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# Real Space Renormalization Group Theory of the Percolation Model

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A cluster expansion renormalization group method in real space is developed to determine the critical properties of the percolation model. In contrast to previous renormalization group approaches, this method considers the cluster size distribution (free energy) rather than the site or bond probability distribution (coupling constants) and satisfies the basic renormalization group requirement of free energy conservation. In the construction of the renormalization group transformation, new couplings are generated which alter the topological structure of the clusters and which must be introduced in the original system. Predicted values of the critical exponents appear to converge to presumed exact values as higher orders in the expansion are considered. The method can in principle be extended to different lattice structures, as well as to different dimensions of space.

**KEY WORDS:** Disordered systems; percolation; nonlocal degrees of freedom; renormalization group theory.

## 1. INTRODUCTION

The understanding of the physical properties of disordered systems is a problem of fundamental importance which has attracted much attention in recent years.[1,2]

The simplest microscopic model of disordered systems is the percolation model.[3] The percolation model describes the behavior of a large system, the elements of which are linked in a random way. In the case in which the number of links present in the system is small, connection between widely separated points cannot occur, whereas when the number of links is sufficiently large, such a connection exists and the system is said to be percolative. The transition between these regimes occurs at a definite

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value of the number of links present. If $p$ is the probability that a link is present, the percolation transition occurs at a critical value $p_c$, which is a critical point characterized by diverging fluctuations.

Such a phase transition thus appears to be a simple example for the application of renormalization group theory.[4] However, as will be shown below, the apparent simplicity of the percolation model is deceptive and, due to the nonlocal character of its degrees of freedom, one meets with difficulties of a new kind when attempting to develop a renormalization group method in real space for the percolation model. In fact, in contrast to the case of interacting systems such as the Ising model (see Section 4), and in spite of many attempts, no satisfactory renormalization group method has been developed directly for the percolation model, i.e., without using its formal equivalence with other models.

In the present paper, the development of such a method is described. Following a brief description of the percolation model in Section 2, Section 3 reviews critically the previous direct approaches based on real space renormalization group methods. Section 4 describes the fundamental requirements which a renormalization group theory for the percolation model should satisfy. The development of a new renormalization group method in real space will be described in Section 5.

## 2. PERCOLATION MODEL

Consider the site percolation problem on an infinite lattice, in which each site is either occupied with probability $p$ or empty with probability $1-p$, independently of all other sites. Occupied sites are either isolated from one another or form groups of nearest-neighbor connected sites called clusters.[5]

Percolation is fully characterized by the behavior of clusters; one is therefore naturally led to consider cluster observables, and the problem consists in evaluating their average value. To calculate the values of various cluster observables, one may introduce a generating function or cluster size distribution, which may be considered as being equivalent to the free energy of a magnetic system in the presence of an external magnetic field[6]

$$f(p, h) = \sum_{|\gamma|} \frac{1}{|\gamma|} P_{|\gamma|}(p) \exp(-h\,|\gamma|) \tag{2.1}$$

where $P_{|\gamma|}(p)$ is the probability that an arbitrary fixed site belongs to a finite cluster of size $|\gamma|$, and $h$ is the external field. The external field is represented by an external site independently connected by a bond to each lattice site in a random way, a bond being present with probability $1-e^{-h}$

and absent with probability $e^{-h}$. The function $f(p, h)$, according to whether $h$ is zero or not, represents the average number of clusters per site in the absence or presence of the external field $h$. The probability $P_{|\gamma|}(p)$ may be expressed as a function of $p$ as

$$P_{|\gamma|}(p) = \sum_{|\partial\gamma|} A_{|\gamma|,\,|\partial\gamma|}\, p^{|\gamma|}(1-p)^{|\partial\gamma|} \tag{2.2}$$

where $A_{|\gamma|,\,|\partial\gamma|}$ is the number of clusters of size $|\gamma|$ and of perimeter $|\partial\gamma|$ containing an arbitrary fixed site.

The coefficients $A_{|\gamma|,\,|\partial\gamma|}$ contain all the information concerning the structure of the lattice, and an exact calculation of these coefficients would thus represent an exact solution of the percolation model. Such a solution is possible, however, only when we assume that the lattice has a simple structure. For example, for the Bethe lattice (Cayley tree), where there are no loops or cycles, computation of the coefficients $A_{|\gamma|,\,|\partial\gamma|}$ represents a combinatorial problem which can be solved exactly.[7]

The derivatives of $f(p, h)$ with respect to $h$ at $h=0$ determine the average values of other interesting observables.[5,8] For example, $f^{(1)}(p, 0)$ is the probability that an arbitrary fixed site belongs to a finite cluster. The percolation probability $P_{|\infty|}(p)$, that is, the probability that an arbitrary fixed site belongs to an infinite cluster, is thus given by

$$P_{|\infty|}(p) = p - f^{(1)}(p, 0) \tag{2.3}$$

$f^{(2)}(p, 0)$ represents the average size of finite clusters containing an arbitrary fixed site and, in general, $f^{(n)}(p, 0)$ represents the average value of the $(n-1)$th power of the cluster size.

