# Hierarchical mean-field model describing relaxation in a small-world network

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This Brief Report presents the hierarchical reaction-diffusion partial differential equations (PDE) system, which reproduces a mean-square displacement and a density relaxation process corresponding to the anomalous diffusion on a small-world network. These results are confirmed by the comparison with the known direct numerical simulations.

## I. INTRODUCTION

The mathematical idea of a small-world network, introduced in the paper [1], is one of the most promising approaches for description of structures conditioned by real world communities. For this reason, over the last years, a lot of research has been done to describe small-world structures, but most of them have focused on static properties. Next step in this direction was established by the study of random walks on small-world networks. Particularly, the direct numerical simulations [2,3] have shown that the averaged diffusion in a small-world network is anomalous one. Namely, the decay rate for an initial localized source is faster then normal (time dependence from $\sim t^{-0.52}$ to $\sim t^{-0.6}$ vs $\sim t^{-0.5}$). As well, the mean-square displacement scales as $\langle x^2(t) \rangle \sim t^\alpha$ with $0 < \alpha < 2$. Thus, these facts demonstrate that this process is close to a superdiffusion.

This problem is also connected with challenges of modern mathematical epidemiology. Namely, the spread of recent diseases (SARS, HIV, etc.) strongly hangs upon short- and long-range traffic flows [4,5]. Most of works concerning the dynamical properties of such random walks deal with the direct numerical simulation or various algebraic approaches. However, a mathematical theory of the disease spread clearly shows the powerfulness of coupled ordinary differential equations (ODE) and PDE (for example, Kermack-McKendrick and Fisher-Kolmogorov models).

Most developed approaches describing a traffic-spread interaction (Rvachev-Longini [6] and Sattenspiel-Dietz [7] models as well as their modern improvements [8]) work with ODE systems, where the spatial jumps are described by the term consisting of a connectivity matrix. The sufficient improvement proposed in [7] incorporates a population subdivision into interacting subgroups with various dynamical properties (see also the overview of metapopulation approaches in [9] and references therein).

Concerning the usage of coupled diffusion equations, such an approach was implemented for two interacting social groups of animals presented by the same species [10].

The deeper insight into the problem provides the hierarchical metapopulation approach. The authors of [11] consider this model within the following assumptions: there exists a set of communities, which are included in the hierarchy equipped with the appropriate metric. For example, houses and workplaces are the down level of communities; the next level is represented by cities; countries are upper, etc. The mixing inside of every community is homogeneous. Additionally, each individual can leave with some probability its local community and enter a new context at each time step. It has been shown that an epidemy spread strongly depends on a transport parameter and hierarchy metric.

Obviously, such multiscaling could play a role of the background, which allows to determine a dependence of diffusion parameters on the averaged network topology. Since a number of long-distance traveling individuals is sufficiently less than a distributed low-mobile local population, these conditions imply the close connection with the problem of random walk on small-world-like networks.

The main goal of this Brief Report is to construct the mean-field model for the random walk in small-world network based on the hierarchy of elementary displacements.

## II. MODEL OF NETWORK

The considered network (see Fig. 1, left) is constructed by the way described in [2]. In means that there exists a regular lattice in one dimension under periodic boundary conditions, each node being connected symmetrically to its two nearest neighbors. Additionally, a new bond is added with the probability $p$. The other end gets attached with equal probability to any of the lattice node. These bonds will be referred as
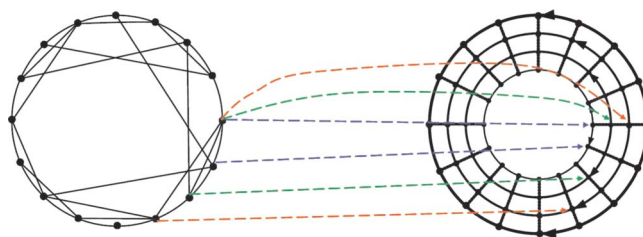


FIG. 1. (Color online) The mapping of a small-world network into a hierarchical lattice: each node of the original network (left) corresponds to a set of nodes placed along radial lines (right); a full density of walkers is subdivided into partial ones belonging to this set according to possible displacement ways. The dashed arrows illustrate these walks: same intensity (colors in online version) picks the initial and end points for paths with different step size and mapping of the correspondent targets.

