A NOTE ON THE MARKOVIAN SIR EPIDEMIC ON A RANDOM
GRAPH WITH GIVEN DEGREES

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Abstract. This paper provides an additional probabilistic interpretation of the limiting
functions for the SIR epidemic on the configuration model derived in the paper by Janson,
Luczak and Windridge (2014) [4].

1. Introduction

The Markovian SIR process is a simple model for a disease spreading around a finite
population in which each individual is either susceptible, infective or recovered. Individuals
are represented by vertices in a graph $G$ with edges corresponding to potentially infectious
contacts. Infective vertices become recovered at rate $\rho \geq 0$ and infect each neighbour at rate
$\beta > 0$; those are the only possible transitions, i.e. recovered vertices never become infective.

The present note concerns SIR epidemics on random graphs with a given degree sequence.
There have been a number of studies of SIR epidemics on random graphs with a given degree
sequence [4; 6; 8; 7; 3; 1]. Here we will give a short discussion and probabilistic interpretation
of the results in [4] as well as alternative formulae for the limiting functions derived in that
paper.

2. Model, notation, assumptions and summary of results from [4]

Let us start by recalling some notation and assumptions from [4].

For $n \in \mathbb{N}$ and a sequence $(d_i)_i$ of non-negative integers, let $G = G(n, (d_i)_i)$ be a simple
graph (i.e. with no loops or double edges) on $n$ vertices, chosen uniformly at random from
among all graphs with degree sequence $(d_i)_i$. (It is tacitly assumed that there is some such
graph, so $\sum_{i=1}^n d_i$ must be even, at least.)

Given the graph $G$, the SIR epidemic evolves as a continuous-time Markov chain. At any
time, each vertex is either susceptible, infected or recovered. Each infective vertex recovers
at rate $\rho \geq 0$ and also infects each susceptible neighbour at rate $\beta > 0$.

There are initially $n_S$, $n_I$, and $n_R$ susceptible, infective and recovered vertices, respectively.
Further, it is assumed that, for each $k \geq 0$, there are respectively $n_{S,k}$, $n_{I,k}$ and $n_{R,k}$ of these
vertices with degree $k$. Thus, $n_S + n_I + n_R = n$ and $n_S = \sum_{k=0}^\infty n_{S,k}$, $n_I = \sum_{k=0}^\infty n_{I,k}$,
$n_R = \sum_{k=0}^\infty n_{R,k}$. We write $n_k$ to denote the total number of vertices with degree $k$; thus, for
each $k$, $n_k = n_{S,k} + n_{I,k} + n_{R,k}$.

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model.
For a sequence \((Y_t^{(n)})_t\) of real-valued stochastic processes defined on a subset \(E\) of \(\mathbb{R}\) and a real-valued function \(y\) on \(E\), \(Y_t^{(n)} \overset{p}{\to} y(t)\) uniformly on \(E' \subseteq E\) means \(\sup_{t \in E'}|Y_t^{(n)} - y(t)| \overset{p}{\to} 0\), as \(n \to \infty\).

The following regularity conditions for the degree sequence asymptotics are imposed in [4].

(D1) The fractions of initially susceptible, infective and recovered vertices converge to some \(\alpha_S, \alpha_I, \alpha_R \in [0, 1]\), i.e.
\[
\frac{n_S}{n} \to \alpha_S, \quad \frac{n_I}{n} \to \alpha_I, \quad \frac{n_R}{n} \to \alpha_R.
\]
Further, \(\alpha_S > 0\).

