Test of Replica Theory: Thermodynamics of 2D Model Systems with Quenched Disorder

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We study the statistics of thermodynamic quantities in two related systems with quenched disorder: A (1+1)-dimensional planar lattice of elastic lines in a random potential and the 2-dimensional random bond dimer model. The first system is examined by a replica-symmetric Bethe ansatz (RBA) while the latter is studied numerically by a polynomial algorithm which circumvents slow glassy dynamics. We establish a mapping of the two models which allows for a detailed comparison of RBA predictions and simulations. Over a wide range of disorder strength, the effective lattice stiffness and cumulants of various thermodynamic quantities in both approaches are found to agree excellently. Our comparison provides, for the first time, a detailed quantitative confirmation of the replica approach and renders the planar line lattice a unique testing ground for concepts in random systems.

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I. INTRODUCTION

Quenched disorder is common to many condensed matter systems. Examples include spin glasses, elastic structures in a random environment or mesoscopic electronic systems. In spite of a large volume of theoretical and experimental work on glasses these systems still pose interesting challenges. On the theoretical side, much of the studies have focused on phase diagrams, the existence of phase transitions and their critical behavior. But even if the equilibrium phases are known, thermodynamic quantities are in general not accessible. Slow glassy equilibration due to the presence of many metastable states on large length scales is the main obstacle to the numerical and experimental study of disordered systems. There exist, however, a number of well-tested analytical tools to study the equilibrium properties. Common to basically all approaches is that they rely on the introduction of replicas in order to reestablish translational invariance. The replicated system is then usually studied by a renormalization group (RG) approach or a Gaussian variational ansatz (GVA) since perturbation theory completely fails. The first method is designed to yield the effective pinning potential at large length scales. The latter approach aims at constructing a Gaussian trial Hamiltonian which describes the glassy phase. The results of the RG approaches are, strictly speaking, valid only close the upper critical dimension or close to a critical point where randomness becomes irrelevant. On the other hand, the GVA has to be combined with the concept of "replica symmetry breaking" which is not generally accepted for elastic structures in random media. Although the results of both approaches are similar, the different underlying concepts indicate that the present general understanding of disordered systems is still incomplete. A more general qualitative picture was developed in form of the droplet theory for spin glasses. It provides a phenomenological scaling approach to static and dynamics properties of the spin-glass ordered phase. The properties of this phase are characterized in terms of connected clusters (droplets) of coherently flipped spins with minimal free energy. It would be desirable to have a detailed quantitative test of this theory. Progress on numerical approaches as monte carlo simulations at finite temperatures were seriously hampered by the slow dynamics. Only recently novel powerful polynomial algorithms became available for the study of large systems at any temperature.

On the experimental side, most of the effort was devoted to spin glasses and pinned vortex systems. Especially the latter class comprises a system which is accessible to exact both analytical methods and numerical algorithms. It is a randomly pinned planar vortex lattice that was highlighted by an experimental study of magnetic flux lines threading through a thin film of the superconductor $2H$-NbSe$_2$. For a certain class of 2D random systems, including the flux line lattice, new promising approaches have been developed. For a planar lattice of non-crossing elastic lines pinned by disorder a replica Bethe ansatz (RBA) can be employed, yielding exact results for thermodynamic quantities and their cumulants for the related random bond dimer model the partition function can be calculated exactly by a polynomial algorithm without the need to run slow relaxation dynamics. Therefore, both method are perfectly suited to overcome to drawbacks of the above mentioned approaches. However, there are also limitations to the RBA and the dimer simulations. The first does not allow to compute correlation functions whereas in the latter the choice of parameters of the related line lattice model is restricted, e.g., only one particular density of lines can be simulated.

The aim of the present work is to show that the thermodynamics of the two studied model systems provide ideal environments for a quantitative test of replica the-
ory including replica symmetry breaking and analytical continuation. Here the 2D model systems can be considered counterparts of exactly solvable 1D quantum systems which have advanced the understanding of strongly correlated systems in general. Our main result is that RBA and dimer model simulations agree so well that they prove each other to be reliable and thus allow to explore many questions in detail that had been unaccessible to date.

The rest of the paper is organized as follows. In the following section we introduce the line lattice model and the dimer model, and explain their mutual relation and their connections to other models. In section III we review briefly the replica Bethe ansatz for the line system and summarize the results in the known limiting cases. We continue in section IV with a detailed quantitative comparison of the Bethe ansatz predictions for various thermodynamic quantities and the corresponding simulation data for the dimer model. To do so, the Bethe ansatz equations are solved numerically outside the validity range of the previously studied limiting cases. We close with a summary and discussion of our results in section V.

II. THE MODELS AND THEIR CONNECTIONS

A. Vortex system

We consider an ensemble of directed vortex lines confined to a plane at average distance \( a \equiv 1/\rho \). The configurations of a single directed line is characterized by its position \( x_i(z) \) since overhangs are forbidden. The preferred path of the line results from the competition between elastic energy, measured by the line tension \( g \), the line interaction in form of a repulsive pair potential \( U(x) \) that does not allow the lines to cross and pinning by a random impurity potential. With a contact repulsion \( U(x) = c \delta(x), c \to \infty \), ensuring the noncrossing condition, the model remains generic and allows for the mapping to a discrete dimer model. Quenched disorder couples locally to the vortices via a random potential \( V(r) \), which we assume to have zero mean and short-range correlations

\[
V(r)V(r') = \Delta \delta_{\xi_d}(r-r').
\]

Whenever the disorder correlation length \( \xi_d \) is the smallest scale in the problem it can safely be set to zero. The total energy can be written as

\[
H = \int dz \sum_i \left\{ \frac{g}{2} \left( \frac{dx_i}{dz} \right)^2 + c \sum_{i,j \neq i} \delta(x_i - x_j) + V(x_i, z) \right\}.
\]

B. Dimer model

The dimer model is defined as follows: Choose a subset (whose elements are called dimers) of the bonds on a square lattice with lattice constant \( b \) and linear size \( L \) such that every of the \( L^2 = N \) lattice sites (labelled by \( (ij) \)) is touched by exactly one of these dimers, see Figs. 1, 2. A square lattice rotated by 45 degrees with lattice constant \( b/\sqrt{2} \) is formed by the centers of the bonds. Its \( 2N \) sites shall for convenience also be labelled by \( (ij) \) and it will be clear from the context if the original lattice or that of the bonds is parametrized. The reduced energy of one such complete covering \( D \) of \( N/2 \) dimers is defined by

\[
H_d = \sum_{(ij) \in D} \epsilon_{ij}/T_d,
\]

where the sum is over all dimers of \( D \). The bond energies \( \epsilon_{ij} \) are randomly drawn from a Gaussian distribution with zero mean and unit variance \( \epsilon_{ij} \epsilon_{kl} = \delta_{ijkl} \). \( T_d \) is the dimer temperature and measures the strength of disorder. The implementation of the polynomial algorithm (with exponent \( \sim 2 \)) on a 32-processor cluster allows to compute thermodynamic quantities numerically exactly – as opposed to, e.g., Monte Carlo sampling – for sizes up to \( L = 512 \) at typically 6000 disorder configurations within a CPU time of days. Merely the measurement of the specific heat in Section V is not covered by the polynomial algorithm. Thermal fluctuations have to be computed from explicitly sampling over a representative set out of \( \exp(NG/\pi) \) possible dimer coverings, again for up to 6000 disorder configurations. This gives, however, also reliable results for sizes up to \( L = 256 \). The typical accuracy of numerical data at the given number of disorder samples is \( \sim 10^{-5} \). For further details of the algorithm for the simulation of the dimer model see, e.g., Ref. 7.

