Singular Dynamical Renormalization Group and Biased Diffusion on Fractals

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An exact renormalization group describes extremely slow, logarithmic diffusion in the presence of a biasing field on ramified fractal structures. Recursion equations are singular at the fixed point and the standard analysis to extract asymptotic behaviors has to be reconsidered. The model reproduces mechanisms working for biased diffusion on percolation clusters. For $1-d$ structures, logarithmic diffusions generalizing that discussed by Sinai [Theory Probab. Its Appl. **27**, 256 (1982)] are obtained by the same methods.

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Slow diffusion, with the average displacement R, growing in time t, as some power of $\ln t$, has been exactly demonstrated by Sinai for a particle hopping on a one-dimensional chain and subject at each site to an independent random bias [1]. There is numerical evidence that logarithmic diffusion could replace the anomalous power law one, in fractal structures, like the infinite incipient cluster (IIC) of percolation, when the diffusing particle is subject to the action of an external biasing field [2,3]. In this case the field is not random, but the structure of the fractal conspires with it and determines a localization effect, e.g., by pushing the particle towards dangling ends [4].

Interestingly enough, the current understanding of such phenomena relies almost entirely on the picture of a particle diffusing in one dimension. This is the situation of the Sinai model, whose behavior is indeed easily understood once realized that, over a distance R along the chain, a potential barrier $\propto\sqrt{R}$ develops by adding the local random biases with zero average. On the basis of Arrhenius law, overcoming such a barrier requires a time $\propto e^{\sqrt{R}}$, from which $R\propto(\ln t)^2$ follows. Another mechanism of slow diffusion under bias is that arising in a comblike structure with teeth of variable length, along which a bias field pushes the particle towards the tips. A suitable power law distribution of teeth lengths is then easily shown to imply waiting times, which make diffusion along the comb basis logarithmic [5]. In this case again the model is basically one dimensional, and still very far from the complexity of fully self-similar structures, like the IIC of percolation. For example, the linear character of the teeth is essential in order to derive the waiting times associated with them.

While it is intuitive to ascribe the bias induced logarithmic diffusion in a fractal to mechanisms of trapping into dangling ends, so far, a proper mathematical description of such phenomena within a fully self-similar geometry has never been accomplished. In the present Letter we address this issue on deterministic fractal models by a suitable dynamical renormalization group (RG) approach.

While the RG is the most natural method to treat dynamics on self-similar structures [6], one should realize that logarithmic long time behavior must somehow imply a peculiar, singular structure for an RG transformation. Indeed, standard dynamical RG yields the time rescaling factor, $l^{1/\nu}$, under length rescaling l [7]. This is consistent with power law diffusion $R\sim t^{\nu}$. Logarithmic diffusion clearly corresponds to the limit $\nu\to 0$, which implies $l^{1/\nu}\to\infty$, and thus a singularity for the RG transformation. A singular RG transformation is very unusual and makes of course practical sense only if the RG can be carried out exactly, as in the example discussed below. The possible occurrence of singularities in RG transformations has been investigated some time ago [8,9]. However, contrary to the attitude of the present work, such singularities, or peculiarities, were seen as obstacles for the RG strategy, and a major concern was to show that they were not located at the fixed point, as, on the contrary, will be the case here [10]. Thus, the RG technique developed below should be of general methodological interest in its own right.

The lattice we consider [Fig. 1(a)] as an example is the so-called T fractal, whose fractal dimension is $\bar{d}=\ln 3/\ln 2$ [11]. A diffusing particle hops between nearest neighbor (nn) sites of the structure. The master equation for the probability, $P_i(t)$, for the particle to be at site i at time t, is

$$P_i(t+\tau)=P_i(t)+\sum_{j\neq i}[W_{ij}P_j(t)-W_{ji}P_i(t)]\,, \qquad (1)$$

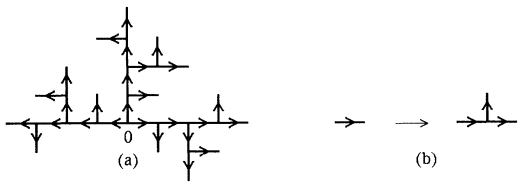

FIG. 1. (a) T fractal at the third generation. The next generation is obtained by performing the operation illustrated in (b) on each bond. The arrows on each bond indicate the direction of the topological bias.

