Discrete SIR model on a homogeneous tree and its continuous limit

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Abstract

We study a discrete Susceptible-Infected-Recovered (SIR) model for the spread of infectious disease on a homogeneous tree and the limit behavior of the model in the case when the tree vertex degree tends to infinity. We obtain the distribution of the time it takes for a susceptible vertex to get infected in terms of a solution of a non-linear integral equation under broad assumptions on the model parameters. Namely, infection rates are assumed to be time-dependent, and recovery times are given by random variables with a fairly arbitrary distribution. We then study the behavior of the model in the limit when the tree vertex degree tends to infinity, and infection rates are appropriately scaled. We show that in this limit the integral equation of the discrete model implies an equation for the susceptible population compartment. This is a master equation in the sense that both the infectious and the recovered compartments can be explicitly expressed in terms of its solution.

Keywords: SIR model; homogeneous tree; Bernoulli equation; non-linear equation; memory effects; fractional SIR models

1 Introduction

Studying the spread of infectious disease has been of great interest for a long time and has motivated a lot of mathematical models. Susceptible-Infected-Recovered (SIR) type models are among those that are commonly studied. A SIR model is a compartmental model, in which a population of individuals is divided into three distinct groups (compartments). The first compartment consists of individuals that are susceptible to the disease, but are not yet infected. The second compartment is represented by infected individuals. Finally, the remaining third compartment is a group of individuals, who have been infected and recovered from the disease.

In this paper we revisit a discrete stochastic SIR model and study its continuous limit (to be explained). In the discrete setting a population is modeled by vertices of a graph, and infection is transmitted from infected vertices to susceptible ones via edges of the graph. Such a model is usually studied under additional assumptions on the graph, infection rates and

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recovery times (e.g., see [1], [3], [7], [13], [14], [16], [18], and references therein). For example, if the underlying graph is complete, infection rates are constant and the recovery times are exponentially distributed, then the model is a discrete version of the classic SIR model of A.G. McKendrick and W.O. Kermack ([11]).

We study the discrete SIR model on a homogeneous tree. The latter is an infinite connected constant vertex degree graph without cycles. The constant vertex degree means that each vertex has the same number of adjacent vertices (neighbors). A homogeneous tree can serve as a mathematical model for an infinite closed homogeneous population, in which all individuals have the same number of social contacts. To the best of our knowledge the SIR model on a homogeneous tree has never been considered, despite many years of study of the SIR model on graphs (networks).

The discrete model is studied under broad assumptions on both infection rates and recovery times. In particular, we assume that an infected vertex emits germs according to a Poisson process with a time-dependent rate. A susceptible vertex can be also infected by itself (according to another Poisson process), which can be interpreted as a source of infection outside of the population. Infection rates are assumed to be time-dependent deterministic functions. An infected vertex recovers in a period of time given by a random variable. Recovery times are assumed to be independent identically distributed random variables with a fairly arbitrary common distribution.

Our main result for the discrete model is concerned with the distribution of the time it takes for a susceptible vertex to get infected (the time to infection). We obtain a simple analytical expression for this distribution in terms of a solution of a non-linear integral equation. In some special cases this integral equation is equivalent to a differential equation of Bernoulli type (depending on a particular case). In one of these cases the corresponding differential equation can be solved analytically.

The structure of a homogeneous tree plays an essential role in our analysis. The key observation is that a susceptible vertex splits the homogeneous tree into a finite number of identical subgraphs, and infection processes on these subgraphs are independent and identically distributed.

We then study the discrete model in the limit, as the vertex degree of the tree tends to infinity, and the infection rate decreases proportionally. We show that in this limit our results for the discrete model imply an equation for the susceptible compartment. We call it the master equation, because both the infectious and the recovered compartments can be explicitly expressed in terms of its solution. This generalizes the results in ([9], [10] and [12]), where the system of equations of the classic Kermack-McKendrick SIR model was reduced to a single equation.

The obtained continuous SIR model is fairly general and provides a flexible technical framework for modeling various infectious and recovery dynamics. In fact, the master equation implies a family of continuous SIR models. A particular SIR model depends on the structure and interpretation of the model parameters. For example, the Kermack-McKendrick SIR model is a special case of our model. Another special case of the model coincides with the SIR model proposed in [6].

The rest of the paper is organized as follows. In Section 2 we consider the discrete SIR model. The model is formally defined in Section 2.1. The main result for the discrete model is
stated and proved in Section 2.2. In Section 3.1 we use this result to derive the master equation for the susceptible compartment in the limit, as the tree vertex degree tends to infinity. We discuss the continuous SIR model implied by the master equation in Section 3.2 and briefly comment of the relationship of our model with fractional SIR models in Section 4. Finally, in Section 5 we consider some special cases in which the integral equation of the discrete model can be written in the differential form.

2 The discrete SIR model

2.1 The model definition

We start with defining the discrete continuous time SIR model on a general graph (since a particular structure of the graph is not important at the definition). Let $\mathcal{T}$ be a connected (and possibly infinite) graph. With some abuse of notation, we will associate a graph with the set of its vertices. Given vertices $x, y \in \mathcal{T}$ we write $x \sim y$, if these vertices are connected by an edge, in which case we call them neighbors. Given a vertex its vertex degree is defined as the number of its neighbors. A vertex can be either susceptible, or infected, or recovered (and immune). At time $t = 0$ each vertex is either susceptible, or infected (in which case we assume that it gets infected at time $t = 0$). When a vertex becomes infected, it starts emitting infectious germs towards all of its neighbors and continues to do so until the moment of its recovery from the disease. When a susceptible vertex gets a germ, it becomes infected, and all subsequently arrived germs do not give any additional effect. An infected vertex emits germs to a given neighbor according to a Poisson process with a time dependent rate. Namely, if a vertex $y \in \mathcal{T}$ becomes infected at time $t_y$ and recovers in a time given in the general case by a random variable $H_y$, then, at time $t \in [t_y, t_y + H_y]$ it infects a susceptible neighbor with the rate $\varepsilon_{t-t_y}$, where $(\varepsilon_t, t \geq 0)$ is a non-negative deterministic function. A susceptible vertex can be also infected by itself, according to a Poisson process with the time-dependent rate $\lambda_t$, where $(\lambda_t, t \geq 0)$ is a non-negative deterministic function. Thus, given $t_y, H_y = h_y$ for $y \sim x$, a susceptible vertex $x$ is infected at time $t$ with the following total infection rate

$$\lambda_t + \sum_{y:y \sim x} \varepsilon_{t-t_y} \cdot 1\{t_y \leq t \leq t_y + h_y\}. \tag{1}$$

