

The virus and socioeconomic inequality: An agent-based model to simulate and assess the impact of interventions to reduce the spread of COVID-19 in Rio de Janeiro, Brazil**O vírus e a desigualdade socioeconômica: um modelo baseado em agentes para simular e avaliar o impacto de intervenções para reduzir a disseminação do COVID-19 no Rio de Janeiro, Brasil**

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ABSTRACT

The emergence of COVID-19 in China, in December of 2019 led to a local epidemic that rapidly spread to multiple countries in the world, including Brazil. Nowadays, there is an accelerated search to understand the dynamics of the spread of the disease and evaluate the effectiveness of intervention measures. Given these special socioeconomic conditions surrounding Brazil, using the predictive models developed for other countries can make a very incomplete picture of the epidemic, since these differences could result in different patterns in low income settings. The aim of this work is to simulate interventions and understand the impact to reduce the spread of COVID-19 considering the socioeconomic conditions of Brazil. With this purpose we use an agent-based model (ABM), a subarea of the Artificial Intelligence, as it allows us to treat each individual in a personalized manner, as well as the environment of which they are part. The simulations have heterogeneous populations, considering different age groups, socioeconomic differences and number of members per family, contacts and movements intra and inter the sub-populations (favelas and non-favelas), numbers of Intensive Care Unit (ICU) and study different scenarios to show how the interventions can influence the spread of the virus in the population of simulated environments.

Keywords. COVID-19; SARS-CoV-2; agent-based modeling; favelas; slums; simulation; artificial intelligence

RESUMO

O surgimento do COVID-19 na China, em dezembro de 2019, levou a uma epidemia local que se espalhou rapidamente para vários países do mundo, incluindo o Brasil. Atualmente, há uma busca acelerada para entender a dinâmica da disseminação da doença e avaliar a eficácia das medidas de intervenção. Dadas essas condições socioeconômicas especiais em torno do Brasil, o uso dos modelos preditivos desenvolvidos para outros países pode fazer uma imagem muito incompleta da epidemia, uma vez que essas diferenças podem resultar em padrões diferentes em contextos de baixa renda. O objetivo deste trabalho é simular intervenções e entender o impacto para reduzir a disseminação do COVID-19, considerando as condições socioeconômicas do Brasil. Com esse objetivo, usamos um modelo baseado em agentes (ABM), uma subárea da Inteligência Artificial, pois permite tratar cada indivíduo de maneira personalizada, bem como o ambiente do qual eles fazem parte. As simulações têm populações heterogêneas, considerando diferentes faixas etárias, diferenças socioeconômicas e número de membros por família, contatos e movimentos intra e inter subpopulações (favelas e não-favelas), número de unidades de terapia intensiva

(UTI) e estudam diferentes cenários mostrar como as intervenções podem influenciar a propagação do vírus na população de ambientes simulados.

Palavras-chave: COVID19; SARS-CoV-2, modelagem baseada em agente; favelas; favelas; simulação; inteligência artificial

1 INTRODUCTION

Since a severe respiratory disease was recently reported in Wuhan, Hubei province of China, on December 2019 the disease identified as COVID-19 quickly spread to other regions. Due to highly transmissible nature of SARS-CoV-2 virus, it has spread to multiple countries, including Brazil, and has been declared a pandemic by the World Health Organization (WHO). The first patient was tested positive for the virus in Brazil on February 2020 and as of 16 April 2020, at least 30,000 cases and 1,924 deaths have been reported [da Saú de 2020]. Currently, there is no vaccine or therapies approved for treatment [Sanders et al. 2020, Shi et al. 2020].

Around the world there is an accelerated search to understand the transmission dynamics of the infection and evaluate the effectiveness of intervention measures. These actions aim to estimate mortality and the healthcare demand, while preserving and considering economic effects. How the countries respond in the initial weeks is critical in influencing the trajectory of national epidemics. However, despite other countries are facing these challenges before Brazil, great uncertainty remains regarding the epidemics peaks due to special factors such as environmental and social conditions and immunity levels of the population. In Brazil, 11.4 million people, nearly 6% of the population, live in favelas¹. The favelas are human settlement areas that combine the lack of sanitation and water, compounded by insufficient living space for families, which means more than three people sharing the same room². Virus transmission may be facilitated in these dense populations, characterized by frequent inter-individual contact, crowded housing, improper sanitation systems, poor education, and poor nutritional status [Go´es et al. 2019]. Furthermore, in this period, most of Brazilian states faces a high incidence of Severe Acute Respiratory Infection (SARI), compared to the same period in previous years [da Saú de

¹ The favelas are Brazilian slums. We chose the term favelas instead of slums due to the fact that we use very specific information of these Brazilian communities that are not easily extrapolated to other contexts. In this work we use favelas in scenarios of Brazil and slum for other countries.

² [www.unhabitat.org. SOWC/06/07/B/Slum2](http://www.unhabitat.org/SOWC/06/07/B/Slum2)

2020]³. This is the case of the Rio de Janeiro which is also the Brazilian state with the highest occurrence rate of tuberculosis [Pereira et al. 2015], two important comorbidity conditions, that could impose poorer clinical outcomes in COVID-19 patients [Guan et al. 2020a].

Thus, given these special socioeconomic conditions surrounding Brazil, using the predictive models developed for other countries can make a very incomplete picture of the epidemic, since these differences will likely result in different patterns in low income settings.

The aim of this work is to simulate interventions and understand the impact to reduce the spread of COVID-19 considering the socioeconomic conditions of Brazil. With this purpose we use an agent-based model (ABM), a subarea of the Artificial Intelligence, combined with the SEIR (Susceptible, Exposed, Infectious and Removed) disease dynamic model, according to the epidemiological characteristics of COVID-19 [Sun et al. 2020, Adhikari et al. 2020]. The ABM approach is suitable to study the spread of the disease, as it allows us to treat each individual in a personalized manner, as well as the environment of which they are part. The simulations have heterogeneous populations, considering different age groups, socioeconomic differences and number of members per family, contacts and movements intra and inter the sub-populations (favelas and non-favelas), numbers of Intensive Care Unit (ICU) and study different scenarios to show how the interventions can influence the spread of the virus in the population of simulated environments.

In this work the simulations are conducted for the Rio de Janeiro city, in the region of the Copacabana, as it presents different socioeconomic areas, due to the existence of the Pavão-Pavãozinho favela complex in this region, which could represents a picture of the Brazil. Some scenarios of interventions are studied: simulating the spread of the virus in a population without isolation, the isolation of the elderly (over 60 years old) and young people (under 18 years), in addition to the previous one, with the displacement of agents on alternate days and the last with the full isolation after thirty infected individuals. Also, we simulate the scenario with homogeneous population, which not consider the favela and conditions of these population. This point out the importance in consider sub-populations

³ <http://info.gripe.fiocruz.br>

in the simulations to a real evaluation of spread and control of outbreaks. The results show the number of infections and deaths over the time, including due to lack of ICUs.

This work is organized as follow: the works related to our research are presented in Section 2. The methodology for the simulations, with the ABM approach, the modeling spread dynamics, details of the population and parameters for the computer simulations are presented in Section 3. The experiments and results for the simulated scenarios in Section 4, followed by the final considerations in Section 5.