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"short links " below because each one connects two nodes with the distance of $2 \leq n_{\max}$ over the regular lattice's path.

For the reason to consider the averaged relaxation process (the time decay function of a localized distribution and mean-square displacement of a random walker), one does not need to consider an exact topological realization. The unique requirement is the same value of $p$ for an ensemble. In other words, any node could be considered as an initial one. This supposition corresponds to the strong mean-field approximation for an irregular distributed system.

## III. TRANSITION TO THE CONTINUOUS MULTISCALE LIMIT

The hierarchy of paths is introduced as follows: the master equation for the probability $U(j,k)$ to find a walker in $j$-th node at $k$-th iteration is

$$U(j,k+1) - U(j,k) = \sum_i W_{ji} U(j,k) - U(i,k) \sum_i W_{ji}, \quad (1)$$

where $W(ji)$ is the probability of going from node $i$ to node $f$ during one time step.

The total quantity $U(j,k)$ can be subdivided into the partial densities in such a way that

$$U(j,k) = \sum_{n=1}^{n_{\max}} u_n(j,k), \quad (2)$$

where the index $n$ denotes the group, which walk along links connecting the nodes with a distance $n$ between them along the background regular lattice. Graphically, this subdivision corresponds to the concentric circles in the Fig. 1, right.

Within this representation, the discrete equation for each group is

$$u_n(j,k+1) - u_n(j,k) = \frac{1}{2}[u_n(j+1,k) + u_n(j-1,k)]$$

$$+ \frac{p}{n_{\max}} \sum_{i=1}^{n_{\max}} (u_i - u_n), \quad (3)$$

where the following suppositions are fulfilled: a walker can (i) make a step with an equal probability only to the nearest node along the corresponding concentric sublattice [the first term in the right-hand side of Eq. (1)], i.e., the transition $j \rightarrow j+1$ for the group marked by index $n$ in Eq. (3) corresponds to $j \rightarrow j+n$ in Eq. (1); or (ii) change its group with the probability $p/n_{\max}$ [second term in the right-hand side of Eq. (1)]. Here, $p$ is the probability of a "short links" presence and $1/n_{\max}$ is a normalizing factor taking into their number. Therefore, their products merge all $W_{ij}$ for links length, which are different from $n$. Note that the sum is taken over all differences in the brackets. Therefore, $n_{\max}$ summands $pu_n/n_{\max}$ give an outflow density from the $n$-th group, which is equal to $pu_n$.

Let the number of nodes in the background regular lattice be large enough to consider the continuous limit. Then, Eq. (3) takes a form of the continuous reaction-diffusion equation
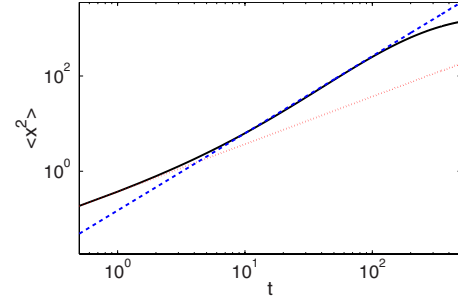


FIG. 2. (Color online) The dependence of the calculated mean-square displacement (solid line) on the time showing the transition from normal diffusion (dotted line, red online) to superdiffusion (dashed line, blue online).

$$\frac{\partial u_n}{\partial t} = D_n \frac{\partial^2 u_n}{\partial x^2} + p\left(\frac{1}{n_{\max}} U - u_n\right). \quad (4)$$

Here, the summation in the reaction term is evaluated with the usage of the definition (2) and $D_n$ is a diffusion coefficient associated with the continuous approximation for diffusion on the circles replacing circular sublattices (see the 1, right). It has a value $D_n = n^2 D_1$ as a consequence of the formula for a mean-square displacement $\langle x^2 \rangle \sim t$. Here, $D_1$ is the diffusion coefficient corresponding to the walk over the background regular lattice.

