Agent-based modeling developed in NetLogo for foodborne disease

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Abstract: Foodborne diseases represent an important public health problem, characterized by the rapid emergence of many cases associated with a common source of contamination. Understanding the mechanisms of spread of these infections is essential for assessing epidemiological risk and for substantiating prevention and control measures. This paper presents an agent-based model, developed in the NetLogo, for simulating a foodborne disease outbreak generated by the consumption of microbiologically contaminated cheese. The model integrates the principles of multi-agent systems modelling according to the ODD (Overview, Design, Concepts, Details) protocol and the SEIR (Susceptible–Exposed–Infected–Recovered) epidemiological model, allowing the individual representation of consumers, their interactions and exposure to the source of contamination. The simulations performed highlight the influence of the distribution of the contaminated product, population mobility and epidemiological parameters on the evolution of the outbreak. The results demonstrate the advantages of agent-based modelling for analysing epidemiological processes and for evaluating different scenarios of the spread of foodborne disease in a controlled virtual environment.

Keywords: agent-based simulation; foodborne infection; epidemiological modelling; SEIR model; ODD protocol.

1. INTRODUCTION

Foodborne diseases are a major public health challenge worldwide. According to the World Health Organization (WHO), approximately 600 million people develop foodborne disease each year, and approximately 420,000 deaths are attributed to these conditions, highlighting their significant impact on population health and health systems (World Health Organization, 2015). In urban environments, high population density, intense mobility and the existence of complex food distribution networks favour the emergence and rapid spread of outbreaks, which requires the development of tools capable of reproducing and analysing these processes.

Modelling complex phenomena is an important research direction in many fields such as production systems, medicine, epidemiology, ecology, economics or social sciences. In the case of systems composed of many interacting entities, classical approaches based on aggregate mathematical equations can describe the general trends of the system but provide limited information on the individual behaviour of the components and its influence on the global dynamics, respectively on the emergent behaviour. To overcome these limitations, Individual-Based Models (IBM) have been developed, in which each entity is explicitly represented and has its own characteristics, behaviour rules and interaction mechanisms. The evolution of the system results from individual actions and from the relationships established between the participants, allowing the observation of emergent phenomena that cannot be directly deduced from the statistical analysis of the component elements. This approach is particularly useful for studying processes in which spatial distribution, mobility and contact between individuals significantly influence the results (Domenteanu et al., 2025).

A frequently used method for implementing IBM is represented by multi-agent systems (MAS). Within them, every entity is modelled as an autonomous agent capable of perceiving the environment, making decisions and executing actions according to pre-established rules. Interactions between agents and between agents and the environment led to the emergence of the collective behaviour of the system. The flexibility of this approach allows the introduction of heterogeneous populations, different levels of mobility and complex scenarios difficult to represent by traditional methods (Di Marzo Serugendo et al., 2006).

In recent years, numerous software platforms dedicated to agent-based modelling have been developed, the most well-known of which are NetLogo, Repast Simphony, GAMA, MASON and AnyLogic. These environments offer varying levels of support for defining agents, modelling interactions between them, spatial representation of the environment, visualization of results and management of simulation

experiments. Through these facilities, researchers can investigate complex systems using individual-based models and analyse emergent behaviours that are difficult to observe with traditional modelling methods (Leon, 2022). From the studied platforms, NetLogo stands out due to the ease of developing agent-based models, the extensive library of examples, the active user community, and the integrated simulation and visualization facilities, useful for analysing spatial epidemiological phenomena (John et al., 2019) .

The spread of infectious diseases represents one of the main challenges for public health systems, as the dynamics of an outbreak are simultaneously influenced by numerous factors, such as population density, mobility of individuals, frequency of contacts and characteristics of the pathogen. Understanding how an infection spreads within a community is essential for estimating epidemiological risk and adopting effective prevention and control measures (Ryu et al., 2022) .

In practice, direct evaluation of different intervention strategies on real populations is difficult, expensive and, in some cases, impossible for ethical or logistical reasons. For this reason, simulation has become an important tool for analysing the behaviour of infection outbreaks and for investigating scenarios that cannot be tested in real conditions. Computer models allow the reproduction of transmission mechanisms and the observation of the effects generated by the modification of certain parameters, such as the contact rate, the degree of mobility or the level of compliance with isolation measures (Zhang et al., 2025).

A major advantage of simulated environments is the possibility of compressing the time required for the phenomena under analysis to unfold and run simulations with different parameters in parallel. Processes that would take several days, weeks or months can be observed in a few seconds or minutes of simulation, facilitating the analysis of many scenarios in a short time. This approach allows for a rapid assessment of the impact of different control measures and a comparison of the effectiveness of proposed strategies before their implementation in real situations (Institute, 2021).

The location of the sources of infection is a determining factor in the dynamics of the spread of the disease. Depending on their location and population distribution, outbreaks can show different patterns of expansion, from relatively uniform spreads to the formation of areas with high concentrations of infected individuals. Multi-agent models allow the investigation of these situations by simultaneously simulating individual movements and interactions between agents, providing a detailed insight into the processes leading to the emergence and development of outbreaks (Salem et al., 2022).

The integration of geographic information into the simulation environment facilitates the identification of vulnerable areas, crisis situations (epidemics) and the observation of the formation of infection clusters. Unlike aggregate models, which mainly provide statistical indicators at the level of the entire population, the multi-agent approach allows the analysis of the spatial distribution of cases and the highlighting of the relationships between the mobility of agents and the spread of infection. In addition, different isolation protocols can be evaluated by modifying the rules of movement or the possibilities of interaction between agents, making it possible to compare their impact on the evolution of the outbreak (Chandran and Roy, 2024).

As agent-based models have become increasingly used in the study of complex systems, the need for standardized methods for describing and documenting them has arisen. The diversity of software platforms, implemented behavioural rules, and used parameters make it difficult to understand, compare, and reproduce results obtained by different research teams. In the absence of a rigorous description, model validation and reuse in other studies become difficult processes (Youvan, 2024).

To address this challenge, the ODD (Overview, Design Concepts, Details) protocol was proposed, which is currently one of the most widely used methods for documenting models based on individuals and MAS. The goal of the protocol is to provide a unified framework through which the structure and functioning of a model can be described in a clear, complete and reproducible manner, independent of the software platform used for implementation (Grimm et al., 2006).

