Prediction of the Impact of the End of year Festivities on the Local Epidemiology of COVID-19 Using Agent-Based Simulation with Hidden Markov Models

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Abstract. Towards the end of 2020, as people changed their usual behavior due to end of year festivities, increasing the frequency of meetings and the number of people who attended them, the COVID-19 local epidemic's dynamic changed. Since the beginnings of this pandemic, we have been developing, calibrating and validating a local agent-based model (AbcSim) that can predict intensive care unit and deaths' evolution from data contained in the state electronic medical records and sociological, climatic, health and geographic information from public sources. In addition, daily symptomatic and asymptomatic cases and other epidemiological variables of interest disaggregated by age group can be forecast. Through a set of Hidden Markov Models, AbcSim reproduces the transmission of the virus associated with the movements and activities of people in this city, considering the behavioral changes typical of local holidays. The calibration and validation were performed based on official data from La Rioja city in Argentina. With the results obtained, it was possible to demonstrate the usefulness of these models to predict possible outbreaks, so that decision-makers can implement the necessary policies to avoid the collapse of the health system.

Keywords: Agent-based models · Hidden Markov models · COVID-19 · Epidemiology · Virus transmission · Holyday behavior

1 Introduction

In late 2019, a new coronavirus variant, Sars-Cov-2, was identified and the pathology it caused was named Covid-19. Due to the rapid spread of the virus, a pandemic was

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declared in March 2020 and since then, more than 200 million cases and 4 million deaths have been reported [1, 2].

Various outbreaks of this disease in different regions of the world have been studied and their epidemiological analysis has been useful to develop models, mainly mathematical, intending to track and predict the spread of epidemics [3–6]. In this context, the present work is conceived to provide an alternative that includes some realistic factors and predicts the effects of various social and health policies.

This pandemic has some specific characteristics that differentiate itself from others, such as a high basic reproduction number (R0) of up to 2.79 [7], the seasonality [8] and the asymptomatic infectious [9]. Besides, age range, comorbidities and other variables affect the probability of becoming infected, going to ICU (intensive care units) or dying [10–12]. Furthermore, local climate, social behaviour, and health habits have been demonstrated to affect the dynamics of the epidemic [13–15].

Therefore, this work proposes a new approach, more complex and realistic than the traditional mathematical model, by considering the multiplicity of factors. An agent-based model (ABM) is used to incorporate local information and specific characteristics for each area of study, namely social, cultural, geographical and climatological variables related to the dynamics of COVID-19 [16–18]. Moreover, ABM allows taking into account the intrinsic randomness of the system and monitoring the space-time characteristics of the simulation runs, even though this kind of model is more computationally expensive and requires more data [19].

The newly developed model is called the Agent-based local model for COVID19 Simulation or AbCSim [20] and allows modelling groups of people with COVID19, either symptomatic or asymptomatic, together with those considered susceptible or cured. The model also considers the complexity of pathology dynamics and the interpersonal relationships within the populations, along with geographical and climatological information relevant to the pandemic [21]. Additionally, it implements a host transmission block based on a set of Hidden Markov Models (HMMs), which reflect the main aspects of agents´ mobility and social activities [22–24].

Access to local specific population information from La Rioja is provided by the Argentinian Public Health Research on Data Science and Artificial Intelligence for Epidemic Prevention (ARPHAI) [25]. This is a project whose main objective is to develop technological tools based on artificial intelligence and data science applied to electronic health records (EHRs). Information extracted from the Acuario database of La Rioja medical records, among other public information, was used.

This work presents a case study, allowing the evaluation of the dynamics for festive dates to make possible the prediction of the effect of gatherings and parties. Therefore decision-makers can implement relevant health and social policies based on this information.

This document is organized as follows: material and methods are presented in Sect. 2, followed by a brief description of the model in Sect. 3. Section 4 details the case study. The results and discussion are shown in Sect. 5. Finally, Sect. 6 includes the conclusions and future work.

2 Material and Methods

2.1 The Agent-Based Model

Agent-based modelling (ABM) is a knowledge-based modelling technique and a useful method for representing biological systems that are irreducibly heterogeneous, where randomness plays a major role and which contain numerous interactions between component subsystems and with the environment [26, 27].

One of the reasons why ABM became popular is because it can simulate and help analyze complex organizations or self-organizing systems. This means that the ABM paradigm can represent "large" systems, which are produced by the interaction of many "small" sub-systems (or agents) that can learn or change their behaviour over time [28].