We assume that all random variables are realized on a certain probability space $(\Omega, \mathcal{F}, P)$, the expectation with respect to the probability $P$ is denoted by $E$; all Poisson processes are independent of each other, and they are also independent of the recovery times.

Both infection rates and recovery times can be fairly arbitrary. However, some minimal technical assumptions are required. These assumptions are as follows.

(A1) Functions $(\varepsilon_t, t \geq 0)$ and $(\lambda_t, t \geq 0)$ are bounded measurable functions.

(A2) Recovery times $\{H_y, y \in \mathcal{T}\}$ are given by independent identically distributed random variables. The common distribution of recovery times is either absolutely continuous, or discrete, or a mixture of these two types of distributions. A special case is when the recovery time is given by a deterministic constant $H$ (including the limit case $H = \infty$).
Remark 1. If $\varepsilon_t \equiv \text{const}$, the recovery time is exponentially distributed, the underlying graph is complete (i.e. any two vertices are neighbors) and $\lambda_t \equiv 0$, then the corresponding discrete SIR model is a discrete version of the classic Kermack-McKendrick model.

Remark 2. Note that the case when the recovery time is given by a deterministic constant $H$ can be modeled by assuming that $\varepsilon_t = 0$ for $t \geq H$. Setting formally $H = \infty$ gives the model, in which an infected individual never recovers and stays infectious forever. This is not entirely realistic. However, by considering a function $\varepsilon$, which decays to zero sufficiently fast, one can model a situation, when contagiousness of a chronically infected individual practically vanishes in a finite time.

2.2 Distribution of the time to infection

In this section we state and prove the main result (Theorem 1 below) for the discrete SIR model on a homogeneous tree.

Let $\varphi_t$ be the probability that an infected at time 0 vertex does not emit a germ towards a given neighbor until time $t$, and let $f_t$ be the probability that an initially susceptible vertex is not self-infected until time $t$. Then

$$\varphi_t = \begin{cases} 1, & t < 0, \\ E \left( e^{-\int_0^{t\wedge H} \varepsilon_u \, du} \right), & t \geq 0, \end{cases} \quad \text{and} \quad f_t = \begin{cases} 1, & t < 0, \\ e^{-\int_0^t \lambda_u \, du}, & t \geq 0, \end{cases}$$

where, for technical convenience, we define both probabilities by unity for $t < 0$, and $H$ is a random variable that has the same distribution as the recovery times.

Theorem 1. Let $T$ be a homogeneous tree with the vertex degree $n+1$, where $n \geq 1$. Assume that at time $t = 0$ a vertex $x \in T$ is infected with probability $p$ and is susceptible with probability $1 - p$ independently of other vertices. Let $\tau$ be the time it takes for a susceptible vertex to get infected. Then

$$P(\tau > t) = (1 - p)f_t[s_t]^{n+1} \quad \text{for} \quad t \geq 0,$$
where the function \( s_t \) satisfies the integral equation

\[
s_t = \varphi_t - (1 - p) \int_0^t f_u s_u \varphi_{t-u} du,
\]

where functions \( \varphi \) and \( f \) are defined in \([2]\) and \( \varphi' \) is the derivative of \( \varphi \).

**Proof of Theorem 7.** Consider a susceptible vertex \( x \in \mathcal{T} \) and define the probability

\[
s_t = P(x \text{ not infected by a given neighbor before time } t),
\]

which does not depend on a neighbor due to homogeneity of both the tree and the initial condition. Recall that infectious neighbors infect the vertex \( x \) independently of each other, and there is an independent chance of self-infection. Therefore, we have that

\[
P(\text{susceptible } x \text{ not infected neither by its neighbors, nor by itself before time } t) = f_t s_{t+1} \quad \text{for } t \geq 0,
\]

and, hence,

\[
P(\tau > t) = (1 - p) f_t s_{t+1} \quad \text{for } t \geq 0,
\]

where the factor \( f_t \) is defined in \([2]\).

Further, recall that a rooted homogeneous tree with the vertex degree \( N \geq 2 \) as a tree, where one of the vertices, called the root, has \( N - 1 \) neighbors, while any other vertex has \( N \) neighbors. Then, observe that removing the vertex \( x \) and all edges connecting \( x \) to its neighbors generates \( n + 1 \) subgraphs given by rooted trees with roots \( y_1, ..., y_{n+1} \), that are neighbors of \( x \). Further, given a neighbor \( y \sim x \) consider an auxiliary SIR model on the rooted tree \( \mathcal{T}_y \) with the root \( y \). Assume that the auxiliary SIR model is specified by the same parameters as the original SIR model on the tree \( \mathcal{T} \). In particular, we assume that at time \( t = 0 \) any vertex in the auxiliary model is either infected with probability \( p \) or susceptible with probability \( 1 - p \), independently of other vertices. Let \( \tilde{\tau} \) be the time to infection of the root vertex \( y \) in the auxiliary SIR model on the graph \( \mathcal{T}_y \). Similarly to equations \((6)-(7)\) in the original model, we have that

\[
P(\tilde{\tau} > t) = (1 - p) f_t s_{t}^n \quad \text{for } t \geq 0.
\]

Further, observe that if the root \( y \) is not infected, then, due to the similarity of the rooted trees, the time before infection of any of its susceptible neighbor has the same distribution as the infection time \( \tilde{\tau} \). Combining this fact with the law of total probability with \((8)\) gives the following equation for the probability \( s_t \)

\[
s_t = p \varphi_t - (1 - p) \int_0^t \varphi_{t-u}(f_u s_u^n)' du + (1 - p) f_t s_t^n \quad \text{for } t \geq 0,
\]

where the function \( \varphi \) is defined in \([2]\). Integrating by parts gives the equation

\[
s_t = \varphi_t - (1 - p) \int_0^t f_u s_u \varphi_{t-u} du,
\]
which is the integral equation (4), as claimed.

