Failure of the Harris criterion for directed polymers on hierarchical lattices

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Exact real space renormalization group analysis shows that the Harris criterion can be violated for two randomly interacting directed polymers on a hierarchical lattice with branching factor b. The interaction energy when the polymers meet on the same bond is random. For a particular case, we find a negative crossover exponent ϕ for disorder when b > 2, even though the specific heat exponent α is positive for $b>2+\sqrt{2}$. Other cases are also considered. General conditions for the validity of the Harris criterion for this system are determined.

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I. INTRODUCTION

According to the Harris criterion, a small disorder at the pure fixed point is relevant if the specific heat exponent α at the pure transition point is positive and vice versa [1]. However, this prediction is contested when, for the disordered Potts model constructed on a particular hierarchical lattice (Fig. 1) with asymmetric bond, the disorder turns out to be relevant in a range of negative α [2]. Consequently, it violates the corollary of the Harris criterion that at the critical point of the pure system the crossover exponent ϕ is equal to α [3,4]. Since real space renormalization group (RSRG) can be implemented exactly on hierarchical lattices [5,6] and this scheme can be thought of as an approximate RSRG for Euclidean lattices [7], the failure of the Harris criterion (see also [8]) cannot just be ignored. Furthermore, based on the results for the Potts model, a belief has emerged that the Harris criterion can be violated only if there are asymmetric bonds in a block [see Fig. 1(b)]. One of our aims is to show that the myth is not necessarily true.

We consider the problem of two randomly interacting directed polymers (DP's) on hierarchical lattices with no asymmetric bonds. DP's are polymers with fluctuations in the transverse directions and a special longitudinal direction along which they are stretched. By choosing various forms of disorder, we show that the relevance or irrelevance of disorder is not very simply dictated by the sign of $2 - d\nu$ or α , where ν is the correlation length exponent and d is the relevant dimension. We show that the crossover exponent need not be either of the two.

There have been a lot of studies on directed polymers in random media or with random interaction because of the simplicity of the system [9-11]. It has been shown that the randomly interacting case enjoys the rather unusual property of solvability via RG, with nontrivial phases [10,11]. This makes them an important object for further studies.

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We define the pure and the random models in the next section. The RG scheme for the pure case is discussed in Sec. III. Section IV deals with the RG of the random problem. Our interest here is in the behavior of the disorder near the pure critical point, and the applicability of the Harris criterion. In Sec. V, a general framework is developed to rationalize these results. In this way we can show under what conditions a hierarchical lattice with no asymmetric bond can lead to a violation of the Harris criterion. We, in the process, identify the appropriate quantity that determines the relevance or irrelevance of disorder. Since, as already mentioned, the exact RG on a hierarchical lattice can be thought of as an approximate Migdal-Kadanoff scheme on a real lattice, the inequalities obtained in this section would be applicable to such approximate schemes also.

II. MODELS: PURE AND RANDOM

The recursive construction of the hierarchical lattice of generation n needs a replacement of each bond of generation n-1 by a motif of N bonds [6]. See Fig. 1. The effective dimension is generally taken as $d_{eff} = (\ln N) / \ln 2$.

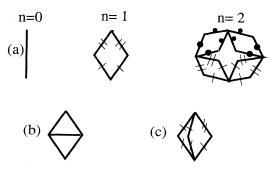


FIG. 1. (a) Construction of hierarchical lattice with b=2. RG procedure takes a lattice from the right to the smaller one on the left. For model B, similarly marked bonds have identical energies. (b) A motif with an asymmetric bond. (c) A special choice of randomness for b = 3 (see text, Sec.V).

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In this paper, we consider only lattices with N=2b, as in Fig. 1(a).

We place two interacting DP's on a hierarchical lattice. They start from one end of the lattice and meet at the other end. There is an attractive interaction -v (v > 0) if a bond of the lattice is shared by the two DP's. As in real space, here also the DP's undergo a binding-unbinding transition for b > 2.

