Mathematical Statistics
Stockholm University

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Research Report 2010:12

ISSN 1650-0377

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Mathematical Statistics
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Research Report **2010:12**,
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Frank Ball[*], David Sirl[†], Pieter Trapman[‡]

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AMS classifications: 60K35, 92D30, 05C80; 60J80, 91D30.

Keywords: Epidemic process, Random intersection graphs, Multi-type branching processes, Coupling.

1 Introduction

Traditional models for the spread of SIR (Susceptible → Infectious → Removed) epidemics [2, 14] are based on the homogeneous mixing assumption, that is, all pairs of individuals in the population contact each other at the same rate, independently of each

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other. Generalizations of this model have been proposed by introducing household structure into the population [4], where contacts between household members are more frequent than other contacts, or by introducing a (social) network structure [1, 19], where contacts are only possible between pairs of individuals that share a connection in the network. These extensions have been combined by the authors in [7, 8]. In most models for epidemics on networks, the network is modelled by a random graph constructed via the configuration model [15, Section 3]. In this construction one can control the degree distribution of the vertices, but the resulting network is locally tree-like, in the sense that the network contains hardly any cliques or short loops. In real social networks cliques are not sparse: "the friends of my friends are likely to be my friends as well". This feature of networks has been captured (among other models) by random intersection graphs [11, 13, 23] (see [10] for a related model). Random intersection graphs might be seen as a model for overlapping groups/cliques, in which a contact between two individuals is possible only if there is at least one group where they are both member of.

The aim of this paper is to study SIR epidemics on random intersection graphs. Specifically, we use branching process approximations to derive (i) a threshold parameter R_*, which determines whether an epidemic with few initial infectives can become established and infect a non-negligible proportion of the population, an event we call a large outbreak; (ii) the probability that a large outbreak occurs; and (iii) the fraction of the population that is infected by a large outbreak. These approximations are made fully rigorous as the population size tends to infinity by proving associated limit theorems.

The only previous rigorous study of epidemics on random intersection graphs is [11]. We extend the analysis of [11] in three directions. First, we allow more general distributions for both group size and group membership (i.e. the number of groups a typical individual belongs to). In [11], both of these quantities follow Poisson distributions; here we allow them to follow mixed-Poisson distributions. Moreover, as discussed in Section 7, we expect similar results to hold when group size and membership follow quite general distributions, though our proofs are valid only for the mixed-Poisson case. Second, we allow for an arbitrary infectious period distribution, unlike in [11] where a Reed-Frost type model is used, so effectively the infectious period is fixed. Third, we give a formal proof of a law of large numbers for the final outcome of a large outbreak, a result that was conjectured but not proved in [11]. Introducing variable infectious periods significantly complicates the analysis. We note that for random infectious periods, our model is not covered by [10, Section 5], since we need directed inhomogeneous random graphs and the proofs in [10] rely heavily on the structure of undirected graphs. Therefore, we need to develop alternative techniques to determine the fraction of the population that is infected by a large outbreak.

The remainder of the paper is organized as follows. Section 2 gives a brief introduction to random intersection graphs, having mixed-Poisson group size and group membership distributions, and to SIR epidemics defined on them. Section 3 collects together and extends some results of Ball and O'Neill [6] concerning final state random variables for homogeneously mixing SIR epidemics, in terms of Gontcharoff polynomials. Section 4 contains the main results of the paper. In Section 4.1 an infinite-type (forward) branching process that approximates the early stages of an epidemic is developed and analyzed, whilst in Section 4.2 a single-type (backward) branching process, which enables the proportion of the population that is infected by a large outbreak to be determined, is described. For both

of these branching processes, the Gontcharoff polynomial results derived in Section 3 are used to determine the probability generating function(als) of their offspring distribution(s). The key limit theorems of the paper are stated in Section 4.3. They show that, if there are few initial infectives, then in a large population, (i) a large outbreak can occur only if the forward branching process is supercritical; (ii) the probability that a large outbreak occurs is close to the probability that the forward branching process survives; and (iii) if there is a large outbreak, then the proportion of the population that is infected by the epidemic is close to the survival probability of the backward branching process. The limit theorems corresponding to the forward and backward branching processes are proved in Sections 5 and 6, respectively. Extension to more general distributions of clique size and membership is discussed briefly in Section 7.

2 Epidemics on random intersection graphs

2.1 Notation

Throughout, $\mathbb{N}$ denotes the set of natural numbers not including 0, while $\mathbb{Z}_+ = \mathbb{N} \cup \{0\}$. For $x \geq 0$, $\lfloor x \rfloor := \max(y \in \mathbb{Z}_+; y \leq x)$ is the floor of x, and $\lceil x \rceil := \min(y \in \mathbb{Z}_+; y \geq x)$ is the ceiling of x.

Furthermore, we write

$$\begin{aligned} f(x) = O(g(x)) \quad &\text{if} \quad \limsup_{x\to\infty} |f(x)/g(x)| < \infty, \\ f(x) = o(g(x)) \quad &\text{if} \quad \lim_{x\to\infty} f(x)/g(x) = 0 \quad \text{and} \\ f(x) = \Theta(g(x)) \quad &\text{if} \quad 0 < \liminf_{x\to\infty} |f(x)/g(x)| \leq \limsup_{x\to\infty} |f(x)/g(x)| < \infty. \end{aligned}$$

A (directed or undirected) graph is *simple* if it contains no parallel edges (edges that share both end-vertices) or self-loops (edges with only one end-vertex). In a directed graph, edges are parallel if they share both end-vertices and have the same direction. In a *multi-graph* self-loops and parallel edges are allowed. We may construct a directed graph from an undirected one by replacing every undirected edge by two directed edges with the same end-vertices but having opposite directions. If we construct a simple graph from a multi-graph, we do this by merging parallel edges and removing self-loops.

We use $\mathbb{P}$ for general unspecified probability measures, for which the interpretation is clear from the context, and $\mathbb{E}$ for the associated expectation. We use $\mathbb{E}_X$ to denote expectation with respect to the random variable X. However, if no confusion is possible we sometimes drop the subscript. For the non-negative random variable X, a mixed-Poisson(X) random variable, Y, is defined by $\mathbb{P}(Y = k) = \mathbb{E}_X[\frac{X^k}{k!}\mathrm{e}^{-X}]$, for $k \in \mathbb{Z}_+$. We say that a random variable is $\mathcal{P}(x)$ if it is Poisson distributed with mean x and $\mathcal{MP}(X)$ if it has a mixed-Poisson(X) distribution. We use $\tilde{X}$ to denote the size-biased variant of the non-negative random variable X, so for $x \geq 0$ we have

$$\mathbb{P}(\tilde{X} \leq x) = \frac{\int_{y\in[0,x]} y \, \mathrm{d}\mathbb{P}(X \leq y)}{\mathbb{E}[X]} = \frac{\mathbb{E}[X\mathbb{1}(X \leq x)]}{\mathbb{E}[X]}. \tag{2.1}$$

Here $\mathbb{1}(\mathcal{A})$, is the indicator function of $\mathcal{A}$, which is 1 if $\mathcal{A}$ holds and 0 otherwise. Let $X_n \Rightarrow X$ denote convergence in distribution. By [16, Theorem 7.2.19] we know that if

$X_n \Rightarrow X$, then $\mathbb{E}[X_n \mathbb{1}(X_n \leq x)] \Rightarrow \mathbb{E}[X \mathbb{1}(X \leq x)]$ for all points of continuity of $\mathbb{P}(X \leq x)$. This implies that if $\mathbb{E}[X_n] \to \mathbb{E}[X]$ and $X_n \Rightarrow X$, then $\tilde{X}_n \Rightarrow \tilde{X}$.

We also use the notation $f_X(s) = \mathbb{E}[s^X]$ $(s \in [0,1])$ for the probability generating function (PGF) of a $\mathbb{Z}_+$-valued random variable X and $\phi_X(\theta) = \mathbb{E}[\mathrm{e}^{-\theta X}]$ $(\theta \geq 0)$ for the moment generating function (MGF) of a real-valued random variable X. Lastly, for any set A we denote its cardinality by $|A|$.

2.2 Random intersection graphs

We consider a variant of random intersection graphs [11, 13] constructed via a bipartite generalization of Norros and Reittu's [21] Poissonian random graph model. Random intersection graphs may be thought of as random graphs composed of overlapping groups/cliques of individuals/vertices.

We construct a sequence of random intersection graphs as follows. Consider two infinite sets of vertices $V = (v_i; i \in \mathbb{N})$ and $V' = (v'_j; j \in \mathbb{N})$. Fix a real number $\alpha > 0$. Assign independent and identically distributed (i.i.d.) weights $(A_i; i \in \mathbb{N})$ to the vertices in V, all distributed as the non-negative random variable A and, independently, i.i.d. weights $(B_j; j \in \mathbb{N})$ to the vertices in V', all distributed as the non-negative random variable B. Assume that $\mu := \mathbb{E}[A] = \alpha \mathbb{E}[B] < \infty$. Define

$$L^{(n)} := \sum_{i=1}^{n} A_i, \tag{2.2}$$

$$L'^{(n)} := \sum_{j=1}^{\lfloor \alpha n \rfloor} B_j. \tag{2.3}$$

Let $(\Omega, \mathcal{F}, \nu)$ be the corresponding probability space, where

$$\Omega = (\mathbb{R}_+)^{\mathbb{N}} \times (\mathbb{R}_+)^{\mathbb{N}}$$

is the product space of non-negative real-valued infinite sequences $(A_i; i \in \mathbb{N})$ and $(B_j; j \in \mathbb{N})$. The σ-field $\mathcal{F}$ is generated by the finite dimensional cylinders on Ω and ν is the appropriate (product) measure determined by the distributions of A and B. We note that, by the strong law of large numbers, both $L^{(n)}/(\mu n) \xrightarrow{a.s.} 1$ and $L'^{(n)}/(\mu n) \xrightarrow{a.s.} 1$ as $n \to \infty$. Here $\xrightarrow{a.s.}$ denotes almost sure convergence with respect to the measure ν. Unless there is a possibility of confusion we use unadorned $\mathbb{E}$ for the expectation with respect to the measure ν.

In this paper we consider processes which depend on $\omega \in \Omega$, that is on the sequences $(A_i; i \in \mathbb{N})$ and $(B_i; i \in \mathbb{N})$. The measure governing a process conditioned on ω is denoted by $\mathbb{P}_\omega$ and the corresponding expectation by $\mathbb{E}_\omega$. We use the notation $X_n \xrightarrow[n\to\infty]{p_\nu} X$ to denote that X_n converges in probability to X as $n \to \infty$, with respect to the measure ν. That is, $X_n \xrightarrow[n\to\infty]{p_\nu} X$ means that for every $\epsilon > 0$, $\delta > 0$, we have $\nu(|X_n - X| > \epsilon) < \delta$ for all sufficiently large $n \in \mathbb{N}$. In particular, we often use the notation $\mathbb{P}_\omega(X_n \in \mathcal{A}) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(X \in \mathcal{A})$, which is to be interpreted as meaning that, for a subset $\mathcal{A}$ of the state space of X_n and X, we have that for every $\epsilon > 0$,

$$\int_{\omega \in \Omega} \mathbb{1}(|\mathbb{P}_\omega(X_n \in \mathcal{A}) - \mathbb{P}(X \in \mathcal{A})| > \epsilon) \nu(\mathrm{d}\omega) \to 0 \qquad \text{as } n \to \infty. \tag{2.4}$$

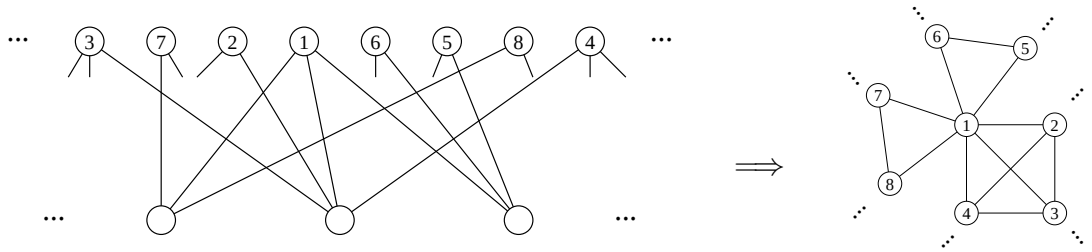

Figure 1: Construction of $G^{(n)}$ from $\mathbb{A}^{(n)}$.

For given $\omega \in \Omega$, an auxiliary sequence of random undirected multigraphs $(\mathbb{A}^{(n)}; n \in \mathbb{N}) := (\mathbb{A}^{(n)}(\omega); n \in \mathbb{N})$ is constructed as follows. For each n, the vertex set of $\mathbb{A}^{(n)}$ consists of $V^{(n)} := (v_i, 1 \le i \le n)$ and $V'^{(n)} := (v'_j, 1 \le j \le \lfloor \alpha n \rfloor)$. Vertices $v_i \in V^{(n)}$ and $v'_j \in V'^{(n)}$ share a $\mathcal{P}(A_i B_j/(\mu n))$ number of edges. Conditioned on the weights of vertices, i.e. on ω, the numbers of edges between distinct pairs of vertices are independent and there is no edge in $\mathbb{A}^{(n)}$ connecting vertices either both in $V^{(n)}$ or both in $V'^{(n)}$. Note that in $\mathbb{A}^{(n)}$, the degree of vertex $v_i \in V^{(n)}$ is $\mathcal{P}(A_i^{(n)})$ with

$$A_i^{(n)} := A_i L'^{(n)}/(\mu n) \xrightarrow{a.s.} A_i \qquad \text{as } n \to \infty, \tag{2.5}$$

while the degree of vertex $v'_j \in V'^{(n)}$ is $\mathcal{P}(B_j^{(n)})$ with

$$B_j^{(n)} := B_j L^{(n)}/(\mu n) \xrightarrow{a.s.} B_j \qquad \text{as } n \to \infty. \tag{2.6}$$

The random variables $A^{(n)}$ and $B^{(n)}$ are defined by

$$\mathbb{P}(A^{(n)} \le x) := n^{-1} |\{1 \le i \le n; A_i^{(n)} \le x\}|, \quad (x \ge 0) \quad \text{and} \tag{2.7}$$

$$\mathbb{P}(B^{(n)} \le x) := \lfloor \alpha n \rfloor^{-1} |\{1 \le j \le \lfloor \alpha n \rfloor; B_j^{(n)} \le x\}|, \quad (x \ge 0). \tag{2.8}$$

Thus, $A^{(n)}(\omega)$ and $B^{(n)}(\omega)$ are random variables with the empirical weight distribution. By the strong law of large numbers, $A^{(n)} \Rightarrow A$ and $B^{(n)} \Rightarrow B$ as $n \to \infty$.

For the purpose of this paper it is not important how the graphs in the sequence depend on each other. For simplicity, we assume that conditioned on $\omega = (A_i; i \in \mathbb{N}) \times (B_j; j \in \mathbb{N})$, the graphs $(\mathbb{A}^{(n)}, n \in \mathbb{N})$ are independent.

The vertices of the random intersection graph $G^{(n)}$ are precisely those in $V^{(n)}$. Two (distinct) vertices share an edge in $G^{(n)}$ if and only if there is at least one path of length 2 between them in $\mathbb{A}^{(n)}$. Thus, $G^{(n)}$ is a simple graph. This construction is visualized in Figure 1. We note that $G^{(n)}$ is slightly different from an ordinary random intersection graph. In [11, 13] the conditional probability that vertices with weights A_i and B_j share an edge in $\mathbb{A}^{(n)}$ is given by $\min(1, A_i B_j/(\mu n))$, as opposed to $1 - \exp[-A_i B_j/(\mu n)]$ in this paper.

