On the reinfection of individuals in stochastic epidemic models

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Abstract

Our interest in this paper is on a number of epidemic models that allow for reinfection of individuals among a closed well-mixed finite population. For stochastic versions of a number of SIS- and SIR-type epidemic models, that account for partial, temporary or no immunity, allowing then for reinfection of individuals, we analytically quantify a main summary statistic: the probability that a given individual suffers exactly M infections during the epidemic, for any value $M \geq 0$. Our analysis has the particular feature that allows to study specific individuals that might behave differently against the disease than the rest of individuals in the population (*i.e.*, to consider that the individual under study has different infectivity, susceptibility or ability to recover). We illustrate our analysis by means of... and explain how this summary statistic relates to another important concept in mathematical epidemiology, *epidemic fade-out*.

Keywords: continuous-time Markov chain; SIS; SIRS; reinfection; epidemic fade-out;

1. Introduction

Mathematical epidemiological models have been extensively studied and used in the literature for analysing disease spread dynamics. Depending on the disease under study and the population of individuals among which

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this disease spreads, different models have been proposed: the SIS epidemic model where individuals are infected and become susceptible immediately after recovery; the SIR model in which after individuals recover they gain immunity against the disease, which lasts forever (this *recovery* might also mean *removal*, representing that individuals die or leave the system not playing a role any more in the disease spread dynamics); the $SEIR$ epidemic model where a latent infection period is considered in which individuals are infected but not infectious; or the $SIRS$ epidemic model where immune individuals recover susceptibility after a period of time.

A wide range of variants to these models have been proposed in order to account for specific characteristics of the disease under study or the population being affected. Stochastic models have usually been considered specially when analysing small populations (*e.g.,* hospital wards [3, 15], prisons [13], schools [2, 19] or families [8]), while deterministic counterparts have been developed for large populations [1]. Compartmental models assume that individuals within the population under study are homogeneous in terms of their behaviour against the disease (*i.e.,* equal infectivity, susceptibility and ability to recover), an assumption that simplifies the mathematical analysis and the estimation of parameters in the model. Heterogeneous populations can be considered instead by means of increasing the number of compartments in the model (*e.g.,* analysing populations structured in households [4, 18]) or, as the extreme case, by developing agent-based models where the epidemic dynamics of each specific individual in the population are tracked [11]. The analysis of agent-based models from a stochastic perspective usually leads to the analysis of continuous-time Markov chains on networks [8, 15] (where each individual represents a node on the network), leading to analytically untractable models that can only be dealt with in an exact way for very small values of the population size N [8, 15] or by means of approximative methods otherwise [14, 17, 21].

Among all the epidemic models in the literature, there are a number of them that have a particular feature in common: the possibility of individuals suffering reinfections [9]. These models are adequate for situations where the disease does not confer immunity to the individuals infected, or when the immunity conferred is only partial or temporary. In Ref. [9], a number of models accounting for this characteristic are presented and comprehensively analysed, also by accounting for vaccination strategies in these situations. In particular, authors in Ref. [9] carry out a deterministic analysis of these models in terms of their dynamics and equilibrium properties, and identify what

they call the *reinfection threshold* in transmission when partial immunity is included [6, 9, 10].

Reinfection of individuals also relates to another important concept in mathematical epidemiology, *epidemic fade-out*. According to Ref. [5], and for epidemics characterised by the occurrence of several *infection waves* [7, 12], epidemic fade-out is defined as the probability that the epidemic dies out in the trough between the first and second waves of the outbreak. There exists a number of works in the literature dealing with how to mathematically define this concept and how to approximate this probability for different epidemic models [5, 16, 20]. In those situations where the different infection waves are caused by reinfection of individuals, the individual probability of reinfection and the epidemic fade-out probability are clearly related.

Despite all the available literature related to models accounting for reinfection of individuals, a comprehensive analytical study for computing the exact number of reinfections suffered by a given individual in the population in different epidemic situations has not been carried out yet. When considering stochastic models, the reinfection dynamics could be analysed by means of computing the probability of a randomly chosen individual in the population suffering exactly M infections, for different possible values of $M \geq 0$. In this paper, we address this question for stochastic versions of SIS- and SIR-type models, such as the ones in Ref. [9], when considering a closed well-mixed homogeneous population of N individuals. Our method allows us to compute this probability in an exact way when analysing an individual in the population that might have a specific behaviour against the disease different than the rest of individuals in the population (*e.g.,* when the individual is a *super-spreader*, a specially susceptible individual, or an individual who recovers faster or more slowly than the rest of individuals in the population).

Main findings.

This paper is structured as follows,...

2. Reinfection probability for a given individual

In this section, and for an SIS stochastic model, as well as for SIR-type models that account for partial and/or temporary immunity, our aim is to compute the probability of reinfection of a given individual in the population. In SubSection 2.1, we compute the probability of reinfection (that is, the probability that a given individual suffers at least 2 infections) in an SIS

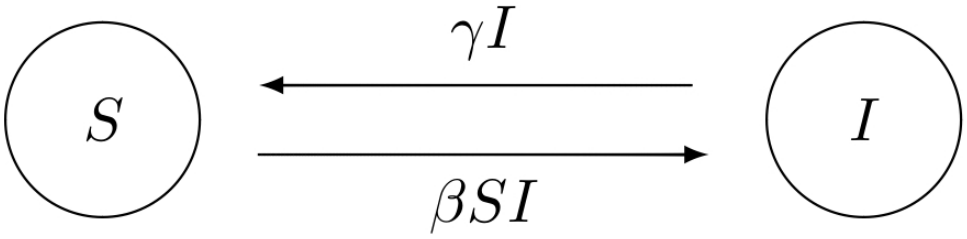

Figure 1: Dynamics of the SIS Model. Each susceptible individual is infected with rate βI, and each infective individual recovers with rate γ.

stochastic model. In SubSection 2.2, the probability of reinfection of an individual is computed for a more general model that accounts for temporary and/or partial immunity gained by individuals after suffering the infection. In SubSection 2.3, we relate these probabilities to the average number of individuals suffering reinfection if the population is considered completely homogeneous. Finally, we explain in the Appendix how to generalise our arguments for computing the probability of a marked individual suffering at least M infections, for any value $M \geq 2$ (so that arguments in this Section correspond to value $M = 2$).

2.1. SIS Model

We consider a closed finite well-mixed population of N individuals, and focus here on a SIS model which is described in Figure 1. Susceptible individuals are infected, due to infectious contacts occurring with infective individuals, while infective individuals recover without gaining any immunity, allowing then for reinfection. In this SIS model, the epidemic dies out at some random time T, and $p(T < \infty) = 1$ since we consider a closed finite population of N individuals. During $[0, T]$, individuals within the population might be re-infected several times, and our interest is to quantify the probability that a given individual suffers (at least) one of these reinfections, as a central summary statistic in these epidemic models.

We define the stochastic Markovian process $\mathcal{X} = \{S(t) : \ t \geq 0\}$, with

$$\begin{aligned} S(t) &= \textit{“number of susceptible individuals at time } t\textit{”}, \\ I(t) &= \textit{“number of infective individuals at time } t\textit{”} \ = \ N - S(t), \end{aligned}$$

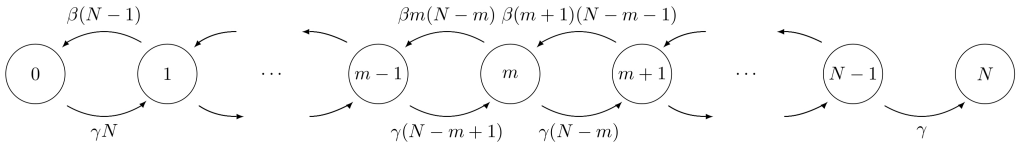

Figure 2: Birth-and-death process $\mathcal{X}$.

for $t \geq 0$, which according to dynamics in Figure 1 is a birth-and-death process with absorbing state $S(t) = N$; see Figure 2. We consider an initially marked individual A within the population, and our aim is to quantify the probability of individual A suffering at least one reinfection during the process. In order to compute this probability, we consider the extended process $\mathcal{X}^{ext} = \{\mathbf{X}^{ext}(t) = (S(t), A(t)) : \ t \geq 0\}$, where $A(t)$ represents the state of individual A at time $t \geq 0$, taking values S, S_I and I. These values represent that individual A, at time t, is susceptible and never suffered the disease before (S), is susceptible but suffered the infection before (S_I) or is infective (I).

Moreover, we consider that individual A might have an specific behaviour against the disease (*e.g.,* that individual A recovers faster or more slowly than the rest of the individuals, or that he/she has a different susceptibility and/or infectivity). Thus, we can define $\gamma(A)$ the recovery rate of individual A, while individual A infects any other individual in the population with rate $\beta_{A\to\bullet}$ and any other individual infects A with rate $\beta_{\bullet\to A}$. This introduces some heterogeneity in the population, allowing to compute the reinfection probability of an individual when this individual is, for example, a superspreader or a particularly susceptible individual within the population. We note however that a completely homogeneous population can be studied just by setting $\gamma(A) = \gamma$ and $\beta_{\bullet\to A} = \beta_{A\to\bullet} = \beta$ in our analysis.

We point out that extended process $\mathcal{X}^{ext}$ allows to: (i) consider an individual A with individual associated rates $\beta_{A\to\bullet}$, $\beta_{\bullet\to A}$ and $\gamma(A)$; (ii) keep track of the state of individual A at any given time, which is necessary when computing the reinfection probability of this individual. The state space of our extended process $\mathcal{X}^{ext}$ is given by

$$\mathcal{S}^{ext} \ = \ (\{1, \ldots, N-1\} \times \{S, S_I, I\}) \cup \{(0, I)\} \cup (\{N\} \times \{S, S_I\}) \cup \{\Delta\},$$

where Δ is an *artificial* absorbing state representing the reinfection of individual A for the first time, and (N, S) and (N, S_I) are absorbing states

Type of event	Original state	Destination state	Rate
Recovery of an infective individual	(m, S), $m \geq 1$	$(m+1, S)$	$\gamma(N-m)$
	(m, S_I), $m \geq 1$	$(m+1, S_I)$	$\gamma(N-m)$
	(m, I)	$(m+1, S_I)$	$\gamma(A)$
	(m, I), $m \leq N-2$	$(m+1, I)$	$\gamma(N-m-1)$
Infection of a susceptible individual	(m, S), $m \geq 1$	$(m-1, I)$	$\beta_{\bullet \to A}(N-m)$
	(m, S), $m \geq 1$	$(m-1, S)$	$\beta(m-1)(N-m)$
	(m, S_I), $m \geq 1$	Δ	$\beta_{\bullet \to A}(N-m)$
	(m, S_I), $m \geq 1$	$(m-1, S_I)$	$\beta(m-1)(N-m)$
	(m, I)	$(m-1, I)$	$\beta m(N-m-1) + \beta_{A \to \bullet} m$

Table 1: Transitions and transition rates among states $(m, a) \in \mathcal{S}^{ext}$, for $0 \leq m \leq N-1$, $n \geq 1$.

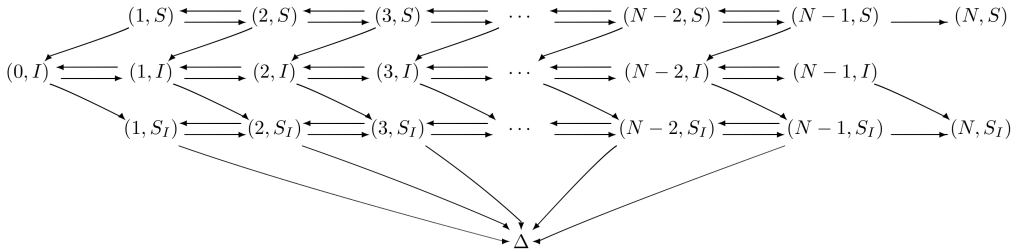

Figure 3: Transitions diagram for process $\mathcal{X}^{ext}$.

representing that the epidemic died out without individual A suffering reinfection. Possible transitions between states in $\mathcal{S}^{ext}$ are given in Table 1, leading to the transitions diagram in Figure 3.

