# A Dynamic Behavior Epidemiological Model By Membrane Systems

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**Abstract.** This paper explores an application of Membrane Systems, also known as P Systems, in the field of epidemiological research. The objective is to use the theoretical foundations of P Systems to enhance our understanding of epidemiological dynamics, and develop a model that integrates various aspects for simulating complex scenarios of communicable diseases. The article draws inspiration from existing research that employs P Systems to model epidemiological processes, particularly in the context of COVID-19. These studies yet highlight the advantages of using membrane models, such as the scalability, flexibility, and ability to capture hierarchical relationships within scenarios.
The proposed model incorporates a population structure, with individual properties and infection transmission rules, in order to generate a disease dynamics, according to a dynamic behavior logic which creates realistic simulation scenarios. The analysis of experimental results reveals valuable insights, including the impact of vaccination coverage, the timing of contagion peaks, and the predictive accuracy of the model. The results emphasize the importance of vaccination in controlling the spread of infectious diseases, and highlight the influence of population awareness and caution on disease dynamics.

**Keywords:** Epidemiological model · information based dynamic behavior · membrane systems · probabilistic strategy

## 1 Introduction

By *Epidemiological modeling* we refer to the prediction of the trend of infectious diseases through mathematical and computational tools. Considering the impact of COVID-19 pandemic, this field of research has undergone new developments and directions in recent years. Epidemiological models can provide new insights into the epidemiology of infectious diseases, and suggest criteria for the design of more efficient control strategies. In this work, a computational model of a parallel and distributed type, called membrane system, is applied to the field of epidemiological research. Membrane systems are an unconventional computation model inspired by the functioning of cells, which makes it natural to think of its use to represent different types of biological processes [1,2,3,4].

The potential of membrane systems to describe population dynamics is not applied only to the epidemiological field. Interesting investigations assessing the risk of population extinction related to the population size dynamics in specific ecological contexts [5,6,7,8] and cellular contexts [9,10,11] have also appeared in the literature.

Very recently, two specific examples of epidemiological modeling have appeared, that inspired the present work. The first one is LOIMOS, an epidemiological simulator developed by Baquero et al. in 2021 [12]. LOIMOS uses transition P Systems with communication rules, active membranes and a stochastic simulator engine to model predictive multilevel scenarios. It also integrates various elements for simulating epidemiological scenarios, such as population structures, individual characteristics, disease dynamics, and intervention strategies. Each membrane represents a compartment within the scenario, such as places (e.g., schools, houses) and individuals (people), with specific labels symbolizing key elements and objects representing attributes like age, roles, infections and health statuses. Rules define interactions and processes within the scenario, including contagion, mobility, scheduling, recovery, and mortality. One of the advantages of models like LOIMOS is their compartmentalization of structures and agents, allowing for easier introductions of new potential features and adaptation to different scenarios. Additionally, hierarchies between elements are naturally defined in P systems, providing a more intuitive representation of complex scenarios.

The second work considers the application of Population Dynamic P Systems (PDP) models to understand epidemic dynamics and evaluate control strategies. Such a study, by Colomer et al. (2021) [14] focuses on modeling the effects of vaccination and contact tracing on handling the COVID-19 outbreak using a stochastic PDP model, which allows to represent pandemic dynamics under various scenarios, including different control measures and epidemiological conditions. The considered scenarios included factors like disease transmission, mobility and government interventions. Furthermore, the model considers the characteristics of the population, disease evolution and impact of interventions, providing insights about the effectiveness of different control strategies. Simulation outcomes reported reductions in estimated deaths and infections with increasing vaccination rates, particularly when combined with social control measures. The objective of this work is the development of a model for the spread and control of infectious diseases based on Membrane Systems, that extends the works appeared so far. The resulting model must be able to recognize and validate the dynamic patterns of infectious diseases and suggest evolutionary predictions in different scenarios. More specifically, the challenges faced in this study are the extension of the application of Membrane Systems in research, by adapting their characteristics into solutions to achieve the proposed goal, including evaluating population dynamics, transmission dynamics, the impact of vaccination and the impact of human behavior. By implementing the provided model, it is possible to improve the understanding of infectious disease dynamics, by producing simulation results of various complex scenarios. This approach also offers the opportunity to validate the predictive ability of the model, and to evaluate the

effectiveness of different strategies that may be adopted to control the diffusion of the infection.