The ODD protocol is organized into three main sections. The first section, Overview, presents the purpose of the model, the entities involved, and the main processes that govern the evolution of the system. The second section, Design Concepts, describes the fundamental concepts underlying the model, such as interactions between agents, adaptation, emergence, or the influence of the environment on individual behaviour. The last section, Details, includes information on model initialization, parameters used, and data sources needed to configure the simulation.

2. BACKGROUND

2.1 MAS in process simulation

Depending on the degree of complexity of the implemented behaviour, MAS can be classified in two categories. Reactive systems represent the simplest form of implementation, with agents responding directly to environmental changes without performing complex planning processes. In contrast, deliberative systems include decision-making mechanisms based on objectives, rules, or strategies, with agents being able to evaluate different alternatives before acting. Between these two extremes are hybrid systems, which combine rapid reactions to environmental changes with planning and adaptation mechanisms. The choice of the type of system depends on the level of detail required and the characteristics of the phenomenon being studied (Spieser et al., 2026).

The use of MAS has many advantages over traditional simulation methods. First, they allow for the explicit representation of population heterogeneity, with each agent having different characteristics, such as age, health status, mobility level, or social behaviour. Second, local interactions between agents can be modelled in a realistic manner, without the need to make simplifying assumptions about the behaviour of the entire population. In addition, modifying individual rules allows for the rapid evaluation of different scenarios and the observation of their effects on the global system (Bonabeau, 2026).

These features make MAS particularly suitable for studying epidemiological processes. In simulations of the spread of infections, each agent can represent an individual in a certain epidemiological state and can interact with other agents according to its position in space and defined mobility rules. Thus, disease transmission occurs as a direct result of contact between individuals and not as an effect of aggregate statistical relationships. Consequently, multi-agent models allow the investigation of aspects that are difficult to analyse by conventional methods, such as the emergence of infection clusters, the influence of the spatial distribution of the population or the impact of isolation measures on the evolution of outbreaks (Zhang et al., 2025).

The analysis of the spread of infectious diseases involves considering two fundamental components: time and space. The evolution of an infection is a dynamic process, influenced both by the sequence of epidemiological events and by the geographical distribution of individuals and sources of contamination. For this reason, modern epidemiological models integrate these dimensions to obtain a more realistic representation of the phenomena studied (Yu et al., 2025).

The temporal component allows the description of the evolution of epidemiological states and their modification during the simulation. Depending on the level of detail pursued, time can be represented continuously or discreetly. In the case of agent-based models, the discrete approach is frequently used, the simulation being divided into successive steps in which agents update their state and interact with the environment. This approach facilitates the implementation of behavioural rules and allows tracking of the individual evolution of agents. Also, the use of virtual time makes it possible to compress processes, so that phenomena that unfold over several weeks or months can be analyzed in a short time interval. Accelerated simulation offers the possibility of rapid evaluation of numerous scenarios and the long-term effects of various control measures (Zhang et al., 2024).

In addition to the temporal component, spatial representation plays an essential role in the study of the spread of infections. In most real situations, contacts between individuals do not occur randomly, but are influenced by geographical position, population density and its mobility. The integration of space in the model allows the description of the distribution of agents in the environment, the simulation of movements and the investigation of how the location of infection sources influences the dynamics of outbreaks. Thus, vulnerable areas, regions with a high probability of transmission and the mechanisms leading to the formation of infection clusters can be identified (Sun et al., 2025).

Another important aspect is the way the population is represented. Traditional epidemiological models frequently use aggregate approaches, in which the population is described by statistical indicators and epidemiological compartments. Although effective for estimating general trends, these models provide limited information on individual behaviour and local interactions. In contrast, IBMs allow for the explicit representation of each participant, including their specific characteristics and behaviours. This approach facilitates the simulation of heterogeneous populations and the analysis of the effects generated by mobility, proximity, and frequency of contact between individuals (Hussien et al., 2025).

By combining temporal, spatial, and individual representation of the population, agent-based epidemiological models provide a flexible framework for investigating disease transmission mechanisms and evaluating different intervention strategies. These features recommend them for studying outbreaks and analysing the impact of containment measures in a controlled virtual environment (Ye et al., 2025).

The development of MAS and individual-based models has been supported by the emergence of specialized software platforms, capable of facilitating the implementation, execution and analysis of simulations. These platforms provide mechanisms for defining agents, managing interactions between them, spatially representing the environment and visualizing the results. The choice of a platform depends on the complexity of the model, the available resources and the research objectives (Maldonado et al., 2024).

2.2 Pathogens involved in food poisoning associated with dairy products

Although epidemiological models can be applied to a wide range of transmissible diseases, in the present paper the attention is directed to food poisoning associated with the consumption of contaminated dairy products, a particular type of infection characterized by the existence of a common source of contamination and by the rapid appearance of cases in the exposed population.

Agent-based modelling offers the possibility to explicitly represent both consumers and contaminated food products (Figure 1). Within the simulation, everyone can interact with one or more food products, the probability of infection being dependent on their degree of contamination. Such an approach allows the investigation of how the distribution of a contaminated batch of cheese can generate local or regional outbreaks and facilitates the evaluation of the effectiveness of measures such as withdrawal of the product from the market, identification of contaminated batches or limitation of distribution (Zhu et al., 2026).

Unlike classical communicable diseases, in which infection occurs mainly through contact between individuals, foodborne infections involve the existence of a common source of contamination. In the case of a batch of microbiologically contaminated cheese, several consumers can become infected independently of each other, without direct contact between them. From a simulation point of view, the food product can be represented as a special agent or as a fixed source of contamination, and the occurrence of cases depends on the interaction of the population with this source. Such an approach allows the analysis of the impact of the distribution of the contaminated product on the size and speed of the outbreak development (Talley et al., 2021).

The first epidemiological models were built on the concept of partitioning the population into groups corresponding to different health states. These models, known as compartmental models, describe the transfer of individuals between epidemiological categories and allow estimating the evolution of the disease at the level of the entire population. Due to their

simplicity and ability to highlight the relationships between epidemiological parameters, compartmental models have become a reference tool in the study of communicable diseases. Currently, mathematical modelling is used both for the retrospective analysis of epidemics and for estimating the impact of intervention measures before their application in practice (Reyné et al., 2021).

