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Abstract

We study the spread of sexually transmitted infections (STIs) and other infectious diseases on a dynamic network by using a branching process approach. The nodes in the network represent the sexually active individuals, while connections represent sexual partnerships. This network is dynamic as partnerships are formed and broken over time and individuals enter and leave the sexual active population due to demography. We assume that individuals enter the sexually active network with a random number of partners, chosen according to a suitable distribution. We discuss branching process approximation for the initial stages of an outbreak of the STI and characterize the basic reproduction number, R_0 and the probability of extinction. In addition, we expose the dependencies between individuals and show how these dependencies complicate the branching process approximation. We illustrate these complications through computations of the probability of a minor outbreak.

Keywords Epidemic Model; Branching process; Basic reproduction number; dynamic network

1 Introduction

Sexually transmitted infections (STIs) are among the world's most common diseases remaining as a major global threat. In addition to accounting for millions of deaths so far, over a million STIs are acquired every day worldwide, and STI pandemics continues to cause a major socio-economic burden on many developing countries (see, e.g. WHO, 2015).

Over the past decades, several authors have used mathematical models to asses the impact of partnerships structure in the spread of HIV (Eaton et al, 2011; Heesterbeek et al, 2015), (see also the Introduction of the PhD thesis of Leung (2016) for an excellent discussion). In order to study the disease dynamics of HIV and other infectious diseases, much attention has been devoted to static networks (see e.g. Newman, 2002; Diekmann et al, 2013; Ball et al, 2010, and references therein). The underlying assumption of that work is that once a connection is formed between two individuals this will remain unaltered and during an epidemic outbreak no new partnerships are formed. However, social interactions do often vary over time: new connections being formed and others being dissolved, providing short term opportunities for disease transmission. To incorporate the dynamics, Leung et al (2012) (see also Leung, 2016) developed and analysed a deterministic model for the spread of an *SI* epidemic on a dynamic network. Here *S* stands for susceptible and *I* stands for infective. Their network model incorporates demographic turnover through individuals entering the population and dying and allows for individuals to have multiple partners at the same time, with the number of partners varying over time. This network model can be seen as an extension of pair formation models to situations where individuals are allowed more than one partner at a time (Kretzschmar and Dietz, 1998). Leung et al (2015) further extend their model by incorporating the assumption that individuals have at most n partners at a given time.

A key parameter in epidemic modelling is the basic reproduction number, R_0. It is usually defined as the expected number of secondary infections caused by an index case in a completely susceptible population and this concept is used both in deterministic and stochastic models for infection spread (Diekmann et al, 2013). It is well known that for a susceptible-infectious-recovered (SIR) epidemic in a homogeneous mixing population the process describing the number of infectious individuals during the early stages of the epidemic is well approximated by a suitable branching process (Ball and Donnelly, 1995). In those branching process approximations, giving birth corresponds to infecting someone and death corresponds to actual death or recovery, while R_0 corresponds to the offspring mean in the branching process. In particular, if $R_0 \leq 1$, then no epidemic is possible, while if $R_0 > 1$ the probability of a large outbreak is strictly larger than 0, but often strictly less than 1. There has been a lot of research on analysing the epidemic

threshold, i.e. $R_0 = 1$, by rigorous branching approximation for the stochastic epidemic models involving networks (see, e.g, Britton, 2010, and references therein). In fact, the technique of Ball and Donnelly (1995) can be used to approximate the initial phase of an epidemic on the contact network that has a large size by a suitable branching process (see, e.g, Ball et al, 2009, 2014).

The present study is an extension of the work of Leung et al (2015) and Leung (2016). Leung and co-authors use deterministic models to study different epidemic models on the dynamic graphs introduced in their work (that we briefly discuss in the following paragraph). In this deterministic approach, one implicit assumption is that the initial fraction of the population which is infectious might be very small, but the number of initially infectious individuals is always large, effectively assuming that the total population size is infinite. In the present study, we consider the epidemic and population dynamics as stochastic processes, where the expected population size is large but finite.

The network model of Leung et al (2015); Leung (2016) can be described as follows (for a detailed description see Section 2). Individuals enter the population at rate μN and die at rate μ per individual. This implies that the population size converges to N, which is assumed to be very large (and in the deterministic models effectively chosen to be infinite). Individuals enter the population without partners. An individual has at most n partners at a time, where n is a strictly positive integer (and can be chosen to be ∞). The possible partnerships are represented by so-called binding sites. At time t, let $n(1-F(t))$ be the average number of partners per individual in the population, i.e. $F(t)$ is the fraction of binding sites that is "free" at time t. If an individual has k partners at time t it acquires a new partner at rate $\rho(n-k)F(t)$ and partners divorce at rate σ per partnership. In the *SI* epidemic framework, a susceptible individual becomes infectious at a rate β times the number of his or her infectious partners. Infectious individuals cannot recover, but of course they stop spreading when they die. A key ingredient in the models of Leung and co-authors is the meanfield at distance one assumption, which is a (non-exact) approximation of the distribution of the number of partners of partners of a newly-infected individual (Leung et al, 2015).

We approach the models by Leung and co-authors from a stochastic perspective. To do this, we make some further assumptions, which make computations easier and the communication of our main message clearer. In contrast to the deterministic models mentioned before, we do not assume that a new individual in the population starts as single. Instead, we assume that the individuals upon entering the population immediately form a (random) number of partnerships with individuals already in the population. The distribution of this random number is chosen in such a way that the *distribution* of the number of partners of an individual does not change over time. That is to say, incoming individuals have a stationary distribution of the number of partners (usually referred to as the de-

gree distribution). The advantage of this assumption is the possibility of deriving explicit and relatively simple formulas for the basic reproduction number and in some cases for the probability of extinction of the epidemic (i.e. the probability that an epidemic stays small), without the mean-field at distance 1 approximation of Leung et al (2015); Leung (2016). We follow Leung et al (2015) to ignore the difference between male and female in our model and in this way effectively consider a homosexual or asexual population. Although this might be unrealistic, we think our main message is highlighted clearer by this omission.

The main purpose of this paper is to analyse possible approximations of the early stages of a stochastic epidemic in the described network by suitable branching processes. Our analysis focuses on the early stage of an epidemic outbreak where only a small number of individuals is initially infected. Note that this assumption does not fit within the deterministic framework, where the number of initial infectives is either exactly 0 or large, because in those models the initial fraction of the (effectively infinite) population infected has to be either 0 or strictly positive. In particular, we are concerned with deriving explicit formulas for the threshold parameter, R_0 and the probability of extinction. For this, we use two representations of the model.

In the first representation we consider a general maximal number of partners, n, but because of certain dependencies to be described in detail afterwards, it is not possible to do more than computing R_0.

The second representation is only valid for $n = 1$, which corresponds to the pair formation model of Kretzschmar and Dietz (1998). What makes this approach different from the first is that here we can describe the dynamics of the disease through a proper branching process. From this we can easily obtain the extinction probability as well as a threshold parameter, denoted by $\hat{R}_0$. This reproduction number $\hat{R}_0$ differs from R_0 and cannot be interpreted as the expected number of individuals infected by a typical infected individual. The interpretation of $\hat{R}_0$ is discussed in subsection 3.2. For further reflections on R_0, we refer the reader to Cushing and Diekmann (2016). Unfortunately, we did not find a way to generalize this approach to $n > 1$.

Finally, in order to avoid undesirable dependencies that appear and complicate the branching process in the two representations of the model, we also study the case in which there is no maximal number of partners, i.e. when $n = \infty$ (c.f. Altmann (1995)). For this model, we can compute the reproduction number as well as an implicit expression for the extinction probability.

The main contributions of the current work are:

- to present a branching process approach for analysing the early stages of an outbreak of a sexually transmitted infection, or a small outbreak, along the dynamic network. In doing this, we show why some appealing straight-

forward branching process approximations of the epidemic process are not correct, because they ignore some subtle dependencies.

- to characterize the basic reproduction number and the probability of extinction for the dynamic network by using a branching process approach.

The paper is structured as follows. Section 2 is devoted to the model definition and assumptions. In Section 3, we present two stochastic representations of the model. In the first, we use a naive (appealing but wrong) branching process approximation to analyse the early phase of an epidemic spreading through a dynamic sexual network. We use the second (less intuitive) representation of the model to compute a threshold parameter $\hat{R}_0$ and the correct probability of extinction during the initial phase of the epidemic. Here we also provide a discussion of the influence of the dependencies. In Section 4, the first representation of the model is used to study the epidemic on the dynamic network when the partnership capacity is infinite, i.e. when $n = \infty$. In this particular case, dependencies fall away and we may use branching processes to analyse the early phase of an epidemic spreading through a dynamic sexual network. In particular, we compute the reproduction number $\mathbb{R}_0$, the offspring distribution and compare reproduction numbers when $n \to \infty$. Finally, we discuss our analytical findings and give an outlook on future work in Section 5.

2 Model definition and assumptions

In our model we assume that individuals enter the population at rate μN (i.e. according to a Poisson process with intensity μN) and that individuals have independent exponentially distributed "lifetimes" (or time they stay in the active population), with expectation $1/\mu$, i.e. individuals leave the active population at rate μ times the number of individuals in this population. This implies that the distribution of the population size, say $N^*(t)$, converges as $t \to \infty$ to a Poisson distribution with mean N, i.e. the stationary and limiting distribution of the population size is Poisson distributed with expectation N (Resnick, 2013, Ch. 5). We assume that N is very large.

When an individual enters the population, he or she immediately forms partnerships with a random number of partners. This random number of partners is independent for different individuals and binomially distributed with parameters n and p_{in}, where n is a positive integer, representing the maximal number of partners an individual can have at any given time (the partnership capacity) and p_{in} is a constant between 0 and 1, to be specified later. So, the probability that an entering individual has ℓ partners is $\binom{n}{\ell}(p_{in})^{\ell}(1-p_{in})^{n-\ell}$. The probability that the incoming individual forms a partnership with an individual that already has k partners at

that moment is proportional to $n-k$. A given individual with ℓ partners acquires new partners among the individuals already in the population at rate $\rho(n-\ell)F(t)$, where $F(t)$ is a time dependent quantity (defined below). Again, the probability that a partnership is formed with an individual that at that moment already has k partners is proportional to $n-k$. Note that we can interpret this construction as follows: a given individual with ℓ partners and a given individual with k partners form a partnership at rate $\rho(n-\ell)(n-k)/(nN)$. Partnerships have independent exponential durations with expectation $1/\sigma$, i.e. partnerships dissolve at rate σ per partnership (if the partnership has not ended by death of one of the partners). If an individual leaves the active population, then all of its partnerships break.

