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Brenda Ivette García-Maya

brenda.gmaya@tec.mx

Tecnológico de Monterrey

Yehtli Morales-Huerta

Universidad Autónoma del Estado de Morelos

Raúl Salgado-García

Universidad Autónoma del Estado de Morelos

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Disease spread in compartmental spaces: Markov and semi-Markov population models

Brenda Ivette García-Maya^{1*}, Yehtli Morales Huerta² and Raúl Salgado-García^{3*}

^{1*}School of Engineering and Sciences, Tecnológico de Monterrey, Guadalajara Campus, Av. General Ramón Corona 2514, Zapopan, Jalisco 45201, México..

²Centro de Investigación en Ciencias, Universidad Autónoma del Estado de Morelos, Avenida Universidad 1001, Cuernavaca, 62209, Morelos, Mexico.

^{3*}Instituto de Investigación en Ciencias Básicas y Aplicadas, Universidad Autónoma del Estado de Morelos, Avenida Universidad 1001, Cuernavaca, 62209, Morelos, Mexico.

*Corresponding author(s). E-mail(s): brenda.gmaya@tec.mx; raulsg@uaem.mx;

Abstract

Mathematical models provide valuable tools for understanding infectious-disease transmission, particularly in structured environments where human mobility and spatial organization influence disease spread. In this work, we propose a stochastic framework to study disease propagation in enclosed spaces composed of interconnected compartments, considering three classes of individuals: susceptible, carriers, and infected. Two complementary formulations are developed: a closed Markov-chain model, in which the total population remains constant, and an open semi-Markov model, which allows individuals to enter and leave the system and incorporates general residence-time distributions. Mathematical expressions for the number and expected number of susceptible, carrier, and infected individuals at time t are obtained. For the open semi-Markov model, the distribution of the time to absorption is also characterized, providing a mathematical description of the time individuals remain within the system. The proposed framework integrates spatial structure, stochastic mobility, and disease transmission, offering a flexible approach for studying infectious-disease propagation in compartmental environments.

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1 Introduction

The mathematical study of infectious-disease transmission has a long history and has played a fundamental role in understanding how epidemics emerge, evolve, and can be controlled. Understanding the mechanisms governing disease transmission is essential for preventing excessive pressure on healthcare systems and, in extreme circumstances, reducing the risk of large-scale epidemics or pandemics (Ferguson et al. 2006; Wu et al. 2020; Peak et al. 2020). Mathematical models provide a systematic framework for representing transmission mechanisms and population interactions, and can be used to predict the evolution of an outbreak, evaluate intervention strategies, and ultimately mitigate the spread of infection within a population (Heesterbeek et al. 2015; Kucharski et al. 2020; Ferguson et al. 2006; Dimitrov et al. 2014).

The rate at which an infectious disease spreads depends on several factors, including the number and behavior of infectious individuals, the frequency and duration of interpersonal contacts, ventilation conditions, the characteristics of the pathogen, and the spatial organization of the environment in which transmission occurs (Morawska and Cao 2020; Somsen et al. 2020; Fadaei 2021; Sun and Zhai 2020). In particular, the structure of an enclosed environment can strongly influence how individuals interact (Li et al. 2021). People may move between different areas, spend different amounts of time in each location, and interact with different subsets of the population. Consequently, the usefulness of a disease-spread model depends largely on its ability to incorporate the mechanisms and environmental characteristics that play a significant role in transmission (Pinter-Wollman et al. 2018).

Empirical and network-based studies further show that contact patterns are heterogeneous and strongly structured by social setting, age, and location, so homogeneous-mixing assumptions may obscure important pathways of transmission (Eubank et al. 2004). Dynamic contact networks also demonstrate that changes in who interacts with whom over time can alter epidemic dynamics in ways that static or mass-action descriptions do not fully capture (Volz and Meyers 2007).

This issue is particularly relevant in enclosed spaces composed of several interconnected sections, such as hospitals, schools, universities, offices, transportation facilities, and other buildings in which individuals move between different areas. In these environments, disease propagation depends not only on the epidemiological characteristics of individuals but also on the structure of the space and their movement through it (Pinter-Wollman et al. 2018). Markov chains provide a natural mathematical framework for representing this mobility (Salgado-García 2021). A Markov chain describes a sequence of transitions between states in which the probability of the next state depends only on the current state and not on the previous history of the process. When states are interpreted as physical compartments, transition probabilities describe how individuals move between different locations (Kim and Song 2012).

This location-based perspective is consistent with epidemic models in which movements between specific places generate the contact structure through which infection can propagate (Eubank et al. 2004). It is also supported by classical indoor-outbreak analyses showing that spatial organization and shared-air pathways can connect individuals who do not necessarily share the same immediate room (Riley et al. 1978).

However, in many applications it is also necessary to account for individuals entering and leaving the environment. An open Markov chain extends the classical Markov-chain framework by allowing arrivals from outside the system as well as departures from it (Salgado-García 2021). This is particularly relevant for environments in which individuals enter a building, move through several sections, and eventually leave it. A further extension is provided by semi-Markov processes, which allow the time spent in each compartment to follow general and potentially state-dependent probability distributions (Barbu and Limnios 2009). This flexibility is important for human mobility because the amount of time spent in a particular location may depend strongly on the characteristics and purpose of that location.

From an epidemiological perspective, explicitly retaining temporal information is also important because infection risk depends on the intensity and duration of exposure, while respiratory-droplet dynamics provide an additional mechanism linking time spent in a shared environment to transmission opportunity (Stilianakis and Drossinos 2010).

In this work, we study the propagation of an infectious disease within an enclosed environment composed of several interconnected sections or compartments. Individuals move through these compartments according to stochastic mobility rules described by Markov and semi-Markov processes. The objective is to combine the spatial organization of the environment, the movement of individuals, and the infection mechanism within a unified mathematical framework.

The proposed model distinguishes three classes of individuals: susceptible individuals, carriers, and infected individuals. We can observe that there are some scientific articles that model individuals using these three classes; see, e.g., (Bisi and Lorenzani 2024; Seto et al. 2007; Buonomo and Della Marca 2024). Susceptible individuals are initially healthy but may acquire the infection through contact with a carrier. Carriers harbor the infectious agent and are capable of transmitting it to susceptible individuals. Infected individuals are those who enter the system as susceptible individuals and subsequently acquire the disease through contact with a carrier. In the present formulation, individuals belonging to the infected class do not transmit the disease to susceptible individuals. Thus, the model explicitly distinguishes between individuals who carry and transmit the infectious agent and those who acquire the infection within the system but are assumed to be non-transmitting.

The interaction among these three classes is dynamic and coupled to the movement of individuals through the compartmental environment. A susceptible individual may remain susceptible while moving between compartments or may become infected after encountering a carrier. Carriers also move through the system and therefore modify the spatial distribution of transmission risk over time. Consequently, infection propagation is intrinsically connected to the mobility process.

To investigate these dynamics, we consider two related mathematical formulations. The first corresponds to a closed system, in which the total number of individuals is conserved and no arrivals or departures occur. The environment is represented by a finite collection of interconnected compartments, and individuals move between them according to a Markov chain whose transition probabilities are specified a priori. The transition matrix therefore represents both the connectivity of the environment and the probabilities associated with movement between its different sections. Within this framework, we investigate how susceptible, carrier, and infected individuals are distributed among the compartments and how infection propagates as a consequence of their interactions. This formulation complements the analysis presented in Ref. (García-Maya et al. 2025).

Although a closed model is appropriate for situations in which the population remains approximately constant, many realistic environments require the incorporation of arrivals and departures. For this reason, the second formulation considers an open system in which individuals may enter the environment, move through its compartments, and eventually leave the system. The exterior of the system can be represented by a collection of absorbing states. Once an individual reaches one of these states, the individual is assumed not to return to the system during the period under consideration.

The open-system formulation is additionally developed using semi-Markov dynamics. Unlike the Markovian case, this framework allows residence times within compartments to follow general probability distributions (Limnios and Oprisan 2012). Such flexibility is particularly relevant when compartments represent locations with different patterns of human activity. For example, individuals may spend only short periods in corridors or transition areas while remaining considerably longer in offices, classrooms, or waiting rooms. Since the duration of exposure can influence opportunities for disease transmission (Bichara et al. 2015), explicitly representing residence times provides a more flexible description of the underlying mobility process.

The combination of an open population structure and semi-Markov mobility therefore extends the closed Markovian model in two important directions. First, the population inside the system can vary over time as individuals enter and leave the environment. Second, the model incorporates heterogeneous temporal patterns through general residence-time distributions. These characteristics make the framework suitable for representing a broad range of structured environments in which both population turnover and residence times are relevant to disease propagation.

Within both formulations, particular attention is given to obtaining mathematical expressions describing the evolution of the three epidemiological classes. Specifically, we derive expressions for the number of susceptible, carrier, and infected individuals at time t , together with their corresponding expected values. These quantities provide information about both the overall evolution of the infection and its spatial distribution throughout the compartmental system.

For the open semi-Markov formulation, we additionally study the time required for an individual to leave the system. Since the exterior is represented by absorbing states, this quantity corresponds to the time to absorption. We derive its distribution function, thereby characterizing the probability that an individual remains within, or

has departed from, the system by a given time. This quantity is particularly relevant because the amount of time spent within the environment determines the period during which interactions with other individuals and potential exposure to infection may occur (Smieszek 2009; Gao et al. 2016).

The relevance of this quantity is further supported by mechanistic respiratory transmission models and indoor outbreak studies, in which exposure duration and shared-air conditions directly affect transmission opportunity (Kretzschmar and Mikolajczyk 2009).

The proposed approach therefore provides a stochastic framework in which spatial structure, population dynamics, residence times, and disease transmission can be studied simultaneously. By obtaining mathematical expressions and expected values for susceptible, carrier, and infected individuals, the model can help identify compartments and mobility patterns associated with greater transmission risk. Consequently, the proposed framework can serve as a useful mathematical tool for policymakers and public-health experts interested in understanding and managing the spread of infectious diseases in enclosed and structurally complex environments.

The article is structured as follows. Section 2 introduces the disease-spread model and presents the mathematical framework for population Markov chains. Section 3 develops the disease-spread model for closed population Markov chains, describing both the diffusive and infective stages and deriving the corresponding evolution equations. Section 4 extends the framework to open semi-Markov chains, introducing the semi-Markov formulation, the open population dynamics, and the corresponding disease-spread model. Finally, the main conclusions and implications of the proposed framework are discussed.

2 Models

2.1 Disease spread model

The model considered here describes a population of individuals moving within a spatially structured environment, denoted by $\mathcal{S}$. The environment is composed of a finite collection of interconnected compartments, which represent the different locations that individuals may occupy. We denote by $s := |\mathcal{S}|$ the total number of compartments and, for convenience, label them by $i = 1, \dots, s$.

At any given time, individuals within $\mathcal{S}$ belong to one of three epidemiological classes: susceptible individuals, carriers, and infected individuals. Susceptible individuals are healthy but may acquire the disease through contact with a carrier. Carriers harbor the infectious agent and are able to transmit it to susceptible individuals. Finally, infected individuals are those who entered the system as susceptible and subsequently acquired the infection through contact with a carrier. In the present model, however, newly infected individuals are assumed not to transmit the disease during the time they remain within $\mathcal{S}$. The precise definitions of these three populations are given below.

- **Susceptible individuals.** These are healthy individuals who may become infected through contact with a carrier. The number of susceptible individuals occupying compartment i at discrete time t is denoted by H_i^t . Accordingly,

$$\mathbf{H}^t = (H_1^t, H_2^t, \dots, H_s^t) \quad (1)$$

describes the spatial distribution of susceptible individuals throughout $\mathcal{S}$ at time t .

- **Carriers.** These are individuals carrying the infectious agent who are able to transmit the disease to susceptible individuals. The number of carriers in compartment i at time t is denoted by C_i^t , and

$$\mathbf{C}^t = (C_1^t, C_2^t, \dots, C_s^t) \quad (2)$$

describes their distribution over the state space.

- **Infected individuals.** These are individuals who entered the state space as susceptible and subsequently became infected through contact with one or more carriers. We assume that, during the time scale relevant to the model, these individuals do not transmit the infection to susceptible individuals. Their number in compartment i at time t is denoted by I_i^t , while

$$\mathbf{I}^t = (I_1^t, I_2^t, \dots, I_s^t) \quad (3)$$

describes the distribution of infected individuals over $\mathcal{S}$.

The evolution of the system is formulated as a discrete-time stochastic process. Each time step consists of two consecutive stages: a *diffusive stage*, describing the movement of individuals through the compartmental structure, and an *infective stage*, during which disease transmission may occur.

During the diffusive stage, individuals move among the compartments of $\mathcal{S}$ according to prescribed stochastic transition rules. The redistribution of the population is therefore determined by the connectivity of the compartmental space together with the probabilities governing transitions between compartments. In the present work, we consider two different mobility frameworks. In the first, individuals move according to a standard Markov chain and the total population is conserved; we refer to this case as the *closed population Markov chain*. In the second, individuals are allowed to enter and leave the system, while their motion among compartments follows semi-Markov dynamics, so that the residence time within a compartment need not be geometrically distributed. We refer to this formulation as the *open semi-Markov chain*. These two cases are considered because they complement the open Markov-chain model of disease transmission previously studied in Ref. [García-Maya et al. \(2025\)](#). Taken together, the three formulations allow us to distinguish the effects of population conservation, population exchange with the environment, and non-Markovian residence-time dynamics on the propagation of infection through a compartmental space.

Once the movement stage has taken place, the system undergoes the infective stage. Infection can occur only through local interactions: a susceptible individual can

become infected only if it occupies the same compartment as at least one carrier during the corresponding time step. Transmission is stochastic. In particular, we assume that the probability that a susceptible individual becomes infected within one time step increases with the number of carriers present in that compartment and decreases with the total number of individuals occupying it. Consequently, compartments with a larger relative concentration of carriers exhibit a higher local probability of transmission. The precise functional form of this infection probability will be specified below.

The distinction between carriers and newly infected individuals is motivated by the time scales considered in the model. We assume that individuals remain within the state space only for a finite period, shorter than the characteristic recovery time of the disease. For this reason, recovered individuals are not explicitly included. Moreover, we assume that the time required for a newly infected individual to become infectious is longer than, or at least comparable to, the typical residence time within the system. Therefore, individuals who acquire the infection while moving through $\mathcal{S}$ remain non-transmitting during the period considered here.