C. Connections

These two apparently diverse models are closely related. The random bond dimer model can be mapped onto an array of lines that interact via a hard-core repulsion, preventing any line crossing. In Fig. 2 this mapping
and the connections to related models are sketched. From the dimer model (A) on top, the discrete lattice version of the line model (C) can be reached directly or via the intermediate random solid-on-solid (SOS) model (B). Both the SOS model and the discrete lines have their continuous counterparts — in the bottom line of the sketch — that can be treated analytically: The 2-dimensional random sine-Gordon (RSG) model (D) (being equivalent to the random-field XY model without vortices) and the continuum (1+1)-dimensional elastic lattice of directed lines (E). The parameters and observables of the isotropic dimer model and its version with a height profile (SOS) can be expressed in terms of the anisotropic vortex line lattice. In the following we describe the relations between the above mentioned models in detail. We start the tour through the mapping table of Fig. 2 from the dimer model (A) with the dimer temperature $T_d$ as the only control parameter. The discrete line lattice can be reached easily via the map

$$ (AC) \quad \text{Add a given dimer pattern and a regular reference dimer covering as given in the middle of Figs. 1, 2 with an "exclusive or" (XOR) operation. Only if a given bond is covered by either the dimer pattern or the reference pattern it shall be covered in the resulting line configuration, which will be noncrossing lines at average density $\rho = 1/(2b)$. A resulting line lattice configuration is shown in the right part of Figs. 1, 2. For the summed energies of all covered bonds in the respective configurations it holds}$$

$$ H_1(\{\epsilon'_{ij}\}) = H_d(\{\epsilon_{ij}\}) + H_{\text{ref}}(\{\epsilon_{ij}\}). \tag{4} $$

Here and in the following, the subscript 'd' stands for quantities of the dimer model, while line-lattice quantities are denoted by the subscript 'l'. $\{\epsilon_{ij}\}$ stands for a given distribution of random energies on all of the bonds of the dimer model while the set of random energies $\{\epsilon'_{ij}\}$ are defined as $\epsilon'_{ij} = -\epsilon_{ij}$ on the occupied bonds of the reference pattern and $\epsilon'_{ij} = \epsilon_{ij}$ elsewhere. If the original random bond energies $\{\epsilon_{ij}\}$ are distributed symmetrically with zero mean, so are the bond energies $\{\epsilon'_{ij}\}$ defining the discrete line lattice model.

$$ (AB) \quad \text{A discrete height profile } \{h_{ij}\} \text{ can be assigned to every plaquette of the square lattice in the following way. Every bond is given a sign } \pm 1 \text{ such that when going through rows or columns of plaquettes the sign of the crossed bonds alternates. Starting at a given plaquette with arbitrary height, one moves to the neighboring plaquettes and adds to the height } +3 \text{ times the bond sign if the crossed bond is covered by a dimer, or } -1 \text{ times the bond sign if it is not. The resulting numbers define a path-independent height profile } \{h_{ij}\}, \text{ see Fig. 3 for an example.}$$

$$ (BC) \quad \text{Define a new discrete height profile } \{H_{ij}\} \text{ on each plaquette by subtracting the height profile } \{h'_{ij}\} \text{ associated with the reference dimer covering, cf. the middle part of Fig. 3.}$$

$$ H_{ij} = h_{ij} - h'_{ij}. \tag{5} $$

### FIG. 2: Overview of the models introduced in the text, showing their degrees of freedom and parameters. Top: discrete models; bottom: continuous models; left: isotropic models, right: anisotropic models.

| model       | isotropic                                                                 | anisotropic                                                                 |
|-------------|---------------------------------------------------------------------------|------------------------------------------------------------------------------|
| A: random bond dimer | configs.: covering $D$  
disorder strength: $1/T_d^2$ | C: discrete line lattice  
configs.: displacement $u_{ij}$  
disorder strength: $1/T_d^2$  
disorder strength: $1/T_d^2$  
line density: $\rho = 1/(2b)$ |
| B: solid on solid | configs.: height $h_{ij}$  
disorder strength: $1/T_d^2$ | D: random sine-Gordon  
configs.: height field $h_{ij}(x, z)$  
disorder strength: $\Delta$  
temperature: $T$  
stiffness: $K$  
edlastic moduli: $c_{11}, c_{44} = T/b^2$ |
| continuous line lattice | configs.: displacement $u_{ij}$  
disorder strength: $1/T_d^2$  
line density: $\rho = 1/(2b)$ | E: continuous line lattice  
configs.: displacement $u_{ij}$  
disorder strength: $\Delta$  
temperature: $T$ |

The profile $\{H_{ij}\}$ is then quantized in steps of width 4. Plaquettes of constant $H$ form domains of average width $2b$ that may be numbered by $k$. The domains are separated by domain walls which can be considered as directed lines. Next, we introduce the displacements $u_k(i)$ of these domain walls from their perfectly aligned positions where $i = 1, \ldots, L$ and $j = 2k$. As illustrated in Fig. 4 the line displacements are determined by the height profile, leading to

$$ u_k(i) = \frac{H_{i,2k} + H_{i,2k+1}}{4} + 2k. \tag{6} $$

It is important to keep in mind that the mapping to a displacement field makes sense only for a well-defined initial configuration of the domain walls implying a fixed density. In the grand canonical ensemble induced by the sum over dimer configurations, $u_k(i)$ is a good degree of freedom only for the configurations corresponding to the mean line density $\rho = 1/(2b)$, which, however, carry the dominant weight in the thermodynamic limit where the density distribution is sharply peaked.
approximation from the line interaction potential \(\text{Eq. (1)}\). The compression modulus is obtained in elastic energy density resulting macroscopic elastic system. We define a continuous displacement field scales (or for more general microscopic interactions) for the special contact repulsion we include the line interaction in the elastic energy, the imposed by the equivalence to the dimer model, the micro-

For the special contact repulsion \(U(x) = c\delta(x), c \rightarrow \infty\), imposed by the equivalence to the dimer model, the microscopic (short scale) \(c_{11}\) vanishes. However, on larger scales (or for more general microscopic interactions) \(c_{11}\) assumes a finite value due to entropic contributions. The resulting macroscopic \(c_{11}\) can be obtained from the free energy density \(f\) of the model of \(\text{Eq. (2)}\) by:\n
\[
    c_{11} = a \frac{\partial^2}{\partial a^2} U(a).
\]

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\[
    c_{11} = a \frac{\partial^2}{\partial a^2} [af(a)].
\]

The disorder energy of \(\text{Eq. (7)}\) can be transformed to the form of \(\text{Eq. (8)}\) by expanding the local density of the lines \(\rho(r)\) in terms of the line displacement \(u(r)\) by use of Poisson’s summation formula, for details see Ref. 2. The relation \(h(r) = 4u(r)/a\) between the line displacement field and the (dimensionless) height profile is the continuum version of \(\text{Eq. (9)}\) which can be seen with the use of \(\text{Eq. (10)}\) and the observation that \(h^{(i)} \approx 2j\) upon coarse graining. This relation is in hindsight, knowing that the lines have a mean distance of \(a = 2b\), the reason for the choice of \(Q = 2\pi/4\) in model D, \(\text{Eq. (9)}\). Due to the coordinate rescaling, the system size \(A = L_xL_z\) is changed when going from model E to D. If we denote the system sizes by \(A_{\text{el}}\) and \(A_{\text{RSG}}\), respectively, we obtain the ratio:\n
\[
    \frac{A_{\text{RSG}}}{A_{\text{el}}} = \sqrt{\frac{c_{11}}{c_{44}}} = \frac{K}{bg}.
\]

Having explained the relationships between the models, we have to specify how the three continuum model parameters, (i) line stiffness \(g = a c_{44}\), (ii) disorder strength \(\Delta\) defined by \(\text{Eq. (11)}\) and (iii) temperature \(T\), are related to the dimer model. First, we observe that only the relative strength of the parameters \(g\) and \(\Delta\) with respect to thermal fluctuations is important, i.e., the ratios \(g/T\) and \(\Delta/T^2\) have to be determined. Out of these we start with the reduced single line stiffness \(g/T\). In the dimer model, out of the \(2L^2\) bonds on average likewise \(L^2/4\) horizontal and vertical bonds are occupied. This holds both with respect to thermal sampling, i.e., summing over dimer configurations, and the disorder average as long as the mean random energy is isotropic. For the discrete lines after the “XOR” addition with the reference state, an average number of \(L^2/4\) horizontal and \(L^2/2\) vertical segments is implied, corresponding to a mean line density of \(\rho = 1/(2b)\). We now consider a given discrete line as performing a one-dimensional random walk with the three possibilities of moving to the left or to the right, or to rest. The probabilities for the possible steps \(x_i = -1, 0, 1\) can be deduced from the average number of occupied horizontal and vertical bonds. From the above analysis of...
occupied bonds we find the corresponding probabilities
\[ w_i = 1/4, 1/2, 1/4 \text{ for the steps } x_i. \]
For the fluctuations of the total horizontal wandering \( X \equiv \sum_i x_i \),
this leads after \( z/b \) steps to
\[ \langle X^2 \rangle = \sum_{i=1}^{z/b} (x_i^2) = z b/2. \]