Randomness is introduced by allowing the interaction energy to be random on each and every bond. The first model, model A, has independent random energy on all the 2b bonds. The randomness in the second model, model B, is taken only along the longitudinal direction so that equivalent bonds on all directed paths have identical random energy [see Fig. 1(a)]. Model B is a hierarchical lattice version of the continuum model of Refs. [10,11]. This model B is also relevant for localization of an interface near a wall (wetting), which has been studied in the past [12]. Other generalizations are also considered.

III. PURE PROBLEM: RENORMALIZATION GROUP

The pure problem can be solved easily by a RSRG approach where one needs only the renormalization of the Boltzmann factor $y = \exp(\frac{v}{kT})$ (T being the temperature in units of the Boltzmann constant). Let y_n and y_{n-1} be the renormalized weights at the nth and (n-1)th generation. By decimating the diamonds the recursion relation is given by

$$y_{n-1} = (y_n^2 + b - 1)/b. (1)$$

The two fixed points of the quadratic recursion relation, Eq. (1), are 1 and b-1 of which the larger one is the unstable fixed point representing the transition point. Since y > 1 there is a transition at $y_c = b - 1$ only for b > 2. The other fixed point $y^* = 1$ corresponds to the high temperature limit.

The length scale exponent ν can be obtained from $2^{1/\nu}=dy_{n-1}/dy_n\mid_{y_c}$ which gives

$$\nu = \frac{\ln 2}{\ln[2(b-1)/b]}. (2)$$

Since the polymer is a one-dimensional object, the extensivity of the various thermodynamic quantities are with respect to the length of the chain (e.g., specific heat per bond). Standard rules [7] then give the specific heat exponent from the singular part of the free energy as

$$\alpha = 2 - \frac{\ln 2}{\ln[2(b-1)/b]} = 2 - \nu,$$
 (3)

which vanishes for $b=2+\sqrt{2}$. Note that $\alpha<0$ for $b<2+\sqrt{2}$. It is clear that hyperscaling holds good with d=1 and not the effective dimension d_{eff} of the lattice. As in the real space case, the length scale exponent ν may be interpreted as the exponent describing the growth of the average distance along the length of the chain between two shared bonds.

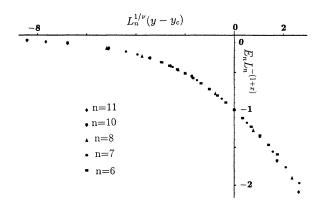


FIG. 2. Data collapse of E_n in terms of appropriate scaled variable for b=4.

It is also gratifying to observe that the same ν describes the finite size scaling form for any thermodynamic quantity [13]. For example, the recursion relation for the average energy E_n at the nth generation is

$$E_{n+1} = \frac{2}{b} \frac{Z_n^2 E_n}{Z_{n+1}},\tag{4}$$

where $Z_{n+1}=(Z_n^2+b-1)/b$ with $Z_0=y$. At the critical point $y=y_c$, the growth of the energy is given by $E_n\sim L_n^{1+x}$ where $L_n=2^n$ is the length of the polymer, and $x=(\ln 2)^{-1}\ln[2(b-1)/b]-1$. This value of the exponent agrees with the finite size scaling prediction of $x=(\alpha-1)/\nu$. Furthermore, Fig. 2 verifies, through data collapse, that for $y\neq y_c$ the energies for small generations do obey a finite size scaling form $E_n/L_n=L_n^x f(L_n^{1/\nu}y)$, where $y=y-y_c$, with the same ν as in Eq. (2).