Remark 2.1. *In this paper we make use of the following equivalent way of constructing* $\mathbb{A}^{(n)}$. *Initially all vertices are* unexplored. *Pick a vertex from* $V^{(n)}$ *according to some law (e.g. uniformly at random), say vertex* v_i *with weight* A_i*; this vertex becomes* active. *Assign a* $\mathcal{P}(A_i^{(n)})$ *number of edges to it (see* (2.5)*). The end-vertices in* $V'^{(n)}$ *of these edges are*

chosen independently with replacement and the probability that v'_j is chosen is $B_j/L'^{(n)}$. After this vertex v_i is made explored, *while the chosen vertices become active.*

Now, if there are any, explore the active vertices from $V'^{(n)}$ one by one. Suppose that we explore vertex v'_j, which has weight B_j, then assign a $\mathcal{P}(B_j^{(n)})$ number of edges to it. These edges connect to vertices independently chosen from $V^{(n)}$. Vertex v_l is chosen with probability $A_l/L^{(n)}$. If the end vertex has already been explored then the edge is ignored and not added to the graph, otherwise it is added and the end vertex in $V^{(n)}$ becomes active. If all the edges from v'_j are drawn, then v'_j is explored.

The next step is to pick an active vertex from $V^{(n)}$, if there are any, according to some, for now, unspecified law and explore it. Say that we chose v_k with weight A_k. Then we proceed as in the first step, i.e. we assign a $\mathcal{P}(A_k^{(n)})$ number of edges to it. Then the end-vertices in $V'^{(n)}$ of these edges are chosen independently with replacement and the probability that v'_j is chosen is $B_j/L'^{(n)}$. If the end vertex has been explored before, then the edge is ignored and deleted. After this, vertex v_k is made explored and the chosen vertices in $V'^{(n)}$, which were previously unexplored, become active. We now explore all active vertices in $V'^{(n)}$ in turn, and so on until there is no active vertex left. After that an unexplored vertex from $V^{(n)}$ is chosen and the process goes on until all vertices in $V^{(n)}$ are explored. Note that if there are unexplored vertices left in $V'^{(n)}$, they will have degree 0, since there is no end-vertex left in $V^{(n)}$ to connect to.

Remark 2.2. *Of course it is possible to construct a simple graph $\mathbb{A}'^{(n)}$ immediately, in which vertex v_i shares an edge with vertex v'_j with probability $1-\exp[-A_iB_j/(\mu n)]$. However, in order to have the machinery ready for branching process approximations we choose the present construction.*

Remark 2.3. *The graph $G^{(n)}$ is a graph of overlapping cliques, in which, asymptotically as $n \to \infty$, the number of cliques a vertex is part of has an $\mathcal{MP}(A)$ distribution and the clique sizes have an $\mathcal{MP}(B)$ distribution. Both of these distributions have finite mean by assumption.*

2.3 SIR epidemics

We consider a stochastic **S**usceptible → **I**nfectious → **R**ecovered/**R**emoved epidemic on the random intersection graph $G^{(n)}$. The vertices of the graph correspond to individuals and the edges to relationships/possible contacts. We assume that initially there is one uniformly at random chosen infectious individual/vertex, while all other individuals are susceptible. Every pair of individuals joined by an edge, makes directed contacts in both directions according to independent Poisson processes with intensity 1. If an infectious individual contacts a susceptible one, the susceptible becomes infectious. Infectious individuals stay infectious for a random infectious period, distributed as $\mathcal{I}$, after which the infectious individual becomes removed and plays no further part in the epidemic. Infectious periods are i.i.d. and independent of the Poisson processes generating the contacts. An infectious contact is a contact by an infectious individual, no matter what the state of the receiving individual is. Note that there is no loss of generality in assuming that the intensity of the Poisson processes governing the contacts is 1, since this can always be achieved by rescaling time. For ease of exposition, primarily to avoid multitype branching

processes that are reducible, we assume that $\mathbb{P}(\mathcal{I} = 0) = 0$. We omit the details but our results are readily extended to the case $\mathbb{P}(\mathcal{I} = 0) > 0$. Note, however, that we do allow for the possibility that $\mathbb{P}(\mathcal{I} = \infty) > 0$.

In order to study properties of the epidemic on a graph, G say, we introduce the *Epidemic Generated Graph*, which is a directed graph constructed as follows. If G is undirected, we replace every edge by two edges connecting the same vertices but in opposite directions, in order to transform it into a directed graph. To every vertex in the graph we assign independently a random variable, distributed as $\mathcal{I}$. Now we thin (the directed version of) G as follows. For each $v_i \in V^{(n)}$, edges starting at v_i are removed independently with probability $\mathrm{e}^{-\mathcal{I}_i}$, where $\mathcal{I}_i$ is the random variable assigned to v_i. Thus an edge starting at v_i is removed if infection would not pass along it were v_i to become infected during the epidemic. The set of vertices that can be reached in the Epidemic Generated Graph from an initially infectious vertex v_0 (including v_0 itself), is distributed as the set of ultimately removed individuals. The set of vertices from which there is a path in the Epidemic Generated Graph to vertex v', including v' itself, is said to be the *susceptibility set* of v' [3, 5]. If one of the vertices in the susceptibility set of v' is an initially infectious individual, then v' will be ultimately removed in the epidemic.

3 Final state random variables and Gontcharoff polynomials

3.1 Results for homogeneously mixing populations

In this section we give a restatement of Theorem 4.2 from Ball and O'Neill [6], adapted to the purposes of this paper (cf. [8]). We note that Ball and O'Neill provide appreciably more general results than their Theorem 4.2. In order to state the theorem, we need the following notation. We consider an SIR epidemic in a homogeneously mixing population with m initial susceptible individuals and a initial infectious individuals. The initial susceptible individuals are labeled $1, 2, \cdots, m$ and the initial infectious individuals have labels $-a+1, -a+2, \cdots, 0$. The random variable $\mathcal{I}_i$ represents the infectious period that individual i will have if it becomes infected. Thus, the probability that individual i, if infected, ultimately has an infectious contact with individual j is $1-\mathrm{e}^{-\mathcal{I}_i}$. (As before, infectious contacts between pairs of individuals are governed by independent unit-rate Poisson processes.) We assume that the random variables $(\mathcal{I}_i; i = -a+1, -a+2, \cdots, m)$ are independent and all distributed as $\mathcal{I}$; they are also independent of the Poisson processes describing infectious contacts. Let $\hat{h}(x) : (0, \infty] \to [0, \infty]$ be a measurable function (the relevant measures are clear from the context) and $\theta > 0$. Furthermore, let

$$\hat{U} := \hat{U}(\hat{h}, \theta) = (\hat{u}_i(\hat{h}, \theta); i \in \mathbb{Z}_+) = (\hat{u}_i; i \in \mathbb{Z}_+)$$

be an infinite vector, where $\hat{u}_k = \mathbb{E}[\mathrm{e}^{-k\mathcal{I}}\mathrm{e}^{-\theta\hat{h}(\mathcal{I})}]$. Let $\mathcal{R}$ be the set of ultimately removed individuals. This set consists of both initially infected and, if any are infected, initially susceptible individuals.

The Gontcharoff polynomials $G_m(x|\hat{U}), m \in \mathbb{Z}_+$, are defined recursively by

$$\frac{x^m}{m!} = \sum_{k=0}^{m} \frac{(\hat{u}_k)^{m-k}}{(m-k)!} G_k(x|\hat{U}), \tag{3.1}$$

for $m \in \mathbb{Z}_+$. We note that $G_m(x|\hat{U})$ is a polynomial of order m, which depends on $\hat{u}_0, \hat{u}_1, \cdots, \hat{u}_{m-1}$. Some properties of Gontcharoff polynomials are mentioned in Section 2 of [6]. In this paper we use only (3.1) and

$$G_m(x|\hat{U}) = \int_{\hat{u}_0}^{x} \int_{\hat{u}_1}^{\xi_0} \cdots \int_{\hat{u}_{m-1}}^{\xi_{m-2}} \mathrm{d}\xi_{m-1} \cdots \mathrm{d}\xi_1 \mathrm{d}\xi_0, \tag{3.2}$$

for $m \in \mathbb{Z}_+$. The following theorem is a special case of Theorem 4.2 in [6], which allows $\hat{h}$ to be random.

Theorem 3.1. *For $\hat{U}$, $\mathcal{R}$ and $\hat{h}$ as above, we have*

$$\mathbb{E}[x^{m+a-|\mathcal{R}|} \mathrm{e}^{-\theta \sum_{i \in \mathcal{R}} \hat{h}(\mathcal{I}_i)}] = \sum_{k=0}^{m} \frac{m!}{(m-k)!} (\hat{u}_k)^{m-k+a} G_k(x|\hat{U}). \tag{3.3}$$

We use the following corollary of this theorem.

Corollary 3.2. *Let $U := U(h) = (u_i(h); i \in \mathbb{Z}_+) = (u_i; i \in \mathbb{Z}_+)$, where $u_i = \mathbb{E}[\mathrm{e}^{-i\mathcal{I}}(1 - h(\mathcal{I}))]$ and $h(x) : (0, \infty] \to [0, 1]$ is Borel-measurable, and let $\mathcal{R}$ be as above. Then*

$$\mathbb{E}[1 - \prod_{i \in \mathcal{R}} (1 - h(\mathcal{I}_i))] = 1 - \sum_{k=0}^{m} \frac{m!}{(m-k)!} (u_k)^{m-k+a} G_k(1|U). \tag{3.4}$$

Proof. Set $x = \theta = 1$ and $\hat{h} = -\log(1-h)$ in Theorem 3.1. □

We can use this corollary to compute the distribution of the number of initially susceptible individuals that are ultimately removed, $\hat{T}(m, a) := \hat{T}(m, a, \mathcal{I})$. If $h(x)$ is constant on $\mathbb{R}_+$, say $h(x) = 1 - s$, then the corollary gives a formula for the PGF $\mathbb{E}[s^{\hat{T}(m,a)}]$.

The distribution of the size of the susceptibility set of an individual in a group of a given size can also be expressed using Gontcharoff polynomials. It turns out to be most convenient here to consider the size of the susceptibility set, $M(m)$ say, of an individual amongst the m other individuals in a group of size $m + 1$, i.e. $M(m)$ does *not* include the individual in question. As will become clear later, we do not need to keep track of the infectious periods of vertices in the susceptibility set. As in [8, Section 3], we have

$$\mathbb{P}(M(m) = k) = \frac{m!}{(m-k)!} (v_k)^{m-k} G_k(1|V) \qquad (k = 0, 1, \cdots, m), \tag{3.5}$$

where $v_k = \mathbb{E}[\mathrm{e}^{-(k+1)\mathcal{I}}]$ and $V = (v_0, v_1, v_2, \cdots)$.

3.2 Application

In the model of this paper we consider the impact of an epidemic in a group, started by a single initial infectious individual with infectious period x. The number of initial susceptible individuals is random and has an $\mathcal{MP}(Y)$ distribution. (Later we choose Y to be $\tilde{B}$ or $\tilde{B}^{(n)}$, the size-biased group weight distribution). We want to compute $\mathbb{E}[\prod_{i\in\mathcal{R}\setminus\{0\}}(1-h(\mathcal{I}_i))\,|\,\mathcal{I}_0 = x]$, where 0 is the initial infectious individual. To compute this we use the following method. We replace the epidemic in a group with m' initial susceptibles and 1 initial infectious individual, whose infectious period is x, by an epidemic with m initial susceptibles and a initial infectives. In this epidemic m is binomially distributed with parameters m' and e^{-x}, $a = m' - m$ and the initial infectives have i.i.d. infectious periods all distributed as $\mathcal{I}$. Thus the initial susceptibles in the new epidemic are those initial susceptibles in the old epidemic who, in that epidemic, avoid direct infection from the initial infective. Since m' is $\mathcal{MP}(Y)$, we may deduce that, conditioned on Y, m and a are independent and respectively $\mathcal{P}(Y\mathrm{e}^{-x})$ and $\mathcal{P}(Y(1-\mathrm{e}^{-x}))$.

Still conditioning on Y, integrating away the randomness in (m, a) and using (3.4) gives, after repeatedly using Fubini's theorem (note that $G_k(1|U) > 0$ for all k, using (3.2) and the fact that $(u_k \in [0,1])$ is decreasing in k),

$$\begin{aligned}
&\mathbb{E}[\prod_{i\in\mathcal{R}\setminus\{0\}}(1-h(\mathcal{I}_i))\,|\,Y,\mathcal{I}_0 = x] \\
&= \sum_{m=0}^{\infty}\sum_{a=0}^{\infty}\frac{\mathrm{e}^{-xm}Y^m}{m!}\frac{(1-\mathrm{e}^{-x})^aY^a}{a!}\mathrm{e}^{-Y}\sum_{k=0}^{m}\frac{m!}{(m-k)!}(u_k)^{m-k+a}G_k(1|U) \\
&= \sum_{m=0}^{\infty}\sum_{k=0}^{m}\frac{\mathrm{e}^{-xm}Y^m}{m!}\frac{m!}{(m-k)!}(u_k)^{m-k}G_k(1|U)\mathrm{e}^{-Y(1-u_k(1-\mathrm{e}^{-x}))} \\
&= \sum_{k=0}^{\infty}\sum_{m=k}^{\infty}\frac{\mathrm{e}^{-xm}Y^m}{(m-k)!}(u_k)^{m-k}G_k(1|U)\mathrm{e}^{-Y(1-u_k(1-\mathrm{e}^{-x}))} \\
&= \sum_{k=0}^{\infty}\mathrm{e}^{-xk}Y^k\mathrm{e}^{-Y(1-u_k)}G_k(1|U).
\end{aligned}$$

Taking expectations over Y gives

$$\mathbb{E}[\prod_{i\in\mathcal{R}\setminus\{0\}}(1-h(\mathcal{I}_i))|\mathcal{I}_0 = x] = \mathbb{E}_Y[\sum_{k=0}^{\infty}\mathrm{e}^{-xk}Y^k\mathrm{e}^{-Y(1-u_k)}G_k(1|U)]. \tag{3.6}$$

This formula can be used to compute the distribution of $T(x) := T(x, Y, \mathcal{I})$, the number of initially susceptible individuals that are ultimately removed when the initial vertex has infectious period x and the number of initial susceptibles has an $\mathcal{MP}(Y)$ distribution. As before, using $h(y) = 1-s$ provides the PGF for $T(x)$. This gives a way to compute $\mathbb{E}[T(x)]$, a quantity we use later.

In a similar way, we use (3.5) to find the PGF of the size of the susceptibility set of an

individual in a group with size distribution $H \sim 1 + \mathcal{MP}(Y)$. It is given by

$$\begin{aligned} g(s;Y) = \mathbb{E}_H[f_{M(H)}(s)] &= \mathbb{E}_H[\mathbb{E}[s^{M(H)}]] \\ &= \mathbb{E}_Y[\sum_{k=0}^{\infty}(sY)^k \mathrm{e}^{-Y(1-v_k)} G_k(1|V)], \end{aligned} \tag{3.7}$$

where v_k and V are as in (3.5).

