Agent-Based Modelling of the spread of COVID-19 in Corsica

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***Abstract*—The modelling epidemiology processes supporting public policy decision-making usually require *SIR* compartmental models which mathematically describe the pandemic phenomenon's dynamics. In general, these models and extensions are used to conceptualize a macro-level of populations evolving between different pre-determined health statuses. In this work, we propose an alternative modelling for the COVID-19 pandemic according to probabilities defined by interactions among individuals. We present an *Agent-Based Model* (*ABM*) to take into account both the heterogeneity of individuals population health statuses and the spatial structure of the environment. The model is verified by reproducing already known results of Corsica's COVID-19 pandemic data and different patterns of COVID-19 virus spread are visualized at any time with the *NetLogo* simulation environment. The implementation details of our alternative approach is then detailed and discussed.**

***Index Terms*—COVID-19, Computational modelling, Agent-Based Model, NetLogo.**

I. Introduction

The *Coronavirus 2019 disease* or *Covid-19* caused by the *SARS-CoV-2* virus appeared on November 16, 2019 in Wuhan, China in the province of Hubei. It spread all over the world and officially became a pandemic on March 11, 2020. In order to cope with the formation of numerous epidemic clusters and to preserve the capacities of hospitals, many countries took containment measures that were unprecedented in the modern industrial world and had major economic, social and environmental consequences. These measures are still causing uncertainties and fears regarding global economy, education, health and populations fundamental rights. On April 15, 2021, France officially reached 100,000 deaths. On April 17, 2021, 3 million deaths due to *COVID-19* were recorded worldwide. In France, official data on the spread of the epidemic are consolidated by the *Ministry of Solidarity and Health* [1] and "*Santé publique France*" [2]. This data can be downloaded from the Web [3]. In *Computer Simulation Science* (*CSS*), conceptual pandemic models have been implemented and simulated for more than half a century. These trivial submodels are historically based on mathematical epidemiological models called *compartmental SIR models* (*S* for *Susceptible*, *I* for *Infected* and *R* for *Recovered*). They were created in 1927 by *Anderson Gray McKendrick* and *William Ogilvy Kermack* [4]. Ever since, these equation-based models have been used in numerous digital tools for public policy decision-making [5]. *SIR* models mathematically describe the epidemiological dynamics of the considered pandemic phenomenon. These are conceptual models built on the basis of a system of differential equations which describes the evolution of the percentage of different categories of the population of individuals over continuous time. Since, different categories of *SIR* models have been proposed to describe individual populations evolving between different predetermined health statuses [6]. The most notable examples are *Susceptible-Infected-Recovered-Death* (*SIRD*) models [7], *Susceptible-Infected-Susceptible* (*SIS*) [8] models, *Susceptible-Exposed-Infected-Removed* (*SEIR*) models [9], *Susceptible-Latent-Infected-Removed* (*SLIR*) [10], and there are many more. While in a basic *SIR* model a person's health status changes from *Susceptible* to *Infected* and then to *Removed*, as people are dead or immune, with an *SIS* model there is no acquired immunity. When a person has been infected, they recover and they are sensitive to the disease again. Both *SEIR* and *SLIR* seem to be more realistic because they integrate an additional intermediate step between the exposing latency period and the apparition of symptoms. Thus, the different specializations of the *SIR* models take into account more degrees of infectivity that may arise between the *Susceptible*, *Infected* and *Recovered* basic stages. Fig. 1 is an illustration of the different steps that we can observe in the basic deterministic models of infectious diseases. In these epidemiological models, the main modelling hypothesis poses as an axiom that all the persons in the population behave,

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contract the virus and develop the disease homogeneously.