Under these assumptions, the model focuses primarily on two quantities. The first is the number and spatial distribution of individuals who become infected while moving through the compartmental environment. The second is the time required for a susceptible individual to acquire the infection. As shown below, both quantities depend not only on the infection mechanism itself, but also on the topology of the compartmental space, the transition rules governing individual mobility, and, in the open-system setting, the mechanisms controlling the arrival and departure of individuals.

2.2 Closed Population Markov chain

We begin by assuming that the environment in which individuals move has a "complex" structure, i.e., is comprised of interconnected compartments whose structure is modeled as a directed graph, and the individuals can stay in the compartments, the vertex of the graph. In contrast to the model open Markov chains [García-Maya et al. \(2025\)](#), in this case there are no "gates" in the directed graph, so, the individuals remain in the state space and the number of individuals is conserved. The individuals move randomly throughout the above described directed graph according to a prescribed stochastic process within the setting of Markov chains. These models are sometimes called *closed population Markov chains* and here we give a definition.

Definition 1 (Population Markov chain) Let $\mathcal{S}$ be a finite set, whose cardinality is denoted by $s := |\mathcal{S}|$, and let $\mathbf{M} : \mathcal{S} \times \mathcal{S} \rightarrow [0, 1] \subset \mathbb{R}$ be an irreducible and aperiodic matrix with spectral radius strictly equal to one. Let $\mathbf{N}^0 = (N_1^0, N_2^0, \dots, N_s^0)$ be a s -dimensional random vector such that $N := \sum_{i=1}^s N_i$ is constant. Here, N_i^0 denotes the initial number of individuals in the i th compartment. We say that $(\mathcal{S}, \mathbf{M}, \mathbf{N}^0)$ is a population Markov chain with state space $\mathcal{S}$, transition matrix $\mathbf{M}$ and initial condition $\mathbf{N}^0$. We denote by $\mathbf{N}^t$ the stochastic vector that denotes the spatial distribution of individuals in the state space at time $t \in \mathbb{N}$. Specifically, N_i^t stands for the number of people that are present at time t in state $i \in \mathcal{S}$.

The process $(\mathbf{N}^t)_{t \in \mathbb{N}}$ evolves according to the recursion equation,

$$\mathbf{N}^{t+1} := \mathcal{R}(\mathbf{N}^t, \mathbf{M}), \quad (4)$$

where $\mathcal{R}(\mathbf{N}^t, \mathbf{M})$ is what we call *redistribution operator* defined as follows. First, let us define, for each $i \in \mathcal{S}$, the random vector $\mathbf{B}_i^t$ as,

$$\mathbf{B}_i^t \sim \text{Multinomial}(M_{i1}, M_{i2}, \dots, M_{is}, \mathbf{N}_i^t), \quad (5)$$

where M_{ij} is the (i, j) th component of the transition matrix $\mathbf{M}$. Next, if we write $\mathbf{R}^t = \mathcal{R}(\mathbf{N}^t, \mathbf{M}) = (R_1^t, R_2^t, \dots, R_s^t)$, then, the j th component of random vector $\mathbf{R}^t$ is defined as,

$$R_j^t = \sum_{i \in \mathcal{S}} B_{ij}^t, \quad (6)$$

where B_{ij}^t is the j th component of random vector $\mathbf{B}_i^t$.

It is useful to clarify the interpretation of the random variables describing the redistribution of individuals among compartments. For each state $i \in \mathcal{S}$, the random vector $\mathbf{B}_i^t$ accounts for the individuals initially located in state i at time t and specifies how they are distributed among the possible destination states at time $t + 1$. More precisely, the random variable B_{ij}^t denotes the number of individuals that move from state i to state j during the time interval from t to $t + 1$. The diagonal term B_{ii}^t therefore represents the number of individuals that remain in state i during that time step. Consequently, the total number of individuals occupying state j at time $t + 1$ is obtained by adding the contributions arriving from every possible state of origin, including state j itself. This motivates the definition of the *redistribution vector* $\mathbf{R}^t$, whose j -th component is $R_j^t = \sum_{i=1}^s B_{ij}^t$, as introduced in Eq. (6) in Definition 1. Thus, R_j^t represents the total population assigned to compartment j after the diffusive step.

Since the compartmental system considered in this section is closed, no individuals enter or leave the state space. Hence, the redistribution process preserves the total population. Individuals may remain in their current compartment or move to another compartment through an admissible transition of the underlying directed graph, but the sum of the populations over all compartments remains constant at every time step. The stochastic evolution of the population is therefore completely determined by the transition probabilities of the underlying Markov chain.

Before analyzing the transmission of disease within this closed population model, it is convenient to establish a basic result concerning its long-time behavior. In particular, we show that the stationary distribution of the population Markov chain can be expressed as a multinomial distribution whose parameters are determined by the stationary probability vector of the underlying single-individual Markov chain. In this sense, the equilibrium distribution of the entire population is inherited directly from the stationary behavior of the corresponding ordinary Markov chain.

Theorem 1 *Let $(\mathcal{S}, \mathbf{M}, \mathbf{N}^0)$ be a population Markov chain with a finite state space $\mathcal{S}$ (with $s := |\mathcal{S}| < \infty$), a transition matrix $\mathbf{M} : \mathcal{S} \times \mathcal{S} \rightarrow [0, 1]$ and initial configuration of individuals $\mathbf{N}^0$, which is assumed to be a constant random vector. Let $\mathbf{N}^t$ be the configuration of the*

number of individuals on the state space at time t , and let by $p_t(\mathbf{n})$ be the corresponding distribution

$$p_t(\mathbf{n}) := \mathbb{P}(\mathbf{N}^t = \mathbf{n}). \quad (7)$$

where $\mathbf{n} := (n_1, n_2, \dots, n_s)$ is a s -dimensional integer vector, i.e., $\mathbf{n} \in \mathbb{N}^s$. Then, the limit distribution $p_\infty(\mathbf{n}) := \lim_{t \rightarrow \infty} p_t(\mathbf{n})$ is given by

$$p_\infty(\mathbf{n}) = \frac{n!}{n_1! n_2! \dots n_s!} \mu_1^{n_1} \mu_2^{n_2} \dots \mu_s^{n_s}. \quad (8)$$

Here, $\boldsymbol{\mu} := (\mu_1, \mu_2, \dots, \mu_s)$ is the left invariant eigenvector of the transition matrix $\mathbf{M}$ associated to the largest eigenvalue $\lambda = 1$. In other words, $\boldsymbol{\mu} = \boldsymbol{\mu} \mathbf{M}$.

Proof: First, we should recall that $p_t(\mathbf{n})$ satisfy the relation

$$p_{t+1}(\mathbf{n}) = \sum_{\mathbf{m} \in \mathbb{N}^s} p_t(\mathbf{m}) K(\mathbf{m}, \mathbf{n}) \quad (9)$$

where the evolution kernel $K(\mathbf{m}, \mathbf{n})$ is given by

$$K(\mathbf{m}, \mathbf{n}) := \mathbb{P}(\mathbf{N}^{t+1} = \mathbf{n} \mid \mathbf{N}^t = \mathbf{m}). \quad (10)$$

As in Ref. [Salgado-García \(2021\)](#), we will derive an evolution equation for the moment generating function of $\mathbf{N}^t$, which we denote by $\mathcal{G}_t(\boldsymbol{\alpha})$,

$$\mathcal{G}_t(\boldsymbol{\alpha}) := \mathbb{E} \left[e^{\mathbf{N}^t \boldsymbol{\alpha}^T} \right] = \sum_{\mathbf{n} \in \mathbb{N}^s} p_t(\mathbf{n}) \exp(\mathbf{n} \boldsymbol{\alpha}^T). \quad (11)$$

It is not hard to see that $\mathcal{G}_{t+1}(\boldsymbol{\alpha})$ can be written as,

$$\mathcal{G}_{t+1}(\boldsymbol{\alpha}) = \sum_{\mathbf{n} \in \mathbb{N}^s} \sum_{\mathbf{m} \in \mathbb{N}^s} p_t(\mathbf{m}) K(\mathbf{m}, \mathbf{n}) \exp(\mathbf{n} \boldsymbol{\alpha}^T), \quad (12)$$

which follows from the evolution rule (9). Recalling the definition of $K(\mathbf{m}, \mathbf{n})$, we can see that

$$K(\mathbf{m}, \mathbf{n}) = \mathbb{P}(\mathbf{N}^{t+1} = \mathbf{n} \mid \mathbf{N}^t = \mathbf{m}) = \mathbb{P}(\mathcal{R}(\mathbf{N}^t, \mathbf{M}) = \mathbf{n} \mid \mathbf{N}^t = \mathbf{m}), \quad (13)$$

which simply states that $K(\mathbf{m}, \mathbf{n}) = \mathbb{P}(\mathcal{R}(\mathbf{m}, \mathbf{M}) = \mathbf{n})$. This result allows us to write,

$$\mathcal{G}_{t+1}(\boldsymbol{\alpha}) = \sum_{\mathbf{n} \in \mathbb{N}^s} \sum_{\mathbf{m} \in \mathbb{N}^s} p_t(\mathbf{m}) \mathbb{P}(\mathcal{R}(\mathbf{m}, \mathbf{M}) = \mathbf{n}) \exp(\mathbf{n} \boldsymbol{\alpha}^T). \quad (14)$$

Now, let us define the function $\mathcal{H}(\boldsymbol{\alpha})$,

$$\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) = \sum_{\mathbf{r} \in \mathbb{N}^s} \mathbb{P}(\mathcal{R}(\mathbf{m}, \mathbf{M}) = \mathbf{r}) \exp(\mathbf{r} \boldsymbol{\alpha}^T) \quad (15)$$

which corresponds to the moment generating function corresponding to the redistribution vector $\mathcal{R}(\mathbf{m}, \mathbf{M})$. Thus we have that

$$\mathcal{G}_{t+1}(\boldsymbol{\alpha}) = \sum_{\mathbf{m} \in \mathbb{N}^s} p_t(\mathbf{m}) \mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}). \quad (16)$$

In Appendix A we show that the function $\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m})$ can be written as

$$\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) = \exp(\mathbf{m} \mathbf{H}^T(\boldsymbol{\alpha})) \quad (17)$$

where $\mathbf{H} : \mathbb{R}^s \rightarrow \mathbb{R}^s$ is a s -dimensional vector function, depending only on $\mathbf{M}$ and $\boldsymbol{\alpha}$, defined as,

$$(\mathbf{H}(\boldsymbol{\alpha}))_i := \log \left(\sum_{j=1}^s M_{i,j} e^{\alpha_j} \right). \quad (18)$$

This result allows us to see that,

$$\mathcal{G}_{t+1}(\boldsymbol{\alpha}) = \sum_{\mathbf{m} \in \mathbb{N}^s} p_t(\mathbf{m}) \exp(\mathbf{m} \mathbf{H}^T(\boldsymbol{\alpha})), \quad (19)$$

which implies that the generating function $\mathcal{G}_{t+1}(\boldsymbol{\alpha})$ satisfies the recurrence relation,

$$\mathcal{G}_{t+1}(\boldsymbol{\alpha}) = \mathcal{G}_t(\mathbf{H}(\boldsymbol{\alpha})). \quad (20)$$

This recursion equation can be straightforwardly solved, to obtain,

$$\mathcal{G}_t(\boldsymbol{\alpha}) = \mathcal{G}_0(\mathbf{H}^{(t)}(\boldsymbol{\alpha})), \quad (21)$$

where $\mathbf{H}^{(t)}(\boldsymbol{\alpha})$ denotes the t -th iteration of $\mathbf{H}(\boldsymbol{\alpha})$. In Appendix A we also prove that the i th component of $\mathbf{H}^{(t)}$, denoted by $H_i^{(t)}$, can be written as,

$$H_i^{(t)}(\boldsymbol{\alpha}) = \log \left(\sum_{j=0}^s M_{i,j}^t e^{\alpha_j} \right) \quad (22)$$

where M_{ij}^t denotes the (i, j) th component of the t th power of the transition matrix $\mathbf{M}$.

