

Absence of anomalous dimension in vertex models: Semidilute solution of directed polymers

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We develop a continuum path-integral approach for the ferroelectric five-vertex model in arbitrary d dimensions by mapping it to a directed polymer problem. A renormalization-group approach with an $\epsilon=3-d$ expansion, 3 being the upper critical dimension, is used to study the polymer solution. The free-energy change due to the interaction of the chains has been computed to $O(\epsilon)$, and the exact expression for the second virial coefficient has been obtained. The fixed point of the problem is found to be exactly $2\pi\epsilon$. By use of finite-size-scaling theory and thermodynamics, the exponents for the vertex model are obtained from those of the polymeric system as the specific-heat exponent $\alpha=(3-d)/2$, and the incommensuration exponent $\bar{\beta}=(d-1)/2$. The model is anisotropic with two length-scale exponents $\nu_{\parallel}=1$ in one direction and $\nu_{\perp}=\frac{1}{2}$ in the remaining $d-1$ directions. It is shown that there are no anomalous dimensions so that the exponents we obtain are exact.

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I. INTRODUCTION

The vertex models (see Fig. 1), conceived a long time ago as simple models of hydrogen-bonded crystals, have, by now, become an important class of models with applications outside equilibrium statistical mechanics [1,2]. However, in contrast to the wealth of information available for two-dimensional models, very little is known about the critical behavior of the models in higher dimensions [3,4]. This seems disturbing because the dimensional dependence of the critical behavior is generally a requirement for a complete understanding of any model. Against this backdrop, we study the simplest vertex model, namely the five-vertex model (5VM) in arbitrary dimensions, obtained by suppressing one of the two ground states, say vertex 2 of Fig. 1 [5,6].

Apart from the interest in the critical behavior of the vertex model, the procedure we adopt interconnects many different problems via the common link of directed random walks [7,8] such as commensurate-incommensurate (CI) transition [9,10], biomembrane phase transition [11-14], polymers in random media

[15,16], flux lattice melting in high- T_c superconductors [8], world lines of anyons [17], etc. It is the developments in the renormalization-group approach for polymers [18] and in the flux lattice melting theory of high- T_c superconductors [8] that paved the way for the approach pursued in this paper.

Higher-dimensional 5VM are defined on diamond-type lattices (see Fig. 2) in the 110 orientation (or its generalization) [6]. The special feature is that the bonds of the lattice are sequentially in the $(x_1, x_2, \dots, x_{d-1})$ directions as one moves up in the $z \equiv x_d$ direction. This preferred direction is the ground-state polarization direction of vertex 1. The model requires putting the 5 vertices on the lattice sites such that the arrows match perfectly on each bond.

It goes without saying that we do not use the lattice statistical methods to study these higher-dimensional models. In fact, as has been done in Ref. [6], we map the problem onto a directed random walk (DRW) problem [7,8] (this is where the suppression of the second vertex of Fig. 1 helps), and then go over to the continuum limit (path-integral method) to use a renormalization-group

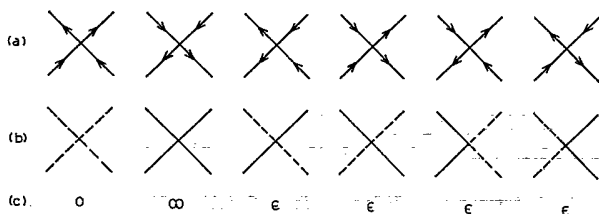


FIG. 1. (a) The arrow configurations with the "ice rule" (two arrows in and two arrows out), (b) the equivalent line configurations with the thick (dashed) line representing the presence (absence) of a line, (c) the energy of the vertex. The second vertex (infinite energy) is not allowed in the five-vertex model.

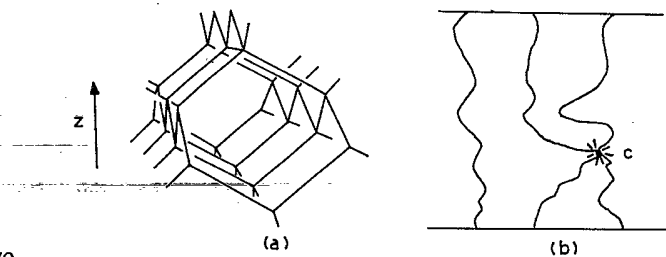


FIG. 2 (a) The diamond lattice in the 110 orientation. The layers have bonds in the x and y directions in sequence. (b) A schematic diagram of many DRW's in 1+1 dimensions. Mutual avoidance forbids a configuration like C.

(RG) approach. The advantage of using the path-integral and RG approach is to get the exponents for general d . Such a scheme is associated with an ϵ ($=3-d$, in this case) expansion, but the remarkable thing, as we will see, is that most of our results are valid to all orders of ϵ . Furthermore, the anisotropy of the vertex model, known from the exact solution in two dimensions, becomes transparent in the path-integral approach from the very beginning.

To show the connection of 5VM with DRW, and to define the latter, let us superpose any arbitrary arrow configuration on the ground state consisting entirely of vertex 1 [1,5,6]. As shown in Fig. 1, by drawing lines on the edges where the arrows do not match we get a set of lines which can wander in the transverse direction but are constrained to move always in the vertical direction (hence the name DRW) [7]. The 5VM is, therefore, equivalent to many DRW's which are not allowed to take steps in the $-z$ direction, but can do a random walk in the transverse directions with a further restriction that two walkers cannot be at the same site. It is the temperature in the statistical model that controls the number of these lines because, as can be easily seen, the n th excited state of 5VM consists of n lines going across the lattice in the vertical direction. The applications mentioned earlier follow if the walks are taken, in two dimensions, as the domain walls that mediate the CI transition, temperature controlling the density of the walls [9,10]. In three dimensions these lines could be the flux lines of the Abrikosov lattice [8].

The exact solution of the two-dimensional 5VM (2D5VM) was obtained by a further mapping of the DRW problem to the Kasteleyn dimer model (K model) [5] which was also utilized to model the biomembrane phase transition [11,12,14]. It was realized that the phase transition mediated by the "lines" are of a different character (a name "3/2" order was proposed [19]). This transition became the topic of extensive studies after Pokrovsky and Talapov pointed out the relevance of wall wandering in two-dimensional CI transitions (now called the Pokrovsky-Talapov transition) with characteristic exponents (see below) [9,10].

The specific heat in the Pokrovsky-Talapov transition (or 2D5VM) is zero for the whole low-temperature phase but has a strong divergence on the high-temperature side with an exponent $\alpha = \frac{1}{2} [c \sim (T - T_c)^{-\alpha}]$, the transition temperature being $T_c = \epsilon/k \ln 2$ (k is the Boltzmann constant). The density of lines or walls, ρ (defined per unit transverse volume) goes to zero as $t \equiv (T - T_c) \rightarrow 0$ with an exponent $\bar{\beta} = \frac{1}{2} (\rho \sim t^{\bar{\beta}})$. Extensive exact finite-size-scaling analysis [20] and correlation function calculations [21] in two dimensions (2D) show that these models are highly anisotropic. There are two length scales, one ξ_{\parallel} parallel to the walk (" z " direction) with exponent $\nu_{\parallel} = 1$ and the other one ξ_{\perp} in the transverse direction with $\nu_{\perp} = \frac{1}{2}$, even though the correlations decay algebraically for the whole high-temperature region.

