) and aerosols (aerodynamic diameter ≤ 5 μm) of

symptomatic individuals. We treated the reduction in the frequency of detection as a measure of reduction in exposure. For coronavirus, in a sample of 17 participants, wearing SFM reduced exposure to 0.09 for droplets particles and to 0.04 for aerosols. There is still no consensus in the literature on how much more pronounced is, at population-level, the transmission of SARS-CoV-2 through droplets as compared to transmission through aerosols. We treat both modes of transmission with even weight and use the arithmetic mean to estimate the average reduction in the exposure by the wearing of SFMs. The arithmetic mean would indicate that, for coronaviruses, the wearing of SFM reduces exposure to 6.5%, but the sample of participants infected by human coronavirus (n = 17) was too small. Thus, for a conservative approach, we used results from the total sample (n = 123) of individuals infected with at least one of the aforementioned respiratory viruses, which indicates a 20% exposure reduction for influenza and 46% for rhino. Thus, we assumed the average exposure index between over the three types of virus, resulting in $K_4 = 24\%$. The results of the exposure assessment can be seen in Fig. 3.

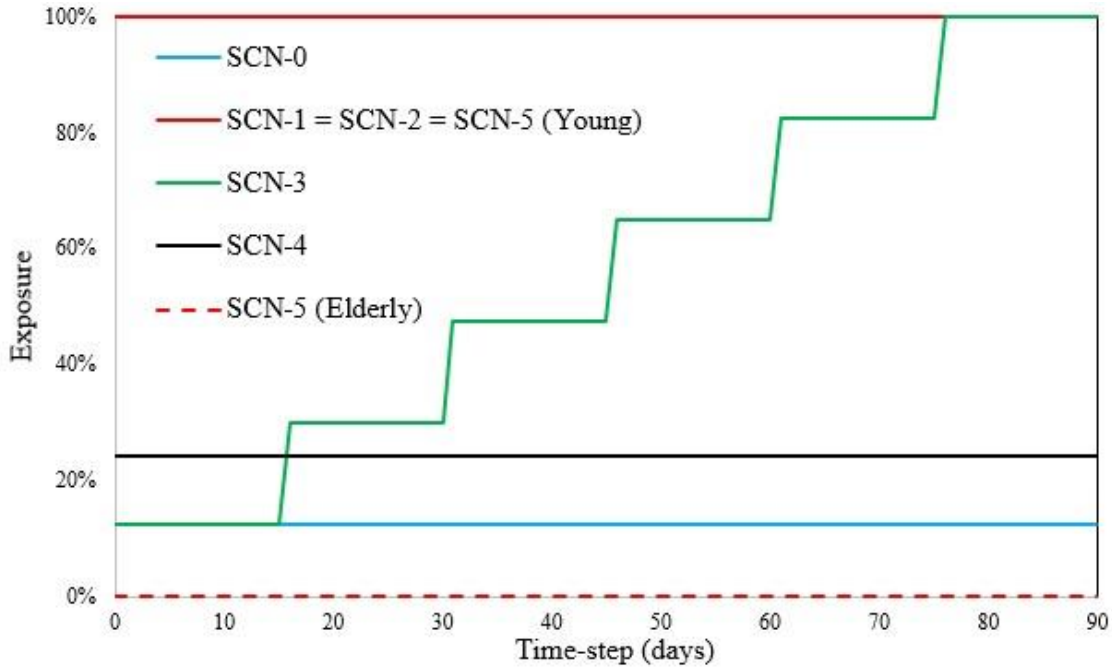

Figure 3. Summary of exposure assessment for each SCN.

We consider young people spend more time on business, having a higher probability of infecting another individual or being infected. We assumed that, in a BAU scenario, young people do business full time (8 hours per day), while elderly only half-time (4 hours per day). Thus, the infection rates are age-specific, i.e. the probability of a young person infects another young is two times higher than an elderly infecting another elderly (see Table 2).

3.6 Quantification and categorization of risks

In this section, the main risk results of each scenario are presented and compared. Fig 4 illustrates the efficiency of each strategy and should be compared against the benchmark SCN-1 in terms of: (A) projection of the accumulated number of infected; (B) projection of the accumulated number of deaths; and (C) Cumulative Distribution Function (CDF) for the time to explosion, and the median time for the explosion is highlighted in brackets.