Our interest is in computing

$$p_{(m,a)} = \text{“}\textit{probability of individual } A \textit{ suffering at least one reinfection given the initial state of the process } (m, a) \in \mathcal{S}^{ext}\text{”},$$

with trivial values $p_\Delta = 1$, $p_{(N,S)} = p_{(N,S_I)} = 0$. If the marked individual is the one starting the outbreak, we will focus on the initial state $(m, a) = (N-1, I)$, while if the outbreak is initiated by a different individual the initial state to consider is $(m, a) = (N-1, S)$. Probabilities $p_{(m,a)}$ for $(m, a) \in \mathcal{S}^{ext}$ satisfy the following equations, which can be obtained by implementing a

first-step argument:

$$\begin{aligned}
\theta_{(m,S)}p_{(m,S)} &= \beta(m-1)(N-m)p_{(m-1,S)} + \beta_{\bullet\to A}(N-m)p_{(m-1,I)} \\
&\quad +\gamma(N-m)p_{(m+1,S)}, \quad 1 \le m \le N-1, \qquad (1)\\
\theta_{(m,I)}p_{(m,I)} &= (\beta m(N-m-1) + \beta_{A\to\bullet}m)\, p_{(m-1,I)} + \gamma(N-m-1)p_{(m+1,I)} \\
&\quad +\gamma(A)p_{(m+1,S_I)}, \quad 0 \le m \le N-1, \qquad (2)\\
\theta_{(m,S)}p_{(m,S_I)} &= \beta(m-1)(N-m)p_{(m-1,S_I)} + \beta_{\bullet\to A}(N-m)p_{\Delta} \\
&\quad +\gamma(N-m)p_{(m+1,S_I)}, \quad 1 \le m \le N-1, \qquad (3)
\end{aligned}$$

with $\theta_{(m,S)} = \beta(m-1)(N-m) + \beta_{\bullet\to A}(N-m) + \gamma(N-m)$ and $\theta_{(m,I)} = \beta m(N-m-1) + \beta_{A\to\bullet}m + \gamma(N-m-1) + \gamma(A)$. A preliminary analysis of Eqs. (1)-(3) allows us to find a recursive scheme for computing these probabilities. In particular, Eq. (3) allows us to compute probabilities of the form $p_{(m,S_I)}$ which, once in hand, allow one for the computation of probabilities of the form $p_{(m,I)}$ by Eq. (2). Finally, once probabilities $p_{(m,I)}$ are in hand, Eq. (1) can be used to compute probabilities of the form $p_{(m,S)}$; see **Algorithm 1**.

Algorithm 1

Recursive scheme for computing probabilities $p_{(m,S_I)}$ ***from Eq.*** (3)***:***

$h_{(N-1,S)} = 1;$

$f_{(N-1,S)} = \frac{\beta(N-2)}{\theta_{(N-1,S)}};$

$g_{(N-1,S_I)} = \frac{\beta_{\bullet\to A}}{\theta_{(N-1,S)}};$

For $m = N-2,\ldots,1$*:*

$h_{(m,S)} = 1 - \frac{\gamma(N-m)}{\theta_{(m,S)}}h^{-1}_{(m+1,S)}f_{(m+1,S)};$

$f_{(m,S)} = \frac{\beta(m-1)(N-m)}{\theta_{(m,S)}};$

$g_{(m,S_I)} = \frac{\beta_{\bullet\to A}(N-m)}{\theta_{(m,S)}} + \frac{\gamma(N-m)}{\theta_{(m,S)}}h^{-1}_{(m+1,S)}g_{(m+1,S_I)};$

$p_{(1,S_I)} = h^{-1}_{(1,S)}g_{(1,S_I)};$

For $m = 2,\ldots,N-1$*:*

$$p_{(m,S_I)} \;=\; h^{-1}_{(m,S)}\left(f_{(m,S)}p_{(m-1,S_I)} + g_{(m,S_I)}\right);$$

Recursive scheme for computing probabilities $p_{(m,I)}$ ***from Eq.*** (2)***:***

$h_{(N-1,I)} \;=\; 1;$

$f_{(N-1,I)} \;=\; \frac{\beta_{A\to\bullet}(N-1)}{\theta_{(N-1,I)}};$

$g_{(N-1,I)} \;=\; \frac{\gamma(A)}{\theta_{(N-1,I)}}p_{(N,S_I)};$

For $m = N-2,\ldots,0$*:*

$$h_{(m,I)} \;=\; 1 - \frac{\gamma(N-m-1)}{\theta_{(m,I)}}h^{-1}_{(m+1,I)}f_{(m+1,I)};$$

$$f_{(m,I)} \;=\; \frac{\beta m(N-m-1)+\beta_{A\to\bullet}m}{\theta_{(m,I)}};$$

$$g_{(m,I)} \;=\; \frac{\gamma(N-m-1)}{\theta_{(m,I)}}h^{-1}_{(m+1,I)}g_{(m+1,I)} + \frac{\gamma(A)}{\theta_{(m,I)}}p_{(m+1,S_I)};$$

$p_{(0,I)} \;=\; h^{-1}_{(0,I)}g_{(0,I)};$

For $m = 1,\ldots,N-1$*:*

$$p_{(m,I)} \;=\; h^{-1}_{(m,I)}\left(f_{(m,I)}p_{(m-1,I)} + g_{(m,I)}\right);$$

Recursive scheme for computing probabilities $p_{(m,S)}$ ***from Eq.*** (1)***:***

$g_{(N-1,S)} \;=\; \frac{\beta_{\bullet\to A}}{\theta_{(N-1,S)}}p_{(N-2,I)};$

For $m = N-2,\ldots,1$*:*

$$g_{(m,S)} \;=\; \frac{\beta_{\bullet\to A}(N-m)}{\theta_{(m,S)}}p_{(m-1,I)} + \frac{\gamma(N-m)}{\theta_{(m,S)}}h^{-1}_{(m+1,S)}g_{(m+1,S)};$$

$p_{(1,S)} \;=\; h^{-1}_{(1,S)}g_{(1,S)};$

For $m = 2,\ldots,N-1$*:*

$$p_{(m,S)} \;=\; h^{-1}_{(m,S)}\left(f_{(m,S)}p_{(m-1,S)} + g_{(m,S)}\right);$$

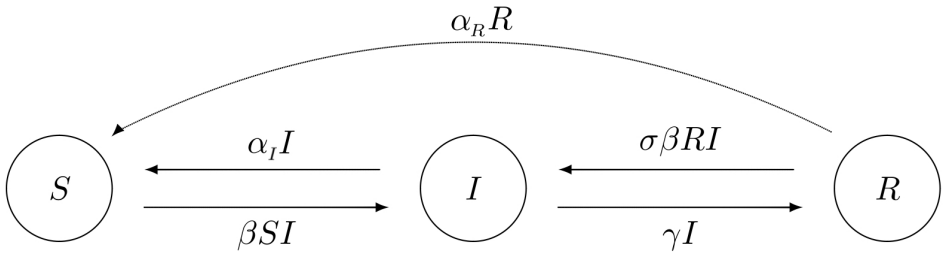

Figure 4: The *temporary-partial immunity SIR model* (TPI-SIR).

2.2. Temporary and/or partial immunity SIR models

We focus now on epidemic models where some kind of immunity is obtained by individuals after suffering the infection. To this aim, we consider models inspired from models in Ref. [9] where some temporary and/or partial immunity hypotheses are assumed:

- *Temporary immunity:* upon infection, individuals develop an immune response leading to temporary immunity, which is lost after a certain time.

- *Partial immunity:* individuals are protected while infected, and regain some susceptibility upon recovery.

As explained in [9, Figure 1(e)], these hypotheses can be incorporated by considering a general model such as the one in Figure 4. Considering only partial immunity, or only temporary immunity, can be done by setting some of the model parameters in Figure 4 equal to zero. We refer for now to the model in Figure 4 as the *temporary-partial immunity SIR model* (TPI-SIR), and we will consider different immunity hypotheses in Section 3 by setting some model parameters equal to zero.

We analyse in this section the probability of reinfection of a marked individual under the TPI-SIR Model. The TPI-SIR Model is represented by the Markovian process $\tilde{\mathcal{X}} = \{\tilde{\mathbf{X}}(t) = (\tilde{S}(t), \tilde{I}(t)) : \ t \geq 0\}$, with $\tilde{R}(t) = N - \tilde{S}(t) - \tilde{I}(t)$ the total number of recovered individuals at time t, defined over the state space $\tilde{\mathcal{S}} = \{(m, n) \in \mathbb{N}_0^2 : \ m + n \leq N\}$. States of the form $(m, 0)$ are considered as absorbing states representing the extinction of the epidemic; that is, we study the process only until the epidemic dies out (*i.e.,*

until $\tilde{I}(t) = 0$), even thought according to Figure 4 there might still occur some events after that, only involving susceptible and recovered individuals.

We propose to track a marked individual A by adding a third variable $\tilde{A}(t)$ to process $\tilde{\mathcal{X}}$ as in Subsection 2.1. In particular, we consider the extended process $\tilde{\mathcal{X}}^{ext} = \{\tilde{\mathbf{X}}^{ext}(t) = (\tilde{S}(t), \tilde{I}(t), \tilde{A}(t)) : \ t \geq 0\}$ where $\tilde{A}(t)$ takes values among states $\{S, S_I, I, R\}$ and represents the state of individual A at time t (that is, individual at time t can be susceptible having or not suffered the infection before, infected or recovered). The state space of $\tilde{\mathcal{X}}^{ext}$ is

$$\tilde{\mathcal{S}}^{ext} \ = \ \Big(\tilde{\mathcal{S}}^{ext}(S) \times \{S, S_I\}\Big) \cup \Big(\tilde{\mathcal{S}}^{ext}(I) \times \{I\}\Big) \cup \Big(\tilde{\mathcal{S}}^{ext}(R) \times \{R\}\Big) \cup \{\tilde{\Delta}\},$$

$\tilde{\Delta}$ is an absorbing state representing reinfection of individual A for the first time, and

$$\begin{aligned}
\tilde{\mathcal{S}}^{ext}(S) &= \{(m,n) \in \mathbb{N}_0^2 : \ m > 0, \ m + n \leq N\}, \\
\tilde{\mathcal{S}}^{ext}(I) &= \{(m,n) \in \mathbb{N}_0^2 : \ n > 0, \ m + n \leq N\}, \\
\tilde{\mathcal{S}}^{ext}(R) &= \{(m,n) \in \mathbb{N}_0^2 : \ m + n < N\},
\end{aligned}$$

relate to the possible numbers of susceptible and infective individuals in the population when individual A is susceptible, infective or recovered, respectively. Transitions among states within $\tilde{\mathcal{S}}^{ext}$ are given in Table 2, and individual A is again considered to potentially behave differently against the disease than the rest of individuals in the population, by considering individual rates $\beta_{\bullet \to A}$, $\beta_{A \to \bullet}$, $\sigma(A)$, $\alpha_R(A)$, $\alpha_I(A)$ and $\gamma(A)$. In order to implement our methodology for a completely homogeneous population, one would set $\beta_{\bullet \to A} = \beta_{A \to \bullet} = \beta$, $\gamma(A) = \gamma$, $\sigma(A) = \sigma$, $\alpha_R(A) = \alpha_R$ and $\alpha_I(A) = \alpha_I$.

We define $p_{(m,n,a)}$ as the probability of individual A suffering at least one reinfection given the initial state of the process $(m, n, a) \in \tilde{\mathcal{S}}^{ext}$. These

Event	Original state	Destination state	Rate
Recovery of an infective individual	(m,n,S), $m \geq 1$	$(m,n-1,S)$	γn
	(m,n,S_I), $m \geq 1$	$(m,n-1,S_I)$	γn
	(m,n,I), $n \geq 2$	$(m,n-1,I)$	$\gamma(n-1)$
	(m,n,I)	$(m,n-1,R)$	$\gamma(A)$
	(m,n,R), $m+n<N$	$(m,n-1,R)$	γn
Infection of a susceptible individual	(m,n,S), $m \geq 1$	$(m-1,n+1,I)$	$\beta_{\bullet\to A} n$
	(m,n,S), $m \geq 2$	$(m-1,n+1,S)$	$\beta(m-1)n$
	(m,n,S_I), $m \geq 1$	$\tilde{\Delta}$	$\beta_{\bullet\to A} n$
	(m,n,S_I), $m \geq 2$	$(m-1,n+1,S_I)$	$\beta(m-1)n$
	(m,n,I), $m \geq 1$	$(m-1,n+1,I)$	$\beta_{A\to\bullet} m + \beta(n-1)m$
	(m,n,R), $m \geq 1$, $m+n<N$	$(m-1,n+1,R)$	βmn
Infection of a recovered individual	(m,n,S), $m \geq 1$, $m+n<N$	$(m,n+1,S)$	$\sigma\beta n(N-m-n)$
	(m,n,S_I), $m \geq 1$, $m+n<N$	$(m,n+1,S_I)$	$\sigma\beta n(N-m-n)$
	(m,n,I), $m+n<N$	$(m,n+1,I)$	$\sigma\beta(n-1)(N-m-n)$ $+\sigma\beta_{A\to\bullet}(N-m-n)$
	(m,n,R), $m+n<N-1$	$(m,n+1,R)$	$\sigma\beta n(N-m-n-1)$
	(m,n,R), $m+n<N$	$\tilde{\Delta}$	$\sigma(A)\beta_{\bullet\to A} n$
Immunity loss of an infective individual	(m,n,S), $m \geq 1$	$(m+1,n-1,S)$	$\alpha_I n$
	(m,n,S_I), $m \geq 1$	$(m+1,n-1,S_I)$	$\alpha_I n$
	(m,n,I), $n \geq 2$	$(m+1,n-1,I)$	$\alpha_I(n-1)$
	(m,n,I)	$(m+1,n-1,S_I)$	$\alpha_I(A)$
	(m,n,R), $m+n<N$	$(m+1,n-1,R)$	$\alpha_I n$
Immunity loss of a recovered individual	(m,n,S), $m \geq 1$, $m+n<N$	$(m+1,n,S)$	$\alpha_R(N-m-n)$
	(m,n,S_I), $m \geq 1$, $m+n<N$	$(m+1,n,S_I)$	$\alpha_R(N-m-n)$
	(m,n,I), $m+n<N$	$(m+1,n,I)$	$\alpha_R(N-m-n)$
	(m,n,R), $m+n<N-1$	$(m+1,n,R)$	$\alpha_R(N-m-n-1)$
	(m,n,R), $m+n<N$	$(m+1,n,S_I)$	$\alpha_R(A)$

