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Research article

Stationary and non-stationary transition probabilities in decision making: Modeling COVID-19 dynamics

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Abstract: This study present a comparative modeling framework for COVID-19 dynamics using stationary and non-stationary transition probabilities within a Markov decision process (MDP). Stationary transitions assume constant rates, while non-stationary transitions capture time-dependent behaviors driven by policy interventions or behavioral changes. We develop a seven-compartmental epidemiological model, derive transition probabilities from binomial and multinomial processes, and implement time-dependent parameterizations to reflect real-world dynamics. Mathematical models for both stationary and non-stationary transition frameworks are developed and simulated over a 365-day period to emphasize dynamic variations in epidemic outcomes. Our findings highlight the significance of non-stationary modeling in accurately representing the dynamic characteristics of pandemic situations and provide recommendations for optimizing public health interventions under uncertainty. This comparative analysis offers useful information for epidemiological modeling and decision making in dynamic risk environments.

Keywords: Stationary; non-stationary; transition probability; COVID-19; MDP

1. Introduction

Infectious disease modeling has a rich history, evolving from simple mathematical frameworks to sophisticated models incorporating various biological and social factors. To provide solid estimates, models need to be properly calibrated based on empirical evidence (see for instance [1–3]). One of the earliest models, the Reed-Frost model, employed a discrete-time approach to describe the probability of an individual being infected in successive time intervals. This model laid the foundation for subsequent studies that sought to capture the complexity of epidemic spread through probabilistic means. For some applications and generalization of the Reed-Frost model, see for instance [4–9]. Classical

compartmental models, such as SIR and SEIR, generally assume constant transition rates between disease states [10, 11]. However, for pandemics such as Covid-19, these assumptions often break down due to dynamic changes, such as behavioral changes, fluctuation in healthcare capacities, and public health policies [1, 12–15]. Consequently, incorporating non-stationary transition probabilities enables a more realistic epidemic dynamics.

In [16], L. Palopoli et al. proposed a Markovian stochastic approach to model the spread of a SARS-CoV-2-like infection within a closed human group using a partially observable Markov decision process (POMDP). The primary objective was to model in detail the effects of transitions between different states and resource limitations, such as hospital beds and the daily availability of tests. Such models are primarily control-oriented, emphasizing the impact of decision commands on transition probabilities and the epidemic's progression.

When it comes to applications, one notable use is the ability to compute exact probabilities and properties of interest given a control policy, such as the decision to implement a lockdown based on the estimated number of infected individuals. This includes determining the probability that the number of deceased individuals will exceed an acceptable threshold or evaluating more general properties expressed in propositional temporal logic. Additionally, it is possible to synthesize control policies that inherently respect these properties. For more literature on these applications, we refer to [10,12,17–20] and the references therein.

In 2006, H. Tuckwell and R. Williams [15] investigated the properties of a simple discrete-time stochastic epidemic Markovian SIR model, in which the total population remained constant and individuals met a random number of others at each time step. In their model, individuals remained infectious for some time units, after which they became either removed or immune. The transition probabilities from susceptible to infected states were determined using the binomial distribution. Their findings have practical applications in controlling the size and duration of epidemics, thereby reducing their human and economic costs. This model offers a more realistic characterization of epidemics compared to classical discrete-time models, such as the Reed-Frost model, which is often used for analyzing agricultural epidemics.

In [21], the authors used multi-state models to estimate transition probabilities between different health states in elderly patients, providing insights into the temporal progression of diseases and the factors influencing these transitions. Complementing this, A. J. Black [22] discussed methodologies for determining the final size of an epidemic using stochastic processes, emphasizing the importance of accurately modeling the pathways to the absorbing state, which signifies the epidemic's end. Similarly, C. Barril et al. [23] explored the final infection size in models that consider asymptomatic transmission, highlighting the implications of transition probabilities between states for understanding the severity and spread of an epidemic. Additionally, S. Purkayastha et al. [14] compared various epidemiological models in their ability to predict the growth rate and final size of the COVID-19 pandemic in India, focusing on how different models handle transition probabilities and the associated uncertainties in projections. For more information on models that have proven useful in determining the major factors affecting the growth rate and final size of an epidemic, see [11, 24–26].

Recently in 2021, A. Zardini et al. [27] employed statistical methods to quantify the probability of transition between different states of COVID-19-affected patients based on age class. The authors provided estimates of the probabilities of transition across the stages characterizing clinical progression after SARS-CoV-2 infection, stratified by age and sex, as well as the time delays between key events.

They analyzed a sample of 1,965 SARS-CoV-2 positive individuals who were contacts of confirmed cases. These individuals were identified irrespective of their symptoms as part of contact tracing activities conducted in Lombardy, Italy, from March 10 to April 27, 2020. They were also monitored daily for symptoms for at least two weeks after exposure to a COVID-19 case and tested for SARS-CoV-2 via real-time PCR. Additionally, F. Riccardo et al. [28] evaluated the effects of lockdown policies in Italy following the outbreak of the pandemic. In [29], the authors propose an extension of the classic susceptible-infected-susceptible (SIS) model, called the general recovering process SIS (grp-SIS) model, a version of the classic SIS framework that allows any recovery-time distribution. Under a mean-field assumption on homogeneous networks, it shows that the shape of the recovery-time distribution significantly alters epidemic dynamics, including the steady-state infection-time profile.

The current study addresses the critical need for robust models in infectious disease research, particularly focusing on COVID-19. By examining both stationary and non-stationary transition probabilities, this research provides a detailed understanding of disease dynamics over time. On the one hand, stationary transition probability

$$\mathbb{P}_{i,j} = \mathbb{P}(X_{q+\triangle q} = j | X_q = i)$$

represents the probability of transitioning from state i to state j within a fixed time period, where X_q is the state at stage q and $\triangle q$ the stage difference. This formulation is essential for understanding how diseases progress under constant conditions. On the other hand, non-stationary transition probabilities

$$\mathbb{P}_{i,j}(t) = \mathbb{P}(X_{q+\triangle q} = j | X_q = i,\ t)$$

allow for changes in transition probabilities over time, reflecting more realistic scenarios where the probability varies with respect to t (with t representing different intervention measures and other factors). This approach is crucial for modeling dynamic public health responses and understanding how interventions can alter the course of an epidemic.

Stationary models serve as a useful baseline for evaluating the effects of new interventions by providing a consistent reference point. However, these models may misestimate impacts if the effects of interventions or the underlying disease dynamics change over time. Policymakers can use stationary models to identify deviations from expected outcomes, which may signal a need for policy adjustments. In contrast, non-stationary models offer a more dynamic approach by incorporating time-varying transition probabilities. This adaptability allows for real-time adjustments based on the latest data and evolving conditions. By reflecting changes in disease patterns, intervention effectiveness, and external factors, we anticipate that non-stationary models will enable more responsive and accurate decision-making. Our primary goal is to assess how different assumptions about transition dynamics impact model outcomes and their relevance to public health policy.

The main contributions of this study include developing an epidemiological model with seven compartments reflecting key clinical stages of COVID-19. We then derive probabilistic transition rules between states using binomial and multinomial distributions, and explicitly distinguish between stationary and non-stationary regimes. We define time-dependent transition parameters using logistic and quadratic forms to reflect real-world dynamics such as behavioral adaptation or resource saturation. Finally, we simulate COVID-19 dynamics under both transition assumptions and compare outcomes over a 365-day period, illustrating the impact of model choice on disease spread over time. We offer policy-relevant interpretations of the modeling differences, particularly with respect to intervention timing and uncertainty in parameter estimation.

This paper is meticulously structured to offer a comprehensive understanding of our findings. Here is an overview of its organization: Section 2 presents key probabilistic tools and foundational concepts. Section 3 details the compartmental model and develops transition probability expressions for both stationary and non-stationary settings. Section 4 presents simulations comparing the two regimes. Section 5 concludes with a discussion of practical implications and directions for future work.

2. Preliminaries

Definition 2.1 (Binomial probability mass function [PMF])**.** *The binomial PMF of a binomial random variable X (that represents the number of successes in n independent Bernoulli trials, each with a probability of success p), also denoted $\mathcal{B}(k; n, p)$ is given by:*

$$\mathbb{P}(X = k) = \mathcal{B}(k; n, p) = \binom{n}{k} p^k (1-p)^{n-k},$$

where:

- *k is an integer representing the number of successes we are interested in,*
- $\binom{n}{k}$ *is the binomial coefficient representing the number of ways to choose k successes out of n trials,*
- p^k *is the probability of getting k successes,*
- $(1-p)^{n-k}$ *is the probability of getting $n-k$ failures.*

For a comprehensive background on the binomial distribution, we refer the reader to [30].

2.1. Chain-binomial models

The chain binomial models as a group assume that the generations of infectious are separated by a significant latent period and time of infectiousness. Thus, they are applicable to diseases in which cases or groups of cases are separated in time well enough to allow identification of successive generations of infection.

- Chain binomial models include the Reed-Frost model and the Greenwood model, which are two paradigms for modelling a disease spread as discrete-time Markov chains.
- They are called chain-binomial models because the transition probabilities are governed by binomial random variables.

In an SI model, we denote the generations of susceptible and infectious by S and I, respectively. Let N be the size of the population, S_t the number of susceptible at time t, I_t the number of infectious at time t, and $\mathbb{P}(I_t)$ the probability that a susceptible becomes infected at time t. We have:

- $S_0 + I_0 = N$: initial condition
- $S_{t+1} + I_{t+1} = S_t$ for times $t = 0, 1, \cdots$: the infectious at time t are removed from the process at time $t+1$.
- $S_t + \sum_{\tau=0}^{t} I_\tau = N, \quad t = 0, 1, \cdots$: at any time t, the number of susceptible plus the number of infectious since time 0 gives the total population.

