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LETTER TO THE EDITOR

Exact fixed point for directed random walks

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Abstract. We have shown that the renormalization group fixed point for mutually avoiding directed random walks in $(d+1)$ dimensions is exactly $2\pi\epsilon$ where $\epsilon = 2-d$, with no higher order terms in ϵ . Since the whole calculation can be carried out to all orders exactly, the model is also significant from a pedagogical point of view.

A directed random walker (DRW) in $D = d + 1$ dimensions always takes steps in one particular direction (to be chosen as the z axis) but can fluctuate in the transverse d directions. Such walks, though of interest on their own, have also emerged as a viable statistical model from various physical problems such as polymers in random media (see, e.g., Kardar and Zhang 1987, Cook and Derrida 1989), two-dimensional commensurate-incommensurate phase transitions (see, e.g., Fisher 1984, Nagle *et al* 1989), biomembrane phase transitions (Izuyama and Akutsu 1982, Bhattacharjee *et al* 1983, Priezhev and Terletsky 1989), flux lattice melting in high T_c materials (Nelson and Seung 1989), world lines of anyons (Wu 1984) and the five-vertex model (Wu 1968, Bhattacharjee 1990). It is the preference for a particular direction that makes DRW a relatively simpler model to study rigorously and, in fact, many non-trivial properties of a DRW are known more or less exactly or rigorously (see, e.g., Privman and Svrakic 1989, also Binder *et al* 1990). In most of the examples cited above, the physics is determined by the properties of many mutually avoiding DRWs where two chains cannot be at the same position if they have the same z -coordinate, as shown in figure 1. Our interest in this letter is in such a many-chain system.

Nelson and Seung (1989), in their studies of flux lattice melting in high T_c superconductors, introduced a path integral approach for many DRWs, along the line of the Edwards model for conventional polymers with excluded volume interaction (see, e.g.,

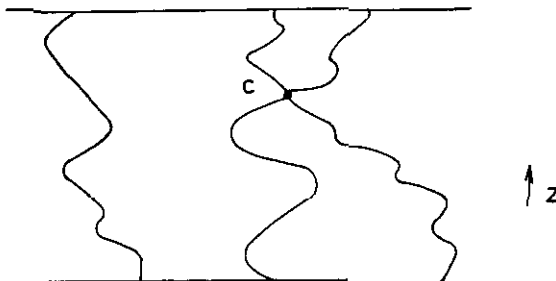


Figure 1. A schematic diagram of many DRWs in 1+1 dimensions. Mutual avoidance forbids a configuration such as C.

Freed 1987, Oono 1984). In this continuum approach, the upper critical dimension follows from a simple dimensional analysis to be $d_c = 2$. Using a momentum shell technique Nelson and Seung (1989) showed that the fixed point of the renormalization group transformation is from $2\pi\epsilon$ to $O(\epsilon)$ where $\epsilon = 2 - d$. Here we show, using the dimensional regularization method, that the fixed point is exactly $2\pi\epsilon$ to all orders of the perturbation theory.

Locating the fixed point exactly is, on its own, of significance and it is also expected to throw much light on the various physical problems mentioned earlier. We wish to come back to this point elsewhere, but would like to point out the pedagogic importance of this result. The renormalization group approach and the associated techniques such as the dimensional regularization, minimal subtraction method, etc, borrowed from field theory and statistical mechanics, have been shown over the years to be *the* tool for understanding, both qualitatively and quantitatively, the properties of polymers especially in the Edwardian path integral formulation (Oono 1984, Freed 1987 and references therein). In this context the model of this letter stands out as a unique example where all of the above techniques can be seen in action and can be carried out to any arbitrary order *unlike* the conventional polymers. Hence the importance of this model as a paradigm just as the $O(N)$ model in the $N \rightarrow \infty$ limit for field theories (Amit 1984).

Our approach here is to use the path integral method to calculate the second virial coefficient in a diagrammatic expansion. Such an expansion, for sure, stumbles on divergences which are to be treated by renormalization. We show how this renormalization can be implemented exactly to all orders in the perturbation theory. The exactness of the renormalized form is proved in two steps; first by establishing uniqueness and then by showing that a particular ansatz (an educated guess) works. The fixed point then follows from calculating the β -function. The exactness of the location of the fixed point is just a corollary of the exactness of the renormalized interaction.

