LETTER TO THE EDITOR

Scaling of fluctuation for directed polymers with random interaction

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Abstract. Using a finite size scaling form for reunion probability, we show numerically the existence of a binding–unbinding transition for directed polymers with random interaction. The cases studied are (A1) two chains in $1 + 1$ dimensions, (A2) two chains in $2 + 1$ dimensions and (B) three chains in $1 + 1$ dimensions. A similar finite size scaling form for fluctuation establishes a disorder-induced transition with identical exponents for cases A2 and B. The length scale exponents in all the three cases are in agreement with previous exact renormalization-group results.

Disorder is often found to give rise to complicated but rich phenomena in nature, an excellent example of which is the existence of the spin–glass transition and the spin–glass phase [1]. Needless to say, one has to look beyond the reality, and study simpler models that retain only the essential features believed to be responsible for such new events [1]. Directed polymers[+] (DP) in random media [2–4] or with random interactions [5, 6] provide a fruitful basis in this regard because of its inherent simplicity. By virtue of mappings to nonlinear, noisy surface growth equations [2, 7], and other applications, DPs have become relevant in a broader context. A crucial result established for directed polymers in random media [3] is the existence of a strong disorder 'spin–glass'-type phase at $d = 1$, and a lower critical dimension, $d = 2$, beyond which a disorder-induced transition exists. For the random interaction case there is also a weak to strong disorder transition [5–7]. Directed polymers are also simpler than the more complex problem of undirected polymers in random medium [8, 9]. Similarly, many heteropolymer (undirected) problems, especially biopolymers, require random interaction [10], and DPs with random interaction quite often serve as a simpler solvable limit [11].

In this letter, we concentrate on the disorder-induced transition in directed polymers with random interaction (RANI), to explore the scaling behaviour of fluctuation due to quenched disorder. The essential feature here is the mutual short-range interaction which is random, as might arise when there is a random charge distribution along the length of the polymer. A different version of our model appears in the context of wetting phenomena in the presence

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[+] A $(d + 1)$-dimensional directed polymer is a random walk stretched in a particular direction with fluctuations in the transverse d-dimensional space.

of disorder at $d = 1$ [12]. For the RANI model, unlike the random medium problem, an exact renormalization group (RG) can be implemented under certain conditions [5, 6]. We would like to verify the length scale exponents obtained from the perturbative RG. This verification is essential for further applicability of RG for the disorder problem to ensure that there are no non-perturbative effects. For comparison, one might point out the situation for the random medium problem. For the weak to strong disorder transition, RG [13, 14] predicts a length scale exponent $2/(d - 2)$ for $d > 2$ while numerical calculations [15, 16] for $d = 3$ gave numbers as different as 4.2 and 6.7. We establish here that, unlike the random medium case, the RANI model is better controlled.

For generality let us start with a system of m polymers each of length N with a random m body (mth-order multicritical) interaction. The model in a continuum formulation is given by

$$\mathcal{H}_m = \frac{1}{2} \sum_{i=1}^{i=m} \int_0^N \left(\frac{\partial \boldsymbol{r}_i(z)}{\partial z} \right)^2 + \int_0^N \mathrm{d}z \, v_m(1 + b(z)) \prod_{i=2}^m \delta(\boldsymbol{r}_i(z) - \boldsymbol{r}_{i-1}(z)) \tag{1}$$

where $\boldsymbol{r}_i(z)$ denotes the d-dimensional transverse spatial coordinate of the ith polymer at contour length z. The first term denotes the elastic energy part of the Gaussian chains and the second term denotes the mutual random contact interaction among the chains. Note that the interaction is always at equal length with a random part $b(z)$ in the coupling constant. The randomness is dependent only on the length z at which the interaction occurs. This is what one expects for a random monomer distribution along the backbone. More general randomness can arise [17] but will not be considered here†. In the following analysis we shall consider a binary distribution for the disorder with equal probability.

We study this system (actually, a discrete version of this) numerically by generating the partition function recursively along the length of the chain. The cases considered are (A1) the two-chain problem ($m = 2$) for $d = 1$, (A2) two chains in $d = 2$, and (B) three chains with three-body interaction ($m = 3$) for $d = 1$. The reason for choosing the last two cases, as explained below, is that $d = 2$ ($d = 1$) is the marginal case for the two-body (three-body) interaction problem. Instead of analysing large systems as has been done in [7] for $m = 2$ and $d = 1$, we use finite size scaling to calculate the exponents for various cases.