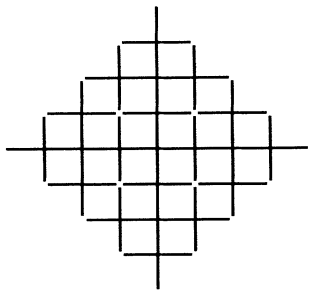

FIG. 2. Example of T fractal with coordination equal to 1 or 4 in $d=2$. Similar structures can be drawn in $d>2$.

where the sums are over nn, j, of site i, and W_{ij} represents the probability that the particle hops from j to i in time τ. It is further assumed that $W_{ij}=W_+$ or W_-, according to whether one goes from j to i following the bond arrow or not. Since the arrows are all pointing in the direction of increasing "chemical" distance from the origin (i.e., the T-fractal central site $j=0$), the following relations have to be satisfied: $2W_+ + W_- \leq 1$ and $3W_+ \leq 1$. We will further assume $W=W_-/W_+ \leq 1$, so that the bias tends to push the particle to higher chemical distance from the origin. This could represent diffusion in the presence of a pressure force, due, e.g., to continuous injection of a fluid at the origin. Putting $\tau=1$, and introducing discrete Laplace transforms [6],

$$\tilde{P}_i^0(\omega_0)=\sum_{n=0}^{\infty} P_i(n)(1+\omega_0)^{-1-n}, \tag{2}$$

Eq. (1) implies

$$\left[\alpha(i)\omega+\sum_{j\neq i}\frac{W_{ji}}{W_+}\right]\tilde{P}_i(\omega)=\sum_{j\neq i}\frac{W_{ij}}{W_+}\tilde{P}_j(\omega)+\delta_{i,0}, \tag{3}$$

where $\omega=\omega_0/W_+$, $\tilde{P}_k^0(\omega_0)=\tilde{P}_k(\omega)/W_+$, and the Kronecker's delta reflects the initial condition, $P_i(0)=\delta_{i,0}$. According to Eq. (1) one should have $\alpha(i)=1$, $\forall i$, in Eq. (3). We introduce such coefficients because our RG transformation distinguishes between sites with different coordination. It will turn out that $\alpha(i)=\alpha_1,\alpha_3$, or α_0, according to whether i has coordination 1,3, or coincides with the origin, respectively. The only parameters entering Eq. (3) will thus be $(\alpha_0,\alpha_1,\alpha_3)\equiv\boldsymbol{\alpha}$, and W.

The RG transformation is based upon eliminating from Eq. (3) the $\tilde{P}$'s corresponding to sites introduced at the last generation of the T fractal. This corresponds to performing the inverse of the operation illustrated in Fig. 1(b) on each elementary T unit of the structure. The sites of the old structure which are not decimated have distances reduced by a factor $l=2$, if measured in terms of the new lattice spacing. The decimation of Eq. (3) enables us to put it into the original form by the following identifications:

$$W'=W^2, \tag{4a}$$

$$\alpha_0'\omega'=\frac{\alpha_0\omega+3}{\alpha_1\omega+W}[(\alpha_1\omega+W)(\alpha_3\omega+2+W)-W] -3W-3, \tag{4b}$$

$$\alpha_1'\omega'=(\alpha_1\omega+W)(\alpha_3\omega+2+W)-2W-W^2, \tag{4c}$$

$$\alpha_3'\omega'=\frac{\alpha_3\omega+2+W}{\alpha_1\omega+W}[(\alpha_1\omega+W)(\alpha_3\omega+2+W)-W] -2-3W-W^2, \tag{4d}$$

$$\tilde{P}_{i'}'=\frac{\alpha_1\omega+W}{(\alpha_1\omega+W)(\alpha_3\omega+2+W)-W}\tilde{P}_i. \tag{4e}$$