**Remark 3.** Consider the SIR model on a homogeneous tree, in which recovery times are given by i.i.d. random variables (including the degenerate case of deterministic recovery time). Recall the function \((\varphi_t, t \geq 0)\) defined in (2) and let

\[
\tilde{\varepsilon}_t = -\frac{d}{dt} \left( \log(\varphi_t) \right) \quad \text{for} \quad t \geq 0.
\]

(11)

It is easy to see that, as long as one is interested in the distribution of the time to infection, they can consider an equivalent model with just susceptible and infected compartments, in which the recovery mechanism is somehow embedded into the new infection rate given by the function \(\tilde{\varepsilon}_t = (\tilde{\varepsilon}_t, t \geq 0)\). For example, consider a SIR model with the infection rate \(\varepsilon_t = (\varepsilon_t, t \geq 0)\) such that \(\varepsilon_t > 0\) for all \(t \geq 0\), and the deterministic recovery time given by a constant \(H > 0\), then

\[
\tilde{\varepsilon}_t = \begin{cases} 
\varepsilon_t, & \text{for } t \leq H, \\
0, & \text{for } t > H.
\end{cases}
\]

(12)

Trivially, if \(H = \infty\), then \(\tilde{\varepsilon}_t = \varepsilon_t\) for all \(t \geq 0\). However, the function \(\tilde{\varepsilon}_t\) can differ significantly from the original function \(\varepsilon_t\) in the case of the random recovery time (e.g., see Corollary 3 in Section 5).

**Remark 4.** In some special cases, the obtained integral equation is equivalent to the Bernoulli type differential equation, which can be solved analytically (see Section 5 for examples).

### 3 Continuous limit of the discrete model

#### 3.1 The master equation

In this section we analyze integral equation (4) in the limit, as the tree vertex degree goes to infinity. Specifically, we show that in this limit the integral equation implies an equation for the susceptible population proportion.

**Theorem 2.** Consider the discrete SIR model on the homogeneous tree \(T\) with the vertex degree \(n + 1\). Suppose that an infected vertex infects a susceptible neighbor with the rate \(\frac{1}{n+1} \varepsilon_t\) after time \(t\) of being infected, where \((\varepsilon_t, t \geq 0)\) is a non-negative function. In addition, suppose that the other model parameters (i.e. the recovery times and the rate of self-infection) do not depend on \(n\). Let \(S_{t,n}\) be the expected susceptible population in this SIR model. Let \((S_t, t \geq 0)\) be a limit point of the sequence of functions \((S_{t,n}, t \geq 0), n \geq 1\), in the sense of the pointwise convergence. Then the function \((S_t, t \geq 0)\) must satisfy the following equation

\[
\log \left( \frac{S_t}{S_0} \right) = -\int_0^t \lambda_u du - \int_0^t (1 - S_u) \gamma_{t-u} du,
\]

(13)

where

\[
\gamma_t := \varepsilon_t P(H > t) \quad \text{for} \quad t \geq 0
\]

(14)

and \(S_0 = 1 - p\) (i.e. it is the probability for a vertex to be susceptible at time \(t = 0\) in the discrete model).
Proof. Note first, that the corresponding \( \varphi \)-function (see equation (2)) is given by

\[
\varphi_{t,n} = \begin{cases} 
1, & t < 0, \\
E \left( e^{-\frac{1}{n+1} \int_0^{\frac{t}{n+1}} \varepsilon_u du} \right), & t \geq 0.
\end{cases}
\]

By Theorem [1]

\[
S_{t,n} = S_{0,n} f_t[s_{t,n}]^{n+1} \quad \text{for} \quad t \geq 0,
\]

(15)

where the function \( s_{t,n} \) satisfies the equation

\[
s_{t,n} = \varphi_{t,n} - S_{0,n} \int_0^t f_u s_{u,n}^n \varphi_{t-n,u} du \quad \text{with} \quad S_{0,n} = 1 - p = S_0.
\]

(16)

By (15)-(16),

\[
s_{t,n} = \left( \frac{S_{t,n}}{S_0 f_t} \right)^{\frac{1}{n+1}} = 1 + \frac{1}{n+1} \left( \log \left( \frac{S_{t,n}}{S_0} \right) - \log(f_t) \right) + o \left( \frac{1}{n+1} \right),
\]

so that

\[
\log \left( \frac{S_{t,n}}{S_0} \right) - \log(f_t) = (n+1)(\varphi_{t,n} - 1) - \int_0^t (S_{u,n})^{\frac{n}{n+1}} (S_0 f_u)^{\frac{1}{n+1}} [(n+1)\varphi_{t-u,n}] du.
\]

(17)

A direct computation (we skip details) gives that

\[
(n+1)(\varphi_{t,n} - 1) = -E \left( \int_0^{\frac{t}{n+1}} \varepsilon_u du \right) + o(1) = \int_0^t \gamma_u du + o(1)
\]

(18)

\[
(n+1)\varphi'_{t,n} = -\gamma_t e^{-\frac{1}{n+1} \int_0^t \varepsilon_u du} = -\gamma_t (1 + o(1))
\]