(D2) The degree of a randomly chosen susceptible vertex converges to a probability distribution \((p_k)_k\), i.e.
\[
\frac{n_{S,k}}{n_S} \to p_k, \quad k \geq 0.
\]
Further, this limiting distribution has a finite and positive mean
\[
\lambda := \sum_{k=0}^{\infty} kp_k \in (0, \infty).
\]

(D3) The average degree of a randomly chosen susceptible vertex converges to \(\lambda\), i.e.
\[
\sum_{k=0}^{\infty} kn_{S,k}/n_S \to \lambda.
\]

(D4) The average degree over all vertices converges to \(\mu > 0\), i.e.
\[
\sum_{k=0}^{\infty} kn_k/n = \sum_{i=1}^{n} d_i/n \to \mu,
\]
and, in more detail, for some \(\mu_S, \mu_I, \mu_R\),
\[
\sum_{k=0}^{\infty} kn_{S,k}/n \to \mu_S,
\]
\[
\sum_{k=0}^{\infty} kn_{I,k}/n \to \mu_I,
\]
\[
\sum_{k=0}^{\infty} kn_{R,k}/n \to \mu_R.
\]

(D5) The maximum degree of the initially infective vertices is not too large:
\[
\max\{k : n_{I,k} > 0\} = o(n).
\]

(D6) Either \(p_1 > 0\) or \(\rho > 0\) or \(\mu_R > 0\).

Clearly, \(\alpha_S + \alpha_I + \alpha_R = 1\) and \(\mu_S + \mu_I + \mu_R = \mu\). Further, assumptions (D1)–(D3) imply
\[
\sum_{k=0}^{\infty} kn_{S,k}/n \to \alpha_S \lambda, \quad \text{and so} \quad \mu_S = \alpha_S \lambda.
\]

Let \(G^*(n, (d_i)_n^n)\) be the random multigraph with given degree sequence \((d_i)_1^n\) defined by the configuration model: we take a set of \(d_i\) half-edges for each vertex \(i\) and combine half-edges into edges by a uniformly random matching (see e.g. [2]). Conditioned on the multigraph being simple, we obtain \(G = G(n, (d_i)_n^n)\), the uniformly distributed random graph with degree sequence \((d_i)_1^n\).

Janson, Łuczak and Windridge (2014) [4] first prove their results for the SIR epidemic on \(G^*\), and, by conditioning on \(G^*\) being simple, they deduce that these results also hold for
the SIR epidemic on $G$. Their argument relies on the probability that $G^*$ is simple being bounded away from zero as $n \to \infty$. By the main theorem of [5] this occurs provided the following condition holds.

(G1) The degree of a randomly chosen vertex has a bounded second moment, i.e.

$$\sum_{k=0}^{\infty} k^2 n_k = O(n). \quad (2.9)$$

The authors of [4] study the SIR epidemic on the multigraph $G^*$, revealing its edges dynamically while the epidemic spreads. The process analysed in [4] works as follows. A half-edge is said to be free if it is not yet paired to another half-edge. A half-edge is called susceptible, infective or recovered according to the type of vertex it belongs to.

At time 0, there are $d_i$ half-edges attached to vertex $i$, for each $i$, and all half-edges are free. Subsequently, each free infective half-edge chooses a free half-edge at rate $\beta$, uniformly at random from among all the other free half-edges. Together the pair form an edge, and are removed from the pool of free half-edges. If the chosen half-edge belongs to a susceptible vertex then that vertex becomes infective, and thus all of its half-edges become infective also. Infective vertices also recover at rate $\rho$.

The process stops when there are no free infective half-edges, at which point the epidemic stops spreading. Some infective vertices may remain but they will recover at i.i.d. exponential times without affecting any other vertex, and are irrelevant from the point of view of the epidemic. Some susceptible and recovered half-edges may also remain, and these are paired off uniformly at time $\infty$ to reveal the remaining edges in $G^*$. This step is unimportant for the spread of the epidemic, but is performed for the purpose of transferring the results from the multigraph $G^*$ to the simple graph $G$.

Clearly, if all the pairings are completed then the resulting graph is the multigraph $G^*$. Moreover, the quantities of interest (numbers of susceptible, infective and recovered vertices at each time $t$) have the same distribution as if we were to reveal the multigraph $G^*$ first and run the SIR epidemic on $G^*$ afterwards.