2 RELATED WORKS

Several works have demonstrated the importance in consider the slums and its specific life conditions to understand the spread and control of epidemics scenarios, such as for Influenza [Adiga et al. 2018, Verma et al. 2018] and Ebola [Long et al. 2018]. In the same way, other studies pointed out to the impact of the population's characteristics on respiratory diseases like influenza, tuberculosis and also human coronaviruses (HCoV) in Brazilian favelas [Goes et al. 2019, Pereira et al. 2015]. However, despite the great number of works being published about COVID-19 in the last weeks, to the best of our knowledge, at this moment, there is no work considering using agent-based modeling to simulate the COVID-19 spread in the contexts of the slums in other countries nor in the Brazilian favelas. Thus, the related works presented in this section are focused on researches that consider the role of slums in the spread and control of infectious diseases or the use of an agent-based model to study epidemic spreading.

Some researches demonstrated the importance in considering the slum and non-slum subpopulations [Long et al. 2018, Adiga et al. 2018, Chen et al. 2016], and clusters of areas with high population density [Engelbrechtsen et al. 2019] in modeling the spread and control of infectious diseases. Chen et al.[Chen et al. 2016] and Adiga et al.[Adiga et al. 2018] use a SEIR and agent-based model to study the impact of influenza epidemic in the slum and non-slum areas of Delhi, the National Capital Territory of India. In order to express the differences they take into account the slum demographics and residents activities. The results show that the peak of infection is overestimated by several weeks, and the cumulative infection rate and peak infection rate are underestimated by 10–50% when slum attributes are ignored. Improper specification of slums in large urban regions results in underestimation of infections in the entire population and could lead to misguided interventions by policy planners.

Many agent-based models were proposed to simulate epidemic outbreaks without considering the slum context nor the COVID-19 context. The work of Andrade et al. [de Andrade et al. 2020] studies the spread and control of tuberculosis in the city of Rio de Janeiro (Brazil) using an agent-based and SEIR disease dynamic model. They conclude that the models are very helpful to identify the positive impact of the control measures in the interruption of disease spread. The model, although simple, have a high predictive value and an enormous capacity to be adapted and applicable to others scenarios, which encompass different aspects of Tuberculosis dispersion. The model presented in [Hackl and Dubernet 2019] is used to study seasonal influenza outbreaks in the metropolitan area of Zurich, Switzerland, where different activities take place during a daily citizens' routine. Despite the simplicity of the implemented epidemic spread model, which only account for susceptible, infected, and recovered individuals (SIR disease dynamic model), the results show how this simulation can help to improve comprehension of the disease spread dynamics and to take better steps towards the prevention and control of an epidemic. The work of [Hunter et al. 2018] proposes an agent-based model to simulate the spread of an airborne infectious diseases in Irish towns (SEIR model). They argue that the model is able to capture complex interactions between factors and emergent results based on agents decisions within the model that other types of models cannot. These interactions and emergent results are essential in understanding the dynamics of an outbreak.

Finally, these works do not consider the slum context nor COVID-19, but also propose an agent-based model to simulate epidemic outbreaks. Although the models are much simpler than ours, as they do not deal with subpopulations and so many different factors and interactions, they demonstrate the effectiveness of using this model to simulate epidemics scenarios.

In this section we presented the works related to our agent-based model for the spread of the COVID-19 in a Brazilian context of two subpopulations: favela and non-favela. We have shown that some studies showed that slums subpopulations can lead a model to underestimate the spread of contagious diseases. We've also shown that the models already created are too simple to account for the characteristics of a favela community. We propose a model that combines some characteristics of these related works in order to provide a better understanding of how the spread of the COVID-19 can affect the lives of people in a Brazilian context of social-economic inequality and environmental conditions.

3 METHODOLOGY

Agent-based models (ABM) are used in many complex problems where simple mathematical formulae are not sufficient to provide more detailed and precise description of the studied context [Railsback and Grimm 2019]. The collective behavior is then analyzed and the results derive conclusions and insights that can help us to understand social contagion phenomena in a more intuitive and practical way. The practicality of the ABM combined with the powerful outcomes provided by it are a good combination for studying the spread of contagious diseases in real contexts.

The ABM approach is suitable for the COVID-19 spread as it permits to add to the model individual characteristics of the agents together with environmental information from the context where the individuals are part of.

In this section the model is presented together with the considerations, background and hypotheses adopted when the project decisions were made. It is also explained how the computational simulations were generated.

3.1 MODELING SPREAD DYNAMICS

The classical epidemiology modeling uses compartmental modules to simplify the mathematical description of infectious disease. The population is divided into compartments, where each compartment represents the characteristics of the individual at a given time. Obeying the principle of equilibrium of the population, each individual can be in only one compartment per unit of time, and the exchange of compartments must take place according to the assumptions made about the nature of the studied phenomenon. These models can be used to predict properties of how a disease spreads and for understanding how different situations may affect the outcome of the epidemic, such as vaccines and isolation actions.

Based on the epidemiological characteristics of COVID-19 [Sun et al. 2020, Adhikari et al. 2020], the model presented in this work was designed using the SEIR disease dynamic model [Oliveira et al. 2008], in which the population is divided into four compartments:

- **Susceptible (S):** includes all individuals who can contract the disease, if they are exposed to it;

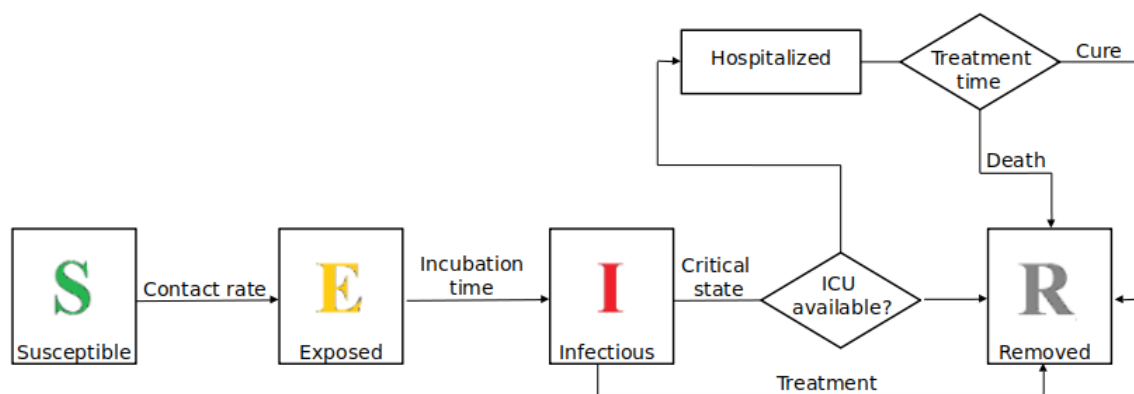
- **Exposed (E):** individuals who have disease and are in the incubation period, in other words, are able to transmit it but have no symptoms (low viral load). They act as potential vectors on the spread of the virus;

- **Infectious (I):** includes individuals who have the disease, are able to transmit it and have symptoms (high viral load).

- **Removed (R):** class of individuals who recover or die.