(19)

for any fixed \( t \geq 0 \), where the function \( \gamma_t \) is defined in (14). In addition, note that \( (S_0 f_u)^{\frac{1}{n+1}} \to 1 \) and \( (S_{u,n})^{\frac{n}{n+1}} \to S_{u,n} \), as \( n \to \infty \). Combining this with (28)-(19) allows to rewrite (17) as follows

\[
\log \left( \frac{S_{t,n}}{S_0} \right) - \log(f_t) = \int_0^t \gamma_u du + \int_0^t S_{u,n} \gamma_{t-u} du + o(1)
\]

(20)

\[
= \int_0^t (1 - S_{u,n}) \gamma_{t-u} du + o(1).
\]

Since \( \log(f_t) = -\int_0^t \lambda_u du \), we obtain that

\[
\log \left( \frac{S_{t,n}}{S_0} \right) = -\int_0^t \lambda_u du - \int_0^t (1 - S_{u,n}) \gamma_{t-u} du + o(1),
\]

(21)
which implies, by the dominated convergence theorem, equation (13) for any pointwise limit point \((S_t, t \geq 0)\) for the sequence of functions \((S_{t,n}, t \geq 0), \ n \geq 1\), as claimed.

Differentiating (13) gives the master equation in the differential form

\[
\frac{S'_t}{S_t} = -\lambda_t - (1 - S_t)\gamma_0 - \int_0^t (1 - S_u)\gamma'_{t-u}du,
\]

or, equivalently,

\[
\frac{S'_t}{S_t} = -\lambda_t - (1 - S_0)\gamma_t + \int_0^t S'_u\gamma_{t-u}du.
\]

**Remark 5.** The existence and the uniqueness of solution of equation (13) follows from general results for integral equations with delay ([5]). It can be shown that the sequence of functions \((S_{t,n}, t \geq 0), \ n \geq 1\), is equicontinuous. Therefore, there exists a subsequence that uniformly converges to the solution of (13). We skip the technical details.

**Remark 6.** It follows from equation (13) that stationary value \(S_\infty\) satisfies the following equation

\[
\log\left(\frac{S_\infty}{S_0}\right) = -\int_0^{\infty} \lambda_u du - (1 - S_\infty)\int_0^{\infty} \gamma_u du.
\]

**Remark 7.** Note that equation (13) (or its differential equivalent (23)) is a standalone equation for the susceptible population \(S_t\), namely that this equation does not involve neither the infected, nor the recovered populations.

**Remark 8.** It should be noted that all the information concerning the infection rates and recovery times of the original discrete SIR model is included in (23) via the function \(\gamma\). For example, if the recovery time in the discrete SIR model is given by a deterministic constant \(H\), then

\[
\gamma_t = \begin{cases} 
\epsilon_t, & \text{for } t < H, \\
0, & \text{for } t \geq H,
\end{cases}
\]

where \(\epsilon_t\) is the rate of infection in the discrete model. In particular, if \(H = \infty\), then \(\gamma_t = \epsilon_t\). In general, these two functions are different (see Example 2 below).

### 3.2 Continuous SIR models implied by the master equation

In this section we show that the master equation (13) for the susceptible population implies equations for other population compartments (which explains the term master equation). A SIR model implied by the master equation (13) depends on the structure and its interpretation of the function \(\gamma\). To clarify what is meant by “interpretation” consider the case when \(\gamma_t = 0\) for all \(t > H\) for some \(H > 0\). This can be interpreted as an infected individual recovering after time \(H\) since the moment of being infected (as in Remark 8). On the other hand, this can be interpreted, as if an infected individual never recovers, but becomes not contagious to others after time \(H\) since the moment of being infected. In this case one can operate with just two compartments, namely susceptible and infected ones. Below we consider examples, where this
argument is reinforced. Note that for simplicity of exposition and without loss of generality we assume throughout this section that

$$\lambda_t \equiv 0,$$  \hspace{1cm} (25)

i.e. there is no self-infection.

### 3.2.1 The model with no recovery

The basic continuous SIR model implied by the master equation is a two-compartmental model, in which the population is divided into two compartments, namely, the compartment of susceptible individuals, described by the variable $S_t$, and the compartment of infected ones, described by the variable $I_t$, so that

$$1 = S_t + I_t \quad \text{and} \quad t \geq 0.$$  \hspace{1cm} (26)

Then $S'_t = -I'_t$, which allows to rewrite equation (23) as follows

$$S'_t = -S_t \left( I_0 \gamma_t + \int_0^t I'_u \gamma_t - u \, du \right).$$  \hspace{1cm} (27)

Equation (27) describes the model, in which an individual infected at time $u \geq 0$ infects any susceptible individual with the rate $\gamma_{t-u}$ at time $t > u$. This model can be interpreted as the model without recovery.

**Example 1** (The model with latent period). Suppose that an infected individual is latent for a non-random period of time of length $L > 0$. In addition, suppose that the rate of infection is constant. Then $\gamma_t = \varepsilon 1_{\{t \geq L\}}$, where $\varepsilon$ is the rate of infection, and equation (27) becomes as follows

$$S'_t = -\varepsilon S_t I_{t-L} \quad \text{and} \quad I'_t = -S'_t.$$

### 3.2.2 Model with a constant rate of infection and random recovery

Suppose that the function $\gamma_t$ is of the following form

$$\gamma_t = \varepsilon \beta_t \quad \text{for} \quad t \geq 0,$$  \hspace{1cm} (28)

where $\varepsilon > 0$ is a given constant and $\beta_t$ is a non-increasing positive function, such that $\beta_0 = 1$ and $\beta_t \rightarrow 0$, as $t \rightarrow \infty$. Then, the master equation implies the continuous SIR model with the three standard compartments, in which an infected individual recovers in a time given by random variable $\xi$ with the tail distribution $P(\xi > t) = \beta_t$, and during its infectious period it infects any susceptible one with the constant rate $\varepsilon$. Indeed, under these assumptions, equation (23) is as follows (recall that (25))