From a modelling perspective individuals can be seen as collections of n "binding sites", where binding sites can either be free or occupied (by a partner). As long as individuals are alive, their binding sites behave independently where partnership formation and separation is concerned. Let $F(t)$ be the fraction of binding sites in the population, which is free at time t. We want this fraction to converge (with high probability) to a constant F, which we use in the formulation of the branching process. Observe that, because the number of partnerships of an individual just after entering the population is binomially distributed with parameters n and p_{in}, as a result, we can consider the binding sites of such an individual to be independent and free with probability $1-p_{in}$. We choose the parameters such that F is equal to $1-p_{in}$, because that is a necessary condition for the distribution of the number of partners of an individual to be stationary. Note that if a binding site is occupied it becomes empty at rate $\sigma+\mu$, where the σ term is caused by separation and the μ term is caused by death of the partner. A binding site, that is already in the population, acquires new partners already present in the population at rate $\rho F(t)$. The rate at which occupied binding sites enters the population is $\mu N n p_{in}$. The number of free binding sites in the population is $F(t)N^*(t)n$. Therefore, per binding site, the rate of acquiring newly arrived partners is $\frac{\mu N n p_{in}}{F(t)N^*(t)n}$. So an empty binding site acquires a new partner at rate $\rho F(t)+\frac{\mu N n p_{in}}{nN^*(t)F(t)}$. If $F(t)$ indeed converges to $F=1-p_{in}$ (and using the fact that $N^*(t)/N$ converges in probability to 1 as $N\to\infty$), then the rate of acquiring a new partner at a binding site is well approximated by $\rho F+\frac{\mu(1-F)}{F}$.

Putting the above together with the theory of Markov on-off processes (Resnick, 2013, p.405), the long run fraction of a binding site to be free is given by:

$$\frac{\sigma+\mu}{\sigma+\mu+\rho F+\frac{\mu(1-F)}{F}}=\frac{(\sigma+\mu)F}{\mu+\sigma F+\rho F^2}.$$

This fraction should be equal to F. As a result,

$$\rho F^2=\sigma(1-F) \tag{1}$$

or,

$$F = \frac{-\sigma + \sqrt{\sigma^2 + 4\rho\sigma}}{2\rho}. \tag{2}$$

So, we choose $p_{in} = 1 - \frac{-\sigma+\sqrt{\sigma^2+4\rho\sigma}}{2\rho}$. The parameters of our model are summarized in Table 1.

Because every binding site is in stationarity, the number of partners of a living individual is binomially distributed with parameters n and $1-F(t)$, i.e. the number of partners of a living individual is k with probability $\binom{n}{k}(1-F(t))^k F^{n-k}(t)$. Furthermore, for a given individual assuming that the individual does not die, the transitions of the number of partners are described by

$$\begin{aligned} &k \longrightarrow k+1 \text{ with rate } \left(\rho F(t) + \frac{\mu(1-F(t))}{F(t)}\right)(n-k), \\ &k \longrightarrow k-1 \text{ with rate } (\sigma+\mu)k. \end{aligned}$$

In the following lemma (the proof is presented in the Appendix), we show that $F(t)$ indeed converges (in some sense) to F as time t and the population size parameter N tends to infinity.

Lemma 1 *As $N \to \infty$ the fraction of free binding sites $F(t)$ satisfies on every bounded interval with probability tending to 1 the following differential equation*

$$\frac{dF(t)}{dt} = -\rho F^2(t) + \sigma\left(1-F(t)\right) - 2\mu\left(p_{in} - (1-F(t)\right). \tag{3}$$

It is not hard to see that the asymptotically stable equilibrium solution of the differential equation (3) is $\frac{-(\sigma+2\mu)+\sqrt{(\sigma+2\mu)^2+4\rho(\sigma+2\mu(1-p_{in}))}}{2\rho}$. So what it says is that as $t \to \infty$:

$$F(t) \to F = \frac{-\sigma + \sqrt{\sigma^2 + 4\rho\sigma}}{2\rho}.$$

In the following analysis we assume that the population has already reached equilibrium and $F(t)$ can be replaced by the constant F.

Next, we consider an *SI* epidemic spreading on the dynamic network described above. In this *SI* model, pairs of individuals make contacts according to independent Poisson processes with per partnership intensity β, as long as the pair is in a partnership. If a susceptible individual contacts an infectious one, it becomes infectious immediately and stays so until it leaves the population. We assume that the infection is introduced in the population by a single infectious individual, when the network is stationary. All other individuals are at that moment susceptible. With some abuse of terminology, we say that a binding site is susceptible (respectively infectious) if the partner at the binding site is susceptible (respectively infectious).

Table 1: The descriptions of the parameters for the model (1).

N	Expected number of individuals in population
n	Number of binding sites per individual
$\rho/(nN)$	Rate of making attempts of new connections per pair of free binding sites
μ	Natural mortality rate per individual
σ	Divorce rate per partnership
β	Disease transmission rate per partnership
$F(t)$	Fraction of free binding sites at time t
p_{in}	Fraction of binding sites of new individuals which is occupied

3 Branching process approaches to the spread of epidemics

3.1 A first naive approach

In this subsection, we study the spread of an STI (or other infectious disease) on the partnership network in the beginning of an epidemic by employing an appealing but wrong branching process approach. Here, we assume that everyone has n binding sites (i.e. an individual has at most n partners at the same time). In the present approach, the dynamic network model can be seen as a discrete space, continuous time Markov chain. So, we can describe the dynamics of the process in terms of rates (depending on the current state of the population), where times between events are exponentially distributed.

In the branching process approach, we want to keep track of properties of the infectious individuals and their binding sites. We implicitly assume that the number of susceptible individuals that are not connected to infectious individuals is very large and their properties, such as the distribution of the number of other susceptible partners etc., does not change as long as the branching process approximation is valid, i.e. we study the initial phase of the epidemic.

The possible states of a binding site of an infectious individual are: free (denoted by ϕ) or occupied by a susceptible (denoted by $-$) or occupied by an infectious individual (denoted by $+$). The binding sites of an individual move among the possible states according to a Markov process. The disease is transmitted from an infectious partner to a susceptible partner at rate β. Such a transmission causes a transition of the state of the binding site from $-$ state to $+$ state. Other possible transitions are from $-$ or $+$ to ϕ, which both happen at rate $\sigma+\mu$ and from ϕ to $-$ at rate $\rho F + \frac{\mu(1-F)}{F}$. Finally, the dynamics of this particular Markov process stops by death of the infectious individual under consideration, which happens at rate μ. The states and the transitions of this Markov process are shown schematically

in Figure 1.

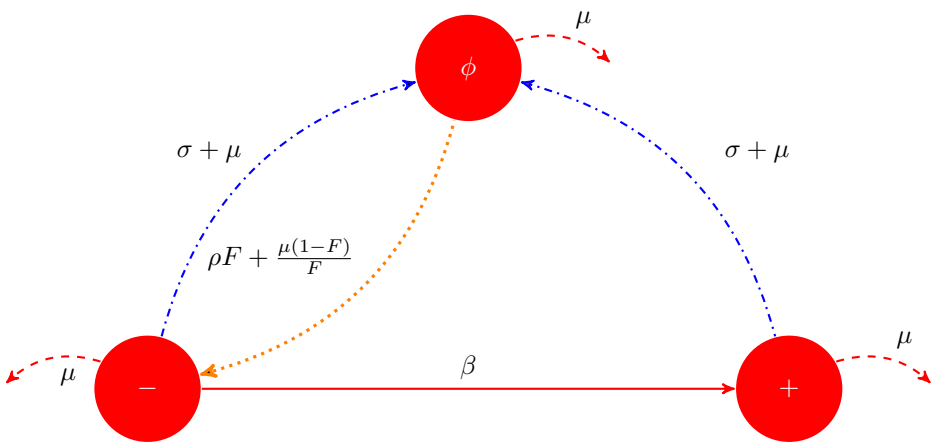

Figure 1: Flow chart describing the possible transitions between states (ϕ), $(+)$, $(-)$ and their corresponding rates. The continuous red line represents transmission of the infection while the dashed line represents death. The dash-dotted blue line represents occupied binding site becoming free while the dotted orange line represents free binding site becoming occupied.

Recall that an infectious individual can produce new infectious binding sites through contacts at his or her susceptible binding sites. The number of new infections caused by one infectious individual is the same as the sum of the number of times we have a transition from the $-$ state to the $+$ state, where the sum is taken over all its binding sites. Thus, in our consideration a child is born (i.e. an infectious binding site is created) whenever there is a passage from the $-$ state to the $+$ state. In the terminology of Galton-Watson branching processes (Jagers, 1975), infectious binding sites generated by an infectious individual are considered as his or her offspring. However, we stress again, as we show later, that the epdemic process is not well approximated by a genuine branching process.

Next, we define the following probabilities:

π_ϕ: Probability that a ϕ binding site becomes $+$ before it disappears, i.e. before the individual under consideration dies.

π_-: Probability that a $-$ binding site becomes $+$ before it disappears.

π_+: Probability that a $+$ binding site becomes $+$ again after having been $-$ or ϕ before it disappears.