Table 2: Transitions among states in $\tilde{\mathcal{S}}^{ext}$, for $n \geq 1$, $m \geq 0$, $m+n \leq N$.

probabilities satisfy, for $m \geq 0$, $n \geq 1$ and $m+n \leq N$, equations

$$\begin{aligned}
\theta_{(m,n,S)}p_{(m,n,S)} &= \beta(m-1)np_{(m-1,n+1,S)} + \beta_{\bullet\to A}np_{(m-1,n+1,I)} + \gamma np_{(m,n-1,S)} \\
&\quad +\alpha_I np_{(m+1,n-1,S)} + \alpha_R(N-m-n)p_{(m+1,n,S)} \\
&\quad +\sigma\beta n(N-m-n)p_{(m,n+1,S)}, \quad m \geq 1, \qquad (4) \\
\theta_{(m,n,I)}p_{(m,n,I)} &= (\beta m(n-1) + \beta_{A\to\bullet}m)\, p_{(m-1,n+1,I)} + \gamma(n-1)p_{(m,n-1,I)} \\
&\quad +\gamma(A)p_{(m,n-1,R)} + \alpha_I(n-1)p_{(m+1,n-1,I)} + \alpha_I(A)p_{(m+1,n-1,S_I)} \\
&\quad +(\sigma\beta(n-1)(N-m-n) + \sigma\beta_{A\to\bullet}(N-m-n))\, p_{(m,n+1,I)} \\
&\quad +\alpha_R(N-m-n)p_{(m+1,n,I)}, \qquad (5) \\
\theta_{(m,n,R)}p_{(m,n,R)} &= \beta mnp_{(m-1,n+1,R)} + \gamma np_{(m,n-1,R)} + \alpha_I np_{(m+1,n-1,R)} \\
&\quad +\alpha_R(N-m-n-1)p_{(m+1,n,R)} + \alpha_R(A)p_{(m+1,n,S_I)} + \sigma\beta n \\
&\quad \times(N-m-n-1)p_{(m,n+1,R)} + \sigma(A)\beta_{\bullet\to A}np_{\tilde{\Delta}}, \quad m+n < N, \qquad (6) \\
\theta_{(m,n,S)}p_{(m,n,S_I)} &= \beta(m-1)np_{(m-1,n+1,S_I)} + \beta_{\bullet\to A}np_{\tilde{\Delta}} + \gamma np_{(m,n-1,S_I)} \\
&\quad +\alpha_I np_{(m+1,n-1,S_I)} + \alpha_R(N-m-n)p_{(m+1,n,S_I)} \\
&\quad +\sigma\beta n(N-m-n)p_{(m,n+1,S_I)}, \quad m \geq 1, \qquad (7)
\end{aligned}$$

with $\theta_{(m,n,S)} = \beta(m-1)n+\beta_{\bullet\to A}n+\gamma n+\alpha_I n+\alpha_R(N-m-n)+\sigma\beta n(N-m-n)$, $\theta_{(m,n,I)} = \beta m(n-1) + \beta_{A\to\bullet}m + \gamma(n-1) + \gamma(A) + \alpha_I(n-1) + \alpha_I(A) + \sigma\beta(n-1)(N-m-n) + \sigma\beta_{A\to\bullet}(N-m-n) + \alpha_R(N-m-n)$, $\theta_{(m,n,R)} = \beta mn+\gamma n+\alpha_I n+\alpha_R(N-m-n-1)+\alpha_R(A)+\sigma\beta n(N-m-n-1)+\sigma(A)\beta_{\bullet\to A}n$, and boundary conditions $p_{\tilde{\Delta}} = 1$, $p_{(m,0,S)} = p_{(m,0,S_I)} = p_{(m,0,R)} = 0$, for any value of m.

Eqs. (4)-(7) can be solved algorithmically in a backwards fashion. In particular, Eq. (7) can be solved first by considering

$$\begin{aligned}
\tilde{\mathcal{S}}^{ext}(S) &= \{(m,n) \in \mathbb{N}_0^2 :\ m > 0,\ m+n \leq N\} \ = \ (\{(m,0) :\ 1 \leq m \leq N\}) \cup \mathcal{C}^{ext}(S), \\
\mathcal{C}^{ext}(S) &= \{(m,n) \in \mathbb{N}^2 :\ m+n \leq N\} \ = \ \bigcup_{k=2}^{N} L(S;k), \\
L(S;k) &= \{(m,n) \in \mathbb{N}^2 :\ m+n = k\}, \quad 2 \leq k \leq N.
\end{aligned}$$

With this states organisation, Eq. (7) can be written in matrix form as

$$\mathbf{p}(S_I) \ = \ \mathbf{A}(S)\mathbf{p}(S_I) + \mathbf{b}(S_I), \qquad (8)$$

with

$$\mathbf{p}(S_I) = \begin{pmatrix} \mathbf{p}_2(S_I) \\ \mathbf{p}_3(S_I) \\ \vdots \\ \mathbf{p}_N(S_I) \end{pmatrix}, \quad \mathbf{p}_k(S_I) = \begin{pmatrix} p_{(k-1,1,S_I)} \\ p_{(k-2,2,S_I)} \\ \vdots \\ p_{(1,k-1,S_I)} \end{pmatrix},$$

$$\mathbf{b}(S_I) = \begin{pmatrix} \mathbf{b}_2(S_I) \\ \mathbf{b}_3(S_I) \\ \vdots \\ \mathbf{b}_N(S_I) \end{pmatrix}, \quad \mathbf{b}_k(S_I) = \begin{pmatrix} \frac{\beta_{\bullet\to A}}{\theta_{(k-1,1,S)}} \\ \frac{\beta_{\bullet\to A}2}{\theta_{(k-2,2,S)}} \\ \vdots \\ \frac{\beta_{\bullet\to A}(k-1)}{\theta_{(1,k-1,S)}} \end{pmatrix},$$

and with matrix $\mathbf{A}(S)$ given by

$$\begin{pmatrix} \mathbf{A}_{2,2}(S) & \mathbf{A}_{2,3}(S) & \mathbf{0}_{J(S;2)\times J(S;4)} & \dots & \mathbf{0}_{J(S;2)\times J(S;N-1)} & \mathbf{0}_{J(S;2)\times J(S;N)} \\ \mathbf{A}_{3,2}(S) & \mathbf{A}_{3,3}(S) & \mathbf{A}_{3,4}(S) & \dots & \mathbf{0}_{J(S;3)\times J(S;N-1)} & \mathbf{0}_{J(S;3)\times J(S;N)} \\ \mathbf{0}_{J(S;4)\times J(S;2)} & \mathbf{A}_{4,3}(S) & \mathbf{A}_{4,4}(S) & \dots & \mathbf{0}_{J(S;4)\times J(S;N-1)} & \mathbf{0}_{J(S;4)\times J(S;N)} \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ \mathbf{0}_{J(S;N-1)\times J(S;2)} & \mathbf{0}_{J(S;N-1)\times J(S;3)} & \mathbf{0}_{J(S;N-1)\times J(S;4)} & \dots & \mathbf{A}_{N-1,N-1}(S) & \mathbf{A}_{N-1,N}(S) \\ \mathbf{0}_{J(S;N)\times J(S;2)} & \mathbf{0}_{J(S;N)\times J(S;3)} & \mathbf{0}_{J(S;N)\times J(S;4)} & \dots & \mathbf{A}_{N,N-1}(S) & \mathbf{A}_{N,N}(S) \end{pmatrix},$$

and with sub-matrices

$$\mathbf{A}_{k,k}(S) = \begin{pmatrix} 0 & \frac{\beta(k-2)}{\theta_{(k-1,1,S)}} & 0 & \dots & 0 & 0 \\ \frac{\alpha_I 2}{\theta_{(k-2,2,S)}} & 0 & \frac{\beta 2(k-3)}{\theta_{(k-2,2,S)}} & \dots & 0 & 0 \\ 0 & \frac{\alpha_I 3}{\theta_{(k-3,3,S)}} & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & 0 & \frac{\beta(k-2)}{\theta_{(2,k-2,S)}} \\ 0 & 0 & 0 & \dots & \frac{\alpha_I(k-1)}{\theta_{(1,k-1,S)}} & 0 \end{pmatrix}, \quad 2 \le k \le N,$$

$$\mathbf{A}_{k,k-1}(S) = \begin{pmatrix} 0 & 0 & 0 & \dots & 0 & 0 \\ \frac{\gamma 2}{\theta_{(k-2,2,S)}} & 0 & 0 & \dots & 0 & 0 \\ 0 & \frac{\gamma 3}{\theta_{(k-3,3,S)}} & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \frac{\gamma(k-2)}{\theta_{(2,k-2,S)}} & 0 \\ 0 & 0 & 0 & \dots & 0 & \frac{\gamma(k-1)}{\theta_{(1,k-1,S)}} \end{pmatrix}, \quad 3 \le k \le N,$$

$$\mathbf{A}_{k,k+1}(S) \;=\; \begin{pmatrix} \frac{\alpha_R(N-k)}{\theta_{(k-1,1,S)}} & \frac{\sigma\beta(N-k)}{\theta_{(k-1,1,S)}} & 0 & \dots & 0 & 0 \\ 0 & \frac{\alpha_R(N-k)}{\theta_{(k-2,2,S)}} & \frac{\sigma\beta(N-k)2}{\theta_{(k-2,2,S)}} & \dots & 0 & 0 \\ 0 & 0 & \frac{\alpha_R(N-k)}{\theta_{(k-3,3,S)}} & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \frac{\sigma\beta(N-k)(k-2)}{\theta_{(2,k-2,S)}} & 0 \\ 0 & 0 & 0 & \dots & \frac{\alpha_R(N-k)}{\theta_{(1,k-1,S)}} & \frac{\sigma\beta(N-k)(k-1)}{\theta_{(1,k-1,S)}} \end{pmatrix}, \quad 2 \le k \le N-1,$$

where $J(S;k) = \#L(S;k) = k-1$, and $\#B$ represents the cardinality of set B. According to the structure of matrix $\mathbf{A}(S)$, system in Eq. (8) can be algorithmically solved in a specialised block-Gaussian elimination fashion; see **Algorithm 2**.

Algorithm 2

$\mathbf{H}_2(S) \;=\; \mathbf{I}_{J(S;2)} - \mathbf{A}_{2,2}(S);$

$\mathbf{J}_2(S_I) \;=\; \mathbf{b}_2(S_I);$

For $k = 3, \dots, N$*:*

$\mathbf{H}_k(S) \;=\; \mathbf{I}_{J(S;k)} - \mathbf{A}_{k,k}(S) - \mathbf{A}_{k,k-1}(S)\mathbf{H}_{k-1}^{-1}(S)\mathbf{A}_{k-1,k}(S);$

$\mathbf{J}_k(S_I) \;=\; \mathbf{A}_{k,k-1}(S)\mathbf{H}_{k-1}^{-1}(S)\mathbf{J}_{k-1}(S_I) + \mathbf{b}_k(S_I);$

$\mathbf{p}_N(S_I) \;=\; \mathbf{H}_N^{-1}(S)\mathbf{J}_N(S_I);$

For $k = N-1, \dots, 2$*:*

$\mathbf{p}_k(S_I) \;=\; \mathbf{H}_k^{-1}(S)\left(\mathbf{A}_{k,k+1}(S)\mathbf{p}_{k+1}(S_I) + \mathbf{J}_k(S_I)\right);$

Once probabilities of the form $p_{(m,n,S_I)}$ are in hand, one proceeds similarly to obtain probabilities $p_{(m,n,R)}$ from Eq. (6), which can be re-written in matrix form by organising

$$\begin{aligned} \tilde{\mathcal{S}}^{ext}(R) &= \{(m,n) \in \mathbb{N}_0^2 :\; m+n < N\} \;=\; (\{(m,0) :\; 0 \le m \le N-1\}) \cup \mathcal{C}^{ext}(R), \\ \mathcal{C}^{ext}(R) &= \{(m,n) \in \mathbb{N}_0^2 :\; n \ge 1,\; m+n < N\} \;=\; \bigcup_{k=1}^{N-1} L(R;k), \\ L(R;k) &= \{(m,n) \in \mathbb{N}_0^2 :\; n \ge 1,\; m+n = k\}, \quad 1 \le k \le N-1. \end{aligned}$$