Since we assumed that $\mathbf{N}^0$ is a constant random vector, the moment generating function $\mathcal{G}_0(\boldsymbol{\alpha})$ is given by,

$$\mathcal{G}_0(\boldsymbol{\alpha}) = \exp(\mathbf{N}^0 \boldsymbol{\alpha}^T) = \exp \left(\sum_{i=1}^s N_i^0 \alpha_i \right), \quad (23)$$

or, equivalently,

$$\mathcal{G}_0(\boldsymbol{\alpha}) = \prod_{i=1}^s \exp(N_i^0 \alpha_i). \quad (24)$$

Thus, the moment generating function $\mathcal{G}_t(\boldsymbol{\alpha})$ can be written as,

$$\mathcal{G}_t(\boldsymbol{\alpha}) = \mathcal{G}_0 \left(\mathbf{H}^{(t)}(\boldsymbol{\alpha}) \right) = \prod_{i=1}^s \exp \left(N_i^0 H_i^{(t)}(\boldsymbol{\alpha}) \right). \quad (25)$$

Now, substituting $H_i^{(t)}(\boldsymbol{\alpha})$, given in Eq. (22), into the above expression, we obtain,

$$\begin{aligned} \mathcal{G}_t(\boldsymbol{\alpha}) &= \prod_{i=1}^s \exp \left(N_i^0 \log \left(\sum_{j=0}^s M_{ij}^t e^{\alpha_j} \right) \right) \\ &= \prod_{i=1}^s \left(\sum_{j=0}^s M_{ij}^t e^{\alpha_j} \right)^{N_i^0}. \end{aligned} \quad (26)$$

Using matrix multiplication notation, the last expression can be written as

$$\mathcal{G}_t(\boldsymbol{\alpha}) = \prod_{i=1}^s \left[(\mathbf{M}^t \mathbf{x}^T)_i \right]^{N_i^0}. \quad (27)$$

where the row vector $\mathbf{x}$ is defined as $\mathbf{x} = (e^{\alpha_1}, e^{\alpha_2}, \dots, e^{\alpha_s})$. Then, by the Perron-Frobenius theorem [Seneta \(1981\)](#) we have that

$$\lim_{t \rightarrow \infty} \mathbf{M}^t \mathbf{x}^T = \mathbf{f} \boldsymbol{\mu} \mathbf{x}^T \quad (28)$$

where $\boldsymbol{\mu}$ and $\mathbf{f}$ are the left and right eigenvectors of $\mathbf{M}$, associated to the largest eigenvalue $\lambda = 1$, i.e., $\mathbf{M} \mathbf{f} = \mathbf{f}$ and $\boldsymbol{\mu} \mathbf{M} = \boldsymbol{\mu}$. Thus, we can write

$$\lim_{t \rightarrow \infty} \mathcal{G}_t(\boldsymbol{\alpha}) = \lim_{t \rightarrow \infty} \prod_{i=1}^s \left[(\mathbf{M}^t \mathbf{x}^T)_i \right]^{N_i^0} = \prod_{i=1}^s \left[(\mathbf{f} \boldsymbol{\mu} \mathbf{x}^T)_i \right]^{N_i^0}. \quad (29)$$

Since $\mathbf{M}$ is a stochastic matrix, is clear that $\mathbf{f}^T = (1, 1, \dots, 1)$, this implies that,

$$\lim_{t \rightarrow \infty} \mathcal{G}_t(\boldsymbol{\alpha}) = \prod_{i=1}^s \left(\sum_{j=1}^s \mu_j e^{\alpha_j} \right)^{N_i^0} = \left(\sum_{j=1}^s \mu_j e^{\alpha_j} \right)^{\sum_{i=1}^s N_i^0}, \quad (30)$$

where we used the fact that $x_j = e^{\alpha_j}$. Now, recalling that $\sum_{i=1}^s N_i^0 = N$ is constant, we obtain,

$$\lim_{t \rightarrow \infty} \mathcal{G}_t(\boldsymbol{\alpha}) = \left(\sum_{j=1}^s \mu_j e^{\alpha_j} \right)^N. \quad (31)$$

This result states that, as t goes to infinity, the moment generating function $\mathcal{G}_t(\boldsymbol{\alpha})$ tends to

$$\left(\sum_{j=1}^s \mu_j e^{\alpha_j} \right)^N,$$

which is the moment generating function of a multinomial distribution with probabilities given by $\boldsymbol{\mu}$ and number of trials N . This concludes the proof.

3 Disease spread in population Markov chains

In this section, we introduce the model of disease transmission within a population Markov chain. As described above, our aim is to characterize the stochastic evolution, and ultimately the probability distributions, of the population vectors $\mathbf{H}^t$, $\mathbf{C}^t$ and $\mathbf{I}^t$, which represent, respectively, the spatial distributions of susceptible, carrier, and infected individuals over the state space $\mathcal{S}$.

The dynamics proceeds in discrete time through two consecutive stages: a diffusive stage, during which individuals are redistributed among the compartments, and an infective stage, during which susceptible individuals may become infected through contact with carriers. More precisely, for the stochastic processes $\{\mathbf{H}^t : t \in \mathbb{N}\}$, $\{\mathbf{C}^t : t \in \mathbb{N}\}$, and $\{\mathbf{I}^t : t \in \mathbb{N}\}$, we assume that, for each $t \in \mathbb{N}$, the diffusive stage takes place during the transition from time $2t$ to $2t + 1$, whereas the infective stage occurs during the subsequent transition from $2t + 1$ to $2t + 2$. Thus, one complete update of the epidemiological system consists of a redistribution step followed by an infection step. In what follows, we describe these two mechanisms separately, beginning with the diffusive stage.

3.1 Diffusive stage

We begin by specifying the initial conditions. At time $t = 0$, we assume that the system contains nonzero populations of susceptible individuals and carriers, while no individual has yet become infected within the compartmental space. Accordingly,

$$\mathbf{H}^0 = \mathbf{h}^0, \quad \mathbf{C}^0 = \mathbf{c}^0, \quad \mathbf{I}^0 = \mathbf{0}, \quad (32)$$

where $\mathbf{0} := (0, 0, \dots, 0) \in \mathbb{N}_0^s$, and $\mathbf{h}^0$ and $\mathbf{c}^0$ are prescribed population vectors, each containing at least one positive entry. Equivalently, the initial numbers of susceptible individuals and carriers are assumed to be strictly positive.

For later use, we define the total number of individuals belonging to each epidemiological class at time t by

$$N_H(t) := \sum_{i=1}^s H_i^t, \quad N_C(t) := \sum_{i=1}^s C_i^t, \quad N_I(t) := \sum_{i=1}^s I_i^t. \quad (33)$$

These quantities satisfy several conservation properties. First, the infective stage only transfers individuals from the susceptible class to the infected class. Therefore, although $N_H(t)$ and $N_I(t)$ may vary with time, their sum remains constant:

$N_H(t) + N_I(t) = N_H(0)$. Here we have used the initial condition $N_I(0) = 0$. Similarly, carriers neither change epidemiological class nor are created or removed from the system. Since the compartmental environment is closed, their total number is conserved,

$$N_C(t) = N_C(0) =: N_C. \quad (34)$$

Hence, it follows immediately that the total population $N := N_H(t) + N_C(t) + N_I(t)$ is independent of time. In particular, it is clear that $N = N_H(0) + N_C$. This conservation law is a direct consequence of the closed nature of the population Markov chain: the diffusive stage only redistributes individuals among the compartments, whereas the infective stage changes their epidemiological labels without creating or removing individuals from the system.

Next, as we assumed that all individuals move according to the population Markov chain model, we have that the evolution equations are given by,

$$\mathbf{H}^{2t+2} = \mathcal{R}(\mathbf{H}^{2t+1}, \mathbf{M}), \quad (35)$$

$$\mathbf{C}^{2t+2} = \mathcal{R}(\mathbf{C}^{2t+1}, \mathbf{M}), \quad (36)$$

$$\mathbf{I}^{2t+2} = \mathcal{R}(\mathbf{I}^{2t+1}, \mathbf{M}). \quad (37)$$

where $\mathcal{R}(\cdot, \mathbf{M})$ is the redistribution operator defined in Definition 1.

In order to obtain analytical approximations for mean number of individuals for each class, we introduce the notation for the first moments of susceptible, carrier and infected populations,

$$\mathbf{h}^t := \mathbb{E} [\mathbf{H}^t], \quad (38)$$

$$\mathbf{c}^t := \mathbb{E} [\mathbf{C}^t], \quad (39)$$

$$\mathbf{i}^t := \mathbb{E} [\mathbf{I}^t]. \quad (40)$$

Now, we will be interested in the dynamical laws governing the behavior of $\mathbf{h}^t$, $\mathbf{c}^t$, and $\mathbf{i}^t$. Actually, it is not hard to see that, for the diffusive stage, the evolution equations for these quantities can be written as,

$$\mathbf{h}^{2t+2} = \mathbf{h}^{2t+1} \mathbf{M}, \quad (41)$$

$$\mathbf{c}^{2t+2} = \mathbf{c}^{2t+1} \mathbf{M}, \quad (42)$$

$$\mathbf{i}^{2t+2} = \mathbf{i}^{2t+1} \mathbf{M}. \quad (43)$$

These results can be obtained directly from the recursive equation (20) for the moment generating function $\mathcal{G}_t(\boldsymbol{\alpha})$ of the distribution for the susceptible, carriers and infected populations.

3.2 Infective stage

To complement the dynamics of the disease spread model, we now state the evolution equations for the infective stage. During the infective stage, susceptible individuals may acquire the infection through contact with carriers occupying the same compartment. Consequently, this stage transfers individuals from the susceptible class to the

infected class, while the number and spatial distribution of carriers remain unchanged. The transmission mechanism is essentially the same as that introduced for the open Markov-chain model in Ref. [García-Maya et al. \(2025\)](#).

According to the time convention introduced above, the infective stage takes place between times $2t$ and $2t + 1$. Its stochastic evolution is therefore described by,

$$\mathbf{H}^{2t+1} = \mathbf{H}^{2t} - \mathcal{A}(\mathbf{H}^{2t}, \mathbf{C}^{2t}, \mathbf{I}^{2t}), \quad (44)$$

$$\mathbf{C}^{2t+1} = \mathbf{C}^{2t}, \quad (45)$$

$$\mathbf{I}^{2t+1} = \mathbf{I}^{2t} + \mathcal{A}(\mathbf{H}^{2t}, \mathbf{C}^{2t}, \mathbf{I}^{2t}). \quad (46)$$

Here, $\mathcal{A}(\mathbf{H}^{2t}, \mathbf{C}^{2t}, \mathbf{I}^{2t})$ is a random vector describing the number of new infections generated in each compartment during the corresponding infective step. More precisely, its i th component, denoted by A_i^{2t} , represents the number of susceptible individuals in compartment i who become infected between times $2t$ and $2t + 1$. Then, conditioned on the current population configuration, we assume that A_i^{2t} has binomial distribution,

$$[\mathcal{A}(\mathbf{H}^{2t}, \mathbf{C}^{2t}, \mathbf{I}^{2t})]_i \sim \text{Bin}(H_i^{2t}, p_i^{2t}), \quad (47)$$

where H_i^{2t} is the number of Bernoulli trials and p_i^{2t} is the probability that a susceptible individual becomes infected during one infective step. The latter is taken to be

$$p_i^{2t} = \gamma \frac{C_i^{2t}}{H_i^{2t} + C_i^{2t} + I_i^{2t}}. \quad (48)$$

Thus, the infection probability increases with the fraction of carriers present in the compartment. The parameter γ controls the overall efficiency of disease transmission and may incorporate effects that are not explicitly represented in the model, such as the typical distance between individuals, contact intensity, environmental conditions, or pathogen-specific transmissibility. In particular, taking $0 \leq \gamma \leq 1$ guarantees that p_i^{2t} is a well-defined probability.

An important difficulty arises when attempting to derive closed evolution equations for the first moments. Indeed, although the conditional expectation of the number of new infections is given by

$$\mathbb{E}[A_i^{2t} | \mathbf{H}^{2t} = \mathbf{h}, \mathbf{C}^{2t} = \mathbf{c}, \mathbf{I}^{2t} = \mathbf{i}] = h_i p_i^{2t}(h_i, c_i, i_i), \quad (49)$$

the probability p_i^{2t} is itself a nonlinear function of the random populations. Consequently, $\mathbb{E}[H_i^{2t} p_i^{2t}]$ cannot, in general, be expressed solely in terms of the first moments of $\mathbf{H}^{2t}$, $\mathbf{C}^{2t}$, and $\mathbf{I}^{2t}$.

To obtain a tractable approximation, we observe that the infection probability, $p_i^{2t}(h_i, c_i, i_i)$, can be expressed as a function $p_i^{2t}(c_i, n_i)$ of c_i and $n_i := h_i + c_i + i_i$, where n_i is the total number of individuals in state i at time $2t$. Consequently, $p_i^{2t}(c_i, n_i)$ remains constant throughout the infective stage. This is because, during this stage, individuals do not move between states; they merely change their epidemiological “labels” (i.e., susceptible individuals become infected). Thus, the total population in

any given state remains constant. This invariance allows us to rewrite the conditional expectation (49). Since $\mathbf{A}^{2t}$ depends exclusively on $\mathbf{H}^{2t}$, $\mathbf{C}^{2t}$, and $\mathbf{N}^{2t}$, where $\{\mathbf{N}^t : t \in \mathbb{N}\}$ denotes the process describing the total population distribution in the chain, we have that,

$$\mathbb{E}[A_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] = \mathbb{E}[H_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] \frac{\gamma c_i}{n_i} \quad (50)$$

At this point, it is important to emphasize that the processes $\{\mathbf{C}^{2t} : t \in \mathbb{N}\}$ and $\{\mathbf{N}^{2t} : t \in \mathbb{N}\}$ evolve over time solely through the diffusive step. This is because carriers do not undergo any changes during the infective stage. Furthermore, because the total population count does not distinguish between different epidemiological labels, the total number of individuals in a given state changes only according to the diffusion rules. Also, we can think of these processes as evolving independently of $\{\mathbf{H}^{2t} : t \in \mathbb{N}\}$ and $\{\mathbf{I}^{2t} : t \in \mathbb{N}\}$ during the infective stage.