The two-dimensional K model was extended to three dimensions (3D) by Izuyama and Akutsu (IA) who studied it by using a free fermion approximation and predicted a finite discontinuity of the specific heat at $T_c = \epsilon/k \ln$

2 [12]. We refer the reader to the original literatures for relevant discussions but just point out that the free fermion approximation necessarily fails in $d=3$ because of the braiding of the lines ("anyonic" contribution) [12,13,6]. In Ref. [6] it is shown using a scaling argument that the free fermion approximation would work for all $d < 3$. This particle analogy will not be pursued in this paper where the peculiarities of $d=3$ will reappear as the peculiarities of the system at its upper critical dimension. A different approach for the three-dimensional IA model was used by Bhattacharjee *et al.* where the first and the second excited states were obtained rigorously for finite cross sections [13]. A strong finite-size-scaling ansatz was used to extract the specific-heat exponent. This procedure showed that $d=3$ is the upper critical dimension of these models,

$$\alpha = (3-d)/2 \quad \text{and} \quad \bar{\beta} = (d-1)/2, \quad (1.1)$$

both of which agree with the exact results in 2D. It has recently been argued, using a scaling theory and the momentum-shell renormalization-group approach of Nelson and Seung, that this value of α is exact [6]. Why the two-excited-state approach of Ref. [13] worked remained unanswered but now a justification can be given in the present framework.

We digress a little bit to point out that the 3D version of IA or its generalizations are not identical to 5VM. One can, however, use the mapping of Wu [5] to get a slightly different dimer model, which has been called the lipid analog model in Ref. [13]. It has been shown, modulo the finite-size-scaling ansatz of Ref. [13], that it belongs to the same universality class as the IA model. It is not really unexpected because minor details of local hopping should not affect the critical behavior. Such details are washed out, in any case, in a continuum formulation.

Before going into the details any further let us show how a simple scaling theory for the DRW's in analogy with the scaling theory of polymers can be used to understand the exponents, identifying, in the process, the relevant length scales and their exponents [22,15,16]. First note that each chain of length N is described by an exponent ν (also called the "roughening exponent") that describes the transverse size $R \sim N^{\nu}$ (as measured, say, by the mean-square end-end distance or by the radius of gyration). Now, for a density ρ , the average separation should set the length scale in the transverse direction and it is given by

$$\xi_{\perp} \sim \rho^{-1/d'} \quad (d' = d - 1). \quad (1.2)$$

The chains, however, feel each other when this average separation is of the order of the size of a chain, thereby defining a length scale ξ_{\parallel} along the contour of the chain such that $\xi_{\parallel}^{\nu} \sim \xi_{\perp}$. This is analogous to the c^* concentration (in our notation ρ^*) for conventional polymers that describe the crossover from dilute to semidilute solutions [22,18] except that for polymers, this concentration is determined for a given length of the chains whereas here it is the other way round. Since for the vertex models, we are interested in the chain length going to infinity (ther-

modynamic limit), the DRW's are always in the semidilute regime where fluctuation is relevant and cannot be ignored. A measure of this fluctuation is the free-energy cost for confinement which is the elastic energy $(\xi_{\perp}/\xi_{\parallel})^2 \sim \rho^{2(1-\nu)/d'}$. Since this is paid by the thermal energy ($\sim t$) one gets [15,16]

$$\bar{\beta} = \frac{d'\nu}{2(1-\nu)}, \quad (1.3)$$

which gives

$$\nu_{\parallel} = \nu_{\perp} = \nu[2(1-\nu)]^{-1} \quad (1.4)$$

for all d . Using $\nu = \frac{1}{2}$ for random walks, we get back the exponent $\bar{\beta}$ of Eq. (1.1) and

$$\nu_{\parallel} = 2\nu_{\perp} = 1 \quad (1.5)$$

for all d . These values are, incidentally, consistent with the hyperscaling relation

$$2 - \alpha = (d-1)\nu_{\perp} + \nu_{\parallel}. \quad (1.6)$$

Our purpose in this paper is to derive the above exponents α , $\bar{\beta}$, ν_{\parallel} , and ν_{\perp} for general d , using a renormalization-group approach. We use the path-integral approach of Nelson and Seung [8] (developed for the flux lattice melting problem) but our interest is different from theirs. They use a momentum-shell technique with a cut off a (coming from, say, the lattice spacing) to study the effect of fluctuation on two chains. Carrying this out for many chains is not so easy. Instead, the dimensional regularization procedure [18] is well suited for our purpose as we have shown elsewhere that the two-chain problem can be handled exactly to all orders [23]. In this approach, the cutoff a is taken to be zero. An RG approach becomes mandatory because the theory is not well defined in this limit as reflected by the divergences in the perturbation theory. Such divergences are cured by renormalization, which, in turn, is expected to produce anomalous exponents. The surprise here is that, even after all this, there is no anomalous dimension. And that is the story we want to tell.

Our approach is to study systematically a semidilute solution of directed polymers. Such a solution is described by the osmotic pressure and the second virial coefficient. As is known for polymers [18], the second virial coefficient identifies the overlap concentration ρ^* and the osmotic pressure gives the ρ dependence. For the second virial coefficient, we take finite but large chains which would come from a 5VM of finite extent in the vertical direction. Finite-size-scaling (FSS) theory [24] is then used to relate the 5VM exponents to the polymer exponents. The whole machinery of RG for polymers is geared towards the computation of different exponents as N , the length of the polymer, goes to infinity. The idea of FSS is to explain the behavior near the critical point as the system size goes to infinity. Since, in this paper N plays the role of both, wedding the two is surely not frivolous. The offspring is the length-scale exponent for 5VM that one cannot get from the thermodynamic quantities. The osmotic pressure calculation then gives us the remaining exponents. We explain the procedure in detail

in Sec. II.

The organization of the paper is as follows. We discuss the method of studying the transition on a lattice, following Ref. 13 in Sec. II where we point out how the relevant quantities can be calculated in the continuum by using polymer methods. The analysis for the second virial coefficient is done in Sec. III. We have shown elsewhere that this can be done exactly to all orders in the perturbation theory and the end result is the same as that from one loop [23]. Some of the details not in Ref. [23] are given in Appendix A. In Sec. IV we study the many-chain problem using the random-field (ghosts) technique. In a quadratic approximation, we calculate all the exponents necessary to complete the story. In Sec. V the results are compiled and related to the vertex model exponents. Section VI is the conclusion where an attempt is made to understand the results in terms of the polymer picture. Such a procedure also acts as an independent check of the results.

II. METHODS AND MODELS

We first review the approach for the lattice problem in Sec. II A. Details may be found in Refs. [13, 14, and 12]. Next, in Sec. II B we define the continuum model with the connection between the two developed in Sec. II C.