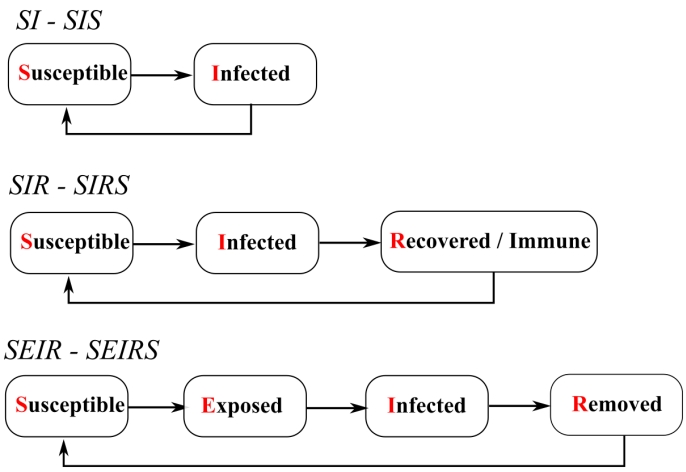


Fig. 1: Basic deterministic epidemiological models.

Taking these basic epidemiological models as a reference, we propose an alternative computational *Agent-Based Model* (*ABM*) to study the COVID-19 dynamics. Our approach offers the possibility to explicitly represent heterogeneities at an individual level, and also allows us to take into account the spatial characteristics of the pandemic. In the early 2000s, the *ABM*, also named *Individual-Based Models* (*IDM*), was developed and opened the way to new modelling perspectives [11], [12]. In this new kind of epidemiological models, the pandemic complex system is considered from the point of view of *Multi-Agents System* (*MAS*). It is then possible to conceptualize the heterogeneous health statuses for each person of the population concerned by the pandemic, taking into account spatial characteristics and intricate nonlinear relationships that may be hard to describe mathematically. Epidemiological effects are observed as emerging from the interactions between agents in the simulation. With the COVID-19 pandemic, the development of this kind of model has become a pregnant topic in the literature [13]–[16]. In addition, these *ABM* epidemiological models, although more complex to implement, benefit from the technological evolution of simulation platforms and computer hardware. In fact, with the increase in computing power and data processing, more and more precise *ABM* instances can be encoded. In this paper, we show how to conceptualize the pandemic phenomenon from the *MAS* point of view. For that, we propose a COVID-19 pandemic *ABM*. The use of an agent-based modelling process will allow us to take into account the heterogeneity of populations in the territories, as well as the environmental spatial characteristics likely to influence the pandemic. The corresponding computer model is implemented in the generic *NetLogo* simulation environment [17]. In an experimental part, the case of Corsica is studied. The paper is organized as follows. In a second part, we recall the computational modelling principles this work is based upon. In a third part we explain the COVID-19 pandemic *ABM* and its subsections describe each component of the model in detail. The implementation of the model as well as some results obtained are discussed in a fourth part. Concluding remarks and possible extensions of this model are presented in a fifth and final part.

II. Computational Modelling Principles

A. Modelling process

The process of complex system modelling aims at providing an *executable model* of the phenomenon observed in the real world, which will be ultimately exploited with computer tools. The executable model is a numerical expression of a set of *constituents*, their *organisation* and their *interactions* within a *descriptive hierarchy* of *abstraction levels*. The modelling process is built under these philosophical bases and raise questions of both *descriptive scales* and constituents organisation as preconditions for the formulation of a *conceptual model*, i.e. a *conceptual modelling* phase relying on a precise scientific *methodological frame*. Hence, conceptual modelling is a cornerstone of an interdisciplinary modelling work in computer simulation science. Fig. 2 is an illustration of what is a modelling process.

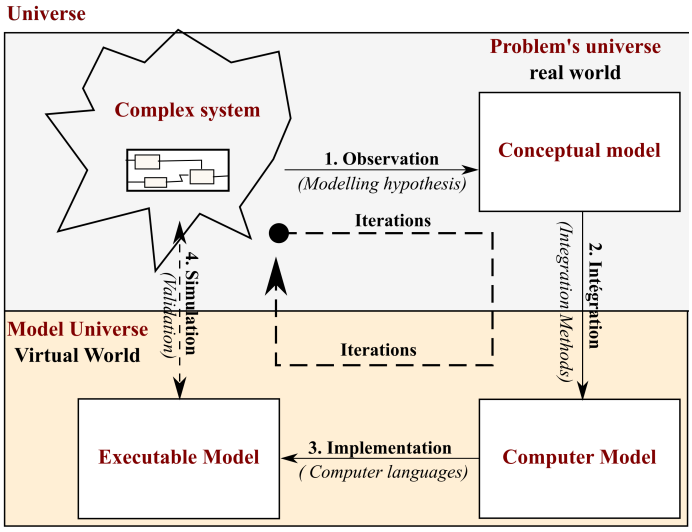


Fig. 2: The process of a complex system modelling in computer simulation science. This modelling process is fully addressed in the seminal works of [18]–[22].