One of the most well-known compartmental models is the SEIR (Susceptible–Exposed–Infectious–Recovered) model, proposed to describe the dynamics of transmissible infectious diseases. Within it, the population is divided into four main compartments. The Susceptible (S) category includes healthy individuals who can contract the disease following contact with infected individuals. The Exposed compartment composed of individuals who contracted the infection and the infection is in the incubation period. The Infectious (I) compartment consists of individuals who are infected and capable of transmitting the pathogen to other individuals. The Recovered (R) category contains individuals who no longer participate in the transmission process, either due to recovery and acquisition of immunity, or due to their elimination from the epidemiological chain (Daughton et al., 2017).

The functioning of the model is based on the transition of individuals between these compartments. A susceptible individual can become exposed following contact with a person in the Infectious category, and after a certain period of incubation, he passes into the Infected category. The person becomes recovered after another period. The dynamics of the process are mainly influenced by the infection transmission rate and the recovery rate, parameters that determine the speed of disease propagation and the duration of the outbreak. Based on these parameters, important characteristics of the epidemiological process can be estimated, such as the number of infected people, the duration of the epidemic or the effectiveness of control measure (Daughton et al., 2017).

Although the SEIR model was originally formulated at the aggregate level, its principles can be easily adapted for agent-based simulations. In this approach, each agent represents an individual and has an epidemiological state associated with one of the compartments S, E, I, or R. The transition from one state to another is determined by local interactions between agents and by rules defined within the simulation. Thus, the transmission of infection is no longer described exclusively by global mathematical relationships but occurs as a direct result of contacts between individuals (Tatsukawa et al., 2023).

Combining the SEIR model with MAS and a geographic representation of the environment offers numerous advantages. This approach allows the integration of agent mobility, the spatial distribution of the population and the influence of local sources of infection on the transmission process. In addition, complex scenarios that include travel restrictions, isolation measures or changes in individual behaviour can be investigated. Therefore, the SEIR model implemented in a multi-agent environment constitutes a suitable solution for the analysis of infection outbreaks and for the evaluation of control strategies in a controlled virtual setting (Zunker et al., 2024).

3. MODEL DESIGN: SPATIAL AND TEMPORAL CALIBRATION

3.1 Model introduction

This section describes the development of a multi-agent model capable of simulating the spread of an infectious disease in an urban agglomeration area (metropolis) that extends over a large area and includes a large number of individuals. The study area is divided into six urban areas, each characterized by the existence of a central agro-food market, which represents the main place of supply for the population and one of the most important points of concentration and interaction of the agents in the model. The model assumes that the epidemic outbreak is initiated in an agro-food market, considered the initial source of exposure of the population through the consumption of contaminated products. After the appearance of the first cases, the infection spreads in the urban environment through contacts between infected and susceptible individuals. The purpose of the model is to reproduce the spatio-temporal dynamics of the infection spread and to provide a tool for evaluating different scenarios of epidemic evolution and control measures and to provide a tool for evaluating different scenarios.

3.2 Model according to ODD protocol

The model description follows the ODD protocol, used to standardize the presentation of agent-based models. The generic description contains the model scope, Entities, state variables and scales, and Process presentation and execution scheduling The proposed model is an Agent-Based Model (ABM), built according to the individual-based paradigm, with the objective of simulating the spatio-temporal propagation of a foodborne disease in an urban environment representative of the municipality of Bucharest. The model aims to evaluate the influence of the initial outbreaks represented by contaminated agri-food markets, population mobility and secondary human-to-human transmission on the evolution of the epidemic. The model contains three categories of entities:

i. the simulation environment, represented by a discrete network of patches;
ii. mobile agents, which represent units of the population containing multiple individuals;
iii. static agents, which represent agri-food markets and constitute the primary outbreaks of infection.

The city is represented by an area of approximately 24 × 24 km², discretized in a NetLogo world of 1200 × 1200 patches, resulting in a spatial resolution of approximately 20 m/patch.

The population of approximately 1.7 million inhabitants is represented by approximately 170–200 mobile agents, each agent corresponding to a representative unit of approximately 10,000 inhabitants.

The time scale is calibrated so that 1 tick ≈ 20 s, and the simulation duration is variable corresponding to the active period of disease propagation.

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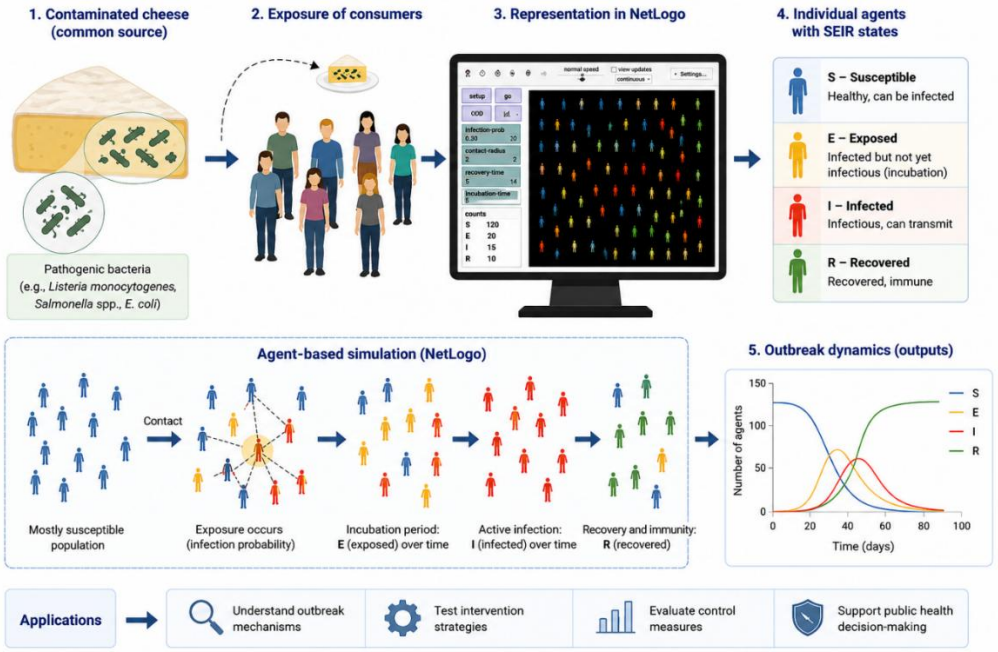

Fig. 1. Conceptual architecture of the agent-based model used to simulate the spread of a foodborne disease resulting from the consumption of a batch of microbiologically contaminated cheese. Images provided by Servier Medical Art (https://smart.servier.com), licensed under CC BY 4.0 (https://creativecommons.org/licenses/by/4.0/). and other publicly available icon resources.