IV. RANDOM CASES

For the disordered case, the recursion relation for the Boltzmann weight can be written as

$$y_{n-1} = b^{-2} (y_n^{(11)} y_n^{(12)} + y_n^{(21)} y_n^{(22)} + \cdots y_n^{(b1)} y_n^{(b2)}) + (b-1)b^{-1},$$
 (5)

where $y_n^{(ij)}$ is the Boltzmann weight in the nth generation for the disorder on the upper (j=1) or lower (j=2) part of the ith branch as in Fig. 1. To understand the effect of the disorder at the pure critical point we introduce a small disorder $y_n^{(ij)} = y_c + \epsilon_n^{(ij)}$. The average of the disorder, $\bar{\epsilon}$, acts like the temperature as it measures the deviation from the pure critical point. (Henceforth, the disorder averaged quantities will be denoted by an overbar.) The second moment is the measure of disorder. In principle, one should look at the variance, but at the pure critical point the variance would be the same as the second moment. Since our motivation is to find the flow of the disorder at the pure fixed point, we need only study the first two moments. Therefore, we do not have to specify the full distribution, the only requirement is the existence of a finite and small variance.

The crossover exponent for the disorder is defined

through the homogeneity of the singular part of the free energy in terms of the scaling fields μ_1 (temperature) and μ_2 (disorder). Under decimation, the free energy behaves as

$$f_{sing}(\mu_1, \mu_2) = \frac{1}{2} f_{sing}(\lambda_1 \mu_1, \lambda_2 \mu_2) = \mu_1^{2-\alpha} G(\mu_2/\mu_1^{\phi}),$$

defining ϕ . The scale factors $\lambda_{1,2}$ are obtained from the eigenvalues of the matrix M with elements $M_{k,l} = \partial \overline{\epsilon_{n-1}^k} / \partial \overline{\epsilon_n^l}$, where $\overline{\epsilon_n^l}$ is the lth moment in the nth generation. The crossover exponent is given by $\phi = \ln \lambda_2 / \ln \lambda_1$.

Let us first consider model A for which energies are independently random on all bonds. Restricting ourselves to the first two moments, the elements of the 2×2 matrix M are obtained from Eq. (5). This matrix is diagonal at the pure fixed point, $\overline{\epsilon} = 0$, $\overline{\epsilon^2} = 0$. The eigenvalues are then

$$\lambda_1 = 2(b-1)/b$$
 and $\lambda_2 = 2y_c^2/b^3$. (6)

The largest eigenvalue λ_1 determines α in agreement with Eq. (3). The crossover exponent

$$\phi = \{\ln[2(b-1)/b]\}^{-1}\ln(2y_c^2/b^3) \tag{7}$$

is negative for all b>2, implying irrelevance. Note that $\phi\neq\alpha$ but it is equal to $2-d_{eff}\nu$. It is a simple exercise to show that at the pure fixed point if the second moment is irrelevant then so are all the higher ones. We skip the details.

For model B, the above procedure gives $\lambda_2 = 2y_c^2/b^2$, and λ_1 the same as model A. The crossover exponent is

$$\phi = \ln[2(b-1)^2/b^2] \left\{ \ln[2(b-1)/b] \right\}^{-1}.$$
 (8)

Now we see, for model B, that $\phi=\alpha$ and not $2-d_{eff}\nu$. Since the randomness in model B is highly correlated, the Harris criterion is less expected to be valid here as opposed to model A. Oddly enough, it turns out to be so. The difference between the two cases begs for a further study of the flow diagram in the $\bar{\epsilon}$ and $\epsilon^{\bar{2}}$ space. The important feature to keep in mind is the instability of the larger root of a quadratic map. If the nontrivial fixed point of $\bar{\epsilon}^{\bar{2}}$ at $\bar{\epsilon}=0$ is in the unphysical negative region, then disorder has to be relevant. But if it is in the physical region (i.e., $\bar{\epsilon}^{\bar{2}}>0$), the disorder becomes irrelevant.

