

Simulating pandemic emergency scenarios considering mobility patterns through an agent-based model

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Abstract

One of the main policies to contain a pandemic spreading is to reduce people mobility. However, it is not easy to predict its actual impact, and this is a limitation for policy-makers who need to act effectively and timely to limit virus spreading. Data are fundamental for monitoring purposes; however, models are needed to predict the impact of different scenarios at a granular scale. Based on this premise, this paper presents the first results of an agent-based model (ABM) able to dynamically simulate a pandemic spreading under mobility restriction scenarios. The model is here used to reproduce the first wave of COVID-19 pandemic in Italy and considers factors that can be attributed to the diffusion and lethality of the virus and population mobility patterns. The model is calibrated with real data (considering the first wave), and it is based on a combination of static and dynamic parameters. First results show the ability of the model to reproduce the pandemic spreading considering the lockdown strategy adopted by the Italian Government and pave the way for scenario analysis of different mobility restrictions. This could be helpful to support policy-making by providing a strategic decision-tool to contrast pandemics.

Keywords

Agent-based simulation, Virus spreading, Mobility Restrictions, Risk index

1. Introduction

The spreading of a pandemic is linked to the transmissibility of the pathogen responsible for the infection and the characteristics of the host population. When the host population is represented by humans, it is complex to predict its spreading since it is highly linked to population patterns and their mobility [1]. During the first phase of the COVID-19 emergency in 2020, governments around the world considered several mobility restrictions measures to struggle the pandemic diffusion. Recent literature tries to quantify the actual effects of these restrictions on the virus spreading, e.g. via a multiple linear regression model also including the number of tests per day and environmental variables [2]. However, this is not an easy task due to biased data, and this is a limitation for policy-makers who need to implement effective and timely measures. Some authors focused on data related to excess deaths, which are likely to be less affected by assumptions, and correlated them with mobile data, showing that mobility is responsible for more than 90% of the initial spreading in Italy and also in France [3]. Mobility restrictions, however, are considered among the most effective policies, although they clearly affect the economic conditions of both people and governments and can also responsible for a “segregation effect” of people with low income [4], [5]. In particular, studies referred to the US

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and Chinese cases analyzed huge amount of data and statistical models to show the strong correlation of such restrictions on the virus spreading [6]–[9]. Giacobelli [10] carried out an analysis to test the impact of social distancing and vaccination in Lombardy (Italy). The study is aim at verifying the effectiveness of containments measures and vaccination on virus spreading. However, other studies show how a lockdown based on distance regulations and restrictions on contact (as in the case of Germany during the first wave) may be as effective as a hard lockdown (as in the case of Italy during the first wave) [11]. This highlights that, notwithstanding the big role of data analysis to understand the pandemic phenomenon, it is also important to have more general models to predict the impact of different policy scenarios, including territorial parameters, independently from the available infection data. Other studies moved in this direction. Mahmood et al. [12] developed a simulator based on geospatial data and diseases factors to forecast infection and hospitalization rate. Silva et al. [13] performed an agent-based analysis to verify the impact of different policy measures. They elaborated an open-source code able to recreate different scenarios and compare the effectiveness of such interventions. Both studies provided a tool for decision-making that is only focused on COVID-19 emergency related factors. In this paper, we test the suitability of an agent-based model (ABM) to dynamically reproduce virus spreading on a large-scale level, considering different factors that can be attributed to the diffusion and lethality of virus and population mobility patterns. The final aim is to build a model that adapts to different contexts and sanitary emergencies linked to any respiratory diseases. The novelty of the model lies in the fact that it provides a tool that can be used for strategic planning purposes to promptly act to a sanitary emergency in order to limit health and economic impacts.

To test the model, the ABM is applied to the Italian case study and reproduces the first wave of COVID-19 pandemic. Next section will briefly describe the fundamentals of the ABM.

