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LIMIT THEOREMS FOR A RANDOM GRAPH EPIDEMIC MODEL

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We consider a simple stochastic discrete-time epidemic model in a large closed homogeneous population that is not necessarily homogeneously mixing. Rather, each individual has a fixed circle of acquaintances and the epidemic spreads along this social network. In case the number of initially infective individuals stays small, a branching process approximation for the number of infectives is in force. Moreover, we provide a deterministic approximation of the bivariate process of susceptible and infective individuals, valid when the number of initially infective individuals is large. These results are used in order to derive the basic reproduction number and the asymptotic final epidemic size of the process. The model is described in the framework of random graphs.

1. Introduction. In this work, we consider a simple stochastic discrete-time model of a so-called SIR epidemic, that is, an epidemic where individuals receive lifelong immunity after having recovered from the disease. Imagine a closed population consisting of n individuals, where each individual has a random number of acquaintances. Let the ith individual have D_i friends, the variables D_i being identically distributed and almost independent, and suppose that two friends rarely have other friends in common. Now introduce an infectious disease into the population by infecting a individuals. If a susceptible individual meets an infective acquaintance at time t, then she will become infective at time $t+1$, and the infective will have recovered at this time point, now being immune to the disease. The probability of an encounter between any given pair of acquaintances at time t is simply given by a fixed number p, and all encounters are independent of each other. The special case where D_i is binomially distributed with parameters $n-1$ and λ/n corresponds to the classical Reed–Frost process (cf. [9]).

Let us try to motivate our choice of model. The classical stochastic epidemic models, such as the Reed–Frost process and the so-called general epidemic (see, e.g., [4]), are far too simplified to be of any practical interest. When aiming at a more realistic mathematical description of an epidemic, one is led to consider effects caused by, for instance, multitype populations, general infectious periods, heterogeneous mixing, births and deaths, immigration and emigration, geographical structure, age-dependence, partial or temporary immunity, change of behavior, and so on. There is a growing literature on theoretical models for infectious diseases, many of the model formulations having the purpose to incorporate one or several of these effects. In particular, generalizations to multitype populations, always assuming homogeneous mixing

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within types, and to general infectious periods have been performed with great success.

We feel, however, that the extremely important phenomena that arise when considering homogeneous populations that are *not* homogeneously mixing have not received enough attention so far. Besides some interesting work on household models (see, e.g., [8]), a model for the spread of venereal diseases in [12] and the recent model of an epidemic on a neighborhood structure in [14], very little has been done. Stochastic models where individuals infect only their nearest neighbors on a spatial lattice have admittedly been carefully studied (cf. [15]), but it is questionable if these interacting particle systems have much relevance when it comes to describing the extremely irregular spread of infection in a human population. A very interesting new class of network models has recently been introduced by Rand [22]; in the discussion at the end of this paper, we will give a brief account of his work.

The model in [14] does not assume any regularity of the neighborhood structure, but still each individual interacts only with a fixed group of others. More precisely, all individuals are assumed to have exactly the same number of acquaintances, and the epidemic spreads along this network. The model is described on a stochastic basis but all results are based on deterministic considerations, in principle assuming an infinite population. The purpose of the present work is to retrieve and extend some of the results from [14] in the form of rigorous limit theorems as the population size grows to infinity. See also [1].

Assume first that the number of initially infective individuals stays small while the total population size grows. Then we show that during the early stages of the epidemic, the process of infectives is well approximated by a branching process. This approximation, sometimes referred to as Kendall's approximation, has been widely discussed in the literature. Since the seminal work by Bartlett [10] and Kendall [18], rigorous branching approximation results have been obtained for the Reed–Frost process, the general epidemic model and many other stochastic epidemic processes; see, for example, [3, 5, 6, 23, 19, 7]. In each of these papers, the technique of proof relies on the assumption of homogeneous mixing in the sense that all susceptible individuals run the same risk of being infected at all times. In the present model, only neighbors of infective individuals may become infected at the next time point; hence, somewhat different methods of proof are needed.

Suppose next that the epidemic is initiated by a fixed proportion of infective individuals. We prove a law of large numbers as the population size tends to infinity, for the bivariate process of susceptible and infective individuals. Again, for many epidemic models, such deterministic approximation results are readily obtained by using standard convergence theorems; see, for example, [16]. Note, however, that density-dependent transition rates are required for these theorems to work, a property that is not fulfilled for network models.

Finally, we are interested in finding expressions for two fundamental quantities: the *basic reproduction number* and the *final epidemic size*. The final size of an SIR epidemic is defined as the number of individuals that have ever

experienced the disease, counted at the end of the epidemic. Note that the initially infective individuals are included in the final size. For many models, the qualitative behavior of the final epidemic size is closely related to the basic reproduction number, R_0, defined as the expected number of new cases generated by one infective individual in a susceptible (large) population. More precisely, we often observe the following threshold behavior in the limit where the population size tends to infinity: if $R_0 \leq 1$, then the final size stays small, while if $R_0 > 1$, there is a risk of having a positive fraction of the population infected, that is, a large outbreak may occur. It turns out that our model shows such a threshold behavior, but the basic reproduction number R_0 is *not* based on the mean number of neighbors as in the Reed–Frost case, but rather on a size-biased mean. Moreover, the general equation for the asymptotic final size looks nothing like the equation for the corresponding Reed–Frost quantity (cf. [4]).

In Section 2, we introduce a stochastic process for exposing one or several given components of a random graph. Limit theorems for this process are presented in Section 3. In Section 4, these results are applied to our epidemic model, and we also give some examples. Section 5 is devoted to the proof of the theorems, and we finish off with a short discussion in Section 6.

2. Preliminaries. Consider an undirected labelled graph $\mathscr{W}$ on n vertices. Denote by $\mathscr{N}$ the set of vertices of $\mathscr{W}$. Also, let $\mathscr{D}_i$ be the set of vertices that are adjacent to i, $1 \leq i \leq n$. We are going to pick a number of vertices of $\mathscr{W}$ and then expose the connected components containing these vertices in a dynamic manner. Let $\mathscr{X}(t)$ and $\mathscr{Y}(t)$ be the set of unexposed and exposed vertices, respectively, at time t, $t = 0, 1, 2, \ldots$. Start the process by choosing a random set $\mathscr{A}$ of vertices to represent the initially exposed vertices, so that $(\mathscr{X}(0), \mathscr{Y}(0)) = (\mathscr{N} \setminus \mathscr{A}, \mathscr{A})$. We will always choose $\mathscr{A}$ to consist of a vertices picked uniformly at random, where a is some fixed number. The time dynamics are defined by

$$\mathscr{Y}(t+1) = \mathscr{X}(t) \cap \Big(\bigcup_{i \in \mathscr{Y}(t)} \mathscr{D}_i \Big),$$
$$\mathscr{X}(t+1) = \mathscr{X}(t) \setminus \mathscr{Y}(t+1), \qquad t \geq 0.$$

The exposed vertices at time t enter a third state at time $t+1$, and can then be regarded as removed from the system. Given a graph $\mathscr{W}$ and an initial configuration $\mathscr{A}$, the process is fully deterministic. We refer to it as the *exposure process* on $\mathscr{W}$. It is obvious that the process terminates in finite time; thus the *final size* τ, defined as the total number of vertices ever exposed, is a finite random variable.