Figure 1 shows the four groups and the factors that cause individuals to change groups. Initially, people who belong to the susceptible compartment and have contact with a sick person will get the virus and move to the exposed compartment group (has no symptoms but has viral load). After the incubation period, with the appearance of symptoms, these individuals will move to the infected group. In this compartment, if the individual received the treatment and was cured, they pass to the removed group. In the other hand, if the individual progresses to having critic symptoms, they are admitted for treatment in the Intensive Care Unit (ICU). In case there are no available ICUs for patients in critical condition, the individual dies and moves to the removed group. Those who got admitted to the available ICUs are moved to the removed group after the treatment period. They can be counted as cured in case of success in the treatment or dead by the disease otherwise.

Figure 1. SEIR model and transition factors between compartments.



For modeling the compartments' transitions shown in Figure 1 we assumed the following assumptions:

- The population is fixed, and during the simulation they won't have contact with members from other populations or be influenced by migrations;

ii) The initial population size is constant. This means that birth rate and mortality rate from natural causes are disregarded;

iii) The population is heterogeneous, composed of different age groups, socioeconomic differences and number of members per family;

iv) Susceptible individuals can be contaminated when in contact with exposed or infectious individuals;

v) All individuals are susceptible and have no immunity to the virus initially;

vi) Individuals make physical contact at home and at work, and interactions in transportation vehicles are disregarded;

vii) Individuals have different viral loads, according to the compartment they are in (Exposed or Infectious);viii) Infectious individuals are automatically put in isolation and with less contact with family members;ix) Individuals with mild and moderate symptoms recover after treatment time;

x) If an ICU bed is available, individuals with severe symptoms are automatically hospitalized. Individuals with severe symptoms who are not hospitalized die automatically. Only a percentage of severe cases recover;

xi) Individuals automatically obey the isolation measures imposed.

3.2 POPULATION

We are interested on understanding the spread of the COVID-19 in a Brazilian contexts of favelas and other wealthier regions. So the the data used to describe the main characteristics of the population is based on census of Rio de Janeiro city. To account for the different socioeconomic differences we picked the Copacabana neighborhood. There is a big socioeconomic gap between the favela within it (the Pavão-Pavãozinho favela complex) and the other parts of the neighborhood. According to data from the Favelas Report in the city of Rio de Janeiro [Cavallieri and Vial 2010], Copacabana has 161,191 inhabitants, of those 12,094 (8%) live in favelas.

Also, Rio de Janeiro is the capital with the biggest elderly population in Brazil (about 18%⁴) and 29% live in Copacabana [da Silveira Barroso Alves et al. 2016]. How- ever, there is a clear difference in the age distribution of the population of Pavão-Pavãozinho favela and other areas of Copacabana, with big discrepancy in their elderly population [Vial

⁴ <https://sidra.ibge.gov.br/tabela/261#notas-tabela>

et al. 2017]. While there is a predominance of young people, between 10 and 29 years old, in Pavão-Pavãozinho, in other areas of Copacabana, the number of young people is significantly narrower. This information is important to be represented in the model, since the elderly will suffer more from severe and critical symptoms than younger people [Guan et al. 2020b]. However, even though there are not many elderly people in Pavão-Pavãozinho (around 5%), this region is of great importance in the simulation, since people who live in areas with low socioeconomic conditions have a higher risk of contamination.

As the study focus on the spread of COVID-19, it is also important to consider the number of ICUs available in the region we chose to model. According to the technical note of [Batista et al. 2020], the Metropolitan I region, in which Copacabana is located has 6 ICUs per 100 thousand inhabitants. That will help our model to be closer to reality when accounting for the hospital infrastructure provided for Copacabana.

The differences that we could represent using this region is picture of the differences that we can find in Brazil.

3.3 PARAMETERS AND COMPUTER SIMULATIONS

This work presents an Agent-Based Model (ABM) of the SEIR structure presented in Section 3.1 (Figure 1). The ABM was implemented using the Anylogic v.8.5.0⁵ software. ABMs are a micro-scale modeling approach where specific and simpler characteristics of the agents and their interaction are responsible for generating the outcomes for the whole universe simulated. The idea is to recreate and predict some events in real world through computational simulations. This strategy is largely used in many fields as biology, ecology, and also for the spread of epidemics.

Firstly, the parameters and initial variables used for the simulations were set, as shown in Table 1. Then, the simulation was run and the macro-level results were observed and analysed. The variables that account for the traits of the agents is shown in Table 2. These traits are responsible for defining the agents' interactions and reactions with the environment and other agents. The variables shown on the bottom part of Table 2 are used to obtain the outcomes of the simulations, as the Contamination Rate (CR), the Recovery Rate (RR) and the Mortality Rate (MR), presented further in Section 4.

⁵ <https://www.anylogic.com>

The CR rate represents how the spread of the virus is progressing day by day, as shown in Equation 1 where $Infectious_d$ is the number of infectious agents on day d while $Infectious_{d-1}$ is the number of infectious agents one day before. A value bigger than 1 means that there is an increase on the number of contaminated agents, and a number below 1 indicates a decrease on the contaminated agents number.

$$CR_d = \frac{Infectious_d}{Infectious_{d-1}} \quad (1)$$

The RR rate indicates the rate at which the infectious agents recover, and is expressed in Equation 2 where $Recovered_d$ is the number of recovered agents on day d and $Recovered_{d-1}$ is the number of recovered agents on the day before. A value bigger than 1 means that there is an increase on the number of recovered agents, and a number below 1 indicates a decrease on the number recovered people.

$$RR_d = \frac{Recovered}{Recovered_{d-1}}$$

The MR rate is the rate in which the agents die, and can be seen in Equation 3 where $Death_d$ is the number of deaths on day d and $Death_{d-1}$ is the number of deaths on the previous day. A value bigger than 1 means that there is an increase on the number of dead agents, and a number below 1 indicates a decrease on the number of deads from one day to the previous one.

$$MR_d = \frac{Death_d}{Death_{d-1}} \quad (3)$$

The parameters for the population has been shown previously in Section 3.2. These parameters are shown also in Table 1 and used in our simulations.

Table 1. Parameters and values.

Parameters	Values
Cycle (δt)	1 day
Update graphs	every 2 hours
Initial infected individuals	3
% of favelas	8% (Section 3.2)
% of non-favelas	92% (Section 3.2)
ICU beds	300

Average individuals per family (slum)	6
Average individuals per family (non-slum)	3
Incubation time	5-7 days
Treatment time (home and ICU)	14 days
Probability of development critical cases	14%
Recover of hospitalized individuals	20%
Threshold for interventions	10 Infectious

The parameters on Table 1 related to the disease, like incubation and treatment time, probability of developing critical cases and recover are based on the studies presented in the literature [Lauer et al. 2020, He et al. 2019] and estimated for another countries, specially from China and Europe, since in Brazil we don't have enough information yet. It is still not clear that percentages, therefore we assume them based on different researches [ICNARC 2020].

Families and their members are randomly generated, respecting the parameters in Table 1 (percentage and average quantity). Work groups also generated randomly. The Age variable (Table 2) is initialized following a distribution that represents the real age groups of the simulated population, as explained in Section 3.2. This variable is used to calculate the birth dates.