In the modelling process of Fig. 2, the complexity is progressively introduced at each iteration of the process. The aim is to produce an intelligible executable model, however sufficiently detailed in accordance with reality. The computational expertise of the initial complex system takes place during the final simulation phase, where scientific experiments are conducted in silico. The data obtained is used for the purposes of study and synthesis, notably to help political decision-making. The discussion on modelling processes has been going for years among the scientific community, particularly because of its critical nature. In fact, taking into account the infinity of possible choices about simplifying

the modelling assumptions initially formulated by modellers, may correspond to an infinity of abstractions, i.e. as many conceptual models and different conceptualisation methods, and that for a same phenomenon observation. Thus, as argued in 2015 by *Stewart Robinson* [23] in a simulation conference, "*conceptual modelling is more an art than a science.*". Thanks to this context, computer simulation became more rigourous over the last few years.

B. Agent-Based Computational Modelling

Agent-Based Computational Modelling (*ABCM*) is at the origin of real-world phenomenon description based on the *agent paradigm*.

From the modeller's point of view, the complex system's conceptual model is thought from its constitutive units, i.e. its constituents [24]. As often reflected in the literature, the *agent paradigm* is especially well adapted to simulate complex system phenomena, whose spatial dynamics come from autonomous and interacting constituents of an organisation. This paradigm imposes to consider the phenomenon in the light of the definition of dynamic or static sub-systems with links and a hierarchical organisation. These sub-systems interact in a global system delimiting de facto for the observer a *Multi-Agent System* (*MAS*). From conceptual modelling, it is a *point of view* involving to formulate the explanation of the phenomenon's dynamics as being the result of a constituents assembly expressed in the form of agent collection, i.e. in the form of autonomous and individual entities. Agents interact among themselves and in function of *interaction links* (*rules*), but also with a superior conceptual entity which represents the wider system, i.e. the *environment*. The set of these critical elements constitutes the key concepts underlying the *MAS* point of view. They are generally sufficient to formulate the conceptual model of a complex system's phenomenon having spatial dynamics. As highlighted by *J. Ferber* in [25], the *MAS* point of view is thus greatly based on the *interaction problem* constituting the main driving force of conceptual thinking at the source of the expression of interaction mechanisms between agents and with the environment; the latter can itself be considered as being an agent. These interaction mechanisms can be of different natures, trans-hierarchical and can evolve in time. The modeller explains these interaction mechanisms in the form of *local interaction rules*. Fig. 3 illustrates how to use the *MAS* key-concepts to build the computer model of a complex system.

In computer simulation science, the *MAS* point of view is nowadays considered as one of the best conceptual modelling methods. In fact, it benefits from major evolutions related to object paradigm and concepts developed over the last decades, as the evolutions of numerous disciplines associated to computer science, in particular *Distributed Artificial Intelligence* (*DIA*) [27] and *Artificial Life* (AL) [28]. In the literature, we usually distinguish between two main types of conceptual models coming from the *MAS* point of view: *Cellular Automata Models* (*CAM*) and *Agent-Based Models* (*ABM*). The *CAM* refer the generic conceptual model specialisations of the basic *Cellular Automata* (*CA*) proposed in the 1940s by *Stanislaw Ulam* [29], and that *John von Neumann* used investigating the logic of self-replication [30]. The conceptual model is constituted by fixed agents called *cells* which constitute a discrete global environment called *cellular environment*. In a *CAM*, cell agents play a major role in the local interaction rules. For their part, the *ABM* are extensions of *CAM* which better translate the *MAS* point of view and its agent paradigm. In fact, in addition to fixed cells, *ABM* also have *mobile agents* which can be moving within the cellular environment. The Fig. 4 is an illustration of the difference of point of view existing between the definition of a *CAM* type and an *ABM* type conceptual model [31].