4 Results

4.1 The forward branching processes

We consider a multi- (possibly infinite) type branching process, which is used to approximate the early stages of an epidemic from a generation point of view. The branching process is described by the following functional form. Let $h(x) : (0, \infty] \to [0, 1]$ be a measurable test function and let X_i, Y_i and $\mathcal{I}_i$ be independent random variables associated to individual i. The random variables denoted by the same letters are i.i.d. and distributed as X, Y and $\mathcal{I}$ respectively. Let $\Gamma(v)$ be the set of children of v in one clique (i.e. all individuals infected by the epidemic initiated by v in that clique). If v has type x and is an ancestor in the branching process, then define (cf. (3.6))

$$\begin{aligned} F(h)(x) := F_{X,\mathcal{I}}(h)(x) := 1 - \mathbb{E}[\prod_{i\in\Gamma(v)} (1 - h(\mathcal{I}_i))|\mathcal{I}_v = x] \\ = 1 - \mathbb{E}_{\tilde{Y}}[\sum_{k=0}^{\infty} \mathrm{e}^{-xk}\tilde{Y}^k \mathrm{e}^{-\tilde{Y}(1-u_k)} G_k(1|U)]. \end{aligned} \tag{4.1}$$

Here u_k, U and $G_k(1|U)$ are as in Corollary 3.2, while $\tilde{Y}$ is the size-biased variant of Y. Define

$$\Phi(h)(x) := \Phi_{X,Y,\mathcal{I}}(h)(x) := \mathbb{E}_X[1 - \mathrm{e}^{-X[F(h)(x)]}], \tag{4.2}$$

$$\tilde{\Phi}(h)(x) := \tilde{\Phi}_{X,Y,\mathcal{I}}(h)(x) := \mathbb{E}_{\tilde{X}}[1 - \mathrm{e}^{-\tilde{X}[F(h)(x)]}], \tag{4.3}$$

where $\tilde{X}$ is the size-biased variant of X.

The formulae above can be interpreted as follows. If $h(x)$ is the indicator function that an individual with type x has a certain property, then $F(h)(x)$ is the probability that at least one of her children in a given clique has this property as well. The clique sizes are i.i.d. and distributed as the number of ultimately removed individuals, which were initially susceptible, in a group with 1 initial infective individual and a random number ($\mathcal{MP}(\tilde{Y})$) of initial susceptible individuals. Note that the ultimately susceptible individuals in a group do not contribute to the clique sizes in the branching process. We assume that the ancestor of the branching process has $\mathcal{MP}(X)$ cliques of children (some of which might be empty), while other individuals in the branching process have $\mathcal{MP}(\tilde{X})$ (possibly empty) cliques of children. (An empty clique of children in the branching process corresponds to a clique in which infection fails to spread in the epidemic process.) Then $\Phi(h)(x)$ is the probability that at least one of the first generation individuals has the same property as the ancestor,

while $\tilde{\Phi}(h)(x)$ is the probability that at least one child of an individual with type x, who is not the ancestor, has this property.

The branching process described above is denoted by

$$\mathcal{Z}^f := \mathcal{Z}^f(X, Y, \mathcal{I}) := (\mathcal{Z}_i^f, i \in \mathbb{Z}_+),$$

where $\mathcal{Z}_i^f$ is a multiset of points in $(0, \infty]$ giving the types of individuals present in generation i of the process. (Note that if the distribution of $\mathcal{I}$ has atoms, at infinity or otherwise, then $\mathcal{Z}_i^f$ may contain repeated elements; on the other hand if the distribution of $\mathcal{I}$ is continuous then almost surely all elements of $\mathcal{Z}_i^f$ are distinct and hence $\mathcal{Z}_i^f$ is a set.) We always assume that $|\mathcal{Z}_0^f| = 1$ and that the type of this individual is distributed as $\mathcal{I}$.

Let $\rho_i := \rho(X, Y, \mathcal{I})$ be the probability that generation i of the branching process $\mathcal{Z}^f(X, Y, \mathcal{I})$ is non-empty, that is $\rho_i = \mathbb{P}(|\mathcal{Z}_i^f| > 0)$. By definition ρ_i is non-increasing, so $\rho := \rho(X, Y, \mathcal{I}) := \lim_{i\to\infty} \rho_i$ exists and is the probability of survival of the branching process. Let $\tilde{\rho}_i(x) = \tilde{\rho}_i(x; X, Y, \mathcal{I})$ be the probability that the lineage of an individual which is not the ancestor and has type x survives for at least i further generations and let $\tilde{\rho}(x) = \lim_{i\to\infty} \tilde{\rho}_i(x)$ be the probability that this lineage survives forever. Note that $\tilde{\rho}_1(x) = \tilde{\Phi}(\mathbf{1})(x)$, where $\mathbf{1}$ is the function which is equal to 1 on its entire domain. It is clear that $\tilde{\rho}(x)$ satisfies

$$\tilde{\rho}(x) = \tilde{\Phi}(\tilde{\rho})(x), \tag{4.4}$$

since in order for the lineage of an individual to survive, at least 1 of the children of that individual must have a surviving lineage. Furthermore,

$$\rho = \int_{(0,\infty]} \Phi(\tilde{\rho})(x)\, \mathrm{d}\mathbb{P}(\mathcal{I} \le x).$$

Let $\tilde{\Phi}_i$ be the i-th iterate of $\tilde{\Phi}$. The functionals $\Phi(h)(x)$ and $\tilde{\Phi}(h)(x)$ are monotonic increasing in $h(x)$. Therefore, $\tilde{\rho}(x) = \lim_{i\to\infty} \tilde{\Phi}_i(\mathbf{1})(x)$ is the pointwise maximal solution of (4.4).

Lemma 4.1. *There is at most one non-zero solution $\tilde{\rho}(x)$ of (4.4).*

Proof. We use an idea from Riordan [22]. To apply this we consider $\tilde{\Phi}'$, a variant of the functional $\tilde{\Phi}$, which acts on functions of m and a, where m and a are as in Section 3.2. Thus $m+a$ is the number of initial susceptibles in a clique, in which there is one initial infective, and a is the number of individuals that are contacted by the initial infective during his/her infectious period. Here the cliques are the basic quantities we study.

Let $p'_{a,m}(k; x_{-a+1}, x_{-a+2}, \cdots, x_0, x_1, \cdots, x_k)$, be the probability (or density) that in a group with a initial infectives, k out of the m initial susceptibles are infected during the epidemic and the infectious periods/types of the ultimately removed individuals (not including the initial infective, which infected the a individuals used in this analysis) are given by $x_{-a+1}, \cdots, x_k$. Then, recalling that $\phi_{\tilde{X}}$ is the MGF of $\tilde{X}$,

$$\tilde{\Phi}'(h')(m,a) = 1 - \sum_{k=0}^{m} \int_{(0,\infty]^{a+k}} p'_{a,m}(k; x_{-a+1}, \cdots x_k) \times$$
$$\prod_{i=-a+1}^{k} \phi_{\tilde{X}} \left(1 - \mathbb{E}_{\tilde{Y}}[\sum_{m_i=0}^{\infty} \sum_{a_i=0}^{\infty} \frac{(\mathrm{e}^{-x_i}\tilde{Y})^{m_i}}{m_i!} \frac{((1-\mathrm{e}^{-x_i})\tilde{Y})^{a_i}}{a_i!} \mathrm{e}^{-\tilde{Y}} (1 - h'(m_i, a_i))] \right)$$
$$\mathrm{d}x_{-a+1} \cdots \mathrm{d}x_k. \tag{4.5}$$

The survival probability of the branching process (now with countably many types, indexed by (m,a)) is the maximal solution of $\tilde{\rho}'(m,a) = \tilde{\Phi}'(\tilde{\rho}')(m,a)$. If either $m \to \infty$ or $a \to \infty$, then for any (m',a') and any $K \in \mathbb{N}$, the probability that a type-(m,a) individual has at least K type-(m',a') children in the next generation tends to 1. Furthermore, it is easy to deduce from (4.5) that for any (m,a), the number of (m',a') children is non-zero with positive probability. Using the same argument as in [22, pp. 911-912], we conclude that there is at most one non-zero solution of $\tilde{\rho}'(m,a) = \tilde{\Phi}'(\tilde{\rho}')(m,a)$.

Next, note that

$$\tilde{\Phi}(h)(x) = 1 - \phi_{\tilde{X}}\left(1 - \mathbb{E}_{\tilde{Y}}[\sum_{m=0}^{\infty}\sum_{a=0}^{\infty}\frac{(\mathrm{e}^{-x}\tilde{Y})^m}{m!}\frac{((1-\mathrm{e}^{-x})\tilde{Y})^a}{a!}\mathrm{e}^{-\tilde{Y}}A(m,a,h)]\right), \quad (4.6)$$

where

$$A(m,a,h) := \sum_{k=0}^{m}\int_{(0,\infty]^{a+k}} p_{a,m}(k; x_{-a+1},\cdots x_k)\prod_{i=-a+1}^{k}(1-h(x_i))\,\mathrm{d}x_{-a+1}\cdots\mathrm{d}x_k. \quad (4.7)$$

Suppose that

$$h(x) = \tilde{\Phi}(h)(x). \quad (4.8)$$

Then (4.6) and (4.7) imply that

$$A(m,a,h) = \sum_{k=0}^{m}\int_{(0,\infty]^{a+k}} p_{a,m}(k; x_{-a+1},\cdots x_k)\times \prod_{i=-a+1}^{k}\phi_{\tilde{X}}\left(1 - \mathbb{E}_{\tilde{Y}}[\sum_{m_i=0}^{\infty}\sum_{a_i=0}^{\infty}\frac{(\mathrm{e}^{-x_i}\tilde{Y})^{m_i}}{m_i!}\frac{((1-\mathrm{e}^{-x_i})\tilde{Y})^{a_i}}{a_i!}\mathrm{e}^{-\tilde{Y}}A(m_i,a_i,h)]\right) \mathrm{d}x_{-a+1}\cdots\mathrm{d}x_k. \quad (4.9)$$

Thus, by (4.5), if h is treated as fixed, $h'(m,a) = 1 - A(m,a,h)$ satisfies

$$h'(m,a) = \tilde{\Phi}'(h')(m,a). \quad (4.10)$$

Let h be a non-zero (i.e. not identically zero) solution of (4.8), assuming such a solution exists. Then h' must be the unique non-zero solution of (4.10), $\tilde{\rho}'$ say. (Note that if h' is identically zero then (4.8) and (4.6) imply that h is identically zero.) Thus $h'(m,a) = 1 - A(m,a,h)$ is independent of h, and $\tilde{\rho}(x)$ is given by the right hand side of (4.6) with $A(m,a,h)$ replaced by $1 - \tilde{\rho}'(m_i,a_i)$, which proves the lemma.

□

Let $\mathcal{I}_i$ be distributed as $\mathcal{I}$. Define

$$R_* := \mathbb{E}_{\mathcal{I}_i}[\mathbb{E}_T[T(\mathcal{I}_i,\tilde{Y},\mathcal{I})]]\mathbb{E}[\tilde{X}]. \quad (4.11)$$

Note that in [11], the notation R_0 is used instead of R_*. We use the notation of [7, 8], because R_0 is usually defined as the expected number of new *direct* infections caused by an infectious individual in the first stages of an epidemic [2, 14], while in (4.11) *all* individuals infected by a local epidemic are "assigned to" the initial infectious individual in the clique. The following result shows that R_* is a threshold parameter for our model, provided the population is sufficiently large (cf. the limit theorems stated in Section 4.3).

Theorem 4.2. *The survival probability satisfies $\rho > 0$ if and only if $R_* > 1$.*

Proof. Firstly, note that whether or not an individual in a group becomes infected is independent of that individual's own infectious period. Hence, the distribution of the infectious period of the individual which brings an infection into a group is distributed as $\mathcal{I}$. Since the interpretation of clique sizes and types in the branching process correspond with group sizes (minus 1) and infectious periods of infected individuals, $\mathbb{E}_{\mathcal{I}_i}[\mathbb{E}_T[T(\mathcal{I}_i, \tilde{Y}, \mathcal{I})]]$ corresponds to the expected number of children within a clique, averaged over the infectious period and over the clique sizes.

Returning to the epidemiological interpretation, we can also condition on the group sizes (ultimately removed + ultimately susceptible). Say that the group sizes are distributed as $1 + H$ (where 1 counts the initial infective and H is the random number of initial susceptibles). The distribution of H is not relevant at the moment. Suppose that $R_* > 1$. Then there exists $K \in \mathbb{N}$ such that

$$\mathbb{E}[\tilde{X}] \sum_{m=0}^{K} \mathbb{E}_{\mathcal{I}_i}[\mathbb{E}_T[T(\mathcal{I}_i, \tilde{Y}, \mathcal{I})|H = m]]\mathbb{P}(H = m) > 1. \tag{4.12}$$

We refer to $\mathbb{E}_{\mathcal{I}_i}[\mathbb{E}_T[T(\mathcal{I}_i, \tilde{Y}, \mathcal{I})|H = m]]$ as $L(m) := L(m, \mathcal{I})$.

For $\epsilon > 0$, let $\hat{\mathcal{I}}_\epsilon$ be the discrete random variable obtained from $\mathcal{I}$ by $\hat{\mathcal{I}}_\epsilon = \epsilon\lfloor \mathcal{I}/\epsilon \rfloor$ (with the convention that $\lfloor \infty \rfloor = \infty$) and note that $\hat{\mathcal{I}}_\epsilon$ is stochastically smaller than $\mathcal{I}$. Since all group sizes are now finite and $L(m)$ depends on the realization of a finite number of edges in the Epidemic Generated Graph, there exists $\epsilon > 0$ such that

$$\mathbb{E}[\tilde{X}] \sum_{m=0}^{K} L(m, \hat{\mathcal{I}}_\epsilon)\mathbb{P}(H = m) > 1.$$

Analagously to the derivation of (4.12), there is some $K'_\epsilon \in \mathbb{N}$ such that for $\hat{\mathcal{I}}'_\epsilon := \hat{\mathcal{I}}_\epsilon \mathbb{1}(\hat{\mathcal{I}}_\epsilon \notin (K'_\epsilon, \infty))$, we have

$$\mathbb{E}[\tilde{X}] \sum_{m=0}^{K'_\epsilon} L(m, \hat{\mathcal{I}}'_\epsilon)\mathbb{P}(H = m) > 1.$$

Therefore, if $R_* > 1$, the branching process under consideration dominates an irreducible finite-type supercritical branching process, which we know from the standard theory [17, Theorem 4.2.2] has a strictly positive probability of survival.

For $R_* \leq 1$ we use the following idea from [10]. Suppose that $R_* \leq 1$ and that $\tilde{\rho}(x) > 0$. Then using (4.4) and (4.3) gives

$$\tilde{\rho}(x) = \tilde{\Phi}(\tilde{\rho})(x) = \mathbb{E}_{\tilde{X}}[1 - \mathrm{e}^{-\tilde{X}[F(\tilde{\rho})(x)]}] < \mathbb{E}[\tilde{X}]F(\tilde{\rho})(x).$$

As in [10], we observe that

$$\begin{aligned} F(\tilde{\rho})(x) &= 1 - \mathbb{E}\left[\prod_{i\in\Gamma(v)} (1-\tilde{\rho}(\mathcal{I}_i)) \,\middle|\, \mathcal{I}_v = x\right] \\ &< \mathbb{E}\left[\sum_{i\in\Gamma(v)} \tilde{\rho}(\mathcal{I}_i) \,\middle|\, \mathcal{I}_v = x\right] = \mathbb{E}[T(x,Y,\mathcal{I})]\mathbb{E}_{\mathcal{I}}[\tilde{\rho}(\mathcal{I})]. \end{aligned}$$

Therefore, $\mathbb{E}_{\mathcal{I}}[\tilde{\rho}(\mathcal{I})] < R_*\mathbb{E}_{\mathcal{I}}[\tilde{\rho}(\mathcal{I})]$ and it follows that $R_* > 1$, which is a contradiction. Thus, if $R_* \leq 1$ then $\tilde{\rho}(x)$ is identically zero on the support of $\mathcal{I}$ and it then follows that $\rho = 0$. □

4.2 The backward branching processes

In this section we study a single type branching process, which is used to approximate the susceptibility set of a uniformly at random chosen vertex from $V^{(n)}$ in the large population limit. Let X, Y and $\mathcal{I}$ be as in the previous subsection. The Galton-Watson branching process

$$\mathcal{Z}^b := \mathcal{Z}^b(X,Y,\mathcal{I}) = (\mathcal{Z}_i^b(X,Y,\mathcal{I}); i \in \mathbb{Z}_+)$$

is described as follows. The single ancestor has a random number of cliques of children distributed as $\mathcal{MP}(X)$. The number of children in different cliques are independent and distributed as $M(\tilde{Y})$, where $M(\cdot)$ is defined as in (3.5) and $\tilde{Y}$ is the size-biased variant of Y. Subsequent individuals in the process have a random number of cliques of children distributed as $\mathcal{MP}(\tilde{X})$. The clique sizes are independent and distributed as the clique sizes of children of the ancestor. Note that since $\mathcal{Z}^b$ is a single-type branching process, $\mathcal{Z}_i^b$ is determined by its cardinality $|\mathcal{Z}_i^b|$, in contrast to $\mathcal{Z}_i^f$ (unless $\mathcal{I}$ is almost surely equal to a fixed constant).