For $t \geq 0$, let $S_t$, $I_t$ and $R_t$ denote the numbers of susceptible, infective and recovered vertices, respectively, at time $t$. Thus $S_t$ is decreasing and $R_t$ is increasing. Also $S_0 = n_S$, $I_0 = n_I$ and $R_0 = n_R$.

For the dynamics described above (with half-edges paired off dynamically, as described), for $t \geq 0$, let $X_{S,t}$, $X_{I,t}$ and $X_{R,t}$ be the number of free susceptible, infective and recovered half-edges at time $t$, respectively. Thus $X_{S,t}$ is decreasing, $X_{S,0} = \sum_{k=0}^{\infty} k n_{S,k}$, $X_{I,0} = \sum_{k=0}^{\infty} k n_{I,k}$ and $X_{R,0} = \sum_{k=0}^{\infty} k n_{R,k}$.

For the uniformly random graph $G$ with degree sequence $(d_i)_1^n$, the variables $X_{S,t}$, $X_{I,t}$ and $X_{R,t}$, for $t \geq 0$, are defined as above conditioned on the final multigraph $G^*$ being a simple graph.

It is shown in [4] that, upon suitable scaling, the processes $S_t, I_t, R_t, X_{S,t}, X_{I,t}, X_{R,t}$ converge to deterministic functions. The limiting functions are written in terms of a parameterisation $\theta_t \in [0, 1]$ of time solving an ordinary differential equation given below. In [4], the function $\theta_t$ is interpreted as the limiting probability that a given initially susceptible
half-edge has been selected for pairing with a (necessarily infective) half-edge by time \( t \). Let

\[
v_S(\theta) := \alpha_S \sum_{k=0}^{\infty} p_k \theta^k, \quad \theta \in [0, 1],
\]

so the limiting fraction of susceptible vertices is \( v_S(\theta_t) \) at time \( t \) (since the events of being selected for pairing will be approximately independent for different half-edges, when \( n \) is large). Similarly, for susceptible half-edges, the limiting function is

\[
h_S(\theta) := \alpha_S \sum_{k=0}^{\infty} k \theta^k p_k = \theta v_S'(\theta), \quad \theta \in [0, 1].
\]

For the total number of free half-edges, let

\[
h_X(\theta) := \mu \theta^2, \quad \theta \in [0, 1].
\]

For the numbers of half-edges of the remaining types, for \( \theta \in [0, 1] \), let

\[
h_R(\theta) := \mu_R \theta + \frac{\mu \rho}{\beta} \theta (1 - \theta),
\]

\[
h_1(\theta) := h_X(\theta) - h_S(\theta) - h_R(\theta).
\]

Thus \( h_X(\theta) = h_S(\theta) + h_1(\theta) + h_R(\theta) \). Note that

\[
v_S(1) = \alpha_S, \quad h_R(1) = \mu_R, \quad h_1(1) = \mu - \mu_S - \mu_R = \mu_1.
\]

The following is shown in [4].

When \( \mu_1 > 0 \), there is a unique \( \theta_\infty \in (0, 1) \) with \( h_1(\theta_\infty) = 0 \). Further, \( h_1 \) is strictly positive on \( (\theta_\infty, 1] \) and strictly negative on \( (0, \theta_\infty) \). Defining the ‘infective pressure’

\[
p_1(\theta) := \frac{h_1(\theta)}{h_X(\theta)},
\]

there is a unique solution \( \theta_t : [0, \infty) \to (\theta_\infty, 1] \) to the differential equation

\[
\frac{d}{dt} \theta_t = -\beta \theta_t p_1(\theta_t),
\]

subject to the initial condition \( \theta_0 = 1 \).