V. GENERAL FORMULATION

In order to construct a general framework for predicting the validity of the Harris criterion, we start with the Taylor expansion of the recursion relation of Eq. (5). If N is the total number of bonds in a block (2b in our examples) and if the recursion relation has the permutation symmetry in the bonds, then

$$\epsilon = g_s(b)(\epsilon_1 + \epsilon_2 + \dots + \epsilon_N) + O(\epsilon_i^2) + \dots,$$
 (9)

which defines $g_s(b)$. Simple arguments show that $g_s(b)$ determines α whose positivity is guaranteed if

$$g_s(b) > \sqrt{2}N^{-1}.$$
 (10)

This gives the critical b as found after Eq. (3).

The requirement for the relevance of the disorder comes from the flow diagram in the $\overline{\epsilon}, \overline{\epsilon^2}$ parameter space. Now, suppose that the bonds are grouped in n sets with N_i bonds in the ith group such that the members of a set have the same randomness. Obviously $\sum N_i = N$. This implies that $\overline{\epsilon_i}\overline{\epsilon_j} = 0$ if i and j belong to two different sets. Starting with a narrrow distribution, the relevance of the disorder at the pure transition, i.e., at $\overline{\epsilon} = 0$, requires

$$g_s(b) > (N_1^2 + N_2^2 + \dots + N_n^2)^{-1/2}.$$
 (11)

Hence, the Harris criterion holds good if either

$$g_s(b) > \max\left[\sqrt{2}N^{-1}, \left(\sum N_i^2\right)^{-1/2}
ight],$$

or

$$g_s(b) < \min \left[\sqrt{2} N^{-1}, \left(\sum_i N_i^2 \right)^{-1/2} \right].$$
 (12)

Let us now consider the models case by case. For model A, we have N=2b and $N_i=1$ $\forall i$, since all bonds have independent randomness. We see that $g_s(b)=(b-1)/b^2$ always satisfies the inequality $\frac{\sqrt{2}}{N} < g_s(b) < \frac{1}{\sqrt{N}}$ if $b > 2+\sqrt{2}$ and therefore the Harris criterion is violated in this regime. For model B, n=2 with $N_i=b$. Consequently, it is the same limits for Eqs. (10) and (11) and therefore the Harris criterion applies in toto.

If the disordered models are classified by \pm according to the sign of α , and I (R) for irrelevance (relevance) of disorder, then the Harris criterion suggests the existence of only two classes (+R) and (-I). On the other hand, the above inequalities allow special classes like (+I) and (-R) where the Harris criterion fails. Model A is in the (+I) class for $b > 2 + \sqrt{2}$. Model B is in either the (+R) or (-I) class depending on b.

It is possible to construct disorder models that can be in any of the four classes mentioned above. For example, take b=3, and out of six take five bonds to have the same random energy while the other one has an independent randomness, as, e.g., in Fig. 1(c). That is, n=2 with $N_1=5, N_2=1$. This gives $\phi=0.868\,812...$ which is neither α nor $2-d\nu$. The model belongs to the (-R)

Since $\sum_{i=1}^{n} N_i = 2b$, $\sum_{i=1}^{n} N_i^2/(4b^2) \geq 1/n$, yielding $\phi \geq 2 - \nu(\ln n)/\ln 2$. The equality in both cases is valid only when all the N_i 's are equal (i.e., $N_i = 2b/n$). In this particular situation, it is natural to interpret $\ln_2 n$ as the effective dimension d_r of the random bonds. In such a case, $\phi = 2 - d_r \nu$, with models A and B serving as the two extremes. Such a simple interpretation is not possible if the N_i 's are not all equal.

VI. SUMMARY

To summarize, we have shown that, for randomly interacting DP's on hierarchical lattices, it is not α but g_s , the derivative of the recursion relation of the pure problem, that controls the relevance or irrelevance of disorder.

Needless to say that g_s also determines α . As a result, there is the possibility of violating the Harris criterion, and we have explicitly constructed several such models. They do not require any asymmetric bonds. This analysis can be extended to asymmetric systems also.

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