In the following, we describe an epidemiological model based on P Systems, incorporating behavioral logic dynamics. We outline the fundamental components of the model, including its structure, the chemical substances involved and the reactions used to represent complex processes in a computational form. We also explore the various characteristics and capabilities of a Membrane System, such as communication among chemical components and rewriting rules. Unlike similar models, the key extensions of this model include:

- Behavioral Dynamics Integration: The population adopts behaviors in response to changes in the epidemiological situation. These include adaptive behaviors based on infection prevalence, which dynamically influence infection rates and vaccination processes.
- Population Movements: Individuals move throughout the simulation scenario with varying probabilities based on the epidemiological context of the destination.
- Scalability and Adaptability: The model allows the number of membranes to be changed to represent different geographic entities (such as cities and provinces), also adjusting their population sizes.
- Dynamic Behavioral Logic Mechanism: The model does not consider static intervention thresholds represented as numerical values. Instead, it uses dynamic behavioral logic, reflecting more realistic and responsive changes in population behavior based on current epidemiological data.

The rest of the paper is organized as follows: in section 2 we provide a theoretical background on Membrane Systems, introducing their key components. This section serves as a foundation for understanding the functioning of Membrane Systems. In section 3, "Model Definition", we outline the structure of the model designed to analyze epidemiological scenarios for generic communicable diseases. Every component is described, starting with the membrane structure, followed by the objects involved in the model. We then delve into information modeling and human behavior, ending in the definition of all the rules that govern the simulation scenarios. The dynamics related to the progression of infection are explained in section 4. New rules are introduced, such as Incubation Rules and rules for the transition to infected and recovered state. Furthermore, the hospitalization process is addressed. Section 5 is about the routines of the individuals within the implemented population. Scheduled activities for different groups of people trigger movement rules and infection rules based on the location where the infection occurs. Section 6 discusses the simulation results, with comparisons over different vaccination coverage levels and an accurate analysis on the role of behavioral dynamics in the proposed case study. The final section briefly summarizes the paper and offers some insights into future directions.

## 2 Prerequisites

In this section, we recall some theoretical notions relating to Membrane Systems are included which will be needed in the following. For further information about Membrane systems, we refer the reader to [29].

**Definition 1.** *Formally, a Membrane System can be defined as:*

$$\Pi = (V, H, \mu, M_1, ..., M_n, R)$$

where:

- $V$: is the alphabet of objects;
- $H$: is the set of labels for membranes;
- $\mu$: represents the membrane structure;
- $M_i$: is a string of symbols over V (initial multiset of symbols in region $i$);
- $R$: finite set of evolution rules.

The functioning of P Systems consists of interactions between membranes and the transfer of chemicals inside them. Elements within a region can be involved in reactions described by rewriting rules, with a resulting replacement of chemicals. Reactions are transitions executed in a region, described by means of a rewriting rule and a target destination, where chemicals on the left are replaced by chemicals on the right. Multiple transitions form a computation. Examples:

- $a \rightarrow xy$ (Non Cooperative, a symbol is turned into a multiset independently from the context);
- $ab \rightarrow xy$ (Cooperative, the reaction evaluates the chemicals in order to reach the goal in a faster way);
- $ac \rightarrow xc$ (Catalyst, in this case the chemical $c$ is called catalyst and triggers a reaction, turning $a$ into $x$);

The possible target destinations are *here*, *out*, $in_j$:

- *here* = the result stays in the same region;
- *out* = the result is sent outside the membrane;
- $in_j$ = the result is sent into the membrane $j$.

Rules are applied with priority; if no priority stands out, then non-determinism decides the order of rule application.

A *configuration* of such a system is described by the multisets of chemicals associated with each region, and by the membrane structure. Starting with the initial configuration, rules are applied in a maximal parallel way to obtain new configurations. When no rules can be applied in a computation step, then the computation halts, and the result is the set of object expelled through the skin membrane (or, alternatively, in a specific output membrane, defined in the system).

An alternative approach for studying epidemiology complex problems is PDP models. These have been recently applied to analyze the dynamics of COVID-19 under various scenarios to compare the impact of different control measures, highlighting the effectiveness of vaccination and contact tracing, especially when combined with social measures like distancing and mask-wearing [14]. By taking as input parameters inherent to the disease, the simulation (which takes place in several steps with a time unit of one day) offers insights about the disease and the effectiveness of interventions. The simulation steps include PCR testing, incubation, infection, recovery and mobility.

## 3 Model Definition

In this section, the definition of a dynamical system model will be discussed with the aim of studying and analyzing the epidemiological scenarios for generic communicable diseases. As stated in the introduction, the objective of this work is to produce an epidemiological model, based on P Systems, to analyze simulation results of populations with dynamic behavioral logic. By implementing this model, the goal is to enhance understanding of infectious disease dynamics, produce simulation results for various complex scenarios, validate the model's predictive ability, and evaluate the effectiveness of different control strategies to manage infection spread.