The coherence length in the percolation model is defined by the asymptotic behavior of the two-point correlation function, which gives the probability that two sites on the lattice belong to a like finite cluster. The coherence length can therefore be interpreted as the average diameter of the finite clusters. It diverges at the percolation threshold $p=p_c$, at which an infinite cluster first appears in the system as $p$ increases.

The behavior of the percolation model in the critical region near $p_c$ is described in analogy to phase transitions of interacting systems by power laws and the associated critical exponents $\alpha$, $\beta$, $\nu$, and $\gamma$:

$$\begin{aligned} f(p, 0) &= (p-p_c)^{2-\alpha} \\ P_{|\infty|}(p, 0) &= (p-p_c)^{\beta} \\ \xi(p, 0) &= (p-p_c)^{-\nu} \\ f^{(2)}(p, 0) &= (p-p_c)^{-\gamma} \end{aligned} \tag{2.4}$$

## 3. PREVIOUS RENORMALIZATION GROUP APPROACHES

Several renormalization group methods have been proposed to study the percolation model. The percolation model, although a trivial one from the point of view of the statistical mechanics of interacting models, belongs in fact to a class of quite sophisticated disordered models, which are equivalent to effective nonrandom interacting models generally more complicated than Ising-like models.

Various methods have been used to express disordered interacting systems in terms of effective nonrandom Hamiltonians. For the percolation problem, it has been shown[6] that the limit $q \to 1$ of the $q$-state Potts model is formally equivalent to the percolation model, and several renormalization groups have been developed for the percolation model using this formulation. With the $q$-state Potts model described by a field Hamiltonian with cubic interactions, the $\varepsilon$-expansion is performed about the upper critical dimension $d_c = 6$ of the latter, yielding the critical behavior of the percolation transition.[9] As the method is a formal expansion about six dimensions of space, it cannot, however, be accurately extended to the physically interesting cases of two or three dimensions of space. The $q \to 1$ limit has also been used by other authors who studied the Potts model with Kadanoff's variational renormalization group.[10]

The equivalence of the percolation model to the Potts model is formal, making it difficult to develop a physical understanding of the geometric properties of the percolation clusters; furthermore, the Potts formulation of the percolation model does not allow one to readily study any of the important physical applications of percolation.

A different approach, which avoids these drawbacks, consists in developing a renormalization group method for the percolation model in real space. Many such renormalization group methods in real space have been proposed to study the percolation model. They make use of either decimation,[11] Migdal–Kadanoff,[12] or site-to-cell transformations.

Among the site-to-cell transformations, the method of Reynolds *et al.*[13] is, in its analytic form for the site and bond problems, a one-cell approximation for the site or bond probability distribution in which intercell correlations are neglected. In a later development, larger cells[14] were considered, using, in particular, Monte Carlo sampling techniques.

Another one-cell method is the block cluster theory,[8] originally developed in two and three dimensions and later extended to higher dimensions.[15,16] Block cluster theory does, in a heuristic way, take into account intercell correlations by simulating the shape of large clusters in the original system at the level of one cell.

Other one-cell transformations have been proposed by developing new

rules for defining cell occupation,[17] or by adding new coupling constants such as connections between sites via bonds[18]; the one-cell approximation for the site and bond probability distributions has also been extended to two cells.[19]

*The most important criticism common to all these real space methods is that they consider the coupling constants (site and bond probability distributions) and directly construct renormalization group equations for them, instead of considering the free energy (cluster size distribution) of the system and, summing over its degrees of freedom at short distance, consequently deriving renormalization group equations for the coupling constants.*

Because of this fundamental shortcoming, all existing real space renormalization group methods for percolation have never been considered satisfactory. For reasons which shall become clear below, difficulties of a new type appear when one attempts to formulate a real space renormalization group for the percolation problem. In the next section, we shall describe these difficulties in detail.

## 4. FUNDAMENTAL REQUIREMENTS OF A RENORMALIZATION GROUP FOR PERCOLATION

We first discuss the fundamental requirements which a renormalization group method must satisfy. This discussion will indicate the way to construct a real space renormalization group for the percolation problem.

The properties a renormalization group transformation must possess are[20] existence, elimination of degrees of freedom, unitary, and smoothness.