$$S'_t = -\varepsilon S_t \left( I_0 \beta_t - \int_0^t S'_u \beta_{t-u} \, du \right).$$  \hspace{1cm} (29)
Define
\[ I_t = I_0 \beta_t - \int_0^t S'_u \beta_{t-u} du \quad \text{for} \quad t > 0 \quad \text{and} \quad I_0 = 1 - S_0 \] (30)
and
\[ R_t = I_0 (1 - \beta_t) - \int_0^t S'_u (1 - \beta_{t-u}) du \quad \text{for} \quad t > 0 \quad \text{and} \quad R_0 = 0. \] (31)

It is easy to see that
\[ 1 = S_t + I_t + R_t \quad \text{for} \quad t \geq 0. \] (32)

Moreover, one can show that both \( I_t \geq 0 \) and \( R_t \geq 0 \) (we skip the details). Therefore, variables \( I_t \) and \( R_t \) can be interpreted as the population proportions of infected and recovered individuals respectively in the continuous SIR model with the constant rate of infection \( \varepsilon \) and the random recovery time with the tail distribution given by the function \( \beta \). Indeed, in this model the infected compartment at time \( t \) consists of 1) those who were infected at time 0 and did not recover before time \( t \) (which gives the first term \( I_0 \beta_t \) in (30), and 2) those, who were infected at time \( u \in (0, t] \) and did not recover before time \( t \) (integrating over time gives the integral term in (30)). A similar argument gives (46), which also follows from (30) and (32) combined with the initial condition \( S_0 + I_0 = 1 \). Differentiating both (30) and (31), and combining them with (29), we get the following system of equations

\[ S'_t = -\varepsilon S_t I_t, \] (33)

\[ I'_t = \varepsilon S_t I_t + I_0 \beta'_t + \varepsilon \int_0^t S_u I_u \beta'_{t-u} du, \] (34)

\[ R'_t = -I_0 \beta'_t - \varepsilon \int_0^t S_u I_u \beta'_{t-u} du. \] (35)

**Remark 9.** The system of equations (33)-(35) is similar to the system of equations of the delay model proposed in [6] for modeling the spread of Covid-19 in Italy.

**Example 2** (The classic SIR model). Consider the discrete SIR model on a homogeneous tree with the vertex degree \( n + 1 \). Assume that the infection rate is constant, i.e. \( \varepsilon_t \equiv \varepsilon \) for some constant \( \varepsilon > 0 \), and that the recovery time \( H \) is exponentially distributed with parameter \( \mu \), i.e. \( P(H > t) = e^{-\mu t} \) for \( t \geq 0 \). In addition, assume that there is no self-infection, i.e. \( \lambda_t = 0 \) for \( t \geq 0 \). Then
\[ E \left( \int_0^{t \wedge H} \varepsilon_u du \right) = \varepsilon E(\min(t, H)) = \frac{\varepsilon}{\mu} \left( 1 - e^{-\mu t} \right), \]
so that \( \gamma_t = \varepsilon e^{-\mu t} \) for \( t \geq 0 \). Setting \( \beta_t = \frac{\mu}{\varepsilon} = e^{-\mu t} \) gives a special case of (28). The system of
equations (33)-(35) becomes as follows

\[ S'_t = -\varepsilon S_t I_t, \quad (36) \]
\[ I'_t = \varepsilon S_t I_t - \mu I_t, \quad (37) \]
\[ R'_t = \mu I_t, \quad (38) \]

which is the system of equations of the classic Kermack-McKendrick model (with the infection rate \( \varepsilon \) and the recovery rate \( \mu \)).

**Remark 10.** Note that in Example 2 it is probably more convenient to start with equation (13), which in this case is as follows

\[ \log \left( \frac{S_t}{S_0} \right) = -\varepsilon \int_0^t (1 - S_u) e^{-\mu(t-u)} du. \quad (39) \]

Then, differentiating (39) gives that

\[ S'_t = -\varepsilon S_t \left( 1 - S_t - \mu \int_0^t (1 - S_u) e^{-\mu(t-u)} du \right). \quad (40) \]

Combining (40) with (39) we obtain the following equation

\[ S'_t = -\varepsilon S_t \left( 1 - S_t + \frac{\mu}{\varepsilon} \log \left( \frac{S_t}{S_0} \right) \right), \quad (41) \]

which is the master equation (in the differential form) corresponding to the Kermack-McKendrick model. Setting \( I_t = 1 - S_t + \frac{\mu}{\varepsilon} \log \left( \frac{S_t}{S_0} \right) \), one can proceed as in Example 2 to get the equations (36)-(38).

**Remark 11.** It should be noted that the master equation (41) is well-known. For example, it is the same as equation (22) in [12] and is also equivalent to equation (26) in [9].

**Remark 12.** Note that equating the time derivative to zero in equation (41), i.e. \( S'_t = 0 \), gives the known equation

\[ 1 - S + \frac{\mu}{\varepsilon} \log \left( \frac{S}{S_0} \right) = 0 \quad (42) \]

for the stationary population proportion of susceptible individuals \( S \) in the SIR model (e.g. see equation (7) in [4] and references therein). In particular, this equation shows that the stationary value \( S \) depends only on the ratio \( \mu/\varepsilon = 1/R_0 \), where \( R_0 \) is the basic reproduction number in the classic SIR model. Note also that equation (42) is just a special case of more general equation (24) for the stationary susceptible state.