As indicated in the Introduction, we wish to consider structures that meet conditions on the number of neighbors of a given individual, that is, random graphs that meet conditions on the number of vertices adjacent to a given vertex. Define the *degree* of a vertex i to be the number of edges incident to i. The totality of degrees of a graph $\mathscr{W}$ is called the *degree sequence* of $\mathscr{W}$.

Let us consider a triangular array of random variables D_i^n; $1 \le i \le n$, $n \ge 1$, where D_i^n takes its values in the set $\{0, 1, 2, \ldots, n-1\}$. In the theorems to come, we will make the following assumptions.

A1. For fixed n, the variables D_i^n, $1 \le i \le n$, are exchangeable.

A2. The quantity $\sum_{i=1}^n D_i^n$ is always an even number.

A3. There exists a nonnegative integer-valued random variable D such that $D_1^n \to D$ in distribution.

A4. $E(D_1^n) \to E(D) = \mu$ and $\mathrm{Var}(D_1^n) \to \mathrm{Var}(D) = \sigma^2$, with μ and σ^2 finite.

A5. There exists $\delta > 0$ such that $\sup_n E((D_1^n)^{4+\delta}) < \infty$.

A6. The variables D_i^n, $1 \le i \le n$, are asymptotically pairwise independent as $n \to \infty$.

Fix the number of vertices n. For a given n-tuple $\mathbf{D}^n = (D_1^n, \ldots, D_n^n)$, pick a uniformly random member $\mathscr{W}^n$ from the set of all labelled graphs on n vertices having $\mathbf{D}^n$ as degree sequence. Of course, (A2) is needed here. (Note carefully that the set of graphs with given degree sequence can sometimes be empty. However, for large n, there will with high probability exist a huge number of graphs with the desired properties. This will be discussed further in the proof; see Section 5.) We then take a set $\mathscr{A}^n$ of initially exposed vertices and run the exposure process $(\mathscr{X}^n, \mathscr{Y}^n)$ on $\mathscr{W}^n$. Assume that the triangular array $\mathscr{D} = \{D_i^n; 1 \le i \le n, n \ge 1\}$ is defined on the probability space $(\Omega_1, \mathscr{F}_1, \mathbf{P}_1)$. Then put *all* of the involved variables on a common probability space $(\Omega, \mathscr{F}, \mathbf{P})$. We are interested in the asymptotic behavior of the process as $n \to \infty$.

A major difficulty in the study of random graphs with prescribed degree sequences is that it is difficult to generate such graphs directly. Instead, one usually studies so-called *random configurations* and then tries to translate results about such random configurations to results about random graphs (see Section 5). The configuration model was introduced by Bender and Canfield [11]; see also [13].

3. Statement of the theorems. Let $\mathscr{W}^n$, $n \ge 1$, be a sequence of graphs derived from the triangular array D_i^n; $1 \le i \le n$, $n \ge 1$, and for each n, let $(\mathscr{X}^n, \mathscr{Y}^n)$ be an exposure process on $\mathscr{W}^n$. Write

$$\big(X^n(t), Y^n(t)\big) = \big(|\mathscr{X}^n(t)|, |\mathscr{Y}^n(t)|\big), \qquad t \ge 0.$$

Assume conditions (A1)–(A6); in particular, suppose that $D_1^n \to D$ in distribution, where D is distributed according to the probability measure $\boldsymbol{\lambda} = (\lambda_0, \lambda_1, \lambda_2, \ldots)$. Denote by φ the probability generating function of $\boldsymbol{\lambda}$.

A simple branching approximation result for the number of exposed vertices is in force. Let $Y(t)$, $t \in \mathbf{N}$, be a Galton-Watson process with a ancestors, the ancestors having offspring according to the distribution $\boldsymbol{\lambda}$ and the members of the subsequent generations having offspring according to $\hat{\boldsymbol{\lambda}} = (\hat{\lambda}_0, \hat{\lambda}_1, \hat{\lambda}_2, \ldots)$, where

$$\hat{\lambda}_k = \frac{(k+1)\lambda_{k+1}}{\sum_{l=1}^{\infty} l\lambda_l}.$$

Write $R_0 = \sum_{k=1}^{\infty} k\hat{\lambda}_k$. We have the following result.

THEOREM 1. *If $Y^n(0) = a$ for all n, then $Y^n(t) \to Y(t)$ in distribution for each $t \geq 0$. Also, the final size τ^n of $(\mathscr{X}^n, \mathscr{Y}^n)$ converges in distribution to the total progeny τ of Y. If $R_0 \leq 1$, then τ is finite a.s., whereas if $R_0 > 1$, then $\mathbf{P}(\tau = \infty) = \vartheta = 1 - (\varphi(s))^a$, where s is the nontrivial root of*

$$s = \frac{\varphi'(s)}{\varphi'(1)}.$$

Note that the basic reproduction number R_0 may be conveniently written as

$$R_0 = \frac{E(D^2)}{E(D)} - 1.$$

Let us give an intuitive explanation of this branching approximation result. Suppose $a = 1$ and assume that n is very large, so that with high probability, all contacts are with unexposed vertices. Our initial vertex has, of course, degree k with probability λ_k. Note, however, that henceforth vertices with a large number of edges are more likely to become exposed than more isolated vertices; more precisely, a vertex with degree $k+1$ is chosen with a probability proportional to $(k+1)\lambda_{k+1}$, and then in turn leads to k new vertices. This explains the appearance of the distribution $\hat{\boldsymbol{\lambda}}$. The reproduction mean for the process $Y(t)$, $t \geq 1$, is simply equal to R_0, and the probability generating function $\hat{\varphi}$ of $\hat{\boldsymbol{\lambda}}$ is given by

$$\begin{aligned}\hat{\varphi}(z) &= \sum_{k=0}^{\infty} z^k \hat{\lambda}_k \\ &= \frac{\sum_{k=0}^{\infty} z^k (k+1)\lambda_{k+1}}{\sum_{l=1}^{\infty} l\lambda_l} = \frac{\varphi'(z)}{\varphi'(1)}.\end{aligned}$$

The classical theory of branching processes (see, e.g., [17]), applied to $Y(t)$, $t \geq 1$, with $Y(1) = 1$, tells us that this process becomes extinct with probability 1 if $R_0 \leq 1$, and that the probability of extinction s is equal to the nontrivial root of the equation $s = \hat{\varphi}(s)$ if $R_0 > 1$. Finally, in order for the branching process $Y(t)$, $t \geq 0$, to become extinct, *all* branches originating from the ancestor

have to become extinct; hence,

$$\begin{aligned}\mathbf{P}(\tau < \infty) &= \sum_{k=0}^{\infty} \mathbf{P}\big(\tau < \infty \,|\, Y(1) = k\big)\mathbf{P}(Y(1) = k) \\ &= \sum_{k=0}^{\infty} s^k \lambda_k = \varphi(s),\end{aligned}$$

so that $\vartheta = 1 - \varphi(s)$.

