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Solution of an infection model near threshold

David A. Kessler* and Nadav M. Shnerb†
Department of Physics, Bar-Ilan University, Ramat-Gan, IL52900 Israel
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We study the susceptible-infected-recovered model of epidemics in the vicinity of the threshold infectivity. We derive the distribution of total outbreak size in the limit of large population size N. This is accomplished by mapping the problem to the first passage time of a random walker subject to a drift that increases linearly with time. We recover the scaling results of Ben-Naim and Krapivsky that the effective maximal size of the outbreak scales as $N^{2/3}$, with the average scaling as $N^{1/3}$, with an explicit form for the scaling function.

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Understanding the spread of an epidemic is, of course, of major importance for the fight against infectious diseases. Of particular importance is the case where novel pathogens, such as the instigators of SARS, HIV, or avian flu, appear in human populations and spread unchecked in the absence of acquired immunity. Since many of the known infectious diseases, both old and new, are strongly related to those already existing in animals, the common hypothesis is that some mutants of the wild type have crossed the barrier between their natural reservoir and the human population [1]. This "zoonosis" scenario involves repeated transfer of subcritical pathogens from the animal reservoir to a human host, followed by subsequent infections in the human population during which a mutation eventually takes place, turning the disease supercritical [2]. Thus, the study of infection models close to criticality is extremely significant for a deeper understanding of this process, aiming ultimately at the prevention of the spread of new, often dangerous, diseases.

Recently, Ben-Naim and Krapivsky [3] (BN-K) studied the statistics of the size of an epidemic in the susceptible-infected-recovered (SIR) model [4–6] when the infectivity is near its threshold value. When the infectivity is below threshold, an outbreak quickly dies out, infecting some finite number of individuals, essentially independent of the population size. Above the threshold, the total average number of affected individuals reaches a finite fraction of the population. BN-K found that at threshold, the total average number of affected individuals is proportional to $N^{1/3}$, for large N, and that there are essentially no outbreaks which infect more than of order $N^{2/3}$ victims. While presenting an argument justifying these scaling laws, no analytic calculations for the distribution of outbreak sizes was given. In this Rapid Communication, we present an exact formula for this distribution, in the limit of large population sizes, which exhibits the scaling properties found by BN-K. This calculation involves solving an auxiliary problem, namely, the first-passage time statistics [7] for a random walker released at $x=1$ to be absorbed at the origin, given a small leftward drift, which increases in magnitude linearly in time. This problem is one of the few such problems with time-dependent forcing [8] for which an analytic solution is available, and so is of independent interest.

*kessler@dave.ph.biu.ac.il
†shnerbn@mail.biu.ac.il

We begin with a description of the SIR model. The N individuals in the population are divided into three subclasses: the susceptible pool, of size S; the infected (and infectious) class, of size I; and those recovered (and no longer infectible), of size R, with $N=S+I+R$. The disease is transmitted from an infected individual to a susceptible one with rate α/N, so that

$$(S,I,R) \xrightarrow{\alpha SI/N} (S-1,I+1,R). \tag{1}$$

Infected individuals recover with a rate β as follows:

$$(S,I,R) \xrightarrow{\beta I} (S,I-1,R+1). \tag{2}$$

Of primary interest is the case where initially $S=N-1$, $I=1$, $R=0$, so that the outbreak is sparked by a single infected individual. The outbreak terminates when the last infected individual recovers, and I returns to 0.

This stochastic process is traditionally approximated (for large populations) by the classic SIR rate equations

$$\dot{S} = -\frac{\alpha}{N}SI,$$

$$\dot{I} = \frac{\alpha}{N}SI - \beta I,$$

$$\dot{R} = \beta I. \tag{3}$$

Since S decreases monotonically, these equations are easiest dealt with by eliminating the time and considering $dI(S)/dS$, which is obtained by dividing the second rate equation by the first as follows:

$$\frac{dI}{dS} = -1 + \frac{N}{R_0 S}, \tag{4}$$

with the solution

$$I = N - S + \frac{N}{R_0}\ln[S/(N-1)], \tag{5}$$

where we have introduced the traditional parameter $R_0 \equiv \alpha/\beta$, equal to the mean number of primary infections caused in a large population of susceptibles by an infected individual. It is clear that if $R_0 < N/(N-1) \approx 1$, the rate equation predicts that the number of infected individuals decreases monotonically in time (decreasing S), whereas if R_0 is greater than this threshold, the number of infected individuals first rises, and as S decreases, eventually N/S rises above R_0 and I falls until it hits 0 at $S_f=(1-r)N$, where the fractional size of the epidemic satisfies

$$r+\exp(-R_0 r)=1. \tag{6}$$

Thus at the classical level, $R_0=1$ marks the threshold between an infection that infects a finite percentage of the population and those that fail to spread.