A. Lattice approach

The transition temperature for 5VM can be located by studying the stability of the ground state. Note that the first excited state requires flipping of one arrow in each horizontal layer (i.e., creating one DRW) at a cost of total energy $N\epsilon$, where N is the lattice size in the z direction. Since the walker can take one of the two possible steps at each point, the entropy is $Nk \ln 2$, so that the free energy of the first excited state is

$$F_1 = N(\epsilon - kT \ln 2), \quad (2.1)$$

which is negative if $T < T_c = \epsilon/k \ln 2$, thereby locating T_c for all dimensions. This argument can be extended to higher excited states since the n th excited state has n DRW's. If λ_n is the degeneracy for the n lines, then the free energy is

$$F_n = Nn\epsilon - NkT \ln \lambda_n^{1/N} \quad (2.2)$$

and the free-energy density can be written as

$$f(\rho) \equiv \frac{F_n}{NV_{\perp}} = -t\rho + s(\rho), \quad (2.3)$$

where $t = k(T - T_c) \ln 2$, $\rho = n/V_{\perp}$, V_{\perp} being the volume in the transverse direction, and

$$s(\rho) = kT \ln(2^n / \lambda_n^{1/N}) \quad (2.4)$$

(the limits $N, V_{\perp} \rightarrow \infty$ understood, and the unimportant T dependence of s is suppressed). This apparently trivial manipulation has been done to isolate $s(\rho)$ which represents the loss in entropy (with respect to noninteracting lines) due to the nonoverlapping restriction. The connection with the continuum model is through

this "entropy" function $s(\rho)$.

The thermodynamics is obtained by minimizing $f(\rho)$ with respect to ρ , the condition being

$$\frac{\partial s(\rho)}{\partial \rho} = t \quad (2.5)$$

which would also give $\bar{\beta}$. The specific heat comes from $c = \epsilon \partial \rho / \partial T \sim \partial \rho / \partial t$.

It is the ρ dependence of $s(\rho)$ that determines the critical behavior of 5VM. Had we had phantom walkers (i.e., noninteracting chains) then, $\lambda_n = 2^{Nn}$ making $s(\rho)$ identically zero, thereby yielding a first-order transition at T_c . This is not the case because of the nonoverlapping constraint of the chains. In general, a power-law dependence

$$s(\rho) \sim \rho^\theta \quad (2.6)$$

is expected. The exponents α and $\bar{\beta}$ are then given by

$$\bar{\beta} = \frac{1}{\theta - 1} \quad \text{and} \quad \alpha = 1 - \bar{\beta}. \quad (2.7)$$

It is known from the exact solution for 2D5VM that $\theta = 3$ for $d = 2$ which gives $\alpha = \frac{1}{2}$ [13]. A mean-field theory produces $\theta = 2$ leading to a finite discontinuity in the specific heat [$\alpha = 0$ (disc)] [13,12]. Dimensional analysis and momentum-shell technique of Ref. [6] lead to $\theta = (d+1)/(d-1)$ to $O(3-d)$ for $d < 3$ as has been proposed in Ref. [13]. This value of θ reproduces the results of Eq. (1.2). We want to calculate θ in a renormalization-group approach.

B. Continuum model

To set up the continuum model, we observe that the directed walks in $d = d' + 1$ dimensions can equivalently be thought of as random walks or polymer chains in the transverse d' directions with the z coordinate playing the role of the contour variable (or the number of steps). The important interaction is, thanks to the directedness, the mutual exclusion at each z coordinate [Fig. 2(b)]. We represent this by a δ function potential between two points of two chains if and only if they have the same z coordinate. The continuum model can, therefore, be written, in analogy with the Edwards model [25] for conventional or self-avoiding polymers, as

$$\mathcal{H}_n = \frac{1}{2} \sum_{\alpha=1}^n \int_0^N dz \left[\frac{\partial \mathbf{r}_\alpha(z)}{\partial z} \right]^2 + v_0 \sum_{\alpha < \beta} \int_0^N dz \delta(\mathbf{r}_\alpha(z) - \mathbf{r}_\beta(z)), \quad (2.8)$$

where $\mathbf{r}_\alpha(z)$ is the (d' dimensional) coordinate of the point at contour length z of chain α , n being the total number of chains. The first term on the right-hand side (rhs) of Eq. (2.8) is the usual entropic contribution (or the elastic energy) of the polymers, each of length N , while the second term ensures the mutual repulsion at the same z of any pair of chains α, β . The two noteworthy features worth remembering are (1) the absence of any intrachain interaction and (2) the special nature of interaction vis-à-vis conventional polymers.

The thermodynamics is obtained from the partition function

$$Z_n = \int \mathcal{D}\mathcal{R} e^{-\beta \mathcal{H}_n}, \quad (2.9)$$

where the integration measure is the sum over all paths, meaning the sum over all configurations of all the chains. The statistical-mechanical model (or the vertex model) in the thermodynamic limit requires the length $N \rightarrow \infty$. We will study both the cases of finite and infinite N .

C. Missing link

So far as the statistical-mechanical problem is concerned we need only worry about the free energy and the osmotic pressure of the polymer system of Eq. (2.8), as explained below.

The free energy of the n th excited state of the vertex model, as pointed out in Sec. II A, requires the "entropy function" $s(\rho)$ which, in the continuum language, would be the excess free energy due to the interaction term in Eq. (2.8), akin to the free energy of swelling of conventional polymers [18,22]. Note that the number of polymers in the vertex model is determined by temperature or rather the temperature difference t , which, in the purely polymer language, would correspond to the chemical potential in a grand canonical ensemble. We prefer to work in the canonical ensemble with a fixed number of chains and compute $s(\rho)$ for it.

The polymer free-energy density (with $N \rightarrow \infty$) can be written as

$$\mathcal{F}(\rho) = \mathcal{F}_0 \rho + N s(\rho), \quad (2.10)$$

where \mathcal{F}_0 is the free energy of a single chain. Now, the osmotic pressure, in this canonical ensemble, is defined as

$$\Pi = \rho^2 \frac{\partial}{\partial \rho} \left[\frac{\mathcal{F}}{\rho} \right], \quad (2.11)$$

which, on using Eq. (2.10), gives

$$\frac{\Pi}{N} = \rho \frac{\partial s}{\partial \rho} - s(\rho), \quad (2.12)$$

ignoring the ideal-gas term. The minimization condition of the free energy for the n th excited state in Eq. (2.5) when inserted in Eq. (2.12) for Π shows that, at the equilibrium value,

$$\Pi = N f_{\min}(\rho), \quad (2.13)$$

where $f_{\min}(\rho)$ is the minimum free-energy density of Eq. (2.3). It is easy to check that if $s(\rho) \sim \rho^\theta$ [Eq. (2.6)], then both $f_{\min}(\rho)$ from Eq. (2.3) and Π of Eq. (2.12) would go as ρ^θ . Thus the density exponent for the osmotic pressure of the directed polymers in the semidilute limit gives the much needed θ exponent for the vertex model, with Eq. (2.13) serving as the connecting link.