The population of approximately 1.7 million is represented by approximately 170–200 mobile agents, each agent corresponding to a representative unit of approximately 10,000 inhabitants. The time scale is calibrated so that 1 tick ≈ 20 s, and the simulation duration is variable corresponding to the active period of disease propagation. The model is initialized by loading the map, configuring the simulation parameters, and distributing agents according to a predefined initial configuration. During each tick, the following are executed: 1) agents movement; 2) updating the state of agri-food markets; 3) transmission of infection; 4) updating the incubation period; 5) agents recovery; 6) updating epidemiological indicators; 7) save results; 8) check stop condition.

The design concepts contain fundamental principles, emergent behaviour, adaptation, objectives, learning, prediction, perception, interactions, stochasticity (probabilistic elements), collective elements and observations. The model reproduces the spread of a foodborne disease by combining two mechanisms: direct infection through exposure to contaminated sources existing in agri-food markets and secondary transmission between individuals. The dynamics of the epidemic result exclusively from local interactions between agents and between agents and contaminated markets, without the existence of a centralized control mechanism.

The model allows manual or automatic modification of simulation parameters by applying intervention measures, such as: closing contaminated markets; reducing population mobility; improving hygiene conditions.

Mobile agents do not pursue an explicit individual objective, their behaviour being determined by the mobility rules and epidemiological transitions defined by the SEIR model. Agents detect the presence of contaminated markets and infected agents in their vicinity resulting in direct and indirect infection.

The model uses stochastic processes for: agent movement (speed is fixed depending upon mobility limitation, but orientation is random) and infection transmission. Simulation monitoring is carried out both as logs and in a graphical manner through: the number of Susceptible agents; the number of Exposed agents; the number of Infected agents; the number of Recovered agents; the epidemiological level (No cases, Local outbreak, Epidemiological alert, Major risk, Epidemic). The concepts related to details include initialization, input data, and submodels. The simulation flow consists of: model reset; loading the map; configuring parameters; loading the initial population distribution; initializing global variables; generating the log file. The input data include: city map; initial population distribution; epidemiological parameters; agri-food market locations; intervention scenarios. The model is composed of the following submodels: mobility submodel; agri-food market submodel; infection transmission submodel; incubation period submodel; recovery submodel; epidemiological monitoring submodel; spatio-temporal calibration submodel.

4. NetLogo model

The tool used is NetLogo and the model is described using the ODD protocol, developed specifically for IBM (individual based models) situations, as part of ABM. The proposed model is an ABM (Center for Connected Learning and Computer-Based Modeling, 2026), built according to the individual-based paradigm, in which each agent represents a representative unit of the population and moves in an urban environment that includes agri-food markets modelled as primary outbreak of infection. In these locations, the existence of contaminated elements is assumed, which represent the

initial source of infection of the agents, after which the transmission of the disease continues through the interactions between infected and susceptible agents. The model was developed and calibrated for the city of Bucharest (Direcția Regională de Statistică București, 2024), chosen as the study area due to its high population density, intense urban mobility and the existence of an extensive network of agri-food markets, factors that can favour the rapid spread of a foodborne outbreak (Bran et al., 2018). In the model, the urban environment is represented by an area of approximately 576 km² and a population of approximately 1.7 million inhabitants. Its high population density, intense urban mobility and large number of food distribution points justify its choice as a case study for the development and calibration of an ABM designed to simulate the spread of foodborne disease in urban areas. (Direcția Regională de Statistică București, 2024). Although the model is calibrated for Bucharest, the methodology can be adapted to other urban areas with similar characteristics.

The epidemiological scenario considers the emergence of a foodborne outbreak from an agri-food market, because of the presence of contaminated food products or elements. Agents who meet these contaminated sources can become infected, representing the primary cases of the outbreak. Subsequently, the model assumes that the infection can also spread through contacts between infected and susceptible individuals, generated by their mobility and interactions in different areas of the city. In this way, the model allows for the investigation of both the role of agri-food markets as initial foci of infection, and the contribution of population mobility to the spatio-temporal expansion of the epidemic outbreak. The model assumes that, after initial exposure to the contaminated source in the agri-food market, infected individuals may contribute to the subsequent spread of the disease through human-to-human contacts, this hypothesis being introduced to allow analysis of the spread of the outbreak under conditions of secondary transmission. The operation of the model is controlled by a set of parameters that describe the mechanisms of infection transmission, the epidemiological characteristics of the disease and the behaviour of the population in the simulated urban environment. The main parameters are described in Table 1. Of these, all, except the population size, will be adjustable by the operator, but also automatically controlled for testing scenarios (example: closing a proven outbreak of infection (market), limiting mobility or increasing hygiene standards if the number of infections exceeds a certain threshold).

This spatial-temporal calibration ensures a compromise between the fidelity of the representation of the epidemiological phenomenon and the computational efficiency of the model, allowing the exploration of many scenarios in a short time, without significantly affecting the realism of the infection propagation dynamics.

Within the model, the severity of the spread of infection is assessed by relating the number of infected agents to the total simulated population. The epidemiological thresholds are defined as a percentage in relation to the population represented by the model, and to facilitate the interpretation of the results they are also expressed in the number of agents. Since, in the adopted configuration, one mobile agent represents approximately 10,000 inhabitants, the epidemiological thresholds can be directly converted to the real population equivalent. This approach allows the same epidemiological criteria to be used even if the aggregation level of the model is subsequently changed. Based on these considerations, the evolution of the outbreak is classified into three epidemiological levels (Table 2).

The values presented in Table 2 represent approximate thresholds, resulting from discretizing the population by the representative agents used in the model. Since one agent corresponds to 10,000 inhabitants, the conversion between percentages of the real population and the number of agents involves rounding to the nearest integer. These approximations do not significantly influence the epidemiological interpretation of the results and allow the definition of unitary criteria for comparing the simulated scenarios.

In scenario analysis, the moment of reaching each epidemiological threshold constitutes one of the main indicators of the dynamics of the spread of the infection and is analyzed together with the maximum number of infected agents, the duration of the epidemic outbreak and the final number of recovered agents.

Table 1. System parameters.