Unitarity amounts to the preservation of the thermodynamic properties of the system under the renormalization group transformation. In particular, it is essential that the partition function or, equivalently, the total free energy of the system, be conserved under the renormalization group transformation. To understand the difficulties associated with the unitarity requirement for the percolation problem, it will prove useful to compare percolation to nondisordered interacting systems, and recall the basic relation upon which the real space renormalization group method developed by Niemeijer and van Leeuwen[21, 22] for the Ising model of a ferromagnet is based, namely

$$e^{H'(s')} = \sum_{\sigma} e^{H(s', \sigma)} \tag{4.1}$$

This equation expresses the mapping of the Hamiltonian of an Ising model to that of a new Ising model in which spins are grouped into cells of length $L$ and a spin degree of freedom $s'$ is attached to each cell; $H(s', \sigma)$ is the

Hamiltonian $H(s)$ of the site system where the site spin variables $s$ are expressed in terms of new variables $s'$ and $\sigma$, and $H'(s')$ is the Hamiltonian of the cell system. The renormalization group equation (4.1) is readily seen to satisfy the unitarity requirement by summing both sides of Eq. (4.1) over $s'$.

It is essential for our purposes to observe that all the degrees of freedom in both the site and the cell systems, i.e., $s$, $\sigma$, and $s'$, are *local* degrees of freedom attached to a site or to a cell, and that the renormalization group equation (4.1) is obtained by partially summing over these local degrees of freedom in the original system.

In the percolation problem, the free energy per site, which represents the average number of clusters per site, is given, in the presence of an external field $h$, by

$$f(p, h) = \sum_{|\gamma|} \sum_{|\partial\gamma|} \frac{1}{\gamma} A_{|\gamma|, |\partial\gamma|} p^{|\gamma|} (1-p)^{|\partial\gamma|} e^{-h|\gamma|} \tag{4.2}$$

which immediately follows from inserting (2.2) into (2.1). The essential observation is that the summations in the right-hand side of (4.2) are to be performed over *nonlocal* quantities: to wit, the size $|\gamma|$ and the perimeter $|\partial\gamma|$ of all clusters containing an arbitrary fixed site. Thus the degrees of freedom in the percolation model are nonlocal and span all ranges of the system. This is in strong contrast to the case of the Ising model, where, as seen above, the summation is over local degrees of freedom.

Because of the existence of these nonlocal degrees of freedom, it is not possible for the percolation model, as it is for the Ising model, to perform a summation over degrees of freedom at short distances in the original system and obtain, even in principle, an accurate renormalization group equation of the type of Eq. (4.1). Summing over short-ranged degrees of freedom in the percolation problem, without taking into account the fact that the degrees of freedom in the system span *all ranges*, leads to a renormalized cluster probability distribution of a given cluster which contains only partial information about the system and not, as in the case of the Ising model, to the Boltzmann probability distribution. Clearly, the procedure will be dependent on the structure of the lattice and the topological structure of the clusters will not be preserved upon renormalization, so that the free energy conservation (unitarity) requirement will be violated as well.

The only way in which one can deal with this essential aspect of the percolation problem is to consider *all ranges* of the degrees of freedom in the process of elimination of degrees of freedom at short distances.

Since the nonlocal degrees of freedom in the system are the cluster degrees of freedom, we must consider the clusters themselves in the process

of constructing our renormalization group. An exact mapping will be defined between clusters in the original and renormalized systems, and for that purpose clusters will be grouped into classes according to their topological structure. In the present context the expression "topological structure" refers to the connectedness of the clusters as defined by the various couplings. As will be seen in the following section, in which we describe in detail the technical aspects of this problem, the generation upon renormalization of new types of couplings will alter the topological structure of the clusters of the renormalized system as compared to the topological structure of the clusters in the original system and, accordingly, new coupling constants must be added in the original system. This will ensure that the topological structure of the clusters is preserved upon renormalization, amounting to the conservation of the free energy.

Of the requirements mentioned at the beginning of this section, we have considered elimination of degrees of freedom and unitarity. We turn next to the requirement of smoothness. In the process of summing over short-distance degrees of freedom, we will also be summing over nonlocal variables $|\gamma|$ and $|\partial\gamma|$, and this may lead to nonanalytic renormalization group equations, in particular for an infinite system. However, we can still sum over nonlocal variables on a finite system and obtain analytical renormalization group equations. The cluster expansion,[22] which is performed on increasingly large, but finite clusters (in the sense of cluster expansion), will provide the ideal framework for such a task.

## 5. REAL SPACE RENORMALIZATION GROUP METHOD

### 5.1. General Method

As described above, the unitarity requirement of the renormalization group transformation amounts, for the percolation problem, to the preservation of the topological structure of the clusters. The renormalization group transformation is constructed exactly for clusters (in the sense of cluster expansion) consisting of a finite number of sites (cells). To perform the summation over the short-ranged degrees of freedom while taking into account cluster degrees of freedom, a mapping is defined between the clusters in the original system and those in the renormalized system, which satisfies the following requirements: (1) each cluster in the original system should be mapped into one and only one cluster of the same topological structure in the renormalized system; (2) to every cluster in the renormalized system, there should correspond at least one cluster of the same topological structure in the original system.