D. Second virial coefficient (read: finite-size scaling)

The scaling theory, as discussed in the Introduction, shows that for $N \rightarrow \infty$, there is a strong overlap of the

chains, and therefore, they are in the semidilute regime. One can monitor the crossover from the dilute to the semidilute regime by studying the virial expansion of Π for finite but large N as

$$\frac{\Pi}{kT\rho} = 1 + A_2\rho + \dots \quad (2.14)$$

For polymers, the crossover from dilute to semidilute regime is determined by the importance of the second term $A_2\rho$, A_2 (a function of N) being the second virial coefficient. In the limit $N \rightarrow \infty$, A_2 is expected to have a power-law behavior $A_2 \sim N^\psi$, so that the appropriate scaled variable for the concentration is

$$\bar{\rho} \equiv \rho N^\psi, \quad (2.15a)$$

the overlap concentration ρ^* being $\sim N^{-\psi}$. For bulk 5VM, $\rho \sim t^{\bar{\beta}}$, which when used in $\bar{\rho}$, gives the scaling variable for temperature as

$$\bar{t} = tN^{\psi/\bar{\beta}}. \quad (2.15b)$$

Polymer chains of large but finite lengths would correspond to a vertex model which is finite in the vertical (z) direction. The critical behavior of such a finite system is, generally, discussed through FSS theory [24]. According to this theory, the critical divergences are rounded off when the correlation length becomes comparable to the finite dimension of the system and the rounding is described by a variable $N\xi_{||}$. This identifies the scaled temperature variable as $tN^{1/\nu_{||}}$ because the correlation length $\xi_{||} \sim t^{-\nu_{||}}$. We immediately extract the length-scale exponent for the z direction, from Eq. (2.15b) as

$$\nu_{||} = \frac{\bar{\beta}}{\psi} = \frac{1}{\psi(\theta-1)}, \quad (2.16a)$$

where the connection between $\bar{\beta}$ and θ as given by Eq. (2.7) is used.

The exponent ν_{\perp} in the transverse direction is still determined by the average separation of the lines as in Eq. (1.2). (See also Sec. VI.) In terms of the incommensuration exponent $\bar{\beta}$, we find

$$\nu_{\perp} = \frac{\bar{\beta}}{d'}. \quad (2.16b)$$

We can now summarize the procedure as follows. We calculate the second virial coefficient and renormalize it to get ψ . Next, we obtain the free energy for the polymers as given by the Hamiltonian in Eq. (2.8), thereby, after renormalization, getting θ . An equivalent procedure would be to compute the osmotic pressure and then renormalize to get θ . Once these two exponents are known, all the exponents for the 5VM can be obtained.

E. Upper critical dimension and the irrelevance of higher-order interactions

A simple dimensional analysis shows that the coupling constant v_0 in Eq. (2.8) has the engineering dimension of $L^{d'-2}$, taking the dimension of r as length (L) while z (or N) has the dimension L^2 . This brings out (and shows the

power of the continuum approach) the anisotropy of the d -dimensional vertex model vividly because in the lattice approach z is just one other spatial direction. We will see, as is known for ($d=$)2-dimensions, that the anisotropy is important.

That v_0 is dimensionless at $d'=2$, identifies the upper critical dimension as $d'^*=2$ or $d^*=d'+1=3$ [6,8]. This necessitates a renormalization-group approach with an $\epsilon=2-d'$ expansion because, as we show, the naive perturbation theory encounters divergences. These divergences are cured by dimensional regularization and renormalization.

Another question is the importance of higher-order interactions. In the Hamiltonian, Eq. (2.8), we considered only two-body interactions. In principle we can have higher-order terms as

$$\sum_{\alpha,\beta,\dots} v_r \int ds \delta(\mathbf{r}_\alpha(s) - \mathbf{r}_\beta(s)) \dots \delta(\mathbf{r}_\beta(s) - \mathbf{r}_\gamma(s)) \quad (2.17)$$

with r chains and the sum is over all possible groupings. Dimensional analysis shows v_r to be dimensionless at $d_r^*=2/(r-1)$ so that around $d'=2$, all these higher-order interactions are irrelevant in the RG sense [26]. The three-body interaction, incidentally, is marginal at $d'=1$, i.e., for 2D5VM. The irrelevance of the higher-order interactions explains why, so far as the exponents are concerned, the two-excited-state approach of Ref. [13] works so well.

III. SECOND VIRIAL COEFFICIENT

The second virial coefficient is defined as

$$A_2 = - \frac{Z_2(N, N, v_0) - Z_1(N)Z_1(N)}{Z_1(N)Z_1(N)}, \quad (3.1)$$

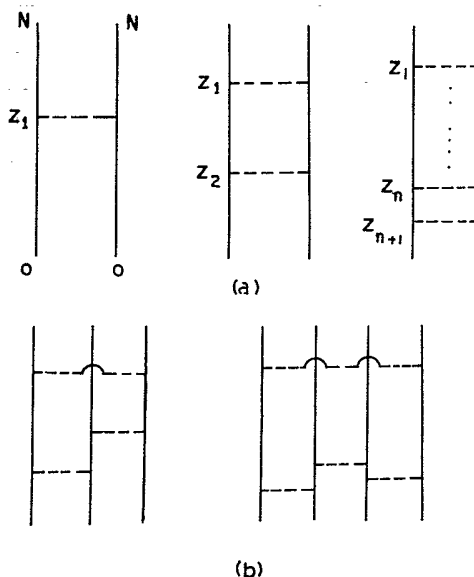


FIG. 3. (a) Diagrams needed for the second virial coefficient. The diagram for n loops requires interactions at $(n+1)$ positions along the chain and its evaluation involves integrations over these positions. (b) A few one-loop diagrams involving many chains. Such diagrams contribute to the free energy.

where $Z_2(N, N, v_0)$ is the partition function for two chains and $Z_1(N)$ is that for one chain. A diagrammatic expansion of A_2 in v_0 can be set up as for conventional polymers, and it is a simple exercise to show that only connected diagrams contribute to A_2 . Furthermore, the special ("equal z ") interaction simplifies the diagrams because no crossed diagram, only ladder-type diagrams, occur as shown in Fig. 3. This two-chain problem and the virial coefficient has been studied elsewhere [23]. Some details regarding the computation of the diagrams are given in Appendix A. We have shown that the renormalization procedure can be carried out exactly and the fixed point can be located exactly. The final answer for the fixed point, remarkably, is identical to the 1-loop level result and agrees with the Nelson-Seung result of Ref. [8].

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

$$u_0 = v_0 L^{2-d'} \quad (3.2)$$

In terms of this u_0 , the second virial coefficient can be written as (see Appendix A and Ref. [23])

$$A_2 = \frac{1}{2} NV L^{-\epsilon} u_0 \left[1 + \sum_{n=1}^{\infty} (-1)^n \left(\frac{u_0}{4\pi} \right)^n \left(\frac{4\pi N}{L^2} \right)^{n\epsilon/2} \times \frac{\Gamma^n(\epsilon/2)}{\Gamma(2+n\epsilon/2)} \right], \quad (3.3)$$

where $\epsilon = 2 - d'$ and V is the volume [henceforth, the subscript \perp of volume in Eq. (2.3) is dropped]. Since $\Gamma(x)$ diverges as x approaches zero, each term of the above series for A_2 is divergent.