2. ABM model

Agent-based modelling is a computer technique that allows to reproduce communities of intelligent and autonomous agents, acting and interacting among themselves and with the environment, according to simple behavioral rules [14]. It allows to recreate complex social interactions and population mobility patterns [15], [16]. By simulating interaction processes at a micro level, emergent behaviors and phenomena at a macro level can emerge [17]–[19].

In this study, a model is proposed for simulating the spread of a generic virus. To test the model, the first wave of COVID-19 in Italy has been simulated. In the ABM, there are two types of agents: administrative regions (r) and individuals (i), i.e. the agents representing the population of the simulated area. The model has been implemented in the NetLogo software which is a multi-agent programmable modeling environment capable of simulating and modelling complex systems [20]. The phases of the model are schematized in Figure 1 and explained in the following.

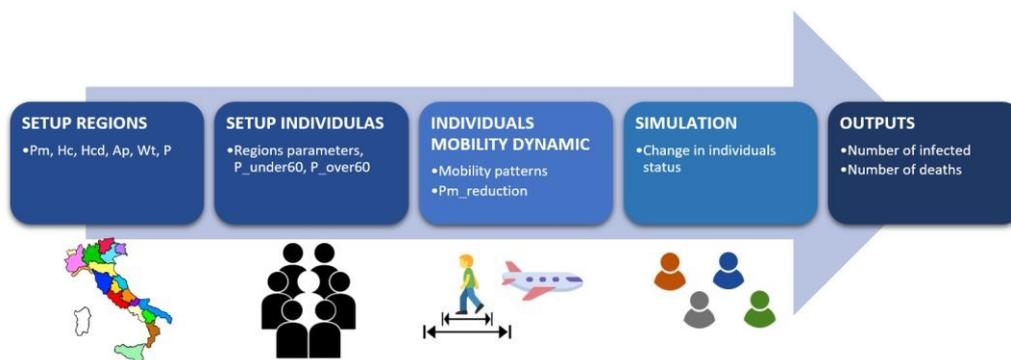


Figure 1: Phases of the ABM

To characterize the agents and simulate pandemic spreading, we referred to the study of Pluchino et al. [21] that developed an a-priori risk index (RI) and calculated it for each Italian region. The Authors demonstrated a correlation between the geographic distribution of RI with a set of available COVID-19 official data (i.e. number of infected individuals, patients in intensive care and the number of deaths.).

For the calculation of RI Pluchino et al. [21] referred to the Crichton's Risk Triangle which evaluates RI as a function of three risk parameters: hazard, exposure and vulnerability [22]. Each of these variables were defined with factors linked to the COVID-19 spreading. The hazard takes into consideration those factors that can intervene in the spread of the infection. It is a function of three factors: population mobility index (Pm), housing concentration (Hc) and health care density (Hcd). Exposure is in this case a measure of the people exposed to the infection, and it's calculated as the total population number by region. Finally, vulnerability is a measure of an individual's likelihood of being infected. Vulnerability is also a function of three parameters, air pollution (Ap), winter temperature (Wt) and age of population (P).

The dynamics of the model is given by the changes in the Pm parameter ($Pm_reduction$), which are evaluated for each agent r and different time windows, according to mobility restriction.

Individual-agents in the model move according to the assigned mobility index multiplied by a variable probability of making a trip belonging to distances' classes from 2 km to 50 km or more. Trips over 50 km are considered as long-distance trips, that are usually made by airplane or train [23], [24]. For sake of simplicity, in this model we assumed that for trips over 50 km, agents moved by airplane.

In Pluchino et al. [21], RI is calculated for each region as a floating-point variable between 0 and 1 and is obtained as, where the exposure is the population of each region:

$$RI = HAZARD \cdot VULNERABILITY \cdot EXPOSURE \quad (1)$$

In the ABM the Authors provided a dynamic version of RI (ri) proposed by Pluchino et al. [21] by referring it to each individual-agent. In this respect, the calculation of the new risk index (ri) excludes the exposure component and all the parameters related to the aggregated region population:

$$ri = hazard \cdot vulnerability \quad (2)$$

$$hazard = 1/3 \cdot Hc + 1/3 \cdot Hcd \quad (3)$$

$$vulnerability = 1/3 \cdot Wt + 1/3 \cdot Ap \quad (4)$$

By combining the RI with the mean infection duration, the model determines the status associated to each individual on the basis of a SIR-based approach proposed by Kermack and McKendrick, on 1927 [25]: susceptible, infected, isolated (or not isolated), immune and dead (Figure 2).