Furthermore, there is a unique solution \( \hat{I}_t \) to

\[
\frac{d}{dt} \hat{I}_t = \frac{\beta h_1(\theta_t) h_S(\theta_t)}{h_X(\theta_t)} - \rho \hat{I}_t, \quad t \geq 0, \quad \hat{I}_0 = \alpha_1.
\]

Defining also \( \hat{R}_t := 1 - v_S(\theta_t) - \hat{I}_t \), Theorem 2.6 in [4] states that, for the epidemic on the multigraph \( G^* \), under conditions [D1] [D6] uniformly on \( [0, \infty) \),

\[
\begin{align*}
S_t/n & \xrightarrow{p} v_S(\theta_t), \quad I_t/n \xrightarrow{p} \hat{I}_t, \quad R_t/n \xrightarrow{p} \hat{R}_t, \\
X_{S,t}/n & \xrightarrow{p} h_S(\theta_t), \quad X_{I,t}/n \xrightarrow{p} h_1(\theta_t), \quad X_{R,t}/n \xrightarrow{p} h_R(\theta_t), \\
X_t/n & \xrightarrow{p} h_X(\theta_t).
\end{align*}
\]

Moreover, the number \( S_\infty := \lim_{t \to \infty} S_t \) of susceptibles that escape infection satisfies

\[
S_\infty/n \xrightarrow{p} v_S(\theta_\infty).
\]
The same holds on the graph \( G \) under the additional assumption \((G1)\) (Theorem 2.7 in [4]).

For the case where there are initially a small number of infectives (of order less than \( n \), so that \( \mu_I = 0 \)), we recall from [4]

\[
R_0 := \left( \frac{\beta}{\rho + \beta} \right) \left( \frac{\alpha_S}{\mu} \right) \sum_{k=0}^{\infty} (k-1) kp_k; \tag{2.23}
\]

the basic reproductive ratio of the epidemic. It is shown in [4] that, when \( R_0 > 1 \), even if \( \mu_I = 0 \), then there is a unique \( \theta_\infty \in (0, 1) \) with \( h_t(\theta_\infty) = 0 \), and that \( h_t \) is strictly positive on \((\theta_\infty, 1)\) and strictly negative on \((0, \theta_\infty)\).

The initial condition of the limiting differential equation, now defined on \((-\infty, \infty)\), is shifted so that \( t = 0 \) corresponds to the time \( T_0 \) in the random process, which is the infimum of times \( t \) such that the fraction of susceptible individuals has fallen from about \( \alpha_S = v_S(1) \) to some fixed smaller \( s_0 \) by time \( t \). It is shown in [4] that there is a unique continuously differentiable \( \theta_t : \mathbb{R} \to (\theta_\infty, 1) \) such that

\[
\frac{d}{dt} \theta_t = -\beta \theta_t p_t(\theta_t), \quad \theta_0 = v_S^{-1}(s_0). \tag{2.24}
\]

Furthermore, \( \theta_t \searrow \theta_\infty \) as \( t \to \infty \) and \( \theta_t \nearrow 1 \) as \( t \to -\infty \).

The processes are extended to be defined on \((-\infty, \infty)\) by taking \( S_t = S_0 \) for \( t < 0 \), and similarly for the other processes.

The following is proven in [4] (Theorems 2.9 and 2.10), for both the simple graph \( G \) and the multigraph \( G^* \). Suppose that conditions \((D1)-(D6)\) and \((G1)\) hold. Assume that \( R_0 > 1 \).

Suppose also that \( \alpha_I = \mu_I = 0 \) but there is initially at least one infective vertex with non-zero degree.