We considered the 12 provinces of the Lombardy region, Italy, for the simulations from which to obtain data. Individuals move across provinces and access places of interest, represented as additional membranes nested in provinces. Given that the model offers margins of scalability and adaptability, the scenario can be changed to various wider and different areas.

### 3.1 Membrane Structure

The membrane structure delineates the layout of the considered simulation scenario. The model considers membranes as places into which human individuals can move to or from. Taking advantage of this aspect, it is possible to introduce a tree-like membrane structure, starting from the outermost element denoted by Eco-Membrane, represented by the skin membrane. The Eco-Membrane contains all the different Province-Membranes included in the scenario. Unlike the more specialized inner membranes, this one only serves as a general delimiter, and it does not play a crucial role in the model.

Province-Membranes, distinguished according to their labels, contain more specific Place-Membranes. This general framework allows modeling places where individuals move for various activities during daily life, thus allowing integrating the simulation of spatial and social aspects in disease transmission. Within each province membrane it is possible to identify different places:

- Schools;
- Work places;

- Hospitals;
- Common Areas, that is places where everyone passes through to go from one area to another.

These elements are common places visited during the individual's daily life. This organization allows the framework to be scalable and efficient in terms of tracking the influence of relevant aspects such as infections, vaccinations, new daily cases and deaths. As a simulation scenario for the data collection of this work, the provinces of the region Lombardy, in Italy, were represented, denoted by their corresponding labels:

$$H_P = \{MI, MB, BS, BG, CR, CO, LC, LO, PV, SO, MN, VA\}.$$

Place-Membranes serve as specialized membranes that represent sites where individuals stay for a specific part of their daily routine. Place-Membranes are identified by the labels in $H_L = \{SC_i, WP_j, CA_k, HP_l\}$ where the subscripts $i, j, k$ and $l$ indicate the $i$-th school, the $j$-th workplace, the $k$-th Common Area and the $l$-th Hospital respectively. The labeling system allows for scalability and improves tracking of information at a deeper level in relation to Province-Membranes. In general, Place-Membranes allow human interaction to trigger infection processes.

### 3.2 Objects

With the term "Object" we refer to elements involved in the P System. Different elements and characteristics within the simulation environment may function as supporting elements, such as time indicators or serve to distinguish different types of individuals.

Symbols and notations are introduced, since they are useful to add characteristics related to different aspects of an epidemiological context, such as infection or vaccination. The main objects involved are:

- Hour object: $Hour_i$ with $0 \leq i \leq 23$, it denotes the time of day and regulates the behavior of individuals.
- Infection Number Object $\phi$ where $1 \leq \phi \leq n$ where $n$ is the number of people in the considered place. It is a local object present in every place that indicates the number of infected people in the considered Place-Membrane. It is used to calculate the probability of contagion.
- Day object: $d_i$ with $1 \leq i \leq 7$ and indicates the day of the week.
- Young object: $g$, represents an individual between the ages of 6 and 19. His trips are mainly to go to school and the common areas.
- Adult object: $a$, represents an adult aged aged between 20 and 59. It mainly travels to workplaces and to the common areas.
- Elderly object: $an.$ indicates an elderly person aged 60 or older. Generally they only move towards the common area.

Each "individual" object reports information in the form of a subscript indicating the province of origin, the province of destination of its movements and a number that sequentially identifies it. The young individual $g_i$ moving from $MB$ to $MI$ is represented as $g_{i,MB,MI}$.

Additional alphabet symbols are used to represent information relating to infection, vaccination status and the use of masks by individuals:

- Incubating infection: addition of the suffix $Iinc$, indicating that an individual, upon contracting an infection, has an initial incubation time for the virus. If it does not have this suffix, then it is healthy. Example of an early infected young person $g_i$ with this suffix: $g_i Iinc$.
- Infection: addition of the suffix $I$. When an individual fully developed an infection (after the incubating period), then we add the suffix $I$.
- Vaccination: the suffix $V$ is added; young uninfected and vaccinated individuals are represented as $g_i V$.

In line with the modeling methodology used in the PDP model [14], individuals within the epidemiological scenario are represented as objects. This approach allows for the characterization of individual attributes and roles.