Using the Markov property, the probability that the destination of a transition out of a given state (say i) to another given state (say j) is proportional to the transition rate from i to j. By making use of this property, it is straightforward to deduce that π_ϕ, π_- and π_+ satisfy the following balance equations (see Figure 1.):

$$\begin{aligned}
\pi_\phi &= \frac{\rho F + \frac{\mu(1-F)}{F}}{\mu + \rho F + \frac{\mu(1-F)}{F}}\pi_-, \\
\pi_- &= \frac{\beta}{\beta+\sigma+2\mu} + \frac{\sigma+\mu}{\beta+\sigma+2\mu}\pi_\phi, \\
\pi_+ &= \frac{\sigma+\mu}{\sigma+2\mu}\pi_\phi.
\end{aligned} \tag{4}$$

Recalling (1): $\rho F^2 = \sigma(1-F)$, we deduce from system (4) that

$$\begin{aligned}
\pi_\phi &= \frac{\beta(\sigma+\mu)(1-F)}{D}, \\
\pi_- &= \frac{\beta(\sigma(1-F)+\mu)}{D}, \\
\pi_+ &= \frac{\beta(\sigma+\mu)^2(1-F)}{(\sigma+2\mu)D},
\end{aligned} \tag{5}$$

where

$$D = \beta\left(\sigma(1-F)+\mu\right) + \mu(\sigma+\mu+\mu F).$$

In order to derive the offspring distribution of a newly infected individual, we let X_ϕ, X_- and X_+ be the random variables denoting, respectively, the number of infectious binding sites generated by an infected individual who starts in ϕ, $-$ and $+$ state. We derive the following probability distributions for $\ell = 0, 1, 2, \cdots$:

$$\begin{aligned}
\mathbb{P}(X_\phi = 1+\ell) &= \pi_\phi \pi_+^\ell (1-\pi_+), \\
\mathbb{P}(X_- = 1+\ell) &= \pi_- \pi_+^\ell (1-\pi_+), \\
\mathbb{P}(X_+ = \ell) &= \pi_+^\ell (1-\pi_+)
\end{aligned} \tag{6}$$

and $\mathbb{P}(X_\phi = 0) = 1-\pi_\phi$ and $\mathbb{P}(X_- = 0) = 1-\pi_-$. Thus, if $n = 1$, when every individual is "born" in state $+$ (because at the time of infection the individual's binding site is occupied by his or her infector), the offspring distribution in our process is geometric with parameter $1-\pi_+$.

The independence of the number of children of individuals can be viewed as the very defining property of branching processes. It is worth mentioning that

the stochastic process leading to (6) is not a branching process as it violates the independence criteria of reproducing individuals, already when $n = 1$. Indeed, information about the state of the partners of one of the individuals provides some information about the state of the partner of other individuals. To understand this, consider what happens if an individual in state + dies. We know with certainty that his or her partner gets a free binding site. While, if the partnership between two infected individuals dissolves, then we know for sure that both the infected individuals, that were in the partnership, gets a free binding site at the same time. We further clarify the dependencies that violates the independence criteria of reproducing individuals for $n = 1$ through the following example.

Example 1 *Consider the case when an infector has exactly 1 "child", the infectee. We consider what happens from the moment of the first infection on.*

$$
\begin{aligned}
&\mathbb{P}(\textit{infectee has } 0 \textit{ children} \mid \textit{infector has 1 child}) = \\
&(1-\pi_\phi)\mathbb{P}\Big(\textit{first event after infection is separation} \mid \textit{infector has 1 child}\Big) \\
&+(1-\pi_\phi)\mathbb{P}\Big(\textit{first event after infection is death of infector} \mid \textit{infector has 1 child}\Big) \\
&+\mathbb{P}\Big(\textit{first event after infection is death of infectee} \mid \textit{infector has 1 child}\Big) \\
&=\frac{\sigma}{\sigma+2\mu}\frac{(1-\pi_\phi)^2}{1-\pi_+}+2\frac{\mu}{\sigma+2\mu}\frac{1-\pi_\phi}{1-\pi_+}=\frac{1-2\frac{\sigma+\mu}{\sigma+2\mu}\pi_\phi+\frac{\sigma}{\sigma+2\mu}\pi_\phi^2}{1-\pi_+} \\
&=\frac{1-2\pi_+ +\frac{\sigma(\sigma+2\mu)}{(\sigma+\mu)^2}\pi_+^2}{1-\pi_+}\neq 1-\pi_+ = \mathbb{P}(\textit{infectee has 0 children}).
\end{aligned}
$$

This example shows that there is dependence between the states of the two events even for $n = 1$.

3.1.1 R_0

In both epidemiology and in branching process theory, the mean number of new infections caused by one infected individual (the children in the branching process) plays an important role. We focus on a newly infected individual and compute the expected number of new infectious binding sites generated by this individual. To this end, let R_0 denote the expected number of new infectious binding sites generated by one infectious individual in the early stages of an epidemic. A newly infected individual in the early stages of an outbreak starts his or her infectious period with one infected (the infector) and a random number of K_s susceptible binding sites. Note that, by the dynamic network properties and the assumption of the early stages of an outbreak, K_s is binomially distributed with parameters $n-1$ and $1-F$. Therefore, by this interpretation, R_0 is given by:

$$
\begin{aligned}
R_0 &= \mathbb{E}(\text{number of infections caused by one infectious individual}),\\
&= \mathbb{E}\big(\mathbb{E}(\text{number of infections caused by one infectious individual} \mid K_s)\big),\\
&= \mathbb{E}\big(\frac{\pi_+}{1-\pi_+} + K_s\frac{\pi_-}{1-\pi_+} + (n-K_s-1)\frac{\pi_\phi}{1-\pi_+}\big),\\
&= \frac{\pi_+}{1-\pi_+} + \frac{n-1}{1-\pi_+}\big(\pi_-(1-F)+\pi_\phi F\big),\\
&= \frac{\beta(1-F)}{\mu(\sigma+\mu+\mu F)(\beta+\sigma+2\mu)}\big((\sigma+\mu)^2+(n-1)(\sigma+2\mu)(\sigma+\mu+\mu F)\big).
\end{aligned}
\tag{7}
$$

This result, giving the explicit expression for the reproduction number R_0 for the general n. The first, second and third term in (7), account respectively for the expected number of new infectious binding sites generated by one infectious individual who starts in the $+$, $-$, and ϕ state. Note that, in computing this expectation, we do not need independence of the number of children at different binding sites (which indeed are not independent). Therefore, this analytic result is exact. However, since we do not deal with a branching process in the above derivation, we are not certain whether a single infectious individual can cause a major outbreak with positive probability if and only if $R_0 > 1$.

The number of partners in our model can have a great effect on R_0. To see the effect of n on R_0, we assume that the average number of partners of an individual be a constant C i.e $n(1-F) = C$. Using this in (7) and treating n as a positive continuous variable, straightforward computation gives

$$
\begin{aligned}
\frac{\partial R_0}{\partial n} &= \frac{-\beta C(\sigma+\mu)^2(\sigma+2\mu)}{\mu\big(n(\sigma+2\mu)-\mu C\big)^2(\beta+\sigma+2\mu)} + \frac{\beta C(\sigma+2\mu)}{n^2\mu(\beta+\sigma+2\mu)},\\
&= \frac{\beta C(\sigma+2\mu)(n-C)\big(2n(\sigma+\mu)+\mu(n-C)\big)}{n^2\big(n(\sigma+\mu)+\mu(n-C)\big)^2(\beta+\sigma+2\mu)}.
\end{aligned}
$$

Since C is always less than n, thus $\frac{\partial R_0}{\partial n} > 0$, i.e R_0 increases as n increases. Thus, the higher number of partners increases the basic reproduction number R_0.

3.1.2 Extinction probability under branching process assumption with $n = 1$.

Assume that $n = 1$ and recall that in this scenario F represents the fraction of single individuals in the population. Although, we have seen that our model is not well-approximated by a proper branching process, it is still possible to define a branching process through the offspring distribution (6). Obviously, we cannot

expect that this branching process approximates the epidemic spread well, but we still want to compute the probability of extinction of this branching process (Jagers, 1975) and compare this with the correct probability of a minor outbreak obtained in Section 3.2.

Standard results from the theory on branching processes (Jagers, 1975) give that the extinction probability q of a branching process originating from one case, with offspring distribution (6), is the smallest non-negative fixed point of the offspring generating function $G(s) = \sum_{i=0}^{\infty} p_i s^i$ where $p_i = P(X_+ = i)$ and $0 \leq s \leq 1$.

Recall that at the moment an individual gets infected, he or she has 1 infectious partner (namely his or her parent). From (6), we know that an infected individual has ℓ ($\ell = 0, 1, 2, \cdots$) children with probability $\mathbb{P}(X_+ = \ell) = \pi_+^\ell (1 - \pi_+)$. So, the extinction probability, denoted here by q_+, is given by the smallest root of

$$q_+ = \sum_{\ell=0}^{\infty} \pi_+^\ell (1 - \pi_+)(q_+)^\ell = \frac{1 - \pi_+}{1 - \pi_+ q_+}.$$

We find that $q_+ = \min(1, \frac{1-\pi_+}{\pi_+})$.

In the following we write the extinction probability in terms of R_0. For this, noting that for $n = 1$, Equation (7) gives

$$\beta = \frac{\mu(\sigma + 2\mu)(\sigma + \mu + \mu F)R_0}{(\sigma + \mu)^2(1 - F) - \mu(\sigma + \mu + \mu F)R_0}. \tag{8}$$

Using this value of β in Equation (5), we can write π_ϕ and π_+ in terms of R_0 as follows:

$$\begin{aligned} \pi_\phi &= \frac{(\sigma + 2\mu)R_0}{(\sigma + \mu)(R_0 + 1)}, \\ \pi_+ &= \frac{R_0}{R_0 + 1}, \end{aligned} \tag{9}$$

where, the first equation of (9) implies that we should take $\sigma \geq \mu(R_0 - 1)$ in order for $\pi_\phi \leq 1$. So, if $R_0 = \frac{\pi_+}{1-\pi_+} > 1$, then $q_+ = 1/R_0$.

