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POISSON APPROXIMATIONS FOR EPIDEMICS WITH TWO LEVELS OF MIXING

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This paper is concerned with a stochastic model for the spread of an epidemic among a population of n individuals, labeled $1, 2, \ldots, n$, in which a typical infected individual, i say, makes *global* contacts, with individuals chosen independently and uniformly from the whole population, and *local* contacts, with individuals chosen independently according to the contact distribution $V_i^n = \{v_{i,j}^n; j = 1, 2, \ldots, n\}$, at the points of independent Poisson processes with rates λ_G^n and λ_L^n, respectively, throughout an infectious period that follows an arbitrary but specified distribution. The population initially comprises m_n infectives and $n - m_n$ susceptibles. A sufficient condition is derived for the number of individuals who survive the epidemic to converge weakly to a Poisson distribution as $n \to \infty$. The result is specialized to the *households* model, in which the population is partitioned into households and local contacts are chosen uniformly within an infective's household; the *overlapping groups* model, in which the population is partitioned in several ways and local mixing is uniform within the elements of the partitions; and the *great circle* model, in which $v_{i,j}^n = v_{(i-j)_{\mathrm{mod}\, n}}^n$.

1. Introduction. This paper is concerned with Poisson approximation for the number of survivors of a stochastic *SIR* epidemic in a finite population, in which individuals mix at two levels, *local* and *global*. *SIR* closed-population epidemics are by far the most studied class of stochastic epidemic models. In such models, there are just three possible states for an individual, susceptible (S), infected (I) and removed (R), and the only possible transitions are $S \to I$ (infection of a susceptible) and $I \to R$ (removal of an infective). There are three classical limit theorems for homogeneously mixing, stochastic *SIR* epidemic models as the population size $n \to \infty$: a branching process limit theorem for the early stages of an epidemic [see, e.g., Whittle (1955), Kendall (1956) and Ball and Donnelly (1995)], from which a threshold theorem governing whether an epidemic is able to take off can be derived; a central limit theorem for the total number of individuals who are ultimately infected by an epidemic that does take off [see, e.g., von Bahr and Martin-Löf (1980)]; and a Poisson limit theorem for the number of individuals

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who remain susceptible at the end of an epidemic that is well above threshold [see, e.g., Daniels (1967) and Lefèvre and Utev (1995)].

The above limit theorems all require that the population size $n \to \infty$. However, the assumption that a large population is homogeneously mixing is clearly unrealistic for real-life epidemics and may lead to incorrect conclusions being drawn. A striking example of considerable contemporary interest is the modeling of emergency responses to a smallpox bioterrorist attack. Recent public debate has focused on the relative merits of targeted vaccination, in which confirmed or suspected cases are isolated and their contacts are traced and vaccinated, and mass vaccination. Using a homogeneously mixing deterministic model for postrelease spread of smallpox among a population of 10 million people, Kaplan, Craft and Wein (2002) found that mass vaccination resulted in far fewer deaths and much faster disease eradication over a wide range of parameter values. This contrasts sharply with Halloran, Longini, Nizam and Yang (2002), who used simulations of a stochastic model for postrelease spread among a structured population of 2000 people and found that although timely mass vaccination could be more effective than targeted vaccination in preventing and containing epidemics, the difference was orders of magnitude smaller than that predicted by the homogeneous deterministic model and, moreover, targeted vaccination prevented more deaths per dose of vaccine than mass vaccination. These studies demonstrate clearly the importance of correctly accounting for population structure when using epidemic models to inform public health policy. Although the model of Halloran, Longini, Nizam and Yang (2002) is clearly the more realistic of the two, it has the disadvantage of being sufficiently complicated to be mathematically intractable. The challenge for mathematicians is to find models that both adequately reflect real-life epidemics and remain susceptible to mathematical analysis.

One way of introducing heterogeneities into an epidemic model (without compromising tractability) is to assume that, aside from disease status, the population is partitioned into different types of individuals, with individuals of the same type behaving homogeneously. The above limit theorems can be extended to this situation but they require that the numbers of individuals of different types all tend to ∞, which again is unrealistic. Consequently, there has been a growing interest recently in studying epidemics among populations whose structure remains locally finite as their size becomes large [see Andersson (1999) for a review]. An important model of this type, that reflects an important feature of human population structure, is the *households* model, in which the population is partitioned into a large number of small households, with uniform mixing within households and, at a much lower rate, within the whole population [see, e.g., Becker and Dietz (1995) and Ball, Mollison and Scalia-Tomba (1997)]. Branching process and central limit theorems have been developed for the households model by Ball (1996) and Ball, Mollison and Scalia-Tomba (1997), respectively, and, in a multitype setting, by Ball and Lyne (2001). In this paper a Poisson limit theorem is developed for an extension of the households model, in which a typical individual,

while infectious, makes global contacts, with individuals chosen independently and uniformly from the entire population, and local contacts, with individuals chosen independently according to a contact distribution (reflecting the underlying population structure) associated with the infecting individual.

The above three classical limit theorems have two main uses. First, they give insight into the behavior of the epidemic model for finite population size n. Second, they can be used to obtain approximations to probabilities and moments associated with the outcomes of a model; exact calculations are usually extremely difficult, and indeed they are impossible for the models of this paper. The branching process approximation holds for epidemics that fail to become established. The central limit theorem provides an approximation to the final outcome of epidemics that take off, provided that its threshold parameter R_0^n (the mean number of infectious contacts made by a typical infective in an otherwise completely susceptible population; cf. Section 2.3) is finite in an asymptotically large population. If $R_0^n \to \infty$ as $n \to \infty$, then the proportion of the population that is ultimately infected by an epidemic converges in probability to 1 and the normal approximation breaks down. However, if $R_0^n = \log(n/b) + o(n)$ as $n \to \infty$, for some $b \in (0, \infty)$, then the number of individuals who remain susceptible at the end of the epidemic converges weakly to a Poisson random variable with mean b. This can form the basis for useful approximations for epidemics that are well above threshold, as illustrated by the following example which was drawn to our attention by Sergey Utev.

Becker and Hasofer (1998) calculated the probability of a complete epidemic (i.e., that infects everyone) for a homogeneous mixing Markov *SIR* epidemic, with $n = 100, 200, 600$ and $R_0 = 1.5, 3, 6$. When $R_0 = 6$, the probability of a complete epidemic, p_C say, is as follows, with the Poisson approximation in parentheses: $n = 100$, $p_C = 0.7888$ (0.7805); $n = 200$, $p_C = 0.6216$ (0.6091); $n = 600$, $p_C = 0.2399$ (0.2260). When $R_0 = 3$, we obtain $n = 100$, $p_C = 0.0172$ (0.0069); $n = 200$, $p_C = 0.0003$ (0.00005). For other choices of (n, R_0), p_C is negligible. The Poisson approximations are remarkably good when $R_0 = 6$, which for many infections is not particularly high [see Anderson and May (1991), Table 4.1, which reports several estimated values of R_0 in excess of 10]. Moreover, the Poisson approximations are extremely simple to calculate, while the exact probabilities require extensive numerical computation. The Poisson approximation developed in this paper is also very easy to apply; it depends only on knowing R_0^n for *global* contacts and the probability that a typical susceptible avoids *local* contact from everyone else in the population.

Poisson approximations for closed-population, homogeneously mixing *SIR* epidemic models have a long history dating back to Daniels (1967). Daniels considered the general stochastic epidemic, in which a typical infective makes contacts at the points of a homogeneous Poisson process throughout an infectious period that follows a negative exponential distribution. Successive contacts are with individuals chosen independently and uniformly from the whole population

and a contacted individual is infected if and only if he or she is still susceptible; otherwise nothing happens. Daniels showed that under certain conditions the number of survivors of the epidemic is approximately Poisson. The first rigorous proof of an asymptotic Poisson limit for the general stochastic epidemic is due to Sellke (1983). Subsequently, asymptotic Poisson limit theorems have been established for a wide range of homogeneously mixing models. In particular, Ball and Barbour (1990) used the Stein–Chen method to derive a Poisson approximation, with an order of magnitude for the error, for the Martin-Löf (1986) epidemic model; Lefèvre and Utev (1995) obtained a necessary and sufficient condition for a Poisson limit theorem to hold for an extension of the general stochastic epidemic in which a typical infectious period follows an arbitrary but specified distribution; and Lefèvre and Utev (1997) derived a necessary and sufficient condition for weak convergence of the number of survivors of a collective epidemic [Picard and Lefèvre (1990)] to a mixed Poisson distribution. The general strategy for proving each of these three results was the same. First, a (mixed) Poisson limit law was established for the number of uncontacted individuals, $X_n(n)$ say, when all n individuals are allowed to make contacts. Then a coupling argument was used to show that the number of survivors of the epidemic has the same limit law as $X_n(n)$. The same approach is adopted in this paper, though the details are markedly different.

The contents of the paper are as follows. The general two-level-of-mixing epidemic model is presented in Section 2, along with three specific examples. These are the households model outlined above; the *overlapping groups* model, an extension of the households model in which the population is partitioned in several ways (e.g., according to household and according to workplace), and mixing is uniform within the elements of the partitions, with rate dependent on the partition; and the *great circle* model, in which individuals are equally spaced around a circle and local mixing is spatial. Section 2 also contains a heuristic explanation of our main Poisson limit theorem that gives insight into why the result holds and the strategy for its proof. The general theory is presented in Section 3 and this splits into three main parts. First, the collection of indicator random variables, describing which individuals avoid contact from all n individuals in the population, is shown to be positively related in the sense of Barbour, Holst and Janson (1992), Definition 2.1.1. This facilitates the second part of the proof, in which a Poisson limit theorem is established for $X_n(n)$. Third, it is shown that the number of survivors of the epidemic has the same limit law as $X_n(n)$. This leads to a simpler proof, via a lower bound branching process, of a key result of Lefèvre and Utev (1995), Section 4, which is presented in the Appendix. In Section 4, the general theory is specialized to the three examples outlined in Section 2, leading to considerable simplification in the sufficient condition for a Poisson limit law to hold. Finally, some brief concluding comments are made in Section 5.

2. Models and heuristics.

2.1. *General model.* We consider a sequence of epidemics (E_n) indexed by the population size n. The individuals are numbered 1 through n. Assign to each individual, in the population of size n, independent and identically distributed *life histories*, $\mathcal{H}^n = (Q, \xi^n, \eta^n)$, where Q is the infectious period, whose distribution is assumed to be independent of n, and ξ^n and η^n are homogeneous Poisson point processes of times, relative to an individual's infection, at which global and local contacts are made, respectively. The elements Q, ξ^n and η^n of $\mathcal{H}^n$ are assumed to be independent. Let ξ^n and η^n have rates $\lambda_G^n = n\beta_G^n$ and λ_L^n, respectively. Each global contact is with an individual chosen independently and uniformly from the n individuals in the population. Each local contact made by individual, i say, is with an individual chosen independently according to the contact distribution $V_i^n = \{v_{i,j}^n;\ j = 1, 2, \ldots, n\}$, where $v_{i,j}^n$ is the probability that individual i on making a local infectious contact does so with individual j. We assume that, for all $i, n \geq 1$, $v_{i,i}^n = 0$ and $\sum_{j=1}^n v_{i,j}^n = 1$. At the end of his or her infectious period, an individual becomes immune to further infection and plays no role in the remainder of the epidemic. If an infected individual makes contact with a susceptible individual i, at time t, say, then the susceptible individual becomes infected and makes local contacts at the points of $t + \eta_i^n$ and global contacts at the points of $t + \xi_i^n$, before becoming immune at time $t + Q_i$.

We assume that there are initially $m_n \geq 1$ infectives and $h_n = n - m_n$ susceptibles in the population, with U_n denoting the set of initial susceptibles. (For our results, the actual set U_n turns out not to be important, except for its cardinality $h_n = |U_n|$.) The epidemic ceases as soon as there are no infectives in the population. Let S_n be the number of individuals who are still susceptible at the end of the epidemic E_n, so $T_n = n - S_n$ is the total number of infectives in the epidemic, that is, the total size of E_n. The aim of the paper is to develop a Poisson limit theorem for S_n. Before presenting some heuristics that motivate our main theorem, we describe some important special cases of the general model, in which the local contact distribution is specified more explicitly.

2.2. *Special cases.*

2.2.1. *Great circle model.* This model is a generalization of the great circle model of Ball, Mollison and Scalia-Tomba (1997). For each $n \geq 1$, the epidemic E_n is among n individuals located in one-dimensional space. Consider the case where each individual has one neighbor on each side; to avoid boundary problems, it is convenient to take the space to be the circumference of a circle. The individuals are numbered sequentially around the circle 1 through n, so that individuals 1 and n are neighbors. Each local contact is with an individual chosen independently from a distribution $\{w_i^n;\ i = -[\frac{n-1}{2}], -[\frac{n-1}{2}] + 1, \ldots, [\frac{n}{2}]\}$, where w_i^n is the probability individual k on making a local infectious contact does

so with individual $(k+i)_{\mathrm{mod}\, n}$, so $v_{k,(k+i)_{\mathrm{mod}\, n}} = w_i^n$. The model considered by Ball, Mollison and Scalia-Tomba (1997) assumed that local contacts are nearest neighbor, and it was motivated by the spread of infection between pigs in a line of stalls.

2.2.2. *Overlapping groups model.* The second model under consideration is the overlapping groups model; compare Andersson (1999). We assume that there are two types of groups, A and B, with all groups of type A (B) being of size m_A (m_B). For example, the two types of groups could represent mixing within households and within workplaces in a human population. We again consider a sequence of epidemics (E_n), indexed by the population size n; however, we only consider those n divisible by $\mathrm{lcm}(m_A, m_B)$, where lcm denotes lowest common multiple. In the epidemic E_n, the individuals are separated into mutually exclusive homogeneously mixing groups of type A. Similarly, the population is also partitioned into mutually exclusive mixing groups of type B. Then, by superimposing the two group structures, we obtain a network of overlapping groups. In this model, it is natural to split the local infection into within group A infectious contacts and within group B infectious contacts. Therefore, let η_A^n and η_B^n be the independent homogeneous Poisson point processes of times, relative to an individual's infection, at which the individual makes infectious contacts within his or her group of type A and within his or her group of type B, respectively. Let η_A^n and η_B^n have rates $\lambda_A^n = (m_A - 1)\beta_A^n$ and $\lambda_B^n = (m_B - 1)\beta_B^n$, respectively. The individual contacted by a type A (B) local contact is chosen uniformly from the other $m_A - 1$ ($m_B - 1$) individuals in the infective's group.