### 3.3 Information-based Human Behavior

Much of recent research on modelling the coupled dynamics of vaccinating behavior and disease dynamics has been conducted by investigators from natural sciences, including physics, applied mathematics and epidemiology [18]. In this model, human behavior plays an important role in infection rewriting rules, by quantifying information to simulate human reactions to stimuli, such as rising infection cases. In general, as the number of infectious cases increases, human behavior becomes more cautious to avoid infection. This interaction can be modelled as a non-negative decreasing function, where the number of infections serves as variable. Consider $M$ as the information about infection cases and $N$ as the total population:

$$\psi(M) = \frac{1}{1 + a\frac{M}{N}} \tag{1}$$

where $a > 0$. Suppose $f = \frac{M}{N}$ and $a = \frac{1}{f^*}$ where $\frac{1}{f^*}$ is the fraction that halves the risk of contagion and $f^*$ is very small:

$$\psi(f) = \frac{1}{1 + \frac{f}{f^*}} \tag{2}$$

is the equivalent form.

### 3.4 Vaccination Dynamics

Vaccination can significantly reduce the spread of infection and a higher percentage of vaccinated individuals results in a lower infection risk. The simulation will

consider different percentages of vaccinated population: 20%, 40%, 60% and 80% coverage producing varied results. Considering $M$ as the number of infected individuals in a scenario and $N$ the total population, $f = \frac{M}{N}$ is the ratio between the two parameters. Since $\frac{1}{f^*}$ is the fraction that halves the contagion risk, let's introduce $x = \frac{f}{f^*}$ where $f^*$ is a very low value. To model the willingness to get vaccinated, an increasing function can be used:

$$\omega(x) = 1 + A\frac{x^n}{1 + x^n} \tag{3}$$

where:

- Consider $f = \frac{M}{N}$ as the ratio of infected individuals to the total population;
- $x = \frac{f}{f^*}$ where $f^*$ is a very low value (e.g., 0.01). The $x$ parameter is normalized, making it suitable for modeling;
- $A$ is the amplitude parameter of the modulation.

For a young individual, the vaccination process can be described as:

$$g_j \xrightarrow{P(v)\ \omega(x)} g_j V \tag{4}$$

with $P(0) \leq P(v) \leq P(MAX)$ representing the probability interval to get vaccinated.

By considering data and information on Vaccine Initial Effectiveness gathered from various sources, such as the studies on the SARS-CoV-2 Delta VOC in Scotland [15], the effectiveness of the ChAdOx1 vaccine in the elderly during SARS-CoV-2 Gamma variant transmission in Brazil [16], and the influence of age on the effectiveness and duration of protection in Vaxzevria and CoronaVac vaccines [17], it is possible to model the reduction in infection. Official data states that a complete 2-dose cycle of Oxford-AstraZeneca COVID-19 vaccine has an expected effectiveness value of 81%, varying in a range between 72-87%.

The vaccine effectiveness can be assigned to each vaccinated individual through a probability density function, where the expected value is $E[x] = 81\%$. Assuming a uniform distribution within the given range, the following formula is used for a continuous uniform distribution:

$$f(x) = \frac{1}{b - a}$$

where:

- $f(x)$ is the probability density function,
- $a$ is the lower bound of the range (in this case set to 72),
- $b$ is the upper bound of the range (in this case set to 87).

Thus, the probability density function for the effectiveness of the vaccine is:

$$f(x) = \frac{1}{87 - 72}$$

An effectiveness value can be assigned by calculating the cumulative probability picking a random number:

$$V(g_j) = rand * (b - a) + a$$

A vaccine duration is also assigned to each individual. Vaccine effectiveness and duration are proportional and strictly related: after having calculated a vaccine effectiveness within the specified range, a correlated duration is generated, representing the period for which the vaccine's protective effect is sustained.

### 3.5 Infection Rules

The infection rates presented in the LOIMOS work [12] classify individuals based on groups that take into account age, health status and possible symptoms resulting from the infection. The rates of transmission in various settings and through various agents of transmission in the population are based on estimates drawn from scientific evidence such as [19,20,21,22,23,24,25,26] and public data.