Then, \( \liminf_{n \to \infty} \mathbb{P}(T_0 < \infty) > 0 \). Also, conditional on \( T_0 < \infty \), uniformly on \((-\infty, \infty)\),

\[
\begin{align*}
S_{T_0+t}/n & \xrightarrow{p} v_S(\theta_t), \quad I_{T_0+t}/n \xrightarrow{p} \hat{I}_t, \quad R_{T_0+t}/n \xrightarrow{p} \hat{R}_t, \tag{2.25} \\
X_{S,T_0+t}/n & \xrightarrow{p} h_S(\theta_t), \quad X_{I,T_0+t}/n \xrightarrow{p} h_I(\theta_t), \quad X_{R,T_0+t}/n \xrightarrow{p} h_R(\theta_t), \tag{2.26} \\
X_{T_0+t}/n & \xrightarrow{p} h_X(\theta_t). \tag{2.27}
\end{align*}
\]

Also, conditional on \( T_0 < \infty \), the number of susceptibles that escape infection satisfies

\[
S_\infty/n \xrightarrow{p} v_S(\theta_\infty). 
\]

Here, again, \( \hat{I}_t \) is the unique solution to

\[
\frac{d}{dt} \hat{I}_t = \frac{\beta h_I(\theta_t) h_S(\theta_t)}{h_X(\theta_t)} - \rho \hat{I}_t, \quad \lim_{t \to -\infty} \hat{I}_t = 0, \tag{2.28}
\]

and \( \hat{R}_t := 1 - v_S(\theta_t) - \hat{I}_t \).

3. New probabilistic interpretation of \( \theta \) and alternative formulae for limiting deterministic functions

We will now give a more complete probabilistic interpretation of the function \( \theta_t \) used to define the deterministic limit for the SIR epidemic.
As stated in the introduction, the function \( \theta_t \) used to define the deterministic limits satisfies
\[
\frac{d\theta_t}{dt} = -\beta \theta_t \frac{h_t(\theta_t)}{h_X(\theta_t)}.
\]
Substituting \( h_X(\theta) = \mu \theta^2 \), \( h_1(\theta) = \mu \theta^2 - \mu R \theta - \frac{\mu \rho}{\beta} \theta (1 - \theta) - \alpha_S \sum_k k p_k \theta^k \), we can rewrite this as
\[
\frac{d\theta_t}{dt} = -\beta \left( \mu \theta^2 - \mu R \theta - \frac{\mu \rho}{\beta} \theta (1 - \theta) - \alpha_S \sum_k k p_k \theta^k \right) \frac{\theta_t}{\mu \theta_t}
\]
\[
= -\left( \beta + \rho \right) \theta_t + \frac{\beta \mu R}{\mu} \frac{\theta_t}{\mu} + \frac{\beta \alpha_S}{\mu} \sum_k k p_k \theta^{k-1}_t.
\]
It follows that
\[
\frac{d}{dt}(\theta_t e^{(\beta + \rho)t}) = \left( \rho + \frac{\beta \mu R}{\mu} \right) e^{(\beta + \rho)t} + \frac{\beta \alpha_S}{\mu} \left( \sum_k k p_k \theta^{k-1}_t \right) e^{(\beta + \rho)t},
\]
and so, integrating,
\[
\theta_t = \left( 1 - \frac{\rho + \frac{\beta \mu R}{\mu}}{\beta + \rho} \right) e^{(\beta + \rho)t} + \frac{\rho + \frac{\beta \mu R}{\mu}}{\beta + \rho} + \frac{\beta \alpha_S}{\mu} \sum_k k p_k \int_0^t \theta^{k-1}_s e^{-(\beta + \rho)(t-s)} ds
\]
\[
= \frac{\rho}{\beta + \rho} + \frac{\beta}{\beta + \rho} \left( \frac{\mu R}{\mu} \right) + \frac{\beta}{\beta + \rho} \frac{\mu - \mu R}{\mu} e^{-(\beta + \rho)t}
\]
\[
+ \frac{\beta \alpha_S}{\mu} \sum_k k p_k \int_0^t \theta^{k-1}_s e^{-(\beta + \rho)(t-s)} ds,
\]
and so
\[
\theta_t = \frac{\mu R}{\mu} + \frac{\mu - \mu R}{\mu} F(t) + \frac{\beta \alpha_S}{\mu} \sum_k k p_k \int_0^t \theta^{k-1}_s e^{-(\beta + \rho)(t-s)} ds,
\]
where
\[
F(t) = \frac{\rho}{\beta + \rho} + \frac{\beta}{\beta + \rho} e^{-(\beta + \rho)t}.
\]
Noting that
\[
\int_0^t \theta^{k-1}_s \frac{dF(t-s)}{ds} ds + \int_0^t \frac{d}{ds} (\theta_s)^{k-1} F(t-s) ds = \left[ \theta^{k-1}_s F(t-s) \right]_0^t,
\]
we see that, for each \( k \geq 1 \),
\[
\beta \int_0^t \theta^{k-1}_s e^{-(\beta + \rho)(t-s)} ds = \theta^{k-1}_t - F(t) - \int_0^t \frac{d}{ds} (\theta_s)^{k-1} F(t-s) ds
\]
\[
= \theta^{k-1}_t - F(t) + \beta (k - 1) \int_0^t \theta^{k-1}_s \frac{h_1(\theta_s)}{h_X(\theta_s)} F(t-s) ds.
\]
This then implies, using \( \alpha_S \sum_k k p_k = \mu_S \), that
\[
\theta_t = \frac{\mu R}{\mu} + \frac{\mu - \mu R}{\mu} F(t) + \frac{\alpha_S}{\mu} \sum_k k p_k \theta^{k-1}_t - \frac{\mu S}{\mu} F(t)
\]
+ \frac{\beta \alpha_S}{\mu} \sum_k k(k-1)p_k \int_0^t \theta_s^{k-1} \frac{h_1(\theta_s)}{h_X(\theta_s)} F(t-s)ds

