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► **To cite this version:**

Benjamin Perrette, Christophe Cruz, Hocine Cherifi. A local Agent-Based Model of COVID-19 spreading and interventions. French Regional Conference on Complex Systems, CSS France, May 2023, Le Havre, France. hal-04055099

**HAL Id: hal-04055099**

**<https://hal.science/hal-04055099v1>**

Submitted on 1 Apr 2023

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# A local Agent-Based Model of COVID-19 spreading and interventions

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Received: date / Accepted: date

**Abstract** This research presents a simulation model that combines meta-population geospatial data with the SEIR epidemiological model to simulate a city of up to 250,000 residents while considering various factors such as virus transmission rate, disease severity, and prevention and control measures. This model can assist decision-makers in exploring different pandemic response strategies, including lockdowns, social distancing, mass testing, contact tracing, and vaccination. This simulation aims to provide decision-makers with a better understanding of the implications of their choices and enable them to make informed real-time decisions to manage a health crisis.

## 1 Introduction

The COVID-19 pandemic is a global challenge that significantly impacts health and the economy. Compartmental and metapopulation models [1,2] are crucial in evaluating the effects of containment policies like facility closures [3–8]. More sophisticated models consider the spatial and social structure and the people’s evolving awareness. However, they are unsuitable for analyzing the transmission dynamics in small populations with complex behavior. Agent-based modeling offers the advantage of observing global behavioral patterns by modeling the interactions between individuals with distinct characteristics [9]. This study presents an agent-based model to evaluate the transmission process of COVID-19. The model relies on collected meta-population geospatial data and the SEIR epidemiological model. The framework enables simulations of various scenarios, such as different levels of virulence, confinement consideration, and the number of available intensive care units. Initially limited to

the city center of Dijon, the study considers a greater Dijon area allowing simulations of up to 250,000 residents[10].

In the SEIR (Susceptible-Exposed-Infectious-Recovered) compartmental model, any individual can be in one of the following states:

S: Susceptible: The individual is healthy;

E: Exposed: The individual is incubating the virus and is characterized by the incubation period;

I: Infectious: The individual is contagious and in the period of infection;

R: Recovered: The individual has recovered or has been removed (dead).

The infectious state period includes three cases: the classic  $U_s$ , the asymptomatic  $A$ , and the rarer  $U_a$ . Patients in the  $U_s$  class present symptoms of the virus and are contagious. Patients in the  $A$  category are contagious but have no symptoms.  $U_a$  is an intermediate case in which the patient begins to be infectious before the end of the incubation period but does not present any symptoms yet. One can integrate individual conditions, such as age, gender, and co-morbidity, into the model by defining the transition rates at the personal level. The simulations reported in the experiments use generic parametrization from [11, 9]. However, one can use parameters obtained by an epidemiologist from on-site experimentation. In this study, we use the vaccination strategies applied in France for the vaccine model. According to data on vaccine efficacy, the vaccine reduces severity by 90%, infectivity by 30%, and susceptibility by 90%. The vaccination is initially disabled, and these data are modifiable during the simulation.

## 2 Experimentation

This section presents our experimentation using the GAMA platform [12]. It combines explicit multi-agent simulations with GIS data management, multi-level modeling, and the capacity to implement Belief-Desire-Intention (BDI) and reactive agents. Thus, GAMA is powerful for prototyping and automatic simulation through its agent-oriented language GAML.

We collected data from the Dijon metropolitan area from OpenStreetMap. We extracted a Shapefile containing all of the buildings throughout Burgundy and a file containing all the roads. The simulation starts when the agents go to work between 6 and 8 am. In the evening, they stop between 4 and 8 pm and can then go to a place of leisure. The principle is the same for those under 18, but they go to school rather than work. One can change all these parameters. As shown below, one can tune many parameters on the agents to adapt the model to its needs. One of the agents is infected at the beginning of the simulation. Depending on their state of health, the agents have a different color. The healthy agents are yellow, those in the incubation period are orange. The symptomatic infected are red, the asymptomatic infected are red with purple borders. The hospitalized infected are red dots with green contours, the agents in specific states are orange with red contours, the recovered are green. The dead are black with red contours. It is possible to change the virus

settings, as reported in (fig. 1). One can close schools so that young people stay at home. The suspension of leisure activities prevents agents from going to public places such as large shopping centers, restaurants, or places of worship.

In the case of a complete lockdown, the agents stay at home and no longer move. All of these parameters are aimed at reducing the spread of the virus. It is also possible to implement preventive measures to decrease virus transmission. Hospitalization of infected individuals can be activated to decrease the likelihood of dying from the virus. One can change the Parameters linked to the hospitals, such as the number of beds. It is also possible to change the entire vaccination model by deciding when the vaccinations should be carried out and how many vaccine doses are available in the city. One can deal with many variants in the simulation. It can also save information about agents and their environments to a CSV file to create a dataset. Afterward, it is possible to search for information on a particular agent (for example, patient 0) and save it to another CSV file. The simulation can be manually paused at any time or automatically. All these parameters are tunable during the simulation.

The different figures illustrate the infection development in the population. It shows the main places where infections occur and the evolution of available hospital beds. They also report the growth of the variant compared to the strain, the variation of the vaccinated population of the first and the second dose, and the distribution of deaths related to the virus according to agents' age. In the first curve (fig. 2a), we can observe the evolution of the number of infections over time in different locations. The gray line represents infections at home. It continues to rise throughout the simulation, even during a lockdown. The dark blue line represents workplace infections, which remain stable during the lockdown but experience a sharp spike after its lifting. The light blue line represents infections at leisure venues, which stay stable when these places are closed. Finally, the purple line represents infections in schools, which remain stable as long as they are closed but increase upon reopening. In the second graph (fig. 2b), we can observe the evolution of the agent states during the simulation. The number of individuals in the incubation period (state E) is orange. It varies according to the restrictions, decreasing during confinement and increasing afterward. The number of infected agents (state I) is shown in red. It falls with improved regulations. The number of agents who have recovered from the disease is shown in green, while the number of agents who died is black (state R). Finally, the number of agents in the specific state (state Ua) is violet.

This model could be a valuable tool for decision-makers in the field of public health to determine when it is the right time to impose restrictions, predict the rise of an epidemic, and act accordingly to stop it. It can be significantly improved, particularly regarding computational speed, to facilitate larger-scale simulations and use knowledge graphs to refine agent behavior.



Fig. 1: Dijon metropolitan area with 250,000 inhabitants

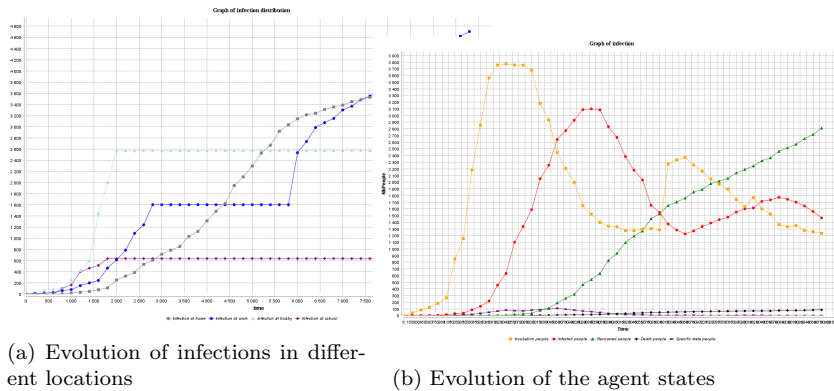


Fig. 2: Evolution of variables during the simulation

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