These characteristics of ABMs make them very versatile and have made them impactful in many areas, including epidemiology. Some of the first works that employed ABMs in public health were used to address infectious diseases. However, over time its uses have expanded to other areas such as chronic disease research and social epidemiology. The use of ABMs has been greatly favoured by the ease with which this modelling strategy allows the integration of individual behaviour into frameworks that view health as the product of the interaction of biological, social and environmental factors [29, 30].

In this work, the AbCSim model [20] is used to predict how social behaviours related to end of year festivities impact the epidemiology of COVID-19.

2.2 Markov Models in AbCSim

Hidden Markov Models (HMMs) are a proper foundation for creating probabilistic models of linear sequence labelling problems. They deliver a conceptual toolkit for complicated models from a simple intuitive graphical representation. They are at the heart of a diverse range of programs, widely used in the biological field [31].

HMMs have been used in many areas, such as automatic speech recognition [32], analysis of electrocardiographic signals [33], analysis of epileptic seizure frequency [34], and DNA sequence analysis and alignment [35]. Some investigations apply this model to different distributions of epidemiological data (binomial, Gaussian, Poisson) and particularly in the analysis of population surveillance [36, 37].

In AbCSim people's mobility events are modelled in discrete time steps with transition probabilities from one state to another that occur during the day in uniform time periods. A transition probability depends only on the state in which the individual is at a given time. There is a particular HMM for each human agent Ha, based on age range (e), neighbourhood (l) and the time slot (h) corresponding to simulation time. As shown in the state graph in Fig. 1, all these HMMs have four states. Each state represents a different type of location or activity, namely: Home (C), Work (T), Leisure (E) and Others (O). In turn, each HMM has its own transition matrix, which represents state change probabilities, that is, to move from one type of location (j) to another (i); a matrix showing output probabilities for each state (for the k possible places where Ha could go in the state j) and a vector of initial location probabilities. Vector is always (1, 0, 0, 0) for the beginning of the day, as it is assumed that all citizens start the day at home.

In another way, a Markov model applied to the progression of the illness in a host (within-host progression), can be defined as a stochastic model in which the patient is assumed to be always in one of a finite number of health states (called Markov states), which must be exhaustive (i.e., all possible) and mutually exclusive (an individual cannot be in two states at the same time) [38]. In this way, popular epidemiological compartmental models first formulated by Kermak & Mac Kendrik [39] can be seen as Markov chain models, as well. As can be seen in Fig. 2, in AbCSim a modification of the compartmental model proposed by Arenas [40] is used to simulate the in-host virus propagation dynamics.

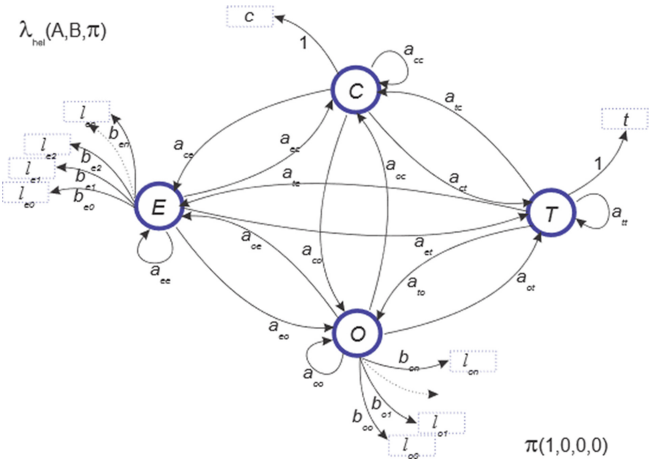

Fig. 1. State graph of a Hidden Markov sub-model. The four states circled, represent C: House; T: Work; E: Leisure; O: Others. Rectangular blocks show possible outputs for each state, i.e., each waypoint. States C and T have only one possible output (defined in the attributes of each human agent, see [21]), therefore, that output has a probability 1 of being chosen. States E and O have different possible outputs selected from a list with locations that depend on the human agent's neighbourhood.