The nonlinear dependence on ω of the new frequency ω', as implied by Eqs. (4b)-(4d), is a standard memory effect associated with dynamical coarse graining. Thus in a complete RG treatment one has to consider recursions for functions $\alpha_i(\omega)$, and Eqs. (4b)-(4d) are put in the form

$$\boldsymbol{\alpha}'(\Lambda\omega)=\mathbf{f}(\boldsymbol{\alpha}(\omega),W), \tag{5}$$

where $\alpha_i(\omega)$ and $\alpha_i'(\Lambda\omega)$ replace $\alpha_i\omega$ and $\alpha_i'\omega'$ on the right- and left-hand sides of Eqs. (4b) and (4c), respectively. In Eq. (5) Λ has to be chosen such to guarantee that $\boldsymbol{\alpha}^{(n)}(\omega)$ approaches a finite, not identically zero fixed point, $\boldsymbol{\alpha}^*(\omega)$, under iteration. In standard treatments this can be implemented by choosing Λ to be the maximum eigenvalue of the ω linearized recursions,

$$\boldsymbol{\alpha}'=T(W)|_{W=W^*}\boldsymbol{\alpha}, \tag{6}$$

near $\omega=0$, where

$$T_{ij}=\left.\frac{\partial f_i(\boldsymbol{\alpha},W)}{\partial\alpha_j}\right|_{\boldsymbol{\alpha}=0},$$

and W^* is the fixed point value of W. This is, e.g., the case when we consider $W^*=1$, according to Eq. (4a). In such a case $\Lambda=2^{1/\nu}=6$ and the average distance traveled after a time t behaves asymptotically as t^ν, with $\nu=\ln 2/\ln 6$ [6]. At the fixed point $W^*=0$, controlling biased diffusion, however, the matrix in Eq. (6) is singular. For $W\to 0$, the diverging components of $\boldsymbol{\alpha}$ are multiplied by factors $2/W$. This, together with the rescaling relation (4a), suggests to look for a fixed point $\boldsymbol{\alpha}^*(\omega)$ of Eq. (5) by putting $\Lambda=\Lambda(W)=2/W^{1/2}$. If this fixed point is attractive in the domain $W<1$, the ω rescaling $\Lambda(W)\overset{W\to 0}{\sim}2^{1/\nu}\to\infty$ implies $\nu=0$, as anticipated in the introduction [12]. To extract the correct long time behavior of the average diffusion distance we use here a simplified procedure in which the $\omega\to 0$ limit is carried out in advance in Eqs. (4b)-(4e), by keeping everywhere only terms to leading order in ω. As anticipated, the most interesting fixed point of Eq. (4a) is $W^*=0$, which controls all biased ($W_-<W_+$) situations. To discuss long time ($\omega\to 0$) scaling, the most suitable quantity turns out to be

$$\bar{R}(\boldsymbol{\alpha}\omega,W)=\sum_j \alpha(j)\omega\tilde{P}_j(\omega)r_j\,, \tag{7}$$

where r_j is the scalar distance of j from the origin. The reason for this choice is the fact that from Eq. (3) it follows that $\sum_j \alpha(j)\omega\tilde{P}_j=1$ and that, under recursions (4a)–(4e), this normalization is preserved [13]. In view of this basic property, it is not difficult to prove that, under renormalization, $\bar{R}\to 2^{-1}\bar{R}$, since 2 is our rescaling factor. The $\omega\to 0$ scaling behavior of $\bar{R}$ can be extracted by envisaging an iterated application of the RG transformation

$$\bar{R}(\boldsymbol{\alpha}\omega,W)\simeq 2^n\bar{R}(\boldsymbol{\alpha}^{(n)}\omega,W^{2^n})\,, \tag{8}$$

