

# Spreading of $N$ Diffusing Species with Death and Birth Features

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The number of distinct sites visited by a random walker after  $t$  steps is of great interest, as it provides a direct measure of the territory covered by a diffusing particle. We review the analytical solution to the problem of calculating  $S_N(t)$ , the mean number of distinct sites visited by  $N$  random walkers on a  $d$ -dimensional lattice, for  $d = 1, 2, 3$  in the limit of large  $N$ . There are three distinct time regimes for  $S_N(t)$ . A remarkable transition, for dimensions  $\geq 2$ , in the geometry of the set of visited sites is found. This set initially grows as a disk with a relatively smooth surface until it reaches a certain size, after which the surface becomes increasingly rough. We also review results for a model for migration and spreading of populations and diseases. The model is based on  $N$  diffusing species, where each species has a probability  $\alpha_-$  of dying (or recovery from a disease) and a probability  $\alpha_+$  to give birth (or infect another species). It is found analytically that when  $\alpha_+ \approx \alpha_- \neq 0$ , after a crossover time  $t_x \sim N/2\alpha_-$ , the territory covered by the population is *localized* around its center of mass while the center of mass diffuses regularly. When  $\alpha_+ > \alpha_-$  the localization breaks down after a second crossover time and the species diffuse and get spread around their center of mass. These results may explain the phenomena of migration and spreading of diseases and population appearing in nature.

## I. NUMBER OF DISTINCT SITES VISITED BY $N$ RANDOM WALKERS

One of the most important properties of a discrete-time lattice random walk is the number of distinct sites visited by a  $t$ -step walk [1–19]. This quantity enters into the description of phenomena ranging from relaxation processes [3–6] and diffusion limited reactions [3,20,21] such as defect annealing [2,7] and exciton trapping, [8,9] to the spread of populations in ecology [22–25].

The analyses in the literature to date refer to the calculation of properties of  $S_1(t)$ , the distinct number of sites visited by a *single* random walker. For this case, the asymptotic forms for the mean number of sites visited,  $\langle S_1(t) \rangle$ , in any number of dimensions  $d$  are well known. Knowledge of  $\langle S_1(t) \rangle$  enables one to find a lowest order approximation to the survival probability for the “trapping problem”, in which a random walker moves in the presence of randomly distributed static traps [3]. This problem can be regarded as the simplest generalization of the Smoluchowski model for the rate of chemical reactions of the form  $A + B \rightarrow B$ , taking into account the possibility of a concentration of  $B$ 's rather than the single  $B$  envisaged by Smoluchowski [3,20,21].  $\langle S_1(t) \rangle$  also appears in the solution of the “target” problem [3], in which a single target is static within a concentration of diffusing traps. The survival probability in this case is given exactly by  $\exp(-k \langle S_1(t) \rangle)$  [3] (where  $k$  depends on the lattice and the concentration of traps), if the traps are initially Poisson distributed.

The properties of the number of distinct sites visited in the more general situation where there are  $N$  random

walkers in the system are not related simply to the single walker case. Here we calculate asymptotic properties of  $S_N(t)$ , the number of distinct sites visited by  $N \gg 1$  independent random walkers.

The quantity  $S_N(t)$  has direct application to any situation that might be conceptualized as a “multiple scavenger problem,” in which mobile traps (or scavengers) react with stationary particles initially distributed homogeneously on the lattice, and a particle disappears when any one of the traps reaches it. It can also be useful for the analysis of simultaneous survival of several particles diffusing in the presence of randomly distributed static traps, which is the generalization of the trapping problem described above (1). The probability for the simultaneous survival of  $M$  of the initial  $N$  particles will be given by a combinatorial factor times  $\langle \exp(-k S_M(t)) \rangle$ , where  $k$  again depends on the concentration of traps and on the lattice. For short times or low concentration of traps, this survival probability can be approximated by  $\exp(-k \langle S_M(t) \rangle)$ .

We consider the case for which all  $N$  random walkers are assumed to be initially at the origin. The single-step displacements are characterized by a finite variance, so that the  $t$ -step transition probabilities (in the absence of boundaries) tend toward the Gaussian form predicted by the central-limit theorem. The random walkers move independently of one another with the consequence that multiple occupancy of a single site is allowed.

Reference [26] finds that the mean number of distinct sites,  $\langle S_N(t) \rangle$ , passes through several distinct growth regimes in time. At very short times, the simple expression is found

$$\langle S_N(t) \rangle \sim At^d \quad [t \ll t_\times], \quad [\text{Regime I}] \quad (1.1)$$

where  $A$  depends on the lattice. Eq. (1.1) simply states that every accessible site is occupied by a walker.