To study the stochastic process at large N, we adopt a similar strategy and eliminate time, focusing solely on the transitions between states. We characterize the system by the number of transitions the system has undergone. In each transition the number of infected individuals either rises or falls by one, so that I undergoes a kind of random walk. After T transitions, S and R are completely specified by T and I, with, for example,

$$S=N-\frac{1}{2}(T+I+1). \tag{7}$$

The probability of an upward transition is $p_+=R_0S/(R_0S+N)$, whereas the probability of a downward transition is $p_-=1-p_+$. These probabilities are unequal and depend on I and T, so that the walk is biased, with a "time-" and space-dependent drift. (From here on, we will colloquially refer to T as time, and trust this will not lead to confusion). The form of these probabilities simplify at threshold, $R_0=1$, where as we shall see, $N-S$ and I are both much smaller than N. Then,

$$p_\pm \approx \frac{1}{2} \mp \frac{1}{8N}(T+I), \tag{8}$$

where T is assumed large enough that we can ignore the 1. Thus, the drift at threshold is very weak.

This formulation immediately gives the well-known answer for an infinite population, where the bias term vanishes and we have a simple random walk starting at 1 with a trap at the origin. The distribution of first-passage times is [7]

$$P(T=2k+1)=2^{-2k-1}\left[\binom{2k}{k}-\binom{2k}{k+1}\right], \tag{9}$$

which for large T becomes

$$P(T=2k+1)\approx \frac{1}{\sqrt{4\pi k^3}}. \tag{10}$$

We now study how the bias, resulting from the reduction of the susceptible pool with time, modifies this answer.

It is straightforward to generate the discrete-time master equation for our biased random walk. Since the bias is very weak, however, it is only effective at large times, and we are justified in passing to the Fokker-Planck equation for the distribution $P(I)$ as follows:

$$\frac{\partial}{\partial T}P(I,T)=\frac{1}{2}\frac{\partial^2}{\partial I^2}P+\frac{1}{4N}\frac{\partial}{\partial I}[(T+I)P]. \tag{11}$$

One final simplification is to realize that the time-dependent drift is more effective than the spatially dependent drift, and so the latter may be dropped. The argument is straightforward: The typically "length" scale I is proportional to $T^{1/2}$. Thus, the time-dependent drift is relevant when $T^{-1}\sim T^{1/2}/N$, or $T\sim N^{2/3}$. The spatially dependent drift become effective only when $T^{-1}\sim 1/N$ or $T\sim N$, much later than the time-dependent drift and so can be neglected.

Thus the equation we need to solve is

$$\frac{\partial P}{\partial T}=\frac{1}{2}\frac{\partial^2 P}{\partial I^2}+\frac{T}{4N}\frac{\partial P}{\partial I}. \tag{12}$$

This equation is difficult to treat in its current form, since it is not separable, but becomes so if we define

$$P \equiv e^{-IT/4N-T^3/(96N^2)}\psi, \tag{13}$$

so that

$$\frac{\partial \psi}{\partial T}=\frac{1}{2}\frac{\partial^2\psi}{\partial I^2}+\frac{I}{4N}\psi, \tag{14}$$

with the boundary conditions $\psi(0,T)=0$, $\psi(I,0)=\delta(I-1)$. We can eliminate N from the equation by the scaling $T\equiv 2a^2\tilde{T}$, $I\equiv a\tilde{I}$, with $a=(2N)^{1/3}$, resulting in (after dropping the tildes)

$$\frac{\partial \psi}{\partial T}=\frac{\partial^2\psi}{\partial I^2}+I\psi, \tag{15}$$