A continuum Hamiltonian for a random walk \( H = \frac{1}{2} \int dz (\partial_x X)^2 \) in comparison
yields \( \langle X^2 \rangle = \frac{T^2}{g} \) and allows to read off
\[ \frac{g b}{T} = 2. \] (12)

The strength of disorder is measured in the continuum theory by the variance \( \Delta \) of the disorder potential. Noting that \( 1/T_d^2 \) is the variance of the (reduced) random bond energies in the dimer model we are lead to identify \( \sqrt{\Delta/T} \) with the dimensionless inverse dimer temperature \( 1/T_d \).
Allowing for the finite disorder correlation length \( \xi_d \), cf. Eq. (14),
which acts as a cutoff in the continuum model, to differ slightly from the lattice constant \( b \) of the dimer model, we have
\[ \frac{\Delta}{T^2} = \frac{\xi_d}{b} \frac{1}{T_d^2}. \] (13)

A closer look at the models, however, suggests that this relation is valid only if the energies \( \epsilon_{ij} \) of the horizontal bonds of the dimer model are set to zero, i.e., if there is no disorder on these bonds. This is because in the continuum model of Eq. (7) the disorder energy is written as the coupling of the local line density \( \rho(\mathbf{r}) \) to the disorder potential \( V(\mathbf{r}) \),
\[ H_{\text{dis}} = \int dx dz V(x, z) \rho(x, z) = \sum_i \int dz V(x_i(z), z). \]
The random part of the energy is thus not an integral over the arc length of the lines but over their \( z \)-coordinate. Therefore, the disorder energy of a line is proportional to its length projected onto the \( z \)-axis and not to its overall length. In the original isotropic dimer model, random energy is collected on both vertical and horizontal bonds and will thus be proportional to the overall length of a fluctuating line. As a consequence, a given disorder in the dimer model corresponds to larger disorder in the continuum line model than assumed by Eq. (13). A possible method to gauge the disorder strength it to consider the annealed disorder average \( -T \ln \tilde{Z} \) of the free energy. This quantity can be obtained analytically in both models. The calculation for the continuum model is straightforward whereas in the dimer model the means of Ref. 16 together with the relation of Eq. (14) can be used. One finds by comparison between the two models the relation
\[ \frac{\Delta}{T^2} = \frac{\xi_d}{b} \frac{2}{T_d^2} \left\{ 1 - \frac{2 G T_d^2}{\pi} + \frac{2 T_d^2}{\pi} \int_0^{1/(2 T_d^2)} dx \frac{\arctan x}{x} \right\}, \] (14)
with Catalan’s constant \( G = 0.915966 \). The contribution from the latter two terms in the curly brackets crosses over at \( T_d \approx 1 \) from zero at small \( T_d \) to \(-1/4 \) at large \( T_d \).
Thus the overall factor of two as compared to the naive estimate of Eq. (13) confirms the conjecture about the contribution of the horizontal random bond energies for strong disorder (small \( T_d \)). For weak disorder (large \( T_d \)) the gauging by the annealed free energy yields a factor of \( 3/2 \) compared to Eq. (13). However, in most expressions below, the latter two terms will only act as corrections at intermediate \( T_d \approx 1 \) and are in those cases frequently neglected. (At large \( T_d \) constant additional terms which are not related to the gauging procedure dominate.) It should be noted that the exact relation Eq. (13) has been derived for one special observable, the annealed free energy, and it cannot be expected to hold universally for all observables with the same value for the regularization length \( \xi_d \). Rather, to different observables the short scale modes around the UV cutoff can contribute with a different weight. The one free parameter \( \xi_d/b \) relating the continuum model to the discrete model will therefore be considered a fitting parameter, which should, however, not turn out to vary dramatically around its expected value of order unity from observable to observable.

Below, results from numerical simulations of both the isotropic dimer model with random energies on vertical and horizontal bonds and the dimer model with vanishing energies on the horizontal bonds will be compared to theory. For the former, Eq. (14) will be used as disorder strength mapping (sometimes without the correction terms) while for the latter Eq. (13) will prove to fit very well. Table II summarizes the relations between the dimer parameters and the continuum model parameters.

III. REPLICAN BETHE ANSATZ

The classical statistics of fluctuating elastic lines in \( d \) dimensions can be described by the quantum statistics of a \((d - 1)\)-dimensional system of interacting bosons19. In the thermodynamic limit, the free energy and its disorder fluctuations are determined by the ground state energy of the Bose gas. An important simplification arises for \((1 + 1)\)-dimensional systems of self-avoiding lines for two reasons. First, in the absence of quenched disorder the interacting Bose gas is replaced by a 1-dimensional free Fermi gas since the non-crossing condition for the lines is then automatically fulfilled by the Pauli exclusion principle.19,20,21 Second, 1-dimensional quantum systems with sufficiently simple interactions (generated here by quenched disorder) can be often treated exactly by Bethe ansatz. Indeed, Kardar used the replica method to show that the self-avoiding line lattice in a random potential maps to a gas of fermions with \( n \) spin components with \( SU(n) \) symmetry interacting via an attractive \( \delta \)-function potential.19 The ground state energy of this system can be calculated exactly by Bethe ansatz. The analogy between the replicated line lattice and \( SU(n) \) fermions was
examined further in Ref. 11. In the following we will summarize the main results of the replica Bethe ansatz (RBA).

Upon replication of the system of Eq. 2 and disorder averaging with the aid of Eq. 11, the equivalent quantum system is described by the Hamiltonian

$$\hat{H} = -\frac{T^2}{2g} \sum_{\alpha=1}^{n} \sum_{j=1}^{N} \frac{\partial^2}{\partial x_j^2} - \frac{\Delta}{T} \sum_{\alpha < \beta} \sum_{j,k} \delta(x_{j,\alpha} - x_{k,\beta}), \quad (15)$$

where $N$ is the number of lines and $n$ the number of replicas. In the quantum system the line stiffness $g$ corresponds to the fermion mass, the temperature $T$ is mapped onto $\hbar$ and the system size in $z$-direction, $L_z$, onto $\hbar \beta$ where $\beta$ is the inverse quantum temperature. We are interested in the ground state with wave function for general $n$. The Bethe ansätze as demonstrated by Sutherland can be analytically continued to real valued $\alpha<\beta$ and by Takahashi and Kardar the thermodynamics of the line lattice, can then be expressed in terms of the density function $\rho(k)$ which yields the number $L_x \rho(k) dk$ of allowed wave numbers in the interval $[k, k + dk]$. One finds

$$E_0(n) = \frac{9 \rho \Delta^2 L_x}{24 T^4} n(1 - n^2) + \frac{T^2 L_x}{2g} \int_{-K}^{K} dk \ k \ 2 \rho(k).$$

The $(n$ dependent) density function $\rho(k)$ is determined by the integral equation

$$nk = \int_{-K}^{K} dk' g_n \left[(k-k')l_d]\ 2 \rho(k') \quad (18a)$$

with the kernel

$$g_n(x) = 2 \sum_{m=0}^{\infty} \arctan \left[ \frac{nx}{m^2 + nm + x^2} \right]. \quad (18b)$$

The length $l_d = T^3/(g \Delta)$ is the characteristic length scale of the interaction in the quantum problem. This length sets the crossover scale beyond which the line fluctuations are dominated by disorder. In the above equations, the integral boundary $K$ is fixed by the mean line density via

$$\rho = \int_{-K}^{K} dk \ \rho(k). \quad (18c)$$

In the limit $n \rightarrow 0$, the integral equation assumes the form: \[\int_{-K}^{K} dk' \left[ \frac{1}{l_d(k-k')} + \pi \coth (\pi l_d(k-k')) \right] \rho(k') = k. \quad (19)\]

This equation can be solved perturbatively in $K l_d$, yielding

$$\rho(k) = \sqrt{1 - (k/K)^2} \left[ \frac{1}{2\pi} K l_d - \frac{\pi}{24} (K l_d)^3 \right. \left. + \frac{\pi^3}{144} \left( 1 + \frac{2}{5} (K l_d)^2 \right) (K l_d)^5 + \ldots \right]. \quad (20)$$