Regime I holds so long as there are many walkers at every accessible site—i.e. so long as  $N P_{\min}(t) \gg 1$ , where  $P_{\min}$  is the smallest non-zero occupation probability on the lattice at time  $t$ . Then  $P_{\min}(t) = z^{-t}$ , where  $z$  is the number of nearest neighbors of a site, so Regime I must terminate at a crossover time  $t_\times$  which scales logarithmically with  $N$ ,

$$t_\times \sim \ln N.$$

To discuss times greater than  $t_\times$ , we will calculate  $\langle S_N(t) \rangle$  using generating function techniques. This analysis leads to a compact scaling expression for  $\langle S_N(t) \rangle$

$$\langle S_N(t) \rangle \sim t^{d/2} f(x) \quad [t \gg t_\times], \quad (1.2)$$

where the tilde denotes the fact that (1.2) holds for  $N$  and  $t$  both large. The scaled variable  $x$  is given by

$$x \equiv \begin{cases} N & [d = 1] \\ N/\ln t & [d = 2] \\ N/\sqrt{t} & [d = 3], \end{cases}$$

and the scaling function  $f(x)$  by

$$f(x) = \begin{cases} (\ln x)^{d/2} & t_\times \ll t \ll t'_\times \\ x & t \gg t'_\times. \end{cases} \quad \begin{array}{l} [\text{Regime II}] \\ [\text{Regime III}] \end{array}$$

Here the second crossover time  $t'_\times$  is

$$t'_\times \sim \begin{cases} \infty & [d = 1] \\ e^N & [d = 2] \\ N^2 & [d = 3]. \end{cases} \quad (1.3)$$

The appearance of Regime III (for  $d \geq 2$ ) can be understood from the following heuristic argument. In Regime II, all but an exponentially small fraction of the walkers are contained within a  $d$ -dimensional sphere of radius  $\xi \sim t^{1/2}$ . Hence  $\langle S_N(t) \rangle$  must be bounded from above by the volume of this sphere,  $V(t) \sim t^{d/2}$ . A second upper bound on  $\langle S_N(t) \rangle$  is  $N\langle S_1(t) \rangle$ , where

$$\langle S_1(t) \rangle \sim \begin{cases} t^{1/2} & [d = 1] \\ t/\ln t & [d = 2] \\ t & [d = 3] \end{cases} \quad (1.4)$$

is the number of distinct sites visited by one random walker. A crossover in  $\langle S_N(t) \rangle$  will occur if the system passes from one constraint to the other. For  $d = 1$ ,  $V(t) < N\langle S_1(t) \rangle$  for all  $t$ , so no crossover occurs—Regime II holds for arbitrarily large  $t$ , confirming the result (1.3) above. For  $d = 2, 3$ , we find  $V(t) < N\langle S_1(t) \rangle$  initially, but for sufficiently large  $t$ ,  $V(t) > N\langle S_1(t) \rangle$ . Thus  $t'_\times$  is obtained from the condition

$$V(t'_\times) \sim N\langle S_1(t'_\times) \rangle. \quad (1.5)$$

For  $d = 2$ , (1.4) and (1.5) lead to  $t'_\times \sim Nt'_\times/\ln t'_\times$ , so that  $t'_\times \sim e^N$ ; this confirms the result (1.3) above. Similarly, for  $d = 3$ ,  $(t'_\times)^{3/2} \sim Nt'_\times$  implies  $t'_\times \sim N^2$ , confirming the result (1.3). One can interpret  $t'_\times$  as the time up to which the walkers visit the same places very frequently. For times longer than  $t'_\times$ , the walkers “almost” do not see each other, and can be treated independently. Thus one would expect the form  $S_N(t) \sim NS_1(t)$  under these conditions.

Following the same kind of reasoning, we can generalize the above argument to any spatial dimension  $d$ . The crossover time to the final regime will be given by

$$t'_\times \sim N^{2/(d-2)} \quad [d > 2]. \quad (1.6)$$

This result is a consequence of the fact that  $\langle S_1(t) \rangle \sim t$  for any dimension larger than 2. Equation (1.6) shows the effect of the space dimension on  $t'_\times$ ; it shows that when the dimension increases, the walkers become “independent” at shorter times  $t'_\times$ .