with $\psi(I,0)=\delta(I-1/a)/a$. The operator on the right-hand side has an spectrum unbounded from above, so we need to regularize the problem by imposing an absorbing wall at some large L, which we will remove to infinity at the end. Clearly, introducing such a wall in the original equation for P has no significant effect, so it cannot materially affect our calculation in terms of ψ. With this regularization, the right-hand operator has a well-defined discrete spectrum, with eigenvalues E_n and normalized eigenfunctions ϕ_n. In terms of this, the flux of ψ to the trap at the origin is given by

$$\mathcal{F}_\psi=\frac{1}{2}\left.\frac{\partial\psi}{\partial I}\right|_{I=0}=\frac{1}{2a}\sum_n \phi_n'(0)\phi_n'\left(\frac{1}{a}\right)e^{E_nT} \approx \frac{1}{2a^2}\sum_n(\phi_n'(0))^2e^{E_nT}. \tag{16}$$

The eigenfunctions ϕ_n are given by

$$\phi_n(I)=A_n\,\mathrm{Ai}(-x+E_n)+B_n\,\mathrm{Bi}(-x+E_n). \tag{17}$$

The condition $\phi_n(0)=0$ implies that

$$B_n=-A_n\,\mathrm{Ai}(E_n)/\mathrm{Bi}(E_n), \tag{18}$$

and so, given that the Wronskian of Ai and Bi is $1/\pi$,

$$\phi_n'(0)=-A_n/(\pi\mathrm{Bi}(E_n)). \tag{19}$$

The normalization condition is

$$1 = \int_0^L \phi_n^2(I)dI = [\phi_n'^2 + (x-E)\phi_n^2]_0^L$$
$$= [(\phi_n'(L))^2 - (\phi_n'(0))^2] \approx \frac{(A_n^2+B_n^2)L^{1/2}}{\pi}, \tag{20}$$

where we have used the fact that L is large to approximate Ai and Bi by their asymptotic expansions for large negative arguments [9]. The density of states is easily calculated from these expansions to be

$$\frac{dn}{dE} \approx \frac{L^{1/2}}{\pi}. \tag{21}$$

We thus have, taking away the cutoff,

$$\mathcal{F}_\psi \approx \frac{1}{2\pi^2 a^2}\int_{-\infty}^{\infty} \frac{dE}{\mathrm{Ai}^2(E)+\mathrm{Bi}^2(E)} e^{ET}. \tag{22}$$

Translating back to the original units and P, this gives our major result for the probability density of extinction of the epidemic at transition T, with $S=N-T/2$ susceptible individuals left, so that $n=T/2$ individuals in all have been infected, as follows:

$$P(n) = \frac{e^{-n^3/(12N^2)}}{\pi^2 a^3}\int_{-\infty}^{\infty} \frac{dE}{\mathrm{Ai}^2(E)+\mathrm{Bi}^2(E)} e^{En/a^2}. \tag{23}$$

The first point to note is that this result satisfies the scaling behavior claimed by BN-K, namely, $P(n)=N^{-1}f(n/N^{2/3})$, so that, in particular, the average epidemic size scales as $\bar{n} \sim N^{1/3}$. To understand our result in more depth, we compute its asymptotic behavior, first for small n. In this limit, the integral is dominated by the integrand at large negative E, so that

$$P(n) \approx \frac{1}{\pi^2 a^3}\int_{-\infty}^{0} \pi(-E)^{1/2} e^{En/(a^2)} = \frac{1}{\sqrt{4\pi n^3}}, \tag{24}$$

as it should, since the drift is not relevant for small n. For large n, the integral is dominated by positive E's of order n^2. There Bi is exponentially larger than Ai, and the integral becomes

$$P(n) \approx \frac{1}{\pi^2 a^3}\int_{-\infty}^{\infty} \pi E^{1/2} e^{-4/3E^{3/2}+En/a^2} dE$$
$$\approx \frac{1}{8\sqrt{\pi}N^2} n^{3/2} e^{-n^3/(16N^2)}. \tag{25}$$

Thus, $P(n)$ is sharply cut off for $n \gg O(N^{2/3})$ in accord with the simulations of BN-K. In Fig. 1, we graph $P(n)$, together with the asymptotic formulas for small and large T. Also displayed is the exact solution of the full master equation for $N=10^3$. We see that indeed the finite systems converge nicely to the scaling limit, with slower convergence at very small n, where the discreteness of n is relevant, and at the largest n, where our dropped spatially dependent bias plays a detectable role.