Let $R_*^b := \mathbb{E}[M(\tilde{Y})]\mathbb{E}[\tilde{X}]$ be the mean number of children of an individual who is not the ancestor. As explained in the appendix of [4], $R_*^b = R_*$; we therefore use only the notation R_*. From (3.7), we know that the PGF of a typical clique size is

$$g(s) := g(s;Y,\mathcal{I}) = \mathbb{E}_{\tilde{Y}}[\sum_{k=0}^{\infty}(s\tilde{Y})^k \mathrm{e}^{-\tilde{Y}(1-v_k)} G_k(1|V)], \tag{4.13}$$

where $V = (v_k; k \in \mathbb{Z}_+)$ is as in (3.5); so the PGF of the number of children of an individual who is not the ancestor is given by

$$\tilde{f}(s) := \tilde{f}(s;X,Y,\mathcal{I}) = \mathbb{E}_{\tilde{X}}[\mathrm{e}^{-\tilde{X}(1-g(s))}]. \tag{4.14}$$

Let $q^b(X,Y,\mathcal{I}) =: q^b := \mathbb{E}_X[\mathrm{e}^{-X(1-g(\tilde{q}))}]$ where $\tilde{q} := \tilde{q}^b(X,Y,\mathcal{I})$ is the minimal solution of $\tilde{f}(s) = s$ in $[0,1]$. From the standard theory of branching processes [17], we know that q^b is the extinction probability of $\mathcal{Z}^b$. Let $\rho^b(X,Y,\mathcal{I}) := 1 - q^b(X,Y,\mathcal{I})$ be the survival probability of $\mathcal{Z}^b$.

4.3 Limit theorems for SIR epidemics on random intersection graphs

Let $\mathcal{E}^{(n)}(\omega, \mathcal{I})$ be the set of ultimately removed vertices, including the single initial infective, in an SIR epidemic (as defined in Section 2.3) on the random intersection graph $G^{(n)}$, constructed using the infectious period distribution $\mathcal{I}$ and the sequences $(A_i; i \in \mathbb{N})$, $(B_j; j \in \mathbb{N})$ denoted by $\omega \in \Omega$. Our focus is on the properties of $|\mathcal{E}^{(n)}|$, the number of individuals ultimately removed in the epidemic. For a branching process, $\mathcal{Z}^f$ say, let $|\mathcal{Z}^f| := \sum_{i=0}^{\infty} |\mathcal{Z}_i^f|$ denote its total size (total progeny), including the ancestor.

Theorem 4.3. *For $k \in \mathbb{N}$, we have*

$$\mathbb{P}_\omega(|\mathcal{E}^{(n)}(\omega, \mathcal{I})| = k) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f(A, B, \mathcal{I})| = k).$$

Theorem 4.4. *Let $\rho^b(A, B, \mathcal{I})$ be the survival probability of the backward branching process $\mathcal{Z}^b(A, B, \mathcal{I})$, as in Section 4.2, and $\rho(A, B, \mathcal{I})$ be the survival probability of the forward branching process $\mathcal{Z}^f(A, B, \mathcal{I})$, as in Section 4.1. For every $0 < \epsilon < \rho^b(A, B, \mathcal{I})$,*

$$\mathbb{P}_\omega\left(\left|n^{-1}|\mathcal{E}^{(n)}(\omega, \mathcal{I})| - \rho^b(A, B, \mathcal{I})\right| < \epsilon\right) \xrightarrow[n\to\infty]{p_\nu} \rho(A, B, \mathcal{I}).$$

Theorems 4.3 and 4.4 are proved in Sections 5 and 6, respectively. Before giving the proofs, we discuss briefly their implications. Note first that, for fixed $k \in \mathbb{N}$, the sequence of random variables $(\mathbb{P}_\omega(|\mathcal{E}^{(n)}(\omega, \mathcal{I})| = k); n \in \mathbb{N})$ is uniformly integrable, so, by taking expectations with respect to the measure ν, Theorem 4.3 implies that

$$\lim_{n\to\infty} \mathbb{P}(|\mathcal{E}^{(n)}(\omega, \mathcal{I})| \le k) = \mathbb{P}(|\mathcal{Z}^f(A, B, \mathcal{I})| \le k) \qquad (k \in \mathbb{N}), \tag{4.15}$$

where $\mathbb{P}$ is the probability measure over the joint space of vertex weights, random graphs and the epidemic processes defined on them. Hence, for any $\epsilon > 0$ and any $k \in \mathbb{N}$,

$$\liminf_{n\to\infty} \mathbb{P}\left(n^{-1}|\mathcal{E}^{(n)}| \le \epsilon\right) \ge \mathbb{P}(|\mathcal{Z}^f(A, B, \mathcal{I})| \le k),$$

so, letting $k \to \infty$,

$$\liminf_{n\to\infty} \mathbb{P}\left(n^{-1}|\mathcal{E}^{(n)}| \le \epsilon\right) \ge 1 - \rho(A, B, \mathcal{I}). \tag{4.16}$$

Suppose that $R_* \le 1$. Then $\rho(A, B, \mathcal{I}) = 0$ and 4.16 implies that, for any $\epsilon > 0$, $\lim_{n\to\infty} \mathbb{P}\left(n^{-1}\left|\mathcal{E}^{(n)}\right| \le \epsilon\right) = 1$, i.e. that

$$n^{-1}|\mathcal{E}^{(n)}| \Rightarrow 0 \qquad \text{as } n \to \infty. \tag{4.17}$$

On the other hand, suppose that $R_* > 1$, so $\rho(A, B, \mathcal{I}) > 0$. Taking expectations in Theorem 4.4 and using uniform intergrability as above yields that, for any $0 < \epsilon < \rho^b(A, B, \mathcal{I})$,

$$\lim_{n\to\infty} \mathbb{P}\left(\left|n^{-1}|\mathcal{E}^{(n)}| - \rho^b(A, B, \mathcal{I})\right| < \epsilon\right) = \rho(A, B, \mathcal{I}). \tag{4.18}$$

Note that (4.18) implies that $\limsup_{n\to\infty} \mathbb{P}\left(n^{-1}|\mathcal{E}^{(n)}| \le \epsilon\right) \le 1 - \rho(A, B, \mathcal{I})$, provided $0 < \epsilon < \rho^b(A, B, \mathcal{I})$, which, together with (4.16), yields that, for such ϵ, $\lim_{n\to\infty} \mathbb{P}\left(n^{-1}|\mathcal{E}^{(n)}| \le \epsilon\right) = 1 - \rho(A, B, \mathcal{I})$. This observation, together with (4.18) and (4.17), yields the following theorem.

Theorem 4.5. *Let T_F be a random variable with distribution specified by $\mathbb{P}(T_F = \rho^b(A, B, \mathcal{I})) = \rho(A, B, \mathcal{I}) = 1 - \mathbb{P}(T_F = 0)$. Then, as $n \to \infty$,*

$$n^{-1}|\mathcal{E}^{(n)}| \Rightarrow T_F.$$

5 Proof of Theorem 4.3

In this proof we use three processes,

- the branching process $\mathcal{Z} := \mathcal{Z}^f(A, B, \mathcal{I})$,
- the branching process $\mathcal{Z}^{(n)} := \mathcal{Z}^f(A^{(n)}, B^{(n)}, \mathcal{I})$,
- the exploration process of the Epidemic Generated Graph on $G^{(n)}$, denoted by $\mathcal{E}^{(n)} := \mathcal{E}^{(n)}(\omega, \mathcal{I}) = (\mathcal{E}_0^{(n)}, \mathcal{E}_1^{(n)}, \cdots)$.

To prove Theorem 4.3 we first show that the distribution of the total size of $\mathcal{Z}^{(n)}$ is approximately that of $\mathcal{Z}$, then that the distribution of the total size of $\mathcal{E}^{(n)}$ is approximately that of $\mathcal{Z}^{(n)}$.

Lemma 5.1. *For $k \in \mathbb{N}$, it holds that $\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}| = k)$.*

Proof. Let the total number of (possibly empty) cliques of children in $\mathcal{Z}$ and $\mathcal{Z}^{(n)}$ be denoted by H and $H^{(n)}$, respectively. Note that if $X_n \Rightarrow X$, then $\mathcal{MP}(X_n) \Rightarrow \mathcal{MP}(X)$ [16, Theorem 7.2.19]. Recall further that $A^{(n)} \Rightarrow A$ and $B^{(n)} \Rightarrow B$ as $n \to \infty$. These latter convergence results also hold for the size-biased variants, as shown just below equation (2.1). It follows that the numbers of cliques of children (which for brevity we call *child cliques*) of the first k individuals in the branching processes we compare (according to some order, which does not depend on the number of cliques they are part of) also converge in distribution, as do the sizes of the first l child cliques we compare. Hence, for $k \in \mathbb{N}$ and $l \in \mathbb{Z}_+$,

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}| = k, H = l).$$

Therefore, for every $L \in \mathbb{N}$, we have

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \le L) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}| = k, H \le L).$$

Note that

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) = \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \le L) + \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} > L)$$

and

$$\mathbb{P}_\omega(|\mathcal{Z}| = k) = \mathbb{P}_\omega(|\mathcal{Z}| = k, H \le L) + \mathbb{P}_\omega(|\mathcal{Z}| = k, H > L).$$

Now, let $c_1 > 0$ and $c_2 > 0$ be constants. We note that the probability of the intersection of the following events can be made arbitrarily close to 0, by taking c_1 and c_2 small enough and L large enough (L is finite, but might depend on c_2):

(i) $|\mathcal{Z}| = k$,

(ii) $H > L$,

(iii) the first k vertices evaluated in the branching process $\mathcal{Z}$ all have infectious periods larger than c_1, and

(iv) at least $c_2 L$ out of the first L cliques evaluated in $\mathcal{Z}$ have size ≥ 2.

The probability that neither (iii) nor (iv) holds can also be made arbitrarily close to 0 by tuning c_1 and c_2.

Combining these observations, it follows that for every $\epsilon > 0$, there exists $L \in \mathbb{N}$, such that for all $l > L$,

$$\mathbb{P}(|\mathcal{Z}| = k) < \mathbb{P}(|\mathcal{Z}| = k, H \leq l) + \epsilon/3.$$

Note that the probability that (iii) does not hold is the same for $\mathcal{Z}^{(n)}$ and $\mathcal{Z}$; whilst given any $\delta > 0$, the fact that $\mathcal{MP}(\tilde{B}^{(n)}) \Rightarrow \mathcal{MP}(\tilde{B})$ implies that there exists $N' \in \mathbb{N}$ such that the probability that (iv) does not hold is at most $\delta/3$ for all $n \geq N'$. It then follows that for given $\epsilon > 0$, there exists $L' \in \mathbb{N}$, such that for all $l > L'$,

$$\nu\Big(\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) < \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) + \epsilon/3\Big) > 1 - \delta/2$$

for all sufficiently large n. Now

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}| = k, H \leq l)$$

implies that for all $\epsilon > 0$ and $\delta > 0$,

$$\nu\Big(\big|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) - \mathbb{P}(|\mathcal{Z}| = k, H \leq l)\big| < \epsilon\Big) > 1 - \delta/2,$$

for all sufficiently large n. Thus, by choosing l large enough, it follows that for all sufficiently large n,

$$\nu\Big(\big|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) - \mathbb{P}(|\mathcal{Z}| = k)\big| < \epsilon\Big) > 1 - \delta$$

and the lemma then follows. □

Lemma 5.2. *For $k \in \mathbb{N}$, $\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| \leq k) - \mathbb{P}_\omega(|\mathcal{E}^{(n)}| \leq k) \xrightarrow[n\to\infty]{p_\nu} 0$.*

Proof. The proof follows from a standard coupling argument, described below. Firstly though, for each $n \in \mathbb{N}$, let $v_0^{(n)}$ be a vertex chosen uniformly at random from $V^{(n)}$ and let $v_1^{(n)}, v_2^{(n)}, \cdots$ be independently chosen vertices from $V^{(n)}$, where the probability that a given vertex is chosen is proportional to its A-weight. Let $a_0^{(n)}, a_1^{(n)}, \cdots$ be the respective A-weights of $v_0^{(n)}, v_1^{(n)}, \cdots$. Let $\mathcal{I}_0^{(n)}$ be the type assigned to vertex $v_0^{(n)}$. Let $v_1'^{(n)}, v_2'^{(n)}, \cdots$ be independently chosen vertices (representing cliques) from $V'^{(n)}$ where the probability that a given vertex is chosen is proportional to its B-weight. The B-weights of $v_1'^{(n)}, v_2'^{(n)}, \cdots$ are denoted by $b_1^{(n)}, b_2^{(n)}, \cdots$, respectively. Let the random variable

$$T^{(n)} := \min(i \in \mathbb{N}; v_i^{(n)} = v_j^{(n)} \text{ for some } j < i)$$

be the smallest index at which a vertex from $V^{(n)}$ is chosen a second time. Similarly, define

$$T'^{(n)} := \min(i \in \mathbb{N}; v_i'^{(n)} = v_j'^{(n)} \text{ for some } j < i).$$

The constructions of $\mathcal{Z}^{(n)}$ and $\mathcal{E}^{(n)}$ are coupled as follows. The ancestor of $\mathcal{Z}^{(n)}$ has a $\mathcal{P}(a_0^{(n)})$ number of (possibly empty) child cliques, l' say. The cliques that the initial infective in $\mathcal{E}^{(n)}$ belongs to are given by $v_1'^{(n)}, v_2'^{(n)}, \cdots, v_{l'}'^{(n)}$, which might contain duplicates; the

B-weights associated with these child cliques are $b_1^{(n)}, b_2^{(n)}, \cdots, b_{l'}^{(n)}$. If $T'^{(n)} > l'$, then there are no duplicates amongst $v_1'^{(n)}, v_2'^{(n)}, \cdots, v_{l'}'^{(n)}$ and the processes stay coupled. If not, the construction can be continued but the details are not important for our purposes.

If the coupling continues the sizes of the cliques are then determined. For each $i = 1, 2, \cdots, l'$, the size of clique i is distributed as the number of initially susceptible individuals which are ultimately infected by a local epidemic in a group with one initially infectious individual, having infectious period $\mathcal{I}_0^{(n)}$, and a $\mathcal{P}(b_i^{(n)})$ distributed number of initially susceptible individuals. The clique sizes are all independent. Say that the total number of vertices in the l' cliques is l, then they get A-weights $a_1^{(n)}, a_2^{(n)}, \cdots, a_l^{(n)}$ and types $\mathcal{I}_1^{(n)}, \mathcal{I}_2^{(n)}, \cdots, \mathcal{I}_l^{(n)}$, which are i.i.d. and distributed as $\mathcal{I}$. If $l < T^{(n)}$ the coupling continues and the generation 1 vertices are $v_1^{(n)}, v_2^{(n)}, \cdots, v_l^{(n)}$. The coupling now proceeds in the obvious way. Note that in this construction we have not yet decided which vertices are in the same group as $v_1^{(n)}$ but are not infected by the local epidemic.