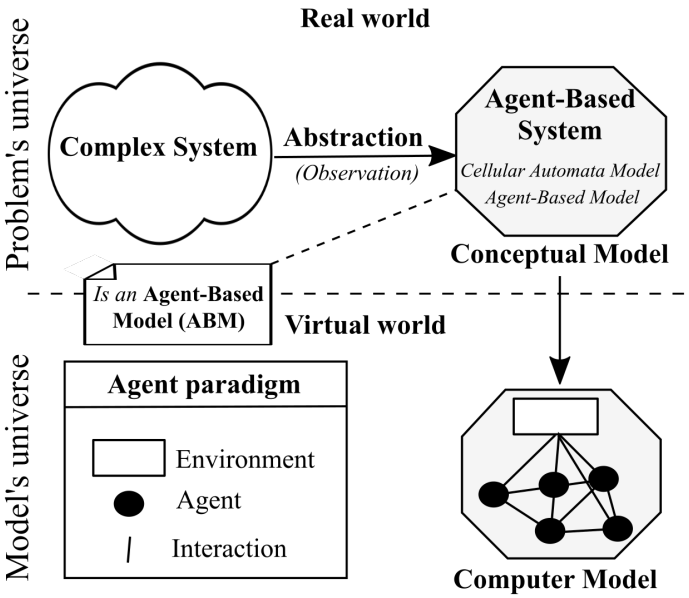


Fig. 3: Formulating a conceptual model and its computer model counterpart from the *MAS* point of view, from [26].

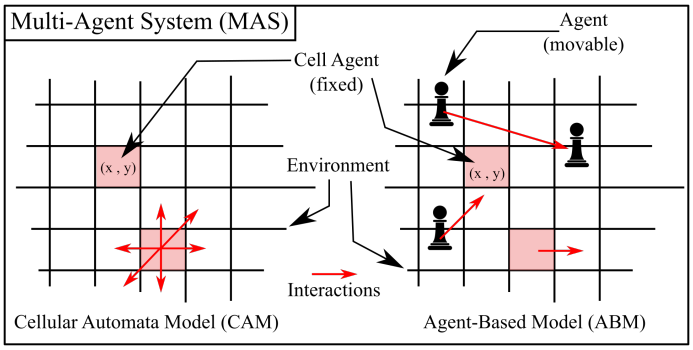


Fig. 4: *Multi-Agent Systems* (*MAS*): *CAM*s versus *ABM*s from [31].

Both *CAM*s and *ABM*s benefit intrinsic capacities giving modeller the formal elements allowing them to describe with much realism numerous phenomena in reality by expressing

TABLE I: Main *ABM* Parameters.

Param.	Name	Comments
S	Surface area	Number of cells.
N_0	Init. population	Number of agents.
α_0	Init. contamination	% of S_i and S_a agents at $t = 0$, distributed according β.
β	Asymptomatic-rate	% of agents don't experience any symptoms after becoming exposed. The rate of asymptomatic infections could be as high as 81% [37].
γ	Mortality rate	% Mort. following infection [38].
χ	Immune period	Up to 8 months after infection [39].
δ	Infect.-period	Range 1-20 days, see [40].
ϕ	Transmission-rate	The threshold at which the viral load in the environment infects the agent.
η	Max. mobility radius	Used to calculate the agent moving according to the value of its κ mobility.
μ	Inf.-r.-asymptomatic	% of asymptomatic finally becoming infected. A small fraction of asymptomatic persons may eventually develop symptoms, see [41].
ν	Surviving-factor	% of viral-load not surviving in the environment. This parameter is used to calculate the decrease of the viral load in a cell of the environment at each time step, see for estimation [42].
π	K-virus-growth	Impact of the agent on the increase of the viral load in a cell.
θ	Min-viral-Load	Minimum viral load deposited in a unit of space (cell).
ρ	Vacc.-coverage	Initial vaccine coverage of the population.

transition rules that can be formulated under very simple mathematical bases. The scientific literature praises indeed in this regard the good performances of these two model types in general. Furthermore, hardware evolutions also have significantly increased the interest for this kind of modelling, in particular in terms of performances, with parallel and distributed computing evolutions [32]–[35]. However, in numerous works, that the *ABM*s are limited in terms of performances when we have to model a propagation phenomenon, and we'll prefer in this case to use a *CAM* [36].