Table 2. Variables and descriptions.

	Variables	Type	Description
A g e n t s	Contacts per day	int	# of contact with another agents per day
	Infection probability	double	probability of transmitting virus
	Age	int	agent age
	Birthday	int	birthday of agent
	Critical	boolean	true if agent develops a critical case
	Favela	boolean	true if agent lives in favela
	State	derived	current state of SEIR model
	Local	derived	current local of agent: home or work
	Home group	derived	family contacts network
	Work group	derived	work contacts network
S i m u l a ti o n	Days	int	# day after first infection
	Susceptible	int	# of susceptible agents
	Exposed	int	# of exposed agents
	Infectious	int	# of infectious agents
	Removed	int	# of removed agents
	Hospitalized	int	# of inpatient agents
	Critical cases	int	# of agents with critical case
	Death and Death by ICU lack	int	# of dead agents by virus and ICU lack
	Recovered	int	# of recovered agents
	Current time	time	current simulation time

representing the amount of.

3.3.1 Daily Events: Movement of agents and locals

An important factor in our model is the interaction between agents, that is, how each agent is exposed to other agents and how their physical contact occur. The dynamics between the agents are modeled in two different locations, at home and at work, forming two different contact network for each agent. Besides that, the model also considers two sub-populations: an agent (individual) could live and work in a favela or in a non-favela region. This results in two types of interactions. The interactions intra-groups are between individuals from the same group (favela or non-favela). For example, an interaction from a person who lives or works in a favela with another person also from the favela. The interaction inter-groups happens between two individuals from different groups. Thus, every day of the simulation (one cycle), the agents move from home to work and from work to home and may have contacts with people from other groups. In this work, contacts in transport vehicles were not considered.

Each simulation cycles take place in one day and each hour of the day is responsible for defining the location where each agent is located. In the beginning of the day (and at the start of simulation), each agent is assigned to their respective family group, so their contact network is their family members. At a certain time in the morning, each agent travels to their workplace, where they are assigned to their work group and change their contact network. Before a day cycle finishes, each agent returns to their home and family network. The Infectious agents who develop the critical case are transferred to hospital, where they are admitted.

3.3.2 Contacts of Agents

The transmission of the virus from an Infectious agent to a Susceptible agent occurs by controlling two variables: InfectionProbability and ContactsPerDay. The probability that an agent transmit the virus to another agent is defined by the infection probability, calculated at each contact with another agent.

Asymptomatic individuals (Exposed in our model) have low viral load, but interact more with other agents in their networks [Shi et al. 2020, Rothe et al. 2020]. The daily amount of interactions for each person is estimated in 20, following the results obtained by [Del Valle et al. 2007]. It is assumed that Infectious individuals have higher viral load, and as they present the symptoms of the disease, they will put themselves in isolation. In this

situation, they interact less with other agents in their networks (average of 5 contacts per day).

The dead agents are removed from the respectively contacts network, and no longer have contact with other agents.

3.3.3 Simulated Interventions

The model was simulated in 5 different scenarios:

1. **Scenario 1** simulates the spread of the virus in a population without isolation interventions, where agents move freely from home to work and work from home.

2. **Scenario 2** also has no isolation of the agents but has a homogeneous population, disregarding the favela's sub-population.

3. **Scenario 3** simulates the isolation of the elderly (over 60 years old) and young people (under 18 years). Only agents in the middle age can move from home to work.

4. **Scenario 4** simulates the displacement of agents on alternate days. The criterion adopted for this intervention is: agents born in even days can only leave on even days and agents born on odd days, only on odd days.

5. **Scenario 5** simulates the full isolation after thirty infected agents, where each agent stay at home until the infection is over, only 5% of the agents circulate to consider essential services.

In this section we presented the parameters for the simulation of the COVID-19 spread in a context of two different groups of people with a high socioeconomic inequality. We presented the main characteristics of the model, as well as the parameters and variables used to run the simulations. Lastly we presented the different scenarios chosen in order to analyze which isolation (or quarantine) method would be more efficient in a context like Rio de Janeiro city. Next section will present the results of the simulations.

4 RESULTS

This section presents the results of the experiments obtained after simulating the 5 scenarios presented last section. It is important to note that, in all scenarios, there are a considerable number of critical cases, since the large part of simulated population belong to the risk group because it contains elderly people and people that live in favelas (as mentioned in Section 3.2). Also, considering that the virus arrived in Brazil through individuals who

traveled to other countries [Candido et al. 2020], the initially infectious agents belong to the non-slum sub population.

Due to the limitation of the maximum number of agents that can be simulated in the AnyLogic software, the total number of agents was set on approximately 35,000 agents and the other parameters that consider the population size were adjusted accordingly, including the parameters presented in Table 1, already adjusted to the proportional values.

4.1 SCENARIO 1 – WITHOUT ISOLATION

The Figure 2(a) shows the number of agents in each compartment of the SEIR model over time. The green line refers to the number of Susceptible agents, the yellow line refers to the Exposed agents, red represents the Infectious agents and gray to the Removed agents. When the number of Exposed and Infected agents increases, the number of Susceptible decreases. As the agents recover from the disease or die due to the disease, the number of Removed agents increases. This tendency is in accordance with the studied phenomenology.

As isolation interventions are not implemented in this scenario, the agents circulate freely, allowing the virus to spread quickly and affecting a large part of the population. As a considerable part of the population belongs to the risk group, the number of hospitalizations with critical cases (red curve in Figure 2(b)) grows rapidly and reaches the maximum number of available ICUs (green line in Figure 2b), reaching 684 critical cases (Figure 2(c)) in just over 60 days. When maximum ICU occupancy is reached, agents with critical cases began to die from lack of health resources (purple curve in Figure 2d). The total number of deaths from the virus was 571, with 175 due to lack of ICU. The total number of deaths represents approximately 1.63% of the total simulated population.

It is known, based on the models developed all around the world for COVID-19, that without isolation the spread of the virus is faster, causing the health system to collapse. However, this scenario works as a basis of comparison for the other ones presented next (with isolation measures). Also, it is important to know how long is the time for the collapse in the Brazilian scenario and the numbers associated to it.

In this baseline scenario, the infection lasted 92 days, with a peak of 25,581 infectious in 53 days. The total number of infectious agents was 33,357 agents, 3,457 living in the favela and 29,900 outside the favela. The collapse of the ICU system occurred in 53 days, coinciding with the day on which the infectious peak occurred.

Observing the highest values calculated for CR presented in Table 3, we noticed that the spread of the virus is higher within the favelas (1.5×), even though the agents initially infected were not residents of the favela. The high MR value (4.68) can be interpreted in Figure 2(d), where the mortality rate represents the high slope of the gray and purple curves.

Figure 2. Results for Scenario 1 (no interventions).