Let $H^{(n)}$ be as in the proof of Lemma 5.1 and let $H^{(*n)}$ be the corresponding number for $\mathcal{E}^{(n)}$. We need to prove that for $k \in \mathbb{N}$ and $l \in \mathbb{Z}_+$,

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) - \mathbb{P}_\omega(|\mathcal{E}^{(n)}| = k, H^{(*n)} = l) \xrightarrow[n\to\infty]{p_\nu} 0,$$

and then deduce the statement of the lemma as in the latter part of the proof of Lemma 5.1. Note that the coupling gives

$$\begin{aligned} &\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, T^{(n)} > k, T'^{(n)} > l) \\ &\quad = \mathbb{P}_\omega(|\mathcal{E}^{(n)}| = k, H^{(*n)} = l, T^{(n)} > k, T'^{(n)} > l). \end{aligned} \tag{5.1}$$

Furthermore, for $C^{(n)}(k,l) := \{T^{(n)} \le k\} \cup \{T'^{(n)} \le l\}$, we have

$$\begin{aligned} \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) \;=\; &\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, T^{(n)} > k, T'^{(n)} > l) \\ &+\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, C^{(n)}(k,l)). \end{aligned}$$

Note that the second term on the right hand side of this expression is bounded above by $\mathbb{P}_\omega(C^{(n)}(k,l))$.

Recall from Section 2.2 that $\mu = \mathbb{E}[A] = \alpha\mathbb{E}[B] < \infty$, which implies that the total weight of vertices in $V^{(n)}$ with weight exceeding $\log n$ is ν-almost surely $o(n)$. (To show this, note that, since $\mu < \infty$, for any $N > 0$,

$$n^{-1}\sum_{i=1}^{n} A_i \mathbb{1}(A_i > N) \xrightarrow{a.s.} \mathbb{E}[A\mathbb{1}(A > N)] \qquad \text{as } n \to \infty$$

and $\mathbb{E}[A\mathbb{1}(A > N)] \to 0$ as $N \to \infty$.) A similar result holds for the weights of the vertices in $V'^{(n)}$. Hence, for every $k, l \in \mathbb{N}$, the probability that both $\max(a_i^{(n)}; 0 \le i \le k) \le \log n$ and $\max(b_j^{(n)}; 1 \le j \le l) \le \log n$ converges to 1 as $n \to \infty$. Thus, the total weights of the first k vertices and the first l cliques chosen in the branching process is ν-almost surely $O(\log n)$. By a birthday problem argument we deduce that $\mathbb{P}_\omega(C^{(n)}(l,k)) \xrightarrow[n\to\infty]{p_\nu} 0$. (Note that if $M_n(k)$ is the number of distinct pairs (i,j) with $0 \le i < j \le k$ and $v_i^{(n)} = v_j^{(n)}$, then under the above restrictions, $\mathbb{E}_\omega[M_n(k)] \le \frac{k(k-1)}{2}\frac{\log n}{L^{(n)}} \xrightarrow[n\to\infty]{p_\nu} 0$). Thus, for every $k, l \in \mathbb{N}$,

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) - \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, T^{(n)} > k, T'^{(n)} > l) \xrightarrow[n\to\infty]{p_\nu} 0.$$

Similarly, we deduce that, again for all $k, l \in \mathbb{N}$,

$$\mathbb{P}_\omega(|\mathcal{E}^{(n)}| = k, H^{(*n)} = l) - \mathbb{P}_\omega(|\mathcal{E}^{(n)}| = k, H^{(*n)} = l, T^{(n)} > k, T'^{(n)} > l) \xrightarrow[n\to\infty]{p_\nu} 0;$$

which, together with (5.1), yields the lemma. □

Theorem 4.3 follows immediately by combining Lemmas 5.1 and 5.2.

6 Proof of Theorem 4.4

Before considering susceptibility sets and backward branching processes, we prove the following extension of Lemma 5.1 which is required later in this section.

Lemma 6.1. $\rho(A^{(n)}, B^{(n)}, \mathcal{I}) \xrightarrow[n\to\infty]{p_\nu} \rho(A, B, \mathcal{I})$.

Proof. For every $k \in \mathbb{Z}_+$, define the random variable

$$\mathcal{I}^k(\mathcal{I}) = \begin{cases} 2^{-k}\lfloor 2^k \mathcal{I} \rfloor & \text{if } \mathcal{I} < 2^k, \\ 2^k & \text{if } \mathcal{I} \in [2^k, \infty), \\ \infty & \text{if } \mathcal{I} = \infty. \end{cases}$$

That is, $\mathcal{I}^k$ is a random variable which can take only finitely many values and for $j = 1, 2, \cdots, 4^k - 1$,

$$\mathbb{P}(\mathcal{I}^k = j2^{-k}) = \mathbb{P}\big(\mathcal{I} \in [j2^{-k}, (j+1)2^{-k})\big),$$

while $\mathbb{P}(\mathcal{I}^k = 2^k) = \mathbb{P}(\mathcal{I} \in [2^k, \infty))$ and $\mathbb{P}(\mathcal{I}^k = \infty) = \mathbb{P}(\mathcal{I} = \infty)$. It is clear that $\mathcal{I}^k \Rightarrow \mathcal{I}$ as $k \to \infty$ and that $\mathcal{I}^k$ is stochastically smaller than $\mathcal{I}^{k+1}$ for all $k \in \mathbb{Z}_+$.

For non-negative random variables X and Y, the function $\tilde{\rho}(X, Y, \mathcal{I}^k)$ is pointwise non-decreasing in k, since it is the survival probability of a branching process and (stochastically) increasing the distribution of the infectious periods, and thus also of the offspring distribution, cannot decrease the survival probability of the process. By monotonicity we have that $\lim_{k\to\infty} \tilde{\rho}(X, Y, \mathcal{I}^k)$ exists pointwise, and by the monotone convergence theorem this limit satisfies (4.4) for $\tilde{\rho}(X, Y, \mathcal{I})$. By Lemma 5.1 we know that for every $k \in \mathbb{N}$, $\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| > k) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}| > k)$. This implies that for every $\epsilon > 0$ and $\delta > 0$, there exists $N_0 \in \mathbb{N}$ such that for $n > N_0$, we have

$$\nu(\rho(A^{(n)}, B^{(n)}, \mathcal{I}) < \rho(A, B, \mathcal{I}) + \epsilon) > 1 - \delta/3. \tag{6.1}$$

Furthermore, for every $\epsilon > 0$, there exists $K \in \mathbb{N}$ such that for $k > K$, we have

$$\rho(A, B, \mathcal{I}^k) > \rho(A, B, \mathcal{I}) - \epsilon/2.$$

Similarly, for every $\epsilon > 0$, $\delta > 0$ and $k \in \mathbb{N}$, there exist $N_k \in \mathbb{N}$ such that for $n > N_k$, we have

$$\nu(\rho(A^{(n)}, B^{(n)}, \mathcal{I}^k) > \rho(A, B, \mathcal{I}^k) - \epsilon/2) > 1 - \delta/3,$$

while for every $k \in \mathbb{N}$ (and $\omega \in \Omega$), $\rho(A^{(n)}, B^{(n)}, \mathcal{I}) \geq \rho(A^{(n)}, B^{(n)}, \mathcal{I}^k)$. Combining these statements establishes that, for every $\epsilon > 0$ and $\delta > 0$, there exists $N \in \mathbb{N}$ such that for all $n > N$, we have

$$\nu(\rho(A^{(n)}, B^{(n)}, \mathcal{I}) > \rho(A, B, \mathcal{I}) - \epsilon) > 1 - 2\delta/3.$$

Combining this with (6.1) completes the proof of the lemma. □

In order to prove Theorem 4.4, we investigate the susceptibility sets of two uniformly at random chosen vertices in the subgraph $\hat{G}^{(n)}$ (of $G^{(n)}$), which is defined as follows. Let $\hat{\mathbb{A}}^{(n)}$ be constructed from $\mathbb{A}^{(n)}$ by ignoring all vertices in $V^{(n)}$ and $V'^{(n)}$ that have weights larger than $\log n$ and ignoring all edges that are incident to such vertices. The graph $\hat{G}^{(n)}$ is constructed from $\hat{\mathbb{A}}^{(n)}$ in the same way that $G^{(n)}$ is constructed from $\mathbb{A}^{(n)}$.

We can create a realization of $\hat{\mathbb{A}}^{(n)}$ as follows. Define the vertex sets $\hat{V}^{(n)} := (v_i \in V^{(n)}; A_i \leq \log n)$ and $\hat{V}'^{(n)} := (v'_j \in V'^{(n)}; B_j \leq \log n)$. Conditional upon the weights of the vertices in $\mathbb{A}^{(n)}$, (i) vertices $v_i \in \hat{V}^{(n)}$ and $v'_j \in \hat{V}'^{(n)}$ share in $\hat{\mathbb{A}}^{(n)}$ a $\mathcal{P}(A_iB_j/(\mu n))$ number of edges and (ii) the number of edges between distinct pairs of vertices are independent. Let

$$\hat{L}^{(n)} := \sum_{i:v_i \in \hat{V}^{(n)}} A_i \quad \text{and} \tag{6.2}$$

$$\hat{L}'^{(n)} := \sum_{j:v'_j \in \hat{V}'^{(n)}} B_j. \tag{6.3}$$

Then the degree of vertex $v_i \in \hat{V}^{(n)}$ in $\hat{\mathbb{A}}^{(n)}$ is $\mathcal{P}(A_i\hat{L}'^{(n)}/(\mu n))$ and the degree of $v'_j \in \hat{V}'^{(n)}$ is $\mathcal{P}(B_j\hat{L}^{(n)}/(\mu n))$. We construct from $\hat{\mathbb{A}}^{(n)}$ an identically distributed copy of $\mathbb{A}^{(n)}$ by adding the vertices from $V^{(n)} \setminus \hat{V}^{(n)}$ and $V'^{(n)} \setminus \hat{V}'^{(n)}$ and, if $v_i \in V^{(n)}$ and $v'_j \in V'^{(n)}$ are not both in $\hat{\mathbb{A}}^{(n)}$, letting v_i and v'_j share a $\mathcal{P}(A_iB_j/(\mu n))$ number of newly-added edges, independently of the number of edges between other vertices.

We compute the probability that the susceptibility sets of two vertices in $\hat{G}^{(n)}$ survive until at least generation

$$t_n = \lceil \log\log n \rceil.$$

Next, we show that, given any $\epsilon > 0$, there exists $K \in \mathbb{N}$ such that the probability that the t_n-th generation of an individual's susceptibility set is empty on $\hat{G}^{(n)}$ *and* the total size of its susceptibility set on $G^{(n)}$ exceeds K is less than ϵ for all sufficiently large n; see Lemma 6.6. We then explore the forward process in $G^{(n)}$, where we ignore the vertices and cliques already explored in the two backward processes. We show that if the epidemic size is not $\Theta(1)$, then, with probability tending to 1 as $n \to \infty$, it is $\Theta(n)$. After this we attempt to connect the forward process with the generation t_n vertices of the backward processes and show that, in the event of a large outbreak, the probability that at least 1 of the vertices in generation t_n of a susceptibility set (if this generation is not empty) is ultimately removed converges to 1 as $n \to \infty$.

We construct a coupling of two independent branching processes and the susceptibility sets of v_1 and v_2 in $\hat{G}^{(n)}$ (which by exchangeability is equivalent to choosing two distinct vertices uniformly at random), assuming that $A_1, A_2 \leq \log n$. We therefore define (cf. equations (2.5)–(2.8)) $\hat{A}_i^{(n)} := A_i \mathbb{1}(A_i \leq \log n)\hat{L}'^{(n)}/(\mu n)$ and $\hat{B}_i^{(n)} := B_i \mathbb{1}(B_i \leq \log n)\hat{L}^{(n)}/(\mu n)$; and let $\hat{c}_A^{(n)} = \sum_{i=1}^{n} \mathbb{1}(A_i \leq \log n)$ and $\hat{c}_B^{(n)} = \sum_{i=1}^{\lfloor \alpha n \rfloor} \mathbb{1}(B_i \leq \log n)$. The random variables $\hat{A}^{(n)}$ and $\hat{B}^{(n)}$ are defined by

$$\begin{aligned} \mathbb{P}_\omega(\hat{A}^{(n)} \leq x) &:= |\{1 \leq i \leq \hat{c}_A^{(n)}; \hat{A}_i^{(n)} \leq x\}|/\hat{c}_A^{(n)} \qquad (x \geq 0) \qquad \text{and} \\ \mathbb{P}_\omega(\hat{B}^{(n)} \leq x) &:= |\{1 \leq i \leq \hat{c}_B^{(n)}; \hat{B}_i^{(n)} \leq x\}|/\hat{c}_B^{(n)} \qquad (x \geq 0). \end{aligned}$$

The processes through which the construction of the susceptibility set of v_i ($i \in \{1,2\}$) takes place are denoted by

$$\hat{\mathcal{S}}^i := \hat{\mathcal{S}}^i(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I}) = (\hat{\mathcal{S}}^i_0, \hat{\mathcal{S}}^i_1, \cdots).$$

The two independent branching processes are $\mathcal{Z}^{b,i} = \mathcal{Z}^{b,i}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})$, for $i \in \{1,2\}$, where $\hat{A}^{(n)}$ and $\hat{B}^{(n)}$ are as above. The corresponding susceptibility set processes in $G^{(n)}$ are denoted by $\mathcal{S}^i$ for $i \in \{1,2\}$. When no confusion is possible, we sometimes suppress the reference to the starting vertex i.

We use the following lemmas.

Lemma 6.2. *Let $0 < \epsilon < 3/\mathrm{e} - 1$. For $k \in \mathbb{N}$, let $(X_i(k); i \in \mathbb{N})$ be a sequence of i.i.d. $\mathcal{P}((1+\epsilon)\log k)$ random variables. Then, for every $C > 0$,*

$$\mathbb{P}(\max_{1 \le i \le \lfloor Ck \rfloor} X_i(k) \le 3 \log k) \to 1 \qquad \text{as } k \to \infty.$$

Proof. Since $\mathrm{e}^k = \sum_{i=0}^{\infty} k^i/k!$, we have $k! > k^k \mathrm{e}^{-k}$. Then

$$\begin{aligned}
\mathbb{P}(X_1(k) > 3\log k) &= \sum_{j=\lceil 3\log k \rceil}^{\infty} \frac{((1+\epsilon)\log k)^j}{j!} \frac{1}{k^{1+\epsilon}} \\
&\le \frac{1}{k^{1+\epsilon}} \sum_{j=\lceil 3\log k \rceil}^{\infty} \frac{((1+\epsilon)\log k)^j}{j^j \mathrm{e}^{-j}} \\
&< \frac{1}{k^{1+\epsilon}} \sum_{j=\lceil 3\log k \rceil}^{\infty} ((1+\epsilon)\mathrm{e}/3)^j \\
&< \frac{3}{3-(1+\epsilon)\mathrm{e}} k^{-1-\epsilon+3(1+\log[1+\epsilon]-\log 3)}.
\end{aligned}$$

The probability that none out of $\lfloor Ck \rfloor$ independent copies of $X_1(k)$ exceeds $3\log k$ is thus given by

$$\begin{aligned}
(1 - \mathbb{P}(X_1(k) > 3\log k))^{\lfloor Ck \rfloor} &> \left(1 - \frac{3}{3-(1+\epsilon)\mathrm{e}} k^{-1-\epsilon+3(1+\log[1+\epsilon]-\log 3)}\right)^{Ck} \\
&> 1 - Ck \frac{3}{3-(1+\epsilon)\mathrm{e}} k^{-1-\epsilon+3(1+\log[1+\epsilon]-\log 3)} \\
&= 1 - \frac{3C}{3-(1-\epsilon)\mathrm{e}} k^{3(1+\log[1+\epsilon]-\log 3)-\epsilon},
\end{aligned}$$

which converges to 1 as $k \to \infty$, since $0 < \epsilon < 3/\mathrm{e} - 1$. □

Recall that the distance between two vertices in a graph is the number of edges in the shortest path connecting those vertices.