III. Conceptual Modelling

A. Model description

Let an agent a_n, with $n = \{1, 2, ..., L\}$, representing one individual agent moving on a $c(_i, j)$ cell of the *CAM*'s square lattice $N = L \times L$ of side L. Each cell owns a viral load $Q_{VL}(i, j)$ which represents the quantity of virus. The higher the viral load, the higher the rate of viral replication, which indicates a more rapid progression of the disease. Agent a_n belongs to the population size N and it can have one of the six possibles states: $S_n \in \{S_s, S_e, S_a, S_i, S_d, S_m\}$. If $S_n = S_s$ (Safe), the agent is not exposed to the pathogen, i.e. is susceptible to be infected with COVID-19. If $S_n = S_k$, with $k = e, a$, the agent is in Exposed or Asymptomatic state to the virus that causes COVID-19, but it is not sick. If $S_n = S_i$ (Infected), the agent has active COVID-19. Finally, if $S_n = S_k$, with $k = d, m$ the agent is either dead (Dead) or immune (Immune). The agents may undergo probabilistic transitions between the considered health states . The main parameters that drive these δ agent's transitions are summarized in table I.

In this paper, we assume that cured agents are replaced in the environment by safe agents to mimic the recruitment rate used in *Ordinary Differential Equations* (*ODE*) models as mentioned in [11].

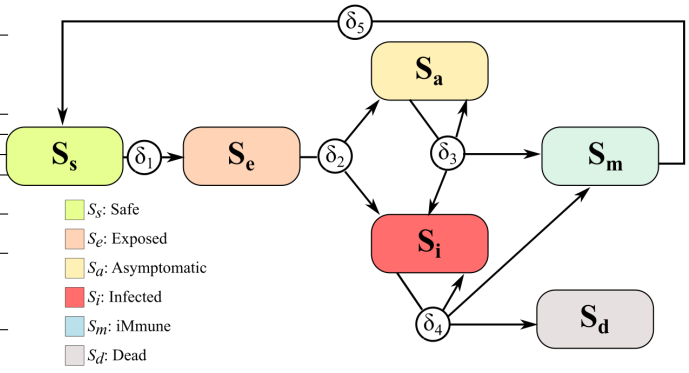


Fig. 5: Schematic representation of an agent's state transition.

In the following, we describe the state transition rules and the dynamics of agent interactions. The transitions rules allowed and their respective values are illustrated in Fig. 7.

B. δ_1 - Exposition of susceptible agents

Agents in S_s state are exposed to the viral-load $Q_{VL}(i, j)$ of the underlying cell.

- $\delta_1(S_s) \rightarrow S_e$: an agent in the S_s changes to the S_e exposed state if the quantity of *viral-load* $Q_{VL}(i, j)$ in the underlying cell is upper to the ϕ transmission-rate.

C. δ_2 - Contagion of exposed agents

Agents that are exposed in S_e state changes to S_a or S_i states. These latter develop symptoms.

- $\delta_2(S_e) \rightarrow S_a$: the local probability P_a of an agent in state S_e to become asymptomatic S_a is given by: $P_a = 1 - \beta^{N_i}$, where β is the asymptomatic-rate, and N_i is the number of infected or asymptomatic agents in the neighboring cells of the *CAM*.
- $\delta_2(S_e) \rightarrow S_i$: the S_i infected agents are the others remaining agents of the set; those who did not become asymptomatic.

D. δ_3 - Contagion of asymptomatic agents

Agents that are asymptomatic in S_a state changes to S_i or S_m states, or stay asymptomatic S_a.

- $\delta_3(S_a) \rightarrow S_i$: the μ infection-rate determines the number of asymptomatic agents becoming infected (N_i'), as: $N_i' = \mu \times N_a$ with N_a the number of asymptomatic agents. An infected agent loss its mobility;
- $\delta_3(S_a) \rightarrow S_m$: the S_m iMmune state of an asymptomatic agent is acquired after χ days (*immune-period-agt*).

E. δ_4 - Infected agents evolution

Agents that are infected (S_i) changes to S_d or S_m states.