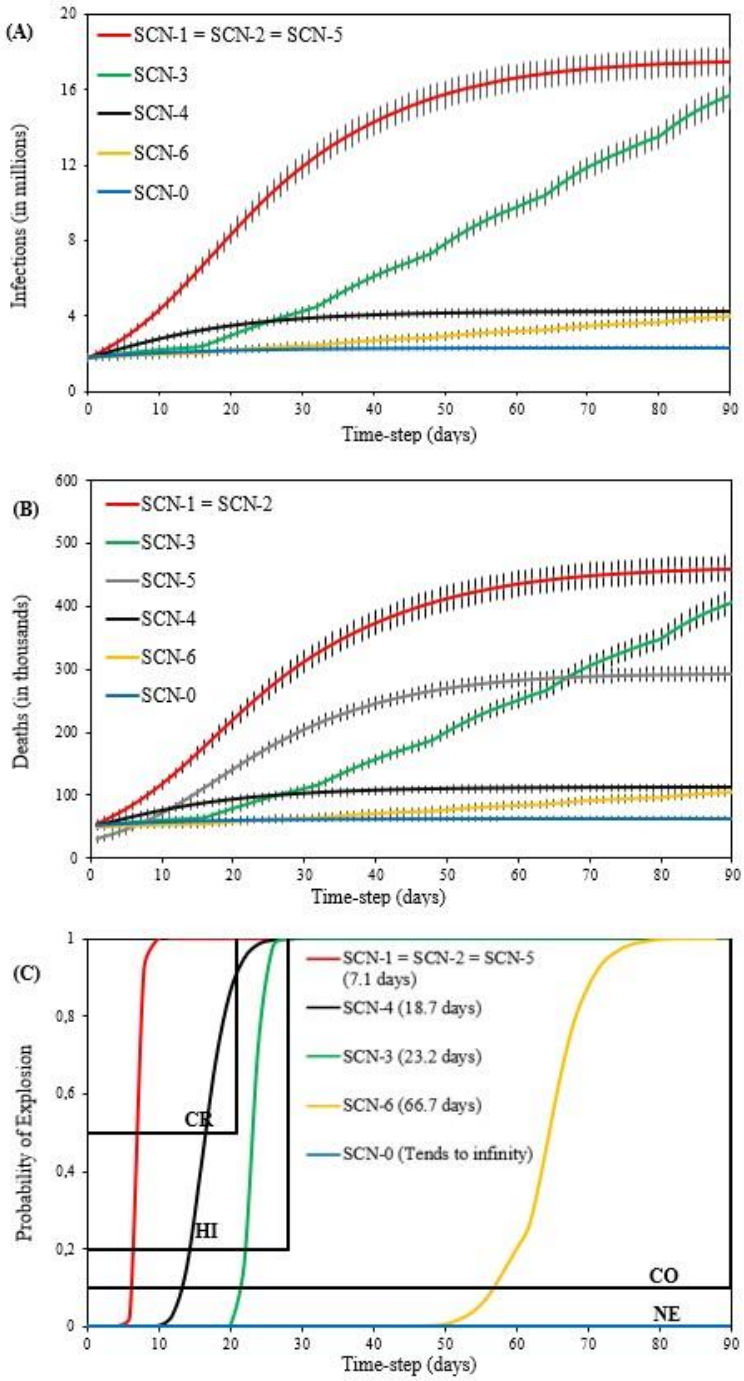

Figure 4. (A) Number of infected individuals in Brazil over time; (B) Death toll in Brazil over time; (C) CDF of the time to explosion (the median time to explosion is the value between parenthesis). (CR = Critical Risk; HI = High Risk; CO = Considerable Risk; NE = Negligible Risk).

In Fig. 4A and 4B, the results for each scenario are presented within a 68.3% CI ($\mu \mp \sigma$), where the lines represent the expected values and the vertical bars the CI.

Regarding the risk curves (Fig 4C), each point can be interpreted as "there is a Y% probability that the number of new infections will reach the explosion threshold by time-step X". Based on these results, one can categorize the risks associated to each scenario: Negligible (NE) for SCN-0, High (HI) for SCN-3 and Critical (CR) for SCN-1, SCN-2, SCN-4 and SCN-5. Note that only the SCN-0 has a 0% risk of explosion.

Table 4 summarizes the results. The main outputs of the model are in the table columns, while the lines represent the comparison of each scenario against the benchmark (in the first line). Values with + or – symbol are interpreted as an efficiency index of each strategy in reducing expected number of infected people and death toll, and increasing the median time to explosion (i.e. the time at which the explosion risk is 50%). A zero value means that there is no difference when compared to the benchmark. The scenarios are ranked according to the risk categories, from worst (CR) to best (NE).