Based on these observations, we can write the expected values of the evolution equations (44) and (46), conditioned on the values obtained during the diffusive stage, as follows:

$$\mathbb{E}[H_i^{2t+1} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] = \mathbb{E}[H_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] (1 - p_i(c_i, n_i)), \quad (51)$$

$$\begin{aligned} \mathbb{E}[I_i^{2t+1} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] &= \mathbb{E}[I_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] \\ &+ \mathbb{E}[H_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}] p_i(c_i, n_i), \end{aligned} \quad (52)$$

Because the processes $\{\mathbf{C}^{2t} : t \in \mathbb{N}\}$ and $\{\mathbf{N}^{2t} : t \in \mathbb{N}\}$ evolve independently of $\mathbf{H}^{2t}$ and $\mathbf{I}^{2t}$, the conditional expectations $\mathbb{E}[H_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}]$ and $\mathbb{E}[I_i^{2t} | \mathbf{C}^{2t} = \mathbf{c}, \mathbf{N}^{2t} = \mathbf{n}]$ reduce to their unconditional forms, $\mathbb{E}[H_i^{2t}]$ and $\mathbb{E}[I_i^{2t}]$. Equations (51) and (53) therefore become:

$$h_i^{2t+1} = h_i^{2t} (1 - p_i(c_i, n_i)), \quad (53)$$

$$i_i^{2t+1} = i_i^{2t} + h_i^{2t} p_i(c_i, n_i). \quad (54)$$

Next, in order to completely define the evolution equations for $\mathbf{H}^{2t+1}$ and $\mathbf{I}^{2t+1}$, we assume that the conditioning values for $\mathbf{C}^{2t}$ and $\mathbf{N}^{2t}$, written as $\mathbf{c}$ and $\mathbf{n}$ in equations (51) and (53), can be replaced by their corresponding expectations, $\mathbf{c}^{2t}$ and $\mathbf{n}^{2t}$, respectively. This approximation assumes that random fluctuations in the populations are negligible compared to their mean values, which holds true for sufficiently large populations. Consequently, the processes $\mathbf{C}^{2t}$ and $\mathbf{N}^{2t}$ can be described solely by the diffusive evolution equations for the mean value (see equation (42)).

$$\mathbf{c}^{2t+2} = \mathbf{c}^{2t+1} \mathbf{M}, \quad \mathbf{c}^{2t+1} = \mathbf{c}^{2t} \quad (55)$$

$$\mathbf{n}^{2t+1} = \mathbf{i}^{2t+1} \mathbf{M}, \quad \mathbf{n}^{2t+1} = \mathbf{n}^{2t} \quad (56)$$

This allows us to replace $\mathbf{c}$ and $\mathbf{n}$ by $\mathbf{c}^{2t}$ and $\mathbf{n}^{2t}$ in equations (51) and (53), obtaining

$$h_i^{2t+1} = h_i^{2t} (1 - p_i(c_i^{2t}, n_i^{2t})), \quad (57)$$

$$i_i^{2t+1} = i_i^{2t} + h_i^{2t} p_i(c_i^{2t}, n_i^{2t}). \quad (58)$$

Or, equivalently, we can write the last equations into its vectorial version as,

$$\mathbf{h}^{2t+1} = \mathbf{h}^{2t} - \mathbf{h}^{2t} \mathbf{P}^{2t}, \quad (59)$$

$$\mathbf{i}^{2t+1} = \mathbf{i}^{2t} + \mathbf{h}^{2t} \mathbf{P}^{2t}, \quad (60)$$

where $\mathbf{P}^{2t}$ is defined as the $s \times S$ diagonal matrix defined as,

$$\mathbf{P}^{2t} := \text{diag}(p_1(c_1^{2t}, n_1^{2t}), p_2(c_2^{2t}, n_2^{2t}), \dots, p_s(c_s^{2t}, n_s^{2t})). \quad (61)$$

Now, to have the full description of the evolution for the mean populations $\mathbf{h}^t$ and $\mathbf{i}^t$, we recall the evolution equations for diffusive stage,

$$\mathbf{h}^{2t+2} = \mathbf{h}^{2t+1} \mathbf{M}, \quad (62)$$

$$\mathbf{i}^{2t+2} = \mathbf{i}^{2t+1} \mathbf{M}. \quad (63)$$

which, combined with equations (59) and (60), we obtain,

$$\mathbf{h}^{2t+2} = \mathbf{h}^{2t} \mathbf{M} - \mathbf{h}^{2t} \mathbf{P}^{2t} \mathbf{M}, \quad (64)$$

$$\mathbf{i}^{2t+2} = \mathbf{i}^{2t} \mathbf{M} + \mathbf{h}^{2t} \mathbf{P}^{2t} \mathbf{M}. \quad (65)$$

The full set of equations for the mean populations, $\mathbf{h}^{2t+2}$, $\mathbf{i}^{2t+2}$ and $\mathbf{c}^{2t+2}$, can be written as,

$$\mathbf{h}^{2t+2} = \mathbf{h}^{2t} (\text{Id} - \mathbf{P}^{2t}) \mathbf{M}, \quad (66)$$

$$\mathbf{i}^{2t+2} = \mathbf{i}^{2t} \mathbf{M} + \mathbf{h}^{2t} \mathbf{P}^{2t} \mathbf{M}, \quad (67)$$

$$\mathbf{c}^{2t+2} = \mathbf{c}^{2t} \mathbf{M}, \quad (68)$$

where Id stands for the identity matrix. The solutions can be straightforwardly obtained, giving,

$$\mathbf{h}^{2t} = \mathbf{h}^0 \prod_{k=0}^{t-1} [(\text{Id} - \mathbf{P}^{2k}) \mathbf{M}], \quad (69)$$

$$\mathbf{i}^{2t} = \mathbf{i}^0 \mathbf{M}^t + \sum_{k=0}^{t-1} \mathbf{h}^{2k} \mathbf{P}^{2k} \mathbf{M}^{t-k}, \quad (70)$$

$$\mathbf{c}^{2t} = \mathbf{c}^0 \mathbf{M}^t, \quad (71)$$

Finally, it is worth noting that the solution $\mathbf{i}^{2t}$ can also be expressed in an alternative form. To see this, first observe that the total infected-plus-susceptible population, denoted by $\mathbf{J}^{2t} := \mathbf{H}^{2t} + \mathbf{I}^{2t}$, remains unchanged during the infective stage. Indeed, since we only consider the infection of susceptible individuals, the susceptible population decreases by exactly the same amount as the infected population increases. Consequently, the evolution of the mean infected-plus-susceptible population, $\mathbf{j}^t := [\mathbf{J}^{2t}]$ follows the same dynamics as the carrier populations (see eq.(71)), namely,

$$\mathbf{j}^{2t} = \mathbf{j}^0 \mathbf{M}^t, \quad (72)$$

or, equivalently, using the fact that $\mathbf{j}^{2t} = \mathbf{h}^{2t} + \mathbf{i}^{2t}$, we have that

$$\mathbf{h}^{2t} + \mathbf{i}^{2t} = (\mathbf{h}^0 + \mathbf{i}^0) \mathbf{M}^t. \quad (73)$$

This expression allows us to rewrite the expression (70) for $\mathbf{i}^{2t}$ as follows:

$$\begin{aligned} \mathbf{i}^{2t} &= (\mathbf{h}^0 + \mathbf{i}^0) \mathbf{M}^t - \mathbf{h}^{2t} \\ &= (\mathbf{h}^0 + \mathbf{i}^0) \mathbf{M}^t - \mathbf{h}^0 \prod_{k=0}^{t-1} [(\text{Id} - \mathbf{P}^{2k}) \mathbf{M}], \end{aligned} \quad (74)$$

which is an alternative way of computing the evolution of the mean infected population.

4 Disease spread model in an open semi-Markov chain

4.1 semi-Markov framework

Semi-Markov chains are a generalization of Markov chains. The main difference between them lies in the distribution of the sojourn time. In Markov chains, the time spent in a state is modeled by a geometric distribution. In contrast, in semi-Markov chains, the sojourn time in a state can be modeled by any distribution.

For a semi-Markov chain to be completely specified, it is necessary to define the state space and its kernel. The kernel is a collection of matrices that determine the probability of transitioning from one state to another for each possible sojourn time. Before we give a formal definition of a semi-Markov chain, some definitions will be introduced.

Let $(Z_t)_{t \in \mathbb{N}_0}$ be a semi-Markov chain (SMC) with state space $\mathcal{S}$. Consider a stochastic process $(S_n)_{n \in \mathbb{N}_0}$ such that $S_0 := 0$, and

$$S_{n+1} := \inf\{t > S_n : Z_t \neq Z_{S_n}\}, \quad n \geq 0,$$

with the convention $\inf \emptyset = +\infty$. To simplify notation, instead of writing $(S_n)_{n \in \mathbb{N}_0}$ we shall write (S_n) , and this will apply for all processes. Therefore, (S_n) are the successive points when a state changes in (Z_t) . Therefore, process (S_n) is called renewal points or jump points of process (Z_t) . Process $(J_n)_{n \in \mathbb{N}_0}$ is the embedded Markov chain,

the chain which records (Z_t) at points (S_n) , i.e., $J_n = Z_{S_n}$. Let $(X_n)_{n \in \mathbb{N}_0}$ be the successive sojourn times in the visited states. By convention $X_0 := S_0 := 0$ and $X_{n+1} := S_{n+1} - S_n$, $n \in \mathbb{N}_0$.

We denote by $\mathcal{M}_{\mathcal{S} \times \mathcal{S}}$ the set of real matrices on $\mathcal{S} \times \mathcal{S}$ and, by $\mathcal{M}_{\mathcal{S} \times \mathcal{S}}(\mathbb{N}_0)$ the set of matrices defined on $\mathbb{N}_0$ which takes values in $\mathcal{M}_{\mathcal{S} \times \mathcal{S}}$. Therefore, the semi-Markov kernel of (Z_t) , is defined as

$$\mathbf{q} := \{q_{i,j}(t) : i, j \in \mathcal{S}, t \in \mathbb{N}_0\} \in \mathcal{M}_{\mathcal{S} \times \mathcal{S}}(\mathbb{N}_0) \quad (75)$$

where each element $q_{i,j}(t)$ is the probability of moving from state i to state j after spending t units of time in i before changing, i.e.,

$$q_{ij}(t) := \mathbb{P}(J_{n+1} = j, S_{n+1} - S_n = t \mid J_n = i), \quad n \geq 0, t \in \mathbb{N}_0; i, j \in \mathcal{S}. \quad (76)$$

The cumulative semi-Markov kernel is defined by

$$Q_{ij}(t) := \mathbb{P}(J_{n+1} = j, X_{n+1} \leq t \mid J_n = i) = \sum_{l=0}^t q_{ij}(l), \quad i, j \in \mathcal{S}, t \in \mathbb{N}_0.$$

It is worth noticing that the semi-Markov kernel considered here is independent of n , which means that the SMC is homogeneous in time. Also observe that we use index $t \in \mathbb{N}_0$ for the calendar points, and index $n \in \mathbb{N}_0$ for the number of jumps of (Z_t) . If semi-Markov kernel is time homogeneous then (J_n) is a homogeneous Markov chain. We denote by p_{ij} , $i, j \in \mathcal{S}$ its transition probability

$$p_{ij} := \mathbb{P}(J_{n+1} = j \mid J_n = i), \quad i, j \in \mathcal{S}, \quad n \in \mathbb{N}_0.$$

Note that p_{ij} can be expressed in terms of the semi-Markov kernel by $p_{ij} = \sum_{k=0}^{\infty} q_{ij}(k)$.

The cumulative distribution function of sojourn time in state $i \in \mathcal{S}$ is

$$H_i(t) := \sum_{l=0}^t \sum_{j \in \mathcal{S}} q_{ij}(l).$$

The conditional cumulative distribution of the waiting time X_{n+1} , $n \in \mathbb{N}$, is

$$F_{ij}(t) := \mathbb{P}(X_{n+1} \leq t \mid J_n = i, J_{n+1} = j) = \begin{cases} \frac{Q_{ij}(t)}{p_{ij}}, & \text{if } p_{ij} \neq 0, \\ 1, & \text{if } p_{ij} = 0. \end{cases} \quad (77)$$

The key distinction between discrete-time Markov and semi-Markov processes lies in the distribution function $F_{ij}(t)$. For a Markov chain, $F_{ij}(t)$ must follow a geometric distribution with parameter $1 - P(i, i)$, where P denotes a transition probability matrix. In contrast, a semi-Markov process imposes no such restriction, allowing $F_{ij}(t)$ to take any probability distribution.

The amount of time that the system has spent in its current state is a random variable. The stochastic process formed by these random variables is known as backward process $(B_t)_{t \in \mathbb{N}_0}$. The backward process is formally defined as follows

$$B_t := t - \max\{S_m : S_m \leq t\} \text{ and } B_t := t \text{ if } S_1 > t. \quad (78)$$

Observe that whenever t corresponds to a renewal epoch, the variable B_t takes the value zero. Following a renewal epoch, B_t increases by one unit at each time step until the occurrence of the next renewal epoch, where it is reset to zero and the cycle repeats.

In some applications, the nature of the problem implies that the sojourn time in a state of a semi-Markov chain has finite support. This situation arises in the problem considered in this work. The amount of time an individual spends in an enclosed environment, such as a shopping mall, is inherently finite. For this reason, we introduce the concept of the support of a state in a semi-Markov chain.

Definition 2 We shall define by τ_i the support of a state $i \in \mathcal{S}$. The support $\tau_i \in \mathbb{N}$ is formally defined as follows

$$\tau_i := \min\{t \in \mathbb{N} : \sum_{k=0}^t \sum_{j \in \mathcal{S}} q_{ij}(k) = 1\}. \quad (79)$$

Roughly speaking, the support of a state is the maximum sojourn time that can be spent in that state throughout the entire process. In this article we shall consider that all states have finite support τ . The support is the same for all states, i.e., $\tau_i = \tau \forall i \in \mathcal{S}$.

Proposition 2 If process (Z_t) is a semi-Markov chain with state space $\mathcal{S} := \mathcal{S}_T \cup \mathcal{S}_A$ where $\mathcal{S}_T$ stands for transient states and $\mathcal{S}_A$ stands for absorbing states. Such that $\mathcal{S}_A \cap \mathcal{S}_B = \emptyset$ and $\mathcal{S}_T, \mathcal{S}_A \neq \emptyset$. Let us denote by (B_t) its backward process which takes values in $\mathbb{N}_0$. Then, the bivariate process (Z_t, B_t) is a Markov process with state space $(\mathcal{S}, \mathbb{N}_0)$ and transition probability function

$$P_{(i, b_1)(j, b_2)} = \begin{cases} \frac{q_{ij}(b_1 + 1)}{\bar{H}_i(b_1)} & \text{if } i \neq j, b_2 = 0, \\ \frac{\bar{H}_i(b_1 + 1)}{\bar{H}_i(b_1)} & \text{if } i = j, b_2 = b_1 + 1, \\ 1 & \text{if } i = j, i \in \mathcal{S}_A, \\ 0 & \text{otherwise,} \end{cases} \quad (80)$$

where $i, j \in \mathcal{S}$ and $b_1, b_2 \in \mathbb{N}_0$. $\bar{H}_i(t)$ is the survival function $\bar{H}_i(t) := P(X_{n+1} > t \mid J_n = i) = 1 - H_i(t)$.

Proof: We only consider transition probabilities between transient states, as the probability of remaining in an absorbing state is trivially equal to one. For the first

case if $i \neq j$ and $b_2 = 0$ we have,

$$\begin{aligned} \mathbb{P}(Z_{t+1} = j, B_{t+1} = 0 \mid Z_t = i, B_t = b_1) &= \frac{\mathbb{P}(J_{n+1} = j, X_{n+1} = b_1 + 1 \mid J_n = i)}{\mathbb{P}(X_{n+1} > b_1 \mid J_n = i)} \quad (81) \\ &= \frac{q_{ij}(b_1 + 1)}{\bar{H}_i(b_1)} \quad (82) \end{aligned}$$

For the second case if $i = j$, and $b_2 = b_1 + 1$ we have,

$$\begin{aligned} \mathbb{P}(Z_{t+1} = i, B_{t+1} = b_1 + 1 \mid Z_t = i, U_t = b_1) &= \frac{\mathbb{P}(X_{n+1} > b_1 + 1)}{\mathbb{P}(X_{n+1} > b_1)} \quad (83) \\ &= \frac{\bar{H}_i(b_1 + 1)}{\bar{H}_i(b_1)} \blacksquare. \quad (84) \end{aligned}$$

Let P_T be the restriction of the matrix P to the transient states. That is, P_T contains the probabilities of transitioning from one transient state within the system to another transient state within the system. Remember that in this work the outside of the system is modeled by absorbing states.