Figure 2: Individual-agents status

During the simulation the individual-agents change their status over time according to their P_m and their meetings, as it follows. At the beginning of the simulation two agents with the status “infected” - which represent the “zero patients” – are located at certain locations, while all other individual-agents have the status called “susceptible”. The individuals start moving on the basis of their assigned P_m and they start to meet each other. When a “susceptible” individual meets an “infected” one, it will contract the virus with a probability based on the product between hazard and the fixed parameter *virulence*, which corresponds to the contagiousness of the virus. It was calculated through a calibration analysis, by comparing the number of real deaths and the simulated one from February 28th to March 11th (i.e. from the first outbreaks detection and to the start of lockdown in Italy). If the product between hazard and virulence is bigger than the value *random-float 1* (a random floating number between 0 and 1), individuals will change their status to "infected". The infected individual is assigned with a probability of being symptomatic ($\leq 10\%$) or asymptomatic ($\geq 90\%$)², which correspond respectively to the status or “isolated” and “not isolated”. A mean infection duration time is considered, during which the individual keeps the acquired status; after this time, the individual dies or recovers from the infection, assuming “dead” or “immune” status; the probability of death is given by comparing the product between vulnerability and lethality with a random floating number between 0 and 1. If this product is higher than this random number, the agent assumes the status “dead”. The value of lethality, i.e. the mortality level of the virus, should be based on real data; due to data uncertainty, it oscillates around 2% [26], varying according to a Gaussian probability distribution with mean 0.02 and standard deviation 0.01. Hazard and vulnerability are parameters of each individual, while virulence and lethality are linked to the characteristics of the virus.

2.1. Case study

For a first test of the model, the case study is related to Italy and the first wave of COVID-19. Italy was the first European country in which the virus was detected, although the dynamics of spread and the date of the first outbreaks remain uncertain. The first confirmed cases of contagion date back to 2020, January 23rd, when two tourists from China were tested positive for the virus in Rome. The first two outbreaks of COVID-19 infections with positive cases of Italian citizens were reported later, on February 21st, in the regions called Lombardy and Veneto³. Since then, the infection has spread throughout Italy with varying intensity. The northern regions were the most affected, in particular in terms of deaths, as also confirmed by Pluchino et. al [21]. Nevertheless, several studies have shown

² <https://www.istat.it/it/archivio/246156>

³ <https://lab24.ilsole24ore.com/storia-corona/virus/>

that there were actually cases even before [27], [28]. On March 7th, a government measure imposed some travel limitations. On March 11th, the restrictive measures were converted into a national lockdown, with a “stay-at-home” order limiting travelling only for essential services or urgent reasons. Figure 3a shows statistics on the number of daily cases in Italy. The trend increases starting from March, and it seems to have a surge in the second wave starting from October 2020. The first trend is justified by the difficulty to accurately detect the actual number of infected [29]. Subsequently, with the growth in the number of tests, the share of recorded infected people has gradually increased (Figure 3b). Nevertheless, uncertainties on the actual number of cases still remain, due to the biased data available on the contagion rate.

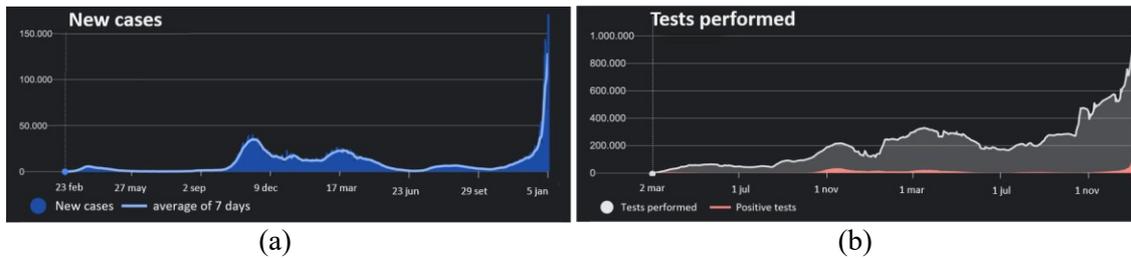


Figure 3: Daily New Cases (a); Daily tests performed (b) from the beginning of the pandemic in Italy (source: google.it)