The pure counterpart of the disordered model, equation (1) is at present well understood through the renormalization-group analysis [19, 20] or by solving the Schrödinger-type equations for the two-body problem [21]. An exact RG shows that there is a bound state for any small attraction for $d < d_c = d_m^{\text{pure}} = 2/(m - 1)$. This binding–unbinding transition is seen over a characteristic length scale $\xi_\parallel \sim |v_m|^{-\nu}$, with $\nu = 2/|\epsilon_m|$, and $\epsilon_m = (m - 1)(d - d_m^{\text{pure}})$. The length scale $\xi_\parallel$ is a measure of the average separation between two contacts along the chain. For repulsive energy, the phase is governed by a stable fixed point where the corresponding scale-invariant theory is described by an infinite strength of the repulsion or a fermion-like behaviour. For $d > d_m^{\text{pure}}$, a threshold for the strength of the attraction is required for the bound state while for smaller attraction or any repulsion, the chains are asymptotically free. Exactly at $d = d_m^{\text{pure}}$, the system is at its marginal dimension where the repelling chains are again like free Gaussian chains but with certain log corrections, and the characteristic length scale diverges exponentially as the transition point is approached.

The random system exhibits certain new features. The fact that the disorder becomes marginally relevant at $d = 1$ for the two-body problem was observed in the context of the

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† In fact, equation (1), for two-body interaction, is the random version of the Hamiltonian used to study the flux lattice melting problem in high T_c superconductors [18]. In a simple picture, the effects of impurities can be thought of as producing random interactions among the flux lines.

disordered wetting phenomena [12]. The exact renormalization-group (RG) analysis [5, 6] reveals, besides establishing this marginal relevance, that there is a disorder induced phase transition beyond the critical dimension $d_m^{\text{dis}} = 1/(m-1)$. The length scale exponent for this transition is found to be $\xi_\parallel^{\text{dis}} \sim (\Delta - \Delta_c^{\text{dis}})^{-\nu_r}$ with $\nu_r = 2/(m-1)(d - d_m^{\text{dis}})$, Δ being the variance of disorder. The critical value of disorder is Δ_c^{dis}. Exactly at the critical dimension d_m^{dis}, any small disorder leads to a strong disorder behaviour over a characteristic length scale $\xi_\parallel^{\text{dis}} \sim \exp(1/\Delta)$. However, in none of the above cases was it possible to investigate the strong disorder limit because of the absence of any perturbative strong coupling fixed point. To investigate further, a real space RG has been performed on the hierarchical lattice that brought out several new features [22]. A dynamic renormalization-group approach also recovered these results and furthermore showed that there is no anomalous exponent for the free energy [7]. This suggests that the effect of disorder is reflected in the various cumulants of the partition functions that characterize the phases and phase transitions [5, 6].

For the pure system, the unbound phase is characterized by the reunion partition function $\mathcal{Z}_{R,m}(N)$ which is the sum of the Boltzmann weights of all paths corresponding to the meeting of m chains at any point in (transverse) space at length N, the other end being tied together at the origin. Similarly, one can define a survival partition function $Z_{S,m}(N)$ for the chains tied at the origin at one end but located anywhere at the other end. The ratio of the two defines the probability of reunion. It has been shown that the reunion and the survival partition functions, and hence the probability, acquire anomalous scaling at the stable fixed point at $d = 1$ [23, 24]. Detailed RG analysis yields the $d = 1$ exact (vicious walker) result that $\mathcal{Z}_{R,2}(N) \sim N^{-3/2}$, and predicts that for marginal cases $d = d_m^{\text{pure}}$, the m chain reunion with m-body interaction has the form $\mathcal{Z}_{R,m}(N) \sim N^{-1}(\ln N)^{-2}$ [24, 25]. These cases include the two chain problem at $d = 2$ and three chain at $d = 1$. The identical log correction, originating from the marginality of the interaction at the appropriate dimensions, is an example of 'grand universality' for the directed polymer multicritical points [20]. This feature is preserved in the random case also.