2.2.3. *Households model.* The last model under consideration is the households model of Ball, Mollison and Scalia-Tomba (1997), where the individuals are separated into mutually exclusive homogeneously mixing groups, called households. For all $i, j, n \geq 1$, $j \neq i$, let $v_{i,i}^n = 0$, let $v_{i,j}^n = 0$ if individuals i and j belong to different housholds and let $v_{i,j}^n = \frac{1}{k-1}$ if individuals i and j belong to the same houshold of size k. (Note that for individuals who belong to households of size 1 the local infectious process is redundant.) The sequence of epidemics (E_n) is now constructed according to the general model of Section 2.1.

2.2.4. *Remark.* The models described above, and especially the great circle model, are very similar to "small world" models; see, for example, Watts (1999), Watts and Strogatz (1998) and Barbour and Reinert (2001). The most frequently asked question concerning "small world" networks is the distribution of the distance between a randomly chosen pair of individuals i and j, say. However, we ask (and answer) a different question which is not just relevant to disease spread but also to the dissemination of information over the network. In particular, we are concerned with the distribution of the number of people who fail to become infected by a disease (hear a rumor/news) passed over a network with both local and global infectious contacts (communication of the information).

2.3. *Heuristics.* In this section, we give a heuristic explanation of the Poisson limit theorem, which involves introducing some basic notation that is required later in the paper. A key concept for understanding the final outcome of the epidemic E_n is that of a susceptibility set. For $1 \le i \le n$, construct individual i's *local* epidemic (sometimes called its *local infectious clump*) $\mathcal{C}_i^n$ by allowing local infectious contacts in a population where initially i is infective and everyone else is susceptible (global infectious contacts are ignored). Let C_i^n be the set of individuals ultimately infected in $\mathcal{C}_i^n$. For $1 \le i \le n$, let $S_i^n = \{j : i \in C_j^n\}$ and call S_i^n the susceptibility set of individual i in E_n. Note that $i \in S_i^n$. Note also that an individual, i say, is ultimately infected in E_n if and only if his or her susceptibility set S_i^n contains at least one individual who is either an initial infective or who is contacted globally.

Suppose that n is large and let z_n denote the mean proportion of individuals in the population who are ultimately infected in the epidemic E_n. Then the probability that a given individual avoids global contact throughout the course of the epidemic is approximately $e^{-R_0^n z_n}$, where $R_0^n = \lambda_G^n E[Q]$ is the mean number of global contacts made by an infectious individual. Moreover, given that the epidemic takes off, as $n \to \infty$, distinct individuals avoid infection independently of each other. Thus,

$$P(i \text{ avoids infection in } E_n) \approx \sum_{k=1}^{n} P(|S_i^n| = k) e^{-kR_0^n z_n}, \qquad i \in U_n,$$

and the mean number of initial susceptibles who are ultimately uninfected in E_n is approximately given by

$$E[S_n] = \sum_{i \in U_n} \sum_{k=1}^{n} P(|S_i^n| = k) e^{-kR_0^n z_n}.$$

Now, $E[S_n] = n(1 - z_n)$, so

$$1 - z_n = \frac{1}{n} \sum_{i \in U_n} \sum_{k=1}^{n} P(|S_i^n| = k) e^{-kR_0^n z_n}. \tag{2.1}$$

The above heuristic argument can be made fully rigorous as $n \to \infty$, given that the epidemic takes off, by generalizing the embedding argument of Scalia-Tomba (1985); see Ball and Neal (2002).

We wish to develop a Poisson limit theorem for S_n, so let $b_n = E[S_n]$ and suppose that $b_n \to b$ as $n \to \infty$, where $b \in (0, \infty)$. Then setting $z_n = 1 - \frac{b_n}{n}$ in (2.1) yields

$$b_n \approx e^{-R_0^n} h_n g(n) + \sum_{i \in U_n} \sum_{k=2}^{n} P(|S_i^n| = k) e^{-kR_0^n}, \tag{2.2}$$

where $g(n) = h_n^{-1} \sum_{i \in U_n} P(|S_i^n| = 1)$ is the probability that an individual chosen at random in U_n has a susceptibility set of size 1. Now

$$\sum_{i \in U_n} \sum_{k=2}^{n} P(|S_i^n| = k) e^{-kR_0^n} \leq h_n e^{-2R_0^n} = \left(e^{-R_0^n} h_n g(n)\right)^2 / h_n g(n)^2.$$

Suppose that $h_n g(n)^2 \to \infty$ as $n \to \infty$. Then letting $n \to \infty$ in (2.2) suggests that a necessary condition for $S_n \xrightarrow{D} \text{Po}(b)$ as $n \to \infty$, where $\text{Po}(b)$ denotes the Poisson distribution with mean b, is

$$R_0^n - \log h_n - \log g(n) + \log b \to 0 \qquad \text{as } n \to \infty. \tag{2.3}$$

Note that, under the above assumptions, if (2.3) holds then $R_0^n \to \infty$ as $n \to \infty$, so the probability that the epidemic takes off tends to 1 as $n \to \infty$.

The standard homogeneously mixing *SIR* epidemic is obtained by setting $\lambda_L^n = 0$, so $P(|S_i^n| = 1) = 1$ $(1 \leq i \leq n)$. Hence, $\log g(n) = 0$ and (2.3) reduces to the usual necessary condition for a strong Poisson limit theorem to hold [see Lefèvre and Utev (1995), Corollary 2.6]. Thus, the term $\log g(n)$ in (2.3) modifies the usual condition to take account of local mixing. For the homogeneously mixing model, R_0^n is the mean of the offspring distribution for the approximating branching process, obtained by assuming that all infectious contacts are with susceptibles and hence result in the spread of infection. Thus, R_0^n is a threshold parameter for such models. For the model with two levels of mixing, the appropriate approximating branching process describes the spread of local infectious clumps [see Ball and Neal (2002)], so the relevant threshold parameter is $R_*^n = R_0^n E[|C^n|]$, where $E[|C^n|] = h_n^{-1} \sum_{i \in U_n} E[|C_i^n|]$ is the mean size of the local epidemic emanating from an individual chosen uniformly in U_n. For many models, symmetries imply that, in obvious notation, $E[|C^n|] = E[|S^n|]$, so the threshold parameter and the Poisson limit theorem depend on different aspects of the distribution of the size of a typical local susceptibility set.

For each $n \geq 1$, construct a random directed graph G_n from the epidemic E_n as follows. For $1 \leq i, j \leq n$, let a directed edge exist from vertex i to vertex j in G_n if and only if in the epidemic E_n individual i would contact individual j, if individual i were to become infectious. A vertex, i say, in G_n is called isolated if there is no directed edge leading into it. Thus, the isolated vertices in the set U_n of the graph G_n correspond to those initial susceptibles in E_n who would not be contacted if we were to make everybody infectious in E_n.

The above informal argument suggests that, under the limiting regime (2.3), S_n has the same limiting distribution as the number of initial susceptibles whose susceptibility sets are not contacted globally by any individual in G_n. If, in addition, $h_n g(n)^2 \to \infty$ as $n \to \infty$, the number of such susceptibles having a susceptibility set of size greater than 1 converges in probability to 0 as $n \to \infty$. Thus, under these conditions, it is highly plausible that S_n has the same asymptotic distribution as the number of isolated vertices, $X_n(n)$ say, in the set U_n of G_n.

Finally, the above argument also suggests that $E[X_n(n)] \to b$ as $n \to \infty$. Thus, the limiting distribution of $X_n(n)$ is likely to be Po(b), provided that the events that different vertices are isolated are only weakly dependent, which, subject to mild conditions on the distribution of a typical infectious period Q, will be the case when local mixing is not too extensive.

3. Generic theory.

3.1. *Statement of main theorem.* Before stating our main theorem, it is necessary to impose some mild technical conditions on Q [cf. Lefèvre and Utev (1995)]. First, we require that $E[Q] < \infty$. Second, note that if $m_n = 1$, $P(S_n = n - 1) \geq P(Q = 0)$ and a Poisson limit for S_n requires $P(S_n = n - 1) \to 0$ as $n \to \infty$. Therefore, we require that $P(Q = 0) = 0$. Finally, let $h(x) = \int_0^x P(Q > y)\,dy$, $j(x) = \int_x^\infty P(Q > y)\,dy$ and $\phi(x) = E[e^{-xQ}]$. Then we require that

$$h(x) \text{ is a slowly varying function (in Karamata's sense),} \tag{3.1}$$

$$\frac{x \log x}{h(x)} P(Q > x) \to 0 \qquad \text{as } x \to \infty, \tag{3.2}$$

$$j(x) \log x \to 0 \qquad \text{as } x \to \infty. \tag{3.3}$$

It is straightforward using Markov's inequality to show that (3.1), (3.2) and (3.3) hold if there exists $\beta > 0$ such that $E[Q^{1+\beta}] < \infty$. Note also that (3.1), (3.2) and (3.3) are required in Lefèvre and Utev (1995) for the strong Poisson limit theorem, Corollary 2.6, which is the homogeneously mixing equivalent of Theorem 3.1.

THEOREM 3.1. *Suppose that there exist* $\alpha > 0$, $0 < \delta < \frac{1}{2}$ *and* $b > 0$ *such that* $\lambda_L^n n^{-\alpha} \to 0$, $n^\delta g(n) \to \infty$ *and* $\lambda_G^n E[Q] - \log(h_n g(n)) + \log b \to 0$ *as* $n \to \infty$. *Suppose, in addition, that there exist* $\varepsilon > \delta + \alpha$, $0 < c, d < 1$, $n_0 \in \mathbb{N}$ *and, for all* $1 \leq i \leq n$, *a set of individuals* L_i^n *in* E_n *such that, for all* $n \geq n_0$ *and for all* $1 \leq i \leq n$, $i \in L_i^n$, $\sum_{j \notin L_i^n} v_{j,i}^n < n^{-\varepsilon}$, $\sum_{j \notin L_i^n} v_{i,j}^n < n^{-\varepsilon}$, $|L_i^n| \leq n^c$, $|M_i^n| \leq n^d$ *and* $h_n n^{-(d+2\delta)} \to \infty$ *as* $n \to \infty$, *where* $M_i^n = \{j : L_i^n \cap L_j^n \neq \varnothing\}$. *Then* $S_n \xrightarrow{D}$ Po(b) *as* $n \to \infty$.

Theorem 3.1 is proved in Sections 3.2–3.4, but first we introduce some more notation, give an overview of the proof of Theorem 3.1 and indicate the role played by each of the conditions of the theorem in its proof.

For $1 \leq i, s \leq n$, let $\theta_i^n(s) = 1$ if individual i avoids an infectious contact from the first s infectives to become infected in the epidemic E_n and $\theta_i^n(s) = 0$ otherwise. Therefore, $\theta_i^n(m_n) = 1$ if and only if individual i avoids an infectious contact from the m_n initial infectives. For $1 \leq s \leq n$, let $X_n(s) = \sum_{i \in U_n} \theta_i^n(s)$ be

the number of initial suscpetibles who avoid contact from the first s infectives in E_n. Then T_n, the total number of individuals who are ultimately infected by the epidemic E_n, is given by $T_n = \inf\{s \geq m_n : s + X_n(s) = n\}$. Note that we have allowed $s > T_n$ in the definitions of $\theta_i^n(s)$ and $X_n(s)$, and we label the individuals who do not become infected in E_n as infectives $T_n + 1, T_n + 2, \ldots, n$. Note also that vertex i is isolated in G_n (see Section 2.3) if and only if $\theta_i^n(n) = 1$, so the number of isolated vertices in the set U_n of G_n is given by $X_n(n)$.

The proof of Theorem 3.1 can be outlined as follows. We first show (Lemma 3.2) that $\{\theta_i^n(n)\} = \{\theta_i^n(n); 1 \leq i \leq n\}$ are positively related in the sense of Barbour, Holst and Janson (1992), Definition 2.1.1. This enables us to bound the total variation distance between the law of $X_n(n)$ and $\mathrm{Po}(b)$, which together with Lemmas 3.5 and 3.6, which show, respectively, that the mean and variance of $X_n(n)$ converge to b as $n \to \infty$, yields (Theorem 3.7) that $X_n(n) \xrightarrow{D} \mathrm{Po}(b)$ as $n \to \infty$. Finally, we show (Lemmas 3.8–3.11) that $P(X_n(n) \neq S_n) \to 0$ as $n \to \infty$, and the required Poisson limit theorem follows. A key tool in the final step is a lower bound branching process for the epidemic E_n (see Lemma 3.9).

The roles of the different conditions in Theorem 3.1 can be described informally as follows. For $1 \leq i \leq n$, the individuals in M_i^n can be interpreted loosely as individual i's *locality*. Then the conditions $|L_i^n| \leq n^c$ $(1 \leq i \leq n)$ and $|M_i^n| \leq n^d$ $(1 \leq i \leq n)$ ensure that individual i's locality is sufficiently small in relation to the total population size when obtaining the mean (Lemma 3.5) and the variance (Lemma 3.6) of the Poisson limit, respectively. The condition $\sum_{j \notin L_i^n} v_{i,j}^n < n^{-\varepsilon}$ $(1 \leq i \leq n)$ $[\sum_{j \notin L_i^n} v_{j,i}^n < n^{-\varepsilon}$ $(1 \leq i \leq n)]$ (see Lemmas 3.5, 3.6 and 3.11) ensures that individual i is unlikely to make [receive] a local infectious contact with [from] an individual outside his or her locality. This is important in allowing us to study the global and local infection separately. Then, since we can consider the global and local infection separately, we are able to establish the Poisson limit theorems in terms of h_n, λ_L^n, $g(n)$ and λ_G^n. The conditions on λ_L^n and, in particular, $g(n)$ (see Lemmas 3.5, 3.6 and 3.11) are necessary to ensure that the local infection does not play too important a role in the spread of the disease, while the condition that $h_n n^{-(d+2\delta)} \to \infty$ ensures that the locations of the initial infectives (and hence also of the initial susceptibles) are not important (see Lemma 3.11, in particular). The above conditions ensure that $\lambda_G^n \to \infty$ as $n \to \infty$, which is necessary to form a useful lower bound branching process in Lemma 3.9.