Model. The DRWs in $D = d + 1$ dimensions can equivalently be thought of as random walkers or polymer chains in the transverse d -directions with the z -coordinate playing the role of the contour variable; the chains would be the projections of the DRWs in the transverse directions. The important interaction for the DRWs is the mutual exclusion at each z -coordinate and this, in the equivalent polymer picture, means that the d -dimensional chains interact repulsively, if and only if, they have the same contour variable z . We represent this short-ranged repulsive potential by a δ -function. In the spirit of the Edwards model (Edwards 1965) for conventional polymers, the dimensionless Hamiltonian for M such DRWs can be written as

$$\mathcal{H} = \frac{1}{2} \sum_{\alpha=1}^M \int_0^{N_0} dz \left(\frac{\partial \mathbf{r}_\alpha}{\partial z} \right)^2 + v_0 \sum_{\alpha, \beta} \int_0^{N_0} dz \delta[\mathbf{r}_\alpha(z) - \mathbf{r}_\beta(z)] \quad (1)$$

where $\mathbf{r}_\alpha(z)$ is the (d -dimensional) coordinate of the point at contour length z of chain α . The first term on the RHS is the usual entropic contribution of each polymer of total length N_0 while the second term ensures the mutual repulsion at the same z of chains α and β , with v_0 as the interaction strength and the summation over all pairs ($\alpha < \beta$).

The thermodynamics of the many chain system is characterized by the osmotic pressure, or equivalently, the second virial coefficient (see, e.g., Freed 1987 and Oono 1984). As is well known, the second virial coefficient is completely determined by two

chains and, therefore, in this paper we consider only the two chain problem ($M = 2$ in (1)).

A simple dimensional analysis of the parameters in the Hamiltonian in (1) shows that $[N_0] \sim L^2$ and $[v_0] \sim L^{d-2}$, identifying $d = 2$ as the upper critical dimension. We would, therefore, be requiring an expansion in $\epsilon = 2 - d$, so that the divergences in the perturbation theory for v_0 would appear as singularities at $\epsilon = 0$. Such divergences will be cured by regularization and renormalization. It might be pointed out here that since there is no intrachain (or self) interaction, there will be no renormalization of N_0 , only a renormalization of v_0 is required. It is this feature that makes DRWs comparatively simpler than polymers.

Second virial coefficient. The second virial coefficient is defined as

$$A_2 = - \frac{Z_2(N_0, N_0, v_0) - Z_1^2(N_0)}{Z_1^2(N_0)} \quad (2)$$

where $Z_2(N_0, N_0, v_0)$ is the partition function of two interacting DRWs and $Z_1(N_0)$ is that of one DRW. The partition function is defined as

$$Z_2(N_0, N_0, v_0) = \int \mathcal{D}r_1 \mathcal{D}r_2 e^{-\mathcal{K}}$$

where the integral is over all possible configurations ('paths') of the chains. Z_1 is also defined similarly.

A diagrammatic expansion of A_2 in v_0 can be set up as for conventional polymers by expanding the Boltzmann factor involving v_0 . It is a simple exercise to show that, thanks to the normalization by $Z_1^2(N_0)$, only connected diagrams contribute to A_2 . Furthermore, the special (equal z) interaction produces only ladder type diagrams as shown in figure 2. The broken lines in the figure represent the interaction and contribute

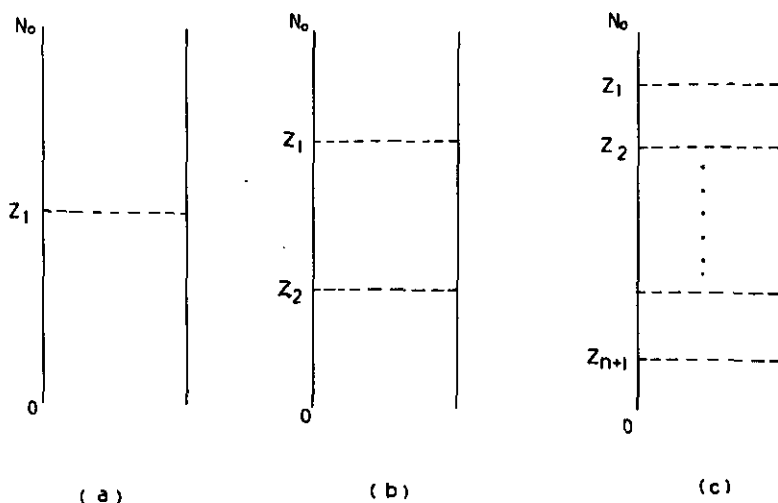


Figure 2. Ladder diagrams needed for the second virial coefficient. The diagram for n loops requires interactions at $(n + 1)$ positions along the chain and its evaluation involves integrations over these positions.