**Example 3** (Constant rate of infection and deterministic recovery). Consider a model, in which the infection rate is given by a constant \( \varepsilon > 0 \), and the recovery time is given by a deterministic constant \( H > 0 \). This model can be obtained by setting \( \gamma_t = \varepsilon \) for \( t \in [0, H] \) and \( \gamma_t = 0 \) for
\( t > H \). This gives the following model equations

\[
S'_t = -\varepsilon S_t I_t,
I'_t = \varepsilon S_t I_t - \varepsilon S_{t-H} I_{t-H},
R'_t = \varepsilon S_{t-H} I_{t-H},
\]

where \( S_t = I_t = 0 \) for \( t < 0 \).

### 3.2.3 The general case: time-varying infection rate and random recovery

In this section we generalize SIR models considered in Sections 3.2.1 and 3.2.2.

Suppose that the function \( \gamma \) is of the following form

\[
\gamma_t = w_t \beta_t \quad \text{for} \quad t \geq 0,
\]

where \( (w_t, t \geq 0) \) is a non-negative function and the function \( (\beta_t, t \geq 0) \) is the tail distribution of some positive random variable (i.e. similarly to what we assumed in Section 3.2.2). Arguing as in Section 3.2.2, we obtain the continuous SIR model described by the following equations

\[
\log \left( \frac{S_t}{S_0} \right) = -\int_0^t (1 - S_u) \gamma_{t-u} du,
\]

\[
I_t = I_0 \beta_t - \int_0^t S'_u \beta_{t-u} du,
\]

\[
R_t = I_0 (1 - \beta_t) - \int_0^t S'_u (1 - \beta_{t-u}) du,
\]

where, \( S_t, I_t \) and \( R_t \) are population proportions of susceptible, infected and recovered individuals respectively, so that \( 1 = S_t + I_t + R_t \) for \( t \geq 0 \). As before, we assumed that \( R_0 = 0 \). In this model an infected individual recovers in a random time given by a random variable \( \xi \) with the tail distribution \( P(\xi > t) = \beta_t \) and, if it is infected at time \( u \), then it infects any susceptible one with the rate \( w_t \) at the time \( u + t \). Recall, that we also assume \( 25 \).

In the differential form the model equations are as follows

\[
S'_t = S_t \left( -I_0 \gamma_t + \int_0^t S'_u \gamma_{t-u} du \right),
\]

\[
I'_t = -S'_t + I_0 \beta'_t - \int_0^t S'_u \beta'_{t-u} du,
\]

\[
R'_t = -I_0 \beta'_t + \int_0^t S'_u \beta'_{t-u} du.
\]

**Remark 13.** By choosing appropriate functions \((w_t, t \geq 0)\) and \((\beta_t, t \geq 0)\) one can model various infection rates and recovery distributions. For example, using the power law functions allows to model memory effects observed in real data (e.g. see \[2\] and references therein).

In the rest of this section we use the idea from \[2\] in order to rewrite equations \[47-\]
in terms of a certain kernel. The idea is based on the fact that these equations contain convolutions, which makes it possible to apply the Laplace transform.

Let \((L\{g\}_t, t \in \mathbb{R}_+}\) be the Laplace transform of a function \((g_t, t \in \mathbb{R}_+)\). It follows from (48) that

\[
L\{I\}_t = I_0 L\{\beta\}_t - L\{S'\}_t L\{\beta\}_t,
\]

and, hence,

\[
L\{S'\}_t = I_0 - \frac{L\{I\}_t}{L\{\beta\}_t}.
\]

Thus, for any appropriate function \((g_t, t \in \mathbb{R}_+)\) we have that

\[
\int_0^t S'_u g_{t-u} du = L^{-1} [L\{S'\}_t L\{g\}_t]
\]

\[
= L^{-1} \left( \left( I_0 - \frac{L\{I\}_t}{L\{\beta\}_t} \right) L\{g\}_t \right) = I_0 g_t - L^{-1} \left( L\{I\}_t \frac{L\{g\}_t}{L\{\beta\}_t} \right).
\]

Since \(L^{-1}(L\{a\}L\{b\})\) is equal to the convolution \(a \ast b\), we can rewrite (50) as follows

\[
\int_0^t S'_u g_{t-u} du = I_0 g_t - \int_0^t I_u K(g)_{t-u} du,
\]

where \(K\) is a kernel defined by

\[
K(g)_t := L^{-1} \left( \frac{L\{g\}_t}{L\{\beta\}_t} \right).
\]

Finally, using (51) with \(g_t = -\gamma_t\) in (47), and with \(g_t = -\beta'_t\) in (48) and (49) gives the system of the model equations in the kernel form

\[
S'_t = -S_t \int_0^t I_u K(\gamma)_{t-u} du,
\]

\[
I'_t = S_t \int_0^t I_u K(\gamma)_{t-u} du - \int_0^t I_u K(\beta')_{t-u} du,
\]

\[
R'_t = \int_0^t I_u K(\beta')_{t-u} du.
\]

Remark 14. It should be noted that equation (52) is an analogue of equation (16) in [2].

4 Remark on fractional SIR models

One of the recognized drawbacks of the classic SIR model is that both the infection rate and the recovery rate do not depend on the state of the system, i.e. the model is memoryless. A popular approach to modeling memory effects consists in using fractional SIR models (e.g., see [17] and references therein). Some of these models are obtained by formal replacement of ordinary derivatives by fractional derivatives of a certain type. This gives a system of fractional differential equations that is equivalent to a system of integro-differential equations.
with a power-law kernel. For example, replacing ordinary derivatives in the classic SIR model by Caputo fractional derivatives gives a system of fractional differential equations, which are equivalent to the following system of integro-differential equations

\[
S_t' = -\epsilon \int_0^t I_u S_u K_{t-u} du, \tag{56}
\]

\[
I_t' = \int_0^t (\epsilon I_u S_u - \mu I_u) K_{t-u} du, \tag{57}
\]

\[
R_t' = \mu \int_0^t I_u K_{t-u} du, \tag{58}
\]