For the pure versions of cases A1, A2 and B, the unbinding critical point is at $v_m = 0$, for which the chains are free. Therefore, around the transition, one can write a finite size scaling form

$$N^{(m-1)d/2} \mathcal{Z}_{R,m}(N) = \mathcal{F}(x) \tag{2}$$

where $x = |v_m| N^{1/\nu}$ for two chains in one dimension and $x = |v_m| \ln N$ for $m = d = 2$ and $m = 3, d = 1$. A similar scaling form can also be written for the probability of reunion. A typical case is shown in figure 1.

The partition function for the chains is generated recursively in their length. For the two-chain problem, since the randomness is only along the z direction, only the relative chain is considered. The centre of mass is a free Gaussian chain. This transformation is not possible for three chains and we consider the full partition function.

For two chains with pair interaction, the recursion relation is given by

$$Z(\boldsymbol{r}, t+1) = \mathrm{e}^{-\eta} \left[\sum_{i=1}^{d} \{ Z(\boldsymbol{r} + \hat{e}_i, t) + Z(\boldsymbol{r} - \hat{e}_i, t) \} + p Z(\boldsymbol{r}, t) \right] / (2d + p) \tag{3a}$$

with $\hat{e}_i$ as unit vectors in the ith direction, and $\boldsymbol{r}$ denoting the position vector for the end point. A weight factor p has been put in for extra weightage of the relative chain. We have set p equal to 4. The random energy $\eta = v_m \pm \Delta$, with equal probability, whenever $\boldsymbol{r}$ is zero. In this relative coordinate, $\mathcal{Z}_{R,2}(N) = Z(\mathbf{o}, N)$, and $Z_{S,2}(N) = \sum_{\boldsymbol{r}} Z(\boldsymbol{r}, N)$. For
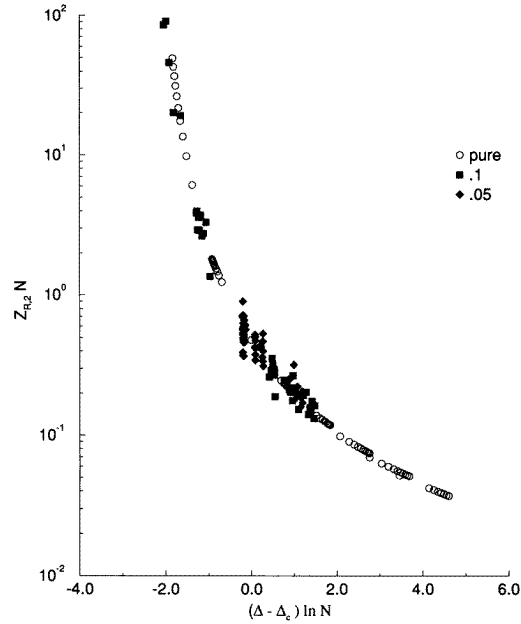
Figure 1. Data collapse for pure and random cases, two chains in $2 + 1$ dimensions. For the pure case, the y-axis is $N\mathcal{Z}_{R,2}(N)$ while for the random case it is $N\langle\mathcal{Z}_{R,2}(N)\rangle$. The x axis is $|v_2|\log N$ for the pure case but $(\Delta - \Delta_c)\log N$ for the random case. The legend shows the values of v_2 for the random case.

three chains in $d = 1$,

$$Z(x, y, z, t + 1) = e^{-\eta} \left[\sum_{i,j,k=\pm 1} Z(x + i, y + j, z + k, t) \right] / 8 \qquad (3b)$$

where the Boltzmann factor for the randomness contributes only for $x = y = z$, i.e. only when three chains meet together. All chains start at origin at $t = 0$. For the three-chain case, $\mathcal{Z}_{R,3}(N) = \sum_x Z(x, x, x, N)$, and $Z_{S,3}(N) = \sum_{x,y,z} Z(x, y, z, N)$.