- The number of infectious at time $t+1$ is given by the Binomial random variable of parameters S_t and $\mathbb{P}(I_t)$. The corresponding transition probability is given by the k^{th} component of the binomial PMF as in the following definitions.

Definition 2.2 (Greenwood model)**.** *In the Greenwood model, the transition probability is given by:*

$$\mathbb{P}(I_{t+1} = k|S_t = x, I_t = y) = \mathcal{B}(k; x, p) = \begin{cases} \binom{x}{k} p^k (1-p)^{x-k} & \text{if} \quad 0 \le k \le x \\ 0 \quad \text{if} \quad k > x, \end{cases} \tag{2.1}$$

where k is an integer and p is constant.

Remark 2.1. *The Greenwood model is obtained if, instead of transfer by close contact, the transfer of infection occurs by contact of susceptibles with infectious material that is relatively widely spread, so that p, is a constant not depending on the number y of infectious.*

Definition 2.3 (Reed-Frost model)**.** *In the Reed-Frost model, the transition probability is given by:*

$$\mathbb{P}(I_{t+1} = k|S_t = x, I_t = y) = \mathcal{B}(k; x, p(y)) = \begin{cases} \binom{x}{k} p(y)^k (1-p(y))^{x-k} & \text{if} \quad 0 \le k \le x \\ 0 \quad \text{if} \quad k > x, \end{cases} \tag{2.2}$$

where k is an integer and the probability any susceptible escapes being infected when there are y infectious is $1 - p(y) = (1 - p(1))^y$*, with* $p(1)$ *being the probability that a susceptible is infected by one given infectious, so that* $p(y) = 1 - (1 - p(1))^y$.

Remark 2.2. *The Reed-Frost model separates the probability of multiple contacts between a susceptible and one infectious from the probability of multiple contacts of a susceptible with different infectious.*

For additional information on chain-binomial models, we refer to [16, 31] and the references therein.

2.2. Markov decision process

Definition 2.4 (Markov decision process)**.** *A Markov decision process (MDP) is a tuple* $\langle \mathcal{S}, \mathcal{A}, \mathcal{P}, \mathcal{R}, \gamma \rangle$ *where:*

- γ *is a discount factor* $\gamma \in [0, 1]$
- $\mathcal{S}$ *is a finite set of states*
- $\mathcal{A}$ *is a finite set of actions*
- $\mathcal{P}$ *is a state transition probability matrix, with the transition from a state s to a successor state s′ defined by*
$$\mathcal{P}^a_{ss'} = \mathbb{P}[S_{t+1} = s'|S_t = s, A_t = a].$$
- $\mathcal{R}$ *is a reward function, with the reward for going from state s to state s′ while taking action a defined by*
$$R^a_s = \mathbb{E}[R_{t+1}|S_t = s, A_t = a].$$

This study focuses on transition probabilities, which are crucial in MDP analysis for quantifying the likelihood of transitioning between states and enabling accurate modeling and optimization of decision-making processes. For more information on MDP, we refer to [32].

3. A COVID-19 scenario

Moving forward, the model adopted will be a generalization of the Reed-Frost model. Indeed, Greenwood model seems not very convenient in our case, given that one of the protocol measure to control the spread of Covid-19 is social distancing, which helps avoid close contact with infectious individuals.

3.1. Model description

We are interested in the following model (Figure 1), that simulates the spread of COVID-19 through a population, divided into seven compartments, each representing a distinct stage of the disease.

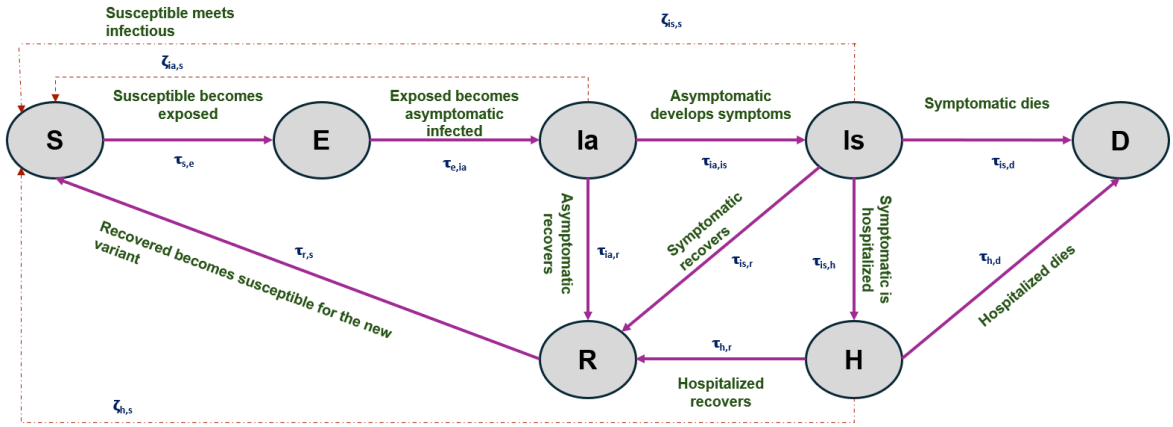

Figure 1. Dynamics of COVID-19 spread.

This model is typically represented using the following system of differential equations:

$$\begin{cases} \dfrac{dS}{dt} &= -\left(\zeta_{ia,s}I_a + \zeta_{is,s}I_s + \zeta_{h,s}H\right)\dfrac{S}{N} + \tau_{r,s}R \\ \dfrac{dE}{dt} &= \left(\zeta_{ia,s}I_a + \zeta_{is,s}I_s + \zeta_{h,s}H\right)\dfrac{S}{N} - \tau_{e,ia}E \\ \dfrac{dI_a}{dt} &= \tau_{e,ia}E - (\tau_{ia,is} + \tau_{ia,r})I_a \\ \dfrac{dI_s}{dt} &= \tau_{ia,is}I_a - (\tau_{is,r} + \tau_{is,h} + \tau_{is,d})I_s \\ \dfrac{dH}{dt} &= \tau_{is,h}I_s - (\tau_{h,r} + \tau_{h,d})H \\ \dfrac{dR}{dt} &= \tau_{is,r}I_s + \tau_{ia,r}I_a + \tau_{h,r}H - \tau_{r,s}R \\ \dfrac{dD}{dt} &= \tau_{h,d}H + \tau_{is,d}I_s \end{cases}, \tag{3.1}$$

where S, E, I_a, I_s, H, R, and D represent the states of susceptible, exposed, asymptomatic infected, symptomatic infected, hospitalized, recovered, and deceased individuals, respectively.

(i) Susceptible: Individuals who have not been infected with the virus but are at risk of becoming infected. They can move to the exposed compartment upon contact with an infected individual.
(ii) Exposed: Individuals who have been exposed to the virus and are in the incubation period. They are infected but not yet infectious. After the incubation period, they transition to the asymptomatic infected compartment.
(iii) Asymptomatic infected: Individuals who have been infected with the virus but do not show symptoms. They can still transmit the virus to susceptible individuals. After a certain period, they either recover or transition to the symptomatic infected compartment.
(iv) Symptomatic infected: Individuals who show symptoms of the infection. These individuals can be further categorized by the severity of symptoms. Depending on the severity and progression of the disease, they may either recover, be hospitalized, or eventually transition to the deceased compartment if the infection becomes fatal.
(v) Hospitalized: Individuals with severe symptoms who require intensive medical care. Their outcomes can vary: they may recover and move to the recovered compartment or, in severe cases, may not survive and move to the deceased compartment.
(vi) Recovered: Individuals who have recovered from the infection but their immunity can last only for some period. They cannot transmit the disease but are still at risk of infection.
(vii) Deceased: Individuals who have died due to the infection.

The transitions between compartments are governed by probabilities, which can be stationary (constant over time) or non-stationary (varying over time). These probabilities depend on various factors, including the disease's natural progression, intervention measures, and population behavior. The following probabilistic parameters are extremely important in studying the progression of the disease under consideration:

(a) $\tau_{s,e}$: probability for a susceptible individual to be exposed to the disease. It depends on the contact rate with infected individuals (asymptomatic, symptomatic or hospitalized), influenced by factors like social distancing, mask usage, vaccination rates, and so on.
(b) $\tau_{e,ia}$: probability for an individual to be infected by the disease without exhibiting symptoms. This can be influenced by demographic factors such as underlying health conditions.
(c) $\tau_{ia,r}$: probability for an individual to recover from asymptomatic infection. This probability is more likely based on the average duration of the infection.
(d) $\tau_{ia,is}$: probability for an individual to develop symptoms subsequent to previous asymptomatic infection.
(e) Symptomatic individuals can have different pathways: mild cases may recover without hospitalization, severe cases may require hospitalization, followed by recovery or death, fatal cases transition to deceased.

- $\tau_{is,h}$: probability for an individual to require hospitalization in the intensive care unit (ICU) due to complications arising from the symptoms of the disease.
- $\tau_{is,r}$: probability for an individual to successfully recover after exhibiting symptoms of the disease.

- $\tau_{is,d}$: probability for an individual to experience complications leading to death after displaying symptoms of the disease.