Lemma 6.3. *For ν-almost all $\omega \in \Omega$, the probability that the total number and the total weight of vertices within distance $2t_n$ of the set $\{v_1, v_2\}$ in $\hat{\mathbb{A}}^{(n)}$ are both smaller than $n^{1/3}$ converges to 1 as $n \to \infty$.*

Proof. All vertices in $\hat{\mathbb{A}}^{(n)}$ have weight at most $\log n$, so their degrees in $\hat{\mathbb{A}}^{(n)}$ are stochastically dominated by i.i.d. $\mathcal{P}(\log n \max(\hat{L}^{(n)}, \hat{L}'^{(n)})/(\mu n))$ random variables. For every $\epsilon > 0$, we have by the strong law of large numbers that $\mathbb{1}(\max(\hat{L}^{(n)}, \hat{L}'^{(n)})/(\mu n) < 1 + \epsilon) \xrightarrow{a.s.} 1$ as $n \to \infty$. We know by Lemma 6.2 that, with probability tending to 1 as $n \to \infty$, none of the at most $n + \lfloor \alpha n \rfloor$ vertices in $\hat{\mathbb{A}}^{(n)}$ has degree exceeding $3 \log n$. So, using a straightforward branching process approximation, the number of vertices within graph distance $2t_n$ of v_1 and v_2 is, with probability tending to 1 as $n \to \infty$, bounded above by

$$2 \sum_{k=1}^{2t_n} (3 \log n)^k = O((3 \log n)^{2t_n+1}).$$

Since $2t_n + 1 = 2\lceil \log \log n \rceil + 1 < 2 \log \log n + 3$, we have

$$\begin{aligned} (3 \log n)^{2t_n+1} &< (3 \log n)^{3+2 \log \log n} \\ &= (3 \log n)^3 \mathrm{e}^{2 \log \log n (\log 3 + \log \log n)} = o(n^{1/3}/\log n), \end{aligned}$$

so the total weight of the vertices is $o(n^{1/3})$. □

For $i \in \{1, 2\}$, let $K^i(t_n)$ be the set of vertices in $V^{(n)}$ within distance $2t_n$ of v_i in $\hat{\mathbb{A}}^{(n)}$, and let $K'^i(t_n)$ be the set of vertices in $V'^{(n)}$ within distance $2t_n$ of v_i in $\hat{\mathbb{A}}^{(n)}$. Lemma 6.3 implies that, with probability tending to 1 as $n \to \infty$, none of the sets $K^1(t_n)$, $K^2(t_n)$, $K'^1(t_n)$ and $K'^2(t_n)$ has total vertex or clique weight exceeding $n^{1/3}$. Furthermore, with probability tending to 1 as $n \to \infty$, the total number of vertices in $K^1(t_n)$ is less than $n^{1/3}$. Conditioned on $K^2(t_n)$ having total weight less than $n^{1/3}$ and $K^1(t_n)$ containing less than $n^{1/3}$ vertices, the probability that $K^1(t_n)$ and $K^2(t_n)$ share an edge is bounded above by $1 - (1 - n^{1/3}/\hat{L}_n)^{n^{1/3}} < n^{2/3}/\hat{L}_n$, which converges ν-almost surely to 0 as $n \to \infty$. So, for ν-almost all $\omega \in \Omega$, the $\mathbb{P}_\omega$-probability that K^1 and K^2 share a vertex converges to 0 as $n \to \infty$. Similarly, we deduce that for ν-almost all $\omega \in \Omega$, the $\mathbb{P}_\omega$-probability that K'^1 and K'^2 share a clique converges to 0 as $n \to \infty$.

Lemma 6.4. *Let $R_* = R_*(A, B, \mathcal{I})$ be as in (4.11). For $0 < c < \log R_*$, it holds that*

$$\mathbb{P}_\omega\big(|\hat{\mathcal{S}}^i_{t_n}| > (\log n)^c \,\big|\, |\hat{\mathcal{S}}^i_{t_n}| > 0\big) \xrightarrow[n\to\infty]{p_\nu} 1.$$

Proof. By Lemma 6.3 and standard coupling arguments, similar to those used in the proof of Lemma 5.2, we can replace $\hat{\mathcal{S}}$ by the branching process $\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})$.

For $n \in \mathbb{N}$, let $\hat{A}^{(n)}_*$ be a random variable having distribution function given by $\mathbb{P}_\omega(\hat{A}^{(n)}_* \le x) = \sup_{i \ge n} \mathbb{P}_\omega(\hat{A}^{(i)} \le x)$ $(x \in \mathbb{R})$ and define $\hat{B}^{(n)}_*$ similarly. Observe that $\hat{A}^{(n)}_* \Rightarrow A$ and $\hat{B}^{(n)}_* \Rightarrow B$ as $n \to \infty$. Furthermore, for all $n \in \mathbb{N}$, $\hat{A}^{(n)}_*$ (respectively, $\hat{B}^{(n)}_*$) is stochastically dominated by $\hat{A}^{(n+1)}_*$ (respectively, $\hat{B}^{(n+1)}_*$). Therefore $R_*(\hat{A}^{(n)}_*, \hat{B}^{(n)}_*, \mathcal{I})$ is also stochastically increasing in n. By the Skorokhod representation theorem [16, Theorem 7.2.14] and the monotone convergence theorem we have that $R_*(\hat{A}^{(n)}_*, \hat{B}^{(n)}_*, \mathcal{I}) \xrightarrow[n\to\infty]{p_\nu} R_*(A, B, \mathcal{I})$. In particular, there exists $N = N(\omega)$ such that for every $n > N$, we have that $R_*(\hat{A}^{(n)}_*, \hat{B}^{(n)}_*, \mathcal{I}) > \mathrm{e}^c$, so, by [17, Theorem 2.7.1] it follows that

$$\mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}_*, \hat{B}^{(n)}_*, \mathcal{I})| > (\log n)^c) - \mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}_*, \hat{B}^{(n)}_*, \mathcal{I})| > 0) \xrightarrow[n\to\infty]{p_\nu} 0.$$

The second probability in this expression converges to $\rho^b(A, B, \mathcal{I})$ by [12, Lemma 4.1] and the lemma then follows by observing that $|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}_*, \hat{B}^{(n)}_*, \mathcal{I})|$ is stochastically smaller than $|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})|$. □

Up to now, we have investigated the behavior of the susceptibility sets of vertices in $\hat{G}^{(n)}$. This is only an intermediate step before analyzing susceptibility sets in $G^{(n)}$. To make the connection between the two graphs we use the following two lemmas.

Lemma 6.5. *For $k \in \mathbb{N}$,*

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = k) - \mathbb{P}_\omega(|\mathcal{S}(A^{(n)}, B^{(n)}, \mathcal{I})| = k) \xrightarrow[n\to\infty]{p_\nu} 0.$$

Proof. In order to simplify the notation we suppress the explicit dependence on $\hat{A}^{(n)}$, $\hat{B}^{(n)}$ and $\mathcal{I}$. We denote by $\mathcal{S}'^i$ the set of cliques containing vertices in the susceptibility set $\mathcal{S}^i$. We prove that

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l) - \mathbb{P}_\omega(|\mathcal{S}| = k, |\mathcal{S}'| = l) \xrightarrow[n\to\infty]{p_\nu} 0, \tag{6.4}$$

from which the lemma follows using similar arguments to those in the proof of Lemma 5.1, which are not repeated here.

Recall that we can construct $G^{(n)}$ from $\hat{G}^{(n)}$, by considering the vertices in $V^{(n)} \setminus \hat{V}^{(n)}$ and $V'^{(n)} \setminus \hat{V}'^{(n)}$ and then connecting them in the usual way with each other and with vertices in $V^{(n)}$ and $V'^{(n)}$ to obtain $\mathbb{A}^{(n)}$. As in the proof of Lemma 5.2, $\mu < \infty$ implies that

$$\sum_{i=1}^{n} A_i \mathbb{1}(A_i > \log[n]) = L^{(n)} - \hat{L}^{(n)} = o(n) \qquad \nu\text{-almost surely.}$$

Therefore,

$$\frac{L^{(n)} - \hat{L}^{(n)}}{L^{(n)}} \xrightarrow{a.s.} 0 \qquad \text{as } n \to \infty.$$

This implies that $1 - \hat{L}^{(n)}/L^{(n)}$ converges in probability to 0. In particular there is an increasing sequence of natural numbers $(p_i; i \in \mathbb{N})$, such that for all $n > p_i$, we have $\mathbb{P}_\omega(1 - \hat{L}^{(n)}/L^{(n)} > 4^{-i}) > 1 - 2^{-i}$. Define the function $\xi : \mathbb{N} \to \mathbb{N}$ by $\xi(n) = 2^i$ if $p_i \le n < p_{i+1}$. This function increases to infinity and

$$\mathbb{P}_\omega(L^{(n)} - \hat{L}^{(n)} < (\xi(n))^{-1} L^{(n)}) \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.5}$$

Similarly, there exists a function $\xi'(n)$ which increases to ∞, such that

$$\mathbb{P}_\omega(L'^{(n)} - \hat{L}'^{(n)}) < (\xi'(n))^{-1} L'^{(n)}) \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.6}$$

Let $\hat{L}^{(n)}_{(k)}$ (respectively, $\hat{L}'^{(n)}_{(k)}$) be the weight of the first k vertices from $\hat{V}^{(n)}$ (respectively, $\hat{V}'^{(n)}$) explored in $\hat{\mathcal{S}}$. Since

$$\mathbb{P}_\omega\left(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l \,\middle|\, \hat{L}^{(n)}_{(k)} \ge (\xi'(n))^{1/2} \cup \hat{L}'^{(n)}_{(l)} \ge (\xi(n))^{1/2}\right) \xrightarrow[n\to\infty]{p_\nu} 0,$$

we have

$$\mathbb{P}_\omega\left(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l, \hat{L}^{(n)}_{(k)} < (\xi'(n))^{1/2}, \hat{L}'^{(n)}_{(l)} < (\xi(n))^{1/2}\right) \\ - \mathbb{P}_\omega(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l) \xrightarrow[n\to\infty]{p_\nu} 0.$$

Combining this with (6.5), (6.6) and the facts that $L^{(n)}/(n\mu) \xrightarrow{a.s.} 1$ and $L'^{(n)}/(n\mu) \xrightarrow{a.s.} 1$ as $n \to \infty$ establishes that

$$\mathbb{P}_\omega\left(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l, \mathcal{S} \cap (V^{(n)} \setminus \hat{V}^{(n)}) \neq \emptyset, \mathcal{S}' \cap (V'^{(n)} \setminus \hat{V}'^{(n)}) \neq \emptyset\right) \xrightarrow[n\to\infty]{p_\nu} 0,$$

which completes the proof of (6.4) and thus of of the lemma. □

Lemma 6.6. *For every $\epsilon > 0$ there exists $K \in \mathbb{N}$ such that*

$$\mathbb{1}(\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{S}(A^{(n)}, B^{(n)}, \mathcal{I})| > K) < \epsilon) \xrightarrow[n\to\infty]{p_\nu} 1.$$

Proof. For ease of presentation we suppress the dependence on the distributions of the weights and infectious periods, writing $\hat{\mathcal{S}}$ for $\hat{\mathcal{S}}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})$ and $\mathcal{S}$ for $\mathcal{S}(A^{(n)}, B^{(n)}, \mathcal{I})$. First note that, as in the proof of Lemma 6.4, we can use branching process approximations to show that for every $K \in \mathbb{N}$ we have

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) \\ - \mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \xrightarrow[n\to\infty]{p_\nu} 0. \quad (6.7)$$

Now,

$$\begin{aligned}
&\mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\
&\quad = \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\
&\qquad - \mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\
&\quad = \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) - \mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0), \qquad (6.8)
\end{aligned}$$

for all sufficiently large n, since $|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0$ implies that $|\mathcal{Z}^b(A^{(n)}, B^{(n)}, \mathcal{I})| > t_n$.

Arguing as in the proof of Lemma 5.1 shows that

$$\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}_\omega(|\mathcal{Z}^b(A, B, \mathcal{I})| > K). \qquad (6.9)$$

To deal with the second term on the right hand side of (6.8), observe that

$$\begin{aligned}
&\mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0) \\
&\quad = \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = \infty) \\
&\qquad + \mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| < \infty) \\
&\quad \leq \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = \infty) + \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (t_n, \infty)). \qquad (6.10)
\end{aligned}$$

Now, given any $\epsilon > 0$, there exists $L \in \mathbb{N}$ such that $\mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (L, \infty)) < \epsilon$. Further, (6.9) and [12, Lemma 4.1] imply that

$$\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (L, \infty)) \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (L, \infty)),$$

so

$$\mathbb{1}(\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (L, \infty)) < \epsilon) \xrightarrow[n\to\infty]{p_\nu} 1,$$

which implies that

$$\mathbb{1}(\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (t_n, \infty)) < \epsilon) \xrightarrow[n\to\infty]{p_\nu} 1.$$

As this holds for any $\epsilon > 0$, it follows from (6.8), (6.9) and (6.10), with another application of [12, Lemma 4.1], that

$$\begin{aligned}\mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\ \xrightarrow[n\to\infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (K, \infty)).\end{aligned} \tag{6.11}$$

Now $\mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (K, \infty))$ can be made arbitrarily close to 0 by choosing K sufficiently large. Thus (6.7) and (6.11) imply that, for every $\epsilon > 0$, we can choose $K \in \mathbb{N}$ such that

$$\mathbb{1}(\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) < \epsilon) \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.12}$$

Finally, note that

$$\begin{aligned}\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) &= \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0) - \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| \le K) \\ &= \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0) - \mathbb{P}_\omega(|\hat{\mathcal{S}}| \le K)\end{aligned}$$

for all sufficiently large n. Similarly, since $|\mathcal{S}| \ge |\hat{\mathcal{S}}|$,

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\mathcal{S}| > K) = \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0) - \mathbb{P}_\omega(|\mathcal{S}| \le K)$$

for all sufficiently large n. Hence, by Lemma 6.5,

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) - \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\mathcal{S}| > K) \xrightarrow[n\to\infty]{p_\nu} 0,$$

whence the lemma follows from (6.12). □

For the remainder of the proof of Theorem 4.4, we re-analyze an exploration process of the forward epidemic process and we couple it to a multi-type branching process, such that the epidemic process is bigger than the branching process for as long as the total weight of both the vertices and the cliques in the exploration process is less than a predefined fraction of the total weight. The survival probability of this branching process can be made arbitrarily close to the probability of a large outbreak as $n \to \infty$. After that we "glue" the susceptibility sets, if they are large, to the forward epidemic process.