with $\boldsymbol{\alpha}^{(n)}=\prod_{m=0}^{n-1}T(W^{2^m})\boldsymbol{\alpha}$. The $\tilde{P}$'s entering in $\bar{R}$ on the right-hand side of Eq. (8) are given by a similar iteration of Eq. (4e) n times. For increasing n the leading contributions to $\boldsymbol{\alpha}^{(n)}$ can be estimated as $(a_0 2^n/W^{2^n}, a_1 2^n, a_3 2^n/W^{2^n})$, the a_i's being suitable constants which depend on initial conditions. The denominators of $\alpha_0^{(n)}$ and $\alpha_3^{(n)}$ imply a strongly singular character of the RG mapping. Indeed, at the $W^*=0$ fixed point, the components would result infinite even for finite n. The singularity does arise from $2/W=\Lambda^2(W)/2$, the factor multiplying the diverging components of $\boldsymbol{\alpha}^{(n)}$.

Now suppose we let $\omega\to 0$ with $\omega 2^n/W^{2^n}$ kept constant, and equal to some $\hat{\omega}$. The behavior of $\bar{R}$ can be finally extracted from Eq. (8) if we have control on $\bar{R}(a_0\hat{\omega},\sim 0,a_3\hat{\omega},\sim 0)$. This can be done by inspecting the acceptable solutions of the system (3) in these limit conditions. A careful analysis of these solutions shows that $\bar{R}$ approaches a finite, nonzero limit and thus does not produce further singularities. On the basis of this, going back to Eq. (8) and taking into account that, to leading order, $2^n\sim\ln\omega/\ln W$, for $\omega\to 0$, $n\to+\infty$, at fixed $\hat{\omega}$, we get finally

$$\bar{R}(\bar{\alpha},\omega)\overset{\omega\to 0}{\sim}\frac{\ln\omega}{\ln W}\,. \tag{9}$$

Assuming $a_i\equiv 1$, $\forall i$, because of Eq. (7) the Laplace transform of the average diffusion distance behaves as

$$\langle\tilde{R}(\omega)\rangle\overset{\omega\to 0}{\sim}\frac{1}{\ln W}\frac{\ln\omega}{\omega}\,, \tag{10}$$

which implies

$$\langle R(t)\rangle\overset{t\to+\infty}{\sim}\frac{\ln t}{|\ln W|}\,. \tag{11}$$

Thus, as anticipated, the singular character of the RG mapping gives rise to logarithmic diffusion. An extra result in Eq. (11) is the logarithmic dependence on W. Since $W=1$ represents the unbiased situation [for which, taking into account that $\Lambda(1)=6$, our methods easily give $R(t)\overset{t\to+\infty}{\sim}t^{\ln 2/\ln 6}$], the amplitude in Eq. (11) has to diverge for $W\to 1^-$, consistent with the expected crossover. In the literature on biased diffusion, logarithmic amplitude dependences on the bias strength [14], like that in Eq. (11), have only been conjectured on the basis of numerical evidence or heuristic arguments [3]. It is remarkable, in our opinion, that our RG treatment naturally yields the amplitude result in addition to logarithmic diffusion.

As mentioned above, a simplifying assumption we made was the possibility of treating the mapping to leading ω order [Eqs. (4)] when discussing the limit of Eq. (8). To corroborate our confidence in the validity of Eq. (11) we chose to try our RG strategy on a problem for which logarithmic diffusion is naturally expected, with an exponent which, like in the case of Sinai's model, can be easily guessed by a potential barrier argument. We indeed consider a deterministic generalization of Sinai's model [15]. This is a $d=1$ structure made of unbiased (line with open circle), right biased (line with rightward-pointing arrow), and left biased (line with leftward-pointing arrow) bonds in one dimension. The structure is built up by iteration according to the inflation rules illustrated in Fig. 3(a), starting, e.g., with a left biased bond at stage zero. Hopping across a biased bond is favored (unfavored) when taking place in the same (opposite) direction of the bias, while unbiased bonds are crossed with equal probability in both directions. In this situation, since the net potential barrier accumulating for a length R is $R^{\ln 2/\ln 3}$ (see Fig. 3), we expect $t\sim\exp(R^{\ln 2/\ln 3})$, i.e., $R\sim(\ln t)^{\ln 3/\ln 2}$. We verified the validity of this result on the basis of the same RG method applied to the T fractal. Details on this calculation, which is quite complicated and involves five a parameters, will be reported elsewhere. Here it suffices to report that in this example the expected logarithmic behavior of R is indeed extracted by an exact RG transformation with singular structure, of the same kind as that discussed above. A logarithmic bias field dependence of the amplitude is found also in this case.