3. Results and discussions

Based on previous literature studies addressing the actual starting period of the COVID-19 spreading ([27], [28]), we simulated eight different scenarios by changing the starting date but keeping the finish date set to June 25th (after the end of the first pandemic wave). For each scenario, the input data are the following: lethality, virulence, starting and finish date of the first wave of the pandemic (Table 1)

Table 1
Variable and Fixed Input data of the scenario simulation

SCENARIO	Variable	Fixed
	Starting date	
1	07/09/2019	
2	21/09/2019	Finish date
3	14/12/2019	25/06/2020
4	28/12/2019	Lethality
5	11/01/2020	0.022
6	25/01/2020	Virulence
7	08/02/2020	0.0035
8	22/02/2020	

The two “zero patients” were located in Lombardy and Lazio, regions where the first cases of COVID-19 occurred and those where hub airports are present; hence they were considered the regions with more connections to other countries.

The output data of the simulation, calculated on June 25th, 2020, are the following:

- Number of infected people for each region (Figure 4);
- Number of dead people for each region (Figure 5).

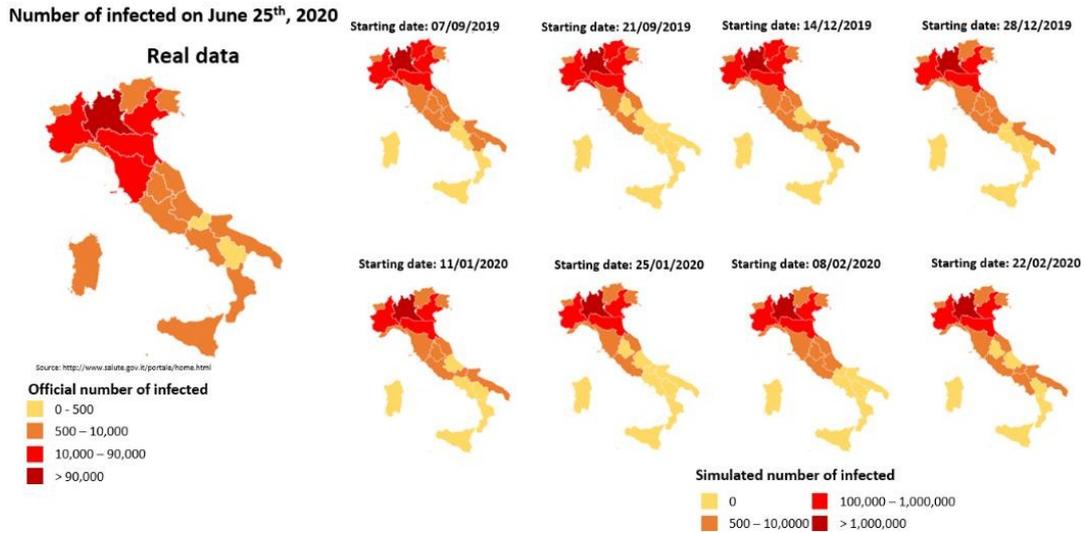


Figure 4: Distribution of number of infected for each scenario

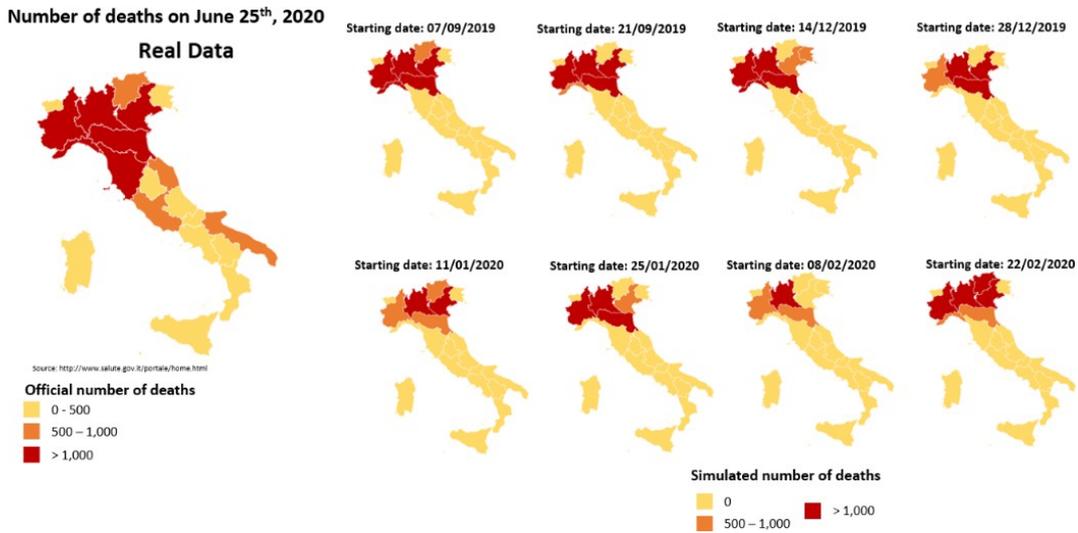


Figure 5: Distribution of number of deaths for each scenario

Both in Figure 4 and Figure 5, the map on the left shows the official data released by the Italian Ministry of Health, respectively related to the number of infected and deaths.

As can be seen in Figure 4, the model is able to accurately reproduce the discrepancy in the number of infected between northern and other regions (central and southern). However, the order of magnitude between official and simulated data is very different (1:10). These findings are in line with the World Health Organization (WHO) which stated