Parameter	Simulation variable	Description	Unit
Direct infection probability	direct_inf_chance (direct P_{trans})	Probability that a susceptible agent will become infected through contact with contaminated source from market. Controls the size of the initial outbreak.	%
Basic reproduction number	indirect_inf_chance (indirect P_{trans})	The average number of secondary cases generated by an infectious agent in a fully susceptible population. In the model, this parameter is used to estimate the probability of human-to-human transmission.	%
Incubation period	ticks_incubation	The interval between the moment of infection and the agent's transition to the infectious state, corresponding to the Exposed state in the SEIR model.	ticks
Infectious period	ticks_recovery	The length of time that the agent remains in the *Infected* state and can transmit the disease to other agents. After this period, the agent enters the *Recovered* state.	ticks
Simulated population	population	The number of agents used in the simulation, established by correlating the real population with the level of aggregation adopted in the model.	agents
Agent mobility	mobility	The movement speed of agents in the urban environment, expressed in patches per tick and calibrated to reproduce the mobility of the real population.	patch/ tick
Level of hygiene conditions	hygiene (H)	Parameter that reflects the effectiveness of hygiene and food safety measures, reducing the probability of infection through exposure to the contaminated source and the probability of human-to-human transmission.	%

Table 2. Infection characteristics.

Epidemiological level	Population percentage	Real equivalent population	Agents
Local outbreak	< 3%	< 50.000 inhabitants	< 5 agents
Epidemiological alert	3–12%	50.000–200.000 inhabitants	5–20 agents
Epidemic	> 12%	> 200.000 inhabitants	> 20 agents

The model is characterized by state variables associated with the environment, agents, and the mechanism of infection propagation. The NetLogo facility is used to move the mobile agents inside a closed contour that represents the boundaries of the area of interest.

The simulation environment is represented by a two-dimensional network discretized into patches. Each patch is associated with two Boolean variables, blocked and inside, which indicate whether it can be traversed by agents and, respectively, whether it belongs to the area of interest. The blocked variable indicates whether the patch belongs to an area inaccessible to agents. These patches delimit the contour of the simulation domain or represent obstacles that cannot be crossed. The inside variable indicates whether the patch belongs to the active domain of the simulation. Mobile agents can move exclusively on the patches for which this variable is true. The model uses exclusively mobile turtle agents for simulation, but they are divided into two categories: associated with individuals (they move) and associated with markets (they do not move).This choice provides a high flexibility of the model and allows for subsequent expansion by associating specific characteristics of each market, such as the level of contamination, the type of products sold, the flow of visitors or the efficiency of sanitation measures, without modifying the general architecture of the model.

Each agent is characterized by the following state variables:

- **movable?** – logical variable used to differentiate mobile agents from static agents. Agents for which this variable is false represent agri-food markets and remain fixed throughout the simulation, while agents for which the value is true represent the mobile population;
- **market_name** – variable used to identify the agri-food market associated with each static agent, facilitating spatial analysis of infection outbreaks;
- **healthy_S?** – indicates that the agent is in the Susceptible (S) state and can contract the infection;
- **exposed?** – indicates that the agent is in the Exposed (E) state, corresponding to the incubation period. At this stage the agent is infected but does not yet transmit the disease;
- **infected?** – indicates that the agent is in the Infected (I) state and can transmit the infection to other susceptible agents;
- **recovered?** – indicates that the agent has passed into the Recovered (R) state and is no longer participating in the spread of the infection;
- **sick-time** – a time counter that records the duration of the infected state and is used to determine the transition to the Recovered (R) state;
- **incubation-time** – a time counter used to monitor the incubation period and to determine the moment of transition from the Exposed (E) state to the Infected (I) state.

To monitor the evolution of the epidemic and control the execution of the simulation, the following global variables are defined:

- **nr_susceptible** – agents in the Susceptible (S) state.
- **nr_exposed** – agents in the Exposed (E) state.
- **nr_infected** – agents in the Infected (I) state.
- **nr_recovered** – agents in the Recovered (R) state.
- **infection_level** – string variable used for the automatic classification of the severity of the epidemy depending on the proportion of infected agents. It can take one of the following values: a) **No cases**; b) **Local outbreak** – less than 3% infected agents; c) **Epidemiological alert** – between 3% and 5% infected agents; d) **Major risk** – the proportion of infected agents is between 5% and 10%; e) **Epidemic** – the proportion of infected agents exceeds 10%.

The model execution is organized into two main stages: an initialization stage, executed only once at the beginning of the simulation, and an iterative stage, executed in a cycle until the stopping condition is met.

Step1. Initialization of the model. This procedure executed only once and has the role of preparing the simulation environment for the experiment. In this stage, the following operations are performed:

- resetting the simulation time (number of ticks);
- removing all existing agents and reinitializing the simulation environment;
- loading the map corresponding to the study area;
- initializing the global variables used to monitor the evolution of the SEIR epidemiological model;
- initializing the log file (log), used to record the evolution of the simulation and subsequent analysis of the results.

Step 2. Configuring simulation parameters. Before starting the simulation, the user configures the model parameters from the graphical interface (Fig.2), according to the values presented in Table 1. The parameters include the probability of infection through the contaminated source, the basic reproduction number, the incubation period, the infectious period, the level of hygiene conditions, the mobility of agents and the size of the simulated population.

Step 3. Initialize the population distribution. To ensure comparability between the analyzed scenarios, the initial spatial distribution of the population is not randomly generated at each execution. The model loads a previously saved configuration, so that all simulations start from the same initial distribution of agents within the city.

Step 4. Simulation cycle (executed in a loop). After completing the initialization stages, the model repetitively executes the main simulation cycle, each iteration corresponding to a simulation tick.

Step 4.1 – Agent Movement. Mobile agents are moved in the simulation environment according to defined mobility rules, without exceeding the limits of the active domain and avoiding areas marked as inaccessible.

Fig. 2. Multi-agent simulation graphical user interface.

Step 4.2 – Updating the status of agri-food markets. The epidemiological status of agri-food markets is updated according to the configuration selected in the user interface. Markets can be activated or deactivated as infection hotspots through the controls available in the interface. The model also allows for modifying the dynamics of the simulation through manual or automatic interventions, such as closing a contaminated market, changing population mobility or increasing the level of hygiene measures, depending on the evolution of the number of infected agents.