It is straightforward to extend our solution to the near-threshold case, where $R_0=1+\Delta$, $|\Delta| \ll 1$. This introduces an additional constant bias to the problem. Equation (14) remains unchanged, where now ψ is related to P by

$$P \equiv e^{-[I(T-2\Delta N)/4N]-([(T-2\Delta N)^3-(2\Delta N)^3]/96N^2)}\psi, \tag{26}$$

so that the probability distribution for outbreak size is

$$P(n;\Delta) = e^{1/4(n^2\Delta/N - n\Delta^2)}P(n;\Delta=0). \tag{27}$$

The appropriate scale for Δ is $O(T/N)$, i.e., $N^{-1/3}$ as noted by BN-K. In Fig. 2 we show the size distribution for various values of the scaled parameter $\delta \equiv \Delta N^{1/3}$. We see that for $\delta > 0$ there is a second peak in addition to the peak at small n. It is interesting to consider the average outbreak size as a function of δ. The scaling with N of $P(n)$ implies that the average outbreak $\bar{n}$ scales as $N^{1/3}$. While $\bar{n}(\delta)$ is given by a double integral, and must be computed numerically, the asymptotic behavior for large positive and negative values of δ is accessible.

For large positive δ, large n's dominate in the integral over n, with a sharp peak at $n=2\delta N^{2/3}$ (the deterministic value, as we presently explain) giving

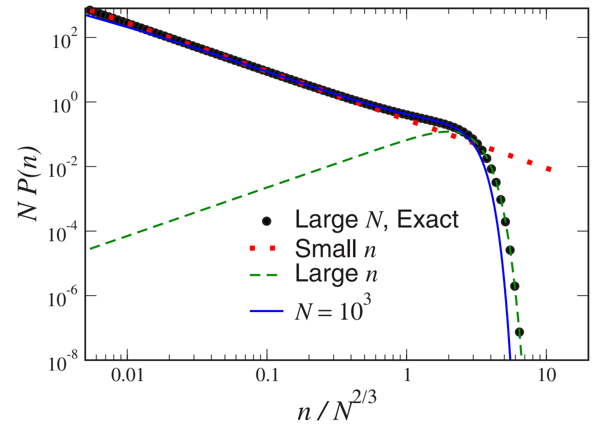

FIG. 1. (Color online) Scaled large-N probability density $NP(n)$ for outbreaks of total size n, versus the scaled outbreak size $n/N^{2/3}$, from Eq. (22), together with the small-n [Eq. (24)] and large-n [Eq. (25)] asymptotics. Also displayed is the exact results for $N=1000$.

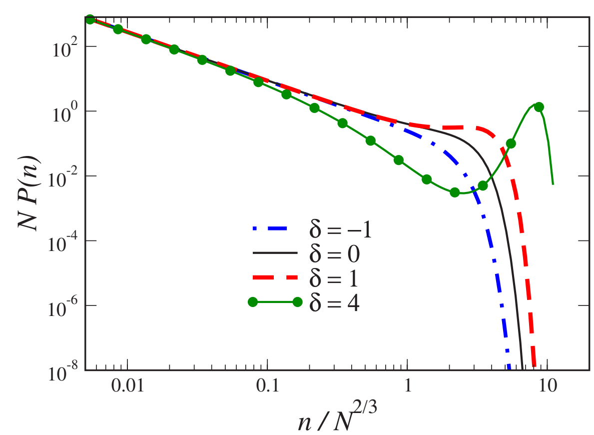

FIG. 2. (Color online) Scaled probability distribution of epidemic sizes $NP(n/N^{2/3})$ for $\delta \equiv (R_0-1)N^{1/3}=-1$, 0, 1, and 4.

$$\bar{n} \approx 2\delta^2 N^{1/3} = 2\Delta^2 N. \tag{28}$$

This is exactly what is needed to match on to the supercritical regime. For $R_0 - 1 \gg N^{-1/3}$, on average a finite fraction of the entire population is infected before the epidemic runs its course. The probability that the epidemic survives to macroscopic proportions is $1 - 1/R_0$, in which case the deterministic prediction of the epidemic size rN [see Eq. (6)] is reliable [10]. Thus the average outbreak is of size

$$\bar{n} = \frac{R_0 - 1}{R_0} rN. \tag{29}$$

The exact results from the master equation for the supercritical regime are in excellent agreement with this result, except in the threshold region $R_0 \approx 1$ (data not shown). In the overlap region where δ is large and Δ small, the supercritical result Eq. (29) indeed reduces to Eq. (28).