3.2. *Positive relatedness.* It is straightforward to see that $\theta_i^n(n) = 1$ if vertex i is isolated in the graph G_n and $\theta_i^n(n) = 0$ otherwise. Therefore, $X_n(n) = \sum_{i \in U_n} \theta_i^n(n)$ is the number of isolated vertices in the set U_n. We now show that $\{\theta_i^n(n)\}$ are positively related. For $n \geq 1$ and each $1 \leq j \leq n$, let $\{\chi_{i,j}^n; i = 1, 2, \ldots, n\}$ be random variables satisfying

$$\mathcal{L}(\chi_{i,j}^n; i = 1, 2, \ldots, n) = \mathcal{L}\big(\theta_i^n(n); i = 1, 2, \ldots, n | \theta_j^n(n) = 1\big).$$

LEMMA 3.2. *For $n \geq 1$, the random variables $\{\theta_i^n(n)\}$ are positively related; that is, for each $1 \leq j \leq n$, the random variables $\{\chi_{i,j}^n; i = 1, 2, \ldots, n\}$ and $\{\theta_i^n(n); i = 1, 2, \ldots, n\}$ can be defined on a common probability space $(\Omega, \mathcal{F}, P)$ such that, for all $i \neq j$, $\chi_{i,j}^n(\omega) \geq \theta_i^n(n)(\omega)$ for all $\omega \in \Omega$.*

PROOF. Consider fixed n and j such that $1 \leq j \leq n$. Let E_n^j be the epidemic in a population of size n, where we know that $\theta_j^n(n) = 1$. Let G_n^j be the graph on n vertices constructed from the epidemic E_n^j in the natural way with $\theta_j^n(n) = 1$. For $i \neq j$, let $\chi_{i,j}^n$ be the indicator function of whether vertex i is isolated in G_n^j. We give an alternative construction for the graph G_n and couple G_n^j to G_n in such a way that, for all $i \neq j$, $\chi_{i,j}^n \geq \theta_i^n(n)$.

Consider the description of the epidemic E_n given in Section 2.1. For $1 \leq i, k \leq n$, let ζ_{ik}^n be the point process of times, relative to individual i's infection, at which individual i makes infectious contacts with individual k. Then ζ_{ik}^n $(1 \leq i, k \leq n)$ are independent and, for $1 \leq i, k \leq n$, ζ_{ik}^n is a homogeneous Poisson process with rate $\gamma_{ik}^n = \beta_G^n + v_{i,k}^n \lambda_L^n$.

Let $\tilde{Q}_i \stackrel{D}{=} Q_i | \theta_j^n(n) = 1$, $\tilde{\mathbf{Q}} = (\tilde{Q}_1, \tilde{Q}_2, \ldots, \tilde{Q}_n)$ and $\mathbf{Q} = (Q_1, Q_2, \ldots, Q_n)$. We say $\mathbf{x} \leq \mathbf{y}$ $(\mathbf{x} < \mathbf{y})$ if, for all $1 \leq i \leq n$, $x_i \leq y_i$ $(x_i < y_i)$. We proceed by showing that $\tilde{\mathbf{Q}} \leq_{\text{st}} \mathbf{Q}$. For $i = 1, 2, \ldots, n$, let W_i be the time of the first point in ζ_{ij}^n. Then $W_1, W_2, \ldots, W_n$ are independent. Let $\mathbf{W} = (W_1, W_2, \ldots, W_n)$ and fix $\mathbf{0} \leq \mathbf{t} = (t_1, t_2, \ldots, t_n)$. Then

$$P(\tilde{\mathbf{Q}} \leq \mathbf{t}) = P(\mathbf{Q} \leq \mathbf{t} | \mathbf{Q} < \mathbf{W}) = \frac{P(\mathbf{Q} \leq \mathbf{t}, \mathbf{Q} < \mathbf{W})}{P(\mathbf{Q} < \mathbf{W})}.$$

Now, since the $W_1, W_2, \ldots, W_n, Q_1, Q_2, \ldots, Q_n$ are independent, we have that

$$P(\mathbf{Q} < \mathbf{W}) = \prod_{i=1}^{n} P(Q_i < W_i)$$

and

$$P(\mathbf{Q} \leq \mathbf{t}, \mathbf{Q} < \mathbf{W}) = \prod_{i=1}^{n} P(Q_i \leq t_i, Q_i < W_i).$$

Therefore, $P(\tilde{\mathbf{Q}} \leq \mathbf{t}) = P(\mathbf{Q} \leq \mathbf{t} | \mathbf{Q} < \mathbf{W}) = \prod_{i=1}^{n} P(Q_i \leq t_i | Q_i < W_i)$, and to show that $\tilde{\mathbf{Q}} \leq_{\text{st}} \mathbf{Q}$, it suffices to show that, for all i, $\tilde{Q}_i \leq_{\text{st}} Q_i$. We therefore require that, for all $1 \leq i \leq n$ and $t_i \geq 0$, $P(Q_i \leq t_i) \leq P(Q_i \leq t_i | Q_i < W_i)$ or, equivalently, $P(Q_i < W_i, Q_i \leq t_i) \geq P(Q_i < W_i) P(Q_i \leq t_i)$. The latter holds, since $P(Q_i < w, Q_i \leq t_i) \geq P(Q_i < w) P(Q_i \leq t_i)$ for all $w, t_i \geq 0$. Thus, $\tilde{Q}_i \leq_{\text{st}} Q_i$ $(1 \leq i \leq n)$, so $\mathbf{Q}$ and $\tilde{\mathbf{Q}}$ can be defined on the same probability space, $(\Omega, \mathcal{F}, P)$ say, such that $\tilde{\mathbf{Q}}(\omega) \leq \mathbf{Q}(\omega)$ for all $\omega \in \Omega$. Augment $(\Omega, \mathcal{F}, P)$ to carry independent Poisson processes ζ_{ik}^n $(1 \leq i, k \leq n)$. Construct G_n^j by setting

$\theta_j^n(n) = 1$ and using $\tilde{\mathbf{Q}}$ and ζ_{ik}^n $(1 \le i, k \le n, k \ne j)$ and construct G_n by using $\mathbf{Q}$ and ζ_{ik}^n $(1 \le i, k \le n)$. Since $\tilde{\mathbf{Q}}(\omega) \le \mathbf{Q}(\omega)$ for all $\omega \in \Omega$, it is immediate that $\chi_{i,j}^n \ge \theta_i^n(n)$ $(i \ne j)$, as required. □

3.3. *Isolated vertices in G_n.* The proof of a Poisson limit for the number of isolated vertices in the set U_n requires the following simple, well-known results.

LEMMA 3.3. *For any nonnegative random variable X and for all $a, b \ge 0$,*

$$E[X^{a+b}] \ge E[X^a]E[X^b] \tag{3.4}$$

and

$$E\big[\exp\big(-(a+b)X\big)\big] \le E[\exp(-bX)]. \tag{3.5}$$

PROOF. Inequality (3.4) follows directly from the fact that $\operatorname{cov}(f(X), g(X)) \ge 0$ for any functions f, g that are monotonic in the same direction [see Hardy, Littlewood and Pólya (1934), page 168], and inequality (3.5) is trivial. □

We now prove three useful consequences of the conditions of Theorem 3.1 in the following lemma.

LEMMA 3.4. *Under the conditions of Theorem* 3.1,

$$\lambda_G^n E[Q] - \log(h_n g(n)) + \log b \to 0 \qquad \text{for some } 0 < b < \infty \text{ as } n \to \infty \tag{3.6}$$

implies that

$$nt(\beta_G^n) - \log\left(\frac{h_n g(n)}{b}\right) \to 0 \qquad \text{as } n \to \infty, \tag{3.7}$$

$$h_n g(n)\phi(\beta_G^n)^n \to b \qquad \text{as } n \to \infty \tag{3.8}$$

and

$$n\{\phi(2\beta_G^n) - \phi(\beta_G^n)^2\} \to 0 \qquad \text{as } n \to \infty, \tag{3.9}$$

where $t(x) = 1 - \phi(x)$ $(x \ge 0)$.

PROOF. Since $n^\delta g(n) \to \infty$ and $h_n n^{-2\delta} \to \infty$ as $n \to \infty$, we have that $g(n)h_n n^{-\delta} \to \infty$ as $n \to \infty$. Hence, for all sufficiently large n, $n^\delta \le h_n g(n) \le n$, and therefore there exists $n_0 \in \mathbb{N}$ such that, for all $n \ge n_0$,

$$\frac{\delta \log n - \log(2b)}{nE[Q]} \le \beta_G^n \le \frac{\log n - \log(b/2)}{nE[Q]}. \tag{3.10}$$

It follows from (3.10) that

$$\beta_G^n = O\left(\frac{\log n}{n}\right)$$

and

$$\frac{\log((\beta_G^n)^{-1})}{\log n} \to 1 \qquad \text{as } n \to \infty, \tag{3.11}$$

so, from (3.10), (3.11) and (3.3), we have that

$$\begin{aligned} n\beta_G^n\left(E[Q] - h\left(\frac{1}{\beta_G^n}\right)\right) &= n\beta_G^n j\left(\frac{1}{\beta_G^n}\right) \\ &= \frac{n\beta_G^n}{\log((\beta_G^n)^{-1})}\log\left(\frac{1}{\beta_G^n}\right) j\left(\frac{1}{\beta_G^n}\right) \to 0 \\ &\qquad \text{as } n \to \infty. \end{aligned} \tag{3.12}$$

Therefore, it follows from (3.12) that (3.3) and (3.6) together imply that

$$n\beta_G^n h\left(\frac{1}{\beta_G^n}\right) - \log\left(\frac{h_n g(n)}{b}\right) \to 0 \qquad \text{as } n \to \infty. \tag{3.13}$$

Then, from Lefèvre and Utev (1995), (6.20),

$$\left| t(\beta_G^n) - \beta_G^n h\left(\frac{1}{\beta_G^n}\right)\right| \le (\beta_G^n)^2 \int_0^{1/\beta_G^n} P(Q > t)t\,dt + \frac{1}{e}P\left(Q > \frac{1}{\beta_G^n}\right). \tag{3.14}$$

We now show that

$$n(\beta_G^n)^2 \int_0^{1/\beta_G^n} P(Q > t)t\,dt + \frac{n}{e}P\left(Q > \frac{1}{\beta_G^n}\right) \to 0 \qquad \text{as } n \to \infty. \tag{3.15}$$

From (3.13), we have that, for all sufficiently large n,

$$n \le c_1 \frac{\log(h_n g(n))}{\beta_G^n h((\beta_G^n)^{-1})} \tag{3.16}$$

for some constant c_1. Since $h_n g(n) \le n$, it follows from (3.11) and (3.16) that, for all sufficiently large n,

$$n \le c_2 \frac{\log((\beta_G^n)^{-1})}{\beta_G^n h((\beta_G^n)^{-1})} \tag{3.17}$$

for some constant c_2. Now put $x_n = (\beta_G^n)^{-1}$. Then, by (3.2),

$$\frac{n}{e}P\left(Q > \frac{1}{\beta_G^n}\right) \le \frac{c_2}{e}\frac{x_n \log(x_n) P(Q > x_n)}{h(x_n)} \to 0 \qquad \text{as } n \to \infty.$$

Also, Proposition 6.5 of Lefèvre and Utev (1995) holds under conditions (3.1) and (3.2), so, by (3.17) and Lefèvre and Utev (1995), (6.25), we have that

$$n(\beta_G^n)^2 \int_0^{1/\beta_G^n} P(Q > t)t\,dt \le c_2 \frac{\log(x_n)}{x_n h(x_n)} \int_0^{x_n} P(Q > t)t\,dt \to 0 \qquad \text{as } n \to \infty.$$

Hence, (3.15) is proved, and so (3.7) follows from (3.13)–(3.15).

Now, for all sufficiently large n,

$$\sum_{i=2}^{\infty} \frac{1}{i} t(\beta_G^n)^i \le \sum_{i=2}^{\infty} t(\beta_G^n)^i = \frac{t(\beta_G^n)^2}{1 - t(\beta_G^n)} \le 2t(\beta_G^n)^2 \tag{3.18}$$

since, by (3.7), $t(\beta_G^n) \to 0$ as $n \to \infty$. In particular, $t(\beta_G^n) \le \frac{1}{n} \log(\frac{2n}{b})$ for all sufficiently large n, and so, for such n,

$$2nt(\beta_G^n)^2 \le \frac{2}{n} \left\{ \log\left(\frac{2n}{b}\right) \right\}^2 \to 0 \qquad \text{as } n \to \infty. \tag{3.19}$$

Therefore, it follows from (3.7), (3.18) and (3.19) that

$$-n \log \phi(\beta_G^n) - \log\left(\frac{h_n g(n)}{b}\right) \to 0 \qquad \text{as } n \to \infty,$$

and (3.8) follows.

Now, from Lefèvre and Utev (1995), (6.16),

$$\begin{aligned} &n|2t(\beta_G^n) - t(2\beta_G^n)| \\ &\quad \le 2\left\{ n(\beta_G^n)^2 \int_0^{1/\beta_G^n} P(Q > t)t \, dt + \frac{n}{e} P\left(Q > \frac{1}{\beta_G^n}\right) \right\}. \end{aligned} \tag{3.20}$$

Therefore, by (3.20) and (3.15),

$$n\{2t(\beta_G^n) - t(2\beta_G^n)\} \to 0 \qquad \text{as } n \to \infty. \tag{3.21}$$

Now

$$n\{\phi(2\beta_G^n) - \phi(\beta_G^n)^2\} = n\{2t(\beta_G^n) - t(2\beta_G^n)\} - nt(\beta_G^n)^2,$$

and the lemma follows from (3.21) and (3.19). □

LEMMA 3.5. *Under the conditions of Theorem* 3.1, $E[X_n(n)] \to b$ *as* $n \to \infty$.