with the kernel \( K_y = \frac{y^{\alpha-2}}{\Gamma(\alpha-1)} \), where \( \alpha \in (0, 1] \) and \( \Gamma \) is the Gamma-function. However, it is not quite clear what physical/biological process is described by equations (56)-(58). In contrast, equations (47)-(49) and their equivalents in the kernel form, i.e. equations (53)-(55), can be naturally interpreted in terms of the interaction between compartments. Indeed, using the terminology of [2], one can say that, for example, the flux into the infected compartment is equal to the flux out of the susceptible compartment (in the absence of any external factors and self-infection). The susceptible compartment decreases at the rate proportional to its current value \( S_t \). The value \( K(\gamma)_{t-u} \) (in (53)-(55)) describes the impact made on the susceptible compartment at time \( t \) by those individuals, who were infected earlier and is still infectious. The coefficient of proportionality, i.e. the integral term \( \int_0^t I_u K(\gamma)_{t-u} du \), measures the total impact of the infected compartment on the susceptible one over the time period \([0, t]\). This generalizes the interaction between susceptible and infected compartments in the classic SIR model, where only the current value \( I_t \) is taken into account.

It should be also noted that the continuous SIR model in the present paper is obtained by passing to the limit in the discrete stochastic SIR model. This is in line with SIR models in the kernel form that are derived from stochastic processes based on natural biological assumptions (e.g., see [2], [6] and references therein).

5 Appendix. Special cases of the discrete SIR model

In this section, we consider some special cases of the discrete SIR model on the homogeneous tree with the vertex degree \( n + 1 \). In these cases the integral equation (4) can be rewritten in an equivalent differential form, which is of interest on its own right.

For simplicity of notations we assume that all vertices are initially susceptible (i.e. \( p = 0 \) in Theorem 1).

**Corollary 1.** Suppose that there is no recovery, i.e. \( H = \infty \), \( \delta_t = \delta 1_{(t \geq 0)} \) and \( \lambda_t = \lambda 1_{(t \geq 0)} \), where \( \delta > 0 \) and \( \lambda > 0 \) are given constants. Then

\[
s_t = e^{-\frac{2\delta}{n}(e^{-\lambda t} - 1 + \lambda t)} , \quad \text{if} \quad n = 1; \tag{59}
\]

\[
s_t = \left( \frac{\delta (n-1) + \lambda}{\delta (n-1)e^{-\lambda t} + \lambda \delta (n-1) t} \right)^{1/n} , \quad \text{if} \quad n \geq 2,
\]
In other words, the probability
\[ P(\tau > t) = e^{-\lambda t}e^{-\frac{n+1}{n-1}(e^{-\lambda t} - 1)}, \quad \text{if} \quad n = 1; \]
\[ P(\tau > t) = e^{-\lambda t} \left( \frac{\varepsilon(n-1) + \lambda}{\varepsilon(n-1)e^{-\lambda t} + \lambda e^{(n-1)t}} \right)^{\frac{n+1}{n-1}}, \quad \text{if} \quad n \geq 2. \] (60) (61)

Proof of Corollary 7. Since \( \varepsilon_t = \varepsilon 1_{t \geq 0} \) and \( \lambda_t = \lambda 1_{t \geq 0} \), we have that
\[ \varphi_t = \begin{cases} 1, & t < 0, \\ e^{-\varepsilon t}, & t \geq 0, \end{cases} \quad \text{and} \quad f_t = \begin{cases} 1, & t < 0, \\ e^{-\lambda t}, & t \geq 0, \end{cases} \] (62)
and \( \varphi'_t = -\varepsilon e^{-\varepsilon t} \) for \( t \geq 0 \). The integral equation (4) in this case is as follows
\[ s_t = e^{-\varepsilon t} + \varepsilon \int_0^t e^{-\lambda u} s_u e^{-\varepsilon(t-u)} du. \] (63)
Differentiating (63) and simplifying gives the following differential equation
\[ s'_t = -\varepsilon s_t + \varepsilon e^{-\lambda t} s^n_t. \] (64)

It is easy to verify that the function defined in (59) is a solution of equation 64.

Remark 15. The equation 64 is the well known Bernoulli equation (e.g., see [15]). Under assumptions of Corollary 7, the model was originally considered in [8].

Remark 16. It follows from equation (61) that
\[ P(\tau > t) = e^{-\lambda t} \left( \frac{\varepsilon(n-1) + \lambda}{\varepsilon(n-1)e^{-\lambda t} + \lambda e^{(n-1)t}} \right)^{\frac{n+1}{n-1}} \]
\[ \sim e^{-\lambda t} \left( \frac{\varepsilon(n-1) + \lambda}{\varepsilon(n-1)e^{-\lambda t} + \lambda e^{(n-1)t}} \right) = \frac{1}{1 + \frac{\lambda}{\varepsilon(n-1)} e^{(n-1)t}} \]
for sufficiently large \( n \). Further, if \( \varepsilon = \varepsilon_n \), where \( \varepsilon_n n \rightarrow c > 0 \), as \( n \rightarrow \infty \), then
\[ 1 - P(\tau > t) = P(\tau \leq t) \rightarrow \frac{\lambda}{c} e^{(c+\lambda)t} - \frac{\varepsilon}{c} = \left( 1 + \frac{\lambda}{c} \right) \frac{1}{1 + \frac{\lambda}{c} e^{(c+\lambda)t}} - \frac{\varepsilon}{c}, \quad \text{as} \quad n \rightarrow \infty. \] (65)

In other words, the probability \( P(\tau \leq t) \) converges to a linear transformation of the logistic curve
\[ \frac{1}{1 + \frac{\lambda}{c} e^{-(c+\lambda)t}}. \]