4.2 Open semi-Markov chain

Suppose we have an enclosed space consisting of several interconnected rooms. Within this enclosed space, people can enter and leave the system. We shall model this system by an open semi-Markov chain. The term "open" comes from the fact that people can enter and leave the system and it is also named a semi-Markov chain because every person moves from one room to another following the rules of a semi-Markov chain. The rooms inside of the system are considered transient states, and the outside of the system is considered absorbing states because once a person goes out of the system, she or he never returns. Formally speaking, we shall define an open semi-Markov chain in the following way.

Definition 3 (Open semi-Markov chain (OSMC)) Let (Z_t) be a semi-Markov chain with semi-Markov kernel $\mathbf{q}$ and state space $\mathcal{S} := \mathcal{S}_T \cup \mathcal{S}_A$ where $\mathcal{S}_T$ stands for transient states and $\mathcal{S}_A$ stands for absorbing states. Observe that $\mathcal{S}_A \cap \mathcal{S}_B = \emptyset$ and $\mathcal{S}_T \cup \mathcal{S}_A = \mathcal{S}$. Let us define by $(\mathcal{I}^t)_{t \in \mathbb{N}_0}$ an income protocol. Process $(\mathcal{I}^t)$ is a stochastic process which models the number of people who enter the system. Therefore the triple $(\mathcal{S}, \mathbf{q}, (\mathcal{I}^t))$ is an open semi-Markov chain.

Inside the system, there are three different kinds of individuals: healthy, carrier and ill individuals. These are random variables are denoted as $\mathbf{H}^t, \mathbf{C}^t$ and $\mathbf{I}^t$, respectively. To see more details about the different kinds of individuals see section 2.1. In this section, we shall study the dynamics of the expected values $\mathbf{h}^t, \mathbf{c}^t$, and $\mathbf{i}^t$, see Equations (38), (39) and (40) for an open semi-Markov chain.

The dynamics of an open semi-Markov chain is similar to the dynamic of a closed Markov chain. It has two steps: *diffusive step* and *infected step*, see sections 3.1 and

3.2. The dynamic of the infected step is very similar to the dynamic of the infected step in a closed Markov chain. The main different between these two processes lies in the diffusion step, in this case we allow people to enter and leave the system. For this reason, we provide a detailed description of the diffusion state below.

4.2.1 Diffusion step for an open semi-Markov chain

We present the evolution equations for the diffusion stage. At each even step, new individuals are introduced into the system according to an incoming protocol ($\mathcal{I}^{2t}$). At each diffusive step new individuals enter the system and the individuals who remain in the system at time $2t - 1$, $t \geq 1$ are redistributed according to a multinomial distribution. In this case the state space is formed by transient states $\mathcal{S}_T$ and absorbing states $\mathcal{S}_A$. The inside of the system is modeled by transient states and the outside is modeled by absorbing states. Therefore, the number of people inside the system at diffusive step is given by equation

$$\mathbf{N}^{2t} = \mathcal{I}^{2t} + \mathcal{R}(\mathbf{N}^{2t-1}, P_T), \quad (85)$$

where $\mathbf{N}^t$ denotes the number of people inside the system at time t , P_T is the restriction of matrix P to transient states, see Proposition 2. Operator $\mathcal{R}(\mathbf{N}^{2t-1}, P_T)$ is the *redistribution operator* defined in Definition 1.

Individuals are redistributed from each state $i \in \mathcal{S}_T$, the movement of each individual is modeled by a semi-Markov chain. Each room is represented by a transient state and, the probability to move from one room to another at calendar time t is given by P_T . So, a person has probability

$$\frac{\overline{H}_i(b_1 + 1)}{\overline{H}_i(b_1)}, \quad (86)$$

to stay in state i . By contrast the probability that an individual changes rooms is

$$\frac{q_{ij}(b_1 + 1)}{\overline{H}_i(b_1)} \quad (87)$$

where $i, j \in \mathcal{S}_T$ and $i \neq j$, $b_1 \in \mathbb{N}$ is the backward time in i at calendar time t , see Proposition (2). From each state $i \in \mathcal{S}_T$, the number of individuals redistributed across the system follows a multinomial distribution, i.e.,

$$R(\mathbf{N}_i^{2t-1}, P_T) \sim \text{Multinomial}(P_{T(i, b_1)(i, b_1+1)}, P_{T(i, b_1)(j, 0)}, N_i^{2t-1}), \quad t > 0, \quad j \in \mathcal{S}_T. \quad (88)$$

Notice that the total number of people redistributed in each state through the system come from all transient states, this number is formally defined as follows

$$\mathcal{R}(\mathbf{N}^{2t-1}, P_T) := \sum_{i \in \mathcal{S}} R(\mathbf{N}_i^{2t-1}, P_T). \quad (89)$$

Observe that $\mathcal{R}(\mathbf{N}^{2t-1}, P_T)$ is a random vector of side $1 \times (s_T \times \tau)$, where to simplify notation $s_T := |\mathcal{S}_T|$. Since the probability that an individual changes state depends on the time spent in the current state, i.e., it depends on its corresponding backward time. The random variable $\mathcal{R}(\mathbf{N}^{2t-1}, P_T)$ has the following structure

$$\mathcal{R}(\mathbf{N}^{2t-1}, P_T) = (N_{(1,0)}^{2t}, \dots, N_{(1,\tau-1)}^{2t}, N_{(2,0)}^{2t}, \dots, N_{(2,\tau-1)}^{2t}, \dots, N_{(s_T,0)}^{2t}, \dots, N_{(s_T,\tau-1)}^{2t}) \quad (90)$$

where $N_{(i,b)}^t$ is the number of people redistributed in state $i \in \mathcal{S}_T$ at time t with backward time $b \in \mathbb{N}$. Let

$$n_{(i,b)}^{2t} := \mathbb{E}[N_{(i,b)}^{2t}] \quad (91)$$

be the average number of people at time t in state i with backward time b . By consequence

$$n_i^{2t} := \sum_{b \in \mathbb{N}_0} n_{(i,b)}^{2t} \quad (92)$$

is the average number of people at time t in state i independent of its backward time.

Taking the expected value of Equation (85), we have

$$(93)$$

where

$$\mathbf{n}_{\mathcal{R}}^{2t} := (n_1^{2t}, n_2^{2t}, \dots, n_{s_T}^{2t}). \quad (94)$$

Each entry of the vector is modeled by Equation (92). We can observe that Equation (92) can be expressed in matrix form as

$$n_i^{2t} := (\tilde{\mathbf{n}}^{2t} P_T) \cdot \mathbf{e}_i. \quad (95)$$

where

$$\tilde{\mathbf{n}}^{2t} := (n_{(1,0)}^{2t}, \dots, n_{(1,\tau-1)}^{2t}, n_{(2,0)}^{2t}, \dots, n_{(2,\tau-1)}^{2t}, \dots, n_{(s_T,0)}^{2t}, \dots, n_{(s_T,\tau-1)}^{2t}). \quad (96)$$

Vector $\mathbf{e}_i$ is a column vector of side $(s_T \times \tau) \times 1$ whose entries are zero except for those corresponding to state $i \in \mathcal{S}_T$, which are equal to one regardless of the associated backward time. Matrix P_T , is the restriction of transient states of matrix P , see Proposition 2.

The redistribution of healthy, carrier, and ill individuals are defined in a similar way. In diffusive stage at starting time $t = 0$, the number of susceptible and carrier coincide with the income protocol while there is any infected person in the system, i.e.,

$$\mathbf{H}^0 = \hat{\mathcal{I}}^0, \quad (97)$$

$$\mathbf{C}^0 = \tilde{\mathcal{I}}^0, \quad (98)$$

$$\mathbf{I}^0 = \underbrace{(0, 0, \dots, 0)}_S. \quad (99)$$

where $\hat{\mathcal{I}}^0$ and $\tilde{\mathcal{I}}^0$ denote entering susceptible and carrier individuals respectively at time $t = 0$. Observe that $\hat{\mathcal{I}}^0$ and $\tilde{\mathcal{I}}^0$ are random vectors of side $1 \times s_T$. We can notice that

$$\mathcal{I}^{2t} = \hat{\mathcal{I}}^{2t} + \tilde{\mathcal{I}}^{2t}.$$

In the subsequent diffusion time steps, susceptible individuals are those who newly enter the system and those who remain inside the system after the infection step, i.e., for $t > 0$

$$\mathbf{H}^{2t} = \hat{\mathcal{I}}^{2t} + \mathcal{R}(\mathbf{H}^{2t-1}, P_T), \quad (100)$$

where $\mathcal{R}(\mathbf{H}^{2t-1}, P_T)$ is the redistribution of healthy people that remains in the system after the infectious step $2t-1$. Healthy individuals redistributed throughout the system may originate from different states. From each state $i \in \mathcal{S}_T$, the number of individuals redistributed across the system follows a multinomial distribution given by

$$R(\mathbf{H}_i^{2t-1}, P_T) \sim \text{Multinomial}(P_{(i,b_1)(i,b_1+1)}, P_{(i,b_1)(j,0)}, H_i^{2t-1}), \quad t > 0, \quad j \in \mathcal{S}_T. \quad (101)$$

Where $i \neq j$. Notice that the total number of healthy people redistributed through the system come from all states in the system, it is formally defined as follows

$$\mathcal{R}(\mathbf{H}^{2t-1}, P_T) = \sum_{i \in \mathcal{S}} R(\mathbf{H}_i^{2t-1}, P_T). \quad (102)$$

Observe that $\mathcal{R}(\mathbf{H}^{2t-1}, P_T)$ is a random vector of side $1 \times (s_T \times \tau)$. Since the probability that an individual changes state depends on the time spent in the current state, i.e., it depends on the corresponding backward time. The variable $\mathcal{R}(\mathbf{H}^{2t-1}, P_T)$ has the following structure

$$\mathcal{R}(\mathbf{H}^{2t-1}, P_T) = (H_{(1,0)}^{2t}, \dots, H_{(1,\tau-1)}^{2t}, H_{(2,0)}^{2t}, \dots, H_{(2,\tau-1)}^{2t}, \dots, H_{(s_T,0)}^{2t}, \dots, H_{(s_T,\tau-1)}^{2t}), \quad (103)$$

where $H_{(i,b)}^{2t}$ is the number of healthy people at time t in state $i \in \mathcal{S}$ with backward time $b \in \mathbb{N}_0$. The symbol τ is the support of every state formally define in Definition (2). Let

$$h_{(i,b)}^{2t} := \mathbb{E}[H_{(i,b)}^{2t}] \quad (104)$$

be the average number of healthy people at time t in state i with backward time b . By consequence

$$h_i^{2t} := \sum_{b \in \mathbb{N}_0} h_{(i,b)}^{2t} \quad (105)$$

is the average number of people at time $2t$ in state i independent of its backward time.

Considering redistribution follows a multinomial distribution, taking the expected value of Equation (100), we have

$$\mathbf{h}^{2t} = \hat{\mathbf{i}}^{2t} + \mathbf{h}_{\mathcal{R}}^{2t}, \quad (106)$$

where $\hat{\mathbf{i}}^{2t} := \mathbb{E}[\hat{\mathcal{I}}^{2t}]$ and

$$\mathbf{h}_{\mathcal{R}}^{2t} := (h_1^{2t}, h_2^{2t}, \dots, h_{s_T}^{2t}). \quad (107)$$

Each entry of the vector is given by Equation (105). We can observe that Equation (105) can be viewed in a matrix form as follows

$$h_i^{2t} := \left(\tilde{\mathbf{h}}^{2t} P_T \right) \cdot \mathbf{e}_i. \quad (108)$$

where

$$\tilde{\mathbf{h}}^{2t} = (h_{(1,0)}^{2t}, \dots, h_{(1,\tau-1)}^{2t}, h_{(2,0)}^{2t}, \dots, h_{(2,\tau-1)}^{2t}, \dots, h_{(s_T,0)}^{2t}, \dots, h_{(s_T,\tau-1)}^{2t}). \quad (109)$$

Vector $\mathbf{e}_i$ is a column vector of side $(s_T \times \tau) \times 1$ whose entries are zero except for those corresponding to state $i \in \mathcal{S}_T$, which are equal to one regardless of the associated backward value.

Redistribution of carriers is carried out in an analogous manner. At diffusion time steps $2t, t \geq 1$, carrier individuals are those who newly enter the system and those who remain inside the system after the infection step, i.e., for $t > 0$

$$\mathbf{C}^{2t} = \tilde{\mathcal{I}}^{2t} + \mathcal{R}(\mathbf{C}^{2t-1}, P_T), \quad (110)$$

where $\tilde{\mathcal{I}}^{2t}$ represent the income protocol of ill people who get infected outside the system and $\mathcal{R}(\mathbf{C}^{2t-1}, P_T)$ is the redistribution of carrier people that remain in the system after the infectious step $2t - 1$. Carrier individuals redistributed throughout the system may originate from different states. From each state $i \in \mathcal{S}_T$, the number of individuals redistributed across the system follows a multinomial distribution

$$R_i(\mathbf{C}^{2t-1}, P_T) \sim \text{Multinomial}(P_{(i,b_1)(i,b_1+1)}, P_{(i,b_1)(j,0)}, C_i^{2t-1}), \quad t > 0, \quad j \in \mathcal{S}_T, \quad (111)$$

where

$$\mathcal{R}(\mathbf{C}^{2t-1}, P_T) = \sum_{i \in \mathcal{S}} R(\mathbf{C}_i^{2t-1}, P_T). \quad (112)$$

Since the probability that an individual changes state depends on the time spent in the current state, i.e., it depends on the corresponding backward value. We have

$$\mathcal{R}(\mathbf{C}^{2t-1}, P_T) = (C_{(1,0)}^{2t}, \dots, C_{(1,\tau-1)}^{2t}, \dots, C_{(2,0)}^{2t}, \dots, C_{(2,\tau-1)}^{2t}, \dots, C_{(s_T,0)}^{2t-1}, \dots, C_{(s_T,\tau-1)}^{2t-1}), \quad (113)$$

where $C_{(i,b)}^t$ is the number of ill people at time t in state $i \in \mathcal{S}_T$ with backward time $b \in \mathbb{N}_0$. Let

$$c_{(i,b)}^t := \mathbb{E}[C_{(i,b)}^t] \quad (114)$$

be the average number of people at time t in state i with backward time b . By consequence

$$c_i^t := \sum_{b \in \mathbb{N}_0} c_{(i,b)}^t \quad (115)$$

is the average number of people at time t in state i independent of its backward time.