PROOF. Note that by Lemma 3.4 the conditions of Theorem 3.1 imply that $h_n g(n) \phi(\beta_G^n)^n \to b$ as $n \to \infty$. Therefore, to prove the lemma, it is sufficient to show that, under the conditions of Theroem 3.1, as $n \to \infty$, $E[X_n(n)] \to b$ if and only if $\phi(\beta_G^n)^n \sum_{i \in U_n} P(|S_i^n| = 1) = h_n g(n) \phi(\beta_G^n)^n \to b$. Now $E[X_n(n)] = \sum_{i \in U_n} E[\theta_i^n(n)] = \sum_{i \in U_n} \prod_{j=1}^n \phi(\beta_G^n + v_{j,i}^n \lambda_L^n)$. Therefore, by (3.4),

$$E[X_n(n)] \ge \sum_{i \in U_n} \prod_{j=1}^{n} \phi(\beta_G^n) \phi(v_{j,i}^n \lambda_L^n) = \phi(\beta_G^n)^n \sum_{i \in U_n} P(|S_i^n| = 1).$$

Now, for all $n \geq n_0$ and for all $1 \leq i \leq n$ by (3.5),

$$\begin{aligned} E[\theta_i^n(n)] &= \prod_{j=1}^{n} \phi(\beta_G^n + v_{j,i}^n \lambda_L^n) \\ &\leq \left\{ \prod_{j \in L_i^n} \phi(v_{j,i}^n \lambda_L^n) \right\} \left\{ \prod_{j \notin L_i^n} \phi(\beta_G^n) \right\} \qquad (3.22) \\ &\leq \left\{ \prod_{j \in L_i^n} \phi(v_{j,i}^n \lambda_L^n) \right\} \phi(\beta_G^n)^{n-n^c}, \end{aligned}$$

since there are at least $n - n^c$ terms in the latter product in (3.22). For $1 \leq i \leq n$, let $H_n^i = \prod_{j \notin L_i^n} \phi(v_{j,i}^n \lambda_L^n)$ and take $d(n) \in \mathbb{N}$ such that $2^{d(n)-1} < n \leq 2^{d(n)}$. We show that, for all $n \geq n_0$ and $1 \leq i \leq n$,

$$H_n^i \geq (1 - 2^{-d(n)} \lambda_L^n n^{-\varepsilon} E[Q])^{2^{d(n)}}.$$

Now, for each n and i, let $c_1^{n,i} \leq c_2^{n,i} \leq \cdots \leq c_{n-|L_i^n|}^{n,i}$ be the variables $\{v_{j,i}^n; j \notin L_i^n\}$ ordered, so $H_n^i = \prod_{j=1}^{n-|L_i^n|} \phi(c_j^{n,i} \lambda_L^n)$. For $j = n - |L_i^n| + 1, n - |L_i^n| + 2, \ldots, 2^{d(n)}$, let $c_j^{n,i} = 0$. Then, since $\phi(0) = 1$, we have that $H_n^i = \prod_{j=1}^{2^{d(n)}} \phi(c_j^{n,i} \lambda_L^n)$. Then, by applying the Cauchy–Schwarz inequality $2^{d(n)-1}$ times, we get

$$H_n^i \geq \left\{ \prod_{j=1}^{2^{d(n)-1}} \phi\left(\tfrac{1}{2}(c_{2j-1}^{n,i} + c_{2j}^{n,i}) \lambda_L^n\right) \right\}^2.$$

We repeat this process to obtain $H_n^i \geq \phi(2^{-d(n)} K_n^i \lambda_L^n)^{2^{d(n)}}$, where $K_n^i = \sum_{j \notin L_i^n} v_{j,i}^n < n^{-\varepsilon}$. Therefore, for all $n \geq n_0$ and for all $1 \leq i \leq n$,

$$\begin{aligned} H_n^i &\geq \phi\left(2^{-d(n)} K_n^i \lambda_L^n\right)^{2^{d(n)}} \\ &\geq \left(1 - 2^{-d(n)} K_n^i \lambda_L^n E[Q]\right)^{2^{d(n)}} \\ &\geq \left(1 - 2^{-d(n)} n^{-\varepsilon} \lambda_L^n E[Q]\right)^{2^{d(n)}}. \end{aligned}$$

Let $H_n = \min\{H_n^i; i \in U_n\}$. Then, for all $n \geq n_0$, $H_n \geq (1 - 2^{-d(n)} n^{-\varepsilon} \lambda_L^n \times E[Q])^{2^{d(n)}}$. Since $\lambda_L^n n^{-\varepsilon} \to 0$ as $n \to \infty$, we have that $H_n \to 1$ as $n \to \infty$.

Let $J_n = \phi(\beta_G^n)^{n^c}$. Then, for all $n \geq n_0$,

$$\begin{aligned} 1 &\leq \frac{E[X_n(n)]}{\phi(\beta_G^n)^n \sum_{i \in U_n} P(|S_i^n| = 1)} \\ &\leq \frac{\sum_{i \in U_n} (\{\prod_{j \in L_i^n} \phi(v_{j,i}^n \lambda_L^n)\} \phi(\beta_G^n)^{n-n^c})}{\phi(\beta_G^n)^n \sum_{i \in U_n} P(|S_i^n| = 1)} \qquad (3.23) \end{aligned}$$

$$= \frac{\phi(\beta_G^n)^{-n^c} \sum_{i\in U_n} P(|S_i^n| = 1)(H_n^i)^{-1}}{\sum_{i\in U_n} P(|S_i^n| = 1)}$$

$$\leq (H_n J_n)^{-1}.$$

For each n, let $b_n = \phi(\beta_G^n)^n \sum_{i\in U_n} P(|S_i^n| = 1)$, so $b_n \to b$ as $n \to \infty$. Then

$$\log(\phi(\beta_G^n)) = -\frac{1}{n} \log\left(\frac{1}{b_n} \sum_{i\in U_n} P(|S_i^n| = 1)\right)$$

and for all sufficiently large n, $b_n \geq \frac{b}{2}$ and $\sum_{i\in U_n} P(|S_i^n| = 1) \leq h_n$, so

$$\frac{1}{b_n} \sum_{i\in U_n} P(|S_i^n| = 1) \leq \frac{2h_n}{b}.$$

Therefore, for all sufficiently large n,

$$\exp\left(-\frac{1}{n} \log\left(\frac{2h_n}{b}\right)\right) \leq \phi(\beta_G^n) \leq 1. \tag{3.24}$$

Thus, $J_n = \phi(\beta_G^n)^{n^c} \to 1$ as $n \to \infty$. The lemma follows since $H_n J_n \to 1$ as $n \to \infty$. □

LEMMA 3.6. *Under the conditions of Theorem* 3.1,

$$\sum_{i\in U_n} \sum_{j\in U_n\setminus\{i\}} \operatorname{cov}\left(\theta_i^n(n), \theta_j^n(n)\right) \to 0 \qquad \text{as } n \to \infty.$$

PROOF. Assume $n \geq n_0$. Then, for all $j \neq i$, using (3.5),

$$E[\theta_i^n(n)\theta_j^n(n)] = \prod_{k=1}^{n} \phi\left(2\beta_G^n + (v_{k,i}^n + v_{k,j}^n)\lambda_L^n\right)$$

$$= \prod_{k\notin L_i^n\cup L_j^n} \phi\left(2\beta_G^n + (v_{k,i}^n + v_{k,j}^n)\lambda_L^n\right)$$

$$\times \prod_{k\in L_i^n\cup L_j^n} \phi\left(2\beta_G^n + (v_{k,i}^n + v_{k,j}^n)\lambda_L^n\right)$$

$$\leq \phi(2\beta_G^n)^{n-|L_i^n\cup L_j^n|} \prod_{k\in L_i^n\cup L_j^n} \phi\left((v_{k,i}^n + v_{k,j}^n)\lambda_L^n\right) \tag{3.25}$$

$$\leq \phi(2\beta_G^n)^{n-2n^c} \prod_{k\in L_i^n\cup L_j^n} \phi\left((v_{k,i}^n + v_{k,j}^n)\lambda_L^n\right), \tag{3.26}$$

since $|L_i^n \cup L_j^n| \leq 2n^c$. Suppose that $L_i^n \cap L_j^n = \varnothing$. Then, by (3.5) and (3.26),

$$E[\theta_i^n(n)\theta_j^n(n)] \leq \phi(2\beta_G^n)^{n-2n^c} \left\{\prod_{k\in L_i^n} \phi(v_{k,i}^n\lambda_L^n)\right\}\left\{\prod_{k\in L_j^n} \phi(v_{k,j}^n\lambda_L^n)\right\}. \tag{3.27}$$

Then, by the proof of Lemma 3.5 and letting $A_n = \phi(2\beta_G^n)^{2n^c}$, we have by (3.27) that

$$E[\theta_i^n(n)\theta_j^n(n)] \le A_n^{-1} H_n^{-2} \phi(2\beta_G^n)^n P(|S_i^n| = 1) P(|S_j^n| = 1). \tag{3.28}$$

Suppose that $L_i^n \cap L_j^n \neq \varnothing$. Then, by (3.5) and (3.26) and the proof of Lemma 3.5, we have that

$$\begin{aligned} E[\theta_i^n(n)\theta_j^n(n)] &\le \phi(2\beta_G^n)^{n-2n^c} \left\{ \prod_{k \in L_i^n} \phi(v_{k,i}^n \lambda_L^n) \right\} \\ &\le A_n^{-1} H_n^{-1} \phi(2\beta_G^n)^n P(|S_i^n| = 1). \end{aligned} \tag{3.29}$$

Now, since

$$n^{-d} \sum_{i \in U_n} P(|S_i^n| = 1) = n^{-d} h_n g(n) = \{h_n n^{-(d+\delta)}\}\{n^\delta g(n)\} \to \infty \qquad \text{as } n \to \infty,$$

we have that, for all sufficiently large n, $\sum_{i \in U_n} P(|S_i^n| = 1) \ge 2n^d$. As in the proof of Lemma 3.5, $\log(\phi(\beta_G^n)) = -\frac{1}{n} \log(\frac{1}{b_n} \sum_{i \in U_n} P(|S_i^n| = 1))$, where $b_n \to b$ as $n \to \infty$. Therefore, for all sufficiently large n, $\frac{1}{b_n} \sum_{i \in U_n} P(|S_i^n| = 1) \ge \frac{n^d}{b}$. Hence,

$$\phi(\beta_G^n)^n \le \exp\left(-\log\left(\frac{n^d}{b} \right) \right) = \frac{b}{n^d} \to 0 \qquad \text{as } n \to \infty.$$

Now, using (3.5), for all $1 \le i \le n$, $E[\theta_i^n(n)] \le \phi(\beta_G^n)^n$. Therefore,

$$\max_{1 \le i \le n} E[\theta_i^n(n)] \le \phi(\beta_G^n)^n \to 0 \qquad \text{as } n \to \infty. \tag{3.30}$$

Since $\{\theta_i^n(n)\}$ are positively related,

$$\begin{aligned} &\sum_{i \in U_n} \sum_{j \in U_n \setminus \{i\}} E[\theta_i^n(n)\theta_j^n(n)] \\ &\quad \ge \sum_{i \in U_n} \sum_{j \in U_n \setminus \{i\}} E[\theta_i^n(n)] E[\theta_j^n(n)] \\ &\quad = \sum_{i \in U_n} \sum_{j \in U_n} E[\theta_i^n(n)] E[\theta_j^n(n)] - \sum_{i \in U_n} E[\theta_i^n(n)]^2 \\ &\quad \ge \left(\sum_{i \in U_n} E[\theta_i^n(n)] \right)^2 - \max_{1 \le j \le n} E[\theta_j^n(n)] \left(\sum_{i \in U_n} E[\theta_i^n(n)] \right). \end{aligned}$$

Since, by (3.30), $\max_{1 \le i \le n} E[\theta_i^n(n)] \to 0$ as $n \to \infty$ and $\sum_{i \in U_n} E[\theta_i^n(n)] = E[X_n(n)] \to b$ as $n \to \infty$, we have that

$$\left(\sum_{i \in U_n} E[\theta_i^n(n)] \right)^2 - \max_{1 \le j \le n} E[\theta_j^n(n)] \left(\sum_{i \in U_n} E[\theta_i^n(n)] \right) \to b^2 \qquad \text{as } n \to \infty.$$

Now, for $n \geq n_0$, we have that $|M_i^n| \leq n^d$ $(1 \leq i \leq n)$. Therefore, by (3.28) and (3.29), for all $n \geq n_0$,

$$\begin{aligned}
&\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)\theta_j^n(n)] \\
&\quad= \sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\},L_i^n\cap L_j^n=\varnothing} E[\theta_i^n(n)\theta_j^n(n)] \\
&\qquad+ \sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\},L_i^n\cap L_j^n\neq\varnothing} E[\theta_i^n(n)\theta_j^n(n)] \\
&\quad\leq \sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} A_n^{-1}H_n^{-2}\phi(2\beta_G^n)^n P(|S_i^n|=1)P(|S_j^n|=1) \qquad (3.31)\\
&\qquad+ \sum_{i\in U_n} |M_i^n|A_n^{-1}H_n^{-1}\phi(2\beta_G^n)^n P(|S_i^n|=1) \\
&\quad\leq \sum_{i\in U_n}\sum_{j\in U_n} A_n^{-1}H_n^{-2}\phi(2\beta_G^n)^n P(|S_i^n|=1)P(|S_j^n|=1) \\
&\qquad+ \sum_{i\in U_n} n^d A_n^{-1}H_n^{-1}\phi(2\beta_G^n)^n P(|S_i^n|=1).
\end{aligned}$$

Note that $1 \geq A_n = \phi(2\beta_G^n)^{2n^c} \geq \phi(\beta_G^n)^{4n^c} \to 1$ as $n \to \infty$ by (3.24). Thus, since $H_n \to 1$ as $n \to \infty$, the right-hand side of (3.31) has the same limit as $\phi(2\beta_G^n)^n\{\sum_{i\in U_n} P(|S_i^n|=1)\}^2 + n^d\phi(2\beta_G^n)^n\{\sum_{i\in U_n} P(|S_i^n|=1)\}$ as $n \to \infty$. Since we have established a lower bound for $\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)\theta_j^n(n)]$, which converges to b^2 as $n \to \infty$, to prove the lemma, it suffices to show that

$$\phi(2\beta_G^n)^n\left\{\sum_{i\in U_n} P(|S_i^n|=1)\right\}^2\left\{1+\left(n^{-d}\sum_{i\in U_n} P(|S_i^n|=1)\right)^{-1}\right\} \to b^2 \qquad (3.32)$$

as $n \to \infty$.