We also have the following law of large numbers.

THEOREM 2. *If $Y^n(0) = a^n$, where $a^n/n \to \bar{a} > 0$ as $n \to \infty$, then the scaled process $(X^n/n, Y^n/n)$ converges in probability (for each fixed t) to a deterministic discrete-time process $(\bar{x}, \bar{y})$. Also, $\tau^n/n \to \bar{\tau}$ in probability, where $\bar{\tau} = 1 - (1 - \bar{a})\varphi(\bar{s})$, $\bar{s}$ satisfies*

$$\bar{s} = (1 - \bar{a})\frac{\varphi'(\bar{s})}{\varphi'(1)}.$$

If $R_0 > 1$, we expect that there exists a unique giant component of $\mathscr{W}^n$, that is, a component containing Cn vertices, $C > 0$ (cf. [21], where, however, the probability space differs slightly from ours). Starting up the process with one single vertex picked at random then actually yields a probability of hitting the giant component which is approximately equal to the proportional size of this set. Hence it should come as no surprise that $\bar{\tau}$ tends to the explosion probability ϑ as $\bar{a} \to 0$.

4. Application to epidemics. Turning to epidemics, we consider a population of n individuals where the ith individual has $\bar{D}_i$ acquaintances; otherwise, no regularity of the neighborhood structure is assumed. Take a random member $\bar{\mathscr{W}}$ of the set of graphs with vertex set $\mathscr{N}$ ($|\mathscr{N}| = n$) having $\bar{\mathbf{D}} = (\bar{D}_1, \ldots, \bar{D}_n)$ as degree sequence to represent the social network. Denote by $\mathscr{X}(t)$ and $\mathscr{Y}(t)$ the set of susceptible and infective individuals, respectively, at time t, $t = 0, 1, 2, \ldots$. A given individual who is infective at time t will become immune at time $t + 1$, and she will infect a given susceptible acquaintance with a fixed probability p, independently for distinct individuals. Thus, it is natural to *thin* the graph $\bar{\mathscr{W}}$, keeping a given edge of $\bar{\mathscr{W}}$ with probability p. This gives rise to a subgraph $\mathscr{W}$ of $\bar{\mathscr{W}}$ with mixed binomial variables D_i as degree variables:

$$\mathbf{P}(D_i = l \,|\, \bar{D}_i = k) = \binom{k}{l} p^l (1 - p)^{k-l}, \tag{1}$$

an edge between vertices i and j having the following interpretation: "if i becomes infected, then i will try to infect j, and vice versa." If we start up the process by putting $(\mathscr{X}(0), \mathscr{Y}(0)) = (\mathscr{N} \setminus \mathscr{A}, \mathscr{A})$, where $\mathscr{A}$ consists of a individuals picked at random, then evidently $(\mathscr{X}, \mathscr{Y})$ is equivalent to an exposure process on $\mathscr{W}$.

We wish to consider a sequence $(\mathscr{X}^n, \mathscr{Y}^n)$ of epidemic processes. Assume that the triangular array $\bar{D}_i^n$; $1 \le i \le n$, $n \ge 1$, satisfies (A1)–(A6), and denote the limiting variable by $\bar{D}$. Define D_i^n and D to be random variables derived from $\bar{D}_i^n$ and $\bar{D}$, respectively, by the thinning procedure above [cf. (1)], and, for each n, let $(\mathscr{X}^n, \mathscr{Y}^n)$ be an exposure process on the random graph $\mathscr{W}^n$ corresponding to $(D_1^n, \dots, D_n^n)$, with initial configuration $\mathscr{A}^n$. It is easily checked that the variables D_i^n; $1 \le i \le n$, $n \ge 1$, satisfy (A1)–(A6) (with limit D); thus, Theorems 1 and 2 may be applied. Note that

$$R_0 = p\bar{R}_0,$$
$$\varphi(z) = \bar{\varphi}(1 - p + pz),$$

where R_0 ($\bar{R}_0$) is the basic reproduction number and φ ($\bar{\varphi}$) is the probability generating function associated with D ($\bar{D}$). At the end of Section 5, we will show that if R_0 is above 1 at the start of the epidemic and if a large outbreak occurs, then R_0 will always be below 1 when the epidemic is over.

EXAMPLE 1. As a first example, consider the ordinary Reed–Frost epidemic process in a homogeneously mixing population of n individuals and with infection parameter $\bar{p}$. It is well known (see, e.g., [9]) that this process can be realized by invoking the classical $\mathscr{G}(n, \bar{p})$ random graph, that is, the random graph on n vertices with independent undirected links of probability $\bar{p}$ (cf. [13]). Indeed, by picking a vertices at random, running the exposure process $(\mathscr{X}, \mathscr{Y})$ on $\mathscr{G}(n, \bar{p})$ and taking cardinalities,

$$\big(X(t), Y(t)\big) = \big(|\mathscr{X}(t)|, |\mathscr{Y}(t)|\big), \qquad t \ge 0,$$

a process coinciding in law with the Reed–Frost process is obtained.

The degree variables D_i corresponding to the graph $\mathscr{G}(n, \bar{p})$ are binomially distributed with parameters $n - 1$ and $\bar{p}$. To translate to the present setting, we generate uniformly random members $\mathscr{W}$ of the set of graphs with degree sequence $(D_1, \dots, D_n)$ and run the exposure process on $\mathscr{W}$. We might as well let our infection probability p be equal to 1, since by tradition the edges of $\mathscr{G}(n, \bar{p})$ indicate links for transmission of the infection rather than social links. It may feel frustrating that the underlying probability space is not exactly the same for these two models. On the other hand, it is not obvious that the $\mathscr{G}(n, \bar{p})$ formulation is the superior one—it seems just as natural to first prescribe the degrees and then choose the graph according to the maximum entropy ("unknown = uniform") principle.

Take a sequence of epidemic processes indexed by n, putting $\bar{p} = \bar{p}_n = \lambda/n$, $\lambda > 0$, in order to keep the number of neighbors bounded as n grows. With D Poisson distributed with parameter λ, the conditions (A1)–(A6) are fulfilled so that the theorems apply. Let us announce the basic reproduction number R_0 and the asymptotic probability ϑ of a large outbreak ($a = 1$):

$$R_0 = \lambda, \qquad 1 - \vartheta = e^{-\lambda\vartheta},$$

by easy calculation.