**Table 1.** Base infection rates for each combination of age group and membrane type and are taken from the LOIMOS work [12]

| | **School** | **Common Area** | **Hospital** | **Workplace** |
|---|---|---|---|---|
| **Young** | 0.03 | 0.02 | 0.05 | – |
| **Adult** | – | 0.02 | 0.05 | 0.02 |
| **Elderly** | – | 0.2 | 0.5 | – |

Therefore, in this work, the general idea behind the rules is to describe a dynamic process of infection among individuals in specific places. The probability of infection, based on the number of infected individuals present in a specific place, vaccination status of the involved individuals and caution factor, determines whether or not to place an individual into an incubation state. The rules are thus applied within the same environment and objects are marked with their health status. The infection rules for different types of PlaceMembranes involving young individuals, both vaccinated and non vaccinated, can be summarized and generalized as follows:

$$g_j \; g_k I \; Hour_i \; d_l \; \phi \xrightarrow{\text{Infection Probability}} g_j Iinc \; g_k I \; Hour_i \; d_l \; \phi \tag{5}$$

- Infection Probability:
  - Modeled as Base Infection Rate $\cdot \frac{\phi}{\text{total\_individuals}} \cdot \psi(M)$
- Components:
  - Base Infection Rate: Specific to the type of membrane (e.g., Hospital or School).
  - $\phi$: Current infection count in the location.
  - $Hour_i$ and $d_l$: respectively $i$-th hour of the day and $l$-th day of the week.

- total_individuals: Total number of individuals in the same membrane.
- $\psi(M)$: Decreasing function that models awareness of contagiousness.
- $g_j$: Healthy young individual, identified by the subscript $j$.
- $g_k I$: Infected young individual, identified by the subscript $k$.
- $g_j Iinc$: Young individual incubating the virus.

## 4 Evolution of Infection

In this section, the dynamics related to the evolution of an infection are described. Once an healthy individual gets in contact with an infected one, the first individual can get also get infected: it can enters an incubation state with a certain probability. The article [28] provides additional evidence for a median incubation period for COVID-19 of approximately 5 days, similar to SARS.

In another work by Holshue et al. [27] it is reported that "The initial respiratory specimens (nasopharyngeal and oropharyngeal swabs) obtained from this patient on day 4 of his illness were positive for 2019-nCoV. [...] The oropharyngeal specimen tested negative for 2019-nCoV on illness day 12" , suggesting that the infection lasts for approximately 7 days. Based on these data, in future simulations on this model, parameters will be set for the duration of the virus incubation phases and the infectivity of the individual, where this can transmit the disease to susceptible individuals.

| **Definition parameter** | **Value** | **References** |
|---|---|---|
| Average duration of the virus incubation (days). | 5 | [Lauer et al. 2020, Heet al. 2020, Holshue et al. 2020] [28] |
| Average duration of virus infection (days). | 7 | [Holshue et al. 2020, Chen et al. 2020; Hellewell et al. 2020, Anderson et al. 2020, Bi et al. 2020] [27] |

### 4.1 Virus Incubation Rules

When a healthy individual gets in contact with an infected one, the virus can be transmitted from the latter to the former with a certain probability. If this happens, then the virus is in an incubation state that lasts for 5 days. The first day is represented by the object $Iinc$ without any subscripts.

In the following rule, a young individual has just got infected; when the day object advances to the next, the subscript 4 indicates that the first day of incubation passed.

$$g_j Iinc\ d_{i+1} \rightarrow g_j Iinc_4\ d_{i+1} \tag{6}$$

– $g_j Iinc$: young individual incubating the virus;
– $g_j Iinc_4$: young individual on the second day of incubation;
– $d_{i+1}$: day object progression.

The second rule explains how the advancement of the day object decrements the $Iinc_x$ counter, reducing it one by one. The counter is decremented by one as a single day passes.

$$g_j Iinc_x \; d_{i+1} \rightarrow g_j Iinc_{x-1} \; d_{i+1} \text{ with } 2 \leq x \leq 4 \tag{7}$$

The last one describes the end of the incubation process. When the incubation process ends, the counter on object $Iinc_1$ reaches the value 1. Then, the one-day advance causes the individual to move from the incubation phase to an infected state, in which the virus is transmissible.

$$g_j Iinc_1 \; d_{i+1} \rightarrow g_j I \; d_{i+1} \tag{8}$$

- $g_j Iinc_1$: young individual incubating the virus on the last day, which is day 1;
- $g_j I$: young infected individual;
- $d_{i+1}$: day object progression.

### 4.2 Transition to Recovery

After the incubation period, the infection evolves through different stages, culminating in recovery and the acquisition of natural immunity. The following rules outline the progression of infection and the transition to a recovered state. For COVID-19, the infected state lasts for 7 days circa [27]. This transition is modeled as follows:

$$g_j I \; d_{i+1} \rightarrow g_j I_6 \; d_{i+1} \tag{9}$$

where:

- $g_j I_x$: young infected individual;
- $g_j I_6$: young infected individual on the second day of infection state;
- $d_{i+1}$: day object progression.

$$g_j I_x \; d_{i+1} \rightarrow g_j I_{x-1} \; d_{i+1} \text{ with } 2 \leq x \leq 6 \tag{10}$$

where:

- $g_j I_x$: young infected individual on day $x$;
- $g_j I_{x-1}$: young individual on the next day $(x-1)$ of infected state;
- $d_{i+1}$: day object progression.