Starting from the site percolation problem, in which only nearest-neighbor couplings between sites are present, new couplings will be generated upon renormalization. In the original system, only nearest-neighbor site couplings are present, in the sense that it is only possible to flow from one occupied site to its nearest-neighbor occupied site; in order to flow from a given occupied site to its next-nearest-neighbor occupied site, it is necessary to flow first through a nearest-neighbor site, which must be occupied, and then flow from the latter to the next-nearest-neighbor occupied site. However, this is no longer the case when we sum over degrees of freedom in the original system and define the renormalization group mapping to the cell system.

To illustrate this, consider the case of the square lattice, in which the sites are grouped into cells of edge length $L = 2$ (see Fig. 1), and consider

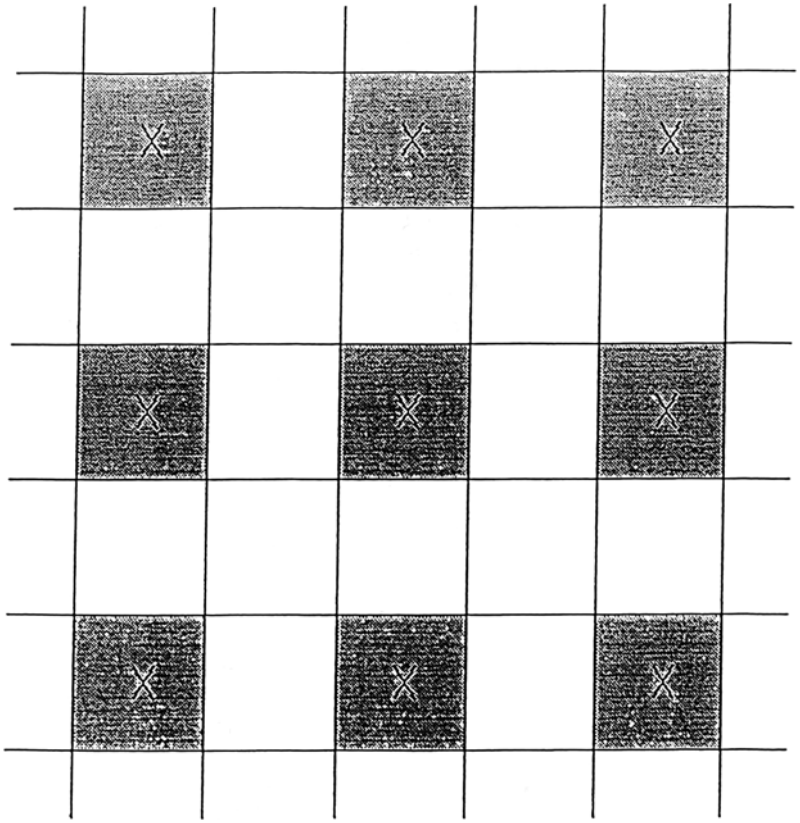

Fig. 1. Grouping of sites of the original system into blocks of edge length $L = 2$. Sites of the renormalized system are denoted by X.

the example of a four-cell cluster (in the sense of cluster expansion) as shown in Fig. 2. A $d$-dimensional cell will be considered occupied when it contains a cluster of occupied sites which spans the cell in all $d$ directions. In Fig. 2, cells 1 and 4 are thus occupied, while cells 2 and 3 are empty. Although cell 3 is empty, it enables one to flow from cell 1 to cell 4, which are next-nearest neighbors; that is, a next-nearest-neighbor coupling is generated in the renormalized system. This next-nearest-neighbor coupling is not present in the original system. In order to define a rigorous mapping between the clusters in the original system and those in the renormalized system, new coupling constants must therefore be introduced in the original system; for example, to account for the generation of next-nearest-neighbor coupling constants, diagonal bonds must be introduced in the original system.

We will thus have to take into account the contribution from different clusters to each type of coupling: this will provide us with a natural way to classify the clusters. To each class of clusters in the renormalized system, there will correspond a class of clusters of the same topological structure in the original system. Next, we consider the probability distribution of each class of clusters and sum over short-distance degrees of freedom in the original system; the result of the summation over short-distance degrees of freedom in the original system for each class of clusters leads to the probability distribution of the corresponding class of clusters in the renor-