If we assume that the branching process starts with an individual with an empty binding site, we can still compute the probability of extinction of the branching process by making use of the following observation. If the initial individual has k children, then the offspring of this initial individual only goes extinct if the offspring of the k children goes extinct. Those k children all correspond to infectious individuals with an infectious binding site at the moment of infection. Recall that

$$\mathbb{P}(X_\phi = k) = \begin{cases} 1 - \pi_\phi & \text{if } k = 0, \\ \pi_\phi (1 - \pi_+)\pi_+^{k-1} & \text{if } k \geq 1. \end{cases}$$

So, we denote by q_ϕ the probability that the offspring of an individual with an empty binding site goes extinct. Then, q_ϕ satisfies

$$q_\phi = \sum_{k=0}^{\infty} \mathbb{P}(X_\phi = k) q_+^k = 1 - \pi_\phi + \frac{\pi_\phi(1-\pi_+)q_+}{1-\pi_+ q_+} = 1 - \pi_\phi + \pi_\phi q_+^2 = \frac{1}{R_0} - \frac{\mu(R_0-1)}{(\sigma+\mu)R_0}.$$

where we have used (9) and $q_+ = 1/R_0$ in the last equality.

Similarly, we can compute q_- the probability that the offspring of an individual with a susceptible binding site goes extinct, we have that

$$q_- = 1 - \pi_- + \frac{\pi_-(1-\pi_+)q_+}{1-\pi_+ q_+} = 1 - \pi_- + \pi_- q_+^2.$$

It is not hard to see that if R_0 is greater than 1, then the extinction probabilities calculated above are less than 1, which is a minimal requirement for consistency.

3.2 Proper branching process approximation for epidemic spread

As stated earlier, we cannot expect that the branching process defined above approximates the epidemic well. Still, this branching process is used to compute the above extinction probabilities. Therefore, the probability calculated above are not necessarily the extinction probabilities of the epidemic process approximated by the branching process. That motivates us for setting up a branching process, which correctly approximates the epidemic process, so that we can get the true extinction probability for the model when $n = 1$. Unfortunately, we do not know how to extend this approach to $n > 1$.

For this branching process, we base our bookkeeping on the empty binding sites. For the moment assume that we start the epidemic with one infectious individual with binding site in state ϕ. Now the individual can either die (in which case no new empty binding sites are created), which occurs at rate μ or form a partnership with a susceptible individual (recall that we are in the early stages of an epidemic), which occur at rate $\rho F + \mu(1-F)/F) = (\sigma+\mu)(1-F)/F$. In case of a partnership between an infectious individual and a susceptible individual four things can happen: (i) a separation, in which case there is one infectious individual with an empty binding site which occurs at rate σ, (ii) the susceptible individual dies, in which case there is also one infectious individual with an empty binding site; this occurs at rate μ (iii) the infectious individual dies, in which case there is no infectious individual with an empty binding site; this occurs at rate μ or (iv) the infectious individual infects the susceptible one (rate β), in which case there is a partnership between two infectious individuals. In creating the branching process approximation below, we consider the resulting infectious individual with an empty binding site in case (i) and case (ii) as new individuals.

In case of a partnership between two infectious individuals two things can happen: (i) a separation, in which case there are two infectious individuals with an empty binding site, which occurs at rate σ (ii) one of the individual dies (rate 2μ), in which case there is one infectious individual with an empty binding site. Again, in creating the branching process approximation below, we consider the resulting infectious individuals with an empty binding site as new individuals. The possible transitions and their rate are schematically depicted in Figure 2.

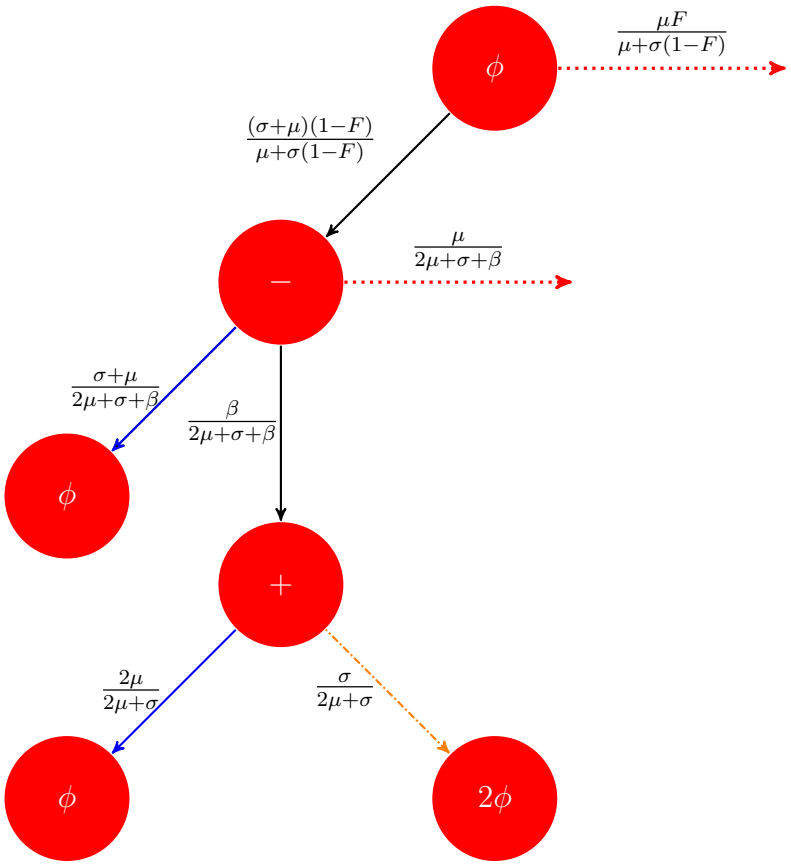

Figure 2: Flow chart describing the offsprings of binding site (ϕ). The dotted red lines represents producing 0 offspring, solid blue lines represent producing 1 offspring while the dash-dotted orange line represents producing 2 offspring.

Observe that an empty binding site can generate, after possibly going through some stages in which the binding site was occupied, zero, one or two "new" empty binding sites. Here the "new" binding sites might actually be the old binding site, which for modelling purposes is considered to be new. To clarify the idea behind our branching process approximation, consider as an example a separation of two infectious individuals. This can be seen as death of the free binding site leading to birth of two free binding sites. The "newborn" free binding sites are independent copies of the initial free binding site, which is why this description leads to a proper branching process.

So, each free binding site generates a random number Y, $Y \in \{0,1,2\}$, of free binding sites in the next generation, independently of other free biding sites. The probabilities of having Y children in the approximating branching process are given by

$$\begin{aligned}
\mathbb{P}(Y=0) &= \frac{\mu\,(\sigma+\mu+(\beta+\mu)F)}{(\sigma(1-F)+\mu)(\beta+\sigma+2\mu)},\\
\mathbb{P}(Y=1) &= \frac{(\sigma+\mu)\,((\sigma+\mu)(\sigma+2\mu)+2\mu\beta)\,(1-F)}{(\sigma(1-F)+\mu)\,(\sigma+2\mu)(\beta+\sigma+2\mu)},\\
\mathbb{P}(Y=2) &= \frac{\sigma\beta(\sigma+\mu)(1-F)}{(\sigma(1-F)+\mu)\,(\sigma+2\mu)(\beta+\sigma+2\mu)}.
\end{aligned} \tag{10}$$

This simple interpretation for the branching process is no longer valid if the number of binding sites of an individual exceeds 1, because death of an individual may cause several pairs of infectious individuals to break at the same moment and in that way cause dependencies, which violate the defining properties of branching processes.

For the branching process with an offspring distribution given through the random variable Y, we can compute the offspring mean (which corresponds to the expected total number of new free binding sites generated by one free binding site). We denote this offspring mean by $\hat{R}_0$, which is given by

$$\hat{R}_0 = E(Y) = \frac{(\sigma+\mu)^2(\sigma+2\mu+2\beta)(1-F)}{(\sigma(1-F)+\mu)\,(\sigma+2\mu)(\beta+\sigma+2\mu)}. \tag{11}$$

Note that, this $\hat{R}_0$ is not the basic reproduction number in the biological sense of the word, but as written above, it is a threshold parameter. The result (11), giving the explicit expression for the reproduction number $\hat{R}_0$ for the case in which every individual has at most one partner.

For the branching process with offspring distribution Y, we can also calculate the probability of extinction, which we denote by $\hat{q}_\phi$. This probability should be

the minimal solution of the following equation (see Jagers, 1975)

$$\hat{q}_\phi = \mathbb{P}(Y=0) + \mathbb{P}(Y=1)\hat{q}_\phi + \mathbb{P}(Y=2)\hat{q}_\phi^2,$$

which is given by

$$\hat{q}_\phi = \min\left(1, \frac{\mu(\sigma+2\mu)\,(\sigma+\mu+(\beta+\mu)F)}{\sigma\beta(\sigma+\mu)(1-F)}\right),$$

Using Equations (7) and (8), we obtain

$$\hat{q}_\phi = \min\left(1, \frac{1}{R_0} - \frac{\mu(R_0-1)}{\sigma R_0}\right).$$

The R_0 in this equation is the basic reproduction number obtained through the original naive branching process approximation and does not correspond to the offspring mean of the branching process used to derive $\hat{q}_\phi$, still it is useful to use this R_0 to simplify the expression for $\hat{q}_\phi$. Note that, the probability of extinction for both approximating branching processes is not the same. In fact, if $R_0 > 1$, then $q_\phi = \hat{q}_\phi + \frac{\mu^2(R_0-1)}{\sigma(\sigma+\mu)R_0}$. As written earlier, the reason for this is that the first approximation is not a proper branching process approximation of the epidemic process. In Fig. 3 we compare the two extinction probabilities q_ϕ and $\hat{q}_\phi$ as functions of σ, where $\sigma \geq \mu(R_0-1)$, while keeping $R_0 = 3$ and $\mu = 1/30$ fixed.

Remark: Of particular interest is the critical infection rate β, denoted by β_c, for which $R_0 = 1$, i.e. the minimum of β which is necessary to possibly cause an epidemic. Here, we show that our formal framework does indeed give the same threshold for both the approximations when $n = 1$. For this, setting $R_0 = 1$ (respectively $\hat{R}_0 = 1$), one obtains

$$\beta_c = \frac{\mu(\sigma+2\mu)(\sigma+\mu+\mu F)}{\sigma(\sigma+\mu)(1-F) - \mu F(\sigma+2\mu)},$$

for both models. This observation makes us believe that also for $n > 1$ a single infected individual can cause a major outbreak with positive probability if and only if $R_0 > 1$, but we did not find a proof for this.