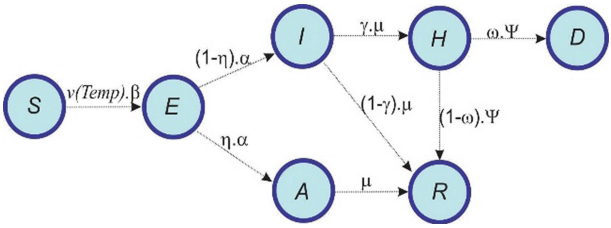

Fig. 2. Spread sub-model with seven states: S: susceptible; E: latent or exposed; I: symptomatic infectious; A: asymptomatic infectious; R: recovered; D: dead, and H: hospitalized. Modified from Arenas et al. [40]

2.3 Data Sources

The model takes information from several data sources. The first source was Acuario [41], the informatics system used in the province of La Rioja for the registration of outpatient care. It has a relational database with more than 200 tables that gather information on 268,000 individuals treated in the province's public health system. The information used from Acuario was mainly three variables: the initial number of people infected, the proportion of people in each age range, and comorbidities in the population. Also, sociological data [42–47], such as the unsatisfied basic needs index and the existence of a drinking water network were used to characterize the different neighbourhoods that are represented in the model.

The data used were de-identified before leaving state headquarters and were stored and processed at the Centre for High-Performance Computing (CCAD) under strict security and access rules. In addition, all data handlers were required to present the Good Clinical Research Practices certification issued by the National Institute on Drug Abuse (NIDA) in collaboration with the Center for Clinical Trials (CCTN), as well as an individual confidentiality commitment.

On the other hand, several public sources were consulted for different purposes, such as: Google Mobility [48]; Google Maps [49]; Google Places [50]; National Weather Service (SMN) [51]; official government pages [52] and different local demographical literature.

3 Model Description

AbCSim is implemented in Java and runs on the computational simulation platform: Repast [53]. This is a platform with a set of open-source modelling and simulation tools based on agents, that runs on different operating systems.

The general scheme of the model is presented in Fig. 3, where its different blocks and implementation levels are identified. The top-level shows the model in its most abstract stage, as a black box, indicating the initial conditions, inputs and outputs. The intermediate level shows the two main blocks that make up the model: one block dedicated to the simulation of the spread of the virus within each host and another dedicated to the transmission of the disease between hosts. Finally, at the lower level, the different sub-models are indicated with their own parameters (Infectivity, Epidemiological characterization, Interpersonal contact, Location and Mobility/Activity, Transport and Infectious trail). In the following sections, they will be properly characterized and detailed individually (together with their contributing modules).

As an agent-based model, a fundamental part of the system is the implementation of human agents (Ha), which possess specific characteristics and attributes of risk factors and co-morbidities. In addition, they can contract and transmit the virus, change their health status and symptoms, and modify their behaviour accordingly.

The relationship between the different human agents with each other and with the environment is also depicted, as the distance between agents, the use of masks, the respect for the place's capacity and the different rules and protocols, are key in modelling the transmission of the virus.

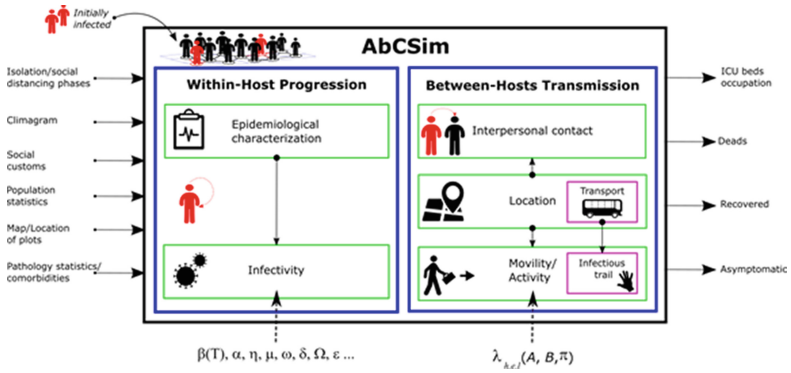

Fig. 3. AbCSim block diagram: General model (black block) with inputs, outputs (horizontal solid line arrows) and initial conditions (curved arrows); main functional blocks (blue left and right-side blocks) and the corresponding sub-models for each block (green and magenta blocks). Vertical solid line arrows represent the relationships between various model elements, and vertical dotted line arrows, the corresponding parameters [21]. (Color figure online)

The behaviour of each agent depends on their age group, habits and the neighbourhood where they live, which are randomly assigned at the beginning of the simulation according to the population statistics of La Rioja city.