Table 5. Summary of the results for each SCN.

	Expected Infected Population (million)	**Expected Death Toll (thousands)**	**Median Time to Explosion (days)**	**Risk Category**
Benchmark: SCN-1 (business as usual)	17.5	460	7.1	CR
SCN-5 (vertical isolation)	0	-165	0	CR
SCN-2 (flight restriction)	0	0	0	CR

	Expected Infected Population (million)	Expected Death Toll (thousands)	Median Time to Explosion (days)	Risk Category
SCN-3 (gradual resumption to business as usual)	-1.8	-50	+16.1	CR
SCN-4 (mandatory use of masks)	-13.3	-350	+11.6	HI
SCN-6 (integrated strategy)	-13.5	-355	+59.6	CO
SCN-0 (stay at home)	-15.1	-400	Explosion does not occur	NE

Note: CR = Critical Risk; HI = High Risk; CO = Considerable Risk; NE = Negligible Risk

3.7 Answers to policymakers

We here summarize the results by answering the questions raised in the Introduction section. The answers are always given in comparison to the benchmark, i.e. BAU strategy (SCN-1).

3.7.1 How many lives can we save and how many infections can we reduce until October 10th if we decide to implement a certain containment strategy?

Table 5 (Expected Death Toll (thousands) and Expected Infected Population (million) columns) shows for each containment strategy, respectively, the reduction (represented by a minus sign) in deaths and infections.

3.7.2 What is the probability of having a collapse in the Brazilian health system by October 10th for each containment scenario?

If a SAH strategy was sustained, a collapse will probably never occur, alongside with a great reduction in infections and deaths. For all other scenarios, it will eventually occur at some time during the next 90 days (Figure 4(C)). This does not mean that the only solution is to maintain the SAH strategy, but that, should another strategy is applied, policymakers have a given deadline (see Median Time to Explosion column in Table 5) to invest in more ICUs in order to avoid a collapse.

3.7.3 Would a gradual economic resumption plan be effective to reduce the risk of collapse?

If that strategy (SCN-3) is applied alone, the final number of infected and deaths are almost the same as a BAU strategy and the risk of a collapse/explosion is still CR (Figure 4). This strategy is only effective to defer the explosion in 15 days (Table 5).

3.7.4 Is vertical isolation effective?

Yes for deaths and no for infections. Vertical isolation is statistically identical to a BAU strategy in terms of infections and risk to the health system, although, in terms of deaths, it causes a significant reduction (i.e. expected 165,000 less deaths) (Table 5). This strategy may also cause side effects on the elderly population due to the home confinement for 90 days (e.g. mental disorders, muscle atrophy, neuromuscular junction damage, fibre denervation, insulin resistance, decreased aerobic capacity, fat deposition, low-grade systemic inflammation). The evaluation of side effects is out of the scope of this paper.

3.7.5 What about BAU with the wearing of masks?

This strategy defers the explosion in 12 days and also causes a substantial reduction in both infections and deaths (Table 5). Risk to the health system is reduced from CR to HI. The high risk is plausible because the wearing of SFMs reduces the exposure index of people from 100% to 24%, which is still sufficient for the virus to

continue to spread at a considerable rate and cause more than 20% probability of explosion occurring within 28 days. The reduction in the exposure index was estimated based on data from experiments that identified human coronaviruses, influenza viruses and rhinoviruses in the exhaled breath and coughs of children and adults with and without SFM.

3.7.6 Which regions are most at risk in the future? Which ones deserve the most effort to control the disease? What is the order of prioritization?

For a BAU scenario, we have this ranking of regions according to the proportion of infected population (i.e.: $\frac{infected\ population\ in\ region\ i}{total\ population\ in\ region\ i} \times 100\%$) (Figure 5): NE (11.39%); N (10.42%), CW (10.41%), S (7.54%) and SE (5.72%). This indicates that the NE, N and CW regions should be prioritized in the distribution of financial resources, especially ICUs. This rank is plausible because data (Appendix, Table A1) shows that NE, N and CW have the greatest infection rates, thus, although they have a low proportion of infected people at the beginning of the simulation, this figure tends to grow faster and surpasses the S and SE regions.