- $\delta_4(S_i) \rightarrow S_d$: dead agents are deduced from the γ mortality rate parameter has a percentage of the infected agents (S_i);

- $\delta_4(S_i) \rightarrow S_m$: if the δ infectious period is over, the agent has become immune. The immunity linearly decreases at each time step.

F. δ_5 - Immunity of agents

- $\delta_5(S_m) \rightarrow S_s$: after the χ immune period, the agent loses immunity and recovers the safe status S_s.

G. Cell contamination

It is assumed that the viral load in a cell of the *CAM* follows the logistic growth law in discrete time (Verhulst model [43]), such that:

$$q_{t+1} = \pi \times q_t \left(1 - q_t\right) \tag{1}$$

where, q_t is the amount of virus particles at time t; π is the maximum amount of virus particles allowed in a unit of space (cell).

IV. Computational modelling

A. NetLogo simulation

With the increasing evolution of performances related to computer hardware and with the emergence of numerous *MAS* generic simulation environments as *Swarm* [44], *Repast* [45], *MASON* [46] or whether *NetLogo* [17], [47], just to name the most famous, *CAM* and *ABM* benefit an increasing renewed interest. All these SMA simulation environments offer an integrated graphical user interface, ergonomic and easy to use, dedicated to the implementation of the executable model. They are very efficient and they gather every day a larger and larger community of modellers. In this work, we have made the choice to use the *NetLogo* modelling and simulation environment [48] which is based on the use of a generic design pattern easily accessible for modellers whichever their disciplinary field. The latter undeniably constitutes a *MAS* simulation environment that is appropriate for interdisciplinary simulation projects [26]. The Fig. 6 is a screenshot of the model in NetLogo.

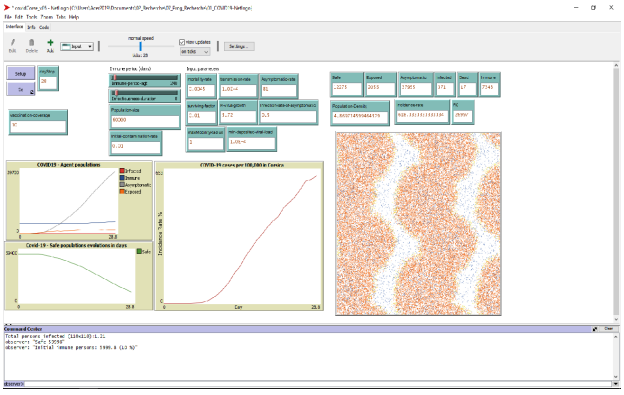


Fig. 6: Screenshot of the model in NetLogo dedicated to simulation experiment parameterisation.

B. Experiments

In this section we verify the capacity of the model to simulate the epidemic phenomenon of COVID-19 in Corsica. Corsica is the fourth largest island in the Mediterranean with an area of $8.722km^2$. It has 350,273 inhabitants in 2021 according to INSEE estimates (39 inhabitants per square KM). Its low demography makes the island the least populated territory in France. An epidemic cluster of the delta variant was declared on *July 9, 2021*. Since the evolution of the epidemic of COVID-19 in the island is particularly worrying. In this experiment, we try to estimate this evolution.

1) Initial conditions and simulation loop: The number of cells and agents are set to correspond to the population density of Corsica. At time $t = 0$, agents in states S_s, S_e, S_a, S_i and S_m are instantiated from the NetLogo interface settings and constitute the initial global state S_0 of the simulation. They are randomly distributed on the $L \times L$ lattice. These agents perform the state transitions δ synchronously at each time step and then randomly move in the environment according to their mobility attribute. The simulation algorithm is summarized on Fig. 7.