In particular, we obtain

$$\mathbf{p}(R) \;=\; \mathbf{A}(R)\mathbf{p}(R) + \mathbf{b}(R), \tag{9}$$

with

$$\mathbf{p}(R) \;=\; \begin{pmatrix} \mathbf{p}_1(R) \\ \mathbf{p}_2(R) \\ \vdots \\ \mathbf{p}_{N-1}(R) \end{pmatrix}, \quad \mathbf{p}_k(R) \;=\; \begin{pmatrix} p_{(k-1,1,R)} \\ p_{(k-2,2,R)} \\ \vdots \\ p_{(1,k-1,R)} \\ p_{(0,k,R)} \end{pmatrix},$$

column vector

$$\mathbf{b}(R) \;=\; \begin{pmatrix} \mathbf{b}_1(R) \\ \mathbf{b}_2(R) \\ \vdots \\ \mathbf{b}_{N-1}(R) \end{pmatrix}, \quad \mathbf{b}_k(R) \;=\; \begin{pmatrix} \frac{\alpha_R(A)p_{(k,1,S_I)}+\sigma(A)\beta_{\bullet\to A}}{\theta_{(k-1,1,R)}} \\ \frac{\alpha_R(A)p_{(k-1,2,S_I)}+\sigma(A)\beta_{\bullet\to A}2}{\theta_{(k-2,2,R)}} \\ \vdots \\ \frac{\alpha_R(A)p_{(1,k,S_I)}+\sigma(A)\beta_{\bullet\to A}k}{\theta_{(0,k,R)}} \end{pmatrix},$$

and with matrix $\mathbf{A}(R)$ given by

$$\begin{pmatrix} \mathbf{A}_{1,1}(R) & \mathbf{A}_{1,2}(R) & \mathbf{0}_{J(R;1)\times J(R;3)} & \cdots & \mathbf{0}_{J(R;1)\times J(R;N-2)} & \mathbf{0}_{J(R;1)\times J(R;N-1)} \\ \mathbf{A}_{2,1}(R) & \mathbf{A}_{2,2}(R) & \mathbf{A}_{2,3}(R) & \cdots & \mathbf{0}_{J(R;2)\times J(R;N-2)} & \mathbf{0}_{J(R;2)\times J(R;N-1)} \\ \mathbf{0}_{J(R;3)\times J(R;1)} & \mathbf{A}_{3,2}(R) & \mathbf{A}_{3,3}(R) & \cdots & \mathbf{0}_{J(R;3)\times J(R;N-2)} & \mathbf{0}_{J(R;3)\times J(R;N-1)} \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ \mathbf{0}_{J(R;N-2)\times J(R;1)} & \mathbf{0}_{J(R;N-2)\times J(R;2)} & \mathbf{0}_{J(R;N-2)\times J(R;3)} & \cdots & \mathbf{A}_{N-2,N-2}(R) & \mathbf{A}_{N-2,N-1}(R) \\ \mathbf{0}_{J(R;N-1)\times J(R;1)} & \mathbf{0}_{J(R;N-1)\times J(R;2)} & \mathbf{0}_{J(R;N-1)\times J(R;3)} & \cdots & \mathbf{A}_{N-1,N-2}(R) & \mathbf{A}_{N-1,N-1}(R) \end{pmatrix},$$

with $J(R;k) = \#L(R;k) = k$. Finally, we have sub-matrices

$$\mathbf{A}_{k,k}(R) = \begin{pmatrix} 0 & \frac{\beta(k-1)}{\theta_{(k-1,1,R)}} & 0 & \dots & 0 & 0 \\ \frac{\alpha_I 2}{\theta_{(k-2,2,R)}} & 0 & \frac{\beta 2(k-2)}{\theta_{(k-2,2,R)}} & \dots & 0 & 0 \\ 0 & \frac{\alpha_I 3}{\theta_{(k-3,3,R)}} & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & 0 & \frac{\beta(k-1)}{\theta_{(1,k-1,R)}} \\ 0 & 0 & 0 & \dots & \frac{\alpha_I k}{\theta_{(0,k,R)}} & 0 \end{pmatrix}, \quad 1 \le k \le N-1,$$

$$\mathbf{A}_{k,k-1}(R) = \begin{pmatrix} 0 & 0 & 0 & \dots & 0 & 0 \\ \frac{\gamma 2}{\theta_{(k-2,2,R)}} & 0 & 0 & \dots & 0 & 0 \\ 0 & \frac{\gamma 3}{\theta_{(k-3,3,R)}} & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \frac{\gamma(k-1)}{\theta_{(1,k-1,R)}} & 0 \\ 0 & 0 & 0 & \dots & 0 & \frac{\gamma k}{\theta_{(0,k,R)}} \end{pmatrix}, \quad 2 \le k \le N-1,$$

$$\mathbf{A}_{k,k+1}(R) = \begin{pmatrix} \frac{\alpha_R(N-k-1)}{\theta_{(k-1,1,R)}} & \frac{\sigma\beta(N-k-1)}{\theta_{(k-1,1,R)}} & 0 & \dots & 0 & 0 \\ 0 & \frac{\alpha_R(N-k-1)}{\theta_{(k-2,2,R)}} & \frac{\sigma\beta(N-k-1)2}{\theta_{(k-2,2,R)}} & \dots & 0 & 0 \\ 0 & 0 & \frac{\alpha_R(N-k-1)}{\theta_{(k-3,3,R)}} & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \frac{\sigma\beta(N-k-1)(k-1)}{\theta_{(1,k-1,R)}} & 0 \\ 0 & 0 & 0 & \dots & \frac{\alpha_R(N-k-1)}{\theta_{(0,k,R)}} & \frac{\sigma\beta(N-k-1)k}{\theta_{(0,k,R)}} \end{pmatrix}, \quad 1 \le k \le N-2.$$

For solving Eq. (9) and the structure of matrix $\mathbf{A}(R)$, we construct **Algorithm 2 (continuation I)**.

Algorithm 2 (continuation I)

$\mathbf{H}_1(R) = \mathbf{I}_{J(R;1)} - \mathbf{A}_{1,1}(R)$;

$\mathbf{J}_1(R) = \mathbf{b}_1(R)$;

For $k = 2, \dots, N-1$*:*

$\mathbf{H}_k(R) = \mathbf{I}_{J(R;k)} - \mathbf{A}_{k,k}(R) - \mathbf{A}_{k,k-1}(R)\mathbf{H}_{k-1}^{-1}(R)\mathbf{A}_{k-1,k}(R)$*;*

$\mathbf{J}_k(R) = \mathbf{A}_{k,k-1}(R)\mathbf{H}_{k-1}^{-1}(R)\mathbf{J}_{k-1}(R) + \mathbf{b}_k(R)$*;*

$\mathbf{p}_{N-1}(R) = \mathbf{H}_{N-1}^{-1}(R)\mathbf{J}_{N-1}(R)$*;*

For $k = N-2, \dots, 1$*:*

$$\mathbf{p}_k(R) \;=\; \mathbf{H}_k^{-1}(R)\,(\mathbf{A}_{k,k+1}(R)\mathbf{p}_{k+1}(R)+\mathbf{J}_k(R));$$

In a similar way, probabilities of the form $p_{(m,n,I)}$ can be obtained from Eq. (5) once both probabilities of the form $p_{(m,n,S_I)}$ and $p_{(m,n,R)}$ are in hand. In particular, by organising

$$\begin{aligned}
\tilde{\mathcal{S}}^{ext}(I) &= \{(m,n)\in\mathbb{N}_0^2:\ n\geq 1,\ m+n\leq N\} \;=\; \mathcal{C}^{ext}(I),\\
\mathcal{C}^{ext}(I) &= \bigcup_{k=1}^{N} L(I;k),\\
L(I;k) &= \{(m,n)\in\mathbb{N}_0^2:\ n\geq 1,\ m+n=k\},\quad 1\leq k\leq N,
\end{aligned}$$

we obtain

$$\mathbf{p}(I) \;=\; \mathbf{A}(I)\mathbf{p}(I)+\mathbf{b}(I), \tag{10}$$

with

$$\mathbf{p}(I) \;=\; \begin{pmatrix} \mathbf{p}_1(I)\\ \mathbf{p}_2(I)\\ \vdots\\ \mathbf{p}_N(I)\end{pmatrix},\quad \mathbf{p}_k(I) \;=\; \begin{pmatrix} p_{(k-1,1,I)}\\ p_{(k-2,2,I)}\\ \vdots\\ p_{(1,k-1,I)}\\ p_{(0,k,I)}\end{pmatrix},$$

column vector

$$\mathbf{b}(I) \;=\; \begin{pmatrix} \mathbf{b}_1(I)\\ \mathbf{b}_2(I)\\ \vdots\\ \mathbf{b}_N(I)\end{pmatrix},\quad \mathbf{b}_k(I) \;=\; \begin{pmatrix} 0\\ \frac{\gamma(A)p_{(k-2,1,R)}+\alpha_I(A)p_{(k-1,1,S_I)}}{\theta_{(k-2,2,I)}}\\ \vdots\\ \frac{\gamma(A)p_{(0,k-1,R)}+\alpha_I(A)p_{(1,k-1,S_I)}}{\theta_{(0,k,I)}}\end{pmatrix},$$

and with matrix $\mathbf{A}(I)$ given by

$$\begin{pmatrix}
\mathbf{A}_{1,1}(I) & \mathbf{A}_{1,2}(I) & \mathbf{0}_{J(I;1)\times J(I;3)} & \dots & \mathbf{0}_{J(I;1)\times J(I;N-1)} & \mathbf{0}_{J(I;1)\times J(I;N)}\\
\mathbf{A}_{2,1}(I) & \mathbf{A}_{2,2}(I) & \mathbf{A}_{2,3}(I) & \dots & \mathbf{0}_{J(I;2)\times J(I;N-1)} & \mathbf{0}_{J(I;2)\times J(I;N)}\\
\mathbf{0}_{J(I;3)\times J(I;1)} & \mathbf{A}_{3,2}(I) & \mathbf{A}_{3,3}(I) & \dots & \mathbf{0}_{J(I;3)\times J(I;N-1)} & \mathbf{0}_{J(I;3)\times J(I;N)}\\
\vdots & \vdots & \vdots & \ddots & \vdots & \vdots\\
\mathbf{0}_{J(I;N-1)\times J(I;1)} & \mathbf{0}_{J(I;N-1)\times J(I;2)} & \mathbf{0}_{J(I;N-1)\times J(I;3)} & \dots & \mathbf{A}_{N-1,N-1}(I) & \mathbf{A}_{N-1,N}(I)\\
\mathbf{0}_{J(I;N)\times J(I;1)} & \mathbf{0}_{J(I;N)\times J(I;2)} & \mathbf{0}_{J(I;N)\times J(I;3)} & \dots & \mathbf{A}_{N,N-1}(I) & \mathbf{A}_{N,N}(I)
\end{pmatrix},$$

with $J(I;k) = \#L(I;k) = k$. Finally, sub-matrices are given as

$$\mathbf{A}_{k,k}(I) = \begin{pmatrix} 0 & \frac{\beta_{A\to\bullet}(k-1)}{\theta_{(k-1,1,I)}} & 0 & \dots & 0 & 0 \\ \frac{\alpha_I}{\theta_{(k-2,2,I)}} & 0 & \frac{(\beta_{A\to\bullet}+\beta)(k-2)}{\theta_{(k-2,2,I)}} & \dots & 0 & 0 \\ 0 & \frac{\alpha_I 2}{\theta_{(k-3,3,I)}} & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & 0 & \frac{\beta_{A\to\bullet}+\beta(k-2)}{\theta_{(1,k-1,I)}} \\ 0 & 0 & 0 & \dots & \frac{\alpha_I(k-1)}{\theta_{(0,k,I)}} & 0 \end{pmatrix}, \quad 1 \le k \le N,$$

$$\mathbf{A}_{k,k-1}(I) = \begin{pmatrix} 0 & 0 & 0 & \dots & 0 & 0 \\ \frac{\gamma}{\theta_{(k-2,2,I)}} & 0 & 0 & \dots & 0 & 0 \\ 0 & \frac{\gamma 2}{\theta_{(k-3,3,I)}} & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \frac{\gamma(k-2)}{\theta_{(1,k-1,I)}} & 0 \\ 0 & 0 & 0 & \dots & 0 & \frac{\gamma(k-1)}{\theta_{(0,k,I)}} \end{pmatrix}, \quad 2 \le k \le N,$$

$$\mathbf{A}_{k,k+1}(I) = \begin{pmatrix} \frac{\alpha_R(N-k)}{\theta_{(k-1,1,I)}} & \frac{\sigma(N-k)\beta_{A\to\bullet}}{\theta_{(k-1,1,I)}} & 0 & \dots & 0 & 0 \\ 0 & \frac{\alpha_R(N-k)}{\theta_{(k-2,2,I)}} & \frac{\sigma(N-k)(\beta+\beta_{A\to\bullet})}{\theta_{(k-2,2,I)}} & \dots & 0 & 0 \\ 0 & 0 & \frac{\alpha_R(N-k)}{\theta_{(k-3,3,I)}} & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & \frac{\sigma(N-k)(\beta(k-2)+\beta_{A\to\bullet})}{\theta_{(1,k-1,I)}} & 0 \\ 0 & 0 & 0 & \dots & \frac{\alpha_R(N-k)}{\theta_{(0,k,I)}} & \frac{\sigma(N-k)(\beta(k-1)+\beta_{A\to\bullet})}{\theta_{(0,k,I)}} \end{pmatrix},$$
$$1 \le k \le N-1.$$

From Eq. (10), we construct **Algorithm 2 (continuation II)**.