EXAMPLE 2. In [14], the case with a constant number of acquaintances is investigated. Actually, the rules for the spread of infection are much more general than in the present work, but the conclusions are very similar to ours. Let k be a fixed positive integer and, for each n, put $\bar{D}_i^n = k$, $1 \le i \le n$. If the total degree $\sum_{i=1}^n \bar{D}_i^n$ is an odd number, pick a vertex j at random and add 1 to the number $\bar{D}_j^n$. The triangular array so obtained satisfies the conditions (A1)–(A6), and Theorem 1 ($a = 1$, p arbitrary) yields that $R_0 = (k-1)p$ and $\vartheta = 1 - (1 - p + ps)^k$, where s satisfies

$$s = (1 - p + ps)^{k-1}.$$

EXAMPLE 3. In the recent paper by Andersson and Britton [2], heterogeneity in epidemic models and its impact on the spread of infection is investigated. Some examples are considered where it turns out that, for a highly infectious disease, a homogeneous process renders a larger outbreak than the equivalent heterogeneous counterparts, while if the disease is less contagious, the maximal final size is obtained in a heterogeneous setup. This contradicts partly the general opinion that the size of an epidemic is always reduced when heterogeneities are introduced into the population.

Incidentally, our random graph epidemic model lends itself to such considerations, and the result is in accordance with the ones proved in [2]. Actually, here we are dealing with a population that is homogeneous by definition, since the degree variables are identically distributed, but the situation where the number of acquaintances is *fixed*, $\bar{D} = \bar{D}_0 \equiv k$, can obviously be regarded as the homogeneous extreme. Write $f(s) = 1 - p + ps$, where p is the probability of infection. In order to simplify the calculations somewhat, we imagine a limiting situation where the proportion $\bar{a}$ of initial infectives tends to zero. The final size proportion, $\bar{\tau}_0$ say, then satisfies $\bar{\tau}_0 = 1 - f^k(s_0)$, where $s_0 = f^{k-1}(s_0)$. We assume that $k \ge 3$; otherwise, $\bar{\tau}_0$ will always be zero irrespective of the value of p, since the basic reproduction number $R_0 = (k-1)p$ then keeps below 1. Let us perturbate $\bar{D}_0$ slightly. For given $\delta > 0$, we define $\bar{D} = \bar{D}_\delta$ to be a degree variable with

$$\begin{aligned} \mathbf{P}(\bar{D}_\delta = k) &= 1 - 2\delta, \\ \mathbf{P}(\bar{D}_\delta = k-1) &= \mathbf{P}(\bar{D}_\delta = k+1) = \delta. \end{aligned}$$

Then the corresponding final size proportion $\bar{\tau}_\delta$ satisfies

$$\bar{\tau}_\delta = 1 - f^k(s_\delta) - f^{k-1}(s_\delta)\big(1 - f(s_\delta)\big)^2\delta,$$

where

$$s_\delta = f^{k-1}(s_\delta) + f^{k-2}(s_\delta)\left[\frac{k-1}{k} - 2f(s_\delta) + \frac{k+1}{k}f^2(s_\delta)\right]\delta.$$

By simple but rather tedious algebraic manipulations, we find that

$$\bar{\tau}_0 - \bar{\tau}_\delta = \frac{f^{k-1}(s_0)(1-s_0)p^2}{1 - (k-1)f^{k-2}(s_0)p}\big(1 - s_0 - 2f^{k-1}(s_0)\big)\,\delta + o(\delta).$$

The leading term is equal to zero for $0 \le p \le 1/(k-1)$, since $s_0 = 1$ if the basic reproduction number $R_0 = (k-1)p$ is below 1. For p larger than $1/(k-1)$, the sign of $\bar{\tau}_0 - \bar{\tau}_\delta$ is determined by the sign of the expression $1 - s_0 - 2f^{k-1}(s_0)$. Using that $s_0 = f^{k-1}(s_0) = (1-p+ps)^{k-1}$, we see that this quantity increases with p, changing its sign at the point

$$p_c = \frac{3}{2}\left(1 - \frac{1}{\sqrt[k-1]{3}}\right).$$

[It is easily checked that indeed $p_c > 1/(k-1)$ for $k \ge 3$.] To conclude, this local analysis indicates that the homogeneous situation $\bar{D}_0$ yields the largest final size if and only if $p \ge p_c$.

5. Proofs of the results. First a few definitions. A *multigraph* is a collection of vertices and edges, where a vertex may be connected to itself (loop), and two given distinct vertices may be joined by more than one edge (multiple edges). Graphs without loops and multiple edges are henceforth called *simple*, in order to distinguish them from the other multigraphs. Let us describe the configuration model. In order to generate a random configuration with n vertices and fixed degree sequence $\mathbf{D} = (D_1, \ldots, D_n)$, we do the following:

1. form a set $\mathscr{L}$ containing D_i copies of the ith vertex, $1 \le i \le n$;
2. choose a random pairing of the elements of $\mathscr{L}$.

Each configuration corresponds to a multigraph whose edges are defined by the pairs above. It is clear that the vertices of the multigraph so obtained have the correct degrees. Also, since any simple graph with given degree sequence $\mathbf{D}$ can be represented by exactly $\prod_{i=1}^{n} D_i!$ configurations, it follows that all the simple graphs are equally probable in the set of multigraphs with degree sequence $\mathbf{D}$. The point is that random configurations are easy to work with, and results for simple graphs can often be inferred using corresponding results for random configurations.

Exposure process on a random configuration. Let us define the exposure process $(\mathscr{X}, \mathscr{Y})$ on a random configuration. A given vertex copy may be in one of three states, which we denote by *closed*, *open* and *discarded*, respectively. Intuitively, we will visit the vertex copies as time goes by. These are initially closed, but they are opened when visited and they are then discarded—see the algorithm below. A vertex is called *unexposed* if it is isolated or if all of its vertex copies are closed. Copies of the same vertex are said to be *associated*.

Now define $\mathscr{X}(t)$, $t \ge 0$, to be the set of unexposed vertices at time t. Also, let $\mathscr{Y}(t)$, $t \ge 1$, be the set of vertices that have remained unexposed exactly up to time $t-1$. The set $\mathscr{Y}(0)$ is chosen at random from the set of all vertices. We refer to the members of $\mathscr{Y}(t)$ as the *exposed* vertices at time t. These vertices enter a third state at the next time point, and can then be regarded as removed. The members of $\mathscr{X}(t)$ with degree k are collected in the set $\mathscr{X}_k(t)$, $k \ge 0$. Evidently, $\mathscr{X}_k(t) = \varnothing$ if $k \ge n$. We write

$$\mathbf{X}(t) = \big(X_0(t), X_1(t), \ldots\big) = \big(|\mathscr{X}_0(t)|, |\mathscr{X}_1(t)|, \ldots\big).$$

Finally, $V(t)$ is defined to be the total number of open vertex copies at time t, $t \geq 0$.