In the opposite limit of vanishing disorder or $l_d \rightarrow \infty$, the exact solution is $\rho(k) = 1/(2\pi)$. Using Eqs. 14a, 15a the ground state energy can be calculated from Eq. 20 perturbatively in $K l_d$. Interestingly, it can be shown order by order in $K l_d$ that the exact result for the ground state energy is obtained from the first two terms

| model | line density | line tension | disorder | system size |
|-------|-------------|-------------|----------|-------------|
| continuum line lattice | $\rho = 1/a$ | $g/T$ | $\Delta/T^2$ | $L_x \times L_z$ |
| isotropic dimer model | $1/(2b)$ | $2/b$ | $\approx 2 \xi_d/(bT_d^2)$ | $bL \times \frac{16\pi T_d}{\xi_d}$ |
| anisotropic dimer model | " | " | $\approx \xi_d/(bT_d^2)$ | " |

TABLE I: Relation between parameters of the continuum line lattice and the dimer model with random vertical and horizontal bond energies (isotropic) or only random vertical bond energies (anisotropic).
in the square brackets of Eq. (21). Indeed one finds that

\[ \int_{-K}^{K} dk k^2 \rho(k) = \frac{\pi^2}{3} \rho^3 + \rho^2 l_d^{-1} \quad (21) \]

to any order in \( \rho l_d \). Using \( \mathcal{T} = \lim_{n \to 0} E_0(n)/(nL_2) \) this leads to the mean free energy density of the line system,

\[ \mathcal{T} = T_0 \rho + \frac{\pi^2 T^2}{6} g \rho^3 + \frac{\Delta}{2T} \rho^2, \quad (22) \]

where the contribution from single non-interacting lines is given by

\[ T_0 = C(g) T - \frac{\Delta}{2 \xi_d T} + \frac{g \Delta^2}{24T^4}. \quad (23) \]

with \( C(g) \) a disorder independent contribution that cannot be obtained from Bethe ansatz. The result for interacting lines [Eq. (22)] was first derived in Ref. 13 while the latter result for a single line was first given in Refs. 20, 24 with finite size corrections calculated in Refs. 25, 26. It should be noted that in the interaction energy of Eq. (22), the entropic thermal contribution – second term – and steric disorder contribution – third term – are simply additive with no interference between the two effects. They agree in their dependency on the system parameters with the respective expressions based on scaling arguments.20, 24

So far we have only used the integral equation (18a) in the limit \( n \to 0 \). However, this equation taken at small \( n \) contains information about the cumulants of the free energy. Therefore, we would like to compute the ground state energy \( E_0(n) \) perturbatively in \( n \ll 1 \). In general, this is not feasible by analytical means. Therefore, below we will solve Eq. (18a) numerically in order to extract the behavior of \( E_0 \) for small \( n \). There is, however, one important limiting case where analytical progress is possible. For strong disorder or low line density with \( l_d \ll 1/\rho \), the integral Eq. (18a) has been shown to assume a particular interesting form. It reduces after a rescaling to the Bethe ansatz equation for the 1-dimensional Bose gas with a repulsive \( \delta \)-function interaction.27 The effective interaction strength of the Bose gas is proportional to \( n^2/l_d \). Therefore, in the interesting limit of small \( n \) one can either use the numerical solution of the Bethe ansatz equations for the Bose gas or Bogoliubov’s perturbation theory to calculate the ground state energy \( E_0(n) \) of the \( SU(n) \) fermions as a polynomial in \( n \) to lowest order in \( \rho l_d \). From \( E_0(n) \) the quenched averaged moments of the partition function of the line system can be evaluated using Eq. (10). For the disorder dependent contributions one finds the result11

\[ \ln Z_n = -\frac{L_x L_z}{2} \left( \frac{\Delta}{T^2} \right)^2 \left( \frac{g}{T} \right)^2 \left\{ \frac{n(1-n^2)l_d \rho + n(l_d \rho)^2}{12} - \frac{4}{3 \pi} n^2 (l_d \rho)^{3/2} + \left( \frac{1}{6} - \frac{1}{2 \pi} \right) n^3 l_d \rho + O(n^4) \right\}. \quad (24) \]

The first term \( \sim (1-n^2) \rho \) in the curly brackets describes the disorder contribution to the single-line free energy cumulants while the following terms stem from line interactions in the presence of disorder. As can be seen from Eq. (10) the above result provides the free energy cumulants in the dilute limit \( \rho l_d \ll 1 \). At higher densities, the mapping to the Bose gas is no longer valid and the ground state energy has to be calculated by direct numerical solution of the integral Eq. (18a). This will be done in Sec. IV C.

A natural limit to the validity of the RBA results is set by the mapping of the line system with short-ranged correlated disorder to the quantum problem with a singular \( \delta \)-function interaction arising from the disorder average. The characteristic length scale in the quantum problem is \( l_d \) which is inversely proportional to the disorder strength \( \Delta \). If \( l_d \) becomes of the order of the cutoff length \( \xi_d \) of the short-ranged disorder correlator of Eq. (1), the assumption of ultra-locally interacting fermions is no longer justified. The \( \delta \)-function interaction, however, is essential for the Fermi gas to be solvable by Bethe ansatz. The RBA results therefore are valid only for temperatures

\[ T \gtrsim T^* = (g \xi_d \Delta)^{1/3}, \quad (25) \]

or, respectively, at sufficiently weak disorder. For lower temperatures a modified replica symmetry breaking solution has been suggested in Ref. 29 for the single line, the predictions of which, however, could not be tested to date by other means. For the interacting line system the modifications at low temperatures implied by the replica symmetry breaking solution can be adapted.11 However, when the RBA results are translated to the random bond dimer model it turns out that the low temperature limit \( T < T^* \) can be never realized in the latter model.

IV. THERMODYNAMICS

A. Large scale equivalence

Before studying thermodynamics, we will demonstrate that the statistics of the random bond dimer model and its associated discrete height profile on large length scales are well described by the continuum model for elastic lines which can be treated analytically by the RBA. From the simulation of the random bond dimer model, the correlations of the height profile \( \{ h_{ij} \} \) of model B can be determined very accurately. The quantity \( \delta h(r) = h(r) - \langle h(r) \rangle \) measures the thermal fluctuations of the height around its state pinned by disorder. A Renormalization group calculation predicts for the disorder averaged correlation function

\[ C(r) = \langle (\delta h(r) - \delta h(0))^2 \rangle = \frac{1}{\pi K} \ln(|r|/b), \quad (26) \]

i.e., logarithmic growth on large scales, irrespective of the value of \( \langle h(0) \rangle \). A possible transition from a glassy
low temperature phase with \( \langle h(0) \rangle > 0 \) to a free thermal phase with \( \langle h(0) \rangle = 0 \) therefore is not reflected directly in this correlation function. However, the coefficient \( 1/(\pi K) \) will be of interest. The stiffness \( K \) obtained from a measurement of the correlation function for large \( |r| \) is the large-scale effective stiffness, renormalized by contributions from thermal and disorder fluctuations on smaller scales. It can be calculated exactly from the RBA free energy Eq. (22). First one can use the thermodynamic definition of the compression modulus of Eq. (8),

\[
c_{11} = a \partial_{a}^{2} [a f(a)],
\]

and then gets via the relation of Eq. (10) the effective stiffness

\[
K = \frac{\pi}{16} \left( 1 + \frac{ag\Delta}{\pi^{2}T^{3}} \right)^{1/2}.
\]  

(27)

Note that due to its linear dependence on density, the single line free energy of Eq. (22) does not contribute to \( K \). The result of Eq. (27) is compared in Fig. 5 to the numerical result as obtained from the dimer model (see also Ref. 8) and from the dimer model with no random energies on the horizontal bonds, i.e., \( \epsilon_{ij} \neq 0 \). The disorder strength \( \Delta \) has been mapped here to \( T_{d} \) according to Eq. (13) and Eq. (13), respectively. The agreement is very good over orders of magnitude while the \( \Delta - T_{d} \) relation from the comparison of annealed free energy averages seems to fit better than the naive estimate. The validity of the replica Bethe Ansatz calculation including its sometimes debated analytical continuation in \( n \) is nicely confirmed by our comparison. Interestingly, no deviation from the RBA result of Eq. (27) is found in the large disorder, i.e., low \( T_{d} \) limit. In terms of the line lattice temperature \( T \) modifications of the result of Eq. (22) must occur at \( T \lesssim T^{*} \), cf. Eq. (24), since otherwise the free energy would not converge to a finite ground state energy for \( T \to 0 \). However, this problem no longer exists after the mapping to the dimer model since the ratio \( \sqrt{\Delta/T} \) of disorder and thermal energy is controlled by the single parameter \( T_{d} \) in the dimer model. Thus the pinning strength and thermal fluctuations cannot be varied independently, and the crossover temperature \( T^{*} \) can vanish.