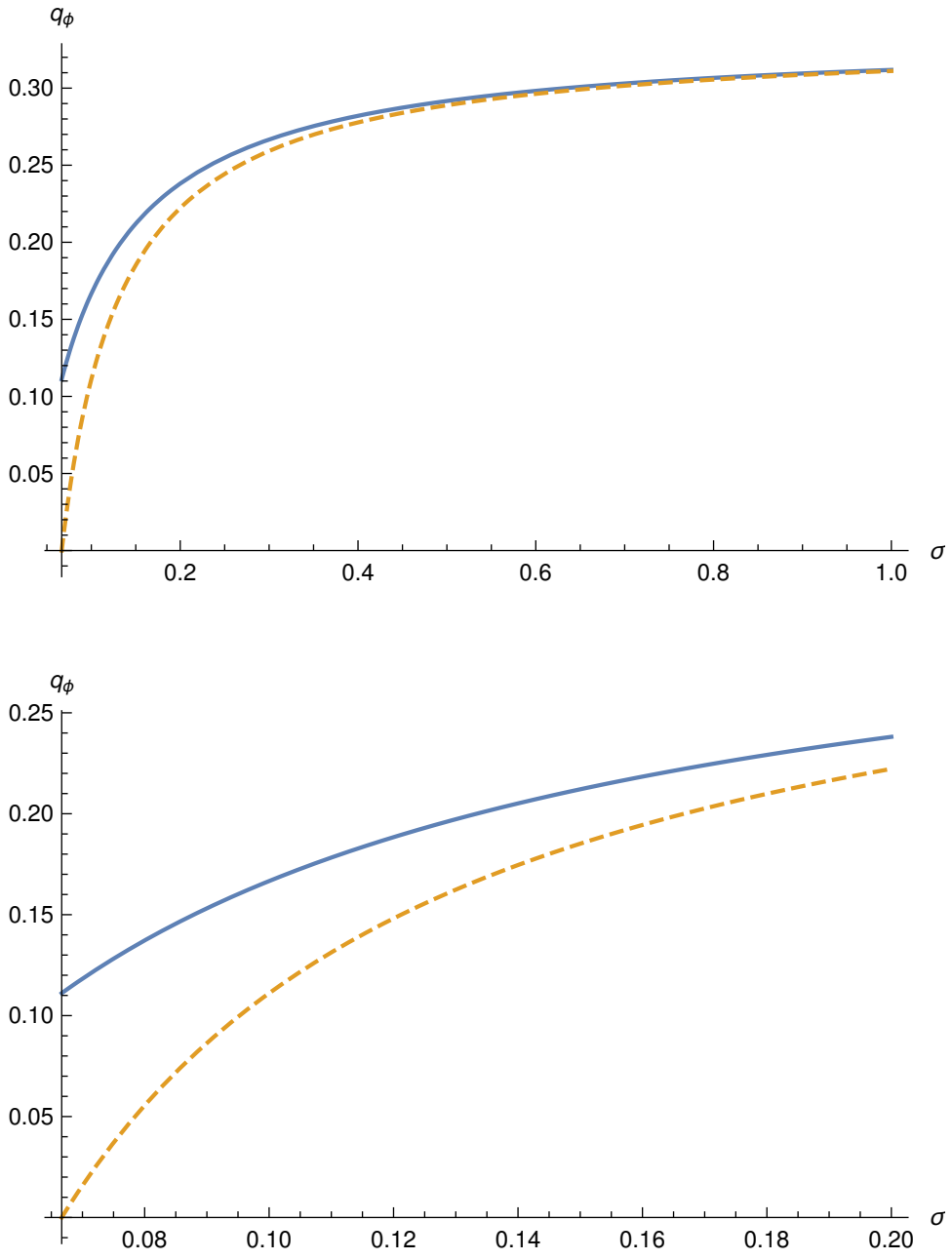

Figure 3: The two extinction probabilities q_ϕ for the two branching process representations of the epidemic process. The solid line is obtained using the naive branching process approximation, while the dashed line gives the correct probability of a minor outbreak. The plots are for $\sigma \geq \mu(R_0 - 1)$, where $R_0 = 3$ and $\mu = 1/30$.

4 Model without maximum partnership capacity

To circumvent the difficulty of dependencies that arises in the branching process approximation for the epidemic process with $n > 1$ in the previous sections, we consider the model with $n = \infty$. In this model, it is again assumed that the new individuals enters the population with a random number of partners. Where those random numbers are assumed to be independent and identically distributed and chosen in such a way that the number of partners of an individual is stationary during the whole "lifetime".

In order to avoid that individuals accumulate new partners at infinite speed, we set for $n < \infty$ the rate at which an individual enters a new partnership per free binding site as $\rho = \frac{\bar{\rho}}{n}$, where $\bar{\rho}$ is a constant. Note that for $n < \infty$, an individual with k partners enters a new partnership at rate $\rho F(n-k)$, which would go to infinity if $\rho > 0$ and $n \to \infty$. Furthermore, assume that an individual enters the population with an expected number μ_{in} of partners.

Arguing as for the finite n case. Individuals acquire new partners at rate $\bar{\rho} + \mu\mu_{in}$ (note that this is independent of the number of partners the individual already has) and lose partners at rate $\sigma + \mu$. If the stationary distribution of the number of partners is distributed as D, then for $k = 0, 1, \cdots$, the probabilities $d_k = \mathbb{P}(D = k)$ needs to satisfy the following balance equation

$$(\bar{\rho} + \mu\mu_{in})d_k = (\sigma + \mu)d_{k+1}(k+1). \tag{12}$$

Noting that $\sum_{k=0}^{\infty} d_k = 1$, it follows from (12) that

$$d_k = \frac{(\frac{\bar{\rho}+\mu\mu_{in}}{\sigma+\mu})^k \mathrm{e}^{-\frac{\bar{\rho}+\mu\mu_{\mathrm{in}}}{\sigma+\mu}}}{k!}, \tag{13}$$

i.e. D is Poisson distributed with expectation $\frac{\bar{\rho}+\mu\mu_{in}}{\sigma+\mu}$. In order to let the degree of entering individuals be stationary from the start, we want μ_{in} to satisfy the following equation:

$$\mu_{in} = \mathbb{E}(D) = \frac{\bar{\rho} + \mu\mu_{in}}{\sigma + \mu},$$

which implies $\mu_{in} = \bar{\rho}/\sigma$. So, D is Poisson distributed with expectation $\bar{\rho}/\sigma$. Furthermore, newly arriving individuals also have this degree distribution.

Having determined the degree distribution, we can now compute the expected number of partners infected by one infectious individual. We denote this expected number by $\mathbb{R}_0$, which corresponds to R_0 as defined for the finite n case.

First we compute the probability that the infectious individual (say v_1) infects a given other individual, say v_2, who was already a partner of v_1 at the moment v_1

got infected. This probability to infect susceptible partner is given by

$$\int_0^\infty \mu e^{-\mu t} \int_0^t \beta e^{-\beta u} e^{-\mu u} e^{-\sigma u} du dt = \frac{\beta}{\beta + \sigma + 2\mu}.$$

Here, 0 can be seen as the time when v_1 got infected, t is the time when v_1 dies and u is the time when v_1 infects v_2. Since the expected number of susceptible partners of an individual at the time of infection is $\bar{\rho}/\sigma$, the expected number of partners v_1 infects, among those individuals who were already partners at the time v_1 was infected is

$$\frac{\bar{\rho}}{\sigma} \int_0^\infty \mu e^{-\mu t} \int_0^t \beta e^{-\beta u} e^{-\mu u} e^{-\sigma u} du dt = \frac{\bar{\rho}\beta}{\sigma(\beta + \sigma + 2\mu)}. \tag{14}$$

Similarly, we can compute the probability that an individual v_1 who dies at time t after being infected, infects a partner v_2 which it contacts at time s since v_1 got infected ($s < t$). This probability is given by

$$\int_s^t \beta e^{-\beta(u-s)} e^{-\mu(u-s)} e^{-\sigma(u-s)} du.$$

So, using the fact that the total rate an individual acquires a new partners is $(\bar{\rho} + \mu\frac{\bar{\rho}}{\sigma})$, the expected number of individuals v_1 infects, among those individuals who were not yet partners of v_1 at the time v_1 got infected is given by

$$\int_0^\infty \mu e^{-\mu t} \int_0^t (\bar{\rho} + \mu\frac{\bar{\rho}}{\sigma}) \int_s^t \beta e^{-\beta(u-s)} e^{-\mu(u-s)} e^{-\sigma(u-s)} du ds dt = \frac{\bar{\rho}\beta(\sigma + \mu)}{\sigma\mu(\beta + \sigma + 2\mu)}. \tag{15}$$

Combining the above two observations (14) and (15), we arrive at the following expression for the basic reproduction number:

$$\mathbb{R}_0 = \frac{\bar{\rho}\beta}{\sigma(\beta + \sigma + 2\mu)} + \frac{\bar{\rho}\beta(\sigma + \mu)}{\sigma\mu(\beta + \sigma + 2\mu)} = \frac{\bar{\rho}\beta(\sigma + 2\mu)}{\sigma\mu(\beta + \sigma + 2\mu)}. \tag{16}$$

Altmann (1995) considers a model very similar to ours but not exactly the same. He considers an SIR epidemic in a population in which individuals do not die but recover (and acquire eternal immunity) and no new individuals can enter the population. It is easy to check that $\mathbb{R}_0$ in (16) obtained above is in agreement with the result in equation (1) of Altmann (1995) after setting the death rate of partners to 0, which leads to replacing $\beta + \sigma + 2\mu$ by $\beta + \sigma + \mu$ in the denominators of both terms in the middle expression of (16) and dropping the factor $(\sigma + \mu)/\sigma$ in the second term of the middle expression of (16).

In order to find the probability of a minor outbreak, we need the distribution of the number of new infectious binding sites that are generated by each infected individual. This then defines the offspring distribution for our branching process.