The dynamics are as follows: pick a vertices at random. These vertices may be isolated, and in this case nothing happens. Otherwise, we follow the algorithm below:

$t = 0$: open the vertex copies of the a vertices (all the other vertex copies are assumed to be closed);

$t \geq 1$: choose partners to the open copies from among open and closed copies. The members of these pairs may have closed associates. Open these associates while you discard the pairs.

The random pairing (or, rather, a part of it) is thus generated dynamically in time. Everything interesting happens along the borderline defined by the open copies, and the process stops when there are no such copies left. Figure 1 shows a realization of the process. Here $\mathcal{N} = \{a, b, \ldots, h\}$ and $\mathbf{D} =$

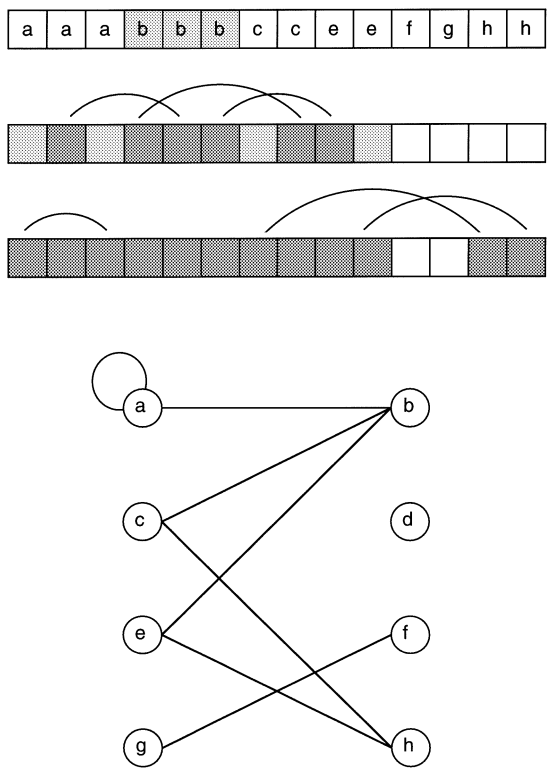

FIG. 1. *Realization of the exposure process and the underlying multigraph. White = closed; light gray = open; dark grey = discarded.*

$(3, 3, 2, 0, 2, 1, 1, 2)$ (vertex d is isolated). Also,

$$\begin{aligned} \mathscr{X}(0) &= \{a, c, d, e, f, g, h\}, & \mathscr{Y}(0) &= \{b\}, \\ \mathscr{X}(1) &= \{d, f, g, h\}, & \mathscr{Y}(1) &= \{a, c, e\}, \\ \mathscr{X}(2) &= \{d, f, g\}, & \mathscr{Y}(2) &= \{h\}. \end{aligned}$$

It is easy to verify that, in case the random configuration gives a simple graph $\mathscr{W}$ without loops and multiple edges, the process coincides with the exposure process of Section 2. Also, the process $(\mathbf{X}(t), V(t))$ is Markov, since the transition rule above is fully specified if we know the number of closed copies belonging to the various vertices together with the overall number of open copies.

For a given n-tuple $\mathbf{D}^n = (D_1^n, \ldots, D_n^n)$, pick a random configuration (i.e., a multigraph) $\tilde{\mathscr{W}}^n$ with n vertices and with $\mathbf{D}^n$ as degree sequence. We then take a set $\mathscr{A}^n$ of initially exposed vertices and run the exposure process $(\mathscr{X}^n, \mathscr{Y}^n)$ on $\tilde{\mathscr{W}}^n$. Remember that the triangular array $\mathscr{D} = \{D_i^n; 1 \le i \le n, n \ge 1\}$ is defined on the probability space $(\Omega_1, \mathscr{F}_1, \mathbf{P}_1)$. If we write $X_k^n(0) = \sum_{i=1}^n J_{ki}^n$, where

$$J_{ki}^n = \begin{cases} 1, & \text{if } D_i^n = k, \\ 0, & \text{otherwise,} \end{cases}$$

then using the assumptions (A1), (A3), (A4) and (A6) and applying a standard Chebyshev argument, we see that $X_k^n(0)/n \to \lambda_k$ in distribution.

By Skorokhod's representation theorem, there exists a probability space $(\tilde{\Omega}_1, \tilde{\mathscr{F}}_1, \tilde{\mathbf{P}}_1)$ and a sequence of variables defined on this space that are distributed like the variables $X_k^n(0)/n$ and that converge to λ_k almost surely $[\tilde{\mathbf{P}}_1]$. For simplicity, we keep the old notation for these new variables. It is legitimate to change the sample space in this way, since we are aiming at weak convergence results anyway. Note that $\mathbf{X}^n(0)/n \to \boldsymbol{\lambda}$ almost surely $[\tilde{\mathbf{P}}_1]$. In the sequel, it will often be convenient to fix a member $\mathscr{D}$ of the convergence set, indicating the corresponding conditional quantities with a subscript $\mathscr{D}$. Assume that the probability space $(\tilde{\Omega}, \tilde{\mathscr{F}}, \tilde{\mathbf{P}})$ holds all of the variables above.

Occasionally, the number $U^n(t)$ of closed copies and the proportion $P^n(t)$ of closed copies among copies that are either closed or open will be needed:

$$\begin{aligned} U^n(t) &= \sum_{k=1}^{\infty} k X_k^n(t), \\ P^n(t) &= \frac{U^n(t)}{U^n(t) + V^n(t)}. \end{aligned}$$

Proof of Theorem 1 for random configurations. The proof will be performed for the case $a = 1$, the general case being similar. Our purpose is to show that V^n converges in distribution to a Galton–Watson process V with initial distribution $\boldsymbol{\lambda}$ and offspring distribution $\hat{\boldsymbol{\lambda}}$. We then note that $V^n(t) - Y^n(t+1)$ tends to zero almost surely for each $t \ge 0$. Together with the fact that $Y^n(0) = a = 1$ for each n, this will give the desired result.

By the definition of V^n,

$$\tilde{\mathbf{P}}_{\mathscr{G}}(V^n(0)=k)\to\lambda_k \quad \text{as } n\to\infty.$$

Now consider the conditional probability

$$\tilde{\mathbf{P}}_{\mathscr{G}}\big(V^n(t+1)=v_{t+1}\,|\,\mathbf{X}^n(t)=\mathbf{x},\,V^n(t)=v\big).$$

Put $U^n(t)=u=\sum_{k=1}^{\infty}kx_k$ and fix one of the v open vertex copies. With probability

$$\frac{(k+1)X^n_{k+1}(t)}{U^n(t)+V^n(t)-1}=\frac{(k+1)x_{k+1}}{u+v-1}, \tag{2}$$

this copy is paired with some closed copy having k associates. Since $X^n_{k+1}(0)/n\to\lambda_{k+1}$, it follows readily that $X^n_{k+1}(t)/n\to\lambda_{k+1}$ almost surely, and likewise $U^n(t)/n\to\sum_{l=1}^{\infty}l\lambda_l$ almost surely. Thus the probability in (2) converges to

$$\frac{(k+1)\lambda_{k+1}}{\sum_{l=1}^{\infty}l\lambda_l}=\hat{\lambda}_k.$$

Now fix *two* of the v open copies. Then one checks that, with a probability tending to 1 as $n\to\infty$, these open copies are paired with closed copies belonging to *distinct* vertices. Thus, by induction,

$$\mathscr{L}_{\mathscr{G}}\big(V^n(t+1)\,|\,\mathbf{X}^n(t)=\mathbf{x},\,V^n(t)=v\big)\to\mathscr{L}\Big(\sum_{m=1}^{v}A_m\Big),$$

where A_m are independent with common distribution $\hat{\boldsymbol{\lambda}}$, and we have proved that $V^n(t)\to V(t)$ in distribution for each fixed $t\ge 0$.