The mobility of each agent is linked to the transition states matrices (activities/places) implemented by means of a set of HMMs (see Sect. 2.2). Each of the HMMs corresponds to an area where the agent lives, the age group to which it belongs and the time zone in which it is at the time of the simulation.

As already mentioned, AbCSim has two main blocks, the first one is about virus propagation within the host, and includes the infectivity sub-model, considering epidemiological characterization (see Sect. 2.2). The second one is about host-to-host transmission and covers the different virus transmission mechanisms between hosts (infectious trail, direct contact or droplet-to-face) in different spaces (home, office, recreation, public transport), and specific circumstances (place's capacity, ventilation, temperature).

Due to the stochastic nature of the epidemiological phenomenon and the model used to try to reproduce it, several "complete" runs must be carried out to obtain the final results, requiring the use of a computer cluster.

4 Case Study: End of Year Festivities

At the end of the year festivities, people tend to get together for dinner and celebrations, and young people go out partying, increasing the number of personal contacts. A particular analysis of this situation is carried out in this work. Parameters of AbCSim were established to reflect the local characteristics of the city of La Rioja and its inhabitants. For more details, including parameters setting and estimation methodology, the reader is referred to [21].

In order to use the AbCSim as a what-if model, different scenarios were proposed, where the regulatory force varied from minor to major. Based on the impact the different

scenarios would have on the number of ICU beds, health decision-makers can establish the level of regulation to implement.

For this, some aspects were considered, on the one hand, dinners were represented for the nights of December 24 and 31, where families are considered to gather to celebrate. The duration and attendance of dinners were varied for the different scenarios. In addition, parties attended mainly by young people were also considered. Finally, since on festive dates people visit stores and entertainment venues frequently, the capacity of these places was varied, with differences among the tested scenarios.

Three scenarios were proposed and analyzed:

- **High Regulated**: due to regulatory constraints that would be proposed, it is assumed that 70% of the population would meet at Christmas and New Year's Eve, in gatherings of 10 people for a period of two hours. Additionally, 20% of young people go out partying, both indoors and outdoors. Also, the minimum distance between people of one and a half meters is respected in every place.
- **Medium Regulated**: it is assumed that 80% of the population would gather at Christmas and New Year's Eve, in meetings of 15 people each for a period of two hours. In addition, 20% of young people would go out partying afterwards, both indoors and outdoors. Finally, the minimum distance between people of one and a half meters would not be respected in shops.
- **Low Regulated**: it is assumed that 90% of the population would meet at Christmas and New Year's Eve, in gatherings of 20 people for a period of two hours and a 40% of young people go out partying also, both indoors and outdoors. In addition, the minimum distance between people of one and a half meters would not be respected in shops, leisure and other venues.

5 Results and Discussion

For each scenario, bed occupancy (Fig. 4), number of symptomatic cases (Fig. 5) and number of accumulated deaths per Covid-19 (Fig. 6) until the end of February were analyzed. In addition, the number of symptomatic versus non-symptomatic cases was compared (Fig. 7).

It can be seen from the results presented that in the low regulated scenario, where there are more meetings than in the other scenarios, there is a relative increase in cases, ICU bed occupancy and deaths due to Covid-19, from January 20th onwards.

This is in line with expectations, as the effect is not immediate, but due to the in-host illnesses and contagion progression, the impact is expected to be seen two to three weeks after the festivities. Also, it can be seen comparing the subplots in Fig. 4 that as much more gatherings are attended, the effect of the festivities generates a stronger impact on ICU bed occupancy. A similar phenomenon can be seen in the number of daily cases and accumulated deaths.

There is no field data available for the analysis of symptomatic versus non-symptomatic patients. However, AbCSim shows that in the low regulated scenario, where there were more contacts with young people who went partying, and therefore more contagion, the number of asymptomatic patients increased, if it is compared to