Algorithm 2 (continuation II)

$\mathbf{H}_1(I) = \mathbf{I}_{J(I;1)} - \mathbf{A}_{1,1}(I);$

$\mathbf{J}_1(I) = \mathbf{b}_1(I);$

For $k = 2, \dots, N$*:*

$\mathbf{H}_k(I) = \mathbf{I}_{J(I;k)} - \mathbf{A}_{k,k}(I) - \mathbf{A}_{k,k-1}(I)\mathbf{H}_{k-1}^{-1}(I)\mathbf{A}_{k-1,k}(I);$

$\mathbf{J}_k(I) = \mathbf{A}_{k,k-1}(I)\mathbf{H}_{k-1}^{-1}(I)\mathbf{J}_{k-1}(I) + \mathbf{b}_k(I);$

$\mathbf{p}_N(I) = \mathbf{H}_N^{-1}(I)\mathbf{J}_N(I);$

For $k = N-1, \ldots, 1$*:*

$$\mathbf{p}_k(I) \;=\; \mathbf{H}_k^{-1}(I)\,(\mathbf{A}_{k,k+1}(I)\mathbf{p}_{k+1}(I) + \mathbf{J}_k(I));$$

Finally, probabilities $p_{(m,n,S)}$ can be computed from Eq. (4) by following exactly the same arguments than the ones used for solving Eq. (7). In particular, we note that Eqs. (4) and (7) only differ in addends $\beta_{\bullet\to A} n p_{\tilde{\Delta}}$ (in Eq. (7)) and $\beta_{\bullet\to A} n p_{(m-1,n+1,I)}$ (in Eq. (4)). Thus, first steps of **Algorithm 2** directly apply for solving Eq. (4), using same matrices $\mathbf{A}_{k,k'}(S)$, but with new vector $\mathbf{b}(S)$ instead of $\mathbf{b}(S_I)$,

$$\mathbf{b}(S) \;=\; \begin{pmatrix} \mathbf{b}_2(S) \\ \mathbf{b}_3(S) \\ \vdots \\ \mathbf{b}_N(S) \end{pmatrix}, \quad \mathbf{b}_k(S) \;=\; \begin{pmatrix} \frac{\beta_{\bullet\to A} p_{(k-2,2,I)}}{\theta_{(k-1,1,S)}} \\ \frac{\beta_{\bullet\to A} 2 p_{(k-3,3,I)}}{\theta_{(k-2,2,S)}} \\ \vdots \\ \frac{\beta_{\bullet\to A} (k-1) p_{(0,k,I)}}{\theta_{(1,k-1,S)}} \end{pmatrix}.$$

2.3. The number of individuals suffering at least one reinfection

We finally point out here that, under the homogeneous case and for the SIS model (same arguments apply for the TPI-SIR model), if the individual starting the infection is chosen randomly from the population, we have

$$p \;=\; \mathbb{P}(A \textit{ suffering at least } 2 \textit{ infections}) \;=\; p_{(m-1,S)} \frac{N-1}{N} + p_{(m-1,I)} \frac{1}{N}.$$

Then, if we are interested in the random variable

$$Y \;=\; \textit{"Number of individuals in the population suffering at least } 2 \textit{ infections"},$$

it is clear that

$$p \;=\; \sum_{y=0}^{N} \mathbb{P}(A \textit{ suffering at least } 2 \textit{ infections} \mid Y = y)\mathbb{P}(Y = y)$$

and, since all the individuals are *symmetric*, we get

$$p \;=\; \sum_{y=0}^{N} \frac{y}{N} \mathbb{P}(Y = y) \;=\; \frac{E[Y]}{N}.$$

Thus, once probabilities $p_{(m,a)}$ are in hand, we can easily obtain $E[Y]$ as

$$E[Y] \;\; = \;\; (N-1)p_{(m-1,S)} + p_{(m-1,I)}.$$

We finally note that the complete probability mass function of Y could also be computed by means of first-step arguments, which is out of the scope of this paper.

3. Results

For numerical results in this Section, we focus on the SIS model, as well as a number of temporary and/or partial immunity models that arise from the general TPI-SIR model, inspired from hypotheses considered in Ref. [7] for explaining a multiple-wave influenza outbreak occurred in Tristan da Cunha in 1971. In particular, we focus on the following models depicted in Figure 5:

- The All-or-Nothing (AoN) immunity model [7] represents the situation in which, after infection, some individuals develop with probability p long-term protection against the infection, while others become fully susceptible.
- The Partially Protective Immunity (PPI) model [7] accounts for the situation in which, following recovery, all individuals have a partial protection against the infection.
- The SIRS model, widely considered in the literature, where immunity fades away after some time.

3.1. Global sensitivity analysis for an homogeneous population

In this SubSection, we consider an individual that behaves equally than the rest of individuals in the population (that is, the population is fully homogeneous). We consider in this section $N = 100$ and $\gamma = 1$, so that the time unit is the average recovery period of an individual. Our interest is in analysing the probability of this individual suffering exactly M infections for the different values of $M \geq 0$, when the different epidemic parameter values change for the SIS and the TPI-SIR models.

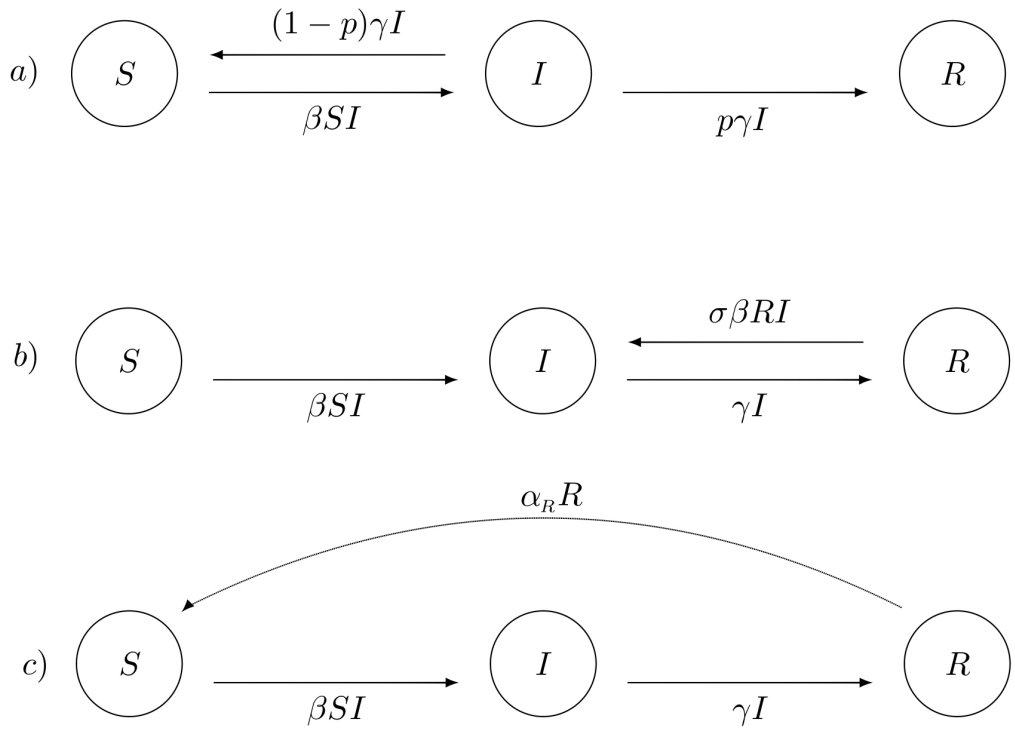

Figure 5: a) All-or-Nothing (AoN) immunity hypothesis [7]; b) Partially protective immunity (PPI) hypothesis [7]; c) SIRS model.

3.1.1. SIS Model: no immunity

In Figure 6 we focus on the SIS model, where individuals develop no immunity after infection. We plot in Figure 6 the probability $p^{M}_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ of individual A, initially susceptible, suffering exactly M infections, for $M \in \{0, 1, 2, 3\}$, versus different values of $R_0 = \beta N$.

The probability of individual A suffering exactly 0 infections during the outbreak is 1 for $R_0 = 0$, and has a sharp decrease once the value $R_0 = 1$ is reached, as we could expect. It is interesting to note that the probabilities of individual A suffering exactly M infections, for $M \in \{1, 2, 3\}$, have maximums for values of R_0 slightly larger than 1. This is directly related to the

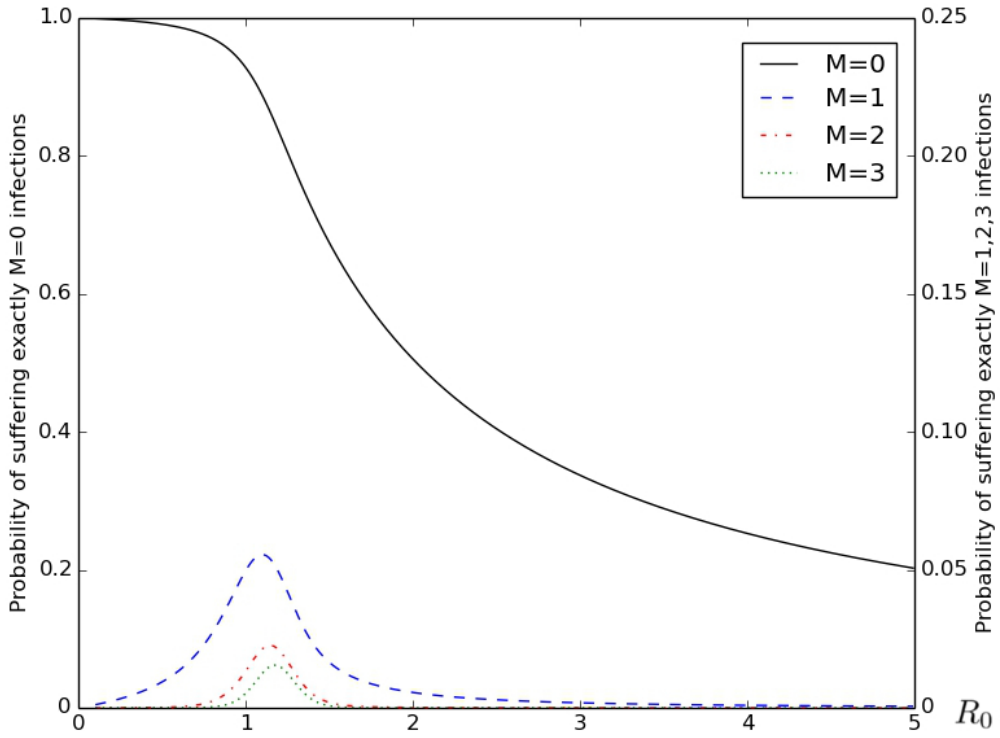

Figure 6: SIS Model. Probability $p^M_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ of individual A, initially susceptible, suffering exactly M infections, for $M \in \{0, 1, 2, 3\}$, versus different values of $R_0 = \beta N$. $N = 100$, $\gamma = 1$. Left y-axis: $M = 0$; Right y-axis: $M \in \{1, 2, 3\}$.

identification of endemic scenarios. For large values of $R_0 > 1$, endemicity corresponds to the individual suffering much more than two or three infections. On the other hand, for this individual suffering exactly 1, exactly 2 or exactly 3 infections, very precise values of R_0 near but larger than 1 are required.

3.1.2. SIRS Model: temporary immunity

In Figure 7 our interest is in analysing the SIRS model, where individuals recover susceptibility after a temporary immunity period. We plot in Figure 7 probabilities $p^M_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ as in Figure 6, while varying the value of $\alpha_R \in \{0.1, 0.2, 0.5, 1.0\}$. We note first that $\alpha_R \to 0$ represents the SIR model, while $\alpha_R \to \infty$ corresponds to the SIS model. Thus, for $\alpha_R = 1.0$ in Figure 7 we already can identify the same behaviours than the ones identified

for the SIS model in Figure 6. Small value $\alpha_R = 0.1$ in Figure 7 represents that individuals only recover susceptibility after a long immunity period. This means that, unless we consider a highly infectious disease (large values of R_0), individual A will only suffer at most 1 infection. This can be observed from the maximum corresponding to the probability of suffering exactly M infections, which occurs for a value of R_0 slightly larger than 3, and this curve slowly decreasing for larger values of R_0.

Shorter immunity periods (*e.g.,* $\alpha_R \in \{0.2, 0.5\}$) allow the individual to get infected several times, which translates into the maximum for the curve corresponding to $M = 1$ occurring closer to $R_0 = 1$ and decreasing faster after this value. It is also worth to point out that for large values of R_0 all the curves for $M \in \{1, 2, 3\}$ join before reaching values near 0, which means that for large values of R_0, the individual can suffer exactly 1, exactly 2 or exactly 3 infections with equal probability.

3.1.3. PPI Model: partial immunity

In Figure 8 we consider the PPI model, where individuals get partial immunity after infection, so that recovered individuals can become infected with some probability $\sigma \in (0, 1)$. We plot in Figure 8 the probabilities for the PPI model, while varying $\sigma \in \{0.1, 0.2, 0.5, 1.0\}$. Although the qualitative behaviour of curves in Figures 7 and 8 is similar, we can see that parameter σ has a more significant impact than α_R for avoiding re-infection of individuals. That is, temporary immunity allows for the individual to suffer more infections than partial immunity for comparable absolute values of α_R and σ. This can be observed by looking at curves corresponding to $M \in \{1, 2, 3\}$ for values $\alpha_R = 0.1$ and $\sigma = 0.1$ in these Figures, as well as for values $\alpha_R = 0.2$ and $\sigma = 0.2$.