Taking the expected value of Equation (110), we have

$$\mathbf{c}^{2t} = \tilde{\mathbf{I}}^{2t} + \mathbf{c}_{\mathcal{R}}^{2t}, \quad (116)$$

where $\tilde{\mathbf{I}}^{2t} := \mathbb{E}[\tilde{\mathcal{I}}^{2t}]$ and

$$\mathbf{c}_{\mathcal{R}}^{2t} := (c_1^{2t}, c_2^{2t}, \dots, c_{s_T}^{2t}). \quad (117)$$

We can observe that

$$c_i^{2t} := (\tilde{c}^{2t} P_T) \cdot \mathbf{e}_i. \quad (118)$$

where

$$\tilde{\mathbf{c}}^{2t} = (c_{(1,0)}^{2t}, \dots, c_{(1,\tau-1)}^{2t}, c_{(2,0)}^{2t}, \dots, c_{(2,\tau-1)}^{2t}, \dots, c_{(s_T,0)}^{2t}, \dots, c_{(s_T,\tau-1)}^{2t}). \quad (119)$$

Observe that $\mathbf{e}_i$ is a column vector of size $(s_T \times \tau) \times 1$. Vector $\mathbf{e}_i$ is a column vector whose entries are zero except for those corresponding to state $i \in \mathcal{S}_T$, which are equal to one regardless of the associated backward value.

In the diffusive step, there are any infections that people only redistribute through the system, i.e.,

$$\mathbf{I}^{2t} = \mathcal{R}(\mathbf{I}^{2t-1}, P_T). \quad (120)$$

Therefore, the redistribution for infected people is

$$R(\mathbf{I}_i^{2t-1}, P_T) \sim \text{Multinomial}(P_{(i,b_1)(i,b_1+1)}, P_{(i,b_1)(j,0)}, I_i^{2t-1}), \quad t > 0, \quad j \in \mathcal{S}_T. \quad (121)$$

Where $i \neq j$. The total number of infected people redistributed through the system is

$$\mathcal{R}(\mathbf{I}^{2t-1}, P_T) = \sum_{i \in \mathcal{S}} R(\mathbf{I}_i^{2t-1}, P_T). \quad (122)$$

$\mathcal{R}(\mathbf{I}^{2t-1}, P_T)$ is a random vector of side $1 \times (s_T \times \tau)$. Since the probability that an individual changes state depends on the time spent in the current state, i.e., it depends on the corresponding backward value. We have

$$\mathcal{R}(\mathbf{I}^{2t-1}, P_T) = (I_{(1,0)}^{2t}, \dots, I_{(1,\tau-1)}^{2t}, I_{(2,0)}^{2t}, \dots, I_{(2,\tau-1)}^{2t}, \dots, I_{(s_T,0)}^{2t}, \dots, I_{(s_T,\tau-1)}^{2t}) \quad (123)$$

where $I_{(i,b)}^t$ is the number of ill people at time t in state $i \in \mathcal{S}_T$ with backward time $b \in \mathbb{N}_0$. Let

$$i_{(i,b)}^{2t} := \mathbb{E}[I_{(i,b)}^{2t}] \quad (124)$$

be the average number of people at time t in state i with backward time b . By consequence

$$i_i^{2t} := \sum_{b \in \mathbb{N}_0} i_{(i,b)}^{2t} \quad (125)$$

is the average number of people with illness at time t in state i independent of its backward time.

Considering redistribution follows a multinomial distribution, taking the expected value of Equation (120), we have

$$\mathbf{i}^{2t} = \mathbf{i}_{\mathcal{R}}^{2t}, \quad (126)$$

That means in this step of time ill people do not enter the system it only redistributes, where

$$\mathbf{i}_{\mathcal{R}}^{2t} := (i_1^{2t}, i_2^{2t}, \dots, i_{s_T}^{2t}). \quad (127)$$

We can observe that

$$i_i^{2t} := (\tilde{\mathbf{i}}^{2t} P) \cdot \mathbf{e}_i. \quad (128)$$

where

$$\tilde{\mathbf{i}}^{2t} = (i_{(1,0)}^{2t}, \dots, i_{(1,\tau-1)}^{2t}, i_{(2,0)}^{2t}, \dots, i_{(2,\tau-1)}^{2t}, \dots, i_{(s_T,0)}^{2t}, \dots, i_{(s_T,\tau-1)}^{2t}). \quad (129)$$

Observe that $\mathbf{e}_i$ is a column vector of size $(s_T \times \tau) \times 1$. Vector $\mathbf{e}_i$ is a column vector whose entries are zero except for those corresponding to state i , which are equal to one regardless of the associated backward value.

Rooms in the enclosed space are represented by states of semi-Markov chain (Z_t) . Therefore we can notice that the average number of susceptible, carrier and infected people inside of the system at time t are random vectors, i.e.,

$$\mathbf{h}^t = (h_1^t, h_2^t, \dots, h_{s_T}^t), \quad (130)$$

$$\mathbf{c}^t = (c_1^t, c_2^t, \dots, c_{s_T}^t), \quad (131)$$

$$\mathbf{i}^t = (i_1^t, i_2^t, \dots, i_{s_T}^t). \quad (132)$$

Where h_i^t , c_i^t and i_i^t stands for the average number of healthy, carrier and ill people in state (room) $i \in \mathcal{S}_T$ at time t .

The average number of individuals in the system at time t is modeled by stochastic vector $\mathbf{n}^t$. Entry $\mathbf{n}_i^t$ models the number of people who are presented at time t in state $i \in \mathcal{S}_T$, i.e., observe that

$$\mathbf{n}_i^t = \mathbf{h}_i^t + \mathbf{c}_i^t + \mathbf{i}_i^t. \quad (133)$$

Having rigorously formulated the mathematical equations that characterize the contagion dynamics together with the redistribution process of individuals, in accordance with the methodological approach presented in [García-Maya et al. \(2025\)](#), in next section we shall present the stationary number of healthy, carrier and ill people in the system.

5 Stationary Equations for a open Semi-Markov Chain

The stationary characterization of the mean number of healthy, carrier, and infected individuals in a open semi-Markov chain provides valuable insight into the long term behavior of the contagion process. Unlike transient analyses, which describe the evolution of the system over finite time horizons, the stationary regime reveals the equilibrium population distribution that emerges after the effects of the initial conditions have vanished. Such information is fundamental for assessing the endemic level

of the disease, quantifying the long-term burden on the population, and evaluating the impact of the underlying mobility and transmission mechanisms. Furthermore, the stationary solution serves as a benchmark for comparing different intervention strategies, optimizing control policies, and identifying the parameters that most strongly influence the prevalence of infection. Consequently, the derivation of the stationary mean numbers of healthy, carrier, and infected individuals constitutes an essential component in the theoretical analysis of closed semi-Markov epidemic models.

Following the same reasoning as in [García-Maya et al. \(2025\)](#), it is straightforward to show that the stationary mean number of healthy, carrier, and ill individuals in the system is given by the following equations, respectively

$$\bar{\mathbf{h}} = \hat{\mathbf{i}} \left(\mathbf{I} - \tilde{\mathbf{P}} \right) \left(\mathbf{I} - P_T \left(\mathbf{I} - \tilde{\mathbf{P}} \right) \right)^{-1}, \quad (134)$$

$$\bar{\mathbf{i}} = \left(\hat{\mathbf{i}} + \bar{\mathbf{h}} P_T \right) \bar{\mathbf{P}} (\mathbf{I} - P_T), \quad (135)$$

and

$$\bar{\mathbf{c}} := \tilde{\mathbf{i}} (\mathbf{I} - P_T)^{-1}. \quad (136)$$

Where $\hat{\mathbf{i}}$ is the stationary distribution of the admission protocol for healthy individuals according with its backward time, i.e.,

$$\hat{\mathbf{i}} := (\hat{i}_{(1,0)}, \dots, \hat{i}_{(1,\tau-1)}, \hat{i}_{(2,0)}, \dots, \hat{i}_{(2,\tau-1)}, \dots, \hat{i}_{(s_T,0)}, \dots, \hat{i}_{(s_T,\tau-1)}). \quad (137)$$

In the admission protocol, we consider only transient states because absorbing states are considered the outside of the system. Matrix $\tilde{P}$ is the contagion matrix. Matrix $\tilde{P}$ is a diagonal matrix of side $s_T \times s_T$ whose off-diagonal entries are all zero, while its diagonal entries are given by the following expression

$$\tilde{P}_{ii} = \frac{\gamma \sum_{b=0}^{\tau} \tilde{c}_{(i,b)}^t}{\sum_{b=0}^{\tau} \tilde{c}_{(i,b)}^t + \sum_{b=0}^{\tau} \tilde{h}_{(i,b)}^t + \sum_{b=0}^{\tau} \tilde{i}_{(i,b)}^t}. \quad (138)$$

The diagonal element i represents the probability that a person is infected in state $i \in \mathcal{S}_T$. Parameter γ is the same parameter as parameter defined in Equation (48)

We are interested in computing the stationary mean number of healthy, carrier and ill people who leave the enclosed space. To achieve this goal we shall define the output matrix. The output matrix is the matrix that represents the probability of passing from the inside of the system to the outside of the system. In mathematical terms, the output matrix represents the probability of passing from a transient state

to an absorbing state. It is formally defined as follows

$$P_{T \times A} := P_{(S_T \times S_A)}. \quad (139)$$

Let $\mathbf{e}_j$ be the j column vector of matrix $P_{T \times A}$. Let

$$\mathbf{e} = \sum_{j \in S_A} \mathbf{e}_j \quad (140)$$

be the exit vector, the vector that represents the probability of getting out of the system by any state. Therefore, the stationary mean number of healthy people leaving the enclosed space is

$$\bar{o} := \bar{\mathbf{h}} \mathbf{e}. \quad (141)$$

The stationary mean number of carrier people leaving the enclosed space is

$$\bar{u} := \bar{\mathbf{c}} \mathbf{e} \quad (142)$$

and the stationary mean number of ill people leaving the enclosed space is

$$\bar{v} := \bar{\mathbf{i}} \mathbf{e}. \quad (143)$$

In following sections we shall present some numerical examples.

6 Results

6.1 Disease spread in closed population Markov chains

As we saw in Section 3.2, we obtained the evolution

$$\mathbf{i}^{2t} = \mathbf{h}^0 \prod_{k=0}^{t-1} [(\text{Id} - \mathbf{P}^{2k}) \mathbf{M}], \quad (144)$$

$$\mathbf{i}^{2t} = \mathbf{h}^0 \mathbf{M}^t + \mathbf{i}^0 \mathbf{M}^t - \mathbf{h}^{2t}, \quad (145)$$

$$\mathbf{c}^{2t} = \mathbf{c}^0 \mathbf{M}^t. \quad (146)$$

It is also important to state that the evolution in time of mean total population $\mathbf{n}^{2t} = \mathbf{h}^{2t} + \mathbf{i}^{2t} + \mathbf{c}^{2t}$ is ruled only by the diffusive stage. This means that the equation for $\mathbf{n}^{2t}$ is given by,

$$\mathbf{n}^{2t} = \mathbf{n}^0 \mathbf{M}^t. \quad (147)$$

To validate the above approximated analytical expressions for the time-dependent behavior for the susceptible and infected populations we achieve some numerical simulations. To this end, we consider the 3-states linear chain shown in Figure 1. The

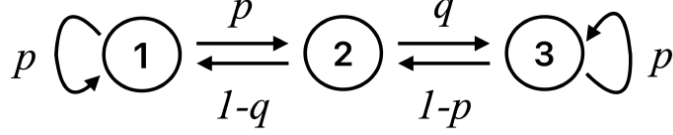


Fig. 1 Three-states linear chain model. We use this Markov chain structure to achieve numerical simulations to see how the infected and susceptible mean populations evolve in time.

corresponding transition matrix is given by

$$\mathbf{M} = \begin{bmatrix} p & 1-p & 0 \\ 1-q & 0 & q \\ 0 & 1-p & p \end{bmatrix} \quad (148)$$

Next, we perform numerical simulations of the stochastic disease-spread process defined by equations (35), (36), (35), (44), (45), and (46). To this end, we consider a population of 10,700 particles in the chain. Of these, 10,000 are assumed to be individuals distributed among the three states as follows: 6500 in state 0, 1500 in state 1, and 2000 in state 2. The remaining 700 particles are assumed to be carriers which are distributed among the three states as follows: 100 in state 0, 450 in state 1, and 150 in state 2. At the initial time, we assume that there are no infected individuals. This specifications allow us to write,

$$\mathbf{h}^0 = [6500, 1500, 2000], \quad (149)$$

$$\mathbf{c}^0 = [100, 450, 150], \quad (150)$$

$$\mathbf{i}^0 = [0, 0, 0], \quad (151)$$

For the numerical simulations, we set $p = 0.43$ and $q = 0.67$. Once the simulations are performed, we compute the time evolution of the total number of particles, irrespective of their epidemiological labels, in order to characterize the evolution of the overall population. This allows us to compare the simulation results with the analytically predicted mean total population, $\mathbf{n}^t$, and mean carrier population, $\mathbf{c}^t$. The comparison is shown in Figure 2, where the solid lines correspond to the populations obtained from the numerical simulations, whereas the dashed lines represent the analytical predictions given by Eqs. (147) and (146).

As can be seen from Figure 2, the analytical approximation accurately reproduces the population dynamics, with its agreement improving as the number of particles increases. This behavior is consistent with the reduction of relative fluctuations expected for larger populations. In particular, the numerical fluctuations depend on the size of the corresponding population, so that the agreement between the stochastic simulations and the analytical mean-field description becomes progressively better in the large-population regime.