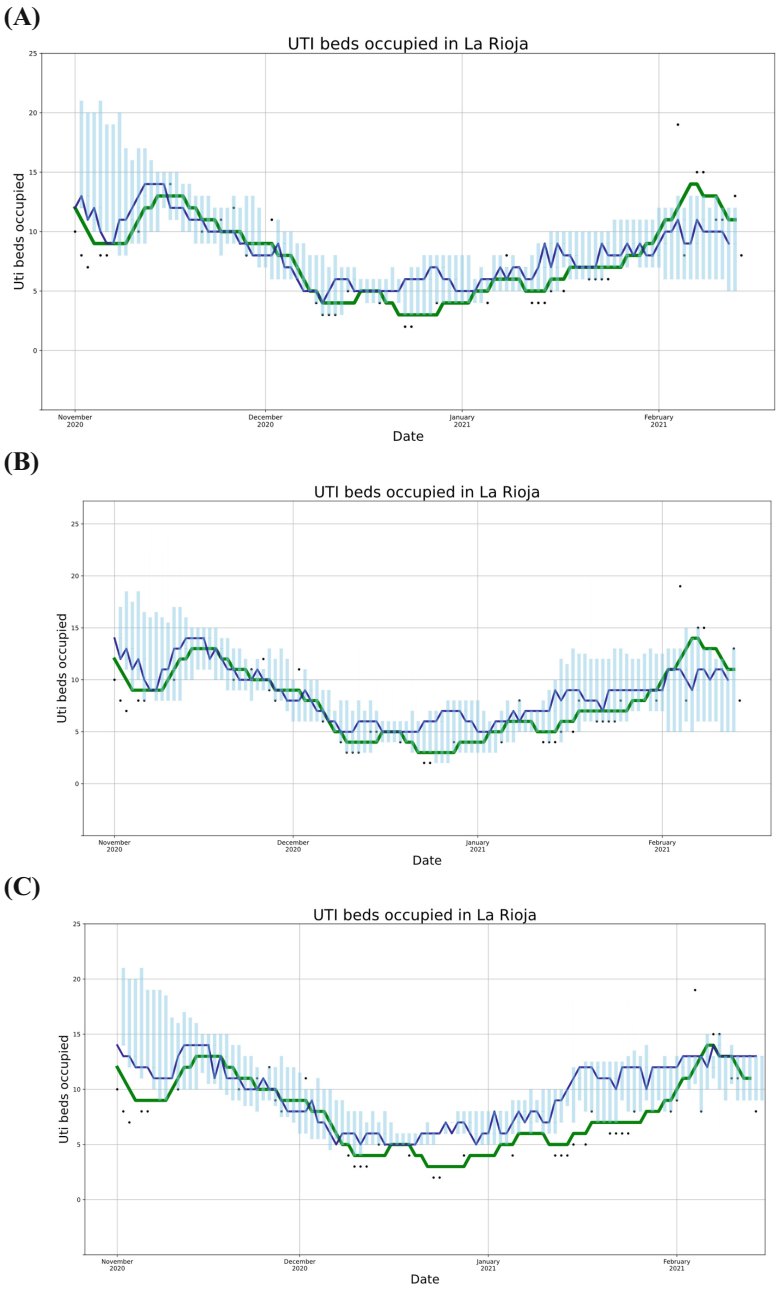

Fig. 4. ICU beds occupied by positive COVID-19 patients in the period under study: (A) corresponds to the High Regulated scenario; (B) corresponds to the Medium Regulated scenario and (C) corresponds to the Low Regulated scenario. ICU beds for Covid-19 + surveyed by the official data are shown in black, with the interpolation from field data in green, the dispersion of the corresponding model output in light blue; and in blue its central tendency.