Assume that individual v_1 is infectious for t time units. We have already computed the probability of infecting a given other individual who was already a partner of v_1 at the moment v_1 got infected (see Equation (4)). Conditioned on t, this probability is

$$\int_0^t \beta \mathrm{e}^{-\beta \mathrm{u}} \mathrm{e}^{-\mu \mathrm{u}} \mathrm{e}^{-\sigma \mathrm{u}} \mathrm{du} = \frac{\beta}{\alpha}(1-\mathrm{e}^{-\alpha \mathrm{t}}),$$

where $\alpha = \beta + \mu + \sigma$. Furthermore, conditioned on t, whether a given partner of v_1 at the time v_1 got infected (say time 0), will itself be infected by v_1 is independent of which other individuals v_1 infects. This implies that the probability generating function of $Z_1(t)$, the number of partners of v_1 at time 0, who are ultimately infected by v_1 for $s \in [0,1]$ is given by

$$\mathbb{E}(s^{Z_1(t)}) = \sum_{\ell=0}^{\infty} \frac{(\frac{\bar{\rho}}{\sigma})^{\ell}}{\ell!} e^{-\frac{\bar{\rho}}{\sigma}} \left(\frac{\beta}{\alpha}(1-e^{-\alpha t})s + 1 - \frac{\beta}{\alpha}(1-e^{-\alpha t}) \right)^{\ell}. \tag{17}$$

Still assuming that v_1 lives until time t since infection, v_1 can also infect individuals that are not yet partners of v_1 at time 0. As described above, an individual acquires new partners according to a homogeneous Poisson process with intensity $\bar{\rho}\frac{\sigma+\mu}{\sigma}$. Up to time t, the distribution of the number of acquired partners is therefore Poisson distributed with expectation $\bar{\rho}\frac{\sigma+\mu}{\sigma}$. If we condition on v_1 acquiring m partners in the time interval $(0,t)$, then, by standard properties of the Poisson process (Resnick, 2013, Section 4.5), those m time points are distributed as m independent uniformly distributed random variables on $(0,t)$. Let $Z_2'(t,m)$ be the random number of individuals v_1 infects that were not partners yet at time 0, conditioned on v_1 dying at time t and acquiring m partners in $(0,t)$. The above demonstration yields

$$\mathbb{E}(s^{Z_2'(t,m)}) = \left(\frac{1}{t} \int_0^t \left(\frac{\beta}{\alpha}(1-e^{-\alpha(t-u)})s + 1 - \frac{\beta}{\alpha}(1-e^{-\alpha(t-u)}) \right) du \right)^{m}. \tag{18}$$

Further, let $Z_2(t)$ be the random number of individuals v_1 infects which were not partners yet at time 0, conditioned on v_1 dying at time t, not conditioned on the number of partners acquired in $(0,t)$. We obtain:

$$\begin{aligned} \mathbb{E}(s^{Z_2(t)}) &= \sum_{m=0}^{\infty} \frac{(\frac{\bar{\rho}(\sigma+\mu)t}{\sigma})^m}{m!} e^{-\frac{\bar{\rho}(\sigma+\mu)t}{\sigma}} \mathbb{E}(s^{Z_2'(t,m)}), \\ &= \sum_{m=0}^{\infty} \frac{(\frac{\bar{\rho}(\sigma+\mu)t}{\sigma})^m}{m!} e^{-\frac{\bar{\rho}(\sigma+\mu)t}{\sigma}} \left(\frac{1}{t} \int_0^t \left(\frac{\beta}{\alpha}(1-e^{-\alpha(t-u)})s + 1 - \frac{\beta}{\alpha}(1-e^{-\alpha(t-u)}) \right) du \right)^{m}. \end{aligned} \tag{19}$$

Note that because we assume $n = \infty$, conditioned on t, $Z_1(t)$ and $Z_2(t)$ are independent of each other, which implies that $\mathbb{E}(s^{Z_1(t)+Z_2(t)}) = \mathbb{E}(s^{Z_1(t)})\mathbb{E}(s^{Z_2(t)})$. Let Z be the random variable describing the total number of individuals infected by v_1. By integrating over time, we obtain by (17) and (19) that:

$$\begin{aligned}\mathbb{E}(s^Z) &= \int_0^\infty \mu e^{-\mu t}\mathbb{E}(s^{Z_1(t)})\mathbb{E}(s^{Z_2(t)})dt,\\ &= \int_0^\infty \mu e^{-\mu t}\left(\sum_{l=0}^{\infty}\frac{(\frac{\bar\rho}{\sigma})^\ell}{\ell!}e^{-\frac{\bar\rho}{\sigma}}\big(\frac{\beta}{\alpha}(1-e^{-\alpha t})s+1-\frac{\beta}{\alpha}(1-e^{-\alpha t})\big)^\ell\right)\\ \times\Bigg(\sum_{m=0}^{\infty}&\frac{(\frac{\bar\rho(\sigma+\mu)t}{\sigma})^m}{m!}e^{-\frac{\bar\rho(\sigma+\mu)t}{\sigma}}\big(\frac{1}{t}\int_0^t\big(\frac{\beta}{\alpha}(1-e^{-\alpha(t-u)})s+1-\frac{\beta}{\alpha}(1-e^{-\alpha(t-u)})\big)du\big)^m\Bigg)dt.\end{aligned} \tag{20}$$

where $\mathbb{E}(s^Z)$ is the probability generating function of Z, the total number of individuals infected by v_1. Equation (20) can further be simplified as follows:

$$\begin{aligned}\mathbb{E}(s^Z) &= \int_0^\infty \mu e^{-\mu t}e^{-\frac{\bar\rho}{\sigma}}\sum_{\ell=0}^{\infty}\frac{(\frac{\bar\rho}{\sigma})^\ell}{\ell!}\left(1-\frac{\beta}{\alpha}(1-e^{-\alpha t})(1-s)\right)^\ell\\ &\times e^{-\frac{\bar\rho(\sigma+\mu)t}{\sigma}}\sum_{m=0}^{\infty}\frac{(\frac{\bar\rho(\sigma+\mu)}{\sigma}t)^m}{m!}\left(1-\frac{\beta}{\alpha}(1-s)+\frac{\beta}{\alpha^2 t}(1-e^{-\alpha t})(1-s)\right)^m dt,\\ &= \int_0^\infty \mu e^{-\mu t}e^{-\frac{\bar\rho\beta}{\sigma\alpha}(1-e^{-\alpha t})(1-s)}e^{-\frac{\bar\rho\beta}{\sigma\sigma}(\sigma+\mu)\left(t-\frac{1}{\alpha}(1-e^{-\alpha t})\right)(1-s)}dt.\end{aligned} \tag{21}$$

To simplify notation, we write, recalling that $\alpha = \beta+\mu+\sigma$, that $c = \frac{\bar\rho\beta(\sigma+\mu)}{\sigma\alpha}$ and $d = \frac{\bar\rho\beta}{\sigma\alpha}(1-\frac{\sigma+\mu}{\alpha}) = \frac{\bar\rho\beta^2}{\sigma\alpha^2}$, After rearranging the terms in (21), a little algebra yields:

$$\begin{aligned}\mathbb{E}(s^Z) &= \mu e^{-d(1-s)}\int_0^\infty e^{-(\mu+c(1-s))t}e^{d(1-s)e^{-\alpha t}}dt,\\ &= \mu e^{-d(1-s)}\int_0^\infty\sum_{\ell=0}^{\infty}\frac{(d(1-s))^\ell}{\ell!}e^{-(\mu+c(1-s)+\ell\alpha)t}dt,\\ &= \mu e^{-d(1-s)}\sum_{\ell=0}^{\infty}\frac{(d(1-s))^\ell}{\ell!(\mu+c(1-s)+\ell\alpha)}.\end{aligned} \tag{22}$$

Thus, we have found an expression for the probability generating function for the number of offspring generated by an infectious individual, involving an infinite series with infinite radius of convergence. Note that, the probability $\mathbb{P}(Z=k)$ for

a specific k can be determined from the probability generating function through

$$\mathbb{P}(Z=k)=\frac{1}{k!}\frac{d^k}{ds^k}\mathbb{E}(s^Z)|_{s=0},$$

but explicit expressions for these probabilities are long and hardly insightful.

Furthermore, we can also find the probability of extinction of the branching process as the smallest positive root of $s=\mathbb{E}(s^Z)$. Again, there is no nice closed form expression for this root, however it can be approximated numerically.

Finally, we explore the consistency in $\mathbb{R}_0$ and R_0 when the number of binding sites n tends to infinity. In the limit when n becomes large, the asymptotic fraction of free binding sites as described in equation (2) becomes

$$\begin{aligned}F&=\frac{-\sigma+\sigma\sqrt{1+4\frac{\bar{\rho}}{n\sigma}}}{2\frac{\bar{\rho}}{n}}\\&\approx\frac{n}{2\bar{\rho}}\left(-\sigma+\sigma\left(1+\frac{2\bar{\rho}}{\sigma n}-\frac{2\bar{\rho}^2}{\sigma^2n^2}+o(\frac{1}{n^2})\right)\right)\approx 1-\frac{\bar{\rho}}{\sigma n}+o(\frac{1}{n}),\end{aligned}$$

where a function $g(x)=o(x)$ if $g(x)/x\to 0$ for $x\to 0$. Therefore, $F\to 1-\frac{\bar{\rho}}{\sigma n}$ as $n\to\infty$. Using $F\to 1-\frac{\bar{\rho}}{\sigma n}$ in (7), a little algebra confirms that

$$\lim_{n\to\infty}R_0=\frac{\bar{\rho}\beta(\sigma+2\mu)}{\sigma\mu(\beta+\sigma+2\mu)},$$

which agrees with equation (16).

5 Conclusion

The reproductive number and the probability of extinction are among the most fundamental concepts in the theory of mathematical modelling of the spread of infectious diseases. These quantities have importance for health officials for planning and allocation of funds to control the spread of those diseases. We explored different strategies to derive explicit expressions for these two important quantities for a dynamic sexual network using branching processes. Although, it is difficult to derive analytical expressions for threshold conditions and the probability of extinction for a disease spreading on a dynamic sexual network, the branching process approach provide insights for determining the analytical expressions both for the threshold quantity and the probability of extinction. To derive these quantities, we proposed two approaches.