Now $n^{-d}\sum_{i\in U_n} P(|S_i^n|=1) \to \infty$ as $n \to \infty$, so $\phi(2\beta_G^n)^n\{\sum_{i\in U_n} P(|S_i^n|=1)\}^2$ and the left-hand side of (3.32) have the same limit as $n \to \infty$. Now $\phi(2\beta_G^n)^n\{\sum_{i\in U_n} P(|S_i^n|=1)\}^2 \to b^2$ as $n \to \infty$ if and only if

$$\left\{\phi(\beta_G^n)^n\sum_{i\in U_n} P(|S_i^n|=1)\right\}^2\left\{\left(1+\frac{\phi(2\beta_G^n)-\phi(\beta_G^n)^2}{\phi(\beta_G^n)^2}\right)^n-1\right\} \to 0 \qquad (3.33)$$

as $n \to \infty$.

Now $\phi(\beta_G^n)^2 \to 1$ as $n \to \infty$ by (3.24), so (3.33) holds, since $n\{\phi(2\beta_G^n) - \phi(\beta_G^n)^2\} \to 0$ as $n \to \infty$ by Lemma 3.4. Thus, $\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)\theta_j^n(n)] \to b^2$ as $n \to \infty$, and the lemma follows. □

THEOREM 3.7. *Under the conditions of Theorem* 3.1, $X_n(n) \xrightarrow{D} \mathrm{Po}(b)$ *as* $n \to \infty$.

PROOF. To prove the theorem, it is sufficient to show that $d_{\mathrm{TV}}(\mathcal{L}(X_n(n)), \mathrm{Po}(b)) \to 0$ as $n \to \infty$, where d_{TV} denotes total variation distance [see Barbour, Holst and Janson (1992), Appendix, for details]. Since $\{\theta_i^n(n)\}$ are positively related for each $n \geq 1$, it follows, using Barbour, Holst and Janson (1992), Corollary 2.C.4, that

$$\begin{aligned} &d_{\mathrm{TV}}\big(\mathcal{L}(X_n(n)), \mathrm{Po}(b)\big) \\ &\quad \leq \frac{1-e^{-b}}{b}\left(\mathrm{var}(X_n(n)) - b + 2\sum_{i\in U_n} E[\theta_i^n(n)]^2\right) \\ &\quad \leq E[X_n(n)] - b + \sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} \mathrm{cov}\big(\theta_i^n(n), \theta_j^n(n)\big) + \sum_{i\in U_n} E[\theta_i^n(n)]^2, \end{aligned}$$

since $1 - e^{-b} < b$ for $b > 0$. Thus, by (3.30),

$$\begin{aligned} &d_{\mathrm{TV}}\big(\mathcal{L}(X_n(n)), \mathrm{Po}(b)\big) \\ &\quad \leq E[X_n(n)] - b + \sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} \mathrm{cov}\big(\theta_i^n(n), \theta_j^n(n)\big) \\ &\qquad + \phi(\beta_G^n)^n E[X_n(n)]. \end{aligned} \tag{3.34}$$

Now Lemma 3.5 and (3.30) ensure that $E[X_n(n)] - b \to 0$ and $\phi(\beta_G^n)^n \times E[X_n(n)] \to 0$ as $n \to \infty$. The theorem then follows from (3.34) since Lemma 3.6 ensures that $\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} \mathrm{cov}(\theta_i^n(n), \theta_j^n(n)) \to 0$ as $n \to \infty$. □

3.4. *Poisson approximation for survivors of the epidemic.* We return to the epidemic E_n. Let $\psi_i^n(t) = 1$ if individual i's susceptibility set avoids global infection from the first t infectives in a population of size n and $\psi_i^n(t) = 0$ otherwise. Let $Y_n(t) = \sum_{i\in U_n} \psi_i^n(t)$. Clearly, for all $t \geq 0$, $\psi_i^n(t) \leq \theta_i^n(t)$ $(1 \leq i \leq n)$. Note that, for T_n, none of the T_n infectives in the epidemic infects any of the remaining S_n susceptibles either locally or globally. Since this is the case, none of the T_n infectives belongs to the susceptiblity set of a remaining susceptible. Therefore, $\theta_i^n(T_n) = 1$ implies that $\psi_i^n(T_n) = 1$, so $\psi_i^n(T_n) = \theta_i^n(T_n)$. Then $Y_n(T_n) = X_n(T_n)$ and to show that $S_n \xrightarrow{D} \mathrm{Po}(b)$ as $n \to \infty$, it is sufficient to show that $d_{\mathrm{TV}}(Y_n(T_n), X_n(n)) \to 0$ as $n \to \infty$. Also, note that both X_n and Y_n are nonincreasing in t.

Let $0 < \delta < \frac{1}{2}$ be as in Theorem 3.1, let R_n be the set of individuals who remain susceptible during E_n and let W_n be the set of initial susceptibles who avoid global infection from the first $n - [n^\delta]$ infectives. Then, if $T_n \geq n - [n^\delta]$, we have that $R_n \subseteq W_n$. Let $A_n = \{\exists\, i, j \in U_n : i, j \in R_n, i \neq j, j \in S_i^n\}$, $B_n^c = \{$the individuals in R_n fail to infect each other globally if they were to become infectious$\}$ and $D_n = \{\exists\, i, j \in U_n : i, j \in W_n, i \neq j, j \in S_i^n\}$.

LEMMA 3.8. *Suppose that there exists* $0 < \delta < \frac{1}{2}$ *such that* $n^\delta g(n) \to \infty$ *as* $n \to \infty$. *Then, for all* $n \in \mathbb{N}$,

$$P\big(Y_n(T_n) \neq X_n(n)\big) \leq P\big(Y_n(T_n) > [n^\delta]\big) + P(D_n) + \big(1 - \phi([n^\delta]\beta_G^n)^{[n^\delta]}\big). \tag{3.35}$$

PROOF. First, note that

$$\begin{aligned} &P\big(Y_n(T_n) \neq X_n(n)\big) \\ &\quad \leq P\big(Y_n(T_n) > [n^\delta]\big) + \sum_{k=1}^{[n^\delta]} P\big(X_n(n) \neq k | Y_n(T_n) = k\big) P\big(Y_n(T_n) = k\big). \end{aligned}$$

Since $T_n = \inf\{t \geq m_n : t + X_n(t) = n\}$, the events $T_n = n - k$ and $X_n(T_n) = k$ are equivalent. Then, since $Y_n(T_n) = X_n(T_n) = S_n$, for each k,

$$\begin{aligned} P\big(X_n(n) \neq k | Y_n(T_n) = k\big) &= P(A_n \cup B_n | T_n = n - k) \\ &\leq P(A_n | T_n = n - k) + P(B_n | S_n = k). \end{aligned}$$

Now the probability that an infective fails to infect globally any set of k individuals is simply $\phi(k\beta_G^n)$. Therefore, if $S_n = k$, the probability that none of the individuals in R_n infect each other globally, if they were to become infectious, is $\phi(k\beta_G^n)^k$, since the Q_i's are independent. Thus, $P(B_n | S_n = k) = 1 - \phi(k\beta_G^n)^k$. Since, for all $0 \leq k \leq [n^\delta]$, $R_n \subseteq W_n$, we have that

$$P(A_n | T_n = n - k) \leq P(D_n | T_n = n - k).$$

Therefore,

$$\begin{aligned} &\sum_{k=1}^{[n^\delta]} P(A_n | T_n = n - k) P\big(Y_n(T_n) = k\big) \\ &\qquad \leq \sum_{k=1}^{[n^\delta]} P(D_n | T_n = n - k) P\big(Y_n(T_n) = k\big) \\ &\qquad = \sum_{k=1}^{[n^\delta]} P(D_n, T_n = n - k) \leq P(D_n), \end{aligned}$$

so

$$\sum_{k=1}^{[n^\delta]} P\big(X_n(n) \neq k | Y_n(T_n) = k\big) P\big(Y_n(T_n) = k\big) \leq P(D_n) + \big(1 - \phi([n^\delta]\beta_G^n)^{[n^\delta]}\big),$$

as required. □

We now proceed by showing that each of the terms on the right-hand side of (3.35) converges to 0 as $n \to \infty$ and then Theorem 3.1 follows.

Let $\tilde{E}_n$ be the homogeneous mixing epidemic in a population of size n, where a typical individual, i say, is infectious for a time Q_i and makes infectious contacts at the points of ξ_i^n. Let $\tilde{S}_n$ be the final number of susceptibles in the epidemic $\tilde{E}_n$. Clearly, $S_n \leq_{\mathrm{st}} \tilde{S}_n$, since the epidemic $\tilde{E}_n$ can be constructed from E_n by simply ignoring local infection.

LEMMA 3.9. *Under the conditions of Theorem* 3.1, *for all* $a \in (0,1)$, $P(\tilde{S}_n \geq an) \to 0$ *as* $n \to \infty$.

PROOF. The lemma is proved for the case $m_n = 1$. The proof extends readily to the case $m_n > 1$. Let $\tilde{T}_n = n - \tilde{S}_n$ be the final size of the epidemic $\tilde{E}_n$. Therefore, to prove the lemma, it is sufficient to show that, for all $a \in (0,1)$, $P(\tilde{T}_n \leq (1-a)n) \to 0$ as $n \to \infty$.

For each n, let $\xi_1^n, \xi_2^n, \ldots$ be independent and identically distributed copies of ξ^n. Let U be uniformly distributed on $(0,1)$. For $i \in \mathbb{Z}$ and $j \geq 1$, let $\{U_{i,j}\}$ be independent and identically distributed copies of U. For each $a \in (0,1)$, we couple a point process $\zeta_i^{n,a}$ to ξ_i^n as follows. The jth point of ξ_i^n is a point on $\zeta_i^{n,a}$ if and only if $U_{i,j} \leq a$. Therefore, $\zeta_i^{n,a}$ is a homogeneous Poisson process with rate $a\lambda_G^n$. Note that $h_n g(n) \to \infty$ as $n \to \infty$, so $\lambda_G^n \to \infty$ as $n \to \infty$.

For fixed $n \geq 1$ and $a \in (0,1)$, let $(Q_0, \zeta_0^{n,a}), (Q_1, \zeta_1^{n,a}), \ldots$ be independent and identically distributed copies of $(Q, \zeta^{n,a})$ and construct the branching process $B_{n,a}$ as follows. Assume that a typical individual, i say, lives for time Q_i and reproduces at the points of $\zeta_i^{n,a}$. Assign to the initial ancestor the life history $(Q_0, \zeta_0^{n,a})$ and assign life histories to individuals in the branching process sequentially from $(Q_1, \zeta_1^{n,a}), (Q_2, \zeta_2^{n,a}), \ldots$. Let $Z_i^{n,a}$ be the number of offspring that the ith individual has in the branching process. Then $Z_1^{n,a}, Z_2^{n,a}, \ldots$ are independent and identically distributed copies of a random variable, $Z^{n,a}$ say, and $P(Z^{n,a} = z | Q = x) = \frac{1}{z!}(a\lambda_G^n x)^z e^{-a\lambda_G^n x}$ $(z = 0, 1, \ldots)$.

Let $C_{n,a}$ be the branching process constructed as in $B_{n,a}$, except that no individual has more than two offspring. This is achieved by ignoring all offspring of an individual after the birth of his or her second offspring. Let $Y_i^{n,a}$ be the number of offspring that the ith individual has in $C_{n,a}$. Let $q_{n,a}$ and $r_{n,a}$ be the extinction probabilities of the branching processes $C_{n,a}$ and $B_{n,a}$, respectively. Then, clearly, $r_{n,a} \leq q_{n,a}$. Now $P(Y_i^{n,a} = 0) = P(Z_i^{n,a} = 0) = E[e^{-a\lambda_G^n Q}]$ and $P(Y_i^{n,a} = 1) = P(Z_i^{n,a} = 1) = E[a\lambda_G^n Q e^{-a\lambda_G^n Q}]$. For $k = 0, 1, 2$, let $y_k^{n,a} = P(Y_i^{n,a} = k)$. It is well known that the extinction probability of $C_{n,a}$ is $\min(y_0^{n,a}/y_2^{n,a}, 1)$. Then, since $P(Q = 0) = 0$ and $a\lambda_G^n \to \infty$, it follows from the proof of Lefèvre and Utev (1995), Lemma 4.5, that $y_0^{n,a} \to 0$ and $y_1^{n,a} \to 0$ as $n \to \infty$. Therefore, for all $a \in (0,1)$, $q_{n,a} \to 0$ as $n \to \infty$.

We follow Kendall (1994) in the construction of the epidemic process $\tilde{E}_n$. Let the initial infective have infectious life history (Q_0, ξ_0^n) and assign sequentially to individuals as they become infected infectious life histories $(Q_1, \xi_1^n), (Q_2, \xi_2^n)$,

$\ldots, (Q_{n-1}, \xi_{n-1}^n)$. Now individual i makes infectious contacts at the points of ξ_i^n while infectious.