In the pure limit \( T_{d} \to \infty \) the stiffness approaches the value \( K = \pi/16 \) in agreement both with the exact calculation in terms of the nonrandom dimer model and the mapping of the line lattice without disorder to free fermions. Hence the most accurate simulation of a system of noncrossing lines by the dimer model is demonstrated. The precise value \( K = \pi/16 \) is of physical significance as shown by the renormalization group (RG) scaling dimension of disorder in RSG model Eq. (9)

\[
\lambda_{\Delta} = 2(1 - \pi/16 K^{-1}),
\]

(28)

see also Ref. 13. The limiting value of \( K = \pi/16 \) indicates that infinitesimal disorder is marginal and the system is thus on the borderline between a glassy and a thermal free phase. Any finite amount of disorder increases \( K \) which in turn renders disorder a relevant perturbation, leading to a glassy phase. This is consistent with the finding of Ref. 8 that the correlation function of the height profile, i.e., the one of \( h \) and not of \( \delta h \), always indicates a low temperature glassy behavior.

### B. Free energy, internal energy and entropy

We now come to a direct comparison of fundamental thermodynamic quantities of the dimer model and of the continuum model for the line lattice. We start with the disorder averaged free energies \( \overline{F} = -T \overline{\ln Z} \). Due to the different meanings of temperature in the line and dimer context we will focus on the logarithm of the partition functions \( \overline{\ln Z} \). When relating the systems we remember the energy relation Eq. (4) between dimer and line configurations. Therefore, the partition functions \( Z_{d} \) of the dimer model and \( Z_{l} \) of the line lattice are related by

\[
\ln Z_{d} + E_{\text{ref}}/T_{d} = \ln Z_{l}
\]

(29)

In the disorder average \( \ln Z_{d} + E_{\text{ref}}/T_{d} \) the reference energy \( E_{\text{ref}} = H_{\text{ref}}(\langle \epsilon_{ij}^{1} \rangle) \), cf. Eq. (4), does not contribute as the bond energies are drawn from a Gaussian distribution with zero mean. Higher moments of the free energy, however, contain contributions from \( E_{\text{ref}} \). In the simulations of the dimer model the moments of the density \( \ln(Z_{l})/\langle bL \rangle^{2} \) are measured by taking into account
the reference energy $E_{\text{ref}}$. The RBA, however, provides the statistics of the free energy density of the line lattice [Eq. (22)] which we denote by $f_l$ in the following. Both quantities are related by

$$
\ln \frac{Z_l}{(bL)^2} = -\frac{A_l}{A_d} \frac{f_l}{T},
$$

(30)

where $A_l = L_x L_y$ and $A_d = (bL)^2$ are the system sizes of the line lattice and dimer model, respectively. Here we have to pay attention to the fact that the two models are only equivalent after a rescaling of the $z$ coordinate as explained for the mapping between the models D and E in Sec. II C. According to Eq. (14) we have

$$
\frac{A_l}{A_d} = \frac{a}{16K} \frac{g}{T} = \frac{a}{16K} \frac{g}{T} \left( 1 + \frac{a g \Delta}{\pi^2 T^3} \right)^{-1/2}
$$

which has to be used in Eq. (30). The disorder independent part of the single line mean free energy $\bar{f}_l$ cannot be calculated unambiguously by the RBA. We thus combine the disorder independent contributions in $\bar{f}_l$ such that in the pure limit ($T_d \to \infty$) the known free energy of the dimer model is matched. In this limit, the partition functions of the dimer model just counts the number of complete dimer coverings of the square lattice. This is a complex combinatorial problem as any flip of one dimer may necessitate a cascade of flips throughout the system. Nevertheless, the result is exactly known to be

$$
\ln Z_d|_{T_d \to \infty} = \frac{G}{\pi} L^2
$$

(31)
in the thermodynamic limit with Catalan’s constant $G = 0.915966$. Next, we translate the line lattice parameters to the dimer model along Table II and get for the dimer model without horizontal energies, ($\epsilon_{ij \in h} = 0$),

$$
\ln \frac{Z_l}{L^2} = \frac{1}{\sqrt{\pi^2 + 4 \xi_d^2/bT_d^2}} \left[ G + \frac{1}{\xi_d^2} \left( 1 - \frac{\xi_d^2}{2b} \right) - \frac{1}{6} \frac{\xi_d^4}{b^2 T_d^4} \right].
$$

(32)

If both vertical and horizontal bonds carry random energies one should make the approximate replacement $1/T_d^2 \to 2/T_d^2$, which can be improved by the correction terms of Eq. (14), as explained above. The second term $\sim T_d^{-2}$ in the square brackets of Eq. (32) comes from terms proportional to disorder in both the single line free energy and the interaction part. The last term $\sim T_d^{-4}$ comes from the term $\Delta^2$ in the single line free energy. When comparing the result of Eq. (32) to the simulation results for the dimer model, at first glance we find no agreement at all. However, as we will discuss shortly, there are indications that one might have to drop the $T_d^{-4}$-term of Eq. (32). Doing so, we get the plots of Fig. 6 for the isotropic and anisotropic random bond energies. Only the large $T_d$ limit was fixed by the known result of Eq. (31), yet the agreement is excellent over orders of magnitude down to small dimer temperatures. The only fitting parameter $\xi_d/b$ arising from the disorder strength relation between the discrete and the continuum model is found, as expected, to be of order one, cf. the caption of Fig. 6.

Why do we have to drop the $\Delta^2$-term of the single line free energy [Eq. (23)] to obtain agreement? One can, in fact, imagine a number of reasons for this discrepancy between the RBA result and the simulation data. The validity of the RBA itself has been critically discussed, especially the interchange of thermodynamic limit and replica number $n \to 0$ limit has been questioned. On the other hand, the simulations are performed for discrete lattice versions of the continuum model which has been solved by RBA. We were not able to find a conclusive answer to what causes the absence of the $\Delta^2$-term in the simulation data. But in connection to this it is interesting to remind of a numerical analysis of the average free energy of a single directed polymer in a random potential via a transfer matrix method in Ref. 30. In Fig. 6 the simulation data of Table II of Ref. 30 are plotted, giving the average free energy as a function of disorder strength. A plot of this kind had not been shown in the cited reference. However, it demonstrates that the data obtained in Ref. 30 agree with ours in not finding support for the term $\sim \Delta^2$ in Eq. (23).

Now we compare further thermodynamic quantities for the dimer model and the line lattice. The entropy and
the internal energy of the dimer model

$$\overline{S}_d = -\frac{\partial}{\partial T_d} T_d = \frac{\partial}{\partial T_d} \left( T_d \ln Z_d \right),$$

$$U_d = \overline{F}_d + T_d \overline{S}_d$$

are easily be calculated from the RBA. In the dimer model simulations, the quenched averaged internal energy $\overline{U}_d = \sum_{(ij)} p(ij) \epsilon_{ij}$ with the disorder configuration dependent dimer occupation probability $p(ij)$ of bond $(ij)$ can be obtained quite easily since the polynomial algorithm allows to calculate the probabilities $p(ij)$. The entropy is then obtained from the free energy by subtraction. A comparison of the data for internal energy and entropy with the RBA prediction is given in Fig. 8 where we used the result of Eq. (32) and $\ln Z_d = \ln Z_r$ to calculate $\overline{S}_d$ and $\overline{U}_d$. We find excellent agreement with $\xi_d/b \approx 1$. The slope of $\overline{S}_d$ at $T_d = 0$ is calculated from Eq. (32) to be

$$1 = \frac{1}{L^2} \frac{\partial}{\partial T_d} \overline{S}_d |_{T_d=0} = G \left( \frac{b}{\xi_d} \right)^{1/2} - \frac{\pi^2}{8} \left( \frac{b}{\xi_d} \right)^{3/2} \left( 1 - \frac{\xi_d}{2b} \right)$$

and matches the simulation data very well.

Summarizing, the quantitative agreement between the RBA results for the line lattice and simulation data for the dimer model is very satisfying; it is even more surprising for the thermodynamic potentials than for the large scale stiffness. The latter is expected to show universality in the sense that it does not depend on microscopic details of the model, while the former receive contributions from all scales. A priori, the sensitivity to the contribution from modes close to the UV cutoff might have been expected to be important. However, our above results indicate that the effect of small scales can be simply accounted for by the single fit parameter $\xi_d/b$ which was found to be very close to the naively expected value of one.