The above results will be derived in detail in this paper. The remarkable feature is the appearance of Regime II. The behavior in Regime I corresponds to the limit [ $N \rightarrow \infty$ ,  $t$  fixed]; the interface of the set of visited sites is smooth and  $S_N(t)$  is easy to understand ( $S_N \sim t^d$ ). The behavior in Regime III corresponds to the opposite limit [ $t \rightarrow \infty$ ,  $N$  fixed]; the interface of the set of visited sites is extremely rough and  $S_N$  is also easy to understand ( $S_N \sim NS_1$ ). In Regime II, the function  $S_N$  takes on an unexpected and nontrivial form. The walkers are largely confined to a sphere of radius  $\sqrt{t}$  (in contrast to Regime I, where they populate a sphere of radius  $t$ ); the interface of the set of visited sites undergoes a progressive roughening, which is readily apparent on visual inspection of the set of visited sites (2).

We also carried out numerical calculations for  $\langle S_N(t) \rangle$  using both the methods of Monte Carlo and exact enumeration. In particular, we confirmed the scaling form (1.2) [26].

## II. MODEL FOR SPREADING AND MIGRATION OF POPULATIONS AND EPIDEMICS

For populations and diseases, birth (infection) and death (recovery) are important features that affect their spatial dynamics. To include these features, “branching diffusion” models have been developed earlier and quantities related to the mean number of (infected) species  $\langle N(\mathbf{r}, t) \rangle$  at position  $\mathbf{r}$  and time  $t$  have been calculated [27–30]. Since, however, the mean number of species gives no information about spatial correlations between two species,  $\langle N(\mathbf{r}, t) \rangle$  cannot describe effects like clustering or segregation that are observed in field experiments [31–33]. Here we review results [34] for a fluctuation reduced branching diffusion (FRBD) model, where the correlations can be calculated analytically.

Consider  $N_0$  species, initially located at the origin of a  $d$ -dimensional coordinate system. At  $t = 0$ , the species start to diffuse independently and death and birth events occur at certain instances of time  $t_k$ . The increments  $\Delta t$  between two successive time instances are exponentially distributed with mean  $\langle \Delta t \rangle = 1/\alpha_+ N(t)$ . At every instance of time  $t_k$ , one randomly chosen species is removed with probability  $p_d$ , and another randomly chosen species is replaced by two species with probability 1. By definition, the birth rate is  $\alpha_+$ . The death rate is  $\alpha_- = p_d \alpha_+ \leq \alpha_+$ , and the mean number of species increases exponentially,  $\langle N(t) \rangle = N_0 \exp(\Delta \alpha t)$ , where  $\Delta \alpha = \alpha_+ - \alpha_-$  is the growth rate.

By construction, the number  $N(t)$  of species shows only weak statistical fluctuations around  $\langle N(t) \rangle$  (that vanish in the ‘‘critical’’ case,  $\alpha_+ = \alpha_-$ ), which prevents the community from dying out. In contrast, in the usual branching diffusion model [27], where death and birth events occur *independently* with rate  $\alpha_+$  and  $\alpha_-$ , there is a nonzero dying-out probability (which is one in the critical case). For the FRBD model the spatial dynamics of the community can be treated analytically and the correlations between the species can be calculated at and above criticality.

Spatial correlations between the species show up most clearly in the mean-squared pair distance,  $\langle r_2^2(t) \rangle \equiv (N(N-1))^{-1} \sum_{i,j} \langle (\mathbf{r}_i - \mathbf{r}_j)^2 \rangle$ . The detailed analytical treatment [34] shows that in the critical case ( $\Delta \alpha = 0$ ),  $\langle r_2^2(t) \rangle$  can be written as

$$\langle r_2^2(t) \rangle = \rho_0^2 \left[ 1 - \exp\left(-\frac{t}{\tau_0}\right) \right], \quad (2.1)$$

with a localization radius  $\rho_0 \equiv \sqrt{(N_0 - 1)/\alpha_+}$  and  $\tau_0 \equiv (N_0 - 1)/2\alpha_+$ . Equation (2.1) shows that  $\langle r_2^2(t) \rangle$  is linear in  $t$  for short times  $t \ll \tau_0$ , while for large times,  $t \gg \tau_0$ ,  $\langle r_2^2(t) \rangle$  saturates and becomes identical to  $\rho_0^2$ . Accordingly, after an initial spreading period, the species stay together in one community, that typically covers a region of radius  $\rho_0$ . The localization behavior for large times reflects strong correlations that are caused by the natural asymmetry between birth/infection and death/recovery processes (birth and infection occur only next to a species while death and recovery occur everywhere).