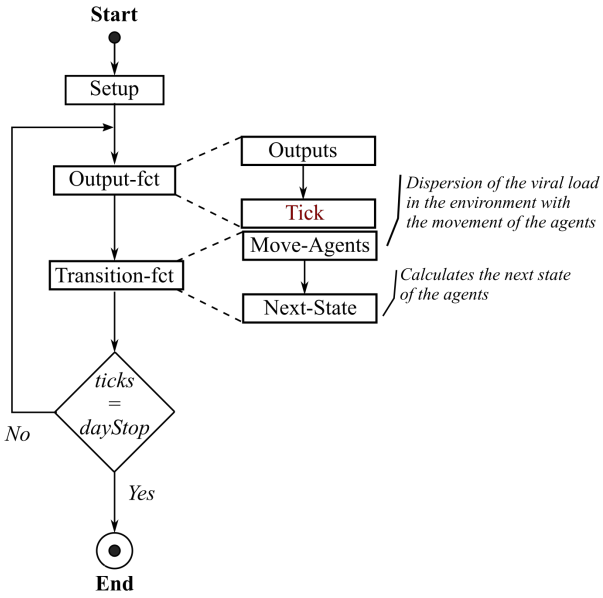
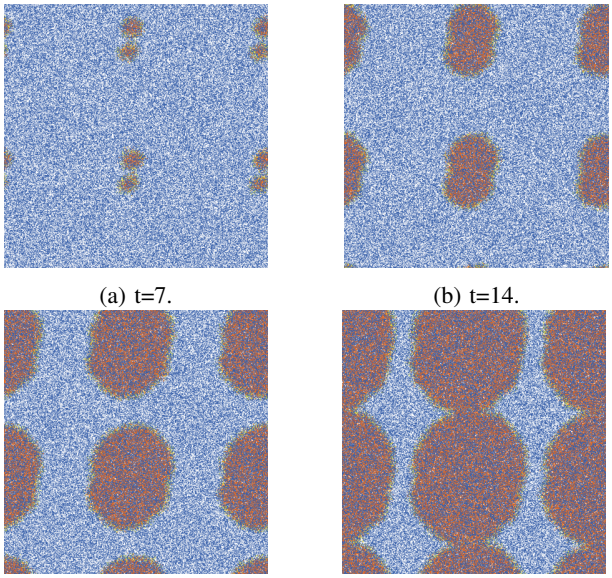


Fig. 7: Simulation algorithm.

Fig. 8 is an illustration of the spatial distribution of agents over time - An example of four snapshots of the lattice for $t = 7$, $t = 14$, $t = 21$ and $t = 28$ days are presented.

2) Calibration: In order to calibrate the model we fit the parameters from the July data obtained from the online tool *COVID-Tracker* (Dashboard Regions) [49]. The incidence rate (real data) to date and the simulated incidence rates per 100,000 population (model outputs) are shown in Fig. 9.

3) Validation: In this section, we use our *ABM* to estimate the evolution of the pandemic in Corsica in the absence of health restrictions for different types of vaccine coverage.



(a) t=7. (b) t=14. (c) t=21. (d) t=28.

Fig. 8: Computer simulation of the COVID-19 model for a 3.10^5 agents population randomly distributed in 110×110 space with a $1.10^{-2}\%$ contamination rate. Each color represents one state: white, S_s;yellow, S_e;orange, S_a;red, S_i;blue, S_m.

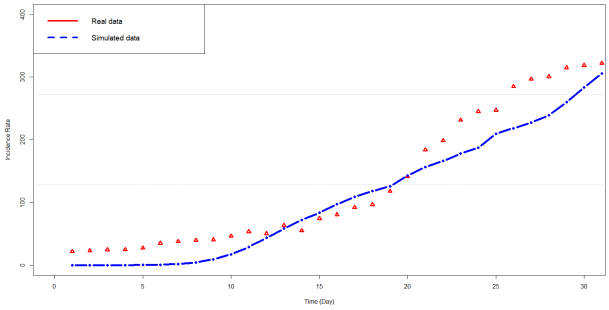


Fig. 9: Validation of the model. The red curve represents the real incidence rates, the blue curve represents the simulated incidence rates. The blue curve nicely follows the red curve - July 2021 period.

The French government is counting on the reinforcement of vaccination to try to curb the resurgence of the COVID-19 due to the Delta variant. In this context, health Minister Olivier Véran hopes France will fully vaccinate more than 50 million people by the end of August. In this paper, we simulate the effects of the French vaccination policy in Corsica. For that, we simulate the different scenarios in Table II. The four scenarios proposed allow us to explore the conditions under which immunity can be achieved in a closed space such as Corsica. The benchmark experiment (scenario 1) corresponds to the real situation until the day of writing this paper, it corresponds to the current vaccine coverage. The common parameters to all experiments performed are detailed in Table III.