### C. Higher moments

Higher cumulants of thermodynamic quantities describe sample-to-sample fluctuations in experimental setups of mesoscopic dimensions while for macroscopic systems their scaling will give information on the selfaveraging behavior. Analytic expressions for higher cumulants of the free energy are available only in the strong disorder or dilute limit $l_d \rho \ll 1$, see Eq. (24). At higher densities we have to resort to a numerical computation of the ground state energy which then yields $\ln Z_r$ via Eq. (16), and thus the cumulants of the free energy. In the following we are interested in a polynomial expression for $E_0(n)$. Thus we have to expand in Eq. (17) the integral of the kinetic energy with respect to $n$. We introduce the dimensionless integral

$$\tilde{E}_{\text{kin}}(n) \equiv b^3 \int_{-K}^{K} dk \, k^2 \tilde{g}(k) = (bK)^3 \int_{-1}^{1} dy \, y^2 \tilde{g}(y) = \sum_{j \geq 0} \varepsilon_{j+1}(\rho_d) n^j,$$

defining the expansion coefficients $\varepsilon_j(\rho_d)$ which depend only on the dimensionless parameter $\rho_d$. With this definition, explicit formulas for the variance (second cumulant) and the skewness (third cumulant) of the reduced free energy can be obtained from the RBA. Using Eqs. (16), (17) together with Eq. (54) and the perturbative result of Eq. (24) we get
\[
\frac{(\ln Z_l)^2}{L^2} = \begin{cases} 
-\frac{A_l}{A_d} T b^2 \varepsilon_2(\rho_d) \\
\frac{A_l}{A_d} g \frac{\varepsilon_2(\rho_d)}{T_0^2} \\
\frac{A_l}{A_d} 4 \left( \frac{\Delta}{a T^2} \right)^{3/2} \left( \frac{b g}{T} \right)^{1/2} + \frac{A_l}{A_d} 2 \left( \xi_d / b \right)^{3/2} \\
\frac{A_l}{A_d} 3 \pi \varepsilon_3(\rho_d) \\
\frac{A_l}{A_d} \frac{4}{T d} \left( \frac{\Delta}{T} \right)^2 \frac{b g}{T} + \frac{A_l}{A_d} \frac{3}{2} \varepsilon_3(T_d) \\
\frac{A_l}{A_d} \frac{3}{4} \left( \frac{\xi_d / b}{T_d} \right)^{3/2} \frac{\varepsilon_3(T_d)}{T_d}
\end{cases}
\]

Here, the mapping \( gb / T \rightarrow 2 \), \( \Delta / T^2 \rightarrow (\xi_d / b) / T_d^2 \), \( a \rightarrow 2 b \), \( \rho_d \rightarrow (b / \xi_d) T_d^2 / 4 \) between the line lattice and the dimer model with random energies only on the vertical bonds has been applied. Also the rescaling of the volume according to Eq. [11] has to be applied for the comparison. In terms of the dimer temperature \( T_d \), the rescaling factor reads

\[
\frac{A_l}{A_d} = \frac{a g \pi T}{n^2} \left( 1 + \frac{a g \Delta}{\pi T^2} \right)^{-1/2} \rightarrow \frac{4}{\pi} \left( 1 + \frac{4 \xi_d / b}{\pi^2 T_d^2} \right)^{-1/2}.
\]

In order to compare the above RBA results to simulation data for the dimer model over the whole range of disorder strength, we solve the Eqs. \([18a],[18b]\) for \( \rho(k) \) numerically. From \( \rho(k) \) the kinetic energy of Eq. \([34]\) and thus the expansion coefficients \( \varepsilon_j \) are obtained. For a numerical treatment it is useful to rewrite Eq. \([18a]\) in the form

\[
y = \frac{1}{n} \int_{-1}^{1} dy' \ g_n[K_l d(y - y')] \tilde{\varepsilon}(y')
\]

with \( y = k / K \) and \( \tilde{\varepsilon}(y) = \varepsilon(Ky) \). At fixed \( K l_d \), the dimensionless function \( \tilde{\varepsilon}(y) \) is computed by the inversion of the discretized integral equation. This inversion is quite delicate since the present kind of inverse problem – a Fredholm integral equation of the first kind – is extremely badly conditioned. An adequate treatment is, however, possible by use of, e.g., the method of singular value decomposition (SVD) of the discretized integral kernel\([35]\). The solution \( \tilde{\varepsilon}(y) \) can only be computed for a given value of \( K l_d \). With the so obtained solution we can calculate the right hand side of

\[
\frac{\rho}{K} = \int_{-1}^{1} dy \tilde{\varepsilon}(y).
\]

The dimer model density \( \rho = 1 / (2 b) \) then fixes \( K \) and we thus obtain the disorder strength \( l / l_d \) that had been implied by our initially chosen value for \( K l_d \). In this approach we cannot – due to the coupling of the BA equations – modify \( n \) and \( l_d \) independently. A modified \( n \) implies a modified \( K \), which results in a different value of \( l_d \). We hence have to adjust the parameter \( K l_d \) in Eq. \([37]\) upon change of \( n \) such that \( l_d \) remains constant. In practice, this is realized by the simple method of nested intervals. The necessary number of discretization points for the integral Eq. \([37]\) depends crucially on considered range of parameters. An increase in the length scale \( l_d \) stretches the integral kernel \( g_n(k \ell_d) / n \) along the abscissa, a decreasing \( n \) does so along the ordinate. Thus, in order to keep up a given level of accuracy, the number of discretization points has to increase like \( l_d / n \). We are unfortunately interested in small \( n \) as we want to extract the coefficients \( \varepsilon_j \) from the behavior around \( n \rightarrow 0 \) and moreover in large \( l_d \) as the result for small \( l_d \) is known analytically. Therefore it is important that the reliability of the numerics can be checked in limiting cases where analytical results for \( \rho(k) \) are available. The limit of large \( l_d \rightarrow \infty \) or \( n \rightarrow 1 \) corresponds to lines without quenched disorder which are described by free fermions with a constant density \( \rho(k) = 1 / (2 \pi) \). The inset of Fig. \([7]\) a plot of the numerical solution in the latter case is displayed, showing very good agreement with the analytical expectation. An other limit which can be compared to analytical results corresponds to \( n \rightarrow 0 \). Then \( \rho(k) \) can be calculated perturbatively\([22,24]\) in \( K l_d \), see Eq. \([20]\). We compare the numerical solution for \( n = 10^{-3} \) and \( K l_d = 0.1 \) with the result of Eq. \([22]\) in Fig. \([7]\) Again the comparison is satisfactory while the mismatch at small \( k / K \) is due to the smallness of \( n \) which necessitates a high discretization level. In practice, \( n \) is chosen as not to require more than \( 10^3 \) discretization points for a relative accuracy of \( 10^{-4} \) in \( E_{\text{kin}}(n) \). Checks against the exact results for the quenched averaged free energy \( E_{\text{kin}}(n) \) and the strong disorder limit of the cumulants \( \varepsilon_j \) are also satisfactory.

Having determined the solution \( \rho(k) \), the coefficients \( \varepsilon_j \) of Eq. \([34]\) can be extracted from the numerically calculated \( E_{\text{kin}}(n) \) by repeated extrapolation to \( n \rightarrow 0 \), subsequent subtraction of this value from the finite-\( n \) result and final division by \( n \). This straightforward procedure is the best we could think of but it is still error-prone. While the desire for a small extrapolation error requires having data points as close as possible to \( n = 0 \), a simple
calculation of error propagation shows that the error of a given data point at finite \( n \) scales as \( n^{-k} \delta E_{\text{kin}} \) where \( k \) stands for the order of the coefficient and \( \delta E_{\text{kin}} \) for the original error of the data. However, we were able to achieve sufficient high accuracy to extract reliable values for the second and third cumulant. The above described scheme was implemented with the use of Numerical Recipe routines.[1] The data for the smallest disorder values needed the highest discretization level and consumed about 200h computation time on a 2GHz processor for the determination of the cumulants at a given value for \( l_d \).