These correlations also affect the dynamics of the community as a whole, which can be measured by the mean-squared displacement of the center of mass,  $\langle r_{\text{cm}}^2(t) \rangle \equiv \langle (N^{-1} \sum_i \mathbf{r}_i)^2 \rangle$ . This quantity is simply related to  $\langle r_2^2(t) \rangle$  and the mean-squared displacement  $\langle r^2(t) \rangle \equiv N^{-1} \sum_i \langle r_i^2 \rangle = t$ ,

$$\langle r_{\text{cm}}^2(t) \rangle = \langle r^2(t) \rangle - \frac{N_0 - 1}{2N_0} \langle r_2^2(t) \rangle. \quad (2.2)$$

Equation (2.2) follows directly from the definitions of the three quantities. By substituting (2.1) in (2.2) and expanding the exponential function up to the second order, one can identify three different time regimes in  $\langle r_{\text{cm}}^2(t) \rangle$ ,

$$\langle r_{\text{cm}}^2(t) \rangle = \begin{cases} \frac{t}{N_0} & \text{for } t \ll \frac{2\tau_0}{N_0 - 1} \\ \frac{N_0 - 1}{2N_0\tau_0} t^2 & \text{for } \frac{2\tau_0}{N_0 - 1} \ll t \ll \tau_0 \\ t & \text{for } t \gg \tau_0. \end{cases} \quad (2.3)$$

Only for very short times,  $t \ll \frac{2\tau_0}{N_0 - 1}$ , the center of mass moves as in the case of independently diffusing particles. In the intermediate time regime  $\frac{2\tau_0}{N_0 - 1} \ll \frac{t}{\tau_0} \ll 1$ ,  $\langle r_{\text{cm}}^2(t) \rangle \propto t^2$  shows ballistic behavior while for long times,  $\langle r_{\text{cm}}^2(t) \rangle \approx \langle r^2(t) \rangle = t$ , independent of  $N_0$ .

Thus we have found that in the critical case ( $\Delta \alpha = 0$ ) the community shows a kind of *migration* behavior for  $t > \tau_0$ : The mean-squared pair distance becomes constant,  $\langle r_2^2(t) \rangle = \rho_0^2$ , and hence the species are located around their center of mass within a ‘‘ball’’ of radius of  $\rho_0$ . In this state of ‘‘dynamical localization’’, the community as a whole moves like a single diffusing entity.

For a growing community with  $\Delta \alpha > 0$ , the mean number of species is not constant, and the localisation radius  $\rho_0$  in (2.1) depends on time,  $\rho_0^2 \rightarrow \rho^2(t) = (\langle N(t) \rangle - 1)/\alpha_+ \simeq (N_0 - 1)/\alpha_+ \exp(\Delta \alpha t)$ . On the other hand (2.2) shows that  $\langle r_2^2(t) \rangle$  is bounded from above by  $2N_0 \langle r^2(t) \rangle / (N_0 - 1) \simeq 2t$  and accordingly,  $\langle r_2^2(t) \rangle$  shows a second crossover at time  $t'_x$ , when  $\rho^2(t)$  becomes larger than  $2t$ ,

$$\langle r_2^2(t) \rangle = \begin{cases} 2t & t \ll \tau_0 \\ \rho^2(t) & \tau_0 \ll t \ll t'_x \\ 2t & t \gg t'_x. \end{cases} \quad (2.4)$$

Thus for a growing community the localization occurs only up to times  $t'_x$ , which is in the order of  $\Delta \alpha^{-1}$ , and the community starts to spread for  $t \gg \Delta \alpha^{-1}$ . We therefore have two crossover times  $\tau_0$  and  $\Delta \alpha^{-1}$  in the non-critical case  $\Delta \alpha > 0$ .

In summary, we have found two different types of phenomena, *migration* and *spreading*. In the case of *migration*, the mean distance between the species saturates after some time, *i.e.* the population territory (epidemics area) does not increase, but the territory as a whole moves with time. In the case of *spreading*, the mean distance between the species increases all the time, but the center of the growing territory almost does not move. Both, *migration* and *spreading* phenomena, occur in the spatial behavior of population dynamics and epidemics [22,35–38].

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FIG. 1. Schematic illustration of the trapping problem in which the number of distinct sites enters explicitly into the expression for the survival probability  $P_{\text{surv}}$ . (a) A single walker, starting in the center of an infinite square lattice, can be trapped by fixed traps distributed randomly in the plane. (b)  $N$  walkers starting at the origin in the presence of the same set of randomly distributed traps. In both cases,  $P_{\text{surv}} \sim \exp(-\langle S_N \rangle)$ .

FIG. 2. Contours of the surface obtained from snapshots at successive times of the territory covered by  $N$  random walkers for the case  $N = 500$  for a sequence of times in Regime II. Note the roughening of the disc surface as time increases.