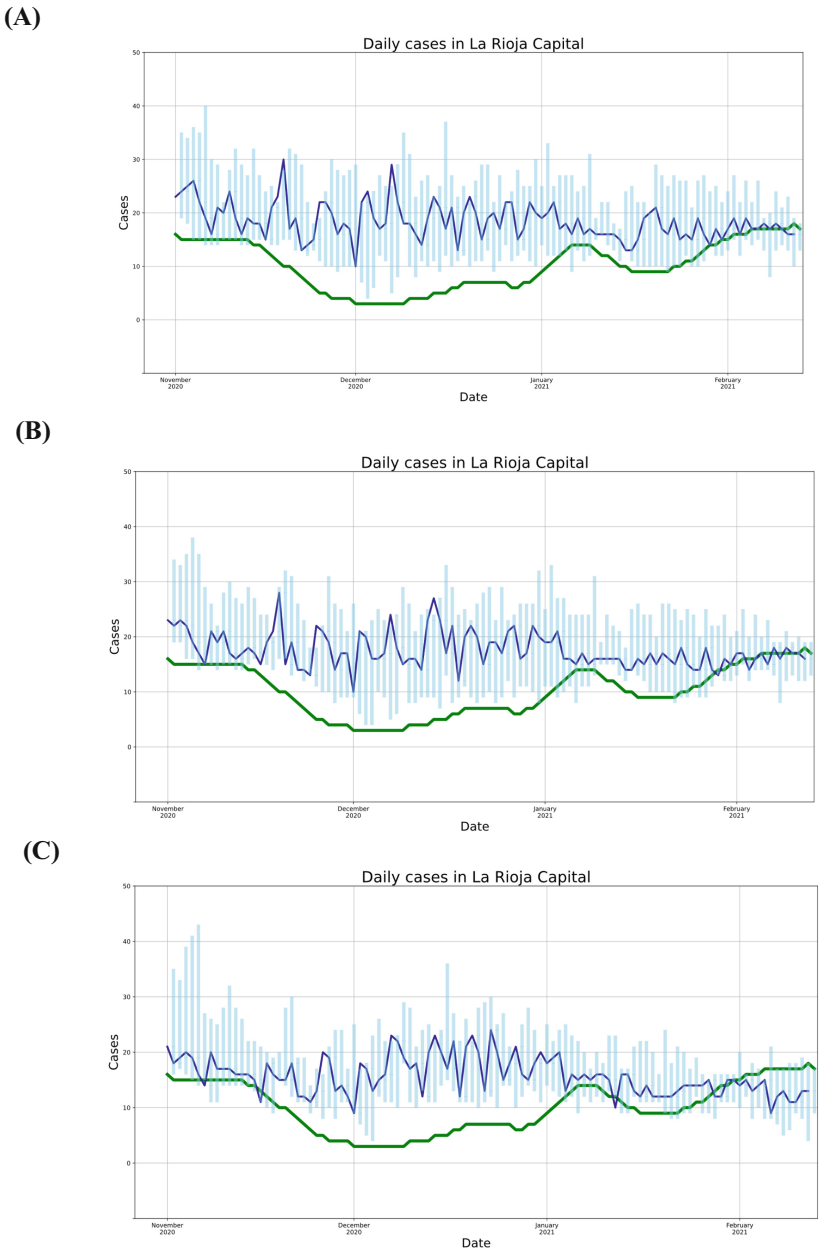

Fig. 5. Daily COVID-19 cases (symptomatic + asymptomatic) estimated by the model in the period under study: (A) corresponds to the High Regulated scenario; (B) corresponds to the Medium Regulated scenario and (C) corresponds to the Low Regulated scenario. Light blue shows the dispersion of the model output and blue, its central tendency. The interpolation from field data is shown in green. (Color figure online)