Also, these distinct vertices form precisely the set $\mathscr{Y}^n(t+1)$, by construction. Hence, $V^n(t)-Y^n(t+1)\to 0$ almost surely for each $t\ge 0$.

Proof of Theorem 2 for random configurations. We wish to prove a law of large numbers for the process $(\mathbf{X}^n/n,\,V^n/n)$; this will give the first part of Theorem 2, since $X^n(t)=\sum_{k=0}^{\infty}X^n_k(t)$ and $Y^n(t)=X^n(t-1)-X^n(t)$. According to the assumption $a^n/n\to\bar{a}>0$,

$$\frac{1}{n}X^n_k(0)\to(1-\bar{a})\lambda_k,$$
$$\frac{1}{n}V^n(0)\to\bar{a}\sum_{k=1}^{\infty}k\lambda_k,$$

in probability as $n\to\infty$. Fix $X^n_k(t)$, $k\ge 0$, and $V^n(t)$. Also write $x_k=X^n_k(t)/n$, $v=V^n(t)/n$, $u=U^n(t)/n$ and $p=P^n(t)/n$. Fix an unexposed vertex of degree $k\ge 1$. Define J^n_l to be equal to 1 if the lth vertex copy of this vertex is paired with an open copy, and 0 otherwise, $1\le l\le k$. Then it is easily shown that

$$\tilde{\mathbf{P}}_{\mathscr{G}}(J^n_l=1)=\frac{v}{u+v-1/n}\to 1-p$$

as $n \to \infty$, and that $\widetilde{\mathrm{Cov}}_{\mathscr{G}}(J_l^n, J_{l'}^n) = O(1/n)$ if $l \neq l'$. Hence, $B^n = \sum_{l=1}^k J_l^n$ converges in distribution to a random variable B that is binomially distributed with parameters k and $1-p$.

Note that we obtain zero new open copies if $B^n = 0$, and otherwise $k-j$ new open copies if $B^n = j$, $1 \le j \le k$; hence, the asymptotic expected number of new open copies is given by

$$\begin{aligned}\sum_{j=1}^{k}(k-j)\pi(j) &= \sum_{j=0}^{k}(k-j)\pi(j) - k\pi(0)\\ &= k-(1-p)k-kp^k\\ &= kp(1-p^{k-1}),\end{aligned}$$

where $(\pi(0), \ldots, \pi(k))$ is the distribution of B. It follows that

$$\begin{aligned}&\tilde{E}_{\mathscr{G}}\left(\frac{1}{n}V^n(t+1)\,\middle|\,\mathbf{X}^n(t)=\mathbf{x}, V^n(t)=v\right)\\ &\quad\to \sum_{k=1}^{\infty} kp(1-p^{k-1})x_k,\end{aligned}$$

as $n \to \infty$. Also, the probability that our vertex will remain unexposed at time $t+1$ is given by $\tilde{\mathbf{P}}_{\mathscr{G}}(B^n = 0) \to \pi(0) = p^k$, so that

$$\tilde{E}_{\mathscr{G}}\left(\frac{1}{n}X_k^n(t+1)\,\middle|\,\mathbf{X}^n(t)=\mathbf{x}, V^n(t)=v\right) \to p^k x_k,$$

as $n \to \infty$. Finally, we write V^n and X_k^n as sums of indicator functions and note that the covariances of these indicators are $O(1/n)$ to get

$$\widetilde{\mathrm{Var}}_{\mathscr{G}}\left(\frac{1}{n}V^n(t+1)\,\middle|\,\mathbf{X}^n(t)=\mathbf{x}, V^n(t)=v\right) \to 0$$

and

$$\widetilde{\mathrm{Var}}_{\mathscr{G}}\left(\frac{1}{n}X_k^n(t+1)\,\middle|\,\mathbf{X}^n(t)=\mathbf{x}, V^n(t)=v\right) \to 0,$$

as $n \to \infty$, which proves the convergence in probability to the following deterministic process:

$$\begin{aligned}x_k(t+1) &= p^k(t)x_k(t),\\ v(t+1) &= \sum_{k=0}^{\infty} kp(t)\big(1-p^{k-1}(t)\big)x_k(t),\end{aligned} \tag{3}$$

where

$$\begin{aligned}u(t) &= \sum_{k=0}^{\infty} kx_k(t),\\ p(t) &= \frac{u(t)}{u(t)+v(t)}.\end{aligned}$$

The initial conditions are given by

$$x_k(0) = (1-\bar{a})\lambda_k,$$
$$v(0) = \bar{a}\sum_{k=0}^{\infty} k\lambda_k.$$

Also note that $u(0) = (1-\bar{a})\sum_k k\lambda_k$ and $p(0) = 1-\bar{a}$.

Now for the proof of the second part of Theorem 2. In order to determine $\lim_{t\to\infty}\sum_k x_k(t)$, we essentially follow [14]. Define $G_t(z) = \sum_k x_k(t)z^k$. Then, by (3), we have the following fundamental recurrence relation:

$$G_{t+1}(z) = \sum_k p^k(t)x_k(t)z^k = G_t\big(p(t)z\big),$$

hence $G_t(z) = G_0(s(t)z)$, where $s(t) = \prod_{t'=0}^{t-1} p(t')$ if $t \geq 1$, $s(0) = 1$. Also note that

$$G_t'(z) = \frac{dG_t(z)}{dz} = s(t)G_0'\big(s(t)z\big). \tag{4}$$

By heavily using (4), we next find a nice recurrence relation for $s(t)$. Since

$$u(t+1) = \sum_k kx_k(t+1) = G_{t+1}'(1) = s(t+1)G_0'\big(s(t+1)\big)$$

and

$$\begin{aligned} v(t+1) &= p(t)\Big[\sum_k kx_k(t) - \sum_k kp^{k-1}(t)x_k(t)\Big] \\ &= p(t)\big[G_t'(1) - G_t'(p(t))\big] \\ &= s(t+1)\big[G_0'(s(t)) - G_0'(s(t+1))\big], \end{aligned}$$

it follows that

$$p(t+1) = \frac{u(t+1)}{u(t+1)+v(t+1)} = \frac{G_0'(s(t+1))}{G_0'(s(t))}.$$

Finally, by cancellation of factors,

$$s(t+1) = p(0)\frac{G_0'(s(t))}{G_0'(s(0))} = (1-\bar{a})\frac{G_0'(s(t))}{G_0'(1)}, \tag{5}$$

which is the promised equation. The sequence $s(t)$ is obviously nonnegative and decreasing; hence, we may let $t\to\infty$ and write $s = \lim_{t\to\infty} s(t)$. Taking limits in (5) yields

$$s = (1-\bar{a})\frac{G_0'(s)}{G_0'(1)}.$$

The theorem now follows immediately by noting that

$$\lim_{t\to\infty}\sum_k x_k(t) = \lim_{t\to\infty} G_t(1) = G_0(s),$$

and that $G_0(z) = (1-\bar{a})\varphi(z)$.