For large negative δ, on the other hand, small n's predominate, and

$$\bar{n} \approx \int_0^\infty dn n e^{-n\Delta^2/4} \frac{1}{2\sqrt{\pi} n^{3/2}} = \frac{1}{(-\Delta)}. \tag{30}$$

This in turn matches on to the subcritical result $\bar{n} \approx 1/(1 - R_0)$ as R_0 approaches one from below. Thus, the near threshold regime interpolates smoothly between the sub- and super-threshold domains. In the former, the probability distribution is sharply peaked at 0, whereas in the latter there are two peaks, one at zero and a second at the deterministic value of n. It is in the near-threshold regime that this second peak is born and splits off from the first. In Fig. 3, we plot $\bar{n}(\delta)$ obtained from a numerical integration of our formula, together with the results for $N=10^3$, 10^4, and 10^5. We see that the agreement is excellent for small $|\delta|$, where the results have converged. Convergence is slower, as expected, for large $|\delta|$.

The results presented here for the subcritical and the supercritical case shed new light on the evolutionary process of zoogenic pathogens in human population. While in infinite population the transition is quite sharp at $\delta=0$, for a finite population of reasonable size (say, $N \sim 10^3 - 10^4$ persons in a typical village or town, exposed to the animal reservoir) the average size of an outbreak at criticality does not yield a good indication for the typical case. While most of the epidemics at criticality are $\mathcal{O}(1)$, there is still a slight chance, scaling with $N^{-1/3}$, to find an $\mathcal{O}(N^{2/3})$ (say, about 100 infected people) outbreak. Clearly, the chance for mutation of the pathogen, or the likelihood of a sick individual to migrate and spread the disease in a big city, are determined almost solely by these rare events. As seen in Fig. 2, this is actually true even slightly above criticality, where δ=0.1. Only way beyond criticality (δ=0.4, Fig. 2) does one find a relatively sharp peak of the distribution function close to the predicted average. Studies of these questions must then take into consideration the finiteness of the susceptible population pool.

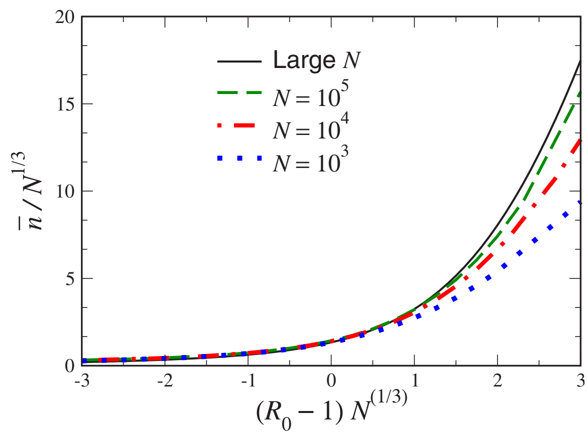

FIG. 3. (Color online) $\bar{n}/N^{1/3}$ as a function of the scaled threshold parameter δ=$(R_0-1)N^{1/3}$ for N=10^3, 10^4, and 10^5, together with a numerical calculation based on our large-N analytic formula for $P(n)$, Eq. (27).

Note added in proof. After the paper went to press, we were informed that many of the results contained herein were previously obtained by A. Martin-Löf [11]. We thank H. Andersson for bringing this reference to our attention. In particular, A. Martin-Löf maps the near-threshold problem to a random walk with a time-dependent boundary, which is equivalent to our formulation of the problem as a random walk with fixed boundary and a time-dependent drift. His final expression for the probability distribution $P(n)$, reduces to our Eq. (27) combined with Eq. (23) for the case treated herein where the infection starts with a single infected individual, and he exhibits a figure equivalent to Fig. 2.

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