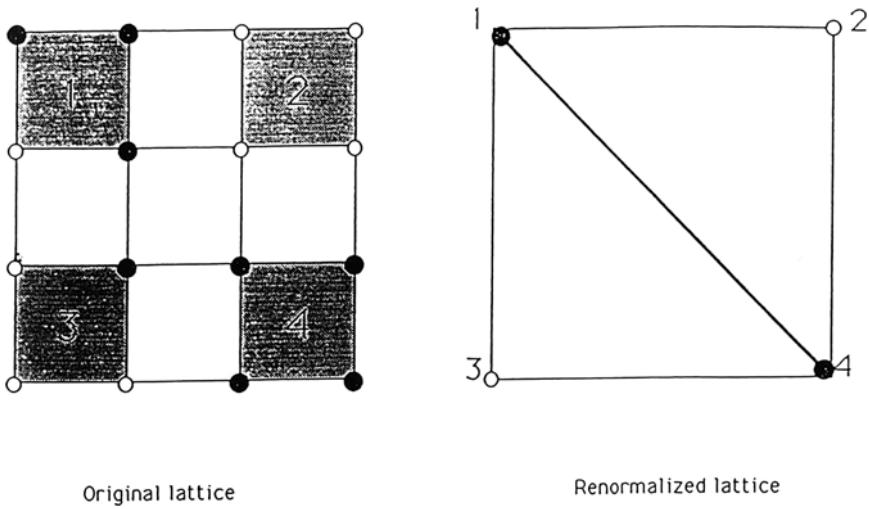


Fig. 2. Illustration of generation of new couplings upon renormalization. In this example, cells 1 and 4 are occupied and connected, while cells 2 and 3 are empty.

malized system. This leads to the implicit renormalization group equation for the coupling constants. In this respect, the present approach is comparable to that developed by Niemeijer and van Leeuwen[21, 22] for the two-dimensional Ising model of a ferromagnet, where the summation over short-distance degrees of freedom for different classes of configurations leads to the renormalization group equations for the different coupling constants; that is, nearest-neighbor, next-nearest-neighbor, etc.

The analytic construction of the renormalization group mapping is simple for the smallest clusters (in the sense of cluster expansion), i.e., those containing one or two cells, but becomes more difficult for clusters (in the sense of cluster expansion) containing three or more cells. At each step of the cluster expansion, one obtains renormalization group equations of the form

$$\mathbf{P}^{(i)}(p_b, r_b, s_b,\ldots) = P^{(i)}(p, r, s,\ldots), \qquad i = 1, 2, 3,\ldots, k \tag{5.1}$$

where $\mathbf{P}^{(i)}$ ($P^{(i)}$) is the probability distribution of the $i$th class of clusters in the renormalized (original) system, $p, r, s,\ldots$ denote the couplings (nearest-neighbor, next-nearest-neighbor, etc.) in the original system, and $p_b, r_b, s_b,\ldots$ denote the couplings (nearest-neighbor, next-nearest-neighbor, etc.) in the renormalized system. The renormalization group equations (5.1) are expected to give rise to a single nontrivial fixed point $(p^*, r^*, s^*,\ldots)$ defined by

$$p^* = p_b = p$$

$$r^* = r_b = r$$

$$s^* = s_b = s$$

$$\text{etc.}$$

which are solutions of Eqs. (5.1). Linearization of these equations about the fixed point yields $k$ eigenvalues, of which only one is expected to be larger than one.[20] This eigenvalue, $\lambda_t$, determines the thermal exponent $y_t$:

$$y_t = \ln \lambda_t / \ln L \tag{5.2}$$

Up to this point, the external field, which is independently coupled to each site, has been set equal to zero. The field exponent is obtained by studying the response of the system to a variation of the external field about $h^* = 0$.[22] One may write

$$\delta[\mathbf{P}_{\text{tot}}(p_b, r_b, s_b,\ldots; h_b)]\,|_{p^*, r^*, d^*} = \delta[P_{\text{tot}}(p, r, s,\ldots; h)]\,|_{p^*, r^*, d^*} \tag{5.3}$$

where $\mathbf{P}_{tot}$ and $P_{tot}$ are the sums over the $k$ terms in Eqs. (5.1), and where $h$ is nonzero. Linearization of Eq. (5.3) with respect to $h$ about $h^* = 0$ yields the field exponent

$$y_h = \ln \lambda_h / \ln L \tag{5.4}$$

It is readily seen that, by summing over $k$ both sides of Eqs. (5.1), we obtain, up to regular terms, the total free energy of the original and renormalized systems. This shows that the renormalization group equations (5.1) satisfy the unitarity requirement. Note that Eq. (5.3) will clearly be nonanalytic at the critical point of an infinite system. However, each of the Eqs. (5.1) need not be singular at the critical point of an infinite system.

## 5.2. Square Lattice

Consider the site percolation problem on the square lattice with nearest-neighbor connections, where the sites are grouped into cells of edge length $L = 2$ (Fig. 1).

**5.2.1. One-Cell Approximation.** For the one-cell approximation, no new couplings will be induced by the renormalization group mapping. Therefore there is only one class of topologically distinct clusters (clusters with nearest-neighbor site couplings).