From random configurations to random graphs. It is shown in [20] that, for a fixed triangular array $\mathscr{D}$, if the maximum degree $M^n = \max_{1\le i\le n} D_i^n$ is $o\left(n^{1/4}\right)$, then the set of simple graphs forms a nonnegligible subset of the set of multigraphs $\tilde{\mathscr{W}}^n$, at least in the limit:

$$\tilde{\mathbf{P}}\left(\tilde{\mathscr{W}}^n \text{ simple}\right) \to \rho > 0 \quad \text{as } n \to \infty.$$

In our setting, this means we have to show that there exists $\varepsilon > 0$ such that

$$\tilde{\mathbf{P}}\left(M^n \le Cn^{1/4-\varepsilon}\right) \to 1 \quad \text{as } n \to \infty. \tag{6}$$

We proceed to show (6). For fixed n, the degree variables $D_1^n, \dots, D_n^n$ are identically distributed; thus,

$$\begin{aligned}\tilde{\mathbf{P}}\left(M^n > c\right) &= \tilde{\mathbf{P}}\left(\bigcup_{i=1}^{n}\left\{D_i^n > c\right\}\right)\\ &\le n\,\tilde{\mathbf{P}}(D_1^n > c).\end{aligned}$$

Put $c = c^n = Cn^{1/4-\varepsilon}$ and note that it is enough to show that the last probability above is $o(1/n)$. For this we use Markov's inequality together with (A5):

$$\tilde{\mathbf{P}}(D_1^n > Cn^{1/4-\varepsilon}) \le \frac{E((D_1^n)^{4+\delta})}{C^{4+\delta}n^{(1/4-\varepsilon)(4+\delta)}} = o(1/n),$$

if $\varepsilon > 0$ is chosen small enough. Equation (6) follows. (Note that, as pointed out in [20], the condition on the maximum degree M^n is sufficient but certainly not necessary. We are not aware of any later results where this condition is weakened.)

Theorem 1 for random graphs now follows easily from Theorem 1 for random configurations. Indeed, by the branching approximation result, the probability that the set $\mathscr{Y}^n(0) \cup \cdots \cup \mathscr{Y}^n(t)$ is free from loops and multiple edges tends to 1 as $n \to \infty$. Hence, the value taken by $Y^n(t)$ is asymptotically independent of whether the entire graph $\tilde{\mathscr{W}}^n$ is simple or not. In other words,

$$\tilde{\mathbf{P}}\left(Y^n(t) = k \,\middle|\, \tilde{\mathscr{W}}^n \text{ simple}\right) - \tilde{\mathbf{P}}\left(Y^n(t) = k\right) \to 0 \quad \text{as } n \to \infty.$$

The corresponding deduction for Theorem 2 is even simpler. It suffices to note that

$$\tilde{\mathbf{P}}\left(\left|\frac{X^n(t)}{n} - \bar{x}(t)\right| + \left|\frac{Y^n(t)}{n} - \bar{y}(t)\right| > \varepsilon\right) \to 0 \quad \text{as } n \to \infty$$

implies

$$\tilde{\mathbf{P}}\left(\left|\frac{X^n(t)}{n} - \bar{x}(t)\right| + \left|\frac{Y^n(t)}{n} - \bar{y}(t)\right| > \varepsilon \,\middle|\, \tilde{\mathscr{W}}^n \text{ simple}\right) \to 0$$

as $n \to \infty$.

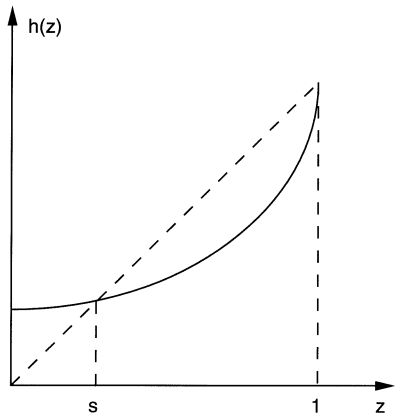

FIG. 2. *The quantity s satisfies $h'(s) < h(s)/s$.*

Basic reproduction number. Finally, we wish to show that two successive large epidemics can never occur in a closed population, since a major outbreak always brings the basic reproduction number below 1. Consider the limiting situation $\bar{a} \to 0$. The basic reproduction number is given by

$$R_0 = \frac{\sum_{k=0}^{\infty} k(k+1)\lambda_{k+1}}{\sum_{l=0}^{\infty} l\lambda_l} = \frac{\varphi''(1)}{\varphi'(1)}.$$

Assume $R_0 > 1$. By letting t tend to infinity in (3), we see that after a large outbreak, the basic reproduction number is changed to

$$R_0^* = \frac{\sum_{k=0}^{\infty} k(k+1)s^{k+1}\lambda_{k+1}}{\sum_{l=0}^{\infty} ls^l\lambda_l} = s\frac{\varphi''(s)}{\varphi'(s)},$$

where s solves the equation $s = \varphi'(s)/\varphi'(1)$. In order to show that $R_0^* < 1$, we put $h(z) = \varphi'(z)$. Since s is the nontrivial solution to the equation

$$\frac{h(s)}{s} = \frac{h(1)}{1},$$

comparing slopes at the point s in Figure 2 reveals that $h'(s) < h(s)/s$, that is, $R_0^* < 1$.

6. Short discussion and open problems. Even though the model of this work is superior to the classical Reed–Frost process when it comes to heterogeneous mixing, it is still a toy model far too simple to have any practical implications. Therefore, it is essential to proceed to study various kinds of generalizations. For instance, it would probably be fairly straightforward, even though notationally inconvenient, to adopt the model to a multitype population setting; here we choose, however, to bring out possible generalizations in two other directions.