We assume that a redistribution over the radial lines connecting the circles does not take any time since each one corresponds to the node as a whole one.

The full density is determined by the expression (2) with the replacement $(j,k) \rightarrow (x,t)$.

## IV. EXAMPLE OF NUMERICAL SOLUTION

The numerical solution of the systems (4) and (2) have been found with the use of the standard MATLAB routine pdepe realizing the algorithm described in [12]. The distributions $u_1(x,0) = (1-p)\exp(-x^2/D_1^2)$ and $u_{n>1}(x,0) = [p/n_{\max}]\exp(-x^2/D_1^2)$ are used as initial values. Thus, their sum representing a full initial density is the Gaussian $U(x,0) = \exp(-x^2/D_1^2)$ too. The parameters $n_{\max} = 8$, $D_1 = 1$, and $p = 0.01$ are used for the calculation on the interval [$-200, 200$] with impenetrable boundary conditions. The value of $p$ is chosen as equal to this one used in [2,3].

The obtained solution of the systems (4) and (2) gives the space-time distributions for partial densities $u_n(x,t)$. Their summation (2) is a desired full density distribution over the network. It was used for the further calculations. Particularly, Fig. 2 represents the mean-square displacement in logarithmical coordinates. The numerical solution $\langle x(t)^2 \rangle$ is drawn with the solid line. For the reference, there are also dashed and dotted lines, which show the power-law functions of time with the exponentials 1.62 (superdiffusion) and 1 (normal diffusion).

The curve of mean-square displacement shows that the process is a normal diffusion only during a short initial time (the solid line coincides with the dotted one). Actually, it takes time compared with the characteristic time of one step
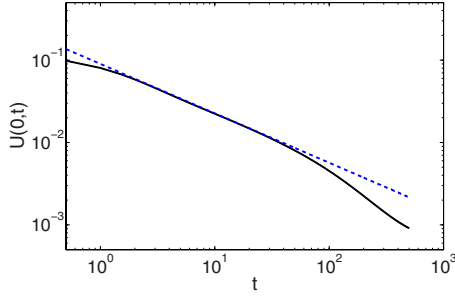
FIG. 3. (Color online) The relaxation of a localized initial distribution: the solid line, representing the calculated density of walkers at the origin, approaches the dashed line corresponding to the power-law dependence $\sim t^{-0.6}$.

in the discrete model. During the interval ($t \sim 1-10$) the diffusion on various scales starts to play a more significant role and a spread is accelerating. Finally, $t > 10$, the process takes a form of stationary superdiffusion. The curve in the Fig. 2 is drawn until the moment of a boundary effect influence. The same three-stage behavior was found by the direct numerical simulation in the paper [3]. Some difference in the relation of the duration of the ranges corresponding to normal diffusion and superdiffusion can be explained by the following reason: the approach considered in this Brief Report is a strong enough averaging, which implies a fast redistribution over all possible paths (rings in the Fig. 1) and a "parallel motion" along them. Conversely, the simulation deals with jumps via one of possible links, and the resulting mean-square displacement is averaging of such realizations. However, the qualitative picture of regimes is the same as well as a comparison of curve's slopes.

The comparison of the approximate model predictions with the results on a relaxation obtained via an exact discrete numerical simulation [2] can be done analyzing the solution $U(0,t)$ represented in the Fig. 3 as a solid line.