1. Hospitalized individuals may recover or succumb to the disease, with probabilities influenced by the quality of healthcare, the severity of the disease, and comorbidities.
   - $\tau_{h,d}$: probability for an individual to succumb to mortality following hospitalization in the ICU.
   - $\tau_{h,r}$: probability for an individual to successfully recover after being discharged from the ICU.
2. $\tau_{r,s}$: probability for an individual to become susceptible again after recovering from the disease.
3. $\zeta_{ia,s}$: probability to contract the infection in one meeting with an individual from I_a.
4. $\zeta_{is,s}$: probability to contract the infection in one meeting with an individual from I_s.
5. $\zeta_{h,s}$: probability to contract the infection in one meeting with an individual from H.

Remark 3.1. *We note that susceptible individuals become exposed by coming into contact with asymptomatically infectious, symptomatically infectious and hospitalized individuals.*

The only deterministic parameter, denoted N, represents the total population in the considered region.

3.2. Balanced system

Let's consider the following diagram, representing the transitions between individuals from a state to another.

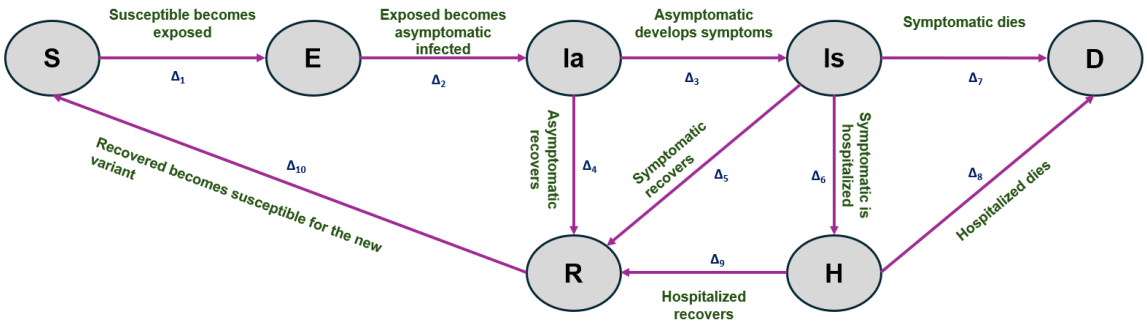

Figure 2. Balanced system showing compartment flows ($\triangle_i$).

The number of people in each state determines the evolution of the population and our system can be conveniently modelled as a discrete-time Markov chain. The state of the Markov chain will be associated with the septuple collected in the following vector

$$V_k = [|S|_k, |E|_k, |I_a|_k, |I_s|_k, |H|_k, |R|_k, |D|_k]^T, \tag{3.2}$$

where $|S|_k, |E|_k, |I_a|_k, |I_s|_k, |H|_k, |R|_k$, and $|D|_k$ represent the cardinalities of S, E, I_a, I_s, H, R, and D, respectively at stage k, with

$$|S|_k + |E|_k + |I_a|_k + |I_s|_k + |H|_k + |R|_k + |D|_k = N. \tag{3.3}$$

In the main section of this work, we will show how to compute the transition probability:

$$\mathbb{P}(V_{k+1} = v'|V_k = v),$$

where v and v' are respectively the state vector values before and after the transition, characterized by the following septuple represents

$$v' - v = [\Delta_{|S|}, \Delta_{|E|}, \Delta_{|I_a|}, \Delta_{|I_s|}, \Delta_{|H|}, \Delta_{|R|}, \Delta_{|D|}]^T.$$

Consider also the vector

$$\Delta = [\Delta_1, \Delta_2, \Delta_3, \Delta_4, \Delta_5, \Delta_6, \Delta_7, \Delta_8, \Delta_9, \Delta_{10}]^T, \tag{3.4}$$

where for each $i = 1, 2, \cdots, 10$, Δ_i represents the flow of individuals between different states, with $\Delta_i \in [0, N] \cap \mathbb{N}$ satisfying the following balanced equation:

$$\begin{cases} B_1: & \Delta_{|S|} &= \Delta_{10} - \Delta_1 \\ B_2: & \Delta_{|E|} &= \Delta_1 - \Delta_2 \\ B_3: & \Delta_{|I_a|} &= \Delta_2 - \Delta_3 - \Delta_4 \\ B_4: & \Delta_{|I_s|} &= \Delta_3 - \Delta_5 - \Delta_6 - \Delta_7 \\ B_5: & \Delta_{|D|} &= \Delta_7 + \Delta_8 \\ B_6: & \Delta_{|H|} &= \Delta_6 - \Delta_8 - \Delta_9 \\ B_7: & \Delta_{|R|} &= \Delta_4 + \Delta_5 + \Delta_9 - \Delta_{10}. \end{cases} \tag{3.5}$$

The flows from different states are subjected to the following constraints:

$$\begin{cases} |S|_k &\geq \Delta_1 \\ |E|_k &\geq \Delta_2 \\ |I_a|_k &\geq \Delta_3 + \Delta_4 \\ |I_s|_k &\geq \Delta_5 + \Delta_6 + \Delta_7 \\ |H|_k &\geq \Delta_8 + \Delta_9 \\ |R|_k &\geq \Delta_{10} \end{cases} \tag{3.6}$$

This ensures that the number of subjects remaining in the compartments S, E, I_a, I_s, H, and R at stage k remains non-negative.

Now, denoting by $l(\cdot)$ an assignment of variables: $\Delta_i = \delta_i$ for $i = 1, \cdots, 10$, let us introduce the following notations:

$$l_1 : (\Delta_1 = \delta_1)$$

is a function linking the variable Δ_1, defined via the balance equation B_1.

$$l_2 : (\Delta_2 = \delta_1 - \Delta_{|E|})$$

is a function linking the variable Δ_2, defined via l_1 and the balance equation B_2.

$$l_3 : (\Delta_3 = \delta_3, \Delta_4 = \delta_1 - \Delta_{|E|} - \delta_3 - \Delta_{|I_a|})$$

is a function linking the variables Δ_3 and Δ_4, defined via l_2 and the balance equation B_3.

$$l_4 : (\Delta_3 = \delta_3, \Delta_5 = \delta_5, \Delta_6 = \delta_6, \Delta_7 = \delta_3 - \delta_5 - \delta_6 - \Delta_{|I_s|})$$

is a function linking the variables $\Delta_3, \Delta_5, \Delta_6$ and Δ_7, defined via l_3 and the balance equation B_4.

$$l_5 : (\Delta_8 = \Delta_{|D|} - \delta_3 + \delta_5 + \delta_6 + \Delta_{|I_s|}, \Delta_9 = \delta_3 - \Delta_{|H|} - \Delta_{|D|} - \delta_5 - \Delta_{|I_s|})$$

is a function linking the variables Δ_8 and Δ_9, defined via l_4 and the balance equations B_5 and B_6.

$$l_6 : (\Delta_{10} = \delta_1 - \Delta_{|E|} - \Delta_{|I_a|} - \Delta_{|H|} - \Delta_{|D|} - \Delta_{|I_s|} - \Delta_{|R|})$$

is a function linking the variable Δ_{10}, defined via l_3, l_4, l_5 and the balance equation B_7.

In this study, the stationary and non-stationary transition probabilities will be critical for understanding how different interventions (e.g., vaccination, social distancing, hand sanitization, masking, testing and contact tracing, ICU, quarantine) affect the progression of the disease. By modeling these probabilities accurately, policymakers can predict outcomes under various scenarios and make informed decisions about resource allocation, healthcare planning, and economic impacts.

3.3. Stationary transition probabilities

Stationary transition probabilities assume that the probabilities of transitioning between states remain constant over time. For diseases where the transition rates are relatively stable over time, stationary models can provide reliable long-term predictions and insights. The models are often mathematically simpler and easier to analyze and allow for the use of established techniques and tools in epidemiological modeling. In such cases, disease dynamics, treatment effects, and other relevant factors are assumed to be stable and unchanging over time.

Let $\delta_i, \delta_j, \cdots$ represent the flow of individuals moving from one state. Consider $\mathcal{V}_{\delta_i,\delta_j,\cdots}$ as the event where the flow of individuals is such that δ_i transitions to a new state, δ_j transitions to another state, and so forth, as specified. That is, $\mathcal{V}_{\delta_i,\delta_j,\cdots}$ = "exactly δ_i individuals move to one state and δ_j individuals to another state and so on, given V_k", where V_k is defined by (3.7).

Theorem 3.1 (Probability of leaving states)**.**
Considering the septuple

$$V_k = [|S|_k, |E|_k, |I_a|_k, |I_s|_k, |H|_k, |R|_k, |D|_k]^T \tag{3.7}$$

where each entry represents the cardinality of the corresponding compartment at epoch k, the probabilities of leaving state S, E, I_a, I_s, H, and R are, respectively, given by the following items.

(i)

$$\mathbb{P}(\mathcal{V}_{\delta_1}) = \begin{cases} 0 & \text{if} \quad \delta_1 > |S|_k \\ \binom{|S|_k}{\delta_1} (\mathbb{P}(g_k))^{\delta_1} (1 - \mathbb{P}(g_k))^{|S|_k - \delta_1} & \text{if} \quad \delta_1 \leq |S|_k \end{cases}, \tag{3.8}$$

where

$$\mathbb{P}(g_k)_M = 1 - \left(1 - \frac{(\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s})(|E|_k + |I_a|_k + |I_s|_k + |H|_k)}{N - |D|_k}\right)^M.$$

with M representing the number of meeting and $g_k(\overline{g}_k)$ the event: "an individual (does not) become infected after meeting an infectious person, given V_k".