Before we compare the RBA predictions for the cumulants to the simulation results for the dimer model we would like to make some remarks on the computation of cumulants in the dimer model simulations. In the replica theory the cumulants of random thermodynamic quantities appear naturally, while in the simulations the moments are immediately accessible. Both are related as follows. If the generating functional of the moments \( \{ m_p \} \) is

\[
M(n) = 1 + nm_1 + n^2 \frac{m_2}{2!} + n^3 \frac{m_3}{3!} + \ldots,
\]

then

\[
\ln M(n) = n \kappa_1 + n^2 \frac{\kappa_2}{2!} + n^3 \frac{\kappa_3}{3!} + \ldots
\]

generates the cumulants \( \{ \kappa_p \} \). The lowest cumulants expressed in terms of moments are

\[
\begin{align*}
\kappa_1 &= m_1 \\
\kappa_2 &= m_2 - m_1^2 \\
\kappa_3 &= m_3 - 3m_1m_2 + 2m_1^3.
\end{align*}
\]

From the dependence of Eq. (38) on the system size \( A_l = L_x \times L_y \) it follows immediately that all the free energy cumulants scale linearly in \( A_l \). Apart from the average free energy, the reduced cumulants \( \kappa_p/\kappa_1^p = F_p^f/F_0^f \) hence vanish in the thermodynamic limit as \( F_p^f/F_0^f \sim A_l^{1-p} \) as one would expect from the central limit theorem. The distribution of the free energy becomes infinitely sharp in the limit of large systems. In other words, the vortex-line array is self averaging which in light of the infinite correlation length reflected by logarithmic correlations had not been evident a priori.

For the determination of the cumulants from the simulation data the following problem is entailed. The moments \( m_p \) scale with the system size like \( m_p \sim A_l^p \). From Eq. (38) we see that a cumulant of order \( p \) has to be calculated as a sum of terms that grow by a factor \( A_l^{p-1} \) faster with the system size then the cumulant itself. Therefore, at a given accuracy of the simulation data for the \( m_p \), which primarily depends upon the number of disorder samples, a limit is set to the system size up to where cumulants can reliably be obtained. This maximum system size decreases with the order of the cumulant. On the other hand, finite size effects have to be minimized as well and, as a consequence, at the achieved precision of \( 10^{-5} \) for the moments \( m_p \) in the dimer model, the variance can be trusted only for system size up to \( L = 64 \) and the third cumulant up to size \( L = 16 \).

In the following, we compare the simulation data for the cumulants \( \langle \ln Z \rangle_p^2/L^2 \) for \( p = 2, 3 \) with the RBA predictions of Eqs. (35), (36). The variance \( (p = 2) \) as a function of \( T_d \) has been computed for the dimer model of size \( L = 64 \) and is shown in Figs. 10 and 11 together with the RBA result. With the only fitting parameter \( \xi_d/b = 0.8 \) we find very good agreement. In addition, the plots show that our numerical solution of the full Bethe ansatz equations nicely confirms the perturbative solution at small \( T_d \). The deviation at larger \( T_d \) shows that the numerical solution is inevitable for a comparison with the simulation data. A closer look at the analytical result of Eq. (36) and the data points of Figs. 10 and 11 shows that \( \langle \ln Z \rangle_2^2/L^2 \) does not follow strictly a power law in \( T_d \).

The third cumulant (skewness, \( p = 3 \)) is shown in Fig. 12. For the reasons explained above, the dimer data are to be trusted only for the small system \( L = 16 \) and here only for \( T_d \lesssim 1 \). In this range, no substantial deviations from the perturbative evaluation of the cumulant, cf. Eq. (36), is expected. Indeed, the agreement between theory and simulation is again very good with \( \xi_d/b = 0.8 \). Although the numerically determined coefficient \( \xi_3 \) has an error of only \( \sim 15\% \), the actual uncertainty of the third cumulant is larger. The reason is the following. In the exact RBA result of Eq. (36) the magnitude of the second term \( \sim \xi_3 \) amounts throughout the studied parameter range to about 85% of the first term. Since the terms are subtracted, the original error of 15% gets amplified to\( \sim 100\% \) in the final expression for the third cumulant. However, this does not restrict the comparison since the perturbative RBA solution could not have been
corrected noticeably in the range $T_d \lesssim 1$ which is set by the simulation data at hand. Note that both the simulation data and the perturbative RBA result consistently do not obey a power law in $T_d$, see Fig. 12.

It must be noted that there is agreement for the third cumulant only if the term $\sim n^3$ from the single line contribution $\sim \frac{n^3}{12} (1 - n^2) \Delta^2$ in Eq. (24) is taken serious, otherwise not even the sign of the cumulant would match. However, the part linear in $n$ stemming from the same contribution we had to drop in the comparison of the average free energy, being consistent with another independent study of the single line free energy. Since a single line (or directed polymer) is expected to have an asymmetrical disorder free energy distribution, we do not argue for a complete irrelevance of the contributions $\sim \Delta^2$ in the single line terms of Eq. (24), consistent with our simulation data for the third cumulant, but suggest a reassessment of the free energy distribution of a single line in random media.

**D. Specific heat**

The specific heat of disordered systems is strongly influenced by the complex nature of thermal excitations about the pinned ground state. In the context of spin glasses the excitations are considered as droplets, i.e., connected regions in which the thermal activated configurations differ from the ground state configuration. Droplets appear on all length scales with the lowest energy ones appearing on largest length scales. Here we would like to test the RBA prediction for the mean specific heat by comparing to our simulation results. The disorder averaged specific heat of the dimer model with random energy on horizontal and vertical bonds can be measured via the thermal fluctuations of the dimer energy,

$$c_d = L^{-2} \frac{(H_d^2 - \langle H_d \rangle^2)}{\langle H_d \rangle^2},$$

where $H_d$ is the Hamiltonian of the dimer model, see Sec. II B. From the RBA result for the free energy Eq. (39) (again without the $\Delta^2$-term in the single line
the region around

Also note that the dimer specific heat probes for the adjustable parameters in the comparison shown in Fig. 13.

Agreement over the entire range of \( \xi_d/b \) is consistent with our findings above. There are no further adjustable parameters in the comparison shown in Fig. 13. Also note that the dimer specific heat probes for the agreement of the RBA and simulations predominantly in the region around \( T_d \approx 1 \), the drop to zero for small and large \( T_d \) being generic rather than specific. So it can be considered complementary to the mean free energy which. For a finite density of excitations at small energies, \( \lim_{E \to 0^+} p_\ell(E) > 0 \), the specific heat as a superposition of exponentials contributions from each scale will be linear at small temperatures which is a famous insight of Anderson et al. Integration over all length scales allows to write the mean specific heat as \( c_T = \int_0^L d\ell \delta c_\ell \) which becomes exact in the limit \( T \to 0 \). In the droplet theory of spin glasses the distribution function \( p_\ell(E) \) is a central quantity. From the finite size scaling of the mean specific heat one can hope to obtain information on this distribution function as with growing system size larger droplets will fit into the system. However, the droplets in our dimer model simulation seem to be dominated by the system boundaries. The number of configurations of lowest excitation energy that differ only on the boundaries from the ground state configuration scales like the linear system size \( L \), yielding a \( 1/L \) decay for the specific heat (instead of a growth from bulk droplets) to its asymptotic value. In fact, this scaling behavior is observed for the specific heat data of our dimer model simulation, see Fig. 14. Indeed, low-lying excitations on the boundary can be easily identified. Consider a bond on the boundary that is occupied by a dimer in the ground state. A configuration that does not cover this very bond may remain unchanged on all the other bonds since simulations are done with open boundary conditions. The missing energy on the bond is the excitation energy, whose probability distribution, however, is nontrivial. The knowledge of this distribution would allow to calculate the finite size scaling of the slope of the specific heat at \( T_d = 0 \). Due to the simplicity of the boundary droplets the distribution could be computed with the dimer algorithm. The conditional probability that a bond is occupied given its random energy is just the probability \( p(ij) \) introduced above in the calculation of the internal energy, see

\[
\overline{c_d} = \frac{T_d}{L^2} \frac{\partial^2}{\partial T_d^2}(T_d \ln Z_d),
\]

where \( \ln Z_d = \ln Z_d \) is given by Eq. (30). After the mapping \( \Delta/T^2 \to 2(\xi_d/b)/T_d^2 \), \( b/T \to 2, \rho \to 1/(2b) \), the mean specific heat of the dimer model reads

\[
c_d = \frac{2\pi^2 - (\xi_d/b)(\pi^2 + 4G)}{[\pi^2 T_d + 8(\xi_d/b)]^{5/2}}.
\]