Next, from the above-referred simulations, we estimated time-evolution of the populations of the susceptible and infected populations. These curves are shown in Figure 3. In such a figure the solid lines represent the simulated population obtained

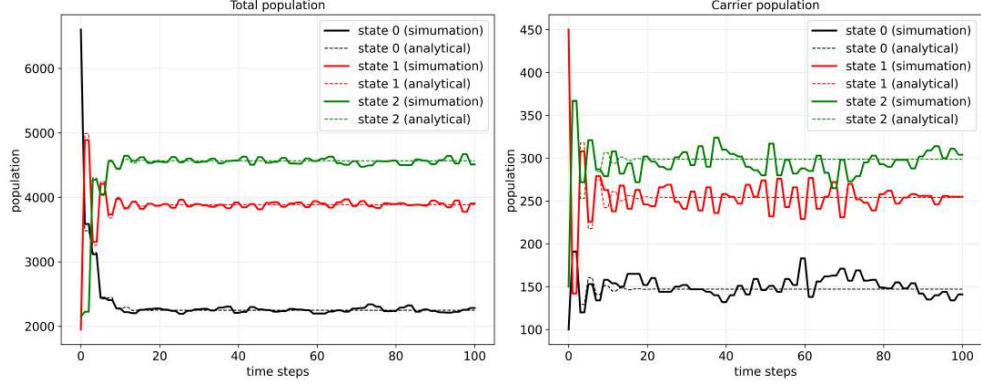


Fig. 2 Time evolution of total and carrier populations in the three-state model. Panels (a) and (b) show the time evolution of the total and carrier populations for each state, respectively. Solid lines represent results obtained from numerical simulations, and dashed lines denote the corresponding analytical solutions evaluated using (147) and (146). The system exhibits an exponential relaxation toward the stationary regime on a relatively short timescale.

from numerical simulations. Dashed lines, on the other hand, stand for the analytically computed mean populations. From these figures we can see that our approximation accurately reproduces the numerically obtained populations. This shows that our formulas for the time-evolution of the susceptible and infected populations accurately reproduce the time-dependent behavior of the infected populations.

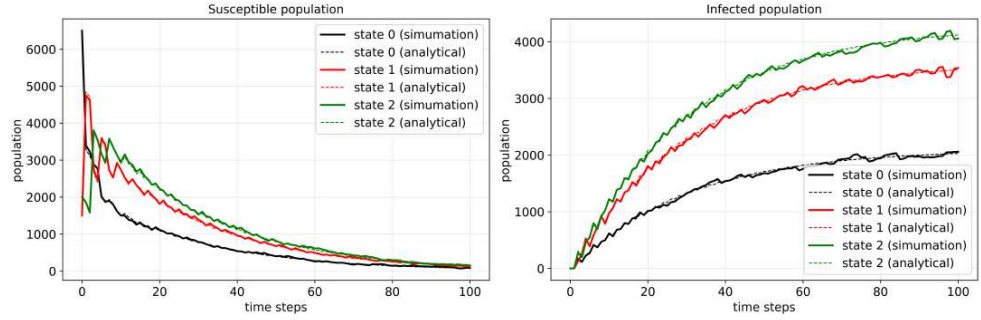


Fig. 3 Time evolution of susceptible and infected populations in the three-state model. Panel (a) shows the time evolution of the susceptible and infected populations for each state. Solid lines represent numerical simulation results, and dashed lines denote the corresponding analytical solutions evaluated using equations (147) and (146), respectively.

6.2 Disease spread open semi-Markov chain

Below, we present an example to calculate the stationary expected value of the number of healthy individuals, computed using Equation (141); carriers computed using Equation (142), and ill individuals computed using Equation (143) in a two compartment (two room) facility with two entrances and two exits. That is, entry and exit are possible from either of the rooms. We call this model Model A.

The parameters of the model are as follows: Let $\mathcal{S} = \{a, b, c, d\}$ be the state space of a semi-Markov chain. Such that there are two transient states $\mathcal{S}_T = \{a, b\}$, representing the inside of the system, and two absorbing states $\mathcal{S}_A = \{c, d\}$ representing the exits of the system. The support of the transient states is $\tau = 3$. For the following simulations, the stationary income protocol for healthy people is

$$\hat{i} \sim (\text{Poisson}(5), \text{Poisson}(5), 0, 0). \quad (152)$$

The stationary income protocol for carrier people is

$$\tilde{i} \sim (\text{Poisson}(5), \text{Poisson}(5), 0, 0). \quad (153)$$

This model is illustrated in the following diagram: For this model, the corresponding

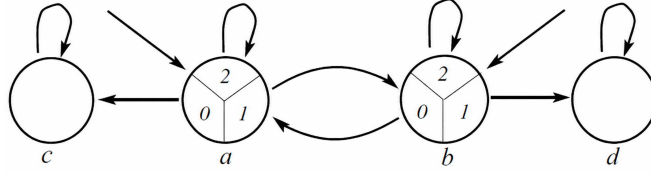


Fig. 4 Open semi-Markov chain with two transient states (representing two rooms within the enclosed space). The maximum residence time in each room is three time units, represented by the backward time values 0, 1, and 2. The system has two exits and two entrances, which are represented by two absorbing states.

semi-Markov kernel is given by

$$q(0) = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad (154)$$

$$q(1) = \begin{pmatrix} 0 & \frac{1}{6} & \frac{1}{6} & 0 \\ \frac{1}{6} & 0 & 0 & \frac{1}{6} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad (155)$$

$$q(2) = \begin{pmatrix} 0 & \frac{1}{6} & \frac{1}{6} & 0 \\ \frac{1}{6} & 0 & 0 & \frac{1}{6} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad (156)$$

$$q(3) = \begin{pmatrix} 0 & \frac{1}{6} & \frac{1}{6} & 0 \\ \frac{1}{6} & 0 & 0 & \frac{1}{6} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}. \quad (157)$$

The transition matrix of the Markov process (Z_t, B_t) associated with the aforementioned semi-Markov kernel, see Equation (2), is given by

$$P = \begin{pmatrix} 0 & \frac{2}{3} & 0 & \frac{1}{6} & 0 & 0 & \frac{1}{6} & 0 \\ 0 & 0 & \frac{1}{2} & \frac{1}{4} & 0 & 0 & \frac{1}{4} & 0 \\ 0 & 0 & 0 & \frac{1}{2} & 0 & 0 & \frac{1}{2} & 0 \\ \frac{1}{6} & 0 & 0 & 0 & \frac{2}{3} & 0 & 0 & \frac{1}{6} \\ \frac{1}{4} & 0 & 0 & 0 & 0 & \frac{1}{2} & 0 & \frac{1}{4} \\ \frac{1}{2} & 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{2} \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}. \quad (158)$$

Observing Matrix (158), we can notice that the exit vector is

$$e = \left(\frac{1}{6}, \frac{1}{4}, \frac{1}{2}, \frac{1}{6}, \frac{1}{4}, \frac{1}{2} \right)^T. \quad (159)$$

The following figure shows the expected stationary number of healthy individuals, carriers, and sick individuals leaving the two-state system with two inputs and two outputs.

In 5 we can observe the stationary mean number of healthy, carrier and ill people leaving the enclose space. In the left green panel, it is observed the departure of healthy individuals which exhibits an inversely proportional relationship with respect to λ , the Poisson parameter for the income protocol of carrier individuals. As the parameter of the Poisson admission protocol for contagious individuals increases, the mean stationary number of departures of healthy people decreases. This graphics were computed using Equation (141). Regarding the departure of carriers, the variability is remarkably narrower, suggesting that the departure rate of this population directly responds to the entry rate with low stochastic dispersion. This is to be expected, as the number of carriers does not change within the system. Carriers are individuals who enter the system infected and, due to the short period of time they spend inside it, cannot recover. Therefore, it is expected that the same number of carriers entering the system is the same number that leaves. The carrier plot was created using Equation (142). Finally, in the last graphic we can observe the mean stationary

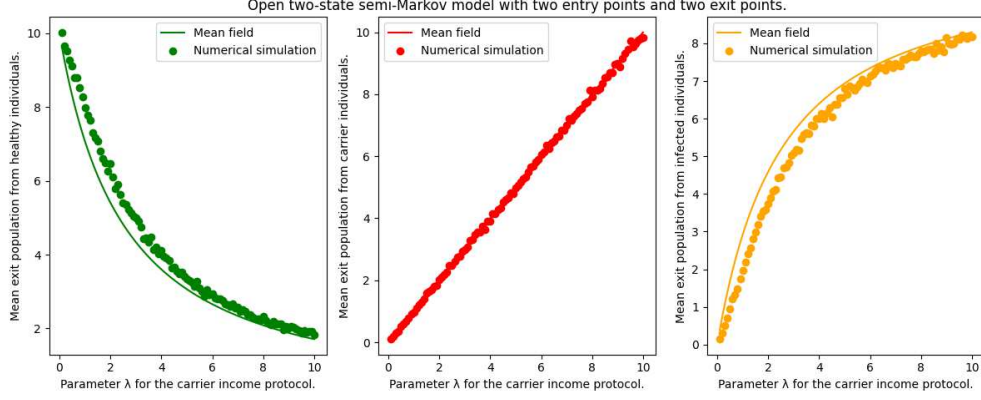


Fig. 5 Plots of the mean stationary number of departures of healthy, carrier, and infected individuals from an open two-state semi-Markov chain with two inputs and output, referred to as model A.

number of ill individuals leaving the enclosed system. Observe that the number of contagious individuals increases as the rate of infected individuals grows, i.e., it increases as the lambda parameter in the income protocol of ill individuals increases.

To compare different income protocols we shall make some modifications to model A. In these case we will consider a single input and output for the system. We shall call this model, model B. The diagram which represents model B is the following

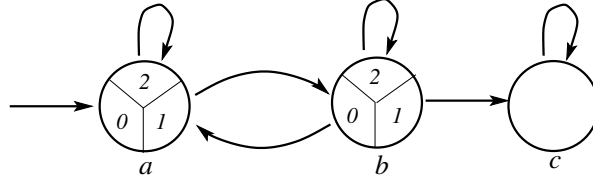


Fig. 6 Open semi-Markov chain with two transient states (representing two rooms within the enclosed space). The maximum residence time in each room is three time units, represented by the backward time values 0, 1, and 2. The system has one exit and one entrance. The exit is represented by an absorbing state.

Figure 6 is a modification from model A, called model B. In model B it is considered a state space $\mathcal{S} = \{a, b, c\}$. It has transient states $\mathcal{S}_T = \{a, b\}$ which represents the inside of the system. The sojourn time in a state is the same as in model A, $\tau = 3$. Such that the backwards times in each transient states are 0, 1, 2. The system has as an absorbing state $\mathcal{S}_A = \{c\}$ which represents the outside. Note that, unlike Model A, the system has a single input and output.

The semi-Markov kernel for model B is

$$q(0) = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad (160)$$

$$q(1) = \begin{pmatrix} 0 & \frac{1}{3} & 0 \\ \frac{1}{6} & 0 & \frac{1}{3} \\ 0 & 0 & 0 \end{pmatrix}, \quad (161)$$

$$q(2) = \begin{pmatrix} 0 & \frac{1}{3} & 0 \\ \frac{1}{6} & 0 & \frac{1}{3} \\ 0 & 0 & 0 \end{pmatrix}, \quad (162)$$

$$q(3) = \begin{pmatrix} 0 & \frac{1}{3} & 0 \\ \frac{1}{6} & 0 & \frac{1}{3} \\ 0 & 0 & 0 \end{pmatrix}. \quad (163)$$

The transition matrix of the Markov process (Z_t, B_t) associated with the preceding semi-Markov kernel, see Equation (2), is given by

$$P = \begin{pmatrix} 0 & \frac{2}{3} & 0 & \frac{1}{3} & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ \frac{1}{6} & 0 & 0 & 0 & \frac{2}{3} & 0 & \frac{1}{6} \\ \frac{1}{4} & 0 & 0 & 0 & 0 & \frac{1}{2} & \frac{1}{4} \\ \frac{1}{2} & 0 & 0 & 0 & 0 & 0 & \frac{1}{2} \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}. \quad (164)$$

The stationary income protocol for healthy people is

$$\hat{i} \sim (\text{Poisson}(10), 0, 0). \quad (165)$$

The stationary income protocol for carrier people is

$$\tilde{i} \sim (\text{Poisson}(10), 0, 0). \quad (166)$$

We can observe that the parameter λ for the entry protocols for healthy and infected individuals is twice as large in Model B as in Model A. This is because Model B has only one entrance; therefore, we set the entry parameter to twice its value so that the number of people inside the system is comparable in both models.

Observing Matrix (164), we can notice that exit vector is

$$e = \left(0, 0, 0, \frac{1}{6}, \frac{1}{4}, \frac{1}{2} \right)^T. \quad (167)$$

Considering model B and using Equations (141), (142) and (143) we shall present the plots for the mean stationary number of healthy, carrier and ill people leaving the enclosed space, respectively.

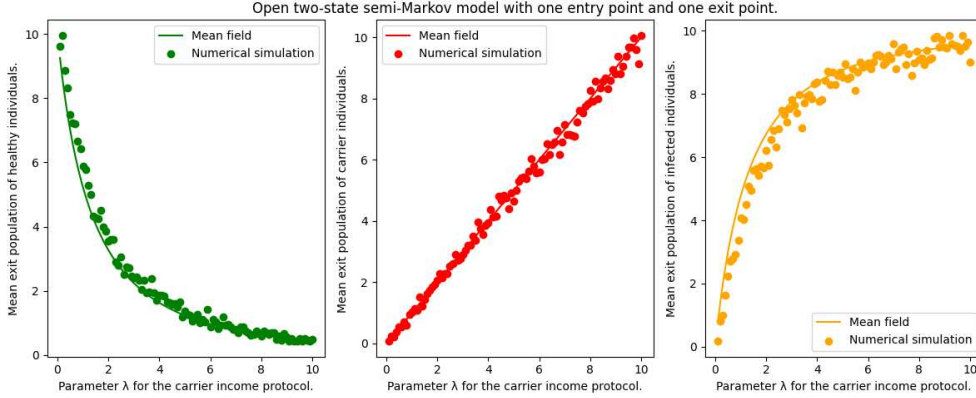


Fig. 7 Plots of the mean stationary number of departures of healthy, carrier, and infected individuals from an open two-state semi-Markov chain with one input and output, referred to as model B.