and hence that

\theta_t = \frac{\mu_R}{\mu} F(t) + \frac{\mu_I}{\mu} + \frac{\alpha_S}{\mu} \sum_k k p_k \theta_t^{k-1} \\
+ \frac{\beta \alpha_S}{\mu} \sum_k k(k-1)p_k \int_0^t \theta_s^{k-1} \frac{h_1(\theta_s)}{h_X(\theta_s)} F(t-s)ds.

(3.2)

Considering formula (3.2), we will now discuss how the function \( \theta_t \) is the asymptotic probability that a half-edge does not transmit infection (i.e. initiate a pairing) by time \( t \). This should be the same as the limiting probability that a given initially susceptible half-edge has not been paired with a (necessarily infective) half-edge by time \( t \), as interpreted in [4], since that probability is that its eventual partner has not transmitted infection by time \( t \).

Given a random half-edge, conditional on it being initially recovered, which has probability \( \mu_R/\mu \), it does not transmit infection by time \( t \) with probability 1.

Conditional on the half-edge being initially infected, which has probability \( \mu_I/\mu \), it does not transmit by time \( t \) with probability \( F(t) \). In the formula for \( F(t) \), the term \( \frac{e^{-\beta t}}{\beta + \rho} \) is the probability that recovery of the vertex occurs before the half-edge’s clock goes off. The term \( \frac{\beta}{\beta + \rho} e^{-(\beta + \rho)t} \) is the probability that the clock of the half-edge goes off before recovery but neither of these events happens by time \( t \).

Conditional on the half-edge being initially susceptible, which happens with probability \( \mu_S/\mu \), we need to further consider the degree of its vertex. With conditional probability \( \frac{\alpha_S k p_k}{\mu_S} \), it has degree \( k \), and then the edge cannot transmit if the vertex does not get infected by time \( t \) or only gets infected by transmitting the infection to the half-edge itself, which happens with probability \( \theta_t^{k-1} \). The half-edge also cannot transmit by time \( t \) if one of the other \( k - 1 \) half-edges gets infected at some time \( s \leq t \), but then the clock of the half-edge in question does not go off before vertex recovery over a period of length \( t - s \); this happens with probability \(- \int_0^t \frac{d}{ds} \left( h_1(\theta_s)^{k-1}ight) F(t-s)ds = \beta(k-1) \int_0^t \theta_s^{k-1} \frac{h_1(\theta_s)}{h_X(\theta_s)} F(t-s)ds \).