Suppose there are S susceptibles remaining when the jth infectious contact by individual i is made. Then we construct the epidemic such that this infectious contact is with a susceptible individual if and only if $U_{i,j} \le \frac{S}{n}$. Let $V_{n,a}$ be the total progeny of the branching process $B_{n,a}$. Then we have coupled $\tilde{E}_n$ and $B_{n,a}$ such that, if the epidemic $\tilde{E}_n$ does not infect more than $(1-a)n$ of the initial susceptibles, every birth in $B_{n,a}$ has a corresponding infection in E_n. Thus, for all $a \in (0,1)$, $P(\tilde{T}_n \le (1-a)n) \le P(V_{n,a} \le (1-a)n)$. Now $P(V_{n,a} \le (1-a)n) \le r_{n,a}$, so, for all $a \in (0,1)$, $P(\tilde{T}_n \le (1-a)n) \to 0$ as $n \to \infty$, as required. $\square$

LEMMA 3.10. *Under the conditions of Theorem* 3.1, $P(Y_n(T_n) \ge [n^\delta]) \to 0$ *as* $n \to \infty$.

PROOF. Fix $a = 1 - 2\delta$ and $\gamma = 1 - \delta$. Then

$$P\big(Y_n(T_n) \ge [n^\delta]\big) \le P\big(Y_n(T_n) \ge an\big) + P\big([n^\gamma] \le Y_n(T_n) \le an\big) + P\big([n^\delta] \le Y_n(T_n) \le [n^\gamma]\big).$$

Since $Y_n(T_n) = S_n \le_{\mathrm{st}} \tilde{S}_n$, it follows from Lemma 3.9 that $P(Y_n(T_n) \ge an) \to 0$ as $n \to \infty$. Define $\tilde{\theta}_i^n(t)$ and $\tilde{X}_n(t)$ in the obvious fashion for $\tilde{E}_n$. Then, clearly, $Y_n(t) \le_{\mathrm{st}} \tilde{X}_n(t)$ for all $t \ge 0$. Now $Y_n(T_n) \le an$ implies that $T_n \ge [(1-a)n]$ and, since Y_n is nonincreasing in t, we have that

$$P\big([n^\gamma] \le Y_n(T_n) \le an\big) \le P\big(Y_n\big([(1-a)n]\big) \ge [n^\gamma]\big).$$

Now $P(Y_n([(1-a)n]) \ge [n^\gamma]) \le P(\tilde{X}_n([(1-a)n]) \ge [n^\gamma])$ and, by Markov's inequality, for all sufficiently large n,

$$P\big(\tilde{X}_n\big([(1-a)n]\big) \ge [n^\gamma]\big) \le P\left(\tilde{X}_n\big([(1-a)n]\big) \ge \frac{1}{2}n^\gamma\right) \le 2\frac{h_n}{n^\gamma}\phi(\beta_G^n)^{(1-a)n-1}.$$

Since $n^\delta g(n) \to \infty$ and $h_n g(n)\phi(\beta_G^n)^n \to b$ as $n \to \infty$, we have that $h_n n^{-\delta} \times \phi(\beta_G^n)^n \to 0$ as $n \to \infty$. Note that

$$2h_n n^{-\gamma}\phi(\beta_G^n)^{(1-a)n-1} = 2\phi(\beta_G^n)^{-1}\{h_n n^{-\delta}\phi(\beta_G^n)^n\}\{n\phi(\beta_G^n)^n\}^{2\delta-1}.$$

Now $\phi(\beta_G^n) \to 1$ as $n \to \infty$ by (3.24). Also, $n\phi(\beta_G^n)^n = h_n g(n)\phi(\beta_G^n)^n(n/\sum_{i\in U_n} P(|S_i^n| = 1)) \ge \frac{b}{2}$ for all sufficiently large n, so, for such n, $0 \le \{n\phi(\beta_G^n)^n\}^{2\delta-1} \le (\frac{b}{2})^{2\delta-1}$. Thus, $P([n^\gamma] \le Y_n(T_n) \le an) \to 0$ as $n \to \infty$.

Finally, since Y_n is nonincreasing in t,

$$P\big([n^\delta] \le Y_n(T_n) \le [n^\gamma]\big) \le P\big(Y_n(n - [n^\gamma]) > \tfrac{1}{2}n^\delta\big) \le P\big(\tilde{X}_n(n - [n^\gamma]) > \tfrac{1}{2}n^\delta\big),$$

so, using Markov's inequality, $P([n^\delta] \le Y_n(T_n) \le n^\gamma) \le 2h_n n^{-\delta}\phi(\beta_G^n)^{n-n^\gamma}$. Since $0 < \gamma < 1$, we have by (3.24) that $\phi(\beta_G^n)^{n^\gamma} \to 1$ as $n \to \infty$. Therefore, since $h_n n^{-\delta}\phi(\beta_G^n)^n \to 0$ as $n \to \infty$, we have that $P([n^\delta] \le Y_n(T_n) \le [n^\gamma]) \to 0$ as $n \to \infty$, and the lemma follows. □

Lemma 3.9 leads, via a similar argument to the proof of Lemma 3.10, to a new and simple proof of Lefèvre and Utev (1995), Proposition 4.3, and this is presented in the Appendix.

LEMMA 3.11. *Under the conditions of Theorem* 3.1, $P(D_n) \to 0$ *as* $n \to \infty$.

PROOF. For fixed n, let $i \sim j$ if $j \in M_i^n$ and $G_n = \{\exists \text{ distinct } i, j \in W_n : i \sim j\}$. Now

$$\begin{aligned} P(D_n) &= P(D_n \,|\, |W_n| \le [n^\delta])P(|W_n| \le [n^\delta]) \\ &\quad + P(D_n \,|\, |W_n| > [n^\delta])P(|W_n| > [n^\delta]) \\ &\le P(D_n \,|\, |W_n| \le [n^\delta]) + P(|W_n| > [n^\delta]) \\ &= P(D_n, G_n^c \,|\, |W_n| \le [n^\delta]) \\ &\quad + P(D_n, G_n \,|\, |W_n| \le [n^\delta]) + P(|W_n| > [n^\delta]) \\ &\le P(D_n \,|\, |W_n| \le [n^\delta], G_n^c) + P(G_n \,|\, |W_n| \le [n^\delta]) + P(|W_n| > [n^\delta]). \end{aligned} \tag{3.36}$$

First, note that $|W_n| = \tilde{X}_n(n - [n^\delta])$. Therefore, $P(|W_n| > [n^\delta]) = P(\tilde{X}_n(n - [n^\delta]) > [n^\delta])$ and by Markov's inequality $P(\tilde{X}_n(n - [n^\delta]) > [n^\delta]) \le 2h_n n^{-\delta} \times \phi(\beta_G^n)^{n-[n^\delta]}$, since $\frac{1}{2}n^\delta \le [n^\delta]$ for all sufficiently large n. Then, as in the proof of Lemma 3.10, we have that

$$2h_n n^{-\delta}\phi(\beta_G^n)^{n-[n^\delta]} \to 0 \qquad \text{as } n \to \infty.$$

Clearly, $P(G_n \,|\, |W_n| \le [n^\delta]) \le P(G_n \,|\, |W_n| = [n^\delta])$. Since each individual in U_n is equally likely to be contained in W_n, we construct the set $\{|W_n| = [n^\delta]\}$ as follows. For each $n \ge 1$, let $\chi_1^n, \chi_2^n, \ldots$ be independent and identically distributed random variables with $P(\chi_1^n = j) = h_n^{-1}$ for $j \in U_n$. Let $N_n = \min\{k > 1 : \exists\, 1 \le i \le k-1, \chi_i^n \sim \chi_k^n\}$. Now, for each individual, i say, there are at most $[n^d]$ individuals, j say (including individual i him- or herself), for whom $j \sim i$. Therefore, for $N_n > k$, given $N_n > k-1$, we require the kth individual not to belong to $\bigcup_{i=1}^{k-1} M_i^n$, and so there are at most $(k-1)[n^d]$ individuals in U_n to avoid. Thus, for all $k > 1$, $P(N_n > k | N_n > k-1) \ge 1 - \frac{k[n^d]}{h_n}$, so $P(N_n > k) \ge \prod_{i=1}^{k-1}(1 - \frac{i[n^d]}{h_n})$. Now, for each k,

$$\begin{aligned} P(G_n \,|\, |W_n| = k) &= Pr(G_n \,|\, |W_n| = k, N_n > k)P(N_n > k) \\ &\quad + P(G_n \,|\, |W_n| = k, N_n \le k)P(N_n \le k). \end{aligned}$$

Suppose that $|W_n| = k$ and let $W_n = \{\chi_1^n, \chi_2^n, \ldots, \chi_k^n\}$. Note that if $N_n > k$, then W_n has been constructed in such a way that, for all $1 \le i < j \le k$, $\chi_i^n \ne \chi_j^n$, so $|W_n| = k$ and there does not exist distinct $i, j \in W_n$ such that $\chi_i^n \sim \chi_j^n$. Hence, $P(G_n | |W_n| = k, N_n > k) = 0$, so $P(G_n | |W_n| = k) \le P(N_n \le k)$. For all $n \ge 1$, let the random variable $\tilde{N}_n$ be such that, for all $k \in \mathbb{N}$, $P(\tilde{N}_n > k) = \prod_{i=1}^{k-1}(1 - \frac{i[n^d]}{h_n})$. Then it is well known [see e.g., Aldous (1985), page 96], that $(\frac{h_n}{[n^d]})^{-1/2}\tilde{N}_n \xrightarrow{D} \tilde{N}$ as $n \to \infty$, where $\tilde{N}$ has density $f(x) = x\exp(-\frac{x^2}{2})$ $(x > 0)$. Since $h_n n^{-d-2\delta} \to \infty$ as $n \to \infty$, we have that $(\frac{[n^d]}{h_n})^{1/2} n^{\delta} \to 0$ as $n \to \infty$, so $P(N_n > [n^{\delta}]) \ge P(\tilde{N}_n > [n^{\delta}]) \to 1$ as $n \to \infty$. Therefore,

$$P(G_n | |W_n| \le [n^{\delta}]) \le P(N_n \le [n^{\delta}]) \to 0 \qquad \text{as } n \to \infty.$$

Note that

$$\begin{aligned} &P(D_n | G_n^c, |W_n| \le [n^{\delta}]) \\ &\quad = \sum_{k=1}^{[n^{\delta}]} P(D_n | G_n^c, |W_n| = k) P\big(|W_n| = k | G_n^c, |W_n| \le [n^{\delta}]\big). \end{aligned} \tag{3.37}$$

The probability that while infectious an individual, i say, fails to infect locally any individual in $\{L_i^n\}^c$ is $\phi(\sum_{j \notin L_i^n} v_{i,j}^n \lambda_L^n)$. Now, conditioning on G_n^c, if each individual, i say, in W_n does not make local infectious contacts outside L_i^n, then all the individuals in W_n will have susceptibility sets of size 1. Since, for all sufficiently large n, $\sum_{j \notin L_i^n} v_{i,j}^n < n^{-\varepsilon}$ $(1 \le i \le n)$, it follows that, for such n,

$$P(D_n | G_n^c, |W_n| = k) \le 1 - \phi(n^{-\varepsilon}\lambda_L^n)^k.$$

Therefore, it follows from (3.37) that

$$\begin{aligned} P(D_n | G_n^c, |W_n| \le [n^{\delta}]) &\le \sum_{k=1}^{[n^{\delta}]} \big(1 - \phi(n^{-\varepsilon}\lambda_L^n)^k\big) P\big(|W_n| = k | G_n^c, |W_n| \le [n^{\delta}]\big) \\ &\le 1 - \phi(n^{-\varepsilon}\lambda_L^n)^{[n^{\delta}]} \\ &\le 1 - (1 - n^{-\varepsilon}\lambda_L^n E[Q])^{[n^{\delta}]} \to 0 \qquad \text{as } n \to \infty, \end{aligned}$$

since $n^{\delta-\varepsilon}\lambda_L^n \to 0$ as $n \to \infty$. Therefore, from (3.36), we have that $P(D_n) \to 0$ as $n \to \infty$. □

We are now in a position to prove our main theorem.

PROOF OF THEOREM 3.1. Theorem 3.7 ensures that $X_n(n) \xrightarrow{D} \text{Po}(b)$ as $n \to \infty$. Therefore, to prove Theorem 3.1, it suffices to show that $P(X_n(n) \ne$

$S_n) \to 0$ as $n \to \infty$. Now Lemma 3.10 shows that under the stated conditions $P(Y_n(T_n) \geq [n^\delta]) \to 0$ as $n \to \infty$. We have from Lemma 3.11 that $P(D_n) \to 0$ as $n \to \infty$. Finally, using Jensen's inequality, $1 - \phi([n^\delta]\beta_G^n)^{[n^\delta]} \leq 1 - \phi(\beta_G^n)^{n^{2\delta}}$ and, since $2\delta < 1$, by (3.24), $1 - \phi(\beta_G^n)^{n^{2\delta}} \to 0$ as $n \to \infty$. Thus, $1 - \phi([n^\delta]\beta_G^n)^{[n^\delta]} \to 0$ as $n \to \infty$, and the theorem now follows using Lemma 3.8. □

4. Specific models. Theorem 3.1 can be simplified greatly if we specify the model to be considered. In this section, we study the great circle, overlapping groups and households models, outlined in Section 2.2.

4.1. *Great circle model.* Consider the great circle of Section 2.2.1 and suppose that $\lim_{n\to\infty} w_i^n = w_i$ $(i \in \mathbb{Z})$, where $\{w_i; i \in \mathbb{Z}\}$ is a proper distribution with $w_0 = 0$. Suppose further that, for $n = 1, 2, \ldots$, $w_i^n \geq w_i (i = -[\frac{n-1}{2}], -[\frac{n-1}{2}] + 1, \ldots, [\frac{n}{2}])$ with $w_0^n = 0$. Therefore, for all $1 \leq i \leq n$, $P(|S_i^n| = 1) = \prod_{j=-[(n-1)/2]}^{[n/2]} \phi(w_j^n \lambda_L^n)$.