Step 4.3 – Transmission of infection. For each agent in the infectious state, susceptible agents in its vicinity are identified. The transition from the Susceptible (S) state to the Exposed (E) state occurs with a probability dependent on the source of infection. In the case of contaminated agri-food markets, the probability of infection is higher than in the case of human-to-human transmission, reflecting direct exposure to the contaminated source. The final infection probability was calculated as the product of the direct/indirect transmission probability and the complement of the hygiene level: $P_{inf}=P_{trans}(1-H/100)$; where P_{inf} is the resulting infection probability, P_{trans} is the direct/indirect transmission probability, and H is the hygiene level. All probabilities are expressed between 0 and 100. The complement of hygiene, (1-H/100), is used because hygiene acts as a protective factor against infection; therefore, it represents the residual susceptibility to transmission after accounting for the protective effect of hygiene. Consequently, higher hygiene levels progressively reduce the baseline transmission probability, whereas in the absence of hygiene-related protection (H=0), the baseline transmission probability remains unchanged.

Step 4.4 – Update the incubation period. For agents in the Exposed (E) state, the incubation period counter is updated. When it expires, the agents move to the Infected (I) state and become capable of transmitting the infection.

Step 4.5 – Agent recovery. For agents in the Infected (I) state, the duration of the infectious period is updated. After it expires, the agents are transferred to the Recovered (R) state and no longer participate in the transmission of the disease.

Step 4.6 – Recording the current state. At the end of each iteration, the values of the main epidemiological indicators are saved in the log file, including the number of susceptible, exposed, infected and recovered agents. The data thus obtained are used to compare different epidemiological scenarios.

Step 4.7 – Updating the graphical representation. The model updates the graphical representation of the evolution of the SEIR compartments, allowing real-time monitoring of the epidemic dynamics and visual comparison of the analyzed scenarios.

Step 4.8 – Checking the stopping condition. At the end of each iteration, the simulation termination condition is checked. This condition is represented by the convergence of infected individuals to 0, while the susceptible number of individuals is decreasing. This represents the end of the infection based on the SEIR assumptions.

5. EXPERIMENTAL RESULTS

The size of the simulation environment (Fig. 3) and the execution parameters of the model were calibrated so as to simultaneously meet three objectives: (i) ensuring a fluent execution, allowing for the analysis in near real time of several epidemiological scenarios; (ii) maintaining a sufficiently detailed graphical representation for the visual tracking of the dynamics of agents and the spread of infection; and (iii) maintaining a correspondence as close as possible between the scale of the simulation and the real characteristics of the urban environment analyzed.

To achieve these objectives, the following model parameters were calibrated: the size of the simulation space, the number of mobile agents and population aggregation factor, the speed of movement of the agents, and the correspondence between simulation time (ticks) and physical time. Since the NetLogo platform uses a movement model based on random directions, the temporal calibration was performed so that the evolution of the simulation was compatible with the characteristic dynamics of the propagation of a foodborne disease.

The size of the simulation environment and the number of agents were set to ensure a compromise between the fidelity of the representation of the studied phenomenon and computational efficiency. For the hardware configuration used in the development and testing of the model (Intel® Core™ i5-9400F processor and 16 GB DDR4 memory, Fig.3), the simulation environment was defined as a NetLogo world of 1200 × 1200 patches, in which approximately 200 mobile

agents evolve over a variable number of ticks. From experimental execution the duration in ticks is around 25,000. Under these conditions, a complete simulation, based on the random movement of the agents, is executed in approximately 20 s, allowing the successive running of many scenarios and the performance of statistical analyses on the results obtained.

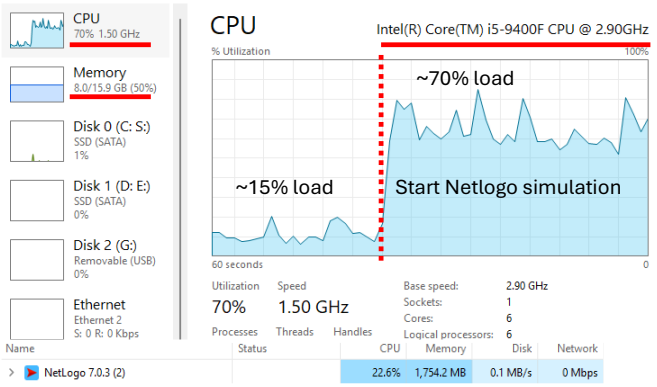

Fig. 3. Resources usage for NetLogo usage from Task Manager.

The model reproduces an urban area of approximately 24 × 24 km², corresponding to the municipality of Bucharest. To fit 24km in 1200 patches it results in a patch dimension of 20m.

Temporal calibration was performed by relating the agents' movement to the average walking speed of an adult. Considering that an agent advances by one patch at each tick (with no mobility restriction – 100%), and one patch corresponds to 20 m, for an average movement speed of approximately 1 m/s it follows that one tick corresponds to an interval of approximately 20 s of real time. Since the objective of the model is to analyse the spread of the epidemic at the macroscopic level and compare epidemiological scenarios, the movement of agents is modelled by a random process, which approximates the aggregate mobility of the population and avoids introducing additional assumptions regarding individual routes or traffic flows. Since the model is used for the comparative evaluation of several epidemiological scenarios, a mechanism for saving and restoring the initial spatial distribution of the population was implemented. This approach guarantees the use of the same initial configuration of agents in all simulations, ensuring the reproducibility of experiments and the comparability of results, regardless of the parameters of the scenario analyzed.

The time horizon of the simulation was determined based on the parameters characteristic of a foodborne disease and the adopted time scale. The model considered an incubation period of one day (86400sec) and an infectious period of two days. Since the simulation exclusively includes the intervals in which the population is active and does not model the day–night cycle, the epidemiological time is compressed by a factor approximately equal to 2. As a consequence, by dividing the considered periods by 20sec/tick, the temporal resolution for the incubation period is 2160 ticks and 4320 ticks for the infectious period.

Based on these assumptions and considering the existence of a single initial source of infection, represented by a contaminated agri-food market, as well as an initial uniform population distribution at the metropolitan level, the complete evolution of the epidemic outbreak, from the appearance of the first case to the disappearance of the last infected agent, takes place over a period of approximately 25,000 ticks (Fig. 4). During this interval, the evolution of the infection goes through all stages from the situation of No cases, Local outbreak, Epidemiological alert, Major risk, to Epidemic, the latter situation being maintained for a long period. Through simulation, we will track the detection of the epidemic and the adjustment of the system parameters to limit the epidemic period (e.g.: elimination of the source(s) of toxiinfection, increase of hygiene standards and the most unpleasant case for the population, limitation of mobility).