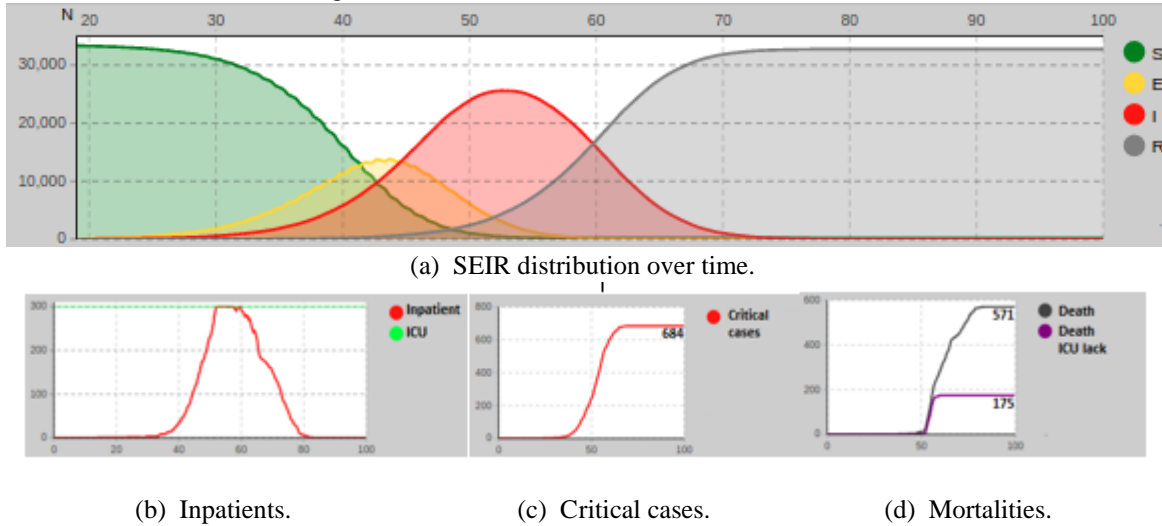


Table 3. Values reached for the calculated rates for Scenario 1 .

Scenario 1				
Contamination Rate (CR)			Recovery Rate (RR)	Mortality Rate (MR)
non-favela	favela	general	2	4.68
2	3	1.42		

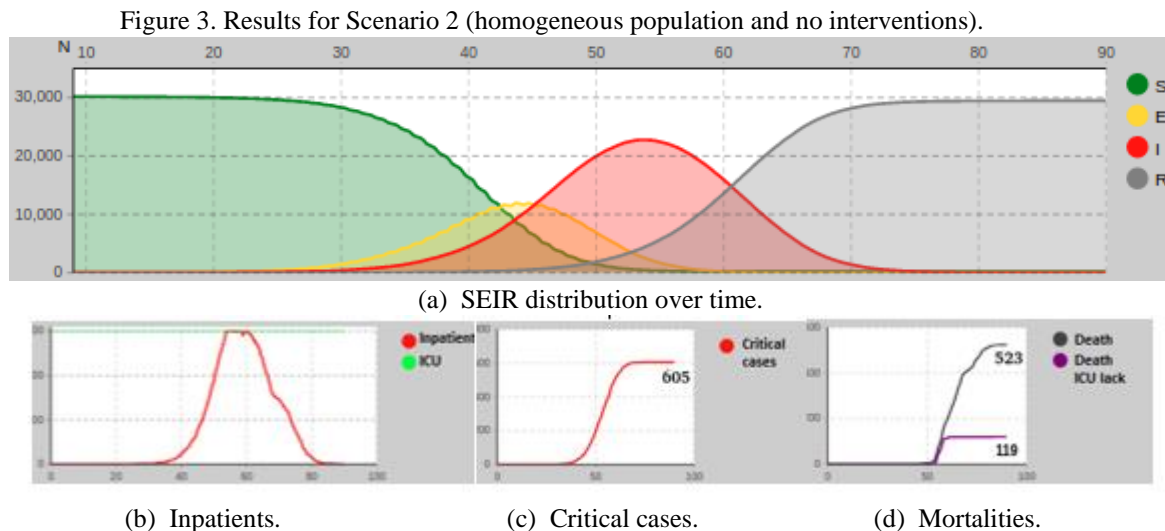
4.2 SCENARIO 2 - WITHOUT ISOLATION AND HOMOGENEOUS POPULATION

This scenario disregards the favela agents and demonstrates that under a homogeneous population the results of infections and deaths could be underestimated.

For example, again the number of hospitalizations with critical cases (red curve in Figure 3(b)) grows rapidly and reaches the maximum number of available ICUs (green line in Figure 3(b)). However, note that the number of critical cases (Figure 3(c)) in just over 60 days is less than in scenario 1, with 79 fewer cases. In addition, in Figure 3(d),

the total number of deaths from the virus was 523 (48 less than scenario 1), with 119 due to lack of ICU (56 less than scenario 1).

This result demonstrates the importance in consider sub-populations in the simulations to a real evaluation of spread and control of outbreaks.



4.3 SCENARIO 3 - ELDERLY AND YOUNG ISOLATION

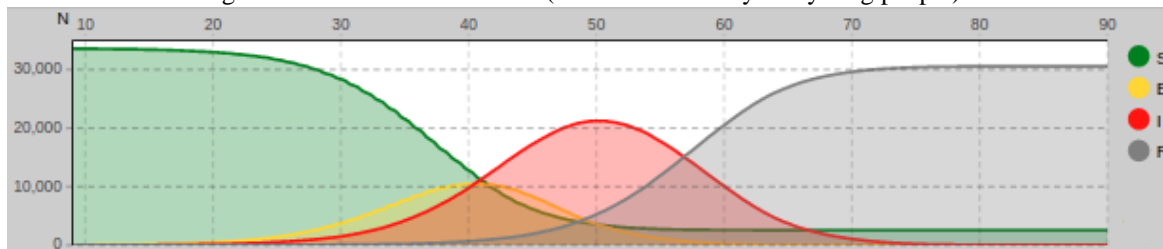
Figure 4(a) shows the number of agents in each compartment of the SEIR model over time. There is a flattening of the Infectious curve when the isolation of the elderly and young agents is started, reducing the peak of Infectious agents. In this scenario, the number of critical cases reached 603 (81 cases less than in scenario 1). The total number of deaths was 504 (67 less), with 83 due to lack of ICUs (92 less). Despite the reduction, the number of infected and dead is still high, due to the fact that the networks of family contacts are maintained and the agents without isolation are the vectors of intra-group transmission. Thus, individuals who are in isolation are also infected.

In this scenario, the infection lasted 93 days, but with a reduction in the amount of infectious agents. The peak of infectious people occurred after 49 days (2 days less than in scenario 1), but with a 17.9% reduction in the infectious peak and a 6.8% reduction in the total number of infected agents. The peak of infectious was 21,018 and the total number of infected agents was 31,091 (3,453 in favela and 27,638 in non-favela). Comparing the number of infections agents of different populations, the reduction of infected agents

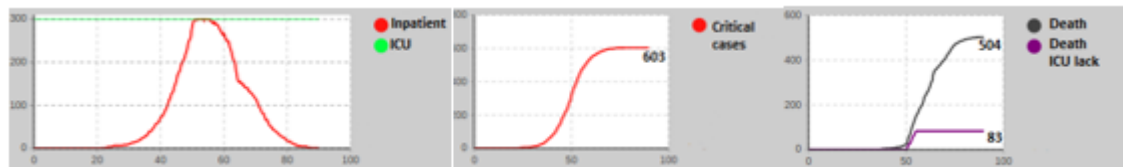
outside the favela was 7.6%, while in the favela it was 0.11%. The ICU lack occurred after 51 days, 2 days after the peak of infectious.