3.1.4. AoN Model: random immunity

In Figure 9 we consider the AoN model, where individuals can gain immunity with probability p after infection. In Figure 9, we plot probability $p^M_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ of individual A, initially susceptible, suffering exactly M infections, for $p \in \{0.1, 0.25, 0.5, 0.75\}$. Asymptotic behaviour of curves in Figure 9 for $R_0 \to \infty$ is different than the ones observed in the other models considered. In particular, the AoN hypothesis does not yield maximums for each probability plotted in Figure 9, so that increasing values of R_0 yield threshold values for each probability of suffering exactly M infections, regardless of the value of M; see, for example, Figure 9 *top-left*.

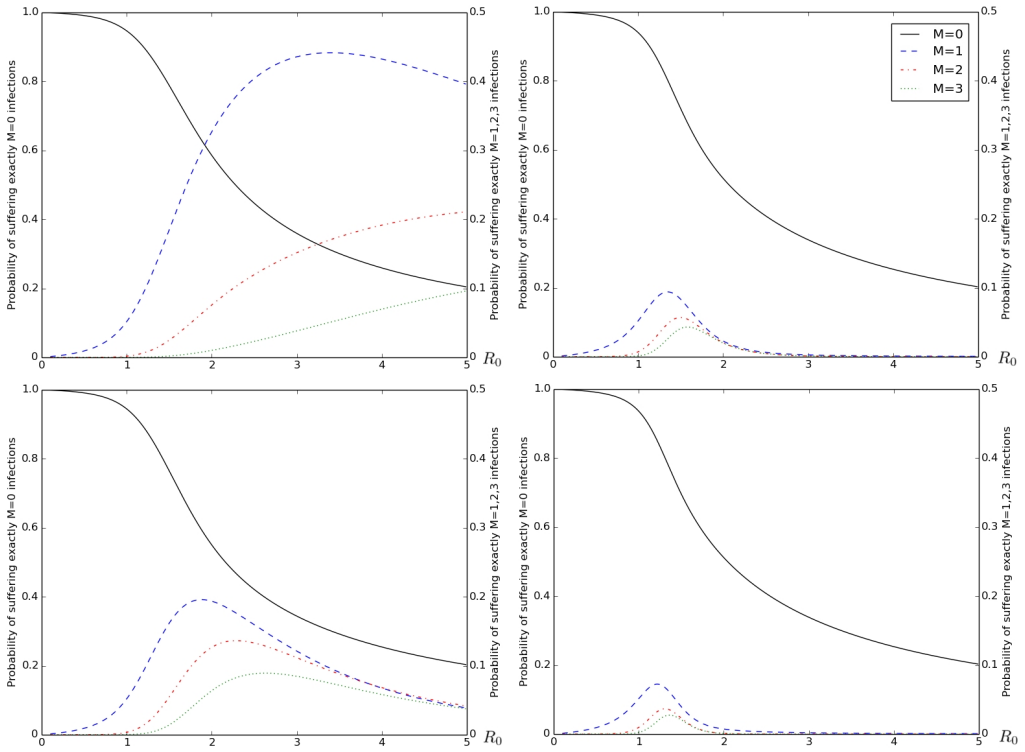

Figure 7: SIRS Model. Probability $p^{M}_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ of individual A, initially susceptible, suffering exactly M infections, for $M \in \{0, 1, 2, 3\}$, versus different values of $R_0 = \beta N$. $\gamma = 1$ and $N = 100$. Immunity is lost at rate $\alpha_R = 0.1$ (*top-left*), $\alpha_R = 0.2$ (*bottom-left*), $\alpha_R = 0.5$ (*top-right*) and $\alpha_R = 1.0$ (*bottom-right*). Left y-axis: $M = 0$; Right y-axis: $M \in \{1, 2, 3\}$.

3.2. The probabilities of suffering exactly M infections as the likelihood for estimation of parameters: Tristan da Cunha as a case study

Here, we can fit every model to Tristan da Cunha data and compare. The idea would be to explain how these probabilities can be used as the likelihood when estimating parameters. Moreover, given the large amount of parameters (β, γ, α_R,...) that we can vary, setting the parameters (at least for the SIRS type models in Figure 4) by means of this fitting would allow us to keep these parameter values when analysing an heterogeneous individual in SubSection 3.3.

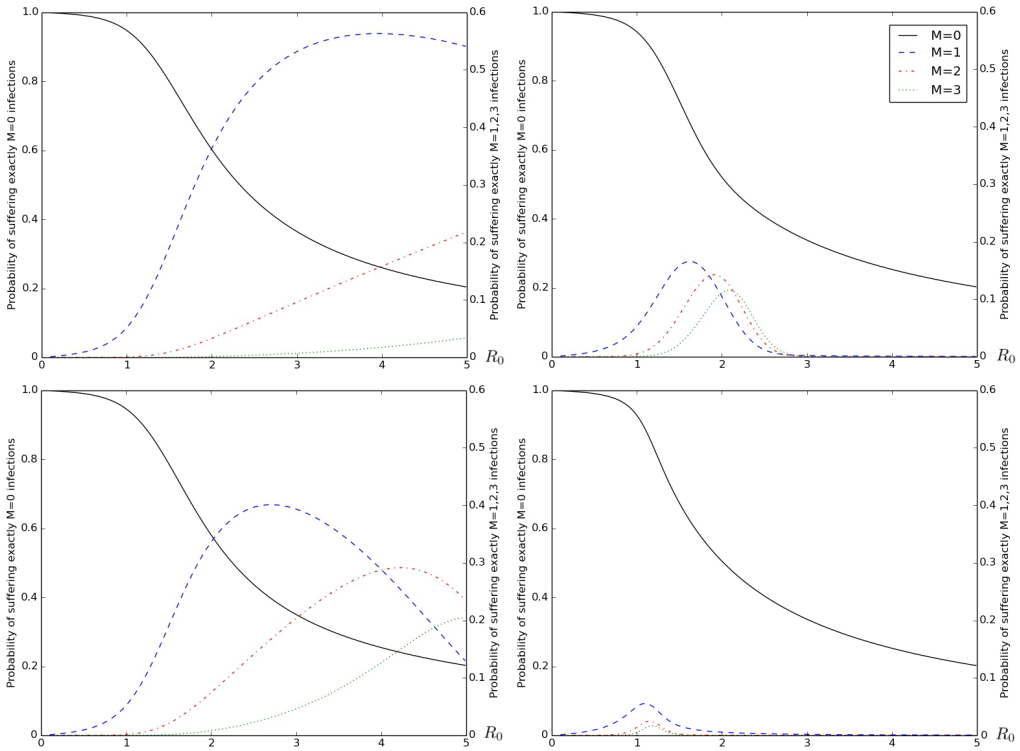

Figure 8: PPI Model. Probability $p^{M}_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ of individual A, initially susceptible, suffering exactly M infections, for $M \in \{0, 1, 2, 3\}$, versus different values of $R_0 = \beta N$. $\gamma = 1$ and $N = 100$. Partial immunity is represented here by parameter $\sigma = 0.1$ (*top-left*), $\sigma = 0.2$ (*bottom-left*), $\sigma = 0.5$ (*top-right*) and $\sigma = 1.0$ (*bottom-right*). Left y-axis: $M = 0$; Right y-axis: $M \in \{1, 2, 3\}$.

We consider... then, we propose the approximated likelihood...

$$L(\theta; \underline{x}) \quad = \quad \ldots$$

3.3. Analysis of a especial individual

In this SubSection, we can plot the histogram of the number of reinfections suffered by individual A (that is, probabilities for $M \in \{0, 1, 2, 3, 4\}$ within a histogram) for models SIS, AoN, PPI and SIRS just when parameter values are chosen from Table 3. Now, the question is how the reinfection dynamics of individual A are, when this individual is somehow special. In particular, we consider how these histograms vary when we consider:

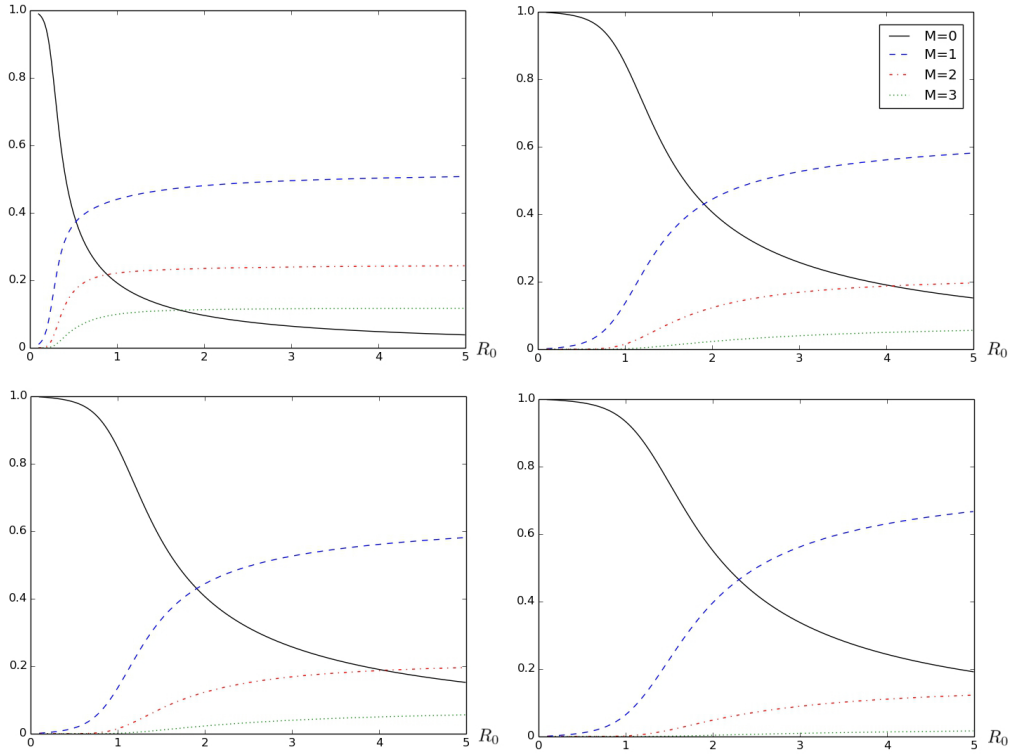

Figure 9: AoN Model. Probability $p^{M}_{(N-1,S)} - p^{M+1}_{(N-1,S)}$ of individual A, initially susceptible, suffering exactly M infections, for $M \in \{0, 1, 2, 3\}$, versus different values of $R_0 = \beta N$. $\gamma = 1$ and $N = 100$. All-or-Nothing probability $p = 0.1$ (*top-left*), $p = 0.25$ (*bottom-left*), $p = 0.5$ (*top-right*) and $p = 0.75$ (*bottom-right*). Left y-axis: $M = 0$; Right y-axis: $M \in \{1, 2, 3\}$.

MLE	SIS	AoN	PPI	SIRS
β				
γ				
σ	–	–		
α_R	–		–	
α_I	–		–	

Table 3: Maximum likelihood estimates (MLEs)...

- Individual A is a *super-infectious* individual ($\beta_{A\to\bullet} = 2\beta$),
- Individual A is a *super-susceptible* individual ($\beta_{\bullet\to A} = 2\beta$),

- Individual A is a *super-recoverable* individual ($\gamma(A) = 2\gamma$).

Acknowledgments

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Appendix A. Probability of suffering at least M infections

In this appendix, we show how to generalise our arguments in order to compute the probability of a marked individual A suffering at least M infections, with $M \geq 2$. We point out here that, in Section 2, we computed the probability of individual A suffering at least $M = 2$ infections (that is, suffering reinfection). Thus, we generalise our arguments in previous section for any value $M \geq 2$, for the SIS and the general TPI-SIR model.

A.1. SIS Model

We consider here the extended process $\mathcal{X}^{ext,M} = \{\mathbf{X}^{ext,M}(t) = (S^M(t), A^M(t)) : t \geq 0\}$, where we define $A^M(t)$ as the state of individual A at time $t \geq 0$, taking values among $a \in \{S_0, \ldots, S_{M-1}, I_1, \ldots, I_{M-1}\}$. In particular, $A^M(t) = S_j$ (or, alternatively, I_j) represents that individual A is, at current time t, susceptible (infected) and suffered exactly j infections up to time t. As before, we can consider that individual A has a different behavior against the disease than the rest of individuals in the population, by considering specific rates $\gamma(A)$, $\beta_{A\to\bullet}$ and $\beta_{\bullet\to A}$.

The space of states for our extended process $\mathcal{X}^{ext,M}$ is given by

$$\begin{aligned}\mathcal{S}^{ext,M} &= (\{1,\ldots,N-1\} \times \{S_0,\ldots,S_{M-1},I_1,\ldots,I_{M-1}\}) \cup (\{0\} \times \{I_1,\ldots,I_{M-1}\}) \\ &\quad \cup (\{N\} \times \{S_0,\ldots,S_{M-1}\}) \cup \{\Delta^M\},\end{aligned}$$

where Δ^M is an artificial absorbing state representing that individual A suffered, at least, M infections. Transitions between states in $\mathcal{S}^{ext,M}$ are given in Table 4, and we note that states of the form (N, a) are absorbing states for process $\mathcal{X}^{ext,M}$ representing the end of the outbreak without individual A suffering M infections.