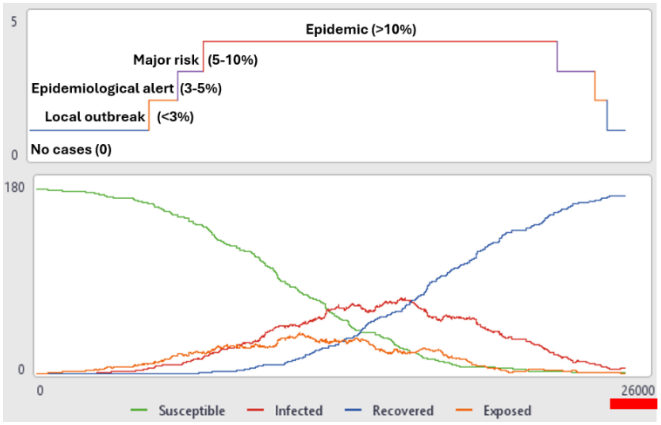

Fig. 4. Epidemiological dynamics according to the SEIR model (below) and classification into epidemiological severity levels (population 170 individuals, map 1200x1200 elementary simulation cells (patch) of size 0.6 pixels, chance of direct infection 35%, chance of indirect infection 8%, mobility 100%, hygiene 0%, recovery ticks 4300, incubation ticks 2100) (above).

The temporal evolution of the SEIR compartments is the main indicator used to compare scenarios and to evaluate the effectiveness of the intervention measures tested in the model.

In the previously described configuration, a full simulation is executed in approximately 100 s, with CPU utilization reaching a stable maximum of approximately 70%, compared to a level of 17% in idle mode. These results confirm that the model can be used to run a large number of scenarios in a short time frame, without compromising the spatiotemporal representativeness of the studied phenomenon.

The model (Fig.5) considers exclusively the periods of population activity, in which agents are in continuous movement, without explicit modelling of the day–night cycle. This assumption leads to compression of time by (approx.) a factor of two and allows for a reduction in simulation duration, while maintaining the essential characteristics of the spread of a foodborne disease at an urban level.

In the proposed model, the severity of the epidemic is quantified by the area under the curve of the "Infected" compartment (Area Under the Infection Curve – AUIC), calculated over the entire duration of the simulation. This indicator expresses the cumulative impact of the infection on the population, integrating both the intensity of the epidemic (the number of infected agents at a given time) and the duration

of its persistence. Unlike point indicators, such as the maximum number of infected, AUIC allows for the objective comparison of epidemiological scenarios that present different temporal dynamics.

Since the model is stochastic, based on random movement of agents and probabilistic transmission events, each simulation run leads to a slightly different evolution of the susceptible, exposed, infected and recovered populations. Consequently, the evaluation of the model cannot be carried out exclusively on the basis of a single simulation, but requires the analysis of the variability of the results obtained from several independent runs, carried out under identical initial conditions.

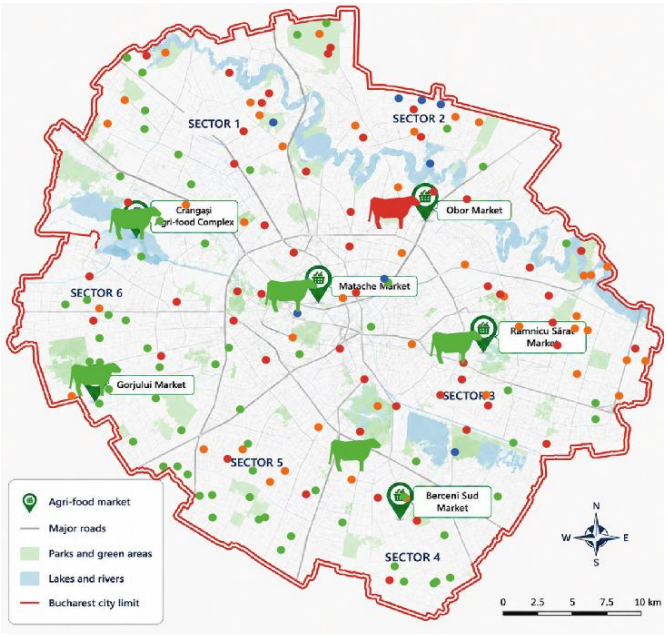

Fig. 5. Screen capture of the MAS simulation that uses Bucharest as layout (double red line is city limits, cows represent agri-food markets (red represents infection), coloured dots represent population agents with different statuses according to Fig. 3 labels).

For this purpose, two complementary measures of the dispersion of the results were calculated: the Mean Absolute Deviation (MAD) and the Root Mean Square Error (RMSE).

The simultaneous use of the two indicators provides a complete characterization of the model reproducibility. While the MAD describes the average variability of the simulations, the RMSE highlights the existence of possible high-amplitude fluctuations. Low values of both indicators indicate that independent runs lead to similar results, suggesting that the model dynamics are stable and that the evolution of the epidemic is predominantly determined by the model structure and the parameters used, not by the random variations introduced into the simulation process.

In the case of the proposed model, the values obtained for MAD and RMSE remained low compared to the simulated population size, which indicates limited variability between the five independent runs and confirms the good repeatability of the results. The observed differences are specific to agent-based models and reflect the probabilistic nature of infection transmission, without affecting the general trend of the epidemic evolution. Therefore, the average of the simulations can be considered a representative estimate of the model behaviour, and the variation range defined by MAD and RMSE provides an objective measure of the uncertainty associated with the simulation process.

MAD and RMSE do not represent a measure of the model error compared to experimental data, since in this study there is no real reference series. The two indicators quantify exclusively the internal variability and reproducibility of the stochastic model, constituting a measure of its robustness to repeated runs under identical conditions.

To evaluate the effectiveness of different control measures on the evolution of the epidemic, eight simulation scenarios were defined. All experiments start from the same SEIR-type epidemiological model, in which each agent successively goes through the states Susceptible (S) → Exposed (E) → Infected (I) → Recovered (R). The simulations are executed until the number of infected people drops below 1%.

The performance of each scenario is assessed through three indicators:

- the area under the infection curve (AUIC) (area below red curve in Fig.6), calculated as the sum of the number of people infected at each moment of the simulation. This indicator quantifies the overall impact of the epidemic, combining both the number of cases and their duration, being indirectly associated with the social impact and the morale of the population;
- the intensity of the epidemic (INTENS) (maximum value of red graphic in Fig.6), defined as the maximum number of people infected simultaneously, a relevant indicator for estimating the pressure exerted on the medical system;
- the duration of the epidemic (DUR) (epidemic duration in Fig.3), expressed in ticks, representing the period in which the number of infected people exceeds the threshold of 10% of the population.