We can observe a relationship between the plots of models A and B. In both as the admission rate of carrier individuals increases, the stationary mean number of healthy departures decreases. Regarding carriers, the variability is remarkably limited. This aligned behavior is expected since the number of carriers remains constant within the system. Finally, the number of exiting contagious individuals grows as the rate of infected entries increases. Plots from models A and B show a very similar behavior, but what is very interesting is comparing in which of both protocols there are more healthy and ill people leaving the enclosed space; this can be observed in the following figure.

In figure 8 we can observe that as the carrier rate increases, there is a lower output of healthy individuals in model B compared to model A. Complementarily, as the admission rate of sick individuals increases, there is a higher output of sick individuals in model B than in model A. The above suggests that, to reduce the number of infections in enclosed spaces, having a greater number of entries and exits in the system is preferable to having a single entry and a single exit.

7 Conclusions

In this work, we presented a stochastic framework for studying the propagation of infectious diseases in enclosed environments composed of interconnected compartments. The proposed approach explicitly incorporates the movement of individuals through the environment and distinguishes three epidemiological classes: susceptible individuals, carriers, and infected individuals. This distinction allows the transmission

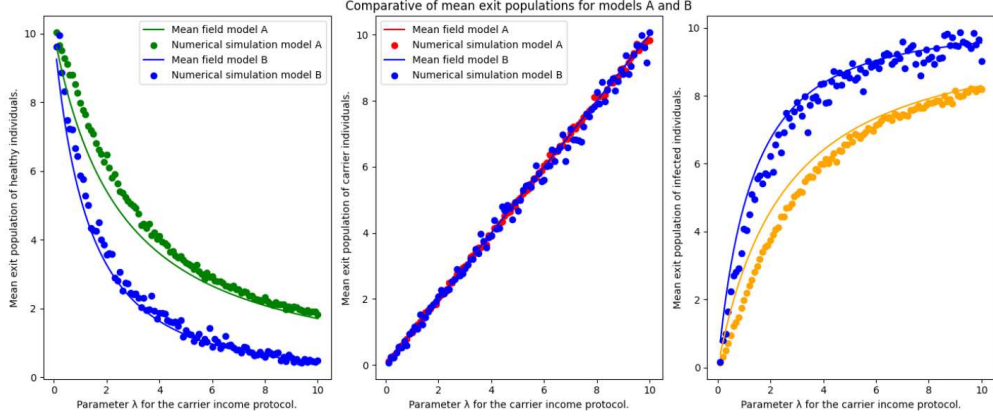


Fig. 8 Comparative graphs of the stationary expected value of the number of healthy, contagious, and infected individuals leaving an enclosed space modeled by a semi-Markov chain with two transient states (rooms inside the enclosed space). The green lines represent model A and the blue lines represent model B.

mechanism to be coupled with the spatial dynamics of the population, since susceptible individuals may acquire the infection when they interact with carriers while moving through the compartmental system.

Two complementary formulations were considered. The first describes a closed population through a Markov chain, where the total number of individuals is conserved and mobility between compartments is determined by a prescribed transition mechanism. This formulation provides a mathematical representation of disease propagation when population changes due to arrivals and departures can be neglected.

The second formulation extends this setting to an open semi-Markov system. The open structure allows individuals to enter and leave the compartmental environment, while the semi-Markov formulation permits residence times to follow more general distributions. Consequently, the model is able to represent environments in which both population turnover and heterogeneous residence times influence the opportunities for interaction and disease transmission. The exterior of the system is represented through absorbing states, which additionally makes it possible to characterize the distribution of the time to absorption and, consequently, the amount of time individuals remain within the system.

The mathematical expressions for the numbers of susceptible, carrier, and infected individuals, together with their expected values, provide a framework for analyzing how infection evolves both temporally and spatially. In particular, the proposed models establish a connection between the structure of the environment, individual mobility, residence times, and the resulting disease dynamics.

Overall, the transition from a closed Markov model to an open semi-Markov formulation provides a more flexible representation of disease propagation in structured environments. The framework can potentially be used to analyze how modifications in mobility patterns, compartment connectivity, residence times, or population turnover affect the evolution of an infection. Future work may focus on applying the proposed

models to specific compartmental environments, estimating their parameters from empirical mobility data, and evaluating intervention strategies designed to reduce the interaction between susceptible individuals and carriers.

Appendix A Some properties of moment generating functions

Let us start by proving that the function $\mathcal{H}(\boldsymbol{\alpha})$,

$$\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) = \sum_{\mathbf{r} \in \mathbb{N}^s} \mathbb{P}(\mathcal{R}(\mathbf{m}, \mathbf{M}) = \mathbf{r}) \exp(\mathbf{r}\boldsymbol{\alpha}^T), \quad (\text{A1})$$

which corresponds to the moment generating function corresponding to the redistribution vector $\mathcal{R}(\mathbf{m}, \mathbf{M})$, can be written as,

$$\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) = \exp(\mathbf{m}\mathbf{H}^T(\boldsymbol{\alpha})), \quad (\text{A2})$$

where $\mathbf{H} : \mathbb{R}^s \rightarrow \mathbb{R}^s$ is a s -dimensional vector function, depending only on $\mathbf{M}$ and $\boldsymbol{\alpha}$, defined as,

$$(\mathbf{H}(\boldsymbol{\alpha}))_i := \log \left(\sum_{j=1}^s M_{i,j} e^{\alpha_j} \right). \quad (\text{A3})$$

First we should recall that the j th component, R_j^t , of the random vector $\mathcal{R}(\mathbf{m}, \mathbf{M})$ can be written as

$$R_j^t = \sum_{i \in \mathcal{S}} B_{i,j}, \quad (\text{A4})$$

where M_{ij} is the (i, j) th component of the transition matrix $\mathbf{M}$ and the random vector $\mathbf{B}_i := (B_{i,1}, B_{i,2}, \dots, B_{i,s})$ has multinomial distribution,

$$\mathbf{B}_i \sim \text{Multinomial}(M_{i1}, M_{i2}, \dots, M_{is}, m_i). \quad (\text{A5})$$

Notice that we omitted the superscript t on $B_{i,j}$, denoting time-dependence, since the random vector $\mathcal{R}(\mathbf{m}, \mathbf{M})$ has been conditioned to $\mathbf{N}^t$ to have the fixed value $\mathbf{m}$. Thus, the conditioned multinomial distribution in Eq. (A5) has no time-dependence.

Now, observe that Eq. (A1) can be written explicitly as

$$\begin{aligned} \mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) &= \sum_{\mathbf{r} \in \mathbb{N}^s} \mathbb{P}(\mathbf{R}^t = \mathbf{r}) \exp(\mathbf{r}\boldsymbol{\alpha}^T) \\ &= \sum_{\mathbf{r} \in \mathbb{N}^s} \mathbb{P}(R_1^t = r_1; R_2^t = r_2; \dots; R_s^t = r_s) \exp(\mathbf{r}\boldsymbol{\alpha}^T) \end{aligned} \quad (\text{A6})$$

and using the expression of R_j in terms of $B_{i,j}$ (A4) we obtain,

$$\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) = \sum_{\mathbf{r} \in \mathbb{N}^s} \mathbb{P} \left(\sum_{i \in \mathcal{S}} B_{i,1} = r_1; \sum_{i \in \mathcal{S}} B_{i,2} = r_2; \dots; \sum_{i \in \mathcal{S}} B_{i,s} = r_s \right) \exp(\mathbf{r}\boldsymbol{\alpha}^T). \quad (\text{A7})$$

Next, we should observe that the probability of a summation of random variables can be written as a conditioned summation of probabilities (the convolution theorem). For instance, the probability of the event $\sum_{i \in \mathcal{S}} B_{i,1} = r_1$ can be written as

$$\mathbb{P}\left(\sum_{i \in \mathcal{S}} B_{i,1} = r_1; \dots\right) = \sum_{b_{1,1}+b_{2,1}+\dots+b_{s,1}=r_1} \dots \mathbb{P}(B_{1,1} = b_{1,1}, \dots, B_{s,1} = b_{s,1}; \dots).$$

Moreover, since we are summing over the variable r_1 , this restriction becomes irrelevant, as r_1 ranges over all possible values. Therefore, we can write:

$$\sum_{r_1 \in \mathbb{N}} \mathbb{P}\left(\sum_{i \in \mathcal{S}} B_{i,1} = r_1; \dots\right) = \sum_{b_{1,1} \in \mathbb{N}} \dots \sum_{b_{s,1} \in \mathbb{N}} \mathbb{P}(B_{1,1} = b_{1,1}, \dots, B_{s,1} = b_{s,1}; \dots).$$

This observation allow us to write Eq. (A7) in terms of summations involving only possible values $B_{i,j}$ as follows:

$$\begin{aligned} \mathcal{H}(\alpha, \mathbf{m}) = & \sum_{b_{1,1} \in \mathbb{N}} \dots \sum_{b_{s,1} \in \mathbb{N}} \dots \sum_{b_{1,s} \in \mathbb{N}} \dots \sum_{b_{s,s} \in \mathbb{N}} \mathbb{P}\left(B_{1,1} = b_{1,1}, \dots, B_{s,1} = b_{s,1}; \right. \\ & \left. B_{1,1} = b_{1,s}, \dots, B_{s,s} = b_{s,s}\right) \exp\left(\sum_{i=1}^s \sum_{j=1}^s b_{i,j} \alpha_j\right). \end{aligned} \quad (\text{A8})$$

Next, defining the vector $\mathbf{b}_i := (b_{i,1}, b_{i,2}, b_{i,s})$ it is possible to rewrite the above expression in a more compact way,

$$\mathcal{H}(\alpha, \mathbf{m}) = \sum_{\mathbf{b}_1 \in \mathbb{N}^s} \dots \sum_{\mathbf{b}_s \in \mathbb{N}^s} \mathbb{P}\left(\mathbf{B}_1 = \mathbf{b}_1, \dots, \mathbf{B}_s = \mathbf{b}_s\right) \exp\left(\sum_{i=1}^s \mathbf{b}_i \alpha^T\right). \quad (\text{A9})$$

Since all the random vectors $\mathbf{B}_i$, for $0 \leq i \leq s$, are assumed to be independent, we have that the joint probability in Eq. (A9) can be written as a product pf the probability of the events $\mathbf{B}_i = \mathbf{b}_i$. This allows us to write,

$$\mathcal{H}(\alpha, \mathbf{m}) = \prod_{i=1}^s \sum_{\mathbf{b}_i \in \mathbb{N}^s} \mathbb{P}\left(\mathbf{B}_i = \mathbf{b}_i\right) \exp\left(\mathbf{b}_i \alpha^T\right). \quad (\text{A10})$$

The summation in Eq. eq:A1:HsumBs-int002 can be identified as the moment generating function of $\mathbf{B}_i \sim \text{Multinomial}(M_{i1}, M_{i2}, \dots, M_{is}, m_i)$ which is a multinomial distribution. The corresponding moment generating function can be written as

$$\sum_{\mathbf{b}_i \in \mathbb{N}^s} \mathbb{P}\left(\mathbf{B}_i = \mathbf{b}_i\right) \exp\left(\mathbf{b}_i \alpha^T\right) = \left(\sum_{j=1}^s M_{i,j} e^{\alpha_j}\right)^{m_i}. \quad (\text{A11})$$

Then, recalling that $\mathbf{H}(\boldsymbol{\alpha}) = (H_1(\boldsymbol{\alpha}), \dots, H_s(\boldsymbol{\alpha}))$ is the s -dimensional vector function whose components are defined as,

$$H_i(\boldsymbol{\alpha}) := \log \left(\sum_{j=1}^s M_{i,j} e^{\alpha_j} \right). \quad (\text{A12})$$

it is clear that

$$\sum_{\mathbf{b}_i \in \mathbb{N}^s} \mathbb{P}(\mathbf{B}_i = \mathbf{b}_i) \exp(\mathbf{b}_i \boldsymbol{\alpha}^T) = \exp(H_i(\boldsymbol{\alpha}) m_i), \quad (\text{A13})$$

which allows us to write Eq. (A10) as follows

$$\mathcal{H}(\boldsymbol{\alpha}, \mathbf{m}) = \prod_{i=1}^s \exp(H_i(\boldsymbol{\alpha}) m_i) = \exp(\mathbf{m} \mathbf{H}^T(\boldsymbol{\alpha})). \quad (\text{A14})$$

Now we prove that the i th component of $\mathbf{H}^{(t)}$, denoted by $H_i^{(t)}$, can be written as,

$$H_i^{(t)}(\boldsymbol{\alpha}) = \log \left(\sum_{j=0}^s M_{ij}^t e^{\alpha_j} \right) \quad (\text{A15})$$

where M_{ij}^t denotes the (i, j) th component of the t th power of the transition matrix $\mathbf{M}$.

We prove the formula (A15) by induction. It is clear that $H_i^{(1)}(\boldsymbol{\alpha}) = H_i(\boldsymbol{\alpha})$. Now, if we write $H_i^{(t+1)}(\boldsymbol{\alpha})$ we have that

$$H_i^{(t+1)}(\boldsymbol{\alpha}) = \log \left(\sum_{j=0}^s M_{ij}^t e^{H_j(\boldsymbol{\alpha})} \right) \quad (\text{A16})$$

Now, observing that

$$\exp(H_j(\boldsymbol{\alpha})) = \sum_{\ell=1}^s M_{j,\ell} e^{\alpha_\ell}, \quad (\text{A17})$$

we have that Eq. (A16) can be expressed as,

$$\begin{aligned} H_i^{(t+1)}(\boldsymbol{\alpha}) &= \log \left(\sum_{j=0}^s M_{ij}^t \sum_{\ell=1}^s M_{j,\ell} e^{\alpha_\ell} \right) = \log \left(\sum_{\ell=1}^s \sum_{j=0}^s M_{ij}^t M_{j,\ell} e^{\alpha_\ell} \right) \\ &= \log \left(\sum_{\ell=1}^s M_{i\ell}^{t+1} e^{\alpha_\ell} \right) \end{aligned} \quad (\text{A18})$$

which proves the relation given in Eq. (A15).

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