Renormalization, fixed point

To absorb the divergence as $\epsilon \rightarrow 0$, we define the renormalized coupling constant u as

$$u_0 = u(1 + f_1 u + \cdots + f_n u^n + \cdots). \quad (3.4)$$

Since there is no intrachain interaction, the chain length remains unrenormalized. An order-by-order calculation shows that the divergences in Eq. (3.3) can be absorbed by choosing

$$f_n = (2\pi\epsilon)^{-n}. \quad (3.5)$$

It has been shown in Ref. [23] that this choice absorbs the divergences for all n . The fixed point is then obtained from the zero of the β function [18,26],

$$\beta(u) \equiv \left[L \frac{\partial u}{\partial L} \right]_{v_0} = \epsilon u(1 - f_1 u), \quad (3.6)$$

yielding $u^* = f_1^{-1} = 2\pi\epsilon$ [23]. Standard analysis [26,18] shows that u^* is the stable fixed point for $\epsilon > 0$, whereas the Gaussian fixed point is the stable one for negative ϵ .

At the fixed point of the coupling constant, the renormalized A_{2R} is obtained as (see Appendix B)

$$A_{2R} = V(4\pi N)^{1-\epsilon/2} \frac{\sin\pi\epsilon/2}{\pi(1-\epsilon/2)} \quad (3.7)$$

and, most importantly, the arbitrary length scale L drops out.

The arbitrary length scale introduced for any renormalization procedure plays a significant role in changing the scaling dimension (or exponent) from the engineering dimension. If this L drops out, then only the engineering dimension is possible and no anomalous exponent appears. This can be traced to the absence of the intrachain interaction in the Hamiltonian. (No renormalization constant for the chain length.) The exponent ψ of Eq. (2.15a) for the second virial coefficient is therefore

$$\psi = \frac{2-\epsilon}{2} = \frac{d'}{2} \quad (3.8)$$

which is exact and also the engineering dimension obtained by demanding that $A_2 \rho$ in Eq. (2.14) is dimensionless.

IV. MANY-CHAIN SYSTEM

The second virial coefficient evaluated in Sec. III sets the scale of concentration for the crossover from the dilute to the semidilute regime. However, to get the extrapolation formula, it is required to go beyond the two-chain problem and obtain the free energy (or the osmotic pressure) through a systematic loop expansion, which entails summations of infinite sets of diagrams, some of which are shown in Fig. 3 [18]. In the path-integral formulation, the summation of the one-loop diagrams can be done indirectly by introducing "ghost" fields in the so-called Gaussian-random-field method [25b,18]. In this section we discuss the many-chain problem in the infinite-chain-length ($N \rightarrow \infty$) limit using the random-field method. Our aim is to compute the exponent θ for the osmotic pressure or the entropy $s(\rho)$ of Eq. (2.6).

A. Formulation

The crossover from the dilute to the semidilute regime is governed by fluctuations in the density which in the diagrammatic language means the dominance of the loops over the trees. To isolate the contribution from fluctuations, in Sec. IV A 1 we introduce a fluctuation variable and then in Sec. IV A 2 introduce a ghost field to disentangle the interaction term. The partition function, Eq. (2.9), can then be expressed as a functional integral over the ghost or Gaussian random field with a different Hamiltonian.

1. Hamiltonian reformulated

Our starting point is the n chain Hamiltonian Eq. (2.8). In the canonical ensemble, we are interested in the finite-density limit obtained by taking the number of chains $n \rightarrow \infty$ and the volume of the d' -dimensional space $V \rightarrow \infty$, with $\rho = n/V$ fixed. A mean-field theory (obtained by keeping the tree diagrams) would be completely described by the average density ρ . To study the effect of fluctuations on the variation in the local concentration arising from the various configurations of the chains, it helps to introduce the fluctuation variable $p(\mathbf{r}, z)$ as [18]

$$p(\mathbf{r}, z) = \sum_{\alpha=1}^n \delta(\mathbf{r} - \mathbf{r}_{\alpha}(z)) - \rho. \quad (4.1)$$

The reason for keeping the contour variable z as an argument will be clear soon.

To express the mutually avoiding term of the Hamiltonian Eq. (2.8) in terms of p , we rewrite each δ function as

$$\delta(\mathbf{r}_\alpha(z) - \mathbf{r}_\beta(z)) = \int d\mathbf{r} \delta(\mathbf{r} - \mathbf{r}_\alpha(z)) \delta(\mathbf{r} - \mathbf{r}_\beta(z)) \quad (4.2)$$

so that

$$\mathcal{H}_n = \mathcal{H}_{0n} + \frac{v_0}{2} \int d\mathbf{r} dz [p(\mathbf{r}, z) + \rho]^2, \quad (4.3)$$

with \mathcal{H}_{0n} as the free Gaussian part (first term) of \mathcal{H}_n of Eq. (2.6). Using the identity $\int p(\mathbf{r}, z) d\mathbf{r} = 0$, reflecting the conservation of chains, \mathcal{H}_n can be expressed as

$$\mathcal{H}_n = \mathcal{H}_{0n} + \frac{1}{2} v_0 V N \rho^2 + \frac{1}{2} v_0 \int_{r,z} p(\mathbf{r}, z)^2 \quad (4.4a)$$

where

$$\int_{r,z} \equiv \int d\mathbf{r} dz. \quad (4.4b)$$

It transpires that the first two terms would give the mean-field contribution while the fluctuation contribution would come from the last term. If the fluctuation part in Eq. (4.4a) is ignored, the free energy via the partition function in Eq. (2.9) would be

$$\mathcal{F}(\rho) = \mathcal{F}_{0\rho} + \frac{1}{2} v_0 N \rho^2, \quad (4.5)$$

giving $s(\rho) \sim \rho^2$ [i.e., $\theta = 2$, see Eq. (2.6)] the mean-field result as already discussed. The manipulations done so far reproduce the mean-field (MF) part easily but it is clearly inadequate. Getting the loop corrections is not straightforward because an expansion in the fluctuation term would be an expansion in powers in v_0 . The random-field technique is a way to convert this power series in v_0 into a loop expansion, to which we now turn.