(ii)

$$\mathbb{P}(\mathcal{V}_{\delta_2}) = \begin{cases} 0 & \text{if} \quad \delta_2 > |E|_k \\ \binom{|E|_k}{\delta_2} \tau_{e,ia}^{\delta_2} (1 - \tau_{e,ia})^{|E|_k - \delta_2} & \text{if} \quad \delta_2 \leq |E|_k \end{cases} \tag{3.9}$$

(iii)

$$\mathbb{P}(\mathcal{V}_{\delta_3,\delta_4}) = \begin{cases} 0 & \text{if} \quad \delta_3 + \delta_4 > |I_a|_k \\ \mathcal{M}_{|I_a|_k,\delta_3,\delta_4} \tau_{ia,is}^{\delta_3} \tau_{ia,r}^{\delta_4} (1 - (\tau_{ia,is} + \tau_{ia,r}))^{|I_a|_k - (\delta_3 + \delta_4)} & \text{if} \quad \delta_3 + \delta_4 \leq |I_a|_k \end{cases} \tag{3.10}$$

(iv)

$$\mathbb{P}(\mathcal{V}_{\delta_5,\delta_6,\delta_7}) = \begin{cases} 0 \quad \text{if} \quad \delta_5 + \delta_6 + \delta_7 > |I_s|_k \\ \\ \mathcal{M}_{|I_s|_k,\delta_5,\delta_6,\delta_7} \tau_{is,r}^{\delta_5} \tau_{is,h}^{\delta_6} \tau_{is,d}^{\delta_7} (1 - (\tau_{is,r} + \tau_{is,h} + \tau_{is,d}))^{|I_s|_k - (\delta_5 + \delta_6 + \delta_7)} \\ \text{if} \quad \delta_5 + \delta_6 + \delta_7 \leq |I_s|_k \end{cases} \tag{3.11}$$

(v)

$$\mathbb{P}(\mathcal{V}_{\delta_8,\delta_9}) = \begin{cases} 0 & \text{if} \quad \delta_8 + \delta_9 > |H|_k \\ \mathcal{M}_{|H|_k,\delta_8,\delta_9} \tau_{h,d}^{\delta_8} \tau_{h,r}^{\delta_9} (1 - (\tau_{h,d} + \tau_{h,r}))^{|H|_k - (\delta_8 + \delta_9)} & \text{if} \quad \delta_8 + \delta_9 \leq |H|_k \end{cases} \tag{3.12}$$

(vi)

$$\mathbb{P}(\mathcal{V}_{\delta_{10}}) = 1, \tag{3.13}$$

considering that no individual gains immunity after recovering from the disease.

Proof.

(i) **Probability of leaving state** S

Let's consider the events:
$c_k(\overline{c}_k)$: "an individual meets one person and (does not) contract the infection, given V_k".
$m_k(\overline{m}_k)$: "an individual meets one person who is (not) infectious, given V_k".
$g_k(\overline{g}_k)$: "an individual (does not) become infected after meeting an infectious person, given V_k".
Suppose M = number of meetings allowed in each period.
We recall also that $\zeta_{ia,s}, \zeta_{is,s}, \zeta_{h,s}$ = probability to contract the infection in one meeting with an individual who is asymptomatic, symptomatic or hospitalized respectively.
We can write:

$$g_k = \{p \in S_k \wedge p \in E_{k+1}\},$$

where p is a generic person.
We have:

$$\mathbb{P}(g_k)_M = 1 - (\mathbb{P}(\overline{c}_k))^M$$

and

$$\overline{c}_k = \overline{m}_k \vee (m_k \wedge \overline{g}_k).$$

Then:

$$\begin{aligned}\mathbb{P}(\overline{c}_k) &= \mathbb{P}(\overline{m}_k \vee (m_k \wedge \overline{g}_k)) \\ &= \mathbb{P}(\overline{m}_k) + \mathbb{P}(m_k \wedge \overline{g}_k) \\ &= \mathbb{P}(\overline{m}_k) + \mathbb{P}(\overline{g}_k|m_k)\mathbb{P}(m_k).\end{aligned}$$

We know that

$$\mathbb{P}(\overline{g}_k|m_k) = 1 - (\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s}),$$

Hence,

$$\begin{aligned}\mathbb{P}(\overline{c}_k) &= \mathbb{P}(\overline{m}_k) + (1 - (\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s}))\mathbb{P}(m_k) \\ &= \frac{|S|_k + |R|_k}{N - |D|_k} + (1 - (\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s}))\frac{|E|_k + |I_a|_k + |I_s|_k + |H|_k}{N - |D|_k} \\ &= \frac{|S|_k + |R|_k + |E|_k + |I_a|_k + |I_s|_k + |H|_k}{N - |D|_k} \\ &\quad -(\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s})\frac{|E|_k + |I_a|_k + |I_s|_k + |H|_k}{N - |D|_k} \\ &= 1 - \frac{(\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s})(|E|_k + |I_a|_k + |I_s|_k + |H|_k)}{N - |D|_k}.\end{aligned}$$

Therefore,

$$\mathbb{P}(g_k)_M = 1 - \left(1 - \frac{(\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s})(|E|_k + |I_a|_k + |I_s|_k + |H|_k)}{N - |D|_k}\right)^M.$$

Now, let us consider the event $\mathcal{V}_{\delta_1}$: "exactly δ_1 susceptible individuals are exposed to the disease, given V_k".

- If $\delta_1 > |S|_k$, then $\mathbb{P}(\mathcal{V}_{\delta_1}) = 0$.
- If $\delta_1 \leq |S|_k$ we have:

$$\mathbb{P}(\mathcal{V}_{\delta_1}) = \mathcal{B}(\delta_1; |S|_k, \mathbb{P}(g_k)) = \binom{|S|_k}{\delta_1} (\mathbb{P}(g_k))^{\delta_1} (1 - \mathbb{P}(g_k))^{|S|_k - \delta_1},$$

where the binomial $\binom{|S|_k}{\delta_1}$ represents the possible combinations of δ_1 individuals out of $|S|_k$ and $\mathbb{P}(g_k)$ is the probability for an individual to become infected after meeting an infectious person (in one meeting).

(ii) **Probability of leaving state E**
Let's consider the event $\mathcal{V}_{\delta_2}$: "exactly δ_2 individuals are infected by the disease without exhibiting symptoms, given V_k".

- If $\delta_2 > |E|_k$, then $\mathbb{P}(\mathcal{V}_{\delta_2}) = 0$.
- If $\delta_2 \leq |E|_k$ we have:

$$\mathbb{P}(\mathcal{V}_{\delta_2}) = \mathcal{B}(\delta_2; |E|_k, \tau_{e,ia}) = \binom{|E|_k}{\delta_2} \tau_{e,ia}^{\delta_2} (1 - \tau_{e,ia})^{|E|_k - \delta_2}.$$

(iii) **Probability of leaving state I_a**
Let's consider the event $\mathcal{V}_{\delta_3,\delta_4}$: "exactly δ_3 individuals develop symptoms subsequent to previous asymptomatic infection and δ_4 individuals recover from asymptomatic infection, given V_k".

- If $\delta_3 + \delta_4 > |I_a|_k$, then $\mathbb{P}(\mathcal{V}_{\delta_3,\delta_4}) = 0$.
- If $\delta_3 + \delta_4 \leq |I_a|_k$ we have:

$$\mathbb{P}(\mathcal{V}_{\delta_3,\delta_4}) = \mathcal{M}_{|I_a|_k,\delta_3,\delta_4} \tau_{ia,is}^{\delta_3} \tau_{ia,r}^{\delta_4} (1 - (\tau_{ia,is} + \tau_{ia,r}))^{|I_a|_k - (\delta_3 + \delta_4)},$$

where the multinomial coefficient

$$\mathcal{M}_{|I_a|_k,\delta_3,\delta_4} = \binom{|I_a|_k}{\delta_3, \delta_4, |I_a|_k - (\delta_3 + \delta_4)}$$

represents the possible combinations of $\delta_3 + \delta_4$ individuals out of $|I_a|_k$.

(iv) **Probability of leaving state I_s**
Let's consider the event $\mathcal{V}_{\delta_5,\delta_6,\delta_7}$: "exactly δ_5 individuals successfully recover after exhibiting symptoms and δ_6 individuals require ICU hospitalization due to complications arising from the symptoms and δ_7 individuals experience complications leading to death after displaying symptoms of the disease, given V_k".

- If $\delta_5 + \delta_6 + \delta_7 > |I_s|_k$, then $\mathbb{P}(\mathcal{V}_{\delta_5,\delta_6,\delta_7}) = 0$.
- If $\delta_5 + \delta_6 + \delta_7 \leq |I_s|_k$ we have:

$$\mathbb{P}(\mathcal{V}_{\delta_5,\delta_6,\delta_7}) = \mathcal{M}_{|I_s|_k,\delta_5,\delta_6,\delta_7} \tau_{is,r}^{\delta_5} \tau_{is,h}^{\delta_6} \tau_{is,d}^{\delta_7} (1 - (\tau_{is,r} + \tau_{is,h} + \tau_{is,d}))^{|I_s|_k - (\delta_5 + \delta_6 + \delta_7)}.$$

(v) **Probability of leaving state H**
Let's consider the event $\mathcal{V}_{\delta_8,\delta_9}$: "exactly δ_8 individuals succumb to mortality following hospitalization in the ICU and δ_9 individuals successfully recover after being discharged from the ICU, given V_k".