This rule captures the transition from being infected to recovering after a specified duration. Once the infection object reaches day 1, the following day the individual is considered recovered with acquired natural immunity:

$$g_j I_1 \; d_{i+1} \rightarrow g_j Imm \; d_{i+1} \tag{11}$$

where:

- $g_j I_1$: young infected individual on the last infection state day;
- $g_j Imm$: young recovered individual with natural acquired immunity;
- $d_{i+1}$: day object progression.

Finally, once an individual is considered recovered, natural acquired immunity is granted.

### 4.3 Hospitalization

Some infected individuals may develop critical conditions, requiring treatment and therefore hospitalization. This process is designed to reflect real-world scenarios where individuals infected with a disease may require medical attention and specialized care; to achieve this, the hospitalization process is simplified by reducing hospitalization to a probabilistic process based only on two constant rates of hospitalization and death.

Considering a generic elderly individual, the hospitalization process can be defined as follows:

$$an_i I \xrightarrow{0.003} an_i IH(in_{HP_j}) \tag{12}$$

where:

- $an_i I$: elderly infected individual;
- $an_i IH$: hospitalized elderly individual;
- The $(in_{HP_j})$ element indicates that the individual is transferred to an hospital membrane.

During hospitalization, a death threshold decides whether the individual in question is excluded from the active part of the population:

$$an_i IH \xrightarrow{0.0005} an_i D \tag{13}$$

where:

- $an_I H$: hospitalized elderly individual;
- $an_i D$: the individual is considered as deceased. The object no longer participates in daily activities and is "removed" from the model.

We stress the fact that objects representing deceased individuals are not actually removed, since they will be useful for data collection. Such individuals are only excluded from the context, as they are no longer able to start infection processes or to access PlaceMembranes.

### 4.4 Movement Rules

The movements of individuals belonging to a specific province can be generally described as follows:

$$g_{X,Y}\ Hour_i\ day_j \xrightarrow{\text{movement\_probability}} (g_{X,Y}\ Hour_i\ day_j, in_Y) \tag{14}$$

where $Y \in H_P \backslash \{X\}$ and $X \neq Y$. The elements in the rewriting rules can be interpreted as follows:

1. $g_{X,Y}$: a generic young individual traveling from province $X$ to province $Y$;
2. $Hour_i$ $day_j$: time and day of the simulation;
3. movement_probability: it is defined as $(1 - \frac{\phi_Y}{\text{total\_population}_Y})$. This means that the willing to move towards an arrival point is defined by the epidemiological context of the destination province.

In simpler terms, a person who is characterized by a destination province different from the origin one will move to a different Province-Membrane according to this rule. The transition is determined by the epidemic situation of the destination province, described as a probability.

## 5 Routines of Individuals

In this section, the behavioral patterns and daily routines of individuals, are described, including the schedules that outline the stages of the day. LOIMOS [12] introduced daily routines that can be reused and implemented. The activities keep people busy from morning to night, including different locations and different scenarios involving various infection contexts.

### 5.1 Schedules for Young Individuals

Children 0–12 years old Monday to Friday:

- 08:00 to 09:00 common area.
- 09:00 to 17:00 school for children.
- 5.00pm to 6.00pm (20%), to 7.00pm (48%), to 8.00pm (32%) common area. Children may be delayed on their way home for 1, 2 or 3 h.
- 18:00,19:00 or 20:00 to 08:00 home.

Children 13–19 years old Monday to Friday (similar to that for children 0-12, but considering High schools, possibly placed in location far from their home):

- 08:00 to 09:00 common area.
- 09:00 to 17:00 High school.
- 5.00pm to 6.00pm (20%), to 7.00pm (48%), to 8.00pm (32%) common area. Teenagers may be delayed on theirs way home for 1, 2 or 3 h.
- 18:00,19:00,20:00 to 08:00 home.

Therefore, once the necessary journeys have been made, the individuals can start their own routine. Let's say a young individual has to go to school; the common area must be crossed. Said so, the considered person will stay from 8:00 to 9:00 in the common area.