Table 4 shows that, for this scenario, the CR was about of $1.143\times$ greater within the agents of favela. Comparing the RM of this scenario with the base scenario, there was a reduction of 62.6% and can be seen with the reduction in slope of curves in Figure 4(d).

Figure 4. Results for Scenario 3 (isolation of elderly and young people).



(a) SEIR distribution over time.



(b) Inpatients.

(c) Critical cases.

(d) Mortalities.

Table 4. Values reached for the calculated rates for Scenario 3.

Scenario 3				
Contamination Rate (CR)			Recovery Rate (RR)	Mortality Rate (MR)
non-favela	favela	general	3	1.75
1.75	2	1.69		

4.4 SCENARIO 4 - ALTERNATE DAYS ISOLATION

In this scenario, the isolation measure adopted is more rigorously, allowing agents to leave the house on alternate days, as explained in the Section 3.3.3. The flattening of the Infectious curve presented in Figure 5(a) is even greater than in Scenario 3, and the peak of this curve is approximately 2.5x less than in Scenario 1. The number of critical cases are 486 (Figure 5(c)) and the total number of deaths are 380 (Figure 5(d)). As in this scenario there is no lack of ICU (Figure 5(b)), therefore there are no deaths as a result of this, as

observed in the previous scenarios. This result shows the importance of not filling the health system.

For this scenario the infection lasted 134 days, however with a great reduction in the peak and in the total of infectious agents. In 84 days, the number of infectious agents peaked at approximately 10,000 agents, 61% less than in scenario 1 and 52.4% less than in scenario 3. The total number of infected agents was 25,705 (-22.94% in relation to scenario 1 and 17.32% to scenario 3). Inside the favela the total number of infected agents was 3,251 (-5.96% and -5.85% in relation to scenarios 1 and 3) and outside the favela it was 22,454 (-24.9% and -18.75% in relation to scenarios 1 and 3). There was no lack of ICUs because the maximum number of simultaneous patients was.

The contamination rates in the Table 5 show that the spread in favela is also greater in this scenario.

Figure 5. Results for Scenario 4 (alternating isolation according to the birthday dates).

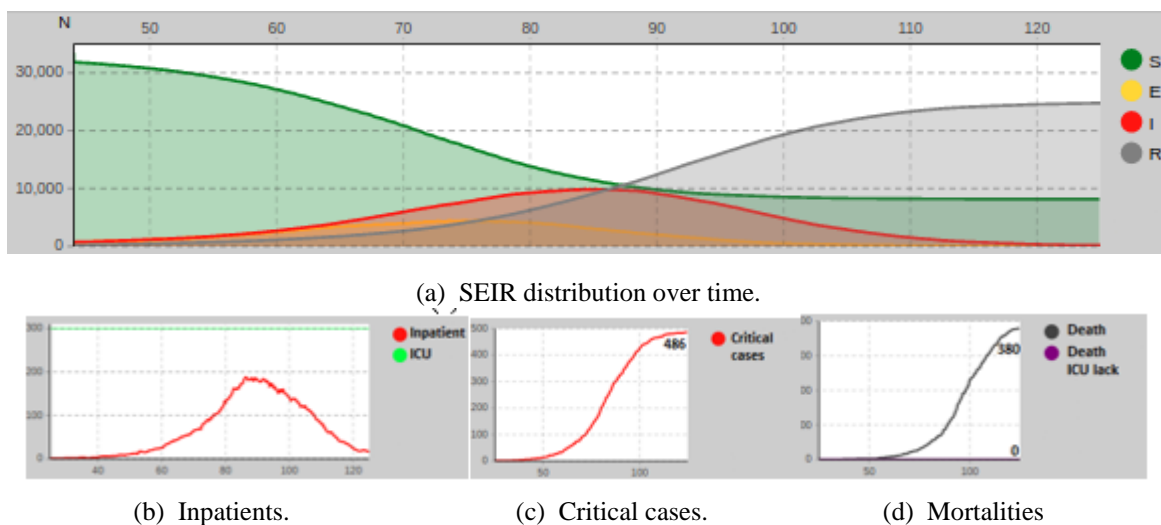


Table 5. Values reached for the calculated rates for Scenario 4.

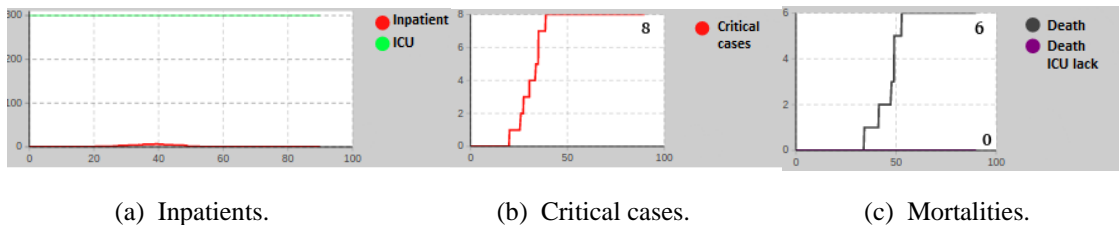
Scenario 4				
Contamination Rate (CR)			Recovery Rate (RR)	Mortality Rate (MR)
non-favela	favela	general	2	1.5
1.5	2.25	1.61		

4.5 SCENARIO 5 - FULL ISOLATION

For this scenario, the SEIR graph will not be shown because the change in the agents' compartment is not apparent. The Figure 6(a) shows the hospitalized agents and the availability of ICUs, Figure 6(b) shows the critical cases and Figure 6(c), the amount of deaths.

In this scenario, the infection disappeared in 38 days and reached the infectious peak of 316 agents after 26 days. The total number of infected agents was 366, being 266 in non-favela and 100 in favela. Table 6 shows that the spread in non-favela is greater in this scenario. This is because there was no time for the virus to spread through the agents of favela, since the simulations start with infectious agents outside the non-favela.

Figure 6. Results for Scenario 5 (full isolation).



(a) Inpatients.

(b) Critical cases.

(c) Mortalities.

Table 6. Values reached for the calculated rates for Scenario 5.

Scenario 5				
Contamination Rate (CR)			Recovery Rate (RR)	Mortality Rate (MR)
non-favela	favela	general		
			4	2

4.6 DISCUSSIONS

As there are no measures to immunize the population yet, it is very likely that a large part will still be contaminated by the virus. However, observing the spread of the virus in the 5 studied scenarios, we can see the importance of adhering to isolation measures so that less individuals become ill causing a collapse on the health system. With the right strategy it is possible to overcome the epidemic so that the health system is able to serve a larger number of individuals in critical cases reducing the number of deaths.