- If $\delta_8 + \delta_9 > |H|_k$, then $\mathbb{P}(\mathcal{V}_{\delta_8,\delta_9}) = 0$.
- If $\delta_8 + \delta_9 \leq |H|_k$ we have:

$$\mathbb{P}(\mathcal{V}_{\delta_8,\delta_9}) = \mathcal{M}_{|H|_k,\delta_8,\delta_9} \tau_{h,d}^{\delta_8} \tau_{h,r}^{\delta_9} (1 - (\tau_{h,d} + \tau_{h,r}))^{|H|_k - (\delta_8 + \delta_9)}.$$

(vi) **Probability of leaving state** R
Let's consider the event $\mathcal{V}_{\delta_{10}}$: "exactly δ_{10} individuals become susceptible again after recovering from the disease, given V_k". Given that no individual gains immunity after recovering from the disease, there is a hundred percent likelihood of becoming susceptible again. Therefore, $\mathbb{P}(\mathcal{V}_\delta) = \tau_{r,s} = 1$.

This completes the proof of Theorem 3.1. □

At this point, we have all we need to proceed with the different transition probabilities.

Theorem 3.2 (Transition probabilities)**.**
The transition probabilities from a state to another are given by the following, where

$$\beta = 1 - \tau_{is,r} - \tau_{is,h} - \tau_{is,d}, \quad Q_1 = |I_a|_k - \delta_3 - \delta_4, \text{ and } Q_2 = |I_s|_k - \delta_5 - \delta_6 - \delta_7.$$

(a) ***Transition probability from state*** S ***to state*** E

$$\begin{aligned}\mathbb{P}(E|S) \quad = \quad & \binom{|S|_k}{\delta_1}\left(\frac{(\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s})(|E|_k + |I_a|_k + |I_s|_k + |H|_k)}{N - |D|_k}\right)^{\delta_1} \\ & \left(1 - \frac{(\zeta_{ia,s} + \zeta_{is,s} + \zeta_{h,s})(|E|_k + |I_a|_k + |I_s|_k + |H|_k)}{N - |D|_k}\right)^{|S|_k - \delta_1}\end{aligned} \tag{3.14}$$

(b) ***Transition probability from state*** E ***to state*** I_a

$$\mathbb{P}(I_a|E) = \binom{|E|_k}{\delta_2}\tau_{e,ia}^{\delta_2}(1 - \tau_{e,ia})^{|E|_k - \delta_2}. \tag{3.15}$$

(c) ***Transition probability from state*** I_a ***to state*** I_s

$$\mathbb{P}(I_s \mid I_a) = \frac{\displaystyle\sum_{\delta_4=0}^{|I_a|_k - \delta_3} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1}\tau_{ia,is}^{\delta_3}\tau_{ia,r}^{\delta_4}(1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1}}{\displaystyle\sum_{\delta_3=0}^{|I_a|_k}\sum_{\delta_4=0}^{|I_a|_k - \delta_3} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1}\tau_{ia,is}^{\delta_3}\tau_{ia,r}^{\delta_4}(1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1}}. \tag{3.16}$$

(d) ***Transition probability from state*** I_a ***to state*** R

$$\mathbb{P}(R \mid I_a) = \frac{\displaystyle\sum_{\delta_3=0}^{|I_a|_k - \delta_4} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1}\tau_{ia,is}^{\delta_3}\tau_{ia,r}^{\delta_4}(1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1}}{\displaystyle\sum_{\delta_4=0}^{|I_a|_k}\sum_{\delta_3=0}^{|I_a|_k - \delta_4} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1}\tau_{ia,is}^{\delta_3}\tau_{ia,r}^{\delta_4}(1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1}}. \tag{3.17}$$

(e) ***Transition probability from state I_s to state R***

$$\mathbb{P}(R|I_s) = \frac{\sum_{\delta_6=0}^{|I_s|_k-\delta_5}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}^{\delta_5}\tau_{is,h}^{\delta_6}\tau_{is,d}^{\delta_7}\beta^{Q_2}}{\sum_{\delta_5=0}^{|I_s|_k}\sum_{\delta_6=0}^{|I_s|_k-\delta_5}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}^{\delta_5}\tau_{is,h}^{\delta_6}\tau_{is,d}^{\delta_7}\beta^{Q_2}}. \tag{3.18}$$

(f) ***Transition probability from state I_s to state H***

$$\mathbb{P}(H|I_s) = \frac{\sum_{\delta_5=0}^{|I_s|_k-\delta_6}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}^{\delta_5}\tau_{is,h}^{\delta_6}\tau_{is,d}^{\delta_7}\beta^{Q_2}}{\sum_{\delta_6=0}^{|I_s|_k}\sum_{\delta_5=0}^{|I_s|_k-\delta_6}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}^{\delta_5}\tau_{is,h}^{\delta_6}\tau_{is,d}^{\delta_7}\beta^{Q_2}}. \tag{3.19}$$

(g) ***Transition probability from state I_s to state D***

$$\mathbb{P}(D|I_s) = \frac{\sum_{\delta_5=0}^{|I_s|_k-\delta_7}\sum_{\delta_6=0}^{|I_s|_k-\delta_5-\delta_7}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}^{\delta_5}\tau_{is,h}^{\delta_6}\tau_{is,d}^{\delta_7}\beta^{Q_2}}{\sum_{\delta_7=0}^{|I_s|_k}\sum_{\delta_5=0}^{|I_s|_k-\delta_7}\sum_{\delta_6=0}^{|I_s|_k-\delta_5-\delta_7}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}^{\delta_5}\tau_{is,h}^{\delta_6}\tau_{is,d}^{\delta_7}\beta^{Q_2}}. \tag{3.20}$$

(h) ***Transition probability from state H to state D***

$$\mathbb{P}(D|H) = \frac{\sum_{\delta_9=0}^{|H|_k-\delta_8}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}^{\delta_9}\tau_{h,d}^{\delta_8}(1-\tau_{h,r}-\tau_{h,d})^{|H|_k-\delta_8-\delta_9}}{\sum_{\delta_8=0}^{|H|_k}\sum_{\delta_9=0}^{|H|_k-\delta_8}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}^{\delta_9}\tau_{h,d}^{\delta_8}(1-\tau_{h,r}-\tau_{h,d})^{|H|_k-\delta_8-\delta_9}}. \tag{3.21}$$

(i) ***Transition probability from state H to state R***

$$\mathbb{P}(R|H) = \frac{\sum_{\delta_8=0}^{|H|_k-\delta_9}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}^{\delta_9}\tau_{h,d}^{\delta_8}(1-\tau_{h,r}-\tau_{h,d})^{|H|_k-\delta_8-\delta_9}}{\sum_{\delta_9=0}^{|H|_k}\sum_{\delta_8=0}^{|H|_k-\delta_9}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}^{\delta_9}\tau_{h,d}^{\delta_8}(1-\tau_{h,r}-\tau_{h,d})^{|H|_k-\delta_8-\delta_9}}. \tag{3.22}$$

(j) ***Transition probability from state R to state S***

$$\mathbb{P}(S|R) = 1, \tag{3.23}$$

considering that no individual gains immunity after recovering from the disease.

Proof.

(a) The probability of landing in state E after leaving state S is as follows:

$$\begin{aligned}\mathbb{P}(E|S) &= \mathbb{P}(\mathcal{V}_{\delta_1}) \\ &= \mathcal{B}(\delta_1; |S|_k, \mathbb{P}(g_k)) \\ &= \binom{|S|_k}{\delta_1} (\mathbb{P}(g_k))^{\delta_1} (1 - \mathbb{P}(g_k))^{|S|_k - \delta_1}.\end{aligned}$$

Therefore, the transition probability from state S to state E is given by (3.14).

(b) The probability of landing in state I_a after leaving state E is as follows:

$$\begin{aligned}\mathbb{P}(I_a|E) &= \mathbb{P}(\mathcal{V}_{\delta_2}) \\ &= \mathcal{B}(\delta_2; |E|_k, \tau_{e,ia}).\end{aligned}$$

Therefore, the transition probability from state E to state I_a is given by (3.15).

(c) The probability of landing in state I_s after leaving state I_a is as follows:

$$\mathbb{P}(I_s|I_a) = \frac{\mathbb{P}(I_s \cap I_a)}{\mathbb{P}(I_a)},$$

where

$$\mathbb{P}(I_s \cap I_a) = \sum_{\delta_4=0}^{|I_a|_k - \delta_3} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1} \tau_{ia,is}^{\delta_3} \tau_{ia,r}^{\delta_4} (1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1} \tag{3.24}$$

is obtained by summing over all possible values of δ_4, and

$$\mathbb{P}(I_a) = \sum_{\delta_3=0}^{|I_a|_k} \sum_{\delta_4=0}^{|I_a|_k - \delta_3} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1} \tau_{ia,is}^{\delta_3} \tau_{ia,r}^{\delta_4} (1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1}. \tag{3.25}$$

Therefore, the transition probability from state I_a to state I_s is given by (3.16).