The randomness reduces the strength of the interaction. The effective interaction $\bar{v}_m$, determined by

$$\exp(-\bar{v}_m) = [\exp(-v_m - \Delta) + \exp(-v_m + \Delta)]/2 \qquad (4)$$

controls the binding–unbinding transition. Since for all the three cases the pure binding–unbinding transition takes place at zero energy (i.e. Boltzmann factor $= 1$), the transition point for a fixed v_m is given by

$$v_m = \ln \cosh \Delta_c . \qquad (5)$$

As a result a bound state can form even for $v_m > 0$. In other words, a thermal unbinding is possible because randomness produces attractive pockets. The scaling of equation (2) can be rewritten as $N\langle\mathcal{Z}_{R,m}(N)\rangle = \mathcal{F}(x)$, where, for cases A2 and B, $x = (\Delta - \Delta_c) \ln N$ for a given v_m with Δ_c satisfying equation (5).

We computed the average reunion and survival partition functions, and also the average probability of reunion where the probability for a given realization is defined as $P(N) = \mathcal{Z}_{R,m}(N)/Z_{S,m}(N)$. The main distinction is that while the first two quantities may be considered as annealed averaging, the last one is strictly a quenched averaged quantity. For a given realization, the recursion relation gives exact values (up to the machine precision) of the partitions functions. An averaging over the disorder is done by considering around 500 samples. The lattice size is chosen such that the average transverse size of a polymer ($\sim N^{1/2}$) does not exceed it (to avoid boundary effects).

For a fixed strength of v_2, we plot, in figure 1, the data for different Δ, with the scaled variables $\langle \mathcal{Z}_{R,m}(N) \rangle N$ as $(\Delta - \Delta_c) \ln N$. This plot shows a nice data collapse on the pure curve with Δ_c chosen as per equation (5) for two different values of v_2. It verifies the exponential divergence of the length scale near the transition. We have also checked similar data collapse for the other cases and various values of v_m. The main inference we draw from this is that for the average chains in the presence of disorder, the nature of the transition remains the same as the pure system except for a shift in the critical value. This also serves as a check on the simulation.

With the above knowledge, we consider a particular value Δ and force the system to be strictly at the transition point of unbinding by choosing appropriate v_m. The specific quantity we calculate is the fluctuation in the reunion partition function or the fluctuation in the probability of reunion. The raw data for the cumulant $\langle P^2 \rangle_c$ have been plotted with N for various Δ with corresponding v_m determined by equation (5). In case there is a disorder induced transition we expect the following scaling to hold good close to this critical point Δ_c^{dis},

$$\langle P^2 \rangle_c = N^{-\phi} \mathcal{G}((\Delta - \Delta_c^{\text{dis}}) N^{1/\nu_r}) \tag{6}$$

where, according to the RG prediction of the divergence of the length scale near the transition point, $\nu_r = 1$ for cases A2 and B. If we believe in Grand Universality [5], the exponent ϕ should also be the same for these two cases. The plot with $\langle P^2 \rangle_c N^{\phi}$ versus $N(\Delta - \Delta_c^{\text{dis}})$ indeed shows a data collapse for a small value of $\Delta_c^{\text{dis}} < 0.05$ and $\phi = 2$. The two cases, A2 and B, for which the pure interaction is marginal, are shown in figures 2 and 3. Numerical accuracy forbids simulations for very small values of Δ and therefore the weak disorder phase cannot be probed in our simulation.

Figure 4 shows the data collapse for the case of two chains at $d = 1$. Since the disorder is expected to be always marginally relevant, the scaled variables for data collapse, from RG [5, 6], would be $\Delta \log N$. We obtain a data collapse for $\phi = 0.57 \pm 0.03$. This verifies the exponential divergence of the length scale for the situation where the disorder is marginal.

To conclude, we have shown that randomly interacting directed polymers undergo a binding–unbinding transition and, at the critical point, the fluctuation in the reunion partition
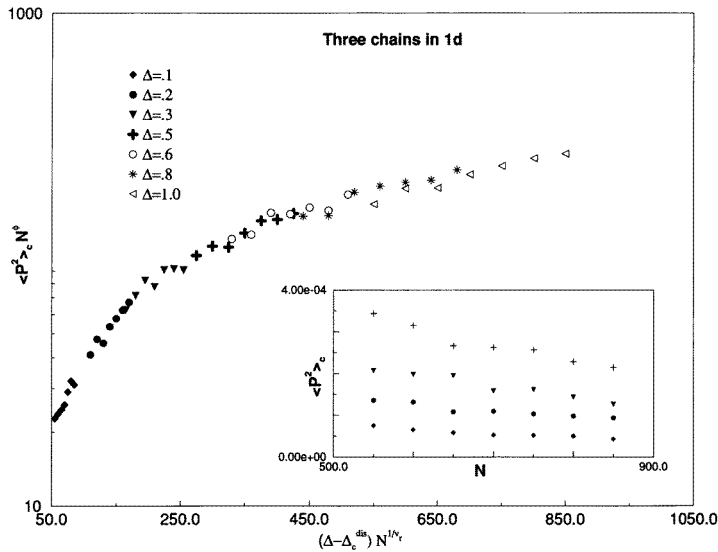