### 5.2 Schedules for Workers

Workers from Monday to Friday follow a routine that is very similar to the young individuals' schedule:

- 07:00 to 08:00 in common area.
- 08:00 to 17:00 at work.
- 17:00 to 19:00 in common area.
- 19:00 to 07:00 at home.

The rules for this category have very similar patterns to the ones involved for young individuals. Once the necessary movements have been made towards the destination Province-Membrane, the workers enter their respective workplace through the common area.

### 5.3 Schedules for Elderly

The elderly goes out to do some tasks in the common area. Every day for 6 specific hours a day there is a 10% probability of going out to perform a task. This outing can be for 1h with a 40% probability, for 2h with a 24% probability and for 3h with a 36% probability [12].

## 6 Discussion

Once the simulation scenario is set, it is possible to draw conclusions from the results obtained from the simulations. The implemented scenario represents the Lombardy region structure, where we initially set a population of 25,000 individuals (the size will be improved in future simulations in order to improve the simulation performance), where cases of infection are introduced. Besides a general diffusion of infections, with the simulations of our model we aimed at studying two specific related aspects: the impact of control measures and the population behavioral dynamics.

The implementation of control measures aimed at mitigating the virus transmission is one of the most studied aspects in epidemiology. Vaccination campaigns are one among the most popular interventions applied in social context to contain the spread of infection. Understanding the effectiveness of such intervention is crucial to define the goodness of the model.

As depicted in Fig. 1, which compares simulations over 365 days with different levels of vaccination coverage, notable differences are presented in the outcomes. From left to right, representing no vaccination, 20%, 40%, 60%, and 80% vaccination coverage, there is a clear trend of decreasing peak values for each case under analysis. Vaccination coverage leads to a reduction in prevalence of the virus, number of new daily cases and number of deaths.

The second aspect, the behavioral dynamics, represents a fundamental point in the proposed case study. In general, dynamic behavior logic integrates with the infection process, in order to create realistic and complex scenarios, as well as

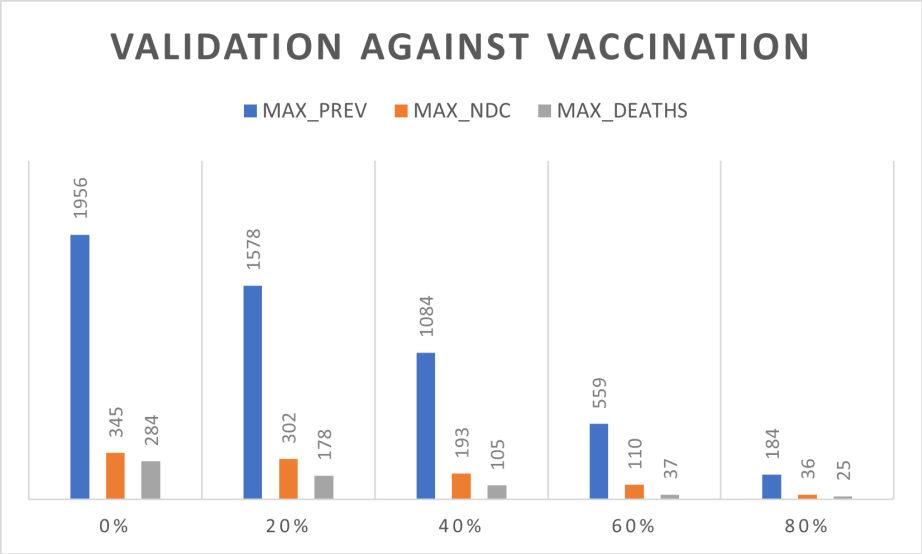


**Fig. 1.** Comparison between simulations of 365 days with medium levels of behavior in response to contagion, subjected to different vaccination coverage. From left to right: no vaccination, 20%, 40%, 60%, and 80%. The values in the columns indicate the peak value of each case under analysis.

converting a trivial probabilistic infection process based on a basic infection rate into a realistic stochastic process composed of multiple parameters. The equation 2 explains that when $f$ and $f^*$ match, the value returned by the function is $\frac{1}{2}$; therefore the value of $f^*$ indicates the fraction of infected individuals such that individuals will adopt a behavior that will halve the probability of infection. At this point it is easier to detail how the behavior is modeled: if $f^* = 0.1$ then the probability of infection will be halved when a tenth of the considered population is infected. For $f > 0.1$ the probability of infection will be further reduced.