For the one-cell approximation in the absence of the external field, the mapping between the clusters in the original system and those in the renormalized system, which consists of a single cluster, leads to the renormalization group equation

$$\begin{aligned} \mathbf{P}(p_b) &= p_b \\ P(p) &= p^4 + 4p^3(1-p) \end{aligned} \tag{5.5}$$

The renormalization group equation (5.5) is readily analyzed. There are three fixed points:

$$p^* = 0$$

$$p^* = 1$$

$$p^* = 0.768$$

The first two fixed points are trivial and correspond to the lattice being either completely empty or completely occupied, respectively. The third fixed point is not trivial. The eigenvalue $\lambda_t$ of the linearized equation (5.5) is $\lambda_t = 1.64$, which leads to

$$y_t = 0.71 \tag{5.6}$$

and the coherence length exponent is $\nu = (y_t)^{-1} = 1.40$. The field eigenvalue $\lambda_t$ and the field exponent $y_h$ are also readily evaluated, as described in Section 5.1, with the result $\lambda_h = 3.45$, leading to [see (5.4)]

$$y_h = 1.79 \tag{5.7}$$

where $y_h$ is indeed the fractal dimension $d_f$ of the percolation clusters.[5]

**5.2.2. Two-Cell Approximation.** For the two-cell approximation, as for the one-cell approximation, no new couplings will be induced upon renormalization.

The renormalization group equation reads, in the absence of an external field,

$$\begin{aligned} \mathbf{P}(p_b) &= p_b^2 \\ P(p) &= p^8 + 8p^7(1-p) + 14p^6(1-p)^2 \end{aligned} \tag{5.8}$$

This renormalization group equation has again three fixed points:

$$p^* = 0$$

$$p^* = 1$$

$$p^* = 0.789$$

The value of the thermal exponent is given again by linearization of Eq. (5.8) about the nontrivial fixed point $p^*$, which leads to the critical exponent

$$\nu = 1.42 \tag{5.9}$$

The field exponent (fractal dimension) is in this case given by

$$d_f = 1.81 \tag{5.10}$$

**5.2.3. Three-Cell Approximation.** It is first for the three-cell approximation that new couplings are generated in the renormalized system and, correspondingly, the unitarity requirement of renormalization group theory will lead to the addition of new couplings in the original system. Two new couplings are generated, as shown in Fig. 3. Figure 3a illustrates a cluster in which cell 2, while not occupied, contains an occupied site which establishes a connection between next-nearest-neighbor occupied cells 1 and 3. This corresponds to the generation of a next-nearest-neighbor coupling between cells 1 and 3. Consequently, in order to preserve the topological properties of the original system upon renor-

malization, a new coupling, that is, a diagonal coupling, is introduced in the original system. Figure 3b illustrates a cluster where cell 1 is occupied, but is not connected to its nearest-neighbor occupied cell 2. This corresponds to the generation of a bond coupling between nearest-neighbor occupied cells 1 and 2 in the renormalized system. In the case of Fig. 3b,