In the first approach, we considered the case in which every individual has n binding sites. This approach suffers from some undesired dependencies, as a

result we ended up with an approximating branching process that in fact was not a proper approximation of the original epidemic process. The dependencies are demonstrated in detail and an example is provided to clarify the dependencies that violates the (for branching processes) crucial independence criteria of reproducing individuals. The obtained insights are a warning for dependencies which are easily overseen.

By the simple modelling framework of this first approach, it is only possible to derive the value of the basic reproduction number R_0. However, the probability of extinction of this approximate branching process is also computed to compare it with the true probability of extinction for the special case in which an individual has at most one partner at a time. Interestingly, starting from one infectious individual, the derivation of R_0 does not depend on the fundamental independence criteria of the number of children at different binding sites. This suggests that the corresponding explicitly derived value of R_0 is exact. However, this does not guarantee the occurrence of a major outbreak with positive probability even if the basic reproduction number $R_0 > 1$. This finding is in contrast to classical epidemic models where a major outbreak has strictly positive probability if and only if $R_0 > 1$.

In the second approach, we demonstrated a simple version of the model in which every individual can have at most one partner at a time. For this model, we managed to establish a proper branching process approximation and derived the offspring distribution of this branching process, which allows us to easily compute the probability of extinction for the branching process (and thus for the epidemic). The expectation of the offspring distribution is a threshold parameter. Finally, for $n = 1$, it is verified that the epidemic threshold parameters obtained by the two different schemes are the same.

In deriving our models and sticking to branching process approximation as a tool for the analysis, we find that the dependencies has a subtle influence on the formulation of branching process. These dependencies disappear if $n = \infty$. In that case we can compute the basic reproduction number $\mathbb{R}_0$ and the degree distribution of the number of partners of an individual. The probability generating function of the distribution of the number of offspring produced by an infectious individual, that involve a convergent infinite series, is also calculated. This helps us derive an implicit expression of extinction probability. Moreover, we show that our computations are consistent in the sense that for $n \to \infty$, $R_0 \to \mathbb{R}_0$.

The current study is only a first step in studying the spread of the disease on a dynamic network using a branching process approach. In future work, we hope to further investigate the disease dynamics by dropping the stationary distribution assumption of the number of partners at debut.

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Appendix

In this appendix, we prove that the fraction of free binding sites in a population with size parameter N, say $F_N(t)$, indeed (under certain conditions) converges to a constant F with probability tending to 1 as $N \to \infty$. To do this we consider a sequence of the epidemic processes indexed by the expected population size N. We often write that an event occurs w.h.p. (with high probability), which means that the probability of the event converges to 1 as $N \to \infty$ and $t \to \infty$.

Since, for finite N the number of edges in the graph will within finite (but exponentially large) time have been both 0 and nN, we cannot obtain that $F_N(t) \to F$ as $t \to \infty$ with high probability. So, we settle for proving that for s large enough and every $\varepsilon > 0$ and $t > 0$ we have that $\sup_{s \le u \le s+t} |F_N(u) - F| < \varepsilon$, with high probability. To do this, we prove that for all $\varepsilon > 0$ and all $t > 0$, $\sup_{u \le t} |F_N(u) - F(u)| < \varepsilon$ w.h.p., where $F(t)$ satisfies

$$F(t) = F(0) - \int_0^t 2\mu\,(p_{in} - (1 - F(s))) - \sigma(1 - F(s)) + \rho(F(s))^2 ds \qquad \text{for } t \ge 0. \tag{23}$$

Here and throughout this appendix we assume that $F_N(0) \to F(0)$ as $N \to \infty$. The proof we provide is inspired by the proof of (Ethier and Kurtz, 2009, Thm 2.1, page 456).

Let $N_N^*(t)$ be the actual population size at time t and recall that the stationary distribution of $N_N^*(t)$ is Poisson distributed with expectation N. Throughout we assume that

$$|N_N^*(0) - N| \le N^{2/3}. \tag{24}$$

From (Ethier and Kurtz, 2009, Thm 11.2.3) we then deduce that for all $t > 0$,

$$|N_N^*(s) - N| \le 2N^{2/3} \qquad \text{for all } s \in [0,t] \text{ w.h.p.} \tag{25}$$

Note that (25) implies that,

$$\left|\frac{N_N^*(s_1)}{N_N^*(s_2)} - 1\right| \le 5N^{-1/3} \qquad \text{for all } s_1, s_2 \in [0,t] \text{ w.h.p.} \tag{26}$$

Let $M_N(t)$ be the number of partnerships in the population at time t. Because each partnership involves two individuals, the sum of the number of partners over all individuals is therefore $2M_N(t)$. Furthermore $F_N(t) = 1 - \frac{2M_N(t)}{nN_N^*(t)}$.

There are four events which change the number of partnerships in the population.

(i) A new individual entering the population, which leads to an expected increase of np_{in} of the number of partnerships and occurs at intensity μN.

(ii) An individual dies, which leads to an expected decrease of $\frac{2M_N(t)}{N_N^*(t)}$ of the number of partnerships and occurs at (time dependent) intensity $\mu N_N^*(t)$.

(iii) Separation, which decreases the number of partnerships by 1 and occurs at intensity $\sigma M_N(t)$ and

(iv) Formation of a new pair, which increases the number of partnerships by 1 and occurs at intensity

$$\frac{\rho}{2}(nN_N^*(t)-2M_N(t))\frac{nN_N^*(t)-2M_N(t)}{nN_N^*(t)} = \frac{\rho n N_N^*(t)}{2}\left(1-\frac{2M_N(t)}{nN_N^*(t)}\right)^2.$$

Denote the times at which one of the above events occur by $t_1 < t_2 < \cdots$ and set $t_0 = 0$. Let $\iota(t) = \max\{i \geq 0; t_i \leq t\}$, be the number of events up to time t. Define

$$\lambda(t) = \frac{nN_N^*(t)}{2}\left(2\mu\frac{N}{nN_N^*(t)} + \frac{2\mu}{n} + \sigma\frac{2M_N(t)}{nN_N^*(t)} + \rho\left(1-\frac{2M_N(t)}{nN_N^*(t)}\right)^2\right). \quad (27)$$

That is, $\lambda(t)$ is the rate at which the first event after time t occurs. By (25) we have

$$0 < \frac{2\mu}{n} \leq \frac{2}{nN_N^*(s)}\lambda(s) \leq \frac{5\mu}{n} + \sigma + \rho < \infty \qquad \text{for all } s \in [0,t] \text{ w.h.p.} \quad (28)$$

Let $\mathscr{F}_i$ be the σ-algebra generated by the whole dynamic random graph process up to time t_i. So $\{(M_N(t), N_N^*(t))\}_{t\in[0,t_i]}$ is measurable with respect to $\mathscr{F}_i$. For $i \geq 0$, the interarrival time $t_{i+1} - t_i$ is exponentially distributed with parameter $\lambda(t_i)$. Conditioned on $\{\lambda(t_i)\}_{i\geq 0}$, the interarrival times are independent. For $i \geq 1$, let $J_i = M_N(t_i) - M_N(t_{i-1})$ and note that $J_i \in [-n, n]$ (i.e. the maximal instantaneous change in $M_N(t)$ is n) and that

$$\begin{aligned}\hat{J}_i = \mathbb{E}[J_i|\mathscr{F}_{i-1}] &= \frac{2\mu\frac{N}{N_N^*(t_{i-1})}p_{in} - 2\mu\frac{2M_N(t_{i-1})}{nN_N^*(t_{i-1})} - \sigma\frac{2M_N(t_{i-1})}{nN_N^*(t_{i-1})} + \rho\left(1-\frac{2M_N(t_{i-1})}{nN_N^*(t_{i-1})}\right)^2}{2\mu\frac{N}{nN_N^*(t_{i-1})} + \frac{2\mu}{n} + \sigma\frac{2M_N(t_{i-1})}{nN_N^*(t_{i-1})} + \rho\left(1-\frac{2M_N(t_{i-1})}{nN_N^*(t_{i-1})}\right)^2} \\ &= \frac{\mu n N p_{in} - 2\mu M_N(t_{i-1}) - \sigma M_N(t_{i-1}) + \rho\frac{nN_N^*(t)}{2}\left(1-\frac{2M_N(t_{i-1})}{nN_N^*(t_{i-1})}\right)^2}{\lambda(t_{i-1})}.\end{aligned}$$

Define

$$\hat{M}_i = J_i - (t_i - t_{i-1})\lambda(t_{i-1})\hat{J}_i, \qquad \text{for } i \geq 1$$

and note that $\mathbb{E}[\hat{M}_{i+1}|\mathscr{F}_i] = 0$ and

$$\mathbb{E}[(\hat{M}_{i+1})^2|\mathscr{F}_i] = \mathbb{E}[(J_{i+1})^2|\mathscr{F}_i] \leq 4n^2. \tag{29}$$

Because $J_i = 1$ with probability at least

$$\frac{\mu N}{\lambda(t_i)} \geq \frac{2\mu N}{nN_N^*(t)} \frac{1}{\frac{5\mu}{n} + \sigma + \rho} \geq \frac{2\mu N}{N + 2N^{2/3}} \frac{1}{5\mu + \sigma n + \rho n} \geq \frac{\mu}{5\mu + \sigma n + \rho n},$$

we obtain that with high probability (here we used (28) and (25)),

$$0 < \frac{\mu}{5\mu + \sigma n + \rho n} \leq \mathbb{E}[(\hat{M}_{i+1})^2|\mathscr{F}_i] \leq 4n^2 < \infty. \tag{30}$$

Furthermore,

$$\begin{aligned} M_N(t) &= M_N(0) + \sum_{i=1}^{\iota(t)} \hat{M}_i + \int_0^{\iota(t)} \lambda(s)\hat{J}_{\iota(s)} ds \\ &= M_N(0) + \sum_{i=1}^{\iota(t)} \hat{M}_i + \int_0^{\iota(t)} \mu n N p_{in} - (2\mu + \sigma)M_N(s) + \rho \frac{nN_N^*(s)}{2} \left(1 - \frac{2M_N(s)}{nN_N^*(s)}\right)^2 ds \end{aligned}$$