2. Hamiltonian through ghosts

Let us introduce a ghost or Gaussian random field $\psi(\mathbf{r}, z)$ in place of $p(\mathbf{r}, z)$ and force it to be $p(\mathbf{r}, z) \forall \mathbf{r}, z$, as

$$\begin{aligned} Z_n = & \int \mathcal{D}\mathcal{R} \mathcal{D}\psi \exp(-\mathcal{H}_{0n} - \frac{1}{2} v_0 V N \rho^2) \\ & \times \exp\left[-\frac{v_0}{2} \int_{r,z} \psi^2(\mathbf{r}, z)\right] \\ & \times \prod_{r,z} \delta(\psi(\mathbf{r}, z) - p(\mathbf{r}, z)). \end{aligned} \quad (4.6)$$

By introducing the Fourier representation for the δ function, and doing the resultant Gaussian integration over ψ , we can write

$$\begin{aligned} Z_n = & e^{(1/2) V N v_0 \rho^2} \\ & \times \int \mathcal{D}\mathcal{R} \mathcal{D}\phi e^{-\mathcal{H}_{0n}} \exp\left[-\int_{r,z} \left[\frac{1}{2v_0} \phi^2 + i\phi p\right]\right], \end{aligned} \quad (4.7)$$

where ϕ is the Fourier conjugate of ψ and the (\mathbf{r}, z) dependence of ϕ and p has been suppressed for simplicity.

The information regarding the chains is in the last $i\phi p$ term and since, by definition Eq. (4.1), p is a sum of n independent quantities, one for each chain, and functional integration over the chains factorizes, sufficing consideration of only one chain.

Defining

$$G(\phi) = \langle e^{-i\phi p} \rangle_0 \quad (4.8)$$

for one chain [p of Eq. (4.1) with $n = 1$], the average being over the free one-chain Hamiltonian $H_0 = \frac{1}{2} \int (\partial\mathbf{r}/\partial z)^2 dz$, the partition function can be rewritten as

$$\begin{aligned} Z_n = & (Z_1)^n e^{-(1/2) v_0 V N \rho^2} \\ & \times \int \mathcal{D}\phi \exp\left[-\int_{r,z} \left[\frac{1}{2v_0} \phi^2 - n \ln G(\phi)\right]\right], \end{aligned} \quad (4.9)$$

which is equivalent to an effective dimensionless Hamiltonian

$$H(\phi) = \int_{r,z} \left[\frac{1}{2v_0} \phi^2 - n \ln G(\phi)\right], \quad (4.10)$$

a functional of ϕ .

We now pause a little to see that the effect of the random fields ϕ and ψ is to replace, as evident from Eq. (4.7), the interacting n chain system by n noninteracting chains, but each chain is in an external random (or fluctuating) potential whose variance is controlled by the original coupling constant. And there lies the difference with a mean-field theory which also replaces a many-body system by an effective single-particle system.

The manipulations done so far are exact in nature but, nevertheless, Eq. (4.9) cannot be studied exactly. We, therefore, resort to a quadratic approximation as mentioned, which reproduces the one-loop correction.

B. Quadratic approximation

Experience in polymers shows that the kind of random-field technique used in Sec. IV A leads, after expanding G to quadratic terms in ϕ , to one-loop corrections in the original path-integral approach [18,27]. With this in mind, we expand $G(\phi)$ and stop at the quadratic term to get

$$\begin{aligned} G(\phi) \approx & 1 - \frac{1}{2} \int dz d\mathbf{r} dz' d\mathbf{r}' \phi(\mathbf{r}, z) \phi(\mathbf{r}', z') \\ & \times \langle p(\mathbf{r}, z) p(\mathbf{r}', z') \rangle. \end{aligned} \quad (4.11)$$

(Note: p refers to one chain only.) The pp average is similar to the structure factor for one chain [18,28] and can be calculated by going over to the Fourier space [$p(\mathbf{q}, z) = \int d\mathbf{r} \exp(i\mathbf{q} \cdot \mathbf{r}) p(\mathbf{r}, z)$] as

$$\begin{aligned} \langle p(\mathbf{q}, z) p(\mathbf{q}', z') \rangle &= \frac{(2\pi)^{d'}}{V} \delta(\mathbf{q} + \mathbf{q}') \langle e^{i\mathbf{q} \cdot [\mathbf{r}(z) - \mathbf{r}(z')] } \rangle \\ &= \frac{(2\pi)^{d'}}{V} \delta(\mathbf{q} + \mathbf{q}') e^{-q^2 |z - z'|/2}. \end{aligned} \quad (4.12)$$

The partition function for the ϕ -dependent Hamiltonian of Eq. (4.10), up to terms quadratic in ϕ , is

$$Z(\{\phi\}) = \int \mathcal{D}\phi \exp \left[-\frac{1}{2v_0} \int_{qz} \phi(\mathbf{q}, z) \phi(-\mathbf{q}, z) - \frac{1}{2} \int_{qzz'} \rho e^{-(q^2/2)|z-z'|} \phi(\mathbf{q}, z) \phi(-\mathbf{q}, z') \right] \\ \propto \left[\text{Det}_{q,z} \left[\frac{1}{2v_0} \delta(\mathbf{q} + \mathbf{q}') \delta(z - z') + \frac{1}{2} \rho e^{q^2|z-z'|/2} \delta(\mathbf{q} + \mathbf{q}') \right] \right]^{-1/2}, \quad (4.13)$$

with the determinant in a Toeplitz form [a shorthand notation $\int_{qzz'} = (2\pi)^{-d'} \int d\mathbf{q} dz dz'$ has been used]. Evaluation of the determinant in Eq. (4.13) is done in Appendix C; we just quote the result here. In the limit $N \rightarrow \infty$, combining all the terms from Eqs. (4.9) and (4.12), the free-energy density is given by ($kT=1$),

$$\frac{\mathcal{F}}{N} = \rho \ln Z_1 + \frac{1}{2} v_0 \rho^2 \\ + \frac{1}{2(2\pi)^{d'} \pi} \int dk d^d q \ln \left[\frac{1}{2v_0} + \frac{\rho q^2/2}{q^4/4 + k^2} \right], \quad (4.14)$$

where q comes from Fourier transformation in space and k comes from a similar transformation for the z coordinate. The last term in this equation is the one-loop correction to the mean-field result as represented by the first two terms on the right-hand side (rhs). The first term on the rhs is the free-energy contribution from noninteracting chains. Therefore the free-energy contribution, needed for the "entropy function" $s(\rho)$, is the last two terms of the above equation.