TABLE II: Vaccination Coverage.

Experiment	**Value**	Comment
Scenario 1	57.2%	Reference benchmark on August 4th.
Scenario 2	90.0%	Expected vaccine coverage to achieve vaccine immunity.
Scenario 3	0%	Group Immunity Policy.
Scenario 4	25.3%	Low vaccination coverage as of May 27.

TABLE III: Experiments - Common model parameters.

Parameter	**Value**	Comment
S	110×110	Cells
N_0	3.5^5	Agents
α_0	2.0^-5	This value is estimated on August 2nd with the *CovidTracker* tool [49].
β	81%	
γ	4.5^{-5}	
χ	240	Days.
δ	8	Days.
ϕ	1.0^-4	
η	1	Moore neighbour.
μ	0.5	
ν	1.0^-2	
π	2.10	
θ	1.0^-4	
ρ	cf. Table	Depends on the simulation experiment.

4) Comments and discussion: Scenario 1 (blue curve) corresponding to the current situation in Corsica, suggests the peak of viral load of the fourth wave around August 15th. From the end of August to the end of September the epidemic slowly decreases with an estimated incidence rate between 100 and 200. Scenario 2 (green curve) assumes 90% vaccination coverage in Corsica. These simulations clearly show that vaccination is the best solution to reach collective immunity in the short term. The incidence rate does not exceed a few cases and the incidence curve is almost flat over the three months simulated. Scenario 3 (red curve) corresponds to the herd immunity policy. In this experiment we assume that the vaccine would no longer be effective against Delta variant infections. In this case the incidence rate relative to the population reaches a peak never known and never recorded in Corsica. The authorities do quickly implement sanitary restrictions and Corsica risks the occurrence of a humanitarian emergency situation. Scenario 4 (orange curve) assumes a low vaccination coverage, identical to that in May. This experience shows that the vaccination coverage of the population in May was not sufficient to counter the epidemic in Corsica if the Delta variant had appeared at that time. The simulation predictions of the incidence rates for the different scenarios in

Table II are graphically shown in Fig. 10.

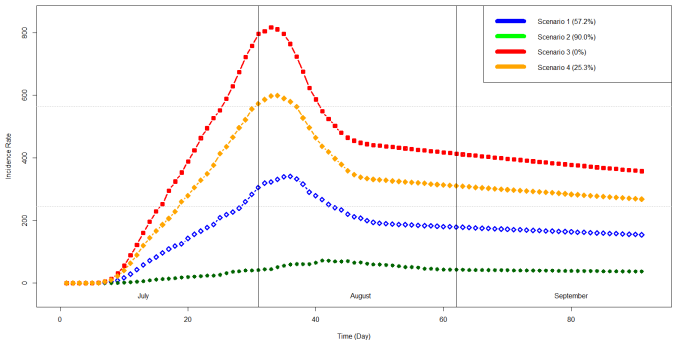


Fig. 10: Simulation experiments - July-September 2021 period. Vaccination Coverage (VC): the curves correspond to the different simulation scenarios described in Table II. Scenario 1 - blue curve, VC 57.2%; scenario 2 - green curve, VC 90.0%; scenario 3 - red curve, VC 0.0%; scenario 4 - orange curve, VC 25.3%.

V. Conclusion and research perspectives

The present work proposes an *Agent-Based Model* (*ABM*) that simulates the epidemiological effects of COVID-19 in Corsica. It tries to apprehend the complexity of the COVID-19 pandemic phenomenon's dynamics within a limited space without being too simplistic. The simulations performed prove that it is possible to simulate an epidemiological phenomenon using an *ABM*. They clearly prove that vaccination is an indispensable individual and collective means of prevention to protect against COVID-19. The results presented are preliminary and will need to be consolidated through numerous replications. The values of the parameters have a strong influence on the results, so a sensitivity analysis of the latter will have to be performed in a future work. We will also consider social constraints in a future version of the model.

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