Alternatively, we have

\[ n \mu_R \theta_t^2 = n \mu_R \theta_t + n \mu_I \theta_t F(t) + n h_S(\theta_t) \]
\[ + n \beta \alpha_S \theta_t \sum_k k(k-1)p_k \int_0^t \theta_s^{k-1} \frac{h_1(\theta_s)}{h_X(\theta_s)} F(t-s)ds. \]

The left hand-side here is approximately the total number of free half-edges at time \( t \). The term \( n \mu_R \theta_t \) is approximately the total number of initially recovered half-edges that are still free at time \( t \). The term \( n \mu_I \theta_t F(t) \) is approximately the total number of initially infective half-edges that are still free at time \( t \). The term \( n h_S(\theta_t) \) is approximately the total number of free susceptible half-edges at time \( t \). The term

\[ n \beta \alpha_S \theta_t \int_0^t \sum_k k(k-1)p_k \theta_s^{k-1} \frac{h_1(\theta_s)}{h_X(\theta_s)} F(t-s)ds \]

is approximately the total number of half-edges belonging to initially susceptible vertices that got infected before time \( t \) and are still free at time \( t \).
The function $\theta_t$ is closely related to the corresponding function in [7, 8], but these papers do not engage with the construction of the configuration model multigraph and simple graph by pairing half-edges.

We saw in Section 1 (equation (2.13)) that
\[ X_{R,t}/n \] is asymptotically close to
\[ h_R(\theta_t) := \mu_R \theta_t + \mu_R \theta_t(1 - \theta_t). \]
The term $\mu_R \theta_t(1 - \theta_t)$ in the above formula is compact but does not appear readily interpretable.

We claim that the limiting function can instead be expressed in the form
\[ \tilde{h}_R(t) = \mu_R \theta_t + \mu_I \theta_t \rho/(\beta + \rho) + \rho/(\beta + \rho)(1 - e^{-(\beta + \rho)t}) \] (3.3)

To understand this formula, note that $n \mu_R \theta_t$ is approximately the number of free recovered half-edges that were initially recovered.

Also,
\[ \frac{\rho}{\beta + \rho}(1 - e^{-(\beta + \rho)t}) \]
is the probability that a vertex infectious at time 0 recovers by time $t$ and that its recovery happens before the clock of an infectious half-edge attached to this vertex goes off. This implies that $n \mu_I \theta_t \rho/(\beta + \rho)(1 - e^{-(\beta + \rho)t})$ is approximately the total number of free recovered half-edges that were infectious at time 0.

Finally,
\[ n \alpha S \sum_k k p_k \theta_t \left( - \int_0^t \frac{d}{ds} (\theta_s)^{k-1} \frac{\rho}{\beta + \rho}(1 - e^{-(\beta + \rho)(t-s)}) ds \right) \]
is approximately the total number of free recovered half-edges whose vertices were susceptible at time 0, got infected and recovered by time $t$.

We are now going to verify that $\tilde{h}_R(t) = h_R(\theta_t)$. This means that we need to verify that
\[ \frac{\mu_R \rho}{\beta} (1 - \theta_t) = \left( \mu_I + \frac{\rho}{\beta + \rho} \right) (1 - e^{-(\beta + \rho)t}) \]