C. Renormalization

Focusing attention on the last fluctuation correction term (to be called I) of the free energy of Eq. (4.14) the k integration can be carried out exactly [29], yielding

$$I = \frac{1}{2(2\pi)^{d'/2}} \frac{2}{\Gamma(d'/2)} 2^{(2+d')/2} (\rho v_0)^{(d'+2)/2} \\ \times \int_0^\infty dq q^{d'+1} [(1+q^{-2})^{1/2} - 1]. \quad (4.15)$$

This integral is ultraviolet divergent and requires regularization. By integrating by parts and doing the integral in the convergent domain of d' , we get

$$I = \frac{1}{2\pi^{d'/2}} \frac{2}{\Gamma(d'/2)(d'+2)} \frac{\Gamma(1+d'/2)}{\Gamma(1/2)} \\ \times \Gamma(-d'/2) (\rho v_0)^{(d'+2)/2}. \quad (4.16)$$

Since our worry is with the last two terms of Eq. (4.14), which give $s(\rho)$, we find by expanding Eq. (4.16) around $\epsilon = 2 - d' = 0$,

$$2s(\rho) \approx \rho^2 L^{-\epsilon} \left[u_0 + \frac{u_0^2}{2\pi} \left[-\frac{1}{\epsilon} + \frac{1+2\gamma-4\ln 2}{4} \right. \right. \\ \left. \left. + \frac{1}{2} \ln \chi \right] \right] + O(\epsilon), \quad (4.17)$$

where $\chi = \rho u_0 L^{2-\epsilon} / \pi$ and γ is the Euler gamma and u_0 is the dimensionless coupling constant of Eq. (3.2). The

renormalization procedure follows Sec. III *in toto*, and so details are not given. We get the same fixed point $u^* = 2\pi\epsilon$ as for the two-chain problem. Using this fixed-point value, and reexponentiating [18,26] we get

$$s(\rho) = \frac{1}{2} \rho^2 L^{-\epsilon} 2\pi\epsilon \left[1 + \frac{1+2\gamma-4\ln 2}{4} \epsilon \right] \chi^{\epsilon/2}. \quad (4.18)$$

This gives $s(\rho) \sim \rho^{2+\epsilon/2}$. The exponent θ , Eq. (2.6), is therefore

$$\theta = 2 + \epsilon/2, \quad (4.19)$$

which agrees with $(d'+2)/d'$ up to order of ϵ . Furthermore, up to $O(\epsilon)$, the arbitrary length L drops out, as we have seen for the second virial coefficient. Though we have not done the calculations for higher-order terms, we believe, based on the result of Sec. III and the location of the fixed point, that this cancellation of L is true for all orders. We can then conclude that θ is really $(d'+2)/d'$, which incidentally is the engineering exponent.

V. EXPONENTS FOR THE VERTEX MODEL

We now compile the results of the previous sections. We showed that the second virial coefficient $A_2 \sim N^\psi$ with $\psi = d'/2 = (d-1)/2$ and the free-energy change [Eq. (2.10)] goes like ρ^θ with $\theta = 2 + \epsilon/2$, which is equal to $(d'+2)/d'$ up to $O(\epsilon)$. The second virial coefficient has been computed exactly [Eq. (3.7)]. Interestingly enough, the length scale that would have given an anomalous dimension for the free energy gets canceled as for A_2 . We therefore believe that the exponent θ will also be the engineering dimension, namely, $(d'+2)/d'$ [13,6]. Using these, the incommensuration and the specific-heat exponents are ($d' = d - 1$, $d < 3$)

$$\bar{\beta} \approx 1 - \frac{\epsilon}{2} = d'/2, \quad \alpha = (3-d)/2 \quad (5.1)$$

if Eq. (4.19) is used. Using $\psi = d'/2 = 1 - \epsilon/2$ (exact) from Sec. III, we find [see Eq. (2.16)] that the length-scale exponents are [30,31]

$$v_{\parallel} = \bar{\beta}/\psi = 1 \quad \text{and} \quad v_{\perp} = \bar{\beta}/d' = \frac{1}{2}. \quad (5.2)$$

VI. CONCLUSION

In this paper we developed a continuum approach for studying the five-vertex model in any dimensions by mapping the problem to that of a semidilute solution of directed polymers. A path-integral method for these polymers have been used. The approach brings out the anisotropic nature of the model clearly. The method utilizes the techniques used in polymers combined with the

standard dimensional regularization procedure and re-normalization. The use of finite-size-scaling theory connects the polymer exponents to the vertex-model exponents as explained in Sec. II. The exponents for the vertex model are given in Sec. V.

The upper critical dimension of the vertex model is shown to be 3, below which the thermodynamic exponents [Eq. (5.1)] depend on d but above which mean-field theory is valid because the Gaussian fixed point is the stable one. The simplicity of the model that led to the exact values of the thermodynamic exponents is the d independence of the length-scale exponents [Eq. (5.2)]. This is strikingly similar to the Gaussian or spherical model [26] in critical phenomena but a deeper connection is not yet clear.

The directed polymers are described by two exponents, ψ giving the length dependence of the second virial coefficient [Eqs. (2.14), (2.15), and (3.8)], and θ giving the density ρ dependence of the excess free energy or the osmotic pressure [Eqs. (2.13) and (4.19)]. It is easy to understand the ψ exponent by comparing the virial series Eq. (2.14) for the polymers with that of a hard-sphere gas. For the latter problem, the second virial coefficient is proportional to the volume of the spheres. For the problem at hand, the volume of each polymer is of the order of $N^{d'\nu}$, giving $\psi = d'/2$ as we have already found. Note also that this is indeed the engineering dimension of the second virial coefficient.

One can also use a simple scaling picture for polymers to get an independent consistency check of the results of this paper. This is best done for the transverse length-scale exponent. For a single chain of length N , the relevant length is the average size $R \sim N^\nu$. For the many-chain or the semidilute case, the density-density correlation would give the necessary length scale. Since the overlap concentration ρ^* of Sec. II sets the scale for concentration, one can write a scaling form for the length scale ξ_\perp as

$$\xi_\perp = N^\nu X(\rho/\rho^*), \quad (6.1)$$

with $\rho^* \sim N^{-\psi}$. For the vertex model we need $N \rightarrow \infty$ in which limit Eq. (6.1) should have an N independent limit. This requires that $X(x) \sim x^{-\nu/\psi}$ for large x , so that $\xi_\perp \sim \rho^{-\nu/\psi}$. A different power-law connection between these two have been used in Eq. (1.2). It is therefore gratifying to note that the exponent ψ we have obtained in Sec. III really makes the two independent arguments consistent, with $\nu = \frac{1}{2}$ (which is surely true).

If we push the analogy with polymers a little further then, following Ref. [22], the transverse correlation length ξ_\perp would be the length scale for the transient network or the average size of a mesh as shown in Fig. 4. For a given mesh size, one can then estimate the length along the chain as $\xi_\parallel^{1/\nu}$, giving a measure for the length scale in the z direction of the vertex model. In this picture ξ_\parallel would then correspond to the average spacing, along the chain, between two collisions, consistent with the picture used for the two-dimensional commensurate-incommensurate transition [10].

To conclude, we note that for the polymer problem,

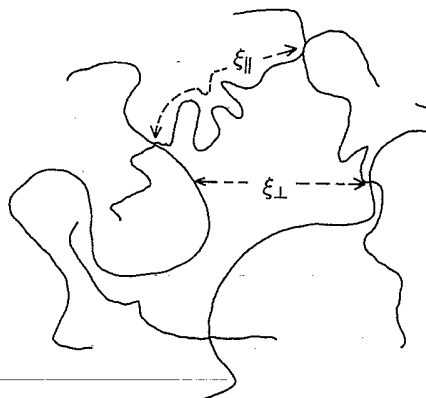


FIG. 4. Schematic diagram showing the mesh and the length scales.

the arbitrary length scale one introduces during the re-normalization procedure cancels out. It is this length scale that produces the anomalous dimensions and its cancellation signifies the nonexistence of anomalous exponents both for the directed polymers and the five-vertex model, even though the theory is described by a nontrivial (i.e., non-Gaussian) fixed point ($u^* = 2\pi\epsilon$, $\epsilon = 3 - d = 2 - d'$). As a consequence, the exponents are the respective engineering dimensions, and so they are exact.