To analyze the impact of behavior modeling in an epidemiological context, we consider $f^*$ as a "Caution Parameter". The following data reflects what has been explained above:

**Table 2.** Summary table of peak metrics from different simulations performed with variable Caution Parameter.

| Caution Parameter | Vaccine Coverage | Metric | Max Value | Day of Occurrence |
|---|---|---|---|---|
| 0.01 | 0 | Prevalence | 1956 | 23 |
| | | New Daily Cases | 345 | 19 |
| | | Deaths | 284 | 359 |
| 0.1 | 0 | Prevalence | 4024 | 23 |
| | | New Daily Cases | 723 | 20 |
| | | Deaths | 245 | 145 |
| 1 | 0 | Prevalence | 5089 | 24 |
| | | New Daily Cases | 962 | 21 |
| | | Deaths | 293 | 63 |
| 10 | 0 | Prevalence | 5197 | 27 |
| | | New Daily Cases | 926 | 27 |
| | | Deaths | 315 | 80 |

From the observed values it is possible to note a strong influence of the general behavior of individuals in response to the epidemic: the more the value of the caution parameter decreases, the more the peak values of the different metrics considered decrease. The only exception concerns the case of the number of deaths for the simulation with a caution parameter equal to 0.01: it reports a high number of deaths, which however reaches its peak after 359 days of simulation out of 365 and after a second wave of infections, due to a less strong prevalence of the virus compared to other cases, where the infection spreads quickly among susceptible people, infecting a considerably greater quantity. Further analysis and data about the model are available at this **web address**.

## 7 Conclusions

The paper outlined an application of membrane systems, a computational model inspired by biological processes, to the field of epidemiological research. The main objective of this research was to define an epidemiological model which integrated the behavioral dynamics of individuals in response to the epidemiological context. The modeling process starts from previous works in membrane computing, and leads to an extension which includes new aspects, linked to the behavioral dynamics of individuals. In particular, the response of the population to changes in various epidemiological scenarios are represented by the model. By defining mathematical functions that vary depending on the number of infected people, different features may be manipulated. Prevalence therefore plays a fundamental role in the mechanisms of the implemented scenarios, as it is exploited as a variable for both infection and vaccination processes.

Our model shows a certain degree of scalability: it is possible to implement scenarios that can vary in size, by adding or decreasing the number of membranes to represent provinces and places, and by modifying the number of individuals in the population. Model adaptability is ensured by the generated results, since vaccination campaigns mitigate virus transmission, by emphasizing the relationship between vaccination coverage and all i) the timing of peak values regarding prevalence, ii) the new daily cases, and iii) deaths. On the other hand, behavioral dynamics (characterizing this model) shapes the spread of infectious diseases by illustrating how individuals' behavior in response to the epidemics can either promote or reduce disease transmission. According to preliminary results obtained by simulations, our model manages to offer a correct representation of the observed trend of infections, and the impact of countermeasures and human behaviors. More specifically:

- **Validation of Outbreak Patterns**, by simulating scenarios with given conditions, showed the model's ability to replicate epidemic dynamics;
- **Validation for Vaccination** confirmed that vaccination campaigns mitigate virus transmission, highlighting the relationship between vaccination coverage and the timing of peaks values regarding prevalence, new daily cases and deaths;
- **Behavioral Dynamics** are the main aspect in this model: they are able to shape the spread of infectious diseases. The model highlighted how the behavior of individuals in response to the epidemic can either favor or reduce the spread of the disease.

In conclusion, some validation results confirm the model's ability to faithfully represent the dynamics of infectious disease transmission and intervention strategies.

Considering the achievements and the potential offered by this research, it would be of interest to explore some of the possible directions for future developments. Although effective, the current model does not provide a few characteristics that could make it even more precise. Possible improvements include:

- **Implementation of Vital Dynamics.** Vital dynamics, including birth and death rates, can increase the realism of the model by replenishing the susceptible population with newborns and taking into account mortality rates. This can support dynamics such as endemicity of the disease.
- **Incorporation of Lockdowns and Closures.** The model could be expanded to incorporate either the implementation of lockdowns or the closure of schools and workplaces once a predetermined threshold of infections is reached.
- **Addition of Tracing Activity.** Incorporating the ability to track and analyze movements and interactions of individuals within a population helps to identify and monitor individuals who have been in close contact with confirmed cases of a communicable disease, to better understand the movements of individuals, to identify potential areas of increased transmission risk.

- **Simulation of additional scenarios.** Simulating additional scenarios will be useful to determine crucial parameters, such as optimal vaccination rates and vaccination priority groups, and to refine the prediction of infection waves.
- **Further validation and sensitivity analysis.** A deeper validation with a sensitivity analysis of the model based on empirical data can highlight unnoticed model limitations and potentialities.

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