Writing $F_N(t) = 1 - \frac{2M_N(t)}{nN_N^*(t)}$, this reads

$$\begin{aligned} F_N(t) = F_N(0)\frac{N_N^*(0)}{N_N^*(t)} &- \frac{2\iota(t)}{nN_N^*(t)} \frac{1}{\iota(t)} \sum_{i=1}^{\iota(t)} \hat{M}_i \\ &- \int_0^{\iota(t)} 2\mu \frac{N}{N_N^*(t)} p_{in} - (2\mu + \sigma)\frac{N_N^*(s)}{N_N^*(t)}(1 - F_N(s)) + \rho \frac{N_N^*(s)}{N_N^*(t)} (F_N(s))^2 ds. \end{aligned}$$

So using (23), we obtain

$$\begin{aligned} |F_N(t) - F(t)| \leq |F_N(0)\frac{N_N^*(0)}{N_N^*(t)} - F(0)| &+ |\frac{\iota(t)}{nN_N^*(t)} \frac{1}{\iota(t)} \sum_{i=1}^{\iota(t)} \hat{M}_i| \\ + |\int_0^{\iota(t)} 2\mu \frac{N}{N_N^*(t)} p_{in} - (2\mu + \sigma)\frac{N_N^*(s)}{N_N^*(t)}(1 - F_N(s)) + \rho \frac{N_N^*(s)}{N_N^*(t)} (F_N(s))^2] ds& \\ - \int_0^t (2\mu p_{in} - (2\mu + \sigma)(1 - F(s) + \rho(F(s))^2 ds|,& \end{aligned}$$

which in turn provides us with the following upperbound

$$\begin{aligned}\sup_{0\le u\le t}|F_N(u)-F(u)| \quad \le \quad & \sup_{0\le u\le t}|F_N(0)\frac{N_N^*(0)}{N_N^*(u)}-F(0)| \\ & + \sup_{0\le u\le t}|\frac{N}{N_N^*(u)}\frac{1}{nN}\sum_{i=1}^{\iota(u)}\hat{M}_i| \\ & + \sup_{0\le u\le t}|\int_{t_{\iota(u)}}^{u}(2\mu p_{in}-(2\mu+\sigma)(1-F(s)+\rho(F(s))^2 ds| \\ & + \sup_{0\le u\le t}\int_0^{t_{\iota(u)}}2\mu p_{in}|\frac{N}{N_N^*(u)}-1|ds \\ & + \sup_{0\le u\le t}\int_0^{t_{\iota(u)}}(2\mu+\sigma)|\frac{N_N^*(s)}{N_N^*(u)}(1-F_N(s))-(1-F(s))|ds \\ & + \sup_{0\le u\le t}\int_0^{t_{\iota(u)}}\rho|\frac{N_N^*(s)}{N_N^*(u)}(F_N(s))^2-(F(s))^2|ds.\end{aligned}$$

We can now analyse the six terms on the right hand side separately.

- $$|F_N(0)\frac{N_N^*(0)}{N_N^*(u)}-F(0)| \le F_N(0)|\frac{N_N^*(0)}{N_N^*(u)}-1|+|F_N(0)-F(0)|$$

  For all $0<u\le t$ the first term on the right hand side is w.h.p. bounded by $5N^{-1/3}$ by (26). The second term converges to 0 because $F_N(0)\to F(0)$ as $N\to\infty$.

- For $\sup_{0\le u\le t}|\frac{N}{N_N^*(u)}\frac{1}{nN}\sum_{i=1}^{\iota(u)}\hat{M}_i|$, note that $\sup_{0\le u\le t}|\frac{N}{N_N^*(u)}|<2$ w.h.p. by (25).

  By Kolmogorov's inequality (See (Durrett, 2010, Thm 2.5.2)) we obtain that

  $$\mathbb{P}\left(\max_{i\le k\le\iota(u)}|\sum_{i=1}^{k}\hat{M}_i|\ge nN^{2/3}\right)\le N^{-4/3}\iota(u).$$

  So, for $u\le t$

  $$\mathbb{P}\left(\max_{i\le k\le\iota(u)}\frac{1}{nN}|\sum_{i=1}^{k}\hat{M}_i|\ge N^{-1/3}\right)\le N^{-4/3}\iota(u)\le N^{-4/3}\iota(t).$$

  Furthermore, $\iota(t)$ is the number of events up to time t, which, by $N_N^*(u)<2N$ for all $u\in[0,t]$ w.h.p. and by (25) and (28), is w.h.p. bounded above by a Poisson distributed random variable with expectation $nNt\left(\frac{5\mu}{n}+\sigma+\rho\right)$. This bound is distributed as the sum of N i.i.d. Poisson distributed random

variables with mean $nt\left(\frac{5\mu}{n}+\sigma+\rho\right)$. So, by the (weak) law of large numbers

$$\frac{\iota(t)}{N} \leq nt\left(\frac{5\mu}{n}+\sigma+\rho\right)+1 \qquad \text{w.h.p.} \tag{31}$$

Combining the above, we obtain that there exists a positive constant C such that

$$\sup_{0\leq u\leq t}|\frac{N}{N_N^*(u)}\frac{1}{nN}\sum_{i=1}^{\iota(u)}\hat{M}_i| \leq Cn^{-1/3} \qquad \text{w.h.p.}$$

- $$|\int_{t_{\iota(u)}}^{u}(2\mu\,(p_{in}-(1-F(s)))-\sigma(1-F(s)+\rho(F(s))^2 ds| \\ \leq (u-t_{\iota(u)})\sup_{t_{\iota(u)}\leq s\leq u}|(2\mu\,(p_{in}-(1-F(s)))-\sigma(1-F(s)+\rho(F(s))^2| \\ \leq (u-t_{\iota(u)})(4\mu+\sigma+\rho).$$

  We are interested in

  $$\sup_{0\leq u\leq t}|\int_{t_{\iota(u)}}^{u}(2\mu\,(p_{in}-(1-F(s)))-\sigma(1-F(s)+\rho(F(s))^2 ds| \\ \leq \sup_{0\leq u\leq t}(u-t_{\iota(u)})(4\mu+\sigma+\rho).$$

  Because $u-t_{\iota(u)}$ is exponentially distributed with parameter at least $\mu N/2$ all over the interval $[0,t]$ by (30), $\sup_{0\leq u\leq t}(u-t_{\iota(u)})$ is stochastically bounded above by the maximum of $\iota(t)$ independent exponentially distributed random variables with mean at least $\mu N/2$. Denote this maximum by X. Let $c(N)$ be a function depending on N, then

  $$\mathbb{P}(X>c(N)) = 1-\left(1-\frac{1}{e^{\mu N c(N)/2}}\right)^{\iota(t)},$$

  which converges to 0 as $e^{\mu N c(N)/2}/\iota(t)\to\infty$, which by (31) holds w.h.p. for $c(n)=N^{-1/2}$.

- $$\sup_{0\leq u\leq t}\int_0^{t_{\iota(u)}}2\mu\,p_{in}|\frac{N}{N_N^*(u)}-1|ds \leq 2\mu\,p_{in}t(5N^{-1/3}) \qquad \text{w.h.p.}$$

  Here we have used (26) and that $t_{\iota(u)}\leq t$ for $u\in[0,t]$.

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$$\begin{aligned}
&\sup_{0\le u\le t}\int_0^{t_{\iota(u)}}(2\mu+\sigma)\Big|\frac{N_N^*(s)}{N_N^*(u)}(1-F_N(s))-(1-F(s))\Big|ds\\
&\quad\le(2\mu+\sigma)\sup_{0\le u\le t}\int_0^{t_{\iota(u)}}\Big|\frac{N_N^*(s)}{N_N^*(u)}-1\Big|(1-F_N(s))+|F(s)-F_N(s))|ds\\
&\quad\le(2\mu+\sigma)t5N^{-1/3}+(2\mu+\sigma)\sup_{0\le u\le t}\int_0^u|F(s)-F_N(s))|ds\qquad\text{w.h.p.}
\end{aligned}$$

Here we have used (26) and that $t_{\iota(u)}\le u\le t$ for $u\in[0,t]$.

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$$\begin{aligned}
&\sup_{0\le u\le t}\int_0^{t_{\iota(u)}}\rho\Big|\frac{N_N^*(s)}{N_N^*(u)}(F_N(s))^2-(F(s))^2\Big|ds\\
&\quad\le\rho\sup_{0\le u\le t}\int_0^u\Big|\left(\frac{N_N^*(s)}{N_N^*(u)}-1\right)(F_N(s))^2+|(F_N(s))^2-(F(s))^2|ds\\
&\le\rho\sup_{0\le u\le t}\int_0^t\Big|\left(\frac{N_N^*(s)}{N_N^*(u)}-1\right)ds+\rho\sup_{0\le u\le t}\int_0^u|F_N(s)-F(s)||F_N(s)+F(s)|ds\\
&\quad\le\rho5tN^{-1/3}+2\rho\sup_{0\le u\le t}\int_0^u|F_N(s)-F(s)|ds,\qquad\text{w.h.p.}
\end{aligned}$$

Here again we have used (26) and that $t_{\iota(u)}\le u\le t$ for $u\in[0,t]$.

Combining the above inequalities we obtain that

$$\sup_{0\le u\le t}|F_N(u)-F(u)|\le\varepsilon(N)+(2\mu+\sigma+2\rho)\sup_{0\le u\le t}\int_0^u|F_N(s))-F(s)|ds,\qquad\text{w.h.p.}\tag{32}$$

where $\varepsilon(N)\to0$ as $N\to\infty$. It follows now by Gronwall's inequality (see (Ethier and Kurtz, 2009, Appendix)) that for all $t>0$,

$$\sup_{0\le u\le t}|F_N(u)-F(u)|\to0$$

in probability as $N\to\infty$. In particular, for all $\varepsilon>0$, all $t>0$ and all s large enough

$$\sup_{s\le u\le s+t}|F_N(u)-F|<\delta,\qquad w.h.p.$$

Here we have used that $F(t)\to F$ as $t\to\infty$.

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