a factor v_0 each. The full lines are the polymers, representing the distribution function

$$G(\mathbf{r}_1, 0; \mathbf{r}_2, z) = (2\pi z)^{-d/2} \exp\left[-\frac{(\mathbf{r}_1 - \mathbf{r}_2)^2}{2z}\right]$$

for a random walk of length z going from \mathbf{r}_1 to \mathbf{r}_2 . Each loop in figure 2 represents an integration over the internal coordinate. For example, the one-loop contribution (figure 2(b)) is proportional to (V is the total volume)

$$V \frac{N_0^{2-d/2}}{[1+(1-d/2)](1-d/2)}.$$

Without going into any further details (to be published elsewhere) we quote the general result for the second virial coefficient as

$$A_2 = N_0 V v_0 \left(1 + \sum_{n=1}^{\infty} (-)^n \frac{v_0^n}{(4\pi)^{nd/2}} N_0^{n(1-d/2)} \frac{\Gamma^n(1-d/2)}{\Gamma(2+n(1-d/2))} \right). \quad (3)$$

As anticipated, each term is divergent at $d = 2$.

Renormalization. We introduce an arbitrary length scale L to define a dimensionless coupling constant u_0 as

$$u_0 = v_0 L^{2-d}$$

and define a renormalized interaction u as

$$u_0 = u(1 + D_1 u + D_2 u^2 + \dots). \quad (4)$$

The coefficients (D_p) are to be determined to absorb the divergences in (3) order by order. It is straightforward but tedious to show that at the n th order (n loop level), the coefficient D_n is determined uniquely by the preceding D_i s ($i < n$) and the terms of (3) with order of v_0 less than n . In other words a D_n once determined at the n th order will remain unaffected even if higher-order terms in (3) are considered. Hence the uniqueness.

By direct computation, we find that up to $O(u^6)$

$$D_p = (2\pi\epsilon)^{-p}. \quad (5)$$

Based on this, we make the *ansatz* that (5) is true for all p . The summation in (4) can be performed easily to get

$$u_0 = \frac{u}{1 - u/2\pi\epsilon} = \frac{2\pi\epsilon u}{2\pi\epsilon - u}. \quad (6)$$

When this renormalized u is substituted in (3) we obtain

$$A_{2R} = N_0 V L^{-\epsilon} \frac{2\pi\epsilon u}{2\pi\epsilon - u} \left(1 + \sum (-)^n \frac{Y^n}{\Gamma(2+n\epsilon/2)} \right) \quad (7)$$

with

$$Y = \frac{\epsilon u}{4\pi\epsilon - 2u} \Gamma(\epsilon/2) \left(\frac{4\pi N_0}{L^2} \right)^{\epsilon/2}.$$

Since $\Gamma(\epsilon/2)$ has a pole [$\Gamma(x) \sim 1/x$ as $x \rightarrow 0$], we find Y , in terms of the renormalized u , to be non-divergent. Moreover, the sum in (7) is well behaved and cancels the apparent divergence at $u = 2\pi\epsilon$. An appeal to uniqueness (just proved) then establishes (6) as the correct renormalization.

Fixed point. The fixed point for RG is determined by the zero of the β -function defined as

$$\beta(u) = L \left(\frac{\partial u}{\partial L} \right) \Big|_{v_0} = \varepsilon \left(\frac{\partial \ln u_0}{\partial u} \right)^{-1}.$$

Using the exact relation between u and u_0 as given by (6), we find

$$\beta(u) = u\varepsilon(1 - u/2\pi\varepsilon)$$

which, incidentally, is identical to the β -function at the one loop level. The fixed point, $\beta(u^*) = 0$, is then

$$u^* = 2\pi\varepsilon$$

which, to emphasize one more time, is an exact result valid to all orders of the perturbation theory. QED.

We thank S Suresh Rao for helpful discussions.

Note added. We thank B Duplantier for pointing out that the sum in (7) for A_{2R} , in the limit $u \rightarrow u^*$ can be performed and is related to equation (18) of Duplantier B 1989 *Phys. Rev. Lett.* **62** 2337.

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