(d) The probability of landing in state R after leaving state I_a is as follows:

$$\mathbb{P}(R|I_a) = \frac{\mathbb{P}(R \cap I_a)}{\mathbb{P}(I_a)},$$

where

$$\mathbb{P}(R \cap I_a) = \sum_{\delta_3=0}^{|I_a|_k - \delta_4} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1} \tau_{ia,is}^{\delta_3} \tau_{ia,r}^{\delta_4} (1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1} \tag{3.26}$$

is obtained by summing over all possible values of δ_3, and

$$\mathbb{P}(I_a) = \sum_{\delta_4=0}^{|I_a|_k} \sum_{\delta_3=0}^{|I_a|_k - \delta_4} \binom{|I_a|_k}{\delta_3, \delta_4, Q_1} \tau_{ia,is}^{\delta_3} \tau_{ia,r}^{\delta_4} (1 - \tau_{ia,is} - \tau_{ia,r})^{Q_1}. \tag{3.27}$$

Therefore, the transition probability from state I_a to state R is given by (3.17).

Remark 3.2. *The transition probabilities* (3.18)-(3.22) *are obtained following the same reasoning as in Part (c) and (d).*

Remark 3.3. *Given that no individual gains immunity after recovering from the disease, there is a one-hundred percent chance of landing in S after leaving R. Hence,*

$$\mathbb{P}(S|R) = 1.$$

This completes the proof of Theorem 3.2. □

Stationary transition probabilities assume that the process reaches a stable equilibrium where the disease dynamics are predictable. This model is not a good fit for predicting the long term dynamics of Covid-19 due to ongoing uncertainties, such as the evolution of the virus with new variants and changes in viral behavior; the public health policies with implementation, adjustment and measures continuously influence disease dynamics; the dynamics of immunity, including the duration of vaccine-induced immunity and natural immunity, are evolving, affecting disease spread and transition rates. Therefore, the need of non-stationary transition probabilities for our study.

3.4. Non-stationary transition probabilities

In contrast to stationary transition probabilities, non-stationary transition probabilities change over time. This means that the likelihood of moving from one state to another can vary due to factors such as time, evolving disease dynamics, intervention strategies, and seasonal effects. In this study, we focus on time as the primary factor influencing our non-stationary transition probabilities. Specifically, we model the various probabilistic parameters as functions of time to achieve a more accurate and realistic representation of disease dynamics and the impact of interventions. In what follows,

$$\beta(w) = 1 - \tau_{is,r}(w) - \tau_{is,h}(w) - \tau_{is,d}(w).$$

(a) Transition probability from state S to state E
The probability of landing in state E after leaving state S is given by:

$$\begin{aligned}\mathbb{P}(E|S,w) = &\binom{|S|_k}{\delta_1}\left(\frac{(\zeta_{ia,s}(w)+\zeta_{is,s}(w)+\zeta_{h,s}(w))(|E|_k+|I_a|_k+|I_s|_k+|H|_k)}{N-|D|_k}\right)^{\delta_1}\\ &\left(1-\frac{(\zeta_{ia,s}(w)+\zeta_{is,s}(w)+\zeta_{h,s}(w))(|E|_k+|I_a|_k+|I_s|_k+|H|_k)}{N-|D|_k}\right)^{|S|_k-\delta_1},\end{aligned} \tag{3.28}$$

where

$$\zeta_{ia,s}(w) = \zeta^0_{ia,s} + a_1 w e^{-kw}, \tag{3.29}$$

and $\zeta_{is,s}(w)$, $\zeta_{h,s}(w)$ are defined as in (3.29), with $\zeta^0_{ia,s}$ being the initial contact rate between a susceptible and an asymptomatic individual, a the constant indicating how high $\zeta_{ia,s}$ rises, and k the rate of decrease. The function defined in (3.29) was borrowed from Ethan Kigundu's research work, former Summer Academy of Actuarial and Mathematical Sciences (SAAMS) scholar from the 2024 cohort at Morgan State University.

(b) Transition probability from state E to state I_a
The probability of landing in state I_a after leaving state E is given by:

$$\mathbb{P}(I_a|E,w) = \binom{|E|_k}{\delta_2} \tau_{e,ia}^{\delta_2}(w)(1-\tau_{e,ia}(w))^{|E|_k-\delta_2}, \tag{3.30}$$

where $\tau_{e,ia}(w)$ is defined as in (3.29).

(c) Transition probability from state I_a to state I_s
The probability of landing in state I_s after leaving state I_a is given by:

$$\mathbb{P}(I_s \mid I_a,w) = \frac{\sum_{\delta_4=0}^{|I_a|_k-\delta_3} \binom{|I_a|_k}{\delta_3,\delta_4,Q_1} \tau_{ia,is}(w)^{\delta_3}\tau_{ia,r}(w)^{\delta_4}(1-\tau_{ia,is}(w)-\tau_{ia,r}(w))^{Q_1}}{\sum_{\delta_3=0}^{|I_a|_k}\sum_{\delta_4=0}^{|I_a|_k-\delta_3} \binom{|I_a|_k}{\delta_3,\delta_4,Q_1} \tau_{ia,is}(w)^{\delta_3}\tau_{ia,r}(w)^{\delta_4}(1-\tau_{ia,is}(w)-\tau_{ia,r}(w))^{Q_1}}, \tag{3.31}$$

where $\tau_{ia,is}(w)$ is defined as in (3.29) and

$$\tau_{ia,r}(w) = \frac{\tau_{ia,r}^{max}}{1+e^{-\beta_2(w-w_0)}} \tag{3.32}$$

with w_0 representing the time at the inflection point, β_2 the growth rate and $\tau_{ia,r}^{max}$ the maximum possible value of $\tau_{ia,r}$.

(d) Transition probability from state I_a to state R
The probability of landing in state R after leaving state I_a is given by:

$$\mathbb{P}(R \mid I_a,w) = \frac{\sum_{\delta_3=0}^{|I_a|_k-\delta_4} \binom{|I_a|_k}{\delta_3,\delta_4,Q_1} \tau_{ia,is}(w)^{\delta_3}\tau_{ia,r}(w)^{\delta_4}(1-\tau_{ia,is}(w)-\tau_{ia,r}(w))^{Q_1}}{\sum_{\delta_4=0}^{|I_a|_k}\sum_{\delta_3=0}^{|I_a|_k-\delta_4} \binom{|I_a|_k}{\delta_3,\delta_4,Q_1} \tau_{ia,is}(w)^{\delta_3}\tau_{ia,r}(w)^{\delta_4}(1-\tau_{ia,is}(w)-\tau_{ia,r}(w))^{Q_1}}, \tag{3.33}$$

where $\tau_{ia,is}(w)$ and $\tau_{ia,r}(w)$ are defined as in (3.29) and (3.32), respectively.

(e) Transition probability from state I_s to state R
The probability of landing in state R after leaving state I_s is given by:

$$\mathbb{P}(R|I_s,w) = \frac{\sum_{\delta_6=0}^{|I_s|_k-\delta_5}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6} \binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2} \tau_{is,r}(w)^{\delta_5}\tau_{is,h}(w)^{\delta_6}\tau_{is,d}(w)^{\delta_7}\beta(w)^{Q_2}}{\sum_{\delta_5=0}^{|I_s|_k}\sum_{\delta_6=0}^{|I_s|_k-\delta_5}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6} \binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2} \tau_{is,r}(w)^{\delta_5}\tau_{is,h}(w)^{\delta_6}\tau_{is,d}(w)^{\delta_7}\beta(w)^{Q_2}} \tag{3.34}$$

where $\tau_{is,r}(w)$ is defined as in (3.32) and $\tau_{is,h}(w)$, $\tau_{is,d}(w)$ are defined as in (3.29).

(f) Transition probability from state I_s to state H
The probability of landing in state H after leaving state I_s is given by:

$$\mathbb{P}(H|I_s,w)=\frac{\sum_{\delta_5=0}^{|I_s|_k-\delta_6}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}(w)^{\delta_5}\tau_{is,h}(w)^{\delta_6}\tau_{is,d}(w)^{\delta_7}\beta(w)^{Q_2}}{\sum_{\delta_6=0}^{|I_s|_k}\sum_{\delta_5=0}^{|I_s|_k-\delta_6}\sum_{\delta_7=0}^{|I_s|_k-\delta_5-\delta_6}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}(w)^{\delta_5}\tau_{is,h}(w)^{\delta_6}\tau_{is,d}(w)^{\delta_7}\beta(w)^{Q_2}} \tag{3.35}$$

where $\tau_{is,r}(w)$ is defined as in (3.32) and $\tau_{is,h}(w)$, $\tau_{is,d}(w)$ are defined as in (3.29).

(g) Transition probability from state I_s to state D

The probability of landing in state D after leaving state I_s is given by:

$$\mathbb{P}(D|I_s,w)=\frac{\sum_{\delta_5=0}^{|I_s|_k-\delta_7}\sum_{\delta_6=0}^{|I_s|_k-\delta_5-\delta_7}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}(w)^{\delta_5}\tau_{is,h}(w)^{\delta_6}\tau_{is,d}(w)^{\delta_7}\beta(w)^{Q_2}}{\sum_{\delta_7=0}^{|I_s|_k}\sum_{\delta_5=0}^{|I_s|_k-\delta_7}\sum_{\delta_6=0}^{|I_s|_k-\delta_5-\delta_7}\binom{|I_s|_k}{\delta_5,\delta_6,\delta_7,Q_2}\tau_{is,r}(w)^{\delta_5}\tau_{is,h}(w)^{\delta_6}\tau_{is,d}(w)^{\delta_7}\beta(w)^{Q_2}} \tag{3.36}$$

where $\tau_{is,r}(w)$ is defined as in (3.32) and $\tau_{is,h}(w)$, $\tau_{is,d}(w)$ are defined as in (3.29).