The most worrying factor that can be pointed out with this study is the spread of the virus within the favelas, as many factors such as hygiene conditions and the crowding of people causes it to spread more quickly. The crowding factor inside the houses can be seen in Figure 7, where the left column shows the non-favela spread and the right column in the favela. In this figure the circles are agents and the colors follow the same used in Figure 1 for Susceptible (green), Exposed (yellow), Infectious (red) and Removed (gray). Initially, all agents are Susceptible. When an agent from each family contracts the virus, he becomes Exposed and has a low viral load (small arrow). The viral load increases (larger arrow) when these agents become Infectious, increasing probability of transmitting the virus to other agents in the family. After, all agents of the families are Infectious and become Removed. This illustration is very close to what happened in scenario 1, in which 99.49% of the total population was infected. In both simulated scenarios, the CR was higher in the favelas ($\approx 1.5\times$ higher).

Table 7 presents a summary of the results for simulated scenarios. Looking at the values, it is possible to see that the isolation of elderly and young (scenario 2) was not very efficient in relation to scenario 1, since there was still a collapse of ICU resources. The intervention on alternate days (scenario 3) was shown to be more efficient than scenarios 1 and 2 and without ICU lack. However, maintaining control for a long period (134 days) makes it difficult to implement. The best results were obtained for scenario 4, where only agents responsible for essential services were able to circulate. In addition to the short period (38 days), many lives were saved and the number of infected agents was much lower than in the other scenarios.

Figure 7. Illustration of the spread of the virus in family environments.

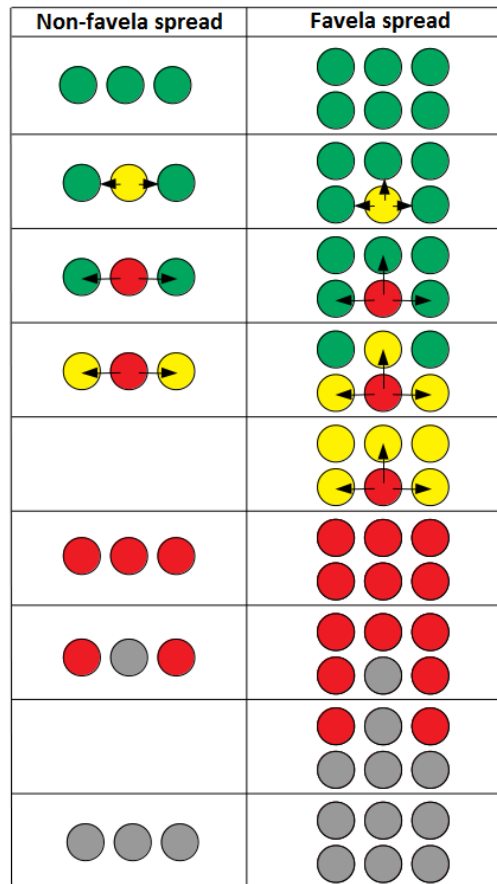


Table 7. Synthesis of the results.

	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
Infection lasted	92 days	92 days	93 days	134 days	38 days
Total infected agents	33357	29991	31091	25705	366
Total dead agent	571	523	504	380	6
Infectious peak	25581 in 53 days	22754 in 54 days	21018 in 49 days	≈10000 in 84 days	316 in 26 days
ICU lack	53 days	54 days	51 days	Did not occur	Did not occur

5 CONCLUSION

This work studied the spread of the recent COVID-19 virus in the Copacabana neighborhood, Rio de Janeiro city using ABM to simulate the epidemic outbreak for

different scenarios and interventions. The higher risk of contamination in the favelas due to their situations where the number of ICU beds are not sufficient to attend all the people who need them.

Even though the model is agent-based, the outcomes were similar to other studies that try to predict the number of people infected and dead in other works that use a pure mathematical approach to draw the predictions. The proposed ABM represented the phenomenology of the studied event and, although some hypotheses are disregarded, the model proved to be effective for the study on the spread of the virus. It is also important to emphasize that the ABM developed in this work can be easily used for other populations.

The results of this study can be used by municipal managers where there are slums and community leaders in the involvement of actors responsible for crisis management and financing solutions, on the importance of social isolation measures, particularly for risk groups, as well as different impacts of measures that can be adopted at different stages of the epidemic. The results should be used with care, considering the limitations of simulations and models that include assumptions that may not apply to all favelas, as well as may be impacted by variables not foreseen in the model, such as comorbidities and immune status of people, which greatly interfere in the outcome of COVID-19 cases. The work can be extended based on new discoveries about the COVID-19. At this moment there is still a scientific effort on getting knowledge about how the virus spreads and how is the development of the disease in different groups of people. The new knowledge can be incorporated to the model in the future to refine and improve it. For validation purposes, future simulation runs can be performed to adjust the parameters to real data for the specific location used for this work.

AUTHOR CONTRIBUTION STATEMENT

V.K. implemented the model, planned and carried out the simulations. V.K, G.S, M.F and E.A contributed to the design and implementation of the research, to the analysis of the results and to the writing of the manuscript. C.M. and J.L reviewed the manuscript considering the epidemiology of pandemic diseases. E.M helped gathering data and information about the scenario in Rio de Janeiro and other parts of the world used to define the parameters of the model.

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REFERENCES

Adhikari, S., Meng, S., Wu, Y.-J., Mao, Y.-P., Ye, R.-X., Wang, Q.-Z., Sun, C., Sylvia, S., Rozelle, S., Raat, H., and Zhou, H. (2020). Epidemiology, causes, clinical manifestation and diagnosis, prevention and control of coronavirus disease (covid-19) during the early outbreak period: a scoping review. *Infectious Diseases of Poverty*, 9.

Adiga, A., Chu, S., Eubank, S., Kuhlman, C. J., Lewis, B., Marathe, A., Marathe, M., Nordberg, E. K., Swarup, S., Vullikanti, A., and Wilson, M. L. (2018). Disparities in spread and control of influenza in slums of delhi: findings from an agent-based modelling study. *BMJ Open*, 8(1).

Batista, A., Antunes, B., Faveret, G., Peres, I., Dantas, L., Bastos, L., Aguilar, S., Baião, F., Mac_aira, P., Hamacher, S., Carnevale, R., and Bozza, F. (2020). Dimensionamento de leitos para os casos de infecção por covid-19 no estado do rio de janeiro para o dia 04 de abril de 2020. Technical Report 2, Núcleo de Operações e Inteligência em Saúde (NOIS).

Candido, D. D. S., Watts, A., Abade, L., Kraemer, M. U. G., Pybus, O. G., Croda, J., Oliveira, W., Khan, K., Sabino, E. C., and Faria, N. R. (2020). Routes for COVID-19 importation in Brazil. *Journal of Travel Medicine*. taaa042.

Cavallieri, F. and Vial, A. (2010). Favelas na cidade do rio de janeiro: o quadro populacional com base no censo 2010. http://portalgeo.rio.rj.gov.br/estudoscariocas/download/%5C3190_FavelasnacidadedoRiodeJaneiro_Censo_2010.PDF.