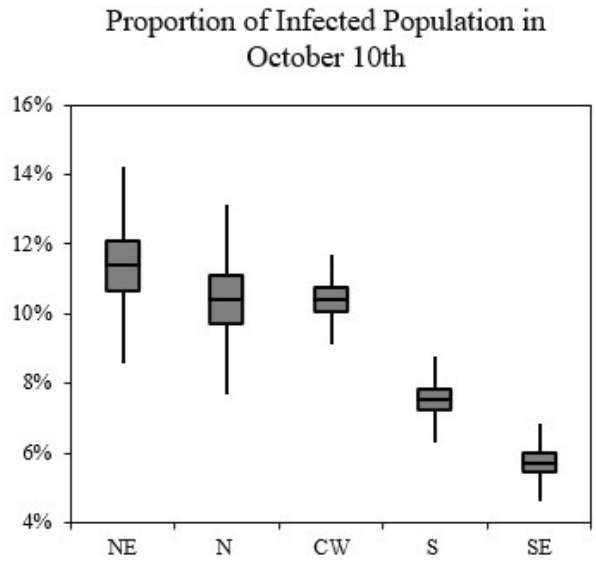

Figure 5. Boxplots for the proportion of infected per region at the end of the simulation in a business as usual scenario (SCN-1).

3.7.7 What is the risk category for an integrated strategy where wearing of masks is mandatory for everyone out of home together with a gradual resumption of the economy?

The integrated strategy SCN-6 (gradual resumption of economy together with mandatory wearing of masks) reduces risk to CO category and expected number of deaths by 355 thousand (Table 5), indicating that this could be somehow effective to satisfy the country's economic needs without posing the health system at high risk.

3.7.8 How many new IUCs would it be necessary to invest in, alongside with the integrated strategy SCN-6, to reduce the risk to negligible levels?

The explosion threshold depends on the number of available ICUs (see Risk of explosion and categorization section). Thus, in order to explore the sensitivity of risk results to ICU capacity, we simulated SCN-6 with increasing numbers of ICUs (Figure 6). We concluded that it is necessary to invest in approximately from 16,000 to 26,000 more ICUs and the integrated strategy (SCN-6) to reduce risks to negligible levels.

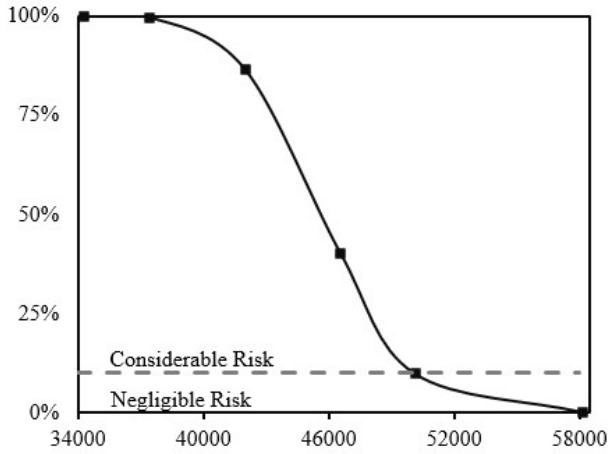

Figure 6. Sensitivity analysis of the risk explosion in 90 days for SCN-6 (gradual resumption of economy together with mandatory wearing of masks) as a function of ICU capacity.

4 DISCUSSION

By the time this paper is published, results may be obsolete. Thus, we consider the model structure in Section 2 and methodology in Section 3 are our greatest contributions. As new information arises, parameters can be easily updated to simulate scenarios for future time periods. Moreover, with a few tweaks, the model structure and methodology can be used for upcoming situations other than COVID-19. Thus, in this section, we firstly discuss the advantages of using the model and methodology and, then, the limitations.

4.1 Advantages

Our model proved to be a useful tool to support public management decisions regarding the prioritization and importance of the most common COVID-19 containment measures, considering all the uncertainty around the data available. Although the data are still very imprecise, our approach was able to propagate the uncertainty in the results and give answers in terms of risk.

DD was modeled in such a way that the infection rate, $\beta^i(t)$, was assumed to vary as a function of the infected population according to a Contest type DD model. Without this assumption, the infection rates would be constant over time, overestimating the risks. This way is more realistic, grounded on the fact that, the more infected people, the less susceptible ones and it is more difficult for the virus to spread. DD Contest-type has been applied to ecological models of fishes, reptiles, birds and mammals (H Resit Akçakaya et al., 2004). To our best knowledge, we were the first to apply DD Contest-type in epidemiological modelling and it has been shown that this innovative approach can bring more realistic results.