(h) Transition probability from state H to state D

The probability of landing in state D after leaving state H is given by:

$$\mathbb{P}(D|H,w)=\frac{\sum_{\delta_9=0}^{|H|_k-\delta_8}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}(w)^{\delta_9}\tau_{h,d}(w)^{\delta_8}(1-\tau_{h,r}(w)-\tau_{h,d}(w))^{|H|_k-\delta_8-\delta_9}}{\sum_{\delta_8=0}^{|H|_k}\sum_{\delta_9=0}^{|H|_k-\delta_8}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}(w)^{\delta_9}\tau_{h,d}(w)^{\delta_8}(1-\tau_{h,r}(w)-\tau_{h,d}(w))^{|H|_k-\delta_8-\delta_9}} \tag{3.37}$$

where $\tau_{h,d}(w)$ is defined as in (3.29) and

$$\tau_{h,r}(w)=\tau_{h,r}^0-a_2we^{-kw}, \tag{3.38}$$

with $\tau_{h,r}^0$ being the initial probability of recovering after being discharged from ICU, a the constant indicating how high $\tau_{h,r}$ rises, k the rate of decrease.

(i) Transition probability from state H to state R

The probability of landing in state R after leaving state H is given by:

$$\mathbb{P}(R|H,w)=\frac{\sum_{\delta_8=0}^{|H|_k-\delta_9}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}(w)^{\delta_9}\tau_{h,d}(w)^{\delta_8}(1-\tau_{h,r}(w)-\tau_{h,d}(w))^{|H|_k-\delta_8-\delta_9}}{\sum_{\delta_9=0}^{|H|_k}\sum_{\delta_8=0}^{|H|_k-\delta_9}\binom{|H|_k}{\delta_8,\delta_9,|H|_k-\delta_8-\delta_9}\tau_{h,r}(w)^{\delta_9}\tau_{h,d}(w)^{\delta_8}(1-\tau_{h,r}(w)-\tau_{h,d}(w))^{|H|_k-\delta_8-\delta_9}} \tag{3.39}$$

where $\tau_{h,d}(w)$ and $\tau_{h,r}(w)$ are defined by (3.29) and (3.38), respectively.

(j) Transition probability from state R to state S
The probability of landing in state S after leaving state R is given by:

$$\mathbb{P}(S|R, w) = 1, \tag{3.40}$$

since no individual gains immunity after recovering from the disease.

4. COVID-19 dynamics over 365 days

Consider a population of 6,500,000 individuals, initially distributed as shown in Table 1. The constants within the probabilistic functions have also been considered in Table 2, to enable the execution of the dynamic simulation.

Table 1. Initial conditions of the state variables.

Initial conditions	Values
$S(0)$	5654000
$E(0)$	817097
$I_a(0)$	22750
$I_s(0)$	4550
$H(0)$	617
$R(0)$	357
$D(0)$	629

Table 2. Constants within the probabilistic functions.

constants	Values
w_0	0
$\tau_{r,s}(w)$	1
β_2	0.5
k	5
a_1	1
a_2	2
$\zeta^0_{ia,s}$	0.15
$\tau^0_{h,r}$	0.15
$\tau^{max}_{ia,r}$	0.04
$\tau^{max}_{is,r}$	0.08

The transition probabilities are adjusted by the intervention intensity w ($0.1 \leq w \leq 9$), which represents the level of external measures (e.g., social distancing, testing, hospitalization, $\cdots$) that shape the non-stationary transition probabilities and eventually impact the dynamic of each compartment over time (in days). Each value of w specifies distinct transitions (e.g. $\tau_{e,ia}(w)$, $\tau_{ia,is}(w)$, $\tau_{is,h}(w)$, $\cdots$), leading to different trajectories.

To illustrate the scientific soundness and practical feasibility of the model, a compilation of 100 runs was performed, clearly demonstrating how the disease evolves over time under varying intervention scenarios: $[0.1 \leq w \leq 2.17]$, $[2.17 \leq w \leq 4.77]$, $[4.77 \leq w \leq 9]$. Selected trajectories for specific values of w (0.1, 1.63, 2.17, 2.35, 4.77, and 8.91) highlight how the interventions influence disease progression over a 360-day period.

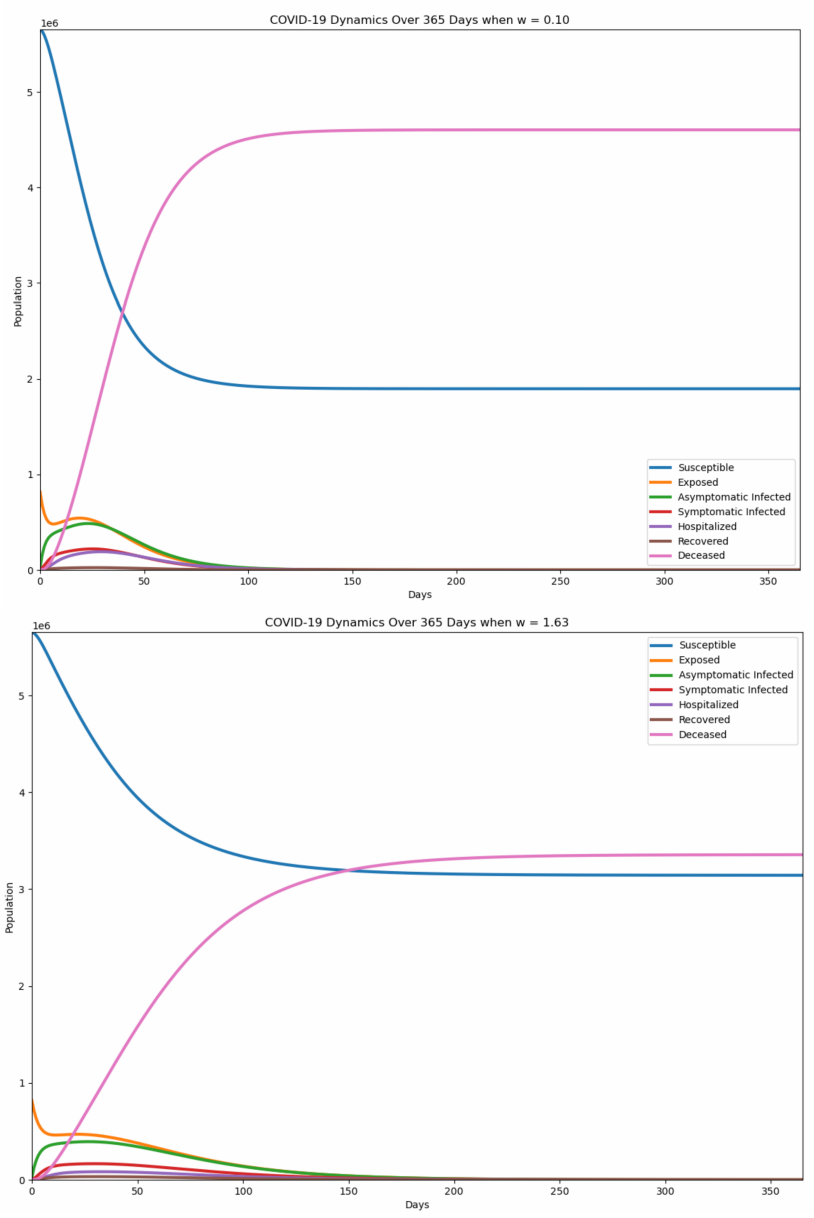

Figure 3. COVID-19 dynamics for low values of the control parameter $0.1 \leq w \leq 2.17$: sharp increase in deceased population and rapid decrease in the susceptible.

- **Observation 1 (Figure 3):**
  With low values of w, the combination of high effective transmission and relative slow effective recovery leads to a sharp increase in the deceased population and a rapid decrease in the susceptible population. In early days, the number of susceptibles is higher than the number of deceased,