As before, there exists a slow relaxation during the time compared with a step of the discrete walks. This means that the main part of walkers is concentrated in the background circle during the initial stage. After this time, there is a redistribution of walkers over the various paths that lead to the faster decay. As a result, the walker motion goes according to the superdiffusive relaxation, described in [2]. Note that the correspondence is not only qualitative but also quantitative: both approaches give the same value of decay exponential, namely, −0.6 (see the region in the Fig. 3, where the solid line $U(0,t) \sim t^{-0.6}$ coincides with the referent dashed one). The direct numerical simulation [2] gives the exponential −0.52 for $p=0.01$, but it has been mentioned there that it can vary to −0.6. At is was discussed above, the faster relaxation in the PDE model originated from the strength of coupling. But here, the quantitative correspondence lies in the reason-

able range of values. Additionally, the analytical estimations presented in [2] also predict the value of the relaxation exponential within a range $[-0.5, -0.75]$, where these bounds correspond to a regular lattice and a Cayley tree. The final stage ($t > 150$) demonstrates the influence of finite-size effects. Thus, the $U(0,t)$ obtained as a solution of the systems (4) and (2) reproduces all details of the relaxation curve obtained in [2].

## V. DISCUSSION AND CONCLUSION

In this Brief Report, the approach to description of the relaxation process in small-world networks is proposed. It is based on the hierarchy of coupled partial differential equations with the scalable diffusion coefficients, which depends on the length of links of a network. This allows to take into account possible long-distance travels by the natural way.

It has shown that the solution of this PDE system corresponds to the results of the direct discrete numerical simulation quite satisfactory for both anomalous relaxation and mean-square displacement of random walkers density in a small-world network.

It should be pointed out that such an approach is ideologically close to the model of superdiffusion in inhomogeneous medium proposed recently in the article [13]. However, it differs from the cited one by the microscopical physical assumptions. The author of [13] studies a mixture of diffusing particles partitioned into a set of groups according to their free flight lengths; including reaction terms allows to describe random exchange between these groups via diffusion processes. Conversely, the present approach considers a random walk corresponding to the normal diffusion as an initial microscopic level within every group of walkers. And the reaction terms mean a simple exchange between various pathways.

On the other hand, the usage of scalable diffusion coefficients has common properties with the recent approach [14], where fat-tailed distributions are obtained as the result of introducing a diffusivity distribution function into the standard integral form of a solution for the simple diffusion equation. But such a substitution is rather artificial in contrast to the system (4), where the hierarchy of coefficients is based on the decomposition of equations *ab initio*.

Finally, it could be pointed out that the described modification is not the only possible one. The method for constructing the coupled PDE system allows to take into account more detailed information about travel length distributions as well. For example, the partial densities in Eq. (2) could be supplied with unequal weights, etc.

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[1] D. J. Watts and S. H. Strogatz, Nature (London) **393**, 440 (1998).

[2] S. Jespersen, I. M. Sokolov, and A. Blumen, Phys. Rev. E **62**, 4405 (2000).

[3] E. Almaas, R. V. Kulkarni, and D. Stroud, Phys. Rev. E **68**, 056105 (2003).

[4] A. Cliff and P. Haggett, Br. Med. Bull. **69**, 87 (2004).

[5] S. Riley, Science **316**, 1298 (2007).

[6] L. A. Rvachev and I. M. Longini, Jr., Math. Biosci. **75**, 3 (1985).

[7] L. Sattenspiel and K. Dietz, Math. Biosci. **128**, 71 (1995).

[8] V. Colizza, M. Barthélemy, A. Barrat, and A. Vespignani, C. R. Biol. **330**, 364 (2007).

[9] A. Dobson, Science **301**, 1488 (2003).

[10] I. Gudelj, K. A. J. White, and N. F. Britton, Bull. Math. Biol. **66**, 91 (2004).

[11] D. Watts, R. Muhamad, D. Medina, and P. Dodds, Proc. Natl. Acad. Sci. U.S.A. **102**, 11157 (2005).

[12] R.D. Skeel and M. Berzins, SIAM J. Sci. Comp. **11**, 1 (1990).

[13] V. P. Shkilev, JETP **107**, 892 (2008).

[14] S. Petrovskii, A. Morozov, and B.-L. Li, Ecol. Complexity **5**, 146 (2008).