Event	Original state	Destination state	Rate
Recovery of an infective individual	(m, S_j), $m \geq 1$	$(m+1, S_j)$	$\gamma(N-m)$
	(m, I_j), $j \geq 1$	$(m+1, S_j)$	$\gamma(A)$
	(m, I_j), $m \leq N-2$, $j \geq 1$	$(m+1, I_j)$	$\gamma(N-m-1)$
Infection of a susceptible individual	(m, S_j), $m \geq 1$, $j \leq M-2$	$(m-1, I_{j+1})$	$\beta_{\bullet \to A}(N-m)$
	(m, S_{M-1}), $m \geq 1$	Δ^M	$\beta_{\bullet \to A}(N-m)$
	(m, S_j), $m \geq 2$	$(m-1, S_j)$	$\beta(m-1)(N-m)$
	(m, I_j), $j \geq 1$	$(m-1, I_j)$	$\beta m(N-m-1) + \beta_{A \to \bullet} m$

Table 4: Transitions among states in $\mathcal{S}^{ext,M}$, for $0 \leq m \leq N-1$, $0 \leq j \leq M-1$.

We define $p^M_{(m,a)}$ as the probability of individual A suffering at least M infections, given the initial state of the process $(m, a) \in \mathcal{S}^{ext,M}$, with trivial probabilities $p^M_{\Delta^M} = 1$, $p^M_{(N,S_j)} = 0$ for all $0 \leq j \leq M-1$. These probabilities satisfy, for $0 \leq m \leq N-1$, $0 \leq j \leq M-1$, the equations

$$\begin{aligned}
\theta_{(m,S)} p^M_{(m,S_j)} &= \beta(m-1)(N-m) p^M_{(m-1,S_j)} + \beta_{\bullet \to A}(N-m)(1_{j=M-1} p^M_{\Delta^M} \\
&\quad + 1_{j<M-1} p^M_{(m-1,I_{j+1})}) + \gamma(N-m) p^M_{(m+1,S_j)}, \quad m \geq 1, \quad (Equation\ (E.S_j)) \\
\theta_{(m,I)} p^M_{(m,I_j)} &= (\beta m(N-m-1) + \beta_{A \to \bullet} m)\, p^M_{(m-1,I_j)} + \gamma(N-m-1) p^M_{(m+1,I_j)} \\
&\quad + \gamma(A) p^M_{(m+1,S_j)}, \quad j \geq 1, \quad (Equation\ (E.I_j))
\end{aligned}$$

with $\theta_{(m,S)}$ and $\theta_{(m,I)}$ defined in Section 2, and $1_{\mathcal{B}}$ a boolean function taking value 1 if condition $\mathcal{B}$ is verified, and 0 otherwise. These equations are directly related to the transitions diagram of $\mathcal{X}^{ext,M}$, given in Figure 10.

This diagram also gives some clue on how to iteratively solve the system of equations given by Eqs. $(E.S_j)-(E.I_j)$. In particular, we can start solving Equations $(E.S_{M-1})$ for $1 \leq m \leq N$ and, once probabilities $p^M_{(m,S_{M-1})}$ are in hand, Equations $(E.I_{M-1})$ can be solved, obtaining probabilities $p^M_{(m,I_{M-1})}$ for $0 \leq m \leq N-1$. Then, we can continue working in an algorithmic fashion solving Eqs. $(E.I_j)$ after Eqs. $(E.S_j)$. In particular, if we develop

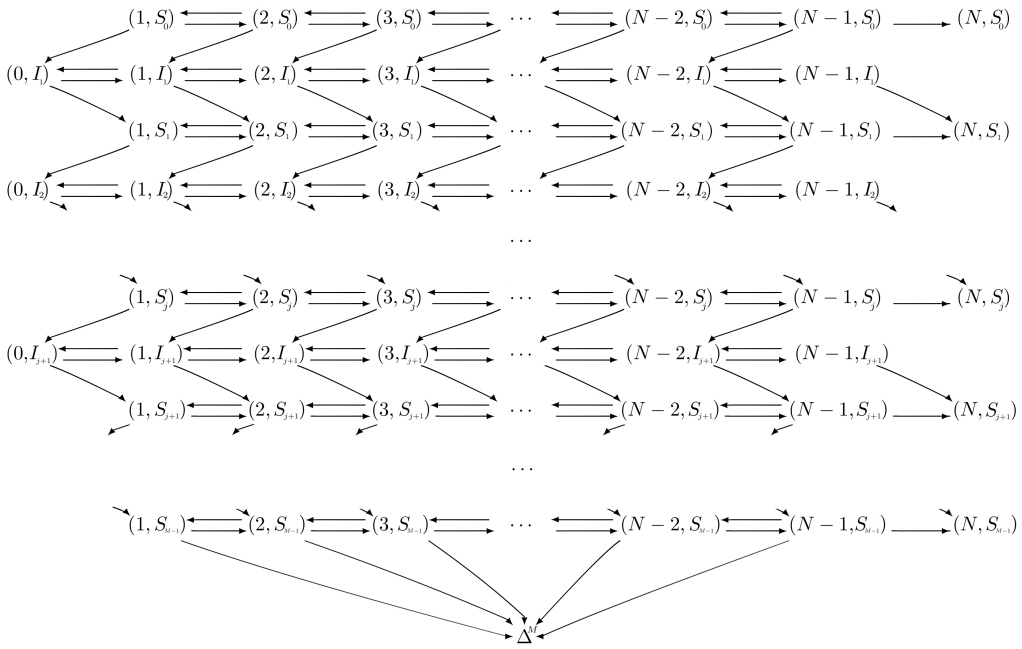

Figure 10: Transitions diagram for process $\mathcal{X}^{ext,M}$.

Algorithms S_j and I_j (following the same arguments than in Section 2), probabilities of interest are computed as follows:

Run Algorithm S_{M-1}*;*

For $j = M-2, \ldots, 0$*:*

Run Algorithm I_{j+1}*;*

Run Algorithm S_j*;*

with **Algorithms** S_j and I_j described below.

Algorithm S_j**,** $0 \leq j \leq M-1$

$g_{(N-1,S_j)} = \frac{\beta_{\bullet \to A}}{\theta_{(N-1,S)}} \left(1_{j=M-1} + 1_{j<M-1} p^M_{(N-2,I_{j+1})} \right)$;

For $m = N-2, \ldots, 1$*:*

$$g_{(m,S_j)} = \frac{\beta_{\bullet\to A}(N-m)}{\theta_{(m,S)}}\left(1_{j=M-1} + 1_{j<M-1}p^M_{(m-1,I_{j+1})}\right) + \frac{\gamma(N-m)}{\theta_{(m,S)}}h^{-1}_{(m+1,S)}g_{(m+1,S_j)};$$

$$p^M_{(1,S_j)} = h^{-1}_{(1,S)}g_{(1,S_j)};$$

For $m = 2, \ldots, N-1$*:*

$$p^M_{(m,S_j)} = h^{-1}_{(m,S)}\left(f_{(m,S)}p^M_{(m-1,S_j)} + g_{(m,S_j)}\right);$$

Algorithm I_j**,** $1 \leq j \leq M-1$

$$g_{(N-1,I_j)} = \frac{\gamma(A)}{\theta_{(N-1,I)}}p^M_{(N,S_j)};$$

For $m = N-2, \ldots, 0$*:*

$$g_{(m,I_j)} = \frac{\gamma(A)}{\theta_{(m,I)}}p^M_{(m+1,S_j)} + \frac{\gamma(N-m-1)}{\theta_{(m,I)}}h^{-1}_{(m+1,I)}g_{(m+1,I_j)};$$

$$p^M_{(0,I_j)} = h^{-1}_{(0,I)}g_{(0,I_j)};$$

For $m = 1, \ldots, N-1$*:*

$$p^M_{(m,I_j)} = h^{-1}_{(m,I)}\left(f_{(m,I)}p^M_{(m-1,I_j)} + g_{(m,I_j)}\right);$$

We note here that quantities $h_{(m,S)}$, $f_{(m,S)}$, $h_{(m,I)}$ and $f_{(m,I)}$ are the ones computed in **Algorithm 1**, since they do not depend on the value of j. Finally, it is worth to point out that, once probabilities $p^M_{(m,a)}$ are in hand for different values of M, the probability of individual A suffering exactly M infections given the initial state (m,a) is given by $p^M_{(m,a)} - p^{M+1}_{(m,a)}$.

A.2. TPI-SIR model

We proceed here as before and define the extended process $\tilde{\mathcal{X}}^{ext,M} = \{\tilde{\mathbf{X}}^{ext,M}(t) = (\tilde{S}^M(t), \tilde{I}^M(t), \tilde{A}^M(t)) : t \geq 0\}$ where $\tilde{A}^M(t)$ takes values among $a \in \{S_0, \ldots, S_{M-1}, I_1, \ldots, I_{M-1}, R_1, \ldots, R_{M-1}\}$. $\tilde{\mathcal{X}}^{ext,M}$ is defined over the space of states

$$\begin{aligned}\tilde{\mathcal{S}}^{ext,M} = &\left(\tilde{\mathcal{S}}^{ext,M}(S) \times \{S_0, \ldots, S_{M-1}\}\right) \cup \left(\tilde{\mathcal{S}}^{ext,M}(I) \times \{I_1, \ldots, I_{M-1}\}\right) \\ &\cup \left(\tilde{\mathcal{S}}^{ext,M}(R) \times \{R_1, \ldots, R_{M-1}\}\right) \cup \{\tilde{\Delta}^M\},\end{aligned}$$

where $\tilde{\Delta}^M$ is the artificial absorbing state representing that individual A suffered at least M infections, and where

$$\begin{aligned}
\tilde{\mathcal{S}}^{ext,M}(S) &= \{(m,n) \in \mathbb{N}_0^2 :\ m > 0,\ m+n \leq N\}, \\
\tilde{\mathcal{S}}^{ext,M}(I) &= \{(m,n) \in \mathbb{N}_0^2 :\ n > 0,\ m+n \leq N\}, \\
\tilde{\mathcal{S}}^{ext,M}(R) &= \{(m,n) \in \mathbb{N}_0^2 :\ m+n < N\},
\end{aligned}$$

relate to the numbers of susceptible and infective individuals when individual A is susceptible, infective or recovered, respectively. Possible transitions among states in our extended process are given in Table 5, where states of the form $(m,0,a)$ are considered as absorbing states, since they represent the situation where no infective individuals remain in the population.

If we define

$$\begin{aligned}
p^M_{(m,n,a)} &= \text{“}\textit{probability of individual } A \textit{ suffering at least } M \textit{ infections, given} \\
&\quad \textit{the initial state of the process } (m,n,a) \in \tilde{\mathcal{S}}^{ext,M}\text{”},
\end{aligned}$$

these probabilities satisfy the following equations, for $m \geq 0$, $n \geq 1$, $m+n \leq N$ and $0 \leq j \leq M-1$,

$$\begin{aligned}
\theta_{(m,n,S)} p^M_{(m,n,S_j)} &= \beta(m-1)np^M_{(m-1,n+1,S_j)} + \beta_{\bullet\to A} n \left(1_{j=M-1} p^M_{\tilde{\Delta}^M} + 1_{j<M-1} p^M_{(m-1,n+1,I_{j+1})}\right) \\
&\quad + \gamma n p^M_{(m,n-1,S_j)} + \alpha_I n p^M_{(m+1,n-1,S_j)} + \alpha_R(N-m-n)p^M_{(m+1,n,S_j)} \\
&\quad + \sigma\beta n(N-m-n)p^M_{(m,n+1,S_j)}, \quad m \geq 1,\ (\textit{Equation } (\tilde{E}.S_j)) \\
\theta_{(m,n,I)} p^M_{(m,n,I_j)} &= \left(\beta m(n-1) + \beta_{A\to\bullet} m\right) p^M_{(m-1,n+1,I_j)} + \gamma(n-1)p^M_{(m,n-1,I_j)} \\
&\quad + \gamma(A)p^M_{(m,n-1,R_j)} + \alpha_I(n-1)p^M_{(m+1,n-1,I_j)} + \alpha_I(A)p^M_{(m+1,n-1,S_j)} \\
&\quad + \left(\sigma\beta(n-1)(N-m-n) + \sigma\beta_{A\to\bullet}(N-m-n)\right) p^M_{(m,n+1,I_j)} \\
&\quad + \alpha_R(N-m-n)p^M_{(m+1,n,I_j)}, \quad j \geq 1, \quad (\textit{Equation } (\tilde{E}.I_j)) \\
\theta_{(m,n,R)} p^M_{(m,n,R_j)} &= \beta mn p^M_{(m-1,n+1,R_j)} + \gamma n p^M_{(m,n-1,R_j)} + \alpha_I n p^M_{(m+1,n-1,R_j)} \\
&\quad + \alpha_R(N-m-n-1)p^M_{(m+1,n,R_j)} + \alpha_R(A)p^M_{(m+1,n,S_j)} \\
&\quad + \sigma\beta n(N-m-n-1)p^M_{(m,n+1,R_j)} + \sigma(A)\beta_{\bullet\to A} n \left(1_{j=M-1} p^M_{\tilde{\Delta}^M}\right. \\
&\quad \left. + 1_{j<M-1} p^M_{(m,n+1,I_{j+1})}\right), \quad m+n < N,\ j \geq 1, \quad (\textit{Equation } (\tilde{E}.R_j))
\end{aligned}$$

with $\theta_{(m,n,S)}$, $\theta_{(m,n,I)}$ and $\theta_{(m,n,R)}$ defined in Section 2, and boundary conditions $p^M_{\tilde{\Delta}^M} = 1$, $p_{(m,0,S_j)} = p_{(m,0,R_j)} = 0$ for any m and j. These equations