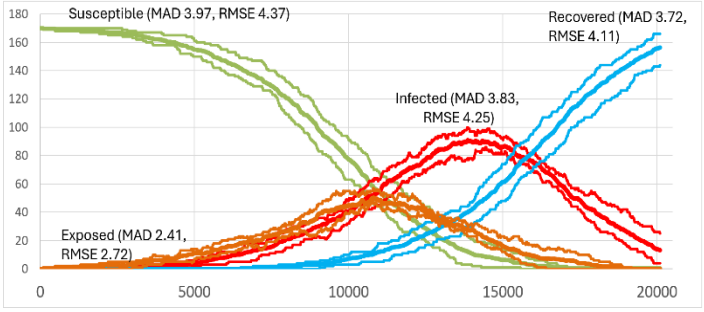

Fig. 6. Graphical representation of the statistical nature of the simulated process.

Experiment 0 (reference scenario). This experiment represents the baseline scenario used to compare all subsequent interventions. A single agri-food market is contaminated at the beginning of the simulation, without any control measures being applied. The level of hygiene is considered normal, so that the probability of transmission remains unchanged and population mobility is maximum. Under these conditions AUIC is 727,000, INTENS is 98 and duration is 12,500 ticks. All values are approximate in the sense that simulation is

susceptible to variability and values are collected by graphical inspection. The same goes for the following experiments.

Experiment 1 (increasing the level of hygiene). This scenario maintains the conditions of the reference experiment, but the probability of transmission is halved by increasing the level of hygiene. Reducing the probability of infection leads to a modest decrease in the AUIC (712,000) and a decrease in the maximum intensity to 78 cases but prolongs the evolution of the epidemic to approximately 13,500 ticks. The results indicate that hygiene measures reduce the speed of the spread of the infection, without significantly changing the total number of people affected.

Experiment 2 (reduced mobility). In this experiment, the probability of transmission remains unchanged, but the speed of population movement is reduced by half. Limiting mobility produces a more significant reduction in the impact of the epidemic, with the AUIC decreasing to 654,000, and the maximum intensity to only 46 simultaneous cases. At the same time, the epidemic evolves more slowly, with the duration increasing to approximately 19,500 ticks. The results highlight the classic effect of "flattening the epidemic curve", by reducing contacts between agents.

Experiment 3 (simultaneous contamination of all markets). In this scenario, all agri-food markets represent initial sources of contamination, without the application of any additional measures. The simultaneous spread from multiple outbreaks determines the highest intensity of all the scenarios analyzed (106 simultaneous cases) and the largest AUIC (732,000), but its duration decreases to approximately 10,700 ticks. The multiplication of outbreaks accelerates the spread of the infection and leads to a rapid peak of the epidemic. People become infected fast and heard immunization can be assumed.

Experiment 4 (closing the contaminated market). Starting from the reference scenario, the contaminated market (Obor) is closed as soon as the epidemic reaches the major risk threshold. The results show that this isolated measure has little effect on the evolution of the epidemic. The AUIC is 729,000, the maximum intensity increases slightly to 102 cases, and the duration of the epidemic is approximately 12,000 ticks. Closing a single source does not significantly limit the evolution of the epidemic.

Experiment 5 (closing the market and increasing hygiene). This scenario combines the closure of the contaminated market with strict hygiene measures, which reduce the probability of transmission by 80%. The intervention produces a significant decrease in all indicators. The AUIC of the epidemic decreases to 540,000, and the maximum intensity is reduced to only 32 simultaneous cases. However, the epidemic evolves more slowly, the duration increasing to approximately 17,000 ticks. The results demonstrate the high efficiency of hygiene measures in limiting human-to-human transmission.

Experiment 6 (market closure and mobility reduction). In this experiment, the contaminated market is closed, and population mobility is reduced by half. Compared to the baseline scenario, the AUIC of the epidemic is reduced to 618,000, and the peak intensity reaches 47 simultaneous cases. The duration of the epidemic increases to approximately 18,200 ticks, confirming that limiting movement reduces the speed of spread and distributes cases over a longer period.

Experiment 7 (simultaneous application of all measures). The last scenario combines all the interventions previously analyzed: closing the contaminated market, reducing the probability of transmission by 80%, and reducing population mobility by half. This scenario produces the best results of all the experiments conducted. The AUIC of the epidemic decreases to only 436,000, representing a reduction of approximately 40% compared to the reference scenario. The maximum intensity remains limited to 32 simultaneous cases, and the duration of the epidemic is approximately 12,000 ticks, comparable to the baseline scenario. The results demonstrate the existence of a synergistic effect between transmission reduction measures and mobility restrictions, their combination managing to simultaneously reduce the overall impact of the epidemic and the pressure on the medical system.

The comparative analysis of the eight scenarios highlights that the measures applied individually produce limited effects on the evolution of the epidemic. Increasing the level of hygiene reduces the intensity of the outbreak, and limiting mobility leads to a pronounced flattening of the epidemic curve, but both measures tend to prolong the duration of the epidemic.

6. CONCLUSIONS

The paper presents a solution for assessing the spread of an infection by simulating epidemiological dynamics based on configurable parameters. The model is implemented in a multi-agent framework developed in NetLogo, which allows for the accelerated reproduction of the infection transmission process and the analysis of the impact of different intervention measures on the evolution of the epidemic.

Closing a single market after reaching a high-risk threshold has a limited impact, suggesting that community transmission is already extensive enough to support the evolution of the epidemic independently of the initial source.

The best results are obtained when the measures are applied simultaneously. Reducing the probability of transmission through hygiene measures, combined with limiting mobility and eliminating the main source of contamination, leads to a decrease in both the total impact of the epidemic (area under the curve) and the maximum number of simultaneous cases, without excessively prolonging the duration of the epidemic phenomenon. These results confirm that integrated intervention strategies are significantly more effective than the isolated application of a single control measure.

The proposed model presents a series of limitations that constitute directions for further development. In its current form, recovered agents acquire permanent immunity, without the possibility of reinfection in the presence of persistent sources of contamination. Also, the movement of agents is random, without reproducing the real mobility flows of the population. The model does not differentiate day–night cycles and does not allow the definition of flows entering and leaving the monitored area or the application of selective mobility restrictions on them.

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