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APPENDIX A

We will first define the rules to calculate any diagram in Fig. 3; the dashed lines contribute a factor v_0 each and the solid lines are the polymers, representing the distribution function

$$G(\mathbf{r}_1, 0; \mathbf{r}_2, z) = (2\pi z)^{-d/2} \exp \left[-\frac{(\mathbf{r}_1 - \mathbf{r}_2)^2}{2z} \right]. \quad (A1)$$

G is properly normalized such that

$$\int d\mathbf{r}_1 G(\mathbf{r}_1, 0; \mathbf{r}_2, z) = \int d\mathbf{r}_2 G = 1 \quad (A2)$$

for a random walk of length z going from \mathbf{r}_1 to \mathbf{r}_2 . Each loop in Fig. 3 represents an integration over the internal coordinate like z_1, z_2 , etc. For example, the one-loop diagram in Fig. 3, after integration over the external end coordinates, requires integrations over the internal coordinates z_1, z_2 as

$$\begin{aligned} v_0^2 VI_1(N) &\equiv -\frac{V_0^2}{2^{d/2}} \int_0^N dz_1 \int_0^{z_1} dz_2 G(0, 2(z_1 - z_2)) \\ &= -\frac{V_0^2}{2^d \pi^{d/2}} \frac{N^{2-d/2}}{(1-d/2)(2-d/2)}. \end{aligned} \quad (A3)$$

The factorial coming from the expansion of the interaction part of partition function is canceled by the factorial that comes from the "z ordering" in (A3). This cancellation is, in fact, true for all orders. We now ex-

PLICITLY demonstrate the calculation of any general loop using the above rules. A general n loop diagram after the integration can be written as

$$v_0^{n+1} I_n(N) \equiv \frac{v_0^{n+1}}{(4\pi)^{d/2}} \int_0^N dz_1 \int_0^{z_1} dz_2 (z_1 - z_2)^{-d/2} \int_0^{z_2} dz_3 (z_2 - z_3)^{-d/2} \dots \int_0^{z_n} ds s^{-d/2}. \quad (\text{A4})$$

It immediately follows that

$$I_{n+1} = \frac{1}{2^{d/2}} \int_0^N dz_1 \int_0^{z_1} dz_2 (z_1 - z_2)^{-d/2} \frac{dI_n(z_2)}{dz_2}. \quad (\text{A5})$$

Now, take

$$I_n(N) = C_n N^{\omega_n}. \quad (\text{A6})$$

By rescaling $x = z_2/z_1$, and doing the necessary integrations, we get

$$I_{n+1} = \frac{1}{(4\pi)^{d/2}} \frac{N^{\omega_n - d/2 + 1} \Gamma(1 - d/2) \Gamma(\omega_n)}{(\omega_n - d/2 + 1) \Gamma(\omega_n - d/2 + 1)} C_n \omega_n, \quad (\text{A7})$$

which implies

$$C_{n+1} = C_n \omega_n \frac{\Gamma(\epsilon/2) \Gamma(\omega_n)}{(4\pi)^{d/2} \Gamma(\omega_n - d/2 + 1)}, \quad (\text{A8})$$

$$\omega_{n+1} = \omega_n + \epsilon/2.$$

With the initial condition [using Eq. (A1)] $C_0 = 1$, $\omega_0 = 1$ iteration gives

$$\omega_n = 1 + n\epsilon/2, \quad C_{n+1} = \frac{\Gamma(\epsilon/2) \Gamma(2 + n\epsilon/2)}{\Gamma[2 + (n+1)\epsilon/2]} C_n. \quad (\text{A9})$$

Equation (A9) gives the second virial coefficient of Eq. (3.3). The details of renormalizing the second virial coefficient can be found in Ref. [23].

APPENDIX B

We evaluate the sum in Eq. (3.3) for the second virial coefficient to get Eq. (3.7). The renormalized u follows from Eq. (3.4) as $u_0 = 2\pi\epsilon u / (2\pi\epsilon - u)$, using which we get

$$A_{2R} = NVL^{-\epsilon} \frac{2\pi\epsilon u}{u^* - u} \int_C \frac{da}{2\pi i a^2} \frac{e^a}{1 + Z\Gamma(\epsilon/2)a^{-\epsilon/2}N}, \quad (\text{B1})$$

where $Z = \epsilon u / (u^* - u)$, $N = \frac{1}{2}(4\pi N/L^2)^{\epsilon/2}$, and \mathcal{C} is a suitable Hankel contour [32]. For $(u \rightarrow u^*)$ Eq. (B1) reduces to

$$A_{2R} = NVL^{-\epsilon} 2\pi \int \frac{da}{e^{2\pi i} \Gamma(\epsilon/2)N} \frac{e^a a^{2-\epsilon/2}}{1 - \epsilon/2} = V(4\pi N)^{1-\epsilon/2} \frac{\sin\pi\epsilon/2}{(1-\epsilon/2)\pi} \quad (\text{B2})$$

as quoted in Eq. (3.7).

APPENDIX C

In this appendix we will calculate the determinant

$$\text{Det}_{q,z} \left[\frac{1}{2v_0} \delta(\mathbf{q} + \mathbf{q}') \delta(z - z') + \frac{1}{2} \rho e^{q^2|z-z'|/2} \delta(\mathbf{q} + \mathbf{q}') \right], \quad (\text{C1})$$

which occurs in Eq. (4.13). Note that this is already diagonal in q 's but not in z 's. Going over to the "Rouse coordinates" [28]

$$\phi_{p,z} = \frac{1}{N} \cos \left[\frac{p\pi z}{N} \right], \quad (\text{C2})$$

the transform of $g(q, z, z') = e^{q^2|z-z'|/2}$ is given by

$$g'(q, p, p') = \frac{1}{N^2} \int \cos \left[\frac{p\pi z}{N} \right] e^{q^2|z-z'|/2} \times \cos \left[\frac{p'\pi z'}{N} \right] dz dz' \quad (\text{C3})$$

which, in the limit $N \rightarrow \infty$ produces (see, e.g., Ref. [28], p. 99)

$$g' = \frac{1}{N^2} \int_0^N dz \cos \left[\frac{p\pi z}{N} \right] \cos \left[\frac{p'\pi z}{N} \right] \times \int_{-\infty}^{\infty} e^{(-q^2/2)|z'|} \cos \left[\frac{p'\pi z''}{N} \right] dz'' = \delta_{p,p'} \frac{q^2}{q^4/4 + p^2\pi^2/N^2}.$$

The determinant now requires integrations over the two variables q and $k = p\pi/N$, leading to Eq. (4.14).

We just add that the procedure adopted is the method of evaluating a Toeplitz determinant (in disguise) [33].

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