Event	Original state	Destination state	Rate
Recovery of an infective individual	(m,n,S_j), $m\geq 1$,	$(m,n-1,S_j)$	γn
	(m,n,I_j), $n\geq 2$, $j\geq 1$	$(m,n-1,I_j)$	$\gamma(n-1)$
	(m,n,I_j), $j\geq 1$	$(m,n-1,R_j)$	$\gamma(A)$
	(m,n,R_j), $m+n<N$, $j\geq 1$	$(m,n-1,R_j)$	γn
Infection of a susceptible individual	(m,n,S_{M-1}), $m\geq 1$	$\tilde{\Delta}^M$	$\beta_{\bullet\to A}n$
	(m,n,S_j), $m\geq 2$	$(m-1,n+1,S_j)$	$\beta(m-1)n$
	(m,n,S_j), $m\geq 1$, $j\leq M-2$	$(m-1,n+1,I_{j+1})$	$\beta_{\bullet\to A}n$
	(m,n,I_j), $m\geq 1$, $j\geq 1$	$(m-1,n+1,I_j)$	$\beta m(n-1)+\beta_{A\to\bullet}m$
	(m,n,R_j), $m\geq 1$, $m+n<N$, $j\geq 1$	$(m-1,n+1,R_j)$	βmn
Infection of a recovered individual	(m,n,S_j), $m\geq 1$, $m+n<N$, $j\geq 1$	$(m,n+1,S_j)$	$\sigma\beta n(N-m-n)$
	(m,n,I_j), $m+n<N$, $j\geq 1$	$(m,n+1,I_j)$	$\sigma\beta(n-1)(N-m-n)$ $+\sigma\beta_{A\to\bullet}(N-m-n)$
	(m,n,R_j), $m+n<N-1$, $j\geq 1$	$(m,n+1,R_j)$	$\sigma\beta n(N-m-n-1)$
	(m,n,R_j), $m+n<N$, $1\leq j\leq M-2$	$(m,n+1,I_{j+1})$	$\sigma(A)\beta_{\bullet\to A}n$
	(m,n,R_{M-1}), $m+n<N$	$\tilde{\Delta}^M$	$\sigma(A)\beta_{\bullet\to A}n$
Immunity loss of an infective individual	(m,n,S_j), $m\geq 1$	$(m+1,n-1,S_j)$	$\alpha_I n$
	(m,n,I_j), $n\geq 2$, $j\geq 1$	$(m+1,n-1,I_j)$	$\alpha_I(n-1)$
	(m,n,I_j), $j\geq 1$	$(m+1,n-1,S_j)$	$\alpha_I(A)$
	(m,n,R_j), $m+n<N$, $j\geq 1$	$(m+1,n-1,R_j)$	$\alpha_I n$
Immunity loss of a recovered individual	(m,n,S_j), $m\geq 1$, $m+n<N$	$(m+1,n,S_j)$	$\alpha_R(N-m-n)$
	(m,n,I_j), $m+n<N$, $j\geq 1$	$(m+1,n,I_j)$	$\alpha_R(N-m-n)$
	(m,n,R_j), $m+n<N-1$, $j\geq 1$	$(m+1,n,R_j)$	$\alpha_R(N-m-n-1)$
	(m,n,R_j), $m+n<N$, $j\geq 1$	$(m+1,n,S_j)$	$\alpha_R(A)$

Table 5: Transitions among states in $\tilde{\mathcal{S}}^{ext,M}$, for $m\geq 0$, $n\geq 1$, $m+n\leq N$, and $0\leq j\leq M-1$.

can be solved one after the other following the diagram in Figure 11. This iterative procedure can be carried out by means of implementing a series of algorithms (**Algorithms** $\tilde{S}_j$, $\tilde{I}_j$ and $\tilde{R}_j$). In particular:

Run Algorithm $\tilde{S}_{M-1}$*;*

For $j=M-2,\ldots,0$*:*

Run Algorithm $\tilde{R}_{j+1}$*;*

Run Algorithm $\tilde{I}_{j+1}$*;*

Run Algorithm $\tilde{S}_j$*;*

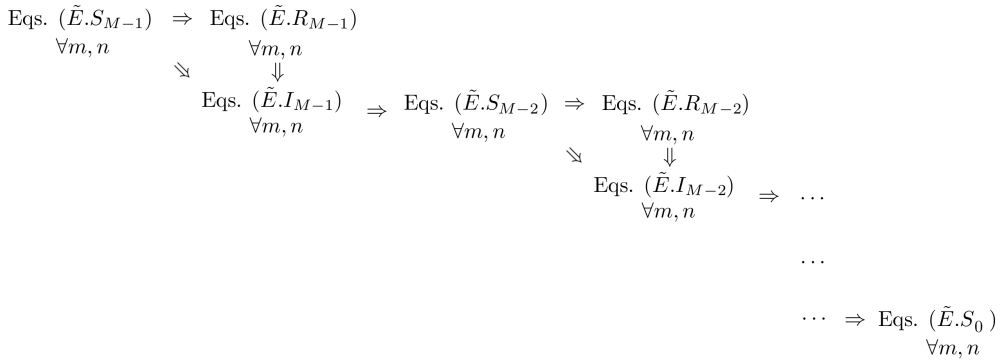

Figure 11: Diagram for solving Eqs. $(\tilde{E}.S_j) - (\tilde{E}.I_j) - (\tilde{E}.R_j)$ for all values of j.

Algorithm $\tilde{S}_j$

$$\mathbf{J}_2^M(S_j) \;=\; \mathbf{b}_2^M(S_j);$$

For $k = 3, \ldots, N$*:*

$$\mathbf{J}_k^M(S_j) \;=\; \mathbf{A}_{k,k-1}(S)\mathbf{H}_{k-1}(S)^{-1}\mathbf{J}_{k-1}^M(S_j) + \mathbf{b}_k^M(S_j);$$

$$\mathbf{p}_N^M(S_j) \;=\; \mathbf{H}_N(S)^{-1}\mathbf{J}_N^M(S_j);$$

For $k = N-1, \ldots, 2$*:*

$$\mathbf{p}_k^M(S_j) \;=\; \mathbf{H}_k(S)^{-1}\left(\mathbf{A}_{k,k+1}(S)\mathbf{p}_{k+1}^M(S_j) + \mathbf{J}_k^M(S_j)\right);$$

Algorithm $\tilde{R}_j$

$$\mathbf{J}_1^M(R_j) \;=\; \mathbf{b}_1^M(R_j);$$

For $k = 2, \ldots, N-1$*:*

$$\mathbf{J}_k^M(R_j) \;=\; \mathbf{A}_{k,k-1}(R)\mathbf{H}_{k-1}(R)^{-1}\mathbf{J}_{k-1}^M(R_j) + \mathbf{b}_k^M(R_j);$$

$$\mathbf{p}_{N-1}^M(R_j) \;=\; \mathbf{H}_{N-1}(R)^{-1}\mathbf{J}_{N-1}^M(R_j);$$

For $k = N-2, \ldots, 1$*:*

$$\mathbf{p}_k^M(R_j) \;=\; \mathbf{H}_k(R)^{-1}\left(\mathbf{A}_{k,k+1}(R)\mathbf{p}_{k+1}^M(R_j) + \mathbf{J}_k^M(R_j)\right);$$

Algorithm $\tilde{I}_j$

$\mathbf{J}_1^M(I_j) \;=\; \mathbf{b}_1^M(I_j)$;

For $k = 2, \ldots, N-1$*:*

$$\mathbf{J}_k^M(I_j) \;=\; \mathbf{A}_{k,k-1}(I)\mathbf{H}_{k-1}(I)^{-1}\mathbf{J}_{k-1}^M(I_j) + \mathbf{b}_k^M(I_j);$$

$\mathbf{p}_{N-1}^M(I_j) \;=\; \mathbf{H}_{N-1}(I)^{-1}\mathbf{J}_{N-1}^M(I_j)$;

For $k = N-2, \ldots, 1$*:*

$$\mathbf{p}_k^M(I_j) \;=\; \mathbf{H}_k(I)^{-1}\left(\mathbf{A}_{k,k+1}(I)\mathbf{p}_{k+1}^M(I_j) + \mathbf{J}_k^M(I_j)\right);$$

We note that:

- Matrices $\mathbf{A}_{k,k'}(S)$, $\mathbf{A}_{k,k'}(I)$, $\mathbf{A}_{k,k'}(R)$, $\mathbf{H}_k(S)$, $\mathbf{H}_k(I)$ and $\mathbf{H}_k(R)$ are defined in Section 2.
- Probability vectors $\mathbf{p}_k^M(S_j)$, $\mathbf{p}_k^M(I_j)$ and $\mathbf{p}_k^M(R_j)$ contain the desired probabilities $p_{(m,n,a)}^M$, and are structured in a similar fashion than vectors $\mathbf{p}_k(S)$, $\mathbf{p}_k(I)$ and $\mathbf{p}_k(R)$ in Section 2.

- Vectors $\mathbf{b}_k^M(\cdot)$ are given as follows

$$\mathbf{b}_k^M(S_j) = \begin{pmatrix} \frac{\beta_{\bullet\to A}}{\theta_{(k-1,1,S)}}\left(1_{j=M-1}+1_{j<M-1}p^M_{(k-2,2,I_{j+1})}\right) \\ \frac{\beta_{\bullet\to A}2}{\theta_{(k-2,2,S)}}\left(1_{j=M-1}+1_{j<M-1}p^M_{(k-3,3,I_{j+1})}\right) \\ \vdots \\ \frac{\beta_{\bullet\to A}(k-1)}{\theta_{(1,k-1,S)}}\left(1_{j=M-1}+1_{j<M-1}p^M_{(0,k,I_{j+1})}\right) \end{pmatrix},$$

$$\mathbf{b}_k^M(I_j) = \begin{pmatrix} 0 \\ \frac{\gamma(A)p^M_{(k-2,1,R_j)}+\alpha_I(A)p^M_{(k-1,1,S_j)}}{\theta_{(k-2,2,I)}} \\ \vdots \\ \frac{\gamma(A)p^M_{(0,k-1,R_j)}+\alpha_I(A)p^M_{(1,k-1,S_j)}}{\theta_{(0,k,I)}} \end{pmatrix},$$

$$\mathbf{b}_k^M(R_j) = \begin{pmatrix} \frac{\alpha_R(A)p^M_{(k,1,S_j)}+\sigma(A)\beta_{\bullet\to A}\left(1_{j=M-1}+1_{j<M-1}p^M_{(k-1,2,I_{j+1})}\right)}{\theta_{(k-1,1,R)}} \\ \frac{\alpha_R(A)p^M_{(k-1,2,S_j)}+2\sigma(A)\beta_{\bullet\to A}\left(1_{j=M-1}+1_{j<M-1}p^M_{(k-2,3,I_{j+1})}\right)}{\theta_{(k-2,2,R)}} \\ \vdots \\ \frac{\alpha_R(A)p^M_{(1,k,S_j)}+k\sigma(A)\beta_{\bullet\to A}\left(1_{j=M-1}+1_{j<M-1}p^M_{(0,k+1,I_{j+1})}\right)}{\theta_{(0,k,R)}} \end{pmatrix}.$$

Finally, once probabilities $p^M_{(m,n,a)}$ are in hand for different values of M, the probability of individual A suffering exactly M infections is given by $p^M_{(m,n,a)} - p^{M+1}_{(m,n,a)}$.

A.3. The number of individuals suffering at least M infections

We finally point out here that, for a completely homogeneous population and the SIS model (same arguments apply for the general TPI-SIR model), if the individual starting the infection is randomly chosen among individuals in the population, it is clear that

$$p^M = \mathbb{P}(A \textit{ suffering at least } M \textit{ infections}) = p^M_{(m-1,S_0)}\frac{N-1}{N} + p^M_{(m-1,I_1)}\frac{1}{N}.$$

Then, if we are interested in the random variable

Y^M = *"Number of individuals in the population suffering at least M infections"*,

it is clear that

$$p^M \;=\; \sum_{y=0}^{N} \mathbb{P}(A \textit{ suffering at least } M \textit{ infections} \mid Y^M = y)\mathbb{P}(Y^M = y)$$

and, since all the individuals are *symmetric*, we get

$$p^M \;=\; \sum_{y=0}^{N} \frac{y}{N}\mathbb{P}(Y^M = y) \;=\; \frac{E[Y^M]}{N}$$

Thus, once probabilities $p^M_{(m,a)}$ are in hand, we can easily obtain $E[Y^M]$ as

$$E[Y^M] \;=\; (N-1)p^M_{(m-1,S_0)} + p^M_{(m-1,I_1)},$$

while the probability mass function of Y^M could also be computed by following first-step arguments, which is out of the scope of this paper.