First, it would be interesting to study continuous-time epidemic models (such as the general epidemic) on a random graph. In such a model, an infected individual typically remains infective for a time period that could have some arbitrary distribution, and during that time tries to infect a given acquaintance according to a time-homogeneous Poisson process. It is then appealing to try to adopt the techniques of [14] to a finite population situation, but it is not evident how to proceed. However, if we are only interested in the final size of the epidemic and not the evolution in time, then some results are certainly within reach, since we may create a directed graph indicating infections on top of the graph describing the acquaintance structure and calculate component sizes of this new graph. More precisely, each individual that becomes infected generates a value P from some distribution on $[0, 1]$ and then infects a given susceptible acquaintance with probability P. In that case, we draw an arrow from the infective to the susceptible friend. The flow of the epidemic is traced by simply following the arrows. Different choices of the distribution of P give the final epidemic size for many interesting continuous-time epidemic processes, including the general epidemic model (cf. [3]).

Another serious drawback of the model under consideration is that the possibility of having small social groups with complete mixing is not taken into account. When we pick a graph at random from the set of all graphs with prescribed degree sequence, the number of short cycles (such as triangles) will with overwhelming probability be very small; in fact, this is the reason why our technique of proof works. In reality, there are many triangles and other short cycles in a social network. Of course, for a general network, it is impossible to make any progress at all in finding analytical expressions, but nevertheless there are some points to be made here. First of all, it is clear that, in some sense, our model provides *overestimates* of the component sizes for structures with the same degrees but with short cycles present. Also, it is not unreasonable that the vertices of a typical social network may be lumped together in small groups, so that when the various groups are identified, the resulting graph of "super vertices" fits nicely into our original setting (see Fig. 3). Instead of choosing among graphs with given degrees according to the uniform measure, one should try to find a feasible way to reward graphs containing a certain amount of triangles and then derive connectivity properties of these graphs.

In this connection, let us finally discuss the recent model of Rand [22]. In [22], a social network similar to the structure of the present paper is considered, with the important difference that there is a fixed probability that two friends of a given individual are themselves acquainted with each other. Then a general epidemic is run on this neighborhood structure and a rather simple system of ordinary differential equations, with the number of *pairs* of individuals of the various types (susceptible–susceptible, susceptible–infective, and so on) as state variables, is derived in a heuristic manner. Even though these equations are to be treated merely as crude approximations of the real dynamics, the modelling approach is indeed very interesting and could show to be extremely fruitful in the future.

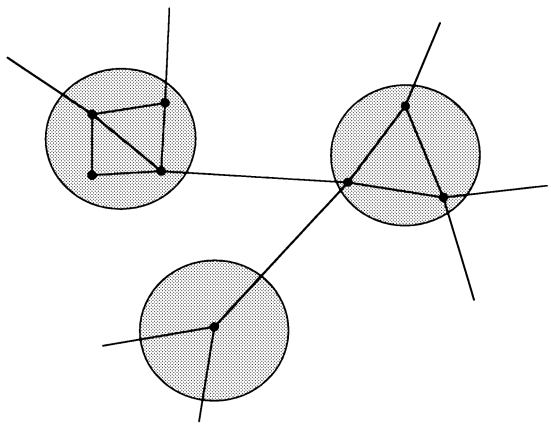

FIG. 3. *Lumping together vertices of a social network.*

REFERENCES

[1] ANDERSSON, H. (1997). Epidemics in a population with social structures. *Math. Biosci.* **140** 79–84.

[2] ANDERSSON, H. and BRITTON, T. (1998). Heterogeneity in epidemic models and its effect on the spread of infection. *J. Appl. Probab.* To appear.

[3] VON BAHR, B. and MARTIN-LÖF, A. (1980). Threshold limit theorems for some epidemic processes. *Adv. in Appl. Probab.* **12** 319–349.

[4] BAILEY, N. T. J. (1975). *The Mathematical Theory of Infectious Diseases and Its Applications*, 2nd ed., Griffin, London.

[5] BALL, F. (1983). A threshold theorem for the Reed–Frost chain-binomial epidemic. *J. Appl. Probab.* **20** 153–157.

[6] BALL, F. (1983). The threshold behavior of epidemic models. *J. Appl. Probab.* **20** 227–241.

[7] BALL, F. and DONNELLY, P. (1995). Strong approximations for epidemic models. *Stochastic Process. Appl.* **55** 1–21.

[8] BALL, F., MOLLISON, D. and SCALIA-TOMBA, G. (1997). Epidemics with two levels of mixing. *Ann. Appl. Probab.* **7** 46–89.

[9] BARBOUR, A. D. and MOLLISON, D. (1990). Epidemics and random graphs. *Stochastic Processes in Epidemic Theory*. *Lecture Notes in Biomath.* **86** 86–89. Springer, Berlin.

[10] BARTLETT, M. S. (1955). *An Introduction to Stochastic Processes*. Cambridge Univ. Press.

[11] BENDER, E. A. and CANFIELD, E. R. (1978). The asymptotic number of labelled graphs with given degree sequences. *J. Combin. Theory Ser. A* **24** 296–307.

[12] BLANCHARD, PH., BOLZ, G. F. and KRÜGER, T. (1990). Modelling AIDS-epidemics or any venereal disease on random graphs. *Stochastic Processes in Epidemic Theory*. *Lecture Notes in Biomath.* **86** 104–117. Springer, Berlin.

[13] BOLLOBÁS, B. (1985). *Random Graphs*. Academic Press, New York.

[14] DIEKMANN, O., DE JONG, M. C. M. and METZ, J. A. J. (1998). A deterministic epidemic model taking account of repeated contacts between the same individuals. *J. Appl. Probab.* **35** 462–468.

[15] DURRETT, R. and LEVIN, S. A. (1994). Stochastic spatial models: a user's guide to ecological applications. *Philos. Trans. Roy. Soc. London Ser. B* **343** 329–350.

[16] ETHIER, S. N. and KURTZ, T. G. (1986). *Markov Processes, Characterization and Convergence*. Wiley, New York.

[17] HARRIS, T. E. (1963). *The Theory of Branching Processes*. Dover, New York.

[18] KENDALL, D. G. (1956). Deterministic and stochastic epidemics in closed populations. *Proc. Third Berkeley Symp. Math. Statist. Probab.* **4** 149–165. Univ. California Press, Berkeley.

[19] MARTIN-LÖF, A. (1986). Symmetric sampling procedures, general epidemic processes and their threshold limit theorems. *J. Appl. Probab.* **23** 265–282.

[20] MCKAY, B. D. (1985). Asymptotics for symmetric 0–1 matrices with prescribed row sums. *Ars Combin.* **19A** 15–25.

[21] MOLLOY, M. and REED, B. (1995). A critical point for random graphs with a given degree sequence. *Random Structures Algorithms* **6** 161–179.

[22] RAND, D. (1997). Correlation equations and pair approximations for spatial ecologies. In *Theoretical Ecology* **2** (J. McGlade, ed.). Blackwell, Malden, Massachusetts.

[23] SCALIA-TOMBA, G. (1985). Asymptotic final size distribution for some chain-binomial processes. *Adv. in Appl. Probab.* **17** 477–495.

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