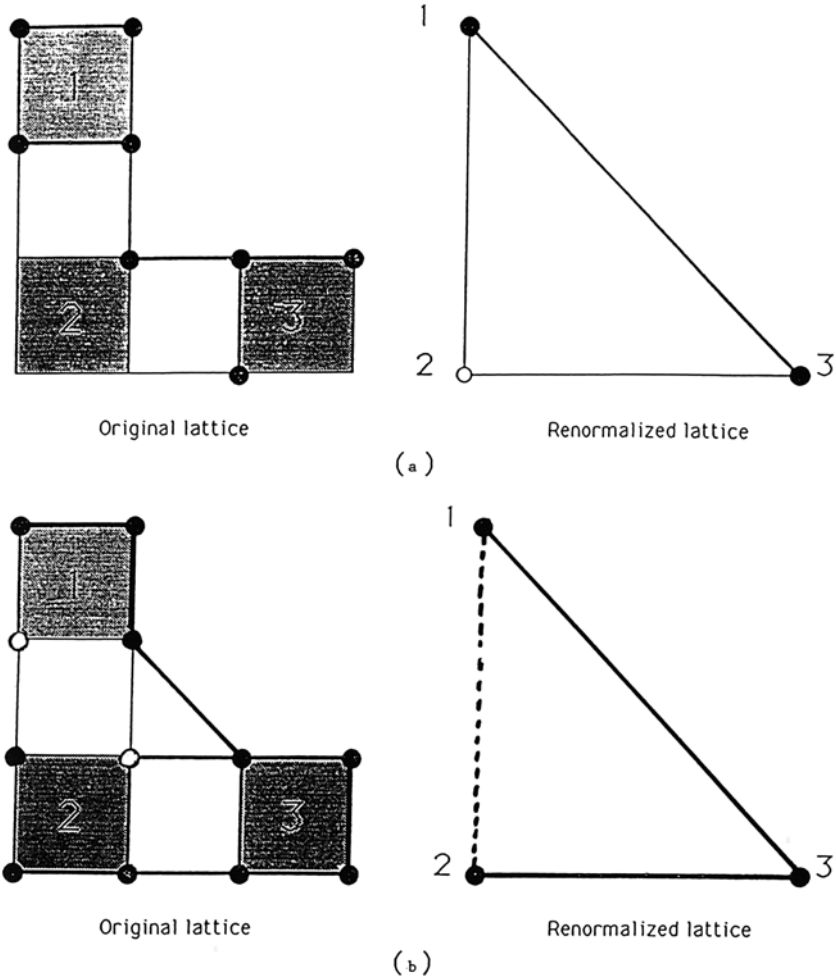


Fig. 3. Illustration of generation of new couplings by the renormalization group transformation corresponding to Eqs. (5.11)–(5.13). Here ● (○) denotes occupied (empty) site or cell. (a) Cluster showing the necessity of introducing next-nearest-neighbor coupling: cells 1 and 3 are occupied and connected via cell 2, which is empty. (b) Cluster in original system showing the necessity of introducing nearest-neighbor bond coupling: two nearest-neighbor cells 1 and 2 are occupied, but not connected. Empty bond coupling is shown by the broken line.

the bond coupling must be specified to be absent, as shown by the hatched line. Consequently, in order to preserve the topological properties of the original system upon renormalization, a new coupling, that is, a bond coupling between nearest-neighbor sites, is introduced. The addition of these new couplings allows the construction of a precise mapping between the clusters of the original and renormalized systems.

There are in this case three classes of topologically distinct clusters. The first class contains those clusters in which all nearest-neighbor cells that are occupied are connected by nearest-neighbor couplings of the original site model. In the second class, diagonal couplings are generated, while the third class includes clusters in which nearest-neighbor bond couplings are generated.

Each cluster in the renormalized system belongs to one and only one of the three classes. To each of these three classes corresponds a class of clusters of the same topological structure in the original system. Any subset of one of these three classes of clusters in the original system maps into one and only one cluster in the renormalized system. This mapping is surjective ("onto") and defines the renormalization group equation for the probability distributions of the corresponding classes of clusters, which, in the absence of an external field, read

$$\begin{aligned}\mathbf{P}_{\mathrm{nn}}(p_b, r_b, d_b) &= p_b^3 r_b^2 d_b + p_b^3 r_b^2 (1-d_b) + 2p_b^2 r_b [r_b(1-p_b)(1-d_b) \\ &\quad + r_b d_b (1-p_b) + (1-r_b)\, d_b (1-p_b) + (1-d_b)(1-r_b)] \\ &= P_{\mathrm{nn}}(p, r, d) \end{aligned} \tag{5.11}$$

$$\begin{aligned}\mathbf{P}_{\mathrm{bond}}(p_b, r_b, d_b) &= p_b^2 d_b [r_b^2 (1-p_b) + r_b (1-r_b)(1-p_b) \\ &\quad + r_b (1-r_b)(1-p_b) + (1-r_b)^2] \\ &= P_{\mathrm{bond}}(p, r, d) \end{aligned} \tag{5.12}$$

$$\begin{aligned}\mathbf{P}_{\mathrm{nnn}}(p_b, r_b, d_b) &= p_b^3 r_b (1-r_b) d_b \\ &= P_{\mathrm{nnn}}(p, r, d) \end{aligned} \tag{5.13}$$

The subscripts nn and nnn stand for nearest-neighbor and next-nearest-neighbor, respectively; $p$ ($p_b$) is the probability that a site (cell) is occupied, $r$ ($r_b$) is the probability that a nearest-neighbor bond is present between two sites (cells), and $d$ ($d_b$) is the probability that two next-nearest-neighbor sites (cells) are connected by a diagonal bond. The left-hand sides of Eqs. (5.11)–(5.13) are most conveniently derived by referring to Fig. 4.

The exact determination of the functions of $P_{\mathrm{nn}}(p, r, d)$, $P_{\mathrm{nnn}}(p, r, d)$, and $P_{\mathrm{bond}}(p, r, d)$ in Eqs. (5.11)–(5.13) requires a large number of clusters