To do that, first note that, integrating by parts,

\[ - \int_0^t \frac{d}{ds} (\theta_s)^{k-1} \frac{\rho}{\beta + \rho}(1 - e^{-(\beta + \rho)(t-s)}) ds \]

\[ = \left[ - \theta_s^{k-1} \frac{\rho}{\beta + \rho}(1 - e^{-(\beta + \rho)(t-s)}) \right]_0^t - \rho \int_0^t \theta_s^{k-1} e^{-(\beta + \rho)(t-s)} ds \]

\[ = \frac{\rho}{\beta + \rho}(1 - e^{-(\beta + \rho)t}) - \rho \int_0^t \theta_s^{k-1} e^{-(\beta + \rho)(t-s)} ds. \]
This means we actually need to verify that
\[
\frac{\mu \rho}{\beta} (1 - \theta_t) = \mu I \frac{\rho}{\beta + \rho} (1 - e^{-(\beta + \rho) t}) + \mu S \frac{\rho}{\beta + \rho} (1 - e^{-(\beta + \rho) t})
\]
\[
- \rho \alpha S \sum_k k p_k \int_0^t \theta_s^{k-1} e^{-(\beta + \rho)(t-s)} ds.
\]

But, as seen in (3.1),
\[
\theta_t = \frac{\mu R}{\mu} + \frac{\mu - \mu R}{\mu} F(t) + \frac{\beta \alpha S}{\mu} \sum_k k p_k \int_0^t \theta_s^{k-1} e^{-(\beta + \rho)(t-s)} ds,
\]
where
\[
F(t) = \frac{\rho}{\beta + \rho} + \frac{\beta}{\beta + \rho} e^{-(\beta + \rho) t},
\]
and so
\[
- \rho \alpha S \sum_k k p_k \int_0^t \theta_s^{k-1} e^{-(\beta + \rho)(t-s)} ds = - \frac{\mu \rho}{\beta} \theta_t + \frac{\rho (\mu - \mu R)}{\beta + \rho} e^{-(\beta + \rho) t}
\]
\[
+ \frac{\rho}{\beta + \rho} \frac{\rho \mu}{\beta + \rho} + \frac{\rho \mu R}{\beta + \rho}.
\]

This means that we need to verify that
\[
\frac{\mu \rho}{\beta} (1 - \theta_t) = \mu I \frac{\rho}{\beta + \rho} (1 - e^{-(\beta + \rho) t}) + \mu S \frac{\rho}{\beta + \rho} (1 - e^{-(\beta + \rho) t})
\]
\[
- \frac{\mu \rho}{\beta} \theta_t + \frac{\rho (\mu - \mu R)}{\beta + \rho} e^{-(\beta + \rho) t} + \frac{\rho}{\beta + \rho} \frac{\rho \mu}{\beta + \rho} + \frac{\rho \mu R}{\beta + \rho},
\]
which holds, noting that \(\mu_S + \mu_I + \mu_R = \mu\).

Similarly, we have an alternative formula for the limit of \(X_{1,t}/n\), the asymptotic scaled number of free infectious half-edges at time \(t\):
\[
\tilde{h}_I(t) = \mu_I \theta_t e^{-(\beta + \rho) t} + \alpha S \theta_t \sum_k k p_k \left( - \int_0^t \frac{d}{ds} (\theta_s)^{k-1} e^{-(\beta + \rho)(t-s)} ds \right). \tag{3.4}
\]

For infectious vertices, we have
\[
\hat{I}_t = \alpha_I e^{-\rho t} + \beta \int_0^t \hat{h}_I(\theta_s) \frac{h_S(\theta_s)}{h_X(\theta_s)} e^{-\rho(t-s)} ds \tag{3.5}
\]
\[
= \alpha_I e^{-\rho t} - \int_0^t \frac{dv_S(\theta_s)}{ds} e^{-\rho(t-s)} ds,
\]
and, for recovered vertices,
\[
\hat{R}_t = \alpha_R + \alpha_I (1 - e^{-\rho t}) + \beta \int_0^t \hat{h}_I(\theta_s) \frac{h_S(\theta_s)}{h_X(\theta_s)} (1 - e^{-\rho(t-s)}) ds \tag{3.6}
\]
\[ \alpha_R + \alpha_I (1 - e^{-\rho t}) - \int_0^t \frac{dv_S(\theta_s)}{ds} (1 - e^{-\rho(t-s)}) ds. \]

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