We need some extra notation. Since the weights of the vertices are exchangeable, the model does not change if we order the vertices such that $A_i^{(n)} \leq A_{i+1}^{(n)}$, and $B_j^{(n)} \leq B_{j+1}^{(n)}$, for $1 \leq i < n$ and $1 \leq j < \lfloor \alpha n \rfloor$. For $\gamma \in (0,1)$, we define

$$\begin{aligned} R^{(n)}(\gamma) &:= \inf\left(i \leq n; \frac{\sum_{j=1}^{i} A_j}{L^{(n)}} \geq 1-\gamma \right) \quad \text{and} \\ R'^{(n)}(\gamma) &:= \inf\left(i \leq \lfloor \alpha n \rfloor; \frac{\sum_{j=1}^{i} B_j}{L'^{(n)}} \geq 1-\gamma \right). \end{aligned}$$

Furthermore, define

$$\begin{aligned} \bar{\gamma} := \bar{\gamma}(\gamma, n) &= 1 - \frac{\sum_{j=1}^{R^{(n)}(\gamma)} A_j}{L^{(n)}} \quad \text{and} \\ \bar{\gamma}' := \bar{\gamma}'(\gamma, n) &= 1 - \frac{\sum_{j=1}^{R'^{(n)}(\gamma)} B_j}{L'^{(n)}}. \end{aligned}$$

We claim that, for $\gamma \in (0,1)$, $\bar{\gamma} \xrightarrow[n\to\infty]{p_\nu} \gamma$. This can be seen by the following reasoning. Let $x = \inf(y \geq 0; \mu^{-1}\mathbb{E}[A\mathbb{1}(A < y)] > 1 - \gamma/2)$. Then x is finite, since $\mu = \mathbb{E}[A] < \infty$. By the strong law of large numbers, we have $n^{-1}\sum_{i=1}^{n} A_i \mathbb{1}(A_i \leq x) \xrightarrow{a.s.} \mathbb{E}[A\mathbb{1}(A \leq x)]$ and $n^{-1}L^{(n)} \xrightarrow{a.s.} \mu$ as $n \to \infty$. Thus,

$$\frac{\sum_{i=1}^{n} A_i \mathbb{1}(A_i \leq x)}{L^{(n)}} \xrightarrow{a.s.} \mu^{-1}\mathbb{E}[A\mathbb{1}(A \leq x)] \geq 1 - \gamma/2$$

as $n \to \infty$, whence $\nu(A_{R^{(n)}} \leq x) \to 1$ as $n \to \infty$. Combining this with

$$1 - \bar{\gamma} = \frac{\sum_{j=1}^{R^{(n)}(\gamma)} A_j}{L^{(n)}} \geq 1 - \gamma$$

and

$$1 - \bar{\gamma} - \frac{A_{R^{(n)}}}{L^{(n)}} = \frac{\sum_{j=1}^{R^{(n)}(\gamma)-1} A_j}{L^{(n)}} < 1 - \gamma$$

completes the proof of the claim. Similarly we can prove that $\bar{\gamma}' \xrightarrow[n\to\infty]{p_\nu} \gamma$. This also shows that the vertices in $V^{(n)} \setminus \hat{V}^{(n)}$ (respectively, $V'^{(n)} \setminus \hat{V}'^{(n)}$) all have labels exceeding $R^{(n)}(\gamma)$ (respectively, $R'^{(n)}(\gamma)$) with probability tending to 1 as $n \to \infty$.

For $c_1 > 0$, let $I(c_1)$ be the set of vertices with type/infectious period less than c_1. Let $\mathcal{I}(c_1)$ denote a random variable having distribution function given by $\mathbb{P}(\mathcal{I}(c_1) \leq x) = \mathbb{P}(\mathcal{I} \leq x | \mathcal{I} \geq c_1)$, for $x \geq c_1$. We use the multi-type branching process $\mathcal{Z}^f(A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma)$, which is obtained from $\mathcal{Z}^f(A^{(n)}, B^{(n)}, \mathcal{I}(c_1))$ by:

(i) Killing upon birth all children with A-weight strictly larger than the weight of vertex $R^{(n)}(\gamma)$. Children with A-weight equal to the weight of vertex $R^{(n)}(\gamma)$ are killed independently with probability given by the fraction of those vertices in $V^{(n)}$ having weight equal to the weight of vertex $R^{(n)}(\gamma)$ that also have label strictly larger than $R^{(n)}(\gamma)$.

(ii) Killing upon birth all cliques of children with B-weight strictly larger than the weight of vertex $R'^{(n)}(\gamma)$. Cliques with B-weight equal to the weight of clique $R'^{(n)}(\gamma)$ are killed independently with probability given by the fraction of those vertices in $V'^{(n)}$ having B-weight equal to the weight of clique $R'^{(n)}(\gamma)$ that also have label strictly larger than $R'^{(n)}(\gamma)$.

If $A_1, A_2, \cdots, A_n$ are distinct, which happens ν-almost surely if the distribution of A has no atoms, then (i) reduces to killing upon birth all children with A-weight strictly larger than the weight of vertex $R^{(n)}(\gamma)$. If $B_1, B_2, \cdots, B_{\lfloor \alpha n \rfloor}$ are distinct then (ii) simplifies similarly.

We observe that the corresponding survival probability function (cf. Section 4.1) $\tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma)$ increases as $\gamma \searrow 0$. Thus, the limit function, as $\gamma \searrow 0$, exists and satisfies (4.4) by the monotone convergence theorem. Invoking Lemma 4.1, this limit function is

$$\lim_{\gamma \searrow 0} \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma) = \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1)).$$

Similarly, since $\tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1))$ is decreasing as $c_1 \searrow 0$, one can show that

$$\lim_{c_1 \searrow 0} \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1)) = \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}).$$

For $\rho(A^{(n)}, B^{(n)}, \mathcal{I})$ as in Section 4.1, this leads to the first assertion of the following lemma. The second assertion then follows using Lemma 6.1.

Lemma 6.7. *For every $\epsilon > 0$, $\omega \in \Omega$ and $n \in \mathbb{N}$, there exist $\gamma > 0$ and $c_1 > 0$ small enough such that*

$$|\rho(A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma) - \rho(A^{(n)}, B^{(n)}, \mathcal{I})| < \epsilon/2.$$

For every $\epsilon > 0$, there exist $\gamma > 0$ and $c_1 > 0$ such that

$$\mathbb{1}(|\rho(A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma) - \rho(A, B, \mathcal{I})| < \epsilon) \xrightarrow[n\to\infty]{p_\nu} 1.$$

Let $c_1 > 0$ and $\gamma \geq 0$ be constants. We consider the forward epidemic process $\bar{\mathcal{E}}^{(n,\gamma)} = \bar{\mathcal{E}}^{(n)}(\omega, \mathcal{I}, c_1, \gamma/3)$, which is obtained from $\mathcal{E}^{(n)}(\omega, \mathcal{I})$ by removing all vertices (and adjacent edges) in $I(c_1)$, $K^1(t_n)$ and $K^2(t_n)$ and not allowing for contacts in the cliques $K'^1(t_n)$ and $K'^2(t_n)$ or in cliques with label $R'^{(n)}(\gamma/3)$ or larger. As before, we deduce that for every $\gamma > 0$ and large enough n, all vertices in $V'^{(n)} \setminus \hat{V}^{(n)}$ have label at least $R'^{(n)}(\gamma/3)$, with probability arbitrarily close to 1. Also define $\bar{\mathcal{E}}^{(n)} = \bar{\mathcal{E}}^{(n,0)} = \bar{\mathcal{E}}(\omega, \mathcal{I}, c_1, 0)$ and let the total weight of the cliques in $\bar{\mathcal{E}}^{(n)}$ be denoted by $\bar{\mathcal{W}}'^{(n)}(c_1)$.

Lemma 6.8. *For every $\epsilon > 0$, there exist constants $\eta > 0$ and $c_1 > 0$, such that*

$$\mathbb{1}\left(\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) - (\rho(A, B, \mathcal{I}) - \epsilon) > 0\right) \xrightarrow[n\to\infty]{p_\nu} 1.$$

Proof. We explore $\bar{\mathcal{E}}^{(n,\gamma)}$ vertex by vertex (and clique by clique) and couple this with an exploration process of the tree of the branching process

$$\mathcal{Z}^{(n,\gamma)} := \mathcal{Z}^f(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I}(c_1), \gamma).$$

With some abuse of notation we use $\bar{\mathcal{E}}^{(n,\gamma)}$ and $\mathcal{Z}^{(n,\gamma)}$ for the exploration processes as well.

We choose one vertex uniformly at random from $\hat{V}^{(n)}$. We assume that this vertex is not in $K^1(t_n)$ or $K^2(t_n)$ and that its type/infectious period exceeds c_1. The probability that this assumption is met can be made arbitrarily close to 1 by choosing n large enough and c_1 small enough. Denote this vertex by $\bar{v}_0$. Define the "forbidden sets" of vertices by

$$\begin{aligned}\Gamma_0 &:= K^1(t_n) \cup K^2(t_n) \cup I(c_1) \cup (V^{(n)} \setminus \hat{V}^{(n)}) \cup \{\bar{v}_0\} \quad \text{and} \\ \Gamma_0' &:= K'^1(t_n) \cup K'^2(t_n) \cup \{v_i' \in V'^{(n)}; i \geq R'^{(n)}(\gamma/3)\}.\end{aligned}$$

For the vertices in $V^{(n)} \setminus \Gamma_0$, we re-randomize the infectious period in such a way that, for every vertex in $V^{(n)} \setminus \Gamma_0$, we let it be an independent random variable with distribution $\mathcal{I}(c_1)$. This will not affect the distribution of the processes.

Let $\sigma_0^{(n)}(i)$ be a relabeling of the vertices in $V^{(n)}$ such that if $v_j \in \Gamma_0$ and $v_i \in V^{(n)} \setminus \Gamma_0$, then $\sigma_0^{(n)}(i) < \sigma_0^{(n)}(j)$, while if $v_i, v_j \in V^{(n)} \setminus \Gamma_0$, then $\sigma_0^{(n)}(i) < \sigma_0^{(n)}(j)$ if $i < j$. The precise order of the labels of the vertices in the forbidden set is not important. Define $\sigma_0'^{(n)}(i)$ similarly.

The A-weight and type of $\bar{v}_0$ are also assigned to the ancestor of $\mathcal{Z}^{(n,\gamma)}$, say that the A-weight is a_0. Then we use a $\mathcal{P}(a_0 L'^{(n)}/(\mu n))$ random variable, d_0, to denote the "maximal" number of cliques vertex $\bar{v}_0$ is part of and, coupled to this, the "maximal" number of child cliques the vertex has in $\mathcal{Z}^{(n,\gamma)}$. The meaning of maximal is clarified below.

We now identify the first child clique. Choose a real number, x' say, uniformly at random from the unit interval. In $\bar{\mathcal{E}}^{(n,\gamma)}$ we try to connect vertex $\bar{v}_0$ to the clique with label i, which satisfies

$$\sum_{j \in \mathbb{N}: \sigma_0'^{(n)}(j) < \sigma_0'^{(n)}(i)} B_j < x' L'^{(n)} \leq \sum_{j \in \mathbb{N}: \sigma_0'^{(n)}(j) \leq \sigma_0'^{(n)}(i)} B_j.$$

Let this vertex be $\bar{v}_1'$. The B-weight of the possible child clique in $\mathcal{Z}^{(n,\gamma)}$ is B_i, where i is such that $\sum_{j=1}^{i-1} B_k < x' L'^{(n)} \leq \sum_{j=1}^{i} B_j$. If $\bar{v}_1' \in \Gamma_0'$, then the clique is ignored in $\bar{\mathcal{E}}^{(n,\gamma)}$. If $x > 1 - \bar{\gamma}$, then the child clique in $\mathcal{Z}^{(n,\gamma)}$ is ignored. We note that as long as the weight of Γ_0' is less than $\bar{\gamma} L'^{(n)}$, a clique can be ignored in $\bar{\mathcal{E}}^{(n,\gamma)}$ only if the child clique in $\mathcal{Z}^{(n,\gamma)}$ is also ignored. Furthermore, the B-weight of the clique in $\mathcal{Z}^{(n,\gamma)}$ is not larger than the B-weight of the clique in $\bar{\mathcal{E}}^{(n,\gamma)}$.

Let the label of $\bar{v}_1'$ be k. We now define

$$\sigma_1'^{(n)}(i) = \begin{cases} \sigma_0'^{(n)}(i), & \text{for } i \text{ such that } \sigma_0'^{(n)}(i) < \sigma_0'^{(n)}(k), \\ \sigma_0'^{(n)}(i) - 1, & \text{for } i \text{ such that } \sigma_0'^{(n)}(i) > \sigma_0'^{(n)}(k), \\ \lfloor \alpha n \rfloor, & \text{for } i = k. \end{cases}$$

That is, we give $\bar{v}_1'$ the maximal label and keep the order of the labels of the other vertices. Furthermore, we add $\bar{v}_1'$ to the forbidden set, i.e. set $\Gamma_1' = \Gamma_0' \cup \{\bar{v}_1'\}$. We choose the next clique in $\bar{\mathcal{E}}^{(n,\gamma)}$ and $\mathcal{Z}^{(n,\gamma)}$, say $\bar{v}_2'$, in the same way as we choose $\bar{v}_1'$, with $\sigma_0'^{(n)}$ replaced by $\sigma_1'^{(n)}$ and Γ_0' replaced by Γ_1', and we continue this process until we have identified all cliques that $\bar{v}_0$ is part of.

We then pick one of the cliques added to $\bar{\mathcal{E}}^{(n,\gamma)}$ which was not ignored in $\mathcal{Z}^{(n,\gamma)}$. We realise a local epidemic in this group as follows. Assume that the B-weight of the clique

is $\bar{b}_1$. Then let d_1' be $\mathcal{P}(\bar{b}_1 L^{(n)}/(\mu n))$. Consider a population with d_1' initial susceptible individuals and 1 initial infectious individual, all with infectious period distributed as $\mathcal{I}(c_1)$, and couple two continuous time epidemics in this population as follows. Consider the first newly infected individual in this population. We associate this individual with vertices in $\bar{\mathcal{E}}^{(n,\gamma)}$ and in $\mathcal{Z}^{(n,\gamma)}$ as follows. Choose a real number, say x, uniformly at random from the unit interval. In $\bar{\mathcal{E}}^{(n,\gamma)}$, we try to connect clique $\bar{v}_1'$ to the vertex with label i, which satisfies

$$\sum_{j\in\mathbb{N}:\sigma_0^{(n)}(j)<\sigma_0^{(n)}(i)} B_j < xL^{(n)} \leq \sum_{j\in\mathbb{N}:\sigma_0^{(n)}(j)\leq\sigma_0^{(n)}(i)} B_j.$$

Suppose that this vertex is $\bar{v}_2$. The A-weight of the possible child in $\mathcal{Z}^{(n,\gamma)}$ is A_i, where i is such that $\sum_{j=1}^{i-1} A_j < xL^{(n)} \leq \sum_{j=1}^{i} A_j$. The vertex we choose is denoted by $\bar{v}_1$.

If $\bar{v}_1 \in \Gamma_0$, then the vertex is ignored in $\bar{\mathcal{E}}^{(n,\gamma)}$ and immediately killed. If $x > 1-\bar{\gamma}$, then the child in $\mathcal{Z}^{(n,\gamma)}$ is ignored. We note that as long as the weight of Γ_0 is less than $\bar{\gamma}L^{(n)}$, a vertex can be ignored in $\bar{\mathcal{E}}^{(n,\gamma)}$ only if the child in $\mathcal{Z}^{(n,\gamma)}$ is also ignored. Furthermore, the A-weight of the vertex in $\mathcal{Z}^{(n,\gamma)}$ is not larger than the A-weight of the vertex in $\bar{\mathcal{E}}^{(n,\gamma)}$. We identify the other vertices infected by local epidemics started by v_0 and the corresponding children in $\mathcal{Z}^{(n,\gamma)}$ as we have identified the cliques v_0 is part of, where at each step the forbidden set of vertices might grow and the chosen vertex gets the highest label for the next vertex pick. The infectious period/type assigned to every vertex (which is not immediately killed) is distributed as $\mathcal{I}(c_1)$ and coupled vertices get the same infectious period/type. We continue in this way until we have identified all vertices infected by local epidemics started by v_0 and we then explore the cliques those individuals are part of one by one, as before.

The exploration process $\bar{\mathcal{E}}^{(n,\gamma)}$ dominates the exploration process $\mathcal{Z}^{(n,\gamma)}$ until the total weight of the forbidden set in $V^{(n)}$ in $\bar{\mathcal{E}}^{(n,\gamma)}$ is at least $\bar{\gamma}L^{(n)}$ or the total weight of the forbidden set in $V'^{(n)}$ in $\bar{\mathcal{E}}^{(n,\gamma)}$ is at least $\bar{\gamma}L'^{(n)}$.