Corollary 2. Suppose that the recovery time is given by a deterministic constant \( H > 0 \), \( \lambda_t = \lambda 1_{t \geq 0} \) and \( \varepsilon_t = \varepsilon 1_{t \leq H} \), where \( \varepsilon > 0 \) and \( \lambda > 0 \) are given constants. Then integral equation (4) is equivalent to the following differential equation
\[ s'_t = -\varepsilon s_t + \varepsilon e^{-\lambda t} s^n_t \quad \text{for} \quad t \leq H, \]
\[ s'_t = -\varepsilon s_t + \varepsilon e^{-\lambda t} s^n_t + \varepsilon e^{-\varepsilon H} - \varepsilon e^{-\lambda(t-H)} - \varepsilon H s^n_{t-H} \quad \text{for} \quad t > H. \] (66)
Proof of Corollary 2. In this case we have that \( f_t = e^{-\lambda t} \) and \( \varphi_t = e^{-\varepsilon \min(t,H)} \) for \( t \geq 0 \), and equation (4) becomes as follows

\[
\begin{align*}
  s_t &= \begin{cases} 
  \varphi_t + \varepsilon \int_0^t e^{-\lambda u} \varphi_{t-u} du & \text{for } t < H, \\
  \varphi_t + \varepsilon \int_{t-H}^t e^{-\lambda u} \varphi_{t-u} du & \text{for } t \geq H.
  \end{cases}
\end{align*}
\] (67)

A direct computation gives that

\[
  s'_t = -\varepsilon \varphi_t + \varepsilon e^{-\lambda t} s^n_t + \varepsilon^2 \int_0^t e^{-\lambda u} \varphi_{t-u} du = -\varepsilon s_t + \varepsilon e^{-\lambda t} s^n_t \quad \text{for } t < H,
\]

which is the first equation in (66).

Further, if \( t > H \), then \( \varphi_t = \varphi_H = e^{-\varepsilon H} \), and, hence,

\[
  s'_t = \varepsilon e^{-\lambda t} s^n_t - \varepsilon e^{-\lambda(t-H)-\varepsilon H} s^n_{t-H} - \varepsilon^2 \int_{t-H}^t f(u) s^n_{t-u} \varphi_{t-u} du
  = \varepsilon e^{-\lambda t} s^n_t - \varepsilon e^{-\lambda(t-H)-\varepsilon H} s^n_{t-H} - \varepsilon (s_t - \varphi_H)
  = -\varepsilon s_t + \varepsilon e^{-\lambda t} s^n_t + \varepsilon e^{-\varepsilon H} - \varepsilon e^{-\lambda(t-H)-\varepsilon H} s^n_{t-H},
\]

and this is the second equation in (66), as claimed.

We are going to consider an example of the model with a random recovery time.

Corollary 3 (Exponential recovery time). Suppose that the recovery time is exponentially distributed with the parameter \( \mu \) and functions \((\varepsilon_t, t \in \mathbb{R}_+)\) and \((\lambda_t, t \in \mathbb{R}_+)\) are as in Corollaries 1 and 2. Then integral equation (4) is equivalent to the following differential equation

\[
  s'_t = -(\mu + \varepsilon) s_t + \varepsilon e^{-\lambda t} s^n_t + \mu.
\] (68)

Proof of Corollary 3. Start with computing the corresponding function \( \varphi \)

\[
  \varphi_t = \mathbb{E} \left( e^{-\varepsilon \min(t,H)} \right) = \mu \int_0^t e^{-\varepsilon u} e^{-\mu u} du + \mu e^{-\varepsilon t} \int_t^\infty e^{-\mu u} du
  = \frac{\mu}{\mu + \varepsilon} + \frac{\varepsilon}{\mu + \varepsilon} e^{-(\mu+\varepsilon)t} \quad \text{for } t \geq 0.
\] (69)

Recall Remark 3 and define

\[
  \tilde{\varepsilon}_t := - (\log(\varphi_t))' = \frac{\varepsilon (\mu + \varepsilon)}{\mu e^{\mu + \varepsilon} t} + \varepsilon 1_{\{t \geq 0\}} \quad \text{for } t \geq 0,
\] (70)

so that \( \varphi'_t = -\tilde{\varepsilon}_t \varphi_t \) for \( t \geq 0 \). A direct computation gives that

\[
  \tilde{\varepsilon}'_t - \tilde{\varepsilon}^2_t = -(\mu + \varepsilon) \tilde{\gamma}_t \quad \text{for } t > 0.
\]
Using the equation in the preceding display and differentiating equation (4) gives that

\[ s_t' = -\tilde{\varepsilon}_t \varphi(t) + \varepsilon f_t s_t^n + \int_0^t f(u) s_u^n \varphi_{t-u} (\tilde{\varepsilon}_t' - \tilde{\varepsilon}_u') \, du \]

\[ = -\varepsilon \tilde{\varepsilon}_t \varphi_t + \varepsilon f_t s_t^n - (\mu + \varepsilon) \int_0^t f_u s_u^n \varphi_{t-u} \tilde{\varepsilon}_{t-u} \, du \]

\[ = -(\mu + \varepsilon) s_t + \varepsilon f_t s_t^n + (\mu + \varepsilon - \tilde{\varepsilon}_t) \varphi_t. \]

Noting that

\[ (\mu + \varepsilon - \tilde{\varepsilon}_t) \varphi_t = \left( \mu + \varepsilon - \frac{\varepsilon (\mu + \varepsilon)}{\mu e^{(\mu+\varepsilon)t} + \varepsilon} \right) \left( \frac{\mu}{\mu + \varepsilon} + \frac{\varepsilon}{\mu + \varepsilon} e^{-(\mu+\varepsilon) t} \right) = \mu, \]

gives the equation \( s_t' = -(\mu + \varepsilon) s_t + \varepsilon f_t s_t^n + \mu \), which is the Bernoulli equation with the additional term \( \mu \), as claimed. \( \square \)

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