Figure 2. Data collapse for fluctuation of the reunion partition function. This is for two chains in $2 + 1$ dimensions. The exponent $\phi = 2$ and $\nu_r = 1$. The inset shows the fluctuations for various Δ and length scales.
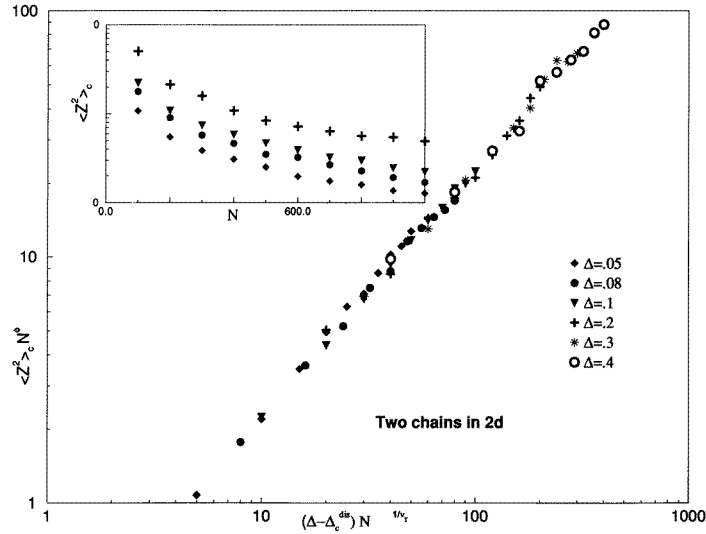
Figure 3. Data collapse for reunion probability for three chains in $1 + 1$ dimensions. The exponents are $\phi = 2$ and $\nu_r = 1$. The inset shows the variance for various Δ and length scales.
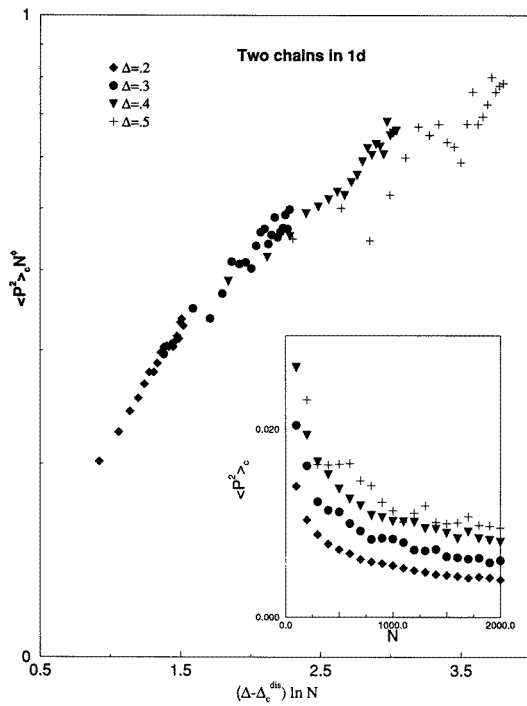

Figure 4. Data collapse for fluctuation of the reunion probability for two chains in $1 + 1$ dimensions. $\phi = 0.57 \pm 0.03$. The inset shows the variance as in figures 2 and 3.

function or the probability of reunion show scaling behaviour with length scale exponents that agree with RG prediction. A finite size scaling form, verified for the pure case, has been used to study the unbinding transition.. We also obtained the exponents that describe the fluctuation of the second cumulant. This exponent ϕ is the same for two chains in $(2+1)$ dimensions and three chains in $(1+1)$ dimensions for both of which the pure interaction is marginal.

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