that in October 2020 the 10 percent of the global world population was infected with the virus⁴, leading to the belief that also in Italy the number of infected was actually higher than the one reported by official data sources, reaching millions of infected. This number is also comparable with the average annual number of seasonal flu cases⁵. In Figure 4 there are some regions with zero number of infected, this is due to the approximation of 1 agent corresponding to 1000 inhabitants. This limitation allows to reduce the computational time of the simulation but makes difficult to replicate a number of real infected under the threshold of 1000.

The accuracy of the model is also demonstrated by the results related to deaths by region, as shown in Figure 5. simulation results are similar to the official data, also considering the approximation of the

⁴ <https://www.cnn.com/2020/10/05/who-10percent-of-worlds-people-may-have-been-infected-with-virus.html>

⁵ <https://www.epicentro.iss.it/influenza/stagione-2019-2020-primo-bilancio>

number of agents. Official data on deaths are less error-prone and independent on tracking reliability as is the case of infected detection. In this view, our findings give a greater validity to the model for its capability of accurately reproducing the number of deaths. Also in this case, it is possible to see how the model is capable of simulating the discrepancy between north and other areas.

Lastly, Figure 6 shows the distribution of the number of infected, setting the starting date respectively on February 22nd (official date) and December 14th. Model results show a peak of infections in June when the starting date is the official one. Actually, the peak was reached in March, as visible by starting the simulation before (December 2019). Therefore, it seems more likely that the pandemic in Italy began before February.