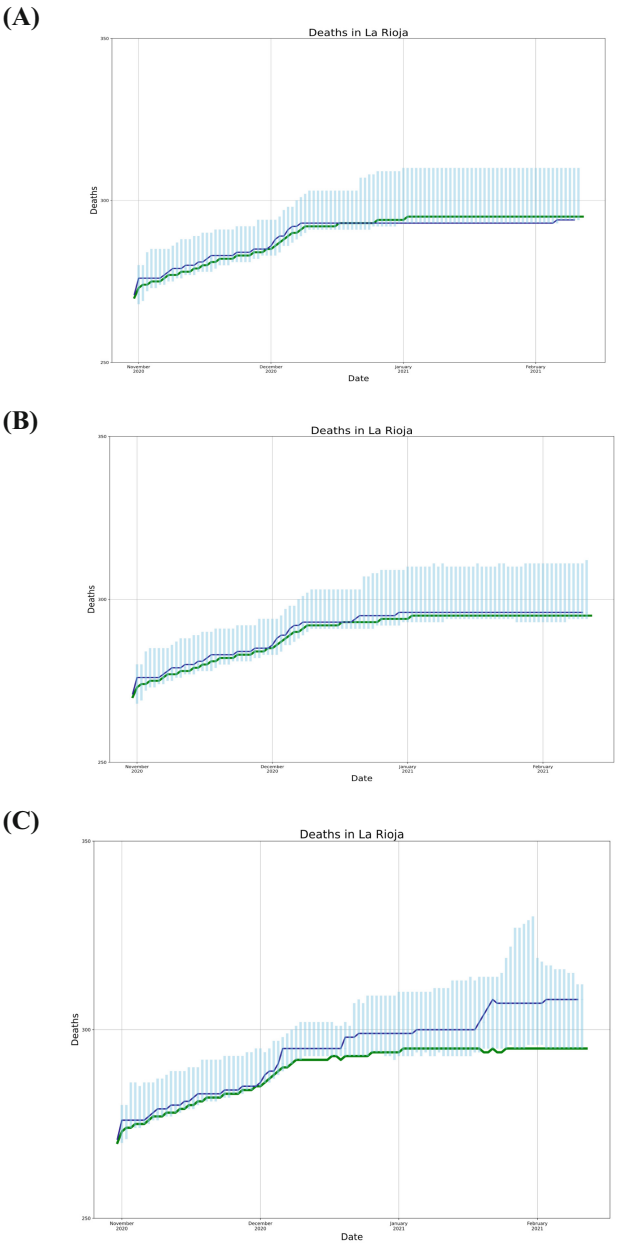

Fig. 6. Accumulated number of deaths due to COVID-19 estimated by the model in the period under study: (A) corresponds to High Regulated scenario; (B) corresponds to the Medium Regulated scenario and (C) corresponds to the Low Regulated scenario. Light blue shows the dispersion of the model output and blue its central tendency. The interpolation from field data is shown in green. (Color figure online)

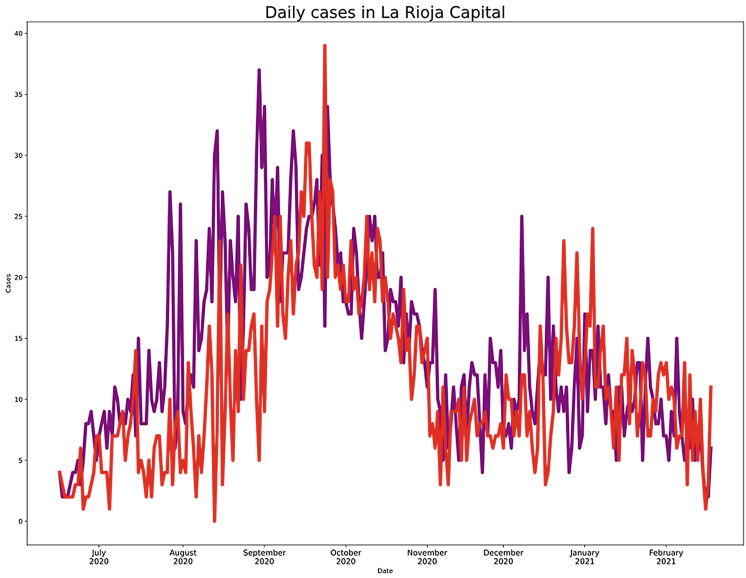

Fig. 7. Daily COVID-19 cases estimated by the model in the period under study for the low regulated scenario. Symptomatic cases are in purple and asymptomatic cases are in red. (Color figure online)

previous months. This may be because most of the contacts are among young people, and due to their age range, they tend not to show symptoms.

A detail to be considered when interpreting these results is that at that time only alpha and delta variants were circulating, and mass vaccination had not yet begun in Argentina country. In addition, the model contemplates the ventilation of homes and buildings, which reduces the rate of contagion, because during the holidays it is summer in the southern hemisphere.

Finally, in retrospect and qualitatively compared with the field data, it is considered that the high regulated scenario is the most representative of what really happened in La Rioja city. This is a good corollary since this scenario is precisely the one that the government proposed for the end of the year festivities. Although it is an a posteriori analysis, it makes it clear that the tool offers the possibility of using the information provided by the simulations to propose some type of restriction, contemplating how much impact it would have, for example, on the increase in ICU beds, compared to the cost of implementing these restrictions.

6 Conclusion and Future Works

In this work, the impact of the end of year festivities on the local epidemiology of COVID-19 was predicted and analyzed using agent-based model simulations with AbCSim. It can be concluded that AbCSim works well as a "what-if model", allowing the analysis of different scenarios and providing decision-makers with a useful tool to properly select the social and health policies they implement.

These models require large amounts of data and calculation power, but on the other hand, they are almost totally explicit and allow a detailed proposal and analysis of particular local situations. In this case for example, it is expected that the model for a relatively small city with this geographical location, such as La Rioja, will behave very differently from the model for a country capital such as Buenos Aires.

In future works, other case studies will be presented, including the impact of ventilation, vaccination, immunity time and school protocols on the dynamics of Covid-19.

7 Disclaimer

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In the same way, the document does not represent the position of the ARPHAI project or of the consortium member institutions.

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