In Fig. 13 we compare this RBA result to the simulation data which we obtained via Eq. (39). We find rather nice agreement over the entire range of \( T_d \) with the choice \( \xi_d/b = 0.98 \) for the only fitting parameter, which is consistent with our findings above. There are no further adjustable parameters in the comparison shown in Fig. 13. Also note that the dimer specific heat probes for the agreement of the RBA and simulations predominantly in the region around \( T_d \approx 1 \), the drop to zero for small and large \( T_d \) being generic rather than specific. So it can be considered complementary to the mean free energy which can easily be understood by considering the lowest lying excitations on a given length scale \( \ell \). On each scale for a given disorder environment the ground state (with zero energy) and the lowest excitation (with energy \( E \)) form a two level system, whose free energy) the specific heat is calculated easily using

\[
c_d = \frac{2\pi^2 - (\xi_d/b)(\pi^2 + 4G)}{[\pi^2 T_d + 8(\xi_d/b)]^{5/2}}.
\]

\[\int_0^\infty dE p_\ell(E) c_{\ell,E} \sim p_\ell(0+) T.\]

The excitation energies obey a length scale dependent disorder distribution \( p_\ell(E) \) and the contribution to the mean specific heat from each scale is

\[\delta c_\ell = \int_0^\infty dE p_\ell(E) c_{\ell,E} \sim p_\ell(0+) T.\]

The conditional probability that a bond is occupied given its random energy is just the probability \( p(ij) \) introduced above in the calculation of the internal energy, see

![Fig. 13: Mean dimer specific heat \( \overline{c_d} \). Shown are the simulation data (diamonds) and the analytical result of Eq. (31) derived from the RBA (full line). The simulated dimer model has random energies on horizontal and vertical bonds, and is of size \( L = 256 \).](image-url)
It can be easily obtained from the dimer algorithm. The distribution of the boundary droplet energies is then given by \( p(ij) p(\text{occ}) / p(E) \) with \( p(\text{occ}) \), \( p(E) \) being the probabilities for the occupation and energy \( \epsilon_{ij} = E \) of a bond, respectively.

![Graph](image.png)

**FIG. 14:** Scaling of the slope of the dimer specific heat \( \overline{c_T} \) at \( T_d = 0 \) with the system size.

The smallest droplet excitation in the bulk is likewise easily identified as the rotation of a plaquette that consists of two opposite dimers. The probability distribution for the energy difference of the two configurations is, however, not easily obtained. It is complicated by the condition that the two dimers before the flip must be part of the groundstate configuration. In the simulations, it should be stressed, statistics of droplet energies can in principle be measured systematically in the following straightforward procedure. For a given disorder configuration the groundstate dimer covering is determined. Then the energy of one arbitrary occupied bond in the bulk is set to infinity and the new groundstate is determined. It will not contain the bond with infinite energy and hence have higher energy than the original groundstate. The energy difference \( E \) together with the diameter \( \ell \) of the non-overlapping region of the two ground states is measured. The statistics of these pairs of values for many disorder realizations yield the distribution \( p(E) \). Quantitative support of the scaling prediction of droplet theory is in reach considering the orders of magnitude over which the dimer model can be simulated.

### V. SUMMARY AND DISCUSSION

In this article we have compared recent exact replica Bethe ansatz results for the planar line lattice with numerical simulations of the classical random bond dimer model. We found excellent agreement for a large set of disorder averaged thermodynamic quantities, namely the effective disorder renormalized elastic stiffness, the free energy, the internal energy, entropy and the specific heat of the dimer model. Characteristics of the disorder distribution of thermodynamic quantities can also be obtained both from the Bethe ansatz and from simulations and their agreement has explicitly been shown for the variance and the skewness (third cumulant) of the free energy. The comparison thus confirms the Replica Bethe Ansatz calculation of Ref. 11 and makes the \((1+1)\)-dimensional line lattice one of the few glassy systems for which the validity of a replica approach (without replica symmetry breaking) can be critically tested in detail. In the comparison, only one free parameter has been used which is the ratio of the short scale regularization lengths of the continuous line model and the lattice constant of the discrete dimer model. The ratio is found to be consistently of the order of unity for all studied thermodynamic quantities. One term in the single line free energy, first given in Ref. 24, could not be confirmed by the simulations, in consistency with numerical data of Ref. 30. It would be interesting to relate the droplet excitations of the dimer or line system to the excitations of the related SU(n) fermi gas in the limit \( n \to 0 \). In view of the manifold links of dimer covering models to condensed matter systems, especially of spin systems, the link to the exactly solved disordered line lattice model might prove useful in future applications.

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1. K. Binder and A. Young, Rev. Mod. Phys. 58, 801 (1986).
2. T. Nattermann and S. Scheidl, Adv. Phys. 49, 607 (2000).
3. "Mesoscopic Quantum Physics," edited by E. Akkermans et al. (North-Holland, Amsterdam, 1994).
4. D. S. Fisher, Phys. Rev. Lett. 56, 1964 (1986).
5. M. Mezard and G. Parisi, J. Physique I 1, 809 (1991).
6. D. S. Fisher and D. A. Huse, Phys. Rev. B 38, 386 (1988).
7. C. Zeng, A. A. Middleton, and Y. Shapir, Phys. Rev. Lett. 77, 3204 (1996).
8. C. Zeng, P. L. Leath, and T. Hwa, Phys. Rev. Lett. 83, 4860 (1999).
9. C. A. Bolle, V. Aksyuk, F. Pardo, P. L. Gammel, E. Zeldov, E. Bucher, R. Boie, D. J. Bishop, and D. R. Nelson, Nature (London) 399, 43 (1999).
10 M. Kardar, Nucl. Phys. B 290, 582 (1987).
11 T. Emig and M. Kardar, Nucl. Phys. B 604, 479 (2001).
12 T. Emig and M. Kardar, Phys. Rev. Lett. 85, 2176 (2000).
13 T. Emig and S. Bogner, Phys. Rev. Lett. 90, 185701 (2003).
14 N. Elkies, G. Kuperberg, M. Larsen, and J. Propp, J. Algebr. Comb. 1, 111 (1992).
15 N. Elkies, G. Kuperberg, M. Larsen, and J. Propp, J. Algebr. Comb. 1, 219 (1992).
16 P. W. Kasteleyn, Physica (Utrecht) 27, 1209 (1961).
17 C. L. Henley, J. Stat. Phys. 89, 483 (1997).
18 L. D. Landau and E. M. Lifshitz, Elasticity Theory (Pergamon Press, Oxford, 1969).
19 D. R. Nelson and H. S. Seung, Phys. Rev. B 39, 9153 (1989).
20 V. L. Pokrovsky and A. L. Talapov, Phys. Rev. Lett. 42, 65 (1979).
21 P. G. de Gennes, J. Chem. Phys. 48, 2257 (1968).
22 B. Sutherland, Phys. Rev. Lett. 20, 98 (1968).
23 M. Takahashi, Prog. Theor. Phys. 44, 899 (1970).
24 M. Kardar and D. R. Nelson, Phys. Rev. Lett. 55, 1157 (1985).
25 J.-P. Bouchaud and H. Orland, J. Stat. Phys. 61, 877 (1990).
26 E. Brunet and B. Derrida, Phys. Rev. E 61, 200 (1997).
27 E. H. Lieb and W. Liniger, Phys. Rev. 130, 1605 (1963).
28 N. N. Bogoliubov, J. Phys. USSR 11, 23 (1947).
29 S. E. Korshunov and V. E. Dotsenko, J. Phys. A 31, 2591 (1998).
30 J. Krug, P. Meakin, and T. Halpin-Healey, Phys. Rev. A 45, 638 (1992).
31 W. Press, B. Flanery, S. Teukolsky, and W. Velterling, Numerical Recipes in C, 2nd ed. (Cambridge Univ. Press, 1993).
32 D. S. Fisher and D. A. Huse, J. Phys. A 20L, 1005 (1987).
33 P. W. Anderson, B. I. Halperin, and C. M. Varma, Phil. Mag. 8, 1 (1972).
34 M. E. Fisher, J. Math. Phys. 7, 1776 (1966).
35 M. Kac and J. C. Ward, Phys. Rev. 88, 1332 (1952).
36 R. Moessner and S. L. Sondhi, Prog. Theor. Phys. Supp. 145, 37 (2002).