All this gives further strong confidence that the results of our RG approach to the T fractal are correct. Thus, the T fractal offers a solid example of a new type of logarithmic diffusion, which cannot be reduced to the usual one-dimensional barrier mechanism. In our model logarithmic diffusion results from the existence of ramifications at all length scales. Without these ramifications a bias would typically produce a full localization, i.e., $\langle R(t)\rangle\overset{t\to+\infty}{\sim}$ const. This is, e.g., the case when biased diffusion on a half straight line is considered, a process which can also be exactly described by our RG method.

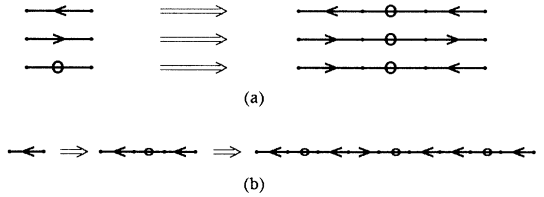

FIG. 3. (a) Inflation rules for the construction of the one-dimensional array of biased bonds. Notice the introduction of unbiased bonds. (b) Inflation growth scheme.

There are good reasons to believe that in the situations realized by numerical experiments, e.g., on biased diffusion on percolation clusters [2,3], the mechanisms leading to logarithmic time dependence of R should be qualitatively similar to those described in the T fractal. The cluster indeed is a fractal structure, essentially made up of dangling ends, which, under the action of an external field, should behave similarly to the branches of our model with respect to the hopping particle.

Results similar to those described for the T fractal above can also be obtained for models within the same family [11]. For example, for the structure in Fig. 2 we obtain again the results (9)–(11) since, under RG, the ratio between rescalings in Euclidean and chemical distances is 1 also in this case.

An advantage of our RG method, even with respect to other exact approaches, is that it also gives control of the bias dependence of the amplitudes.

Apart from this, it seems worth pointing out that, from a methodological viewpoint, to extract logarithmic, rather than power law dependence, from an RG strategy, implies the use of a singular transformation, a feature which openly contradicts the usual postulates made in the approach. Here we showed that giving up the analyticity of the transformation can lead to the possibility of describing phenomena like logarithmic diffusion on a fractal.

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[11] This is the most simple example in $d=2$ of a whole class of ramified fractals in d dimensions, which can all be treated with our methods (see Fig. 2).

[12] We performed a numerical check of the existence of such an attractive fixed point. This analysis is hindered by the singular behavior of Λ, which allows us to control satisfactorily only a limited number (≤ 10) of iterations of Eq. (5). Nevertheless we obtained evidence that indeed the nth iterated of Eq. (5) approach a fixed point, with $\alpha_3^*(\omega)$ and $\alpha_0^*(\omega)$ not identically zero and $\alpha_1^*(\omega)\equiv 0$.

[13] Notice that, if in the initial model $\alpha_0=\alpha_1=\alpha_3=1$, $\bar{R}$ is nothing but the Laplace transform of the average diffusion distance multiplied by ω. The inequivalence of the sites imposes $\bar{R}$ as the natural quantity to discuss in the RG framework.

[14] Ratios like W are normally put in the form $W=(1-E)/(1+E)$ with E playing the role of topological bias field in our case.

[15] A model very similar to the one discussed below, involving pseudorandom sequences of biases in $d=1$, based on the Tue-Morse succession, has been recently discussed by S. Goldstein, K. Kelly, J. L. Lebowitz, and D. Szasz, Physica (Amsterdam) **38D**, 141 (1989). For this model they prove Sinai-like diffusion, but do not compute the bias dependence of the amplitude.