THEOREM 4.1. *Suppose that there exist $\alpha > 0, 0 < \delta < \frac{1}{2}$ and $b > 0$ such that $\lambda_L^n n^{-\alpha} \to 0, n^\delta P(|S_1^n| = 1) \to \infty$ and $\lambda_G^n E[Q] - \log(h_n P(|S_1^n| = 1)) + \log b \to 0$ as $n \to \infty$. Suppose also that there exist $\gamma \geq 0$ and $\rho > \frac{\delta+\alpha}{1+\gamma} + 2\delta$ such that $\gamma > \delta + \alpha - 1$, $\sum_{i\in\mathbb{Z}} |i|^{1+\gamma} w_i < \infty$ and $h_n n^{-\rho} \to \infty$ as $n \to \infty$. Then $S_n \xrightarrow{D} \mathrm{Po}(b)$ as $n \to \infty$.*

PROOF. To prove the theorem, it is sufficient to show that the conditions of Theorem 3.1 are satisfied. First, note that $P(|S_i^n| = 1) = \prod_{l=-[(n-1)/2]}^{[n/2]} \phi(w_l^n \lambda_L^n)$ $(1 \leq i \leq n)$, so $g(n) = P(|S_1^n| = 1)$. Fix ε and c such that $\frac{\delta+\alpha}{1+\gamma} < \frac{\varepsilon}{1+\gamma} < c < \rho - 2\delta$ and, for $1 \leq i \leq n$, let $L_i^n = \{j \in \mathbb{N} : j \leq n \text{ and } -\frac{1}{10}n^c < (j-i)_{\mathrm{mod}\, n} < \frac{1}{10}n^c\}$. Then, for $n \geq 1$, $|L_i^n| \leq \frac{1}{3}n^c$ $(1 \leq i \leq n)$, so $|M_i^n| \leq n^c$ $(1 \leq i \leq n)$. Recall that, for $n \geq 1$, $w_l^n \leq w_l$ $(l = -[\frac{n-1}{2}], -[\frac{n-1}{2}] + 1, \ldots, [\frac{n}{2}])$. Thus, for $1 \leq i \leq n$,

$$\sum_{j\notin L_i^n} v_{i,j}^n = \sum_{|l|\geq n^c/10} w_l^n = 1 - \sum_{|l|<n^c/10} w_l^n \leq 1 - \sum_{|l|<n^c/10} w_l = \sum_{|l|\geq n^c/10} w_l.$$

Now $\sum_{|l|\geq n^c/10} w_l < n^{-\varepsilon}$ for all sufficiently large n, since otherwise

$$\begin{aligned}\sum_{i\in\mathbb{Z}} |i|^{1+\gamma} w_i &\geq \sum_{|i|\geq n^c/10} |i|^{1+\gamma} w_i \\ &\geq \frac{1}{10^{1+\gamma}} n^{c(1+\gamma)} \sum_{|i|\geq n^c/10} w_i \geq \frac{1}{10^{1+\gamma}} n^{c(1+\gamma)-\varepsilon}\end{aligned}$$

for arbitrarily large n, which contradicts $\sum_{i\in\mathbb{Z}} |i|^{1+\gamma} w_i < \infty$ since $c(1+\gamma) - \varepsilon > 0$. Thus, $\sum_{j\notin L_i^n} v_{i,j}^n < n^{-\varepsilon}$ for all sufficiently large n. Further, $\sum_{j\notin L_i^n} v_{j,i}^n = \sum_{j\notin L_i^n} v_{i,j}^n$ by the symmetry of the great circle model, so $\sum_{j\notin L_i^n} v_{j,i}^n < n^{-\varepsilon}$ for all sufficiently large n. Finally, since $c + 2\delta < \rho$, $h_n n^{-(c+2\delta)} \to \infty$ as $n \to \infty$, and the theorem then follows from Theorem 3.1. □

In the nearest neighbor case where, for all $n \geq 3$, $w_1^n = w_{-1}^n = \frac{1}{2}$, the conditions of Theorem 4.1 can be greatly simplified. The result is presented in Theorem 4.2. The proof of Theorem 4.2 is very similar to that of Theorem 4.3 and is hence omitted.

THEOREM 4.2. *Suppose that there exist* $0 < \delta < \frac{1}{2}$ *and* $b > 0$ *such that* $n^\delta \phi(\frac{1}{2}\lambda_L^n)^2 \to \infty$, $h_n n^{-2\delta} \to \infty$ *and* $\lambda_G^n E[Q] - \log h_n - 2\log\phi(\frac{1}{2}\lambda_L^n) + \log b \to 0$ *as* $n \to \infty$. *Then* $S_n \xrightarrow{D} \mathrm{Po}(b)$ *as* $n \to \infty$.

The extension of Theorem 4.2 to d-dimensional nearest neighbor percolation epidemic models is straightforward, and in that case $g(n) = P(|S_1^n| = 1) = \phi(\frac{1}{2d}\lambda_L^n)^{2d}$.

4.2. *Overlapping groups model.* Consider the overlapping groups model of Section 2.2.2. Suppose that no two individuals belong to both the same group of type A and the same group of type B. Therefore, for all $1 \leq i \leq n$, $P(|S_i^n| = 1) = \phi(\beta_A^n)^{m_A - 1}\phi(\beta_B^n)^{m_B - 1}$. Let $i \overset{o}{\sim} j$ if individuals i and j belong to the same group either of type A or of type B. For $1 \leq i \leq n$, let $L_i^n = \{j : j \overset{o}{\sim} i\}$. Then $|L_i^n| = m_A + m_B - 1$. Clearly, since there is no local infection between two individuals who do not share a group, we have, for all $n \geq 1$ and for all $1 \leq i \leq n$, that $\sum_{j\notin L_i^n} v_{i,j}^n = \sum_{j\notin L_i^n} v_{j,i}^n = 0$. Note that $|M_i^n| = 2m_A m_B - m_A - m_B + 1$. The local independence in the overlapping groups model of two individuals in different groups leads to a simplification of Theorem 3.1, as demonstrated below.

THEOREM 4.3. *Suppose that there exist* $0 < \delta < \frac{1}{2}$ *and* $b > 0$ *such that* $n^\delta P(|S_1^n| = 1) \to \infty$, $h_n n^{-2\delta} \to \infty$ *and* $\lambda_G^n E[Q] - \log(h_n P(|S_1^n| = 1)) + \log b \to 0$ *as* $n \to \infty$. *Then* $S_n \xrightarrow{D} \mathrm{Po}(b)$ *as* $n \to \infty$.

Before proving Theorem 4.3, we require the following two lemmas. However, we first note that Lemma 3.4 holds under the conditions of Theorem 4.3.

LEMMA 4.4. *Under the conditions of Theorem* 4.3, $E[X_n(n)] \to b$ *and*

$$\sum_{i\in U_n} \sum_{j\in U_n\setminus\{i\}} \mathrm{cov}\left(\theta_i^n(n), \theta_j^n(n)\right) \to 0 \qquad \text{as } n \to \infty.$$

PROOF. Using (3.4) and (3.5), it is straightforward to show that

$$h_n\phi(\beta_G^n)^n P(|S_1^n|=1) \le E[X_n(n)] \le h_n\phi(\beta_G^n)^{n-m_A-m_B+1} P(|S_1^n|=1). \tag{4.1}$$

By identical arguments to those employed in the proof of Lemma 3.5, (3.24) again holds and $E[X_n(n)] \to b$ since $\phi(\beta_G^n)^{m_A+m_B-1} \to 1$ as $n \to \infty$. Therefore, (4.1) leads to a result equivalent to that of Lemma 3.5 without requiring that there exists $\alpha > 0$ such that $\lambda_L^n n^{-\alpha} \to 0$ as $n \to \infty$.

Note that $|L_i^n \cup L_j^n| \le 2(m_A + m_B - 1)$ and, using (3.25), we have that if $L_i^n \cap L_j^n = \varnothing$, then

$$E[\theta_i^n(n)\theta_j^n(n)] \le \phi(2\beta_G^n)^{n-2(m_A+m_B-1)} P(|S_i^n|=1) P(|S_j^n|=1). \tag{4.2}$$

Suppose that $L_i^n \cap L_j^n \ne \varnothing$. Then it is straightforward to show that

$$E[\theta_i^n(n)\theta_j^n(n)] \le \phi(2\beta_G^n)^{n-2(m_A+m_B-1)} P(|S_i^n|=1). \tag{4.3}$$

Since $\{\theta_i^n(n)\}$ are positively related,

$$\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)\theta_j^n(n)] \ge \sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)]E[\theta_j^n(n)]. \tag{4.4}$$

As in the proof of Lemma 3.6, it is straightforward to show that the right-hand side of (4.4) converges to b^2 as $n \to \infty$. Since $|M_i^n| = 2m_Am_B - m_A - m_B + 1$, we have from (4.2) and (4.3) that

$$\begin{aligned}
&\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)\theta_j^n(n)] \\
&\quad\le \sum_{i\in U_n}\sum_{j\in U_n} A_n^{-2}\phi(2\beta_G^n)^n P(|S_i^n|=1)P(|S_j^n|=1) \\
&\qquad + (2m_Am_B - m_A - m_B + 1)\sum_{i\in U_n} A_n^{-2}\phi(2\beta_G^n)^n P(|S_i^n|=1) \\
&\quad= A_n^{-2}\{h_n^2 P(|S_1^n|=1)^2\phi(2\beta_G^n)^n\}\left\{1 + \frac{2m_Am_B - m_A - m_B + 1}{h_n P(|S_1^n|=1)}\right\},
\end{aligned} \tag{4.5}$$

where $A_n = \phi(\beta_G^n)^{2(m_A+m_B-1)}$. Note that, by (3.24), $A_n \to 1$ as $n \to \infty$ and by the conditions of Theorem 4.3, $h_n P(|S_1^n|=1) \to \infty$ as $n \to \infty$. Therefore, the right-hand side of (4.5) has the same limit as $h_n^2 P(|S_1^n|=1)^2\phi(2\beta_G^n)^n$ as $n \to \infty$. Since we have established a lower bound for $\sum_{i\in U_n}\sum_{j\in U_n\setminus\{i\}} E[\theta_i^n(n)\theta_j^n(n)]$ which converges to b^2 as $n \to \infty$, to prove the lemma, it suffices to show that $h_n^2 P(|S_1^n|=1)^2\phi(2\beta_G^n)^n \to b^2$ as $n \to \infty$. Now $h_n^2 P(|S_1^n|=1)^2\phi(2\beta_G^n)^n \to b^2$ if and only if

$$\{h_n P(|S_1^n|=1)\phi(\beta_G^n)^n\}^2\left\{\left(1 + \frac{\phi(2\beta_G^n) - \phi(\beta_G^n)^2}{\phi(\beta_G^n)^2}\right)^n - 1\right\} \to 0 \quad \text{as } n \to \infty. \tag{4.6}$$

Now $\phi(\beta_G^n)^2 \to 1$ as $n \to \infty$, by (3.24), so (4.6) holds, since $n\{\phi(2\beta_G^n) - \phi(\beta_G^n)^2\} \to 0$ as $n \to \infty$ by Lemma 3.4. Thus, $\sum_{i \in U_n} \sum_{j \in U_n \setminus \{i\}} E[\theta_i^n(n)\theta_j^n(n)] \to b^2$ as $n \to \infty$, and the lemma follows. □

Define R_n, W_n, A_n, B_n and D_n as in Section 3.4. Then it is straightforward to show that Lemmas 3.8–3.10 hold under the conditions of Theorem 4.3.

LEMMA 4.5. *Under the conditions of Theorem* 4.3, $P(D_n) \to 0$ *as* $n \to \infty$.

PROOF. As in the proof of Lemma 3.11, let $i \sim j$ if $j \in M_i^n$ and let $G_n = \{\exists \text{ distinct } i, j \in W_n : i \sim j\}$. Then, by similar arguments to those used in the proof of Lemma 3.11, (3.17), we have that

$$P(D_n) \le P(D_n \,|\, |W_n| \le [n^\delta], G_n^c) + P(G_n \,|\, |W_n| \le [n^\delta]) + P(|W_n| > [n^\delta]). \tag{4.7}$$

First, note that, as in the proof of Lemma 3.11, $P(|W_n| > [n^\delta]) \to 0$ as $n \to \infty$. Now, if no two individuals in W_n share the same group, it is impossible for individuals in W_n to infect each other locally, so $P(D_n | G_n^c, |W_n| \le [n^\delta]) = 0$. Now, for all $1 \le i \le n$, $|M_i^n| = 2m_A m_B - m_A - m_B + 1$, so by similar arguments to those used in the proof of Lemma 3.11, with $[n^d]$ replaced by $2m_A m_B - m_A - m_B + 1$, it is straightforward to show that $P(G_n \,|\, |W_n| \le [n^\delta]) \to 0$ as $n \to \infty$. □

PROOF OF THEOREM 4.3. First, note that since $\{\theta_i^n(n)\}$ are positive related and (3.30) still holds then (3.34) still holds. Also, by (3.30) and Lemma 4.4, the right-hand side of (3.34) converges to 0 as $n \to \infty$, so $X_n(n) \xrightarrow{D} \mathrm{Po}(b)$ as $n \to \infty$. Further, as previously mentioned, Lemma 3.8 holds under the conditions of Theorem 4.3, so (3.35) holds. Now, $P(Y_n(T_n) > [n^\delta]) \to 0$ and $P(D_n) \to 0$ as $n \to \infty$ by Lemmas 3.10 and 4.5, respectively. Note that, by Jensen's inequality, $1 - \phi([n^\delta]\beta_G^n)^{[n^\delta]} \le 1 - \phi(\beta_G^n)^{n^{2\delta}}$, so, using (3.24), $1 - \phi([n^\delta]\beta_G^n)^{[n^\delta]} \to 0$ as $n \to \infty$, since $2\delta < 1$. Thus, $P(Y_n(T_n) \ne X_n(n)) \to 0$ as $n \to \infty$, and the theorem follows. □

The extension to k-types of overlapping groups is straightforward and involves no new concepts.