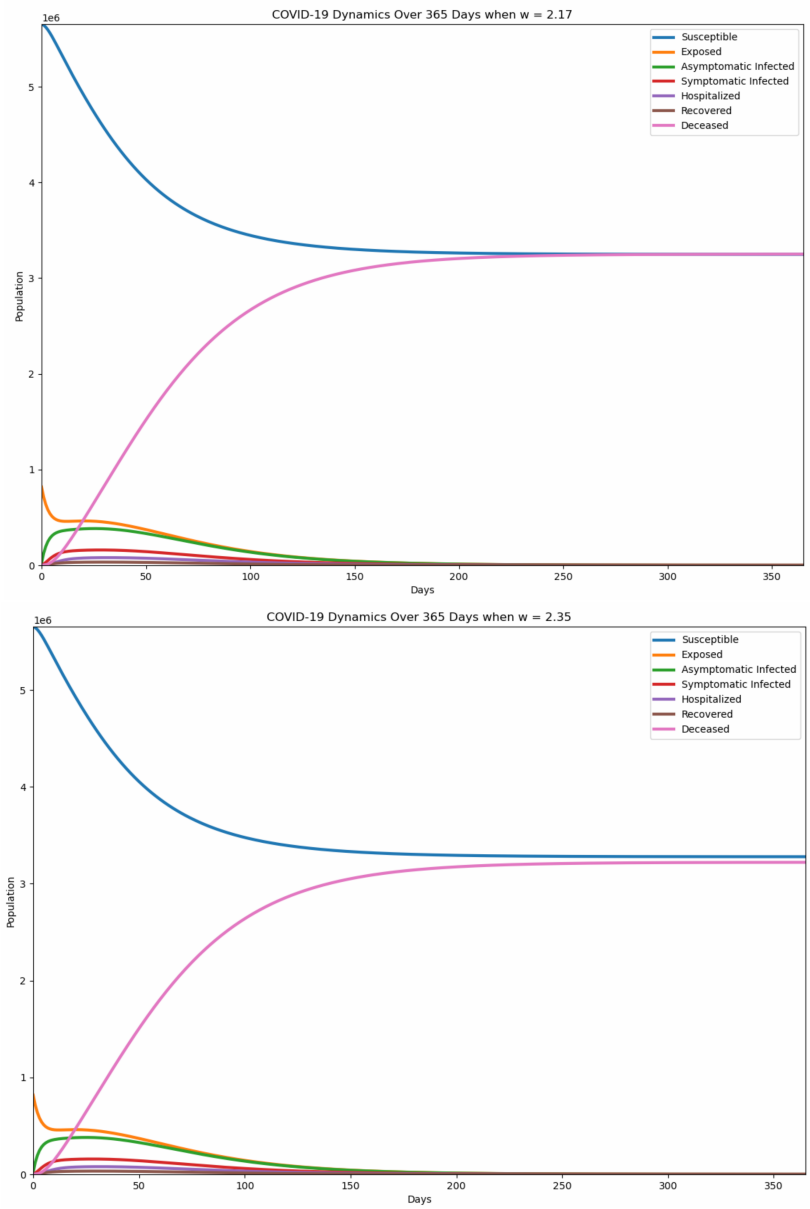

Figure 4. COVID-19 dynamics for moderate values of the control parameter $2.17 \leq w \leq 4.77$: balanced progression and approaching stabilization of all compartments over time (days).

but as the disease progresses, the two populations overlap, and the number of deceased eventually surpasses that of the susceptibles, indicating high lethality and a prolonged impact of the disease. This rapid decline in susceptibles and sharp rise in deceased create a cascading effect on intermediate states, such as the infected and recovered populations. The reduction in susceptibles decreases the pool of individuals available for new infections, while the increase in deceased reduces the number of individuals who can transition to other compartments.

- **Observation 2 (Figure 4):** For moderate values of w, the susceptible population remains consistently larger than the deceased population, due to a slower increase and decrease in the deceased

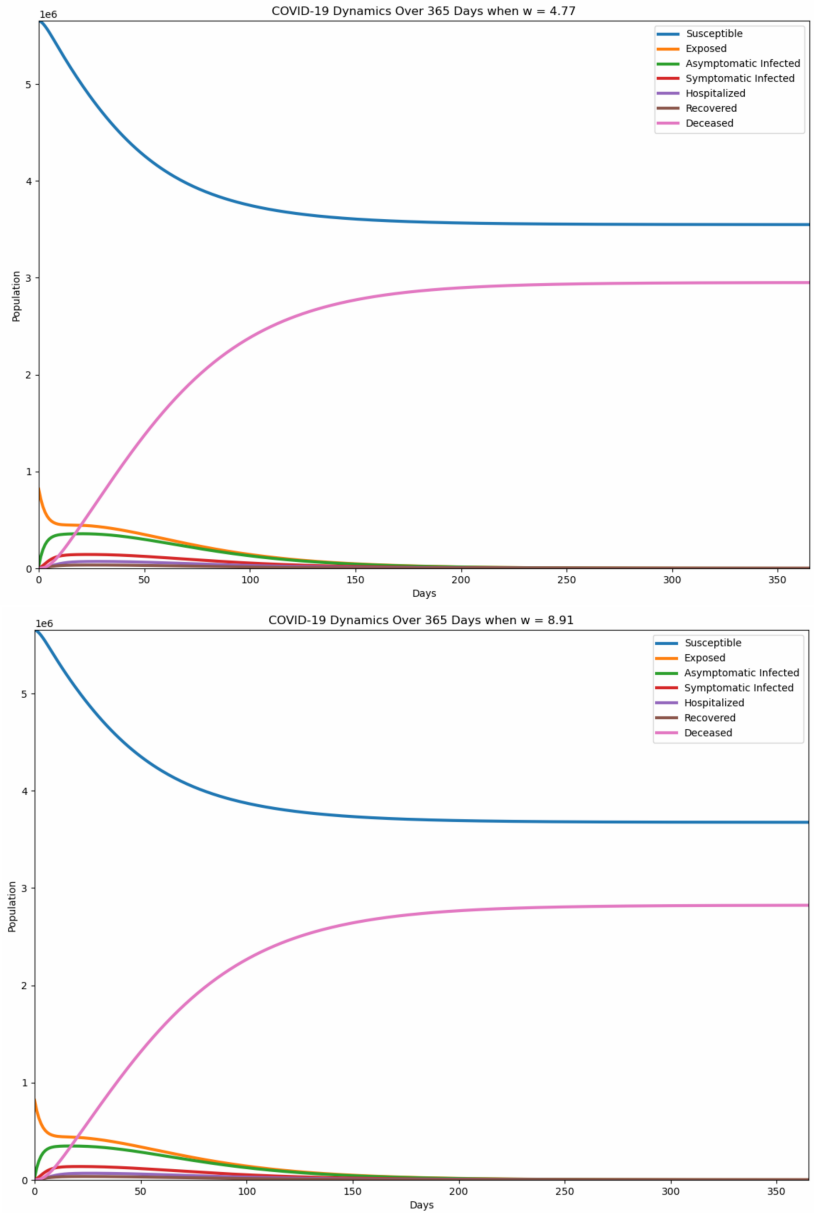

Figure 5. COVID-19 dynamics for high values of the control parameter [$4.77 \leq w \leq 9$]: the overall system exhibits equilibrium.

and susceptible compartments, respectively. This phase signifies a more controlled epidemic progression. By approximately day 250, trajectories approach a steady state, with negligible day-by-day variation across compartments. Both the susceptible and deceased populations balance, indicating that the epidemic has eased and the populations are no longer undergoing significant changes.

- **Observation 3 (Figure 5):** Finally, for higher values of w, the sizes of the susceptible and deceased populations settle, indicating that the system has reached an equilibrium with no significant new infections or deaths occurring. In this range, the number of susceptibles remains higher than the number of deceased, with negligible variation in intermediate compartments such as the

infected and recovered populations, and leading to a long-term steady state in the epidemic's dynamics.

Data sources

The values in Table 1 were calibrated for a synthetic population of $N = 6.5 \times 10^6$, using proportion consistent with reported epidemiological estimates for COVID-19 during early pandemic phase (see [1, 12, 14]). Stationary parameters (see [11]) are fixed over time providing a baseline scenario, whereas non-stationary parameters follow logistic or exponential forms to mimic intervention effects and behavioral changes [16, 23]. This semi-empirical strategy allows the model to remain biologically interpretable, enabling a comparative study of stationary and non-stationary assumptions without relying on case-specific trial data.

5. Concluding remarks

This study develops transition probability models using the chain-binomial approach, tailored for MDPs with non-stationary transition probabilities. Incorporating non-stationary transition probabilities offers significant advantages in accurately capturing the evolving dynamics of COVID-19. Unlike stationary models, which assume constant transition probabilities, non-stationary models account for changes over time due to factors such as evolving virus variants, seasonal variations, and public health interventions. By reflecting these time-dependent changes, non-stationary transition probabilities provide a more nuanced understanding of disease progression and help policymakers adapt strategies effectively as conditions evolve.

The simulations demonstrate that the dynamics of Covid-19 are highly sensitive to the control parameter w, which represents intervention intensity with the following key regimes:

- When $w \in [0.1, 2.17]$, the disease spread rapidly with quick decrease of susceptibles and sharp increase of deceased. The susceptible and deceased trajectories overlap earlier for low values of w.
- When $w \in [2.17, 4.77]$, the disease progression slows down, showing the effect of effective interventions.
- When $w \in [4.77, 9]$, the system approaches a steady state, with higher values of w ($w \geq 9$) providing only marginal additional benefit.

Our findings emphasize that while stationary models provide a stable baseline for evaluating long-term interventions and resource allocation, they may be inadequate in scenarios where disease patterns fluctuate over time. In contrast, the non-stationary models, built upon the chain-binomial framework, offer the adaptability necessary for real-time forecasting and timely policy adjustments. This approach enables more accurate modeling of the pandemic's dynamics and improves the efficacy of response strategies. This ensures that policies remain effective as circumstances shift, optimizing resource allocation and potentially leading to cost savings by avoiding both over- and under-preparation scenarios. Therefore, integrating non-stationary transition probabilities into MDP frameworks enhances the ability to implement timely and effective interventions, improving overall public health outcomes.

In conclusion, both stationary and non-stationary transition probabilities play distinct yet complementary roles in optimizing decision making for managing the dynamics of COVID-19. Stationary models provide simplicity and consistency, making them well-suited for long-term planning and resource allocation. They offer a stable reference point, which is valuable for assessing overall trends and guiding strategic decisions. Conversely, non-stationary models introduce the flexibility and adaptability necessary for dynamic response and accurate forecasting. By accounting for time-varying factors, these models allow for real-time adjustments based on evolving data, which is crucial for timely and effective policy-making. Integrating both stationary and non-stationary approaches creates a balanced framework that leverages the stability of stationary models alongside the adaptability of non-stationary models. This integrated approach enhances public health outcomes by providing a comprehensive tool for both strategic planning and responsive action, improving economic efficiency in managing the COVID-19 pandemic. Future research focusing on cost-benefit analysis will further refine these models, enhancing their utility and effectiveness in crafting optimized pandemic responses.

Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this article.

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