Chen, J., Chu, S., Chungbaek, Y., Khan, M., Kuhlman, C., Marathe, A., Mortveit, H., Vullikanti, A., and Xie, D. (2016). Effect of modelling slum populations on influenza spread in delhi. *BMJ Open*, 6(9)

da Saúde, M. (2020). Coronavírus no brasil. Technical report, Ministério da Saúde. <https://www.saude.gov.br/noticias?start=20>. Accessed in: April 13, 2020.

da Silveira Barroso Alves, D., Serrano Barbosa, M. T., Raúl Caffarena, E., and da Silva, A. S. (2016). Caracterização do envelhecimento populacional no município do rio de janeiro: contribuições para políticas públicas sustentáveis. *Cadernos Saúde Coletiva*, 24(1). <http://www.scielo.br/pdf/cadsc/v24n1/1414-462X-cadsc-1414-462X201600010272.pdf>.

de Andrade, A. A. S., Silva, G. D., Kloh, V. P., and Filho, J. K. (2020). Modelagem epidemiológica da dispersão da tuberculose pulmonar. Aceito para publicação no XIII Encontro Acadêmico de Modelagem Computacional (EAMC) 2020.

Del Valle, S. Y., Hyman, J. M., Hethcote, H. W., and Eubank, S. G. (2007). Mixing patterns between age groups in social networks. *Social Networks*, 29(4):539–554.

Engelbrechtsen, S., Engø-Monsen, K., Frigessi, A., and Freiesleben de Blasio, B. (2019). A theoretical single-parameter model for urbanisation to study infectious disease spread and interventions. *PLOS Computational Biology*, 15(3):1–36.

Guan, W.-j., Liang, W.-h., Zhao, Y., Liang, H.-r., Chen, Z.-s., Li, Y.-m., Liu, X.-q., Chen, R.-c., Tang, C.-l., Wang, T., Ou, C.-q., Li, L., Chen, P.-y., Sang, L., Wang, W., Li, J.-f., Li, C.-c., Ou, L.-m., Cheng, B., Xiong, S., Ni, Z.-y., Hu, Y., Xiang, J., Liu, L., Shan, H., Lei, C.-l., Peng, Y.-x., Wei, L., Liu, Y., Hu, Y.-h., Peng, P., Wang, J.-m., Liu, J.-y., Chen, Z., Li, G., Zheng, Z.-j., Qiu, S.-q., Luo, J., Ye, C.-j., Zhu, S.-y., Cheng, L.-l., Ye, F., Li, S.-y., Zheng, J.-p., Zhang, N.-f., Zhong, N.-s., and He, J.-x. (2020a). Comorbidity and its impact on 1,590 patients with covid-19 in china: A nationwide analysis. medRxiv.

Guan, W.-j., Ni, Z.-y., Hu, Y., Liang, W.-h., Ou, C.-q., He, J.-x., Liu, L., Shan, H., Lei, C.-l., Hui, D. S., Du, B., Li, L.-j., Zeng, G., Yuen, K.-Y., Chen, R.-c., Tang, C.-l.,

Wang, T., Chen, P.-y., Xiang, J., Li, S.-y., Wang, J.-l., Liang, Z.-j., Peng, Y.-x., Wei, L., Liu, Y., Hu, Y.-h., Peng, P., Wang, J.-m., Liu, J.-y., Chen, Z., Li, G., Zheng, Z.-j., Qiu, S.-q., Luo, J., Ye, C.-j., Zhu, S.-y., and Zhong, N.-s. (2020b). Clinical characteristics of coronavirus disease 2019 in china. *New England Journal of Medicine*.

Go'és, L. G. B., Zerbinati, R. M., Tateno, A. F., de Souza, A. V., Ebach, F., Corman, V. M., Moreira-Filho, C. A., Durigon, E. L., da Silva Filho, L. V. R. F., and Drexler, J. F. (2019). Typical epidemiology of respiratory virus infections in a brazilian slum. *Journal of Medical Virology*.

Hackl, J. and Dubernet, T. (2019). Epidemic spreading in urban areas using agent-based transportation models. *Future Internet*, 11:92.

He, F., Deng, Y., and Li, W. (2019). Coronavirus disease 2019: What we know? *Journal of Medical Virology*, n/a(n/a).

Hunter, E., Mac Namee, B., and Kelleher, J. (2018). An open-data-driven agent-based model to simulate infectious disease outbreaks. *PLOS ONE*, 13(12):1–35.

ICNARC (2020). Icnarc report on covid-19 in critical care 27 march 2020.

Lauer, S. A., Grantz, K. H., Bi, Q., Jones, F. K., Zheng, Q., Meredith, H. R., Azman, A. S., Reich, N. G., and Lessler, J. (2020). The Incubation Period of Coronavirus Disease 2019 (COVID-19) From Publicly Reported Confirmed Cases: Estimation and Application. *Annals of Internal Medicine*.

Long, E. F., Nohdurft, E., and Spinler, S. (2018). Spatial resource allocation for emerging epidemics: A comparison of greedy, myopic, and dynamic policies. *Manufacturing & Service Operations Management*, 20(2):181–198.

Oliveira, I. M. d. et al. (2008). Modelos epidemiologicos seir.

Pereira, A. G. L., Medronho, R. d. A., Escosteguy, C. C., Valencia, L. I. O., and Magalhães, M. d. A. F. M. (2015). Spatial distribution and socioeconomic context of tuberculosis in rio de janeiro, brazil. *Revista de saude publica*, 49:48.

Railsback, S. F. and Grimm, V. (2019). *Agent-based and individual-based modeling: a practical introduction*. Princeton university press.

Rothe, C., Schunk, M., Sothmann, P., Bretzel, G., Froeschl, G., Wallrauch, C., Zimmer, T., Thiel, V., Janke, C., Guggemos, W., Seilmaier, M., Drost, C., Vollmar, P., Zwirgmaier, K., Zange, S., Wolfel, R., and Hoelscher, M. (2020). Transmission of 2019-ncov infection from an asymptomatic contact in germany. *New England Journal of Medicine*, 382(10):970–971.

Sanders, J. M., Monogue, M. L., Jodlowski, T. Z., and Cutrell, J. B. (2020). Pharmacologic Treatments for Coronavirus Disease 2019 (COVID-19): A Review. *JAMA*.

Shi, Y., Wang, Y., Shao, C., Huang, J., Gan, J., Huang, X., Bucci, E., Piacentine, M., Ippolito, G., and Melino, G. (2020). Covid-19 infection: the perspectives on immune responses. *Cell Death Differentiation*.

Sun, J., He, W.-T., Wang, L., Lai, A., Ji, X., Zhai, X., Li, G., Suchard, M. A., Tian, J., Zhou, J., Veit, M., and Su, S. (2020). Covid-19: Epidemiology, evolution, and cross-disciplinary perspectives. *Trends in Molecular Medicine*.

Verma, R., Chahal, V., Kumar, R., Bhalla, K., Dhankar, M., Dhaka, R., and Agrawal, G. (2018). Community perception about swine flu in an urban slum of haryana: A cross-sectional study. *Family Medicine and Primary Care*, 6:1515–1520.

Vial, A., Dias, A., Fartes, B., Patrocínio, B., Ribeiro, B., Borba, C., Tepedino, C., Bovolenta, D., Autran, G., Santos, J., Couto, L., Paiva, L., Salandia, L., Pandolfi, M., Franc̃a, M., Veiga, P., Brito, P., and Moraes, R. (2017). *Caderno ficha dos territórios*. Technical Report 2, Instituto Pereira Passos.