It is important to state that our model cannot make precise predictions for what will exactly happen in the future; any model that tries to be precisely predictive will likely miss some information, because decisions are made every time, changing the future. Our model is only descriptive, with the purpose of only tracking the efficiency of each single control measure and, also, of an integrated strategy which seems to be viable for the Brazilian government to implement: gradual resumption of economy together with mandatory wearing of masks during the business time.

Finally, we proposed a set of criteria to categorize the computed risks of the pandemic to the health system, which could be useful not only for COVID-19, but also as a reference for categorizing risks to the health system of any country (mostly the ones where ICU beds are the most critical bottleneck). This categorization is useful to communicate risks to the general public and politicians, who are mostly unfamiliar with probabilistic language. The rationale behind the risk categorization was explained in the QMRA methodology section, so readers must ensure that they fully understand it in order to be secure that they can correctly interpret the results of the risk category.

4.2 Limitations

We have not considered the influence of containment strategies to the Brazilian economy, since business restrictions have caused the income of many people to reduce dramatically. We quantify and categorize only risks to the health system. Our model also does not assess the cost of the control measures, although it provides quantitative and robust results that can be used to feed a cost-efficiency analysis.

The exposure estimates of wearing SFMs (SCN-4) are very uncertain. Because the experiment was performed with a small sample, and we had to include in our estimates the results of experiments with similar but not identical viruses (i.e. influenza virus and rhinovirus) that have different penetrability through SFMs. There are also different types of masks (e.g. N95, cloth), which are not considered in our estimates, and can be more or less effective than the SFMs deemed in the study. Also, we assume that the face mask plan includes mandatory wear during business time with penalties to individuals and companies well defined by law and intense police oversight, in such a way that everyone follows the law and wears a SFM during all the time out of home. The portion of the population that would not take the law seriously is very difficult to estimate and was not considered in this scenario.

We model the beneficial effect of national flight restrictions only at a macro point of view, i.e., it prevents the migration of infected people from one region to another. We have not modeled the beneficial effect of preventing the transmission of COVID-19 inside airports and airplanes.

Currently, our model was built and simulated using a paid software called RAMAS (H R Akçakaya & Root, 2013). Although we share all the model files (Siqueira

et al., 2020), it is only useful for those who have the RAMAS license. We acknowledge this impairs the ease of reproducing the results.

Given these limitations, proposals for future studies include: to conduct a risk assessment of containment strategies to the Brazilian economy; to perform a cost-effectiveness analysis for the control measures; to investigate new studies related to the effectiveness of masks and update the parameter K_4; to build and simulate the model in an open scriptable software, then it can be easily reproduced by others. Another proposal for a future study is to evaluate the effectiveness of alternative vaccine types and mass vaccination programs.

5 CONCLUSIONS

We have quantified, assessed, categorized and ranked the risks related to different control scenarios that seem plausible for the short-term, and provided reliable results so that the BHM can make informed decisions. The results indicated that SCN-6, which includes the gradual resumption of economy in five steps together with mandatory wearing of SFMs during business time with well-defined penalties and intensive police oversight, is expected to lead to 5.1 million infected and 135 thousand deaths by mid October 2020. When compared to a business as usual or do-nothing plan, this represents less 12.4 million and 320 thousands infected people and deaths respectively. In SCN-6, the risk to the health system is considerable (i.e. >10% probability of explosion within 90 days), which indicates that this plan could satisfy the country's economic needs but poses the health system at a risk that is not negligible. Thus, at best, this plan would also include investment in more ICUs. We estimated that SCN-6 together with at least 16,000 additional ICUs reduces the risks to negligible levels.

The model is probabilistic in nature, incorporating in the results the inherent uncertainty in COVID-19 dynamics, making this its main advantage. On the other hand, the main limitation is the uncertainty in some estimates of the reduced exposure due to the wearing of masks, which is a consequence of the lack of knowledge due to the unprecedent nature of the COVID-19 (published experiments have small samples). This is also a limitation of all other models in the literature that have dealt with describing the dynamics of the pandemic. Nevertheless, our model is able to inform managers about the uncertainty in the results, unlike other approaches, so decision makers can be aware of the risks of their decisions.

Our model did not attempt to be a precise forecasting tool, but rather a descriptive one. The COVID-19 dynamics is, then, described under predefined scenarios (different conditions of business restriction, flight restriction, wearing of masks), in order to evaluate the impact of such measures and provide meaningful conclusions that can be used to aid public health decisions. Therefore, the model is significant for decisions taken under uncertainty, but it is very important that due care is taken on how to interpret the results.

6 ACKNOWLEDGMENTS

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