4.3. *Households model.* Let $i \overset{h}{\sim} j$ if individuals i and j belong to the same household. For each $n \ge 1$ and for all $1 \le i \le n$, let $L_i^n = \{j : j \overset{h}{\sim} i\}$. Note that, for all $1 \le i, j \le n$, if $L_i^n \cap L_j^n \ne \varnothing$ then $L_j^n = L_i^n$. Thus, for all $1 \le i \le n$, $M_i^n = L_i^n$. (Note that $i \sim j$ if and only if $i \overset{h}{\sim} j$, since $M_i^n = L_i^n$.) It is easy to see that, for all $1 \le i \le n$, $\sum_{j \notin L_i^n} v_{i,j}^n = \sum_{j \notin L_i^n} v_{j,i}^n = 0$. Let π_k^n be the probability that an individual in U_n belongs to a household of size k. Now, if individual i belongs to a household of size $k \ge 2$, $P(|S_i^n| = 1) = \phi(\frac{1}{k-1}\lambda_L^n)^{k-1}$, so $g(n) = \pi_1^n + \sum_{k=2}^\infty \pi_k^n \phi(\frac{1}{k-1}\lambda_L^n)^{k-1}$.

THEOREM 4.6. *Suppose that there exist* $0 < \delta < \frac{1}{2}$ *and* $b > 0$ *such that*

$$n^{\delta} g(n) = n^{\delta} \left\{ \pi_1^n + \sum_{k=2}^{\infty} \pi_k^n \phi\left(\frac{1}{k-1} \lambda_L^n \right)^{k-1} \right\} \to \infty$$

and $\lambda_G^n E[Q] - \log(h_n g(n)) + \log b \to 0$ *as* $n \to \infty$. *Suppose, in addition, that there exist* $\zeta > \frac{1}{1-2\delta}$ *and* $c > \frac{1}{\zeta}$ *such that, for all* $n \geq 1$, $\sum_{k=1}^{\infty} k^{\zeta} \pi_k^n < \infty$ *and* $h_n n^{-(c+2\delta)} \to \infty$ *as* $n \to \infty$. *Then* $S_n \xrightarrow{D} \mathrm{Po}(b)$ *as* $n \to \infty$.

PROOF. Now, for all sufficiently large n, $|M_i^n| = |L_i^n| \leq n^c$ $(1 \leq i \leq n)$, since otherwise

$$\sum_{k=1}^{\infty} k^{\zeta} \pi_k^n \geq n^{c\zeta} \pi_{[n^c]+1}^n \geq n^{c\zeta} h_n^{-1} \geq n^{c\zeta - 1}$$

for arbitrarily large n, which contradicts $\sum_{k=1}^{\infty} k^{\zeta} \pi_k^n < \infty$ since $c\zeta - 1 > 0$.

By similar arguments to those employed in Lemma 4.4, it is straightforward to show that, under the conditions of the theorem,

$$E[X_n(n)] \to b \quad \text{and} \quad \sum_{i \in U_n} \sum_{j \in U_n \setminus \{i\}} \mathrm{cov}\left(\theta_i^n(n), \theta_j^n(n)\right) \to 0 \tag{4.8}$$

as $n \to \infty$.

Note that since $\{\theta_i^n(n)\}$ are positive related and (3.30) still holds then (3.34) still holds. Also, by (3.30) and (4.8), the right-hand side of (3.34) converges to 0 as $n \to \infty$, so $X_n(n) \xrightarrow{D} \mathrm{Po}(b)$ as $n \to \infty$. Define R_n, W_n, A_n, B_n and D_n as in Section 3.4. Then it is straightforward to show that Lemmas 3.8–3.10 hold under the conditions of the theorem, so (3.35) holds and $P(Y_n(T_n) \geq [n^{\delta}]) \to 0$ as $n \to \infty$. Since $|M_i^n| \leq n^c$ and $h_n n^{-(c+2\delta)} \to \infty$ as $n \to \infty$, by similar arguments to those used in Lemma 4.5, $P(D_n) \to 0$ as $n \to \infty$. Note that, by Jensen's inequality, $1 - \phi([n^{\delta}]\beta_G^n)^{[n^{\delta}]} \leq 1 - \phi(\beta_G^n)^{n^{2\delta}}$, so, using (3.24), $1 - \phi([n^{\delta}]\beta_G^n)^{[n^{\delta}]} \to 0$ as $n \to \infty$, since $2\delta < 1$. Thus, $P(Y_n(T_n) \neq X_n(n)) \to 0$ as $n \to \infty$, and the theorem follows. □

Suppose that $\lambda_L^n \to \infty$ and $\pi_1^n \to \pi_1 > 0$ as $n \to \infty$. Then, by Jensen's inequality and Lefèvre and Utev (1995), Lemma 4.5, we have that, for all $k \geq 2$,

$$\phi\left(\frac{1}{k-1} \lambda_L^n \right)^{k-1} \leq \phi(\lambda_L^n) \to 0 \qquad \text{as } n \to \infty.$$

Then it is straightforward to show that $\lambda_G^n E[Q] - \log(h_n g(n)) + \log b \to 0$ if and only if $\lambda_G^n E[Q] - \log h_n \to \log \frac{\pi_1}{b}$. Furthermore, all the survivors of the epidemic belong to households of size 1 in the limit as $n \to \infty$.

Suppose that all the households are of equal size, K say. Then we have the following immediate corollary to Theorem 4.3, by setting $\lambda_A^n = \lambda_L^n$, $\lambda_B^n = 0$ and $m_A = K$.

COROLLARY 4.7. *Suppose that there exist* $0 < \delta < \frac{1}{2}$ *and* $b > 0$ *such that* $n^{\delta}\phi(\frac{1}{K-1}\lambda_L^n)^{K-1} \to \infty$, $h_n n^{-2\delta} \to \infty$ *and* $\lambda_G^n E[Q] - \log h_n - (K-1) \times \log \phi(\frac{1}{K-1}\lambda_L^n) + \log b \to 0$ *as* $n \to \infty$. *Then* $S_n \xrightarrow{D} \mathrm{Po}(b)$ *as* $n \to \infty$.

An intriguing consequence of Theorem 4.2 and Corollary 4.7 is that, for any given sequence $(\lambda_G^n, \lambda_L^n)$, the nearest neighbor great circle epidemic and the equal-sized households epidemic, where all households are of size 3, have the same Poisson limit distribution, provided one exists. No corresponding result holds for either the branching process approximation or the Gaussian approximation, and this is due to the fact, noted in Section 2.3, that the threshold parameter and the Poisson limit theorem depend on different aspects of the distribution of the size of a typical local susceptibility set.

5. Concluding comments. We have developed a Poisson limit theorem for a very general model for epidemics with two levels of mixing. Although the theorem has a technically complicated proof, its use as a tool for approximating the final outcome of severe epidemics is extremely simple. One just has to determine R_0^n, the mean number of global contacts that emanate from a typical infectious individual, and $g(n)$, the probability that a randomly chosen initial susceptible has local susceptibility set of size 1. (For most models, these quantities are easily calculated.) Then, provided that the epidemic is well above threshold and local spread is sufficiently restrictive, Theorem 3.1 implies that the number of survivors of the epidemic is approximately Poisson distributed with mean $h_n g(n) e^{-R_0^n}$, where n is the total population size and h_n is the initial number of susceptibles. Moreover, our method of proof yields, via (3.34) and (3.35), a bound for the total variation distance between the exact and approximating distributions.

The conditions of Theorem 3.1 can be shown to be close to optimal by considering the homogeneously mixing case ($\lambda_L^n = 0$) for which Lefèvre and Utev (1995) establish necessary and sufficient conditions for a Poisson limit theorem. If $\lambda_L^n = 0$, then $g(n) = 1$ and Theorem 3.1 reduces to the strong Poisson limit theorem of Lefèvre and Utev (1995), Corollary 2.6, with the additional condition that there exists $\zeta > 0$ such that $h_n n^{-\zeta} \to \infty$ as $n \to \infty$. [Lefèvre and Utev (1995), Corollary 2.6, requires in our terminology that $h_n \to \infty$ as $n \to \infty$.] The additional restriction on h_n is required to ensure that, where there is local infection, the configuration of the initial susceptibles is not important for the Poisson limit theorem (see, in particular, Lemmas 3.6 and 3.11). Obviously, this is not required for the homogeneously mixing case; all that is required is that $h_n \to \infty$ as $n \to \infty$, yielding the strong Poisson limit theorem of Lefèvre and Utev (1995), Corollary 2.6.

A natural extension of the Poisson limit is a compound Poisson limit. Compound Poisson limits are often considerably harder to prove than Poisson limits and the above models are no exception. However, the households model

permits a compound Poisson limit, the details of which will be presented elsewhere. Suppose that all the households are of size $K \geq 2$ and that the infection period is constant, $Q = q > 0$. Then, provided λ_G^n and λ_L^n are appropriately scaled with n, it is fairly straightforward to show that a compound Poisson limit exists and, furthermore, that $S_n \xrightarrow{D} \mathrm{Po}(b_1) + K\,\mathrm{Po}(b_2)$ for some $0 \leq b_1, b_2 < \infty$ as $n \to \infty$. In particular, if $b_1, b_2 > 0$, then $\lambda_G^n = \frac{1}{qK}\log(\frac{n}{b_2}) + o(n)$ and $\lambda_L^n = \frac{1}{qK}\log(\frac{n}{b_3}) + o(n)$ as $n \to \infty$, where $b_3 = (b_2^{1/K}/b_1)^{K/(K-1)}$. Therefore, to obtain an interesting compound Poisson limit for the households model requires very careful scaling of the global and local infection rates. Moreover, for large n, the survivors of the epidemic either belong to a household which completely avoids infection or a survivor is the only survivor within his or her household.

APPENDIX

Here we show that Lemma 3.9 leads to a simpler proof of Lefèvre and Utev (1995), Proposition 4.3. Lefèvre and Utev (1995) consider homogeneously mixing epidemics (so, in our notation, $\lambda_L^n = 0$), with the same conditions on Q as we impose in Section 2.1, except that $E[Q] < \infty$ and (3.3) are not required. They also assume that there are n initial susceptibles and m_n initial infectives, so the infection rate, β_G^n in our notation, is indexed by the initial number of susceptibles and the number of susceptibles at the end of the epidemic is given by $X_n(T_n)$, where now $T_n = \min\{t \geq m_n : t + X_n(t) = n + m_n\}$. Suppose also that the sequence (β_G^n) satisfies the condition [(2.9) of Lefèvre and Utev (1995)]

$$(n + m_n)t(\beta_G^n) - \log(n/b_n) \to 0 \qquad \text{with } b_n \to b, \text{ as } n \to \infty, \tag{A.1}$$

where $b \in (0, \infty)$. Lefèvre and Utev (1995), Proposition 4.3, states that subject to these conditions

$$P\big(X_n(T_n) \geq l\big) \to 0 \qquad \text{as } l \to \infty, \text{ uniformly in } n. \tag{A.2}$$

To prove (A.2), fix $0 < a < \delta < 1$. Then, for all $l \geq 1$,

$$\begin{aligned} &P\big(X_n(T_n) \geq l\big) \\ &\quad \leq P\big(l \leq X_n(T_n) \leq [n^\delta]\big) \\ &\qquad + P\big([n^\delta] \leq X_n(T_n) \leq an\big) + P\big(X_n(T_n) \geq an\big). \end{aligned} \tag{A.3}$$

Now $X_n(T_n) \leq an$ implies that $T_n \geq (1-a)n + m_n \geq (1-a)(n + m_n)$, so

$$\begin{aligned} &P\big([n^\delta] \leq X_n(T_n) \leq an\big) \\ &\quad \leq P\left(\frac{1}{2}n^\delta \leq X_n\big((1-a)(n+m_n)\big)\right) \\ &\quad \leq \frac{2}{n^\delta}E\big[X_n\big((1-a)(n+m_n)\big)\big] \qquad \text{by Markov's inequality} \\ &\quad = 2\{n\phi(\beta_G^n)^{n+m_n}\}^{1-a}n^{a-\delta} \to 0 \qquad \text{as } n \to \infty, \end{aligned}$$

since (A.1) implies that $n\phi(\beta_G^n)^{n+m_n} \to b$ as $n \to \infty$.

Suppose that $m_n \le an$ for all $n \ge 1$. Then, by Lefèvre and Utev (1995), Proposition 6.6, $\lambda_G^n = n\beta_G^n \to \infty$ as $n \to \infty$, and it is trivial to adapt the proof of Lemma 3.9 to show that $P(X_n(T_n) \ge an) \to 0$ as $n \to \infty$. Suppose that $m_n > an$ for all $n \ge 1$. Then (A.1) implies that $\phi(\beta_G^n)^{m_n} \to 0$ as $n \to \infty$. Therefore, since $T_n \ge m_n$, Markov's inequality yields

$$\begin{aligned} P\big(X_n(T_n) \ge an\big) &\le P\big(X_n(m_n) \ge an\big) \\ &\le \frac{E[X_n(m_n)]}{an} = \frac{\phi(\beta_G^n)^{m_n}}{a} \to 0 \qquad \text{as } n \to \infty. \end{aligned}$$

Hence, $P(X_n(T_n) \ge an) \to 0$ as $n \to \infty$ for any sequence (m_n) satisfying (A.1).

Thus, the final two terms on the right-hand side of (A.3) converge to 0 as $n \to \infty$, so (A.2) will follow if $P(l \le X_n(T_n) \le [n^\delta]) \to 0$ as $l \to \infty$ uniformly in n. Now, as in the proof of Lemma 3.5, it is straightforward to show that, for all sufficiently large n,

$$\exp\left(-\frac{2}{n+m_n}\log\left(\frac{n}{b}\right)\right) \le \phi(\beta_G^n) \le 1,$$

so $\phi(\beta_G^n)^{[n^\delta]} \to 1$ as $n \to \infty$ and

$$E\big[X_n(n+m_n-[n^\delta])\big] = n\phi(\beta_G^n)^{n+m_n}\phi(\beta_G^n)^{-[n^\delta]} \to b \qquad \text{as } n \to \infty. \tag{A.4}$$

Further, $X_n(T_n) \le [n^\delta]$ implies that $T_n \ge n + m_n - [n^\delta]$, so

$$P\big(l \le X_n(T_n) \le [n^\delta]\big) \le P\big(l \le X_n(n+m_n-[n^\delta])\big) \le \frac{1}{l}E\big[X_n(n+m_n-[n^\delta])\big],$$

and (A.2) follows using (A.4).

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