Note that we may choose $c_1 > 0$ small enough such that $\mathbb{P}(\mathcal{I} < c_1) < \gamma/2$. By the law of large numbers this implies that $c_1 > 0$ might be chosen such that the total weight of vertices in $I(c_1)$ is less than $(\gamma/2)L^{(n)}$ with probability tending to 1 as $n \to \infty$. By Lemma 6.3, we know that the weights of K^1, K^2, K'^1 and K'^2 are each a.s. $o(n)$ and we know that the set of vertices with label $\geq R'^{(n)}(\gamma/3)$ has total weight at least $(\gamma/3)L^{(n)}$ and the probability that this total weight is is less than $(\gamma/2)L^{(n)}$ can be made arbitrary close to 1 by choosing n sufficiently large.

If the ordering of the exploration processes $\bar{\mathcal{E}}^{(n,\gamma)}$ and $\mathcal{Z}^{(n,\gamma)}$ stops because the total weight of the forbidden set in $V'^{(n)}$ exceeds $\gamma L'^{(n)}$, then, using Lemma 6.7, the lemma is immediate with $\eta = \gamma/3$. If this ordering stops because the total weight of the forbidden set in $V^{(n)}$ exceeds $\gamma L^{(n)}$, then the total weight of vertices in $\bar{\mathcal{E}}^{(n,\gamma)}$ that are not in the original forbidden set exceeds $(\gamma/3)L^{(n)}$. We now proceed as follows. Since all of the vertices in $\hat{V}'^{(n)}$ have weight at most $\log n$, the number of vertices with labels exceeding $R'^{(n)}(\gamma/3)$ grows to infinity and, by the law of large numbers, we find that the total weight of cliques in this set which contain vertices in $\bar{\mathcal{E}}^{(n,\gamma)}$ is $\Theta(n)$. This completes the proof of the lemma. □

Proof of Theorem 4.4. We use the notation of Lemma 6.8. Recall that $\bar{\mathcal{E}}^{(n)} = \bar{\mathcal{E}}^{(n,0)}$ and that $\mathcal{E}^{(n)} = \mathcal{E}^{(n)}(\omega, \mathcal{I})$ is the set of ultimately infected vertices in a population of n individuals.

We first provide bounds for

$$\begin{aligned}\mathbb{E}_\omega[n^{-1}|\mathcal{E}^{(n)}| \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] &= \mathbb{E}_\omega[n^{-1}\sum_{i=1}^{n}\mathbb{1}(v_i \in \mathcal{E}^{(n)}) \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \\ &= \mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)} \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n)\end{aligned}$$

and for

$$\begin{aligned}&\mathbb{E}_\omega[n^{-2}|\mathcal{E}^{(n)}|^2 \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \\ &\quad= \mathbb{E}_\omega[n^{-2}\sum_{i=1}^{n}\sum_{j=1}^{n}\mathbb{1}(v_i, v_j \in \mathcal{E}^{(n)}) \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \\ &\quad= n^{-1}\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)} \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \\ &\qquad+ (1-n^{-1})\mathbb{P}_\omega(v_1, v_2 \in \mathcal{E}^{(n)} \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n).\end{aligned}$$

Let $\epsilon' > 0$. By Lemma 6.4 and the asymptotic theory of supercritical general branching processes [18] modified to the lattice case, we have that, if the susceptibility set of v_1 in $\hat{G}^{(n)}$ survives for $t_n = \lceil \log\log n \rceil$ generations, then there exists $c_2 > 0$ such that the probability that the number and the total weight of the vertices in this generation is at least $c_2 \log\log n$ is greater than $1-\epsilon'$ for all sufficiently large n. We denote the set of vertices in generation t_n of this susceptibility set by $\hat{V}^{(n)}_{t_n}$. The same holds for the susceptibility set of v_2. Furthermore, the events of survival up to generation t_n of the two susceptibility sets are asymptotically independent by a birthday problem type of argument and Lemma 6.3.

Conditioned on $\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n$, the law of large numbers establishes that the following event occurs with probability exceeding $1-\epsilon'$. The number of vertices in $\hat{V}^{(n)}_{t_n}$ that both (i) are in the same clique as an infected vertex explored in $\bar{\mathcal{E}}^{(n)}$ and (ii) have infectious period at least c_1, grows to infinity as $n \to \infty$. Since each vertex in $\hat{V}^{(n)}_{t_n}$ is infected independently with probability at least $1 - \mathrm{e}^{-c_1} > 0$, we have that

$$\mathbb{1}\left(\mathbb{P}_\omega\left(v_1 \in \mathcal{E}^{(n)} \,\middle|\, |\hat{\mathcal{S}}^1_{t_n}| > 0, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n\right) > 1 - 2\epsilon'\right) \xrightarrow[n\to\infty]{p_\nu} 1.$$

Furthermore, if the susceptibility set of v_1 does not survive up to generation t_n in $\hat{G}^{(n)}$, then Lemma 6.6 shows that the probability that the initial infective is in v_1's susceptibility set converges to 0. More precisely, for every $K \in \mathbb{N}$ we have that

$$\begin{aligned}\mathbb{P}_\omega\big(v_1 \in \mathcal{E}^{(n)} \,\big|\, |\hat{\mathcal{S}}^1_{t_n}| = 0\big) &= \frac{\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)}, |\hat{\mathcal{S}}^1_{t_n}| = 0)}{\mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| = 0)} \\ &\le \frac{\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)}, |\mathcal{S}^1| \le K) + \mathbb{P}_\omega(|\mathcal{S}^1| > K, |\hat{\mathcal{S}}^1_{t_n}| = 0)}{\mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| = 0)}.\end{aligned}$$

The first term in the numerator of the right hand side of this inequality converges to 0 as $n \to \infty$, while by Lemma 6.6 we have that, for every $\epsilon > 0$ and $\delta > 0$, there exists $K \in \mathbb{N}$ such that the second term in the numerator is smaller than ϵ with ν-probability at least $1-\delta$ for all sufficiently large n. The denominator is trivially strictly positive. We therefore conclude that

$$\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)} \,\big|\, |\hat{\mathcal{S}}^1_{t_n}| = 0) \xrightarrow[n\to\infty]{p_\nu} 0.$$

From the proof of Lemma 6.8 we deduce that

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| > 0) - \mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| > 0 \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \xrightarrow[n\to\infty]{p_\nu} 0,$$

whence

$$\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)} \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) - \mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| > 0) \xrightarrow[n\to\infty]{p_\nu} 0.$$

Now, arguing as at the start of the proof of Lemma 6.4,

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| > 0) - \mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(A^{(n)}, B^{(n)}, \mathcal{I})| > 0) \xrightarrow[n\to\infty]{p_\nu} 0,$$

whilst the end of the proof of Lemma 6.4 shows that

$$\mathbb{P}_\omega(|\mathcal{Z}^b_{t_n}(A^{(n)}, B^{(n)}, \mathcal{I})| > 0) \xrightarrow[n\to\infty]{p_\nu} \rho^b(A, B, \mathcal{I}).$$

Thus, $\mathbb{P}_\omega(|\hat{\mathcal{S}}^1_{t_n}| > 0) \xrightarrow[n\to\infty]{p_\nu} \rho^b(A, B, \mathcal{I})$, whence

$$\mathbb{E}_\omega[n^{-1}|\mathcal{E}^{(n)}| \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \xrightarrow[n\to\infty]{p_\nu} \rho^b(A, B, \mathcal{I}).$$

Since the first t_n generations of the susceptibility sets of v_1 and v_2 in $\hat{G}^{(n)}$ are non-overlapping with probability tending to 1 as $n \to \infty$, we notice that

$$\mathbb{P}_\omega(v_1, v_2 \in \mathcal{E}^{(n)} \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) - (\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)} \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n))^2 \xrightarrow[n\to\infty]{p_\nu} 0.$$

This gives that

$$\mathbb{E}_\omega[n^{-2}|\mathcal{E}^{(n)}|^2 \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \xrightarrow[n\to\infty]{p_\nu} (\rho^b(A, B, \mathcal{I}))^2.$$

Therefore, $\mathrm{var}(n^{-1}|\mathcal{E}^{(n)}| \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \xrightarrow[n\to\infty]{p_\nu} 0$ and we conclude that, for all $\delta > 0$,

$$\mathbb{P}_\omega(|n^{-1}\mathcal{E}^{(n)} - \rho^b(A, B, \mathcal{I})| < \delta \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.13}$$

On the other hand, we know by Lemma 6.8 that for every $\epsilon' > 0$, there exist constants $\eta > 0$ and $c_1 > 0$ such that

$$\mathbb{1}(\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) > \rho(A, B, \mathcal{I}) - \epsilon') \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.14}$$

Furthermore, by Theorem 4.3 there exists $k \in \mathbb{N}$ such that

$$\mathbb{1}\Big(\sum_{i=1}^{k} \mathbb{P}_\omega(|\mathcal{E}^{(n)}| = k) > 1 - \rho(A, B, \mathcal{I}) - \epsilon'\Big) \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.15}$$

Now observe that

$$\begin{aligned}\mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)}, \bar{\mathcal{W}}'^{(n)}(c_1) \le \eta n) \;\le\; & \mathbb{P}_\omega(v_1 \in \mathcal{E}^{(n)}, |\mathcal{E}^{(n)}| \le k) \\ & + \mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) \le \eta n, |\mathcal{E}^{(n)}| > k).\end{aligned}$$

By exchangeability, the first term on the right hand side of this inequality is bounded above by k/n which converges to 0 as $n \to \infty$. Further, for any $K \in \mathbb{N}$,

$$\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n, |\mathcal{E}^{(n)}| \leq K) \xrightarrow[n\to\infty]{p_\nu} 0,$$

so (6.14) and (6.15) imply that for every $\epsilon > 0$, there exists $k \in \mathbb{N}$ such that

$$\mathbb{1}(\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n, |\mathcal{E}^{(n)}| > k) < \epsilon) \xrightarrow[n\to\infty]{p_\nu} 1.$$

It follows that

$$\mathbb{E}_\omega[n^{-1}|\mathcal{E}^{(n)}| \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n] \xrightarrow[n\to\infty]{p_\nu} 0,$$

so for every $\delta > 0$ we have

$$\mathbb{P}_\omega(n^{-1}|\mathcal{E}^{(n)}| < \delta \,\big|\, \bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n)) \xrightarrow[n\to\infty]{p_\nu} 1. \tag{6.16}$$

Combining (6.13) and (6.16) completes the proof of Theorem 4.4. □

7 Extension

In this paper we have studied the spread of an SIR epidemic on a random intersection graph. A variant of the random intersection graph is proposed in [20], where a configuration model construction is used to create the graph. In our terminology and notation, independent degrees are assigned to vertices in V and V', where the distributions for the degrees of vertices in V are identical and the same holds for the distribution of the degrees of vertices in V'. Each vertex in $V \cup V'$ is assigned a number of half-edges given by its degree. In the auxiliary graph $\mathbb{A}^{(n)}$ the half-edges of the first n vertices in V are paired uniformly at random with the first $L^{(n)}$ half-edges in V', where $L^{(n)}$ is the number of half-edges assigned to the first n vertices in V. Note that the final vertex in V' used in this construction might not retain its full degree in $\mathbb{A}^{(n)}$.

We expect that similar results to those presented in this paper hold for epidemics on such graphs. Some additional dependencies arise since connecting to a vertex takes away one of its available half-edges, however we anticipate that the impact of those dependencies is very small.

Assume that the degrees of vertices in V are distributed as D and degrees of vertices in V' are distributed as H, where $\mu_D = \mathbb{E}[D]$ and $\mu_H = \mathbb{E}[H]$ are both finite. For notational convenience we assume that the empirical distributions used to construct $\mathbb{A}^{(n)}$ are the same. We derive a formula in the spirit of (4.1) (see also (3.6)). Let $\tilde{D}$ and $\tilde{H}$ denote the size-biased variants of D and H, respectively. Thus, for example, the distribution of $\tilde{D}$ is given by

$$\mathbb{P}(\tilde{D} = d) = \mu_D^{-1} d\mathbb{P}(D = d) \qquad (d \in \mathbb{N}).$$

As in (3.6), let $U = U(h) = (u_k; k \in \mathbb{Z}_+)$, where $u_k = \mathbb{E}[\mathrm{e}^{-k\mathcal{I}}(1 - h(\mathcal{I}))]$. Conditioning on clique size, the number of individuals in a clique directly infected by the initial infective

and then the final size, we find that

$$\begin{aligned}
1-F(h)(x) &= \mathbb{E}[\prod_{i\in\Gamma(v)}(1-h(\mathcal{I}_i))\,\big|\,\mathcal{I}_0=x] \\
&= \sum_{m=0}^{\infty}\mathbb{P}(\tilde{H}-1=m)\sum_{a=0}^{m}\binom{m}{a}(1-\mathrm{e}^{-x})^a\mathrm{e}^{-x(m-a)} \\
&\qquad\qquad \times\sum_{k=0}^{m-a}\frac{(m-a)!}{(m-a-k)!}(u_k)^{m-k}G_k(1|U) \\
&= \sum_{m=0}^{\infty}\sum_{k=0}^{m}\sum_{a=0}^{m-k}\mathbb{P}(\tilde{H}-1=m)\binom{m-k}{a}(1-\mathrm{e}^{-x})^a\mathrm{e}^{-x(m-a)} \\
&\qquad\qquad \times\frac{m!}{(m-k)!}(u_k)^{m-k}G_k(1|U)
\end{aligned}$$

and then

$$\begin{aligned}
1-F(h)(x) &= \sum_{m=0}^{\infty}\sum_{k=0}^{m}\mathbb{P}(\tilde{H}-1=m)\mathrm{e}^{-kx}\frac{m!}{(m-k)!}(u_k)^{m-k}G_k(1|U) \\
&= \sum_{k=0}^{\infty}\mathrm{e}^{-kx}G_k(1|U)\sum_{m=k}^{\infty}\mathbb{P}(\tilde{H}-1=m)\frac{m!}{(m-k)!}(u_k)^{m-k} \\
&= \sum_{k=0}^{\infty}\mathrm{e}^{-kx}G_k(1|U)f^{(k)}_{\tilde{H}-1}(u_k),
\end{aligned}$$

where $f_{\tilde{H}-1}$ is the PGF of $\tilde{H}-1$ and $f^{(k)}_{\tilde{H}-1}$ is its kth derivative.

Let $\Phi(h)(x) := 1-f_D(1-F(h)(x))$ and $\tilde{\Phi}(h)(x) := 1-f_{\tilde{D}-1}(1-F(h)(x))$. It is straightforward to show that those functionals have the same interpretation as (4.2) and (4.3), and hence that they determine the survival probability, $\rho(D,H,\mathcal{I})$ say, of a forward branching process approximating the early stages of an epidemic in this model.

Similar modifications can also be made to the backward branching process. It is readily shown that the PGF of a typical clique size (recall (4.13)) is now given by

$$g(s)=\sum_{k=0}^{\infty}s^kG_k(1|V)f^{(k)}_{\tilde{H}-1}(v_k),$$

where V and v_k are as in (3.5). It then follows that the PGF of the number of children of an individual, who is not the ancestor, is given by $\tilde{f}(s)=f_{\tilde{D}-1}(g(s))$ and the corresponding PGF for the ancestor is $f_D(g(s))$. The survival probability of the backward branching process, $\rho^b(D,H,\mathcal{I})$ say, is then determined exactly as at the end of Section 4.2.

We expect that, under mild conditions on the distributions of D and H, Theorems 4.3–4.5 hold for the model described in this section, with the forward and backward branching processes being modified as indicated above.

Acknowledgments This research was supported by the UK Engineering and Physical Sciences Research Council under research grant number EP/E038670/1 (Frank Ball and David Sirl) and by the Riksbankens Jubileumsfond (Pieter Trapman).

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