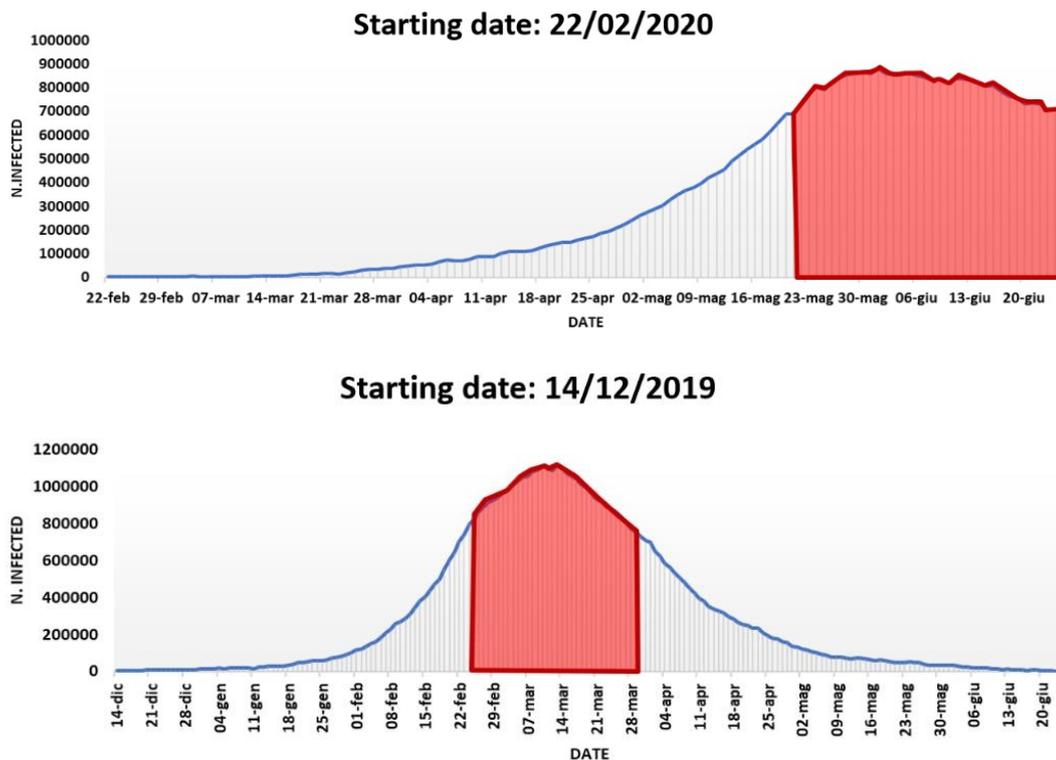


Figure 6: Distribution of number of infected by setting starting date on 22/02/2020 (official date) and on 14/12/2019

4. Conclusion

Mobility restrictions and lockdowns are among the main interventions adopted by governments to contrast the diffusion of a pandemic, like the COVID-19 one. However, at the beginning of the virus spreading, the adoption of an adequate pandemic plan could lead to less drastic economic consequences [30]. In this paper, an ABM is presented to dynamically simulate a virus diffusion. The aim is to provide useful suggestions to contrast pandemic emergencies in the context of a preliminary strategic plan. The model is inspired by the work of Pluchino et. al [21] defining an a-priori risk index based on context-specific characteristics (e.g. air pollution, ageing population, hospital density). The agents of the model are therefore endowed with an a-priori risk index and move according to an assigned mobility index.

To test the model, we referred to the first-wave of COVID-19 spreading in Italy, calibrating the variables so to accurately reproduce the real scenario.

Results show that the model is able to accurately simulate the pandemic spreading, especially in terms of number of deaths and differences among the regions. A higher number of infected results from the simulations with respect to the real case. This is attributable to the biased data regarding infections due to scarce tracking (i.e. a low number of tests) especially during the first wave. Finally, the model shows how it is likely that the pandemic started well before the official date in February 2020.

By using this result, the model can be used to simulate different scenarios beyond the status quo at a granular scale, e.g. by reproducing differential lockdowns based on the a-priori index.

Besides, the model could be tested in other contexts where the virus spreading followed different patterns.

Although calibrated on COVID-19 data, the ABM can be easily adapted to any health emergencies caused by respiratory diseases. It is configured as a decision support tool able to provide useful information for government agencies to undertake the proper interventions in the event of a pandemic diffusion. Future researches will include a scenarios analysis in order to test the impact of different mobility restrictions on the virus spreading [31] and will implement the vaccination phase.

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