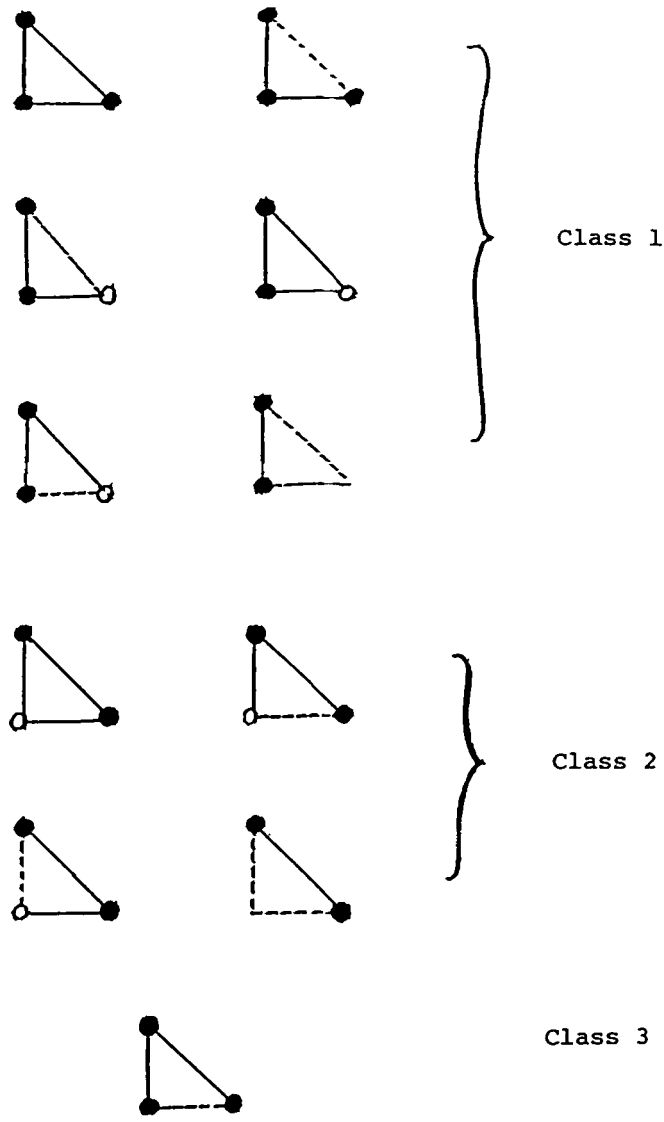


Fig. 4. Classes of clusters in renormalized system for the three-cell approximation corresponding to Eqs. (5.11)–(5.13).

to be counted. This calculation is performed exactly on a computer in which all clusters are enumerated and classified as described above.

The renormalization group equations (5.11)–(5.13) give rise to a single nontrivial fixed point $(p^*, r^*, d^*)$ given by

$$p^* = 0.794$$

$$r^* = 0.632$$

$$d^* = 0.487$$

Linearizing both sides of Eqs. (5.11)–(5.13) about the fixed point $(p^*, r^*, d^*)$ enables us to obtain the thermal exponent by determining the eigenvalues of the $3 \times 3$ matrix

$$\begin{pmatrix} \frac{\partial \mathbf{P}_{nn}}{\partial p_b} & \frac{\partial \mathbf{P}_{nn}}{\partial r_b} & \frac{\partial \mathbf{P}_{nn}}{\partial d_b} \\ \frac{\partial \mathbf{P}_{bond}}{\partial p_b} & \frac{\partial \mathbf{P}_{bond}}{\partial r_b} & \frac{\partial \mathbf{P}_{bond}}{\partial d_b} \\ \frac{\partial \mathbf{P}_{nnn}}{\partial p_b} & \frac{\partial \mathbf{P}_{nnn}}{\partial r_b} & \frac{\partial \mathbf{P}_{nnn}}{\partial d_b} \end{pmatrix}^{-1}_{p^*, r^*, d^*} \cdot \begin{pmatrix} \frac{\partial P_{nn}}{\partial p} & \frac{\partial P_{nn}}{\partial r} & \frac{\partial P_{nn}}{\partial d} \\ \frac{\partial P_{bond}}{\partial p} & \frac{\partial P_{bond}}{\partial r} & \frac{\partial P_{bond}}{\partial d} \\ \frac{\partial P_{nnn}}{\partial p} & \frac{\partial P_{nnn}}{\partial r} & \frac{\partial P}{\partial d} \end{pmatrix}_{p^*, r^*, d^*} \tag{5.14}$$

The eigenvalues of this matrix are

$$\lambda_1 = 1.646$$

$$\lambda_2 = 0.594$$

$$\lambda_3 = 0.387$$

Only one eigenvalue, $\lambda_t$, is relevant, i.e., larger than unity. The thermal exponent is given by

$$y_t = \ln \lambda_t / \ln 2 = 0.72 \tag{5.15}$$

which yields the correlation length exponent $\nu = 1.39$.

The field eigenvalue and exponent are obtained by studying the response of the system to a variation of the external field about $h^* = 0$, as described above in Section 5.1. One finds

$$\lambda_h = 3.58 \tag{5.16}$$

leading to

$$y_h = \ln \lambda_h / \ln 2 = 1.84 \tag{5.17}$$

Table I. Results for the Percolation Model on the Square Lattice[a]

| One cell | | Two cell | | Three cell | | Four cell | |
|---|---|---|---|---|---|---|---|
| $\nu$ | $d_f$ | $\nu$ | $d_f$ | $\nu$ | $d_f$ | $\nu$ | $d_f$ |
| 1.40 | 1.79 | 1.42 | 1.81 | 1.39 | 1.84 | 1.36 | 1.89 |

[a] Conjectured exact values are $\nu = 4/3$ and $d_f = 1.89$.

**5.2.4. Four-Cell Approximation.** For the four-cell approximation, as in the case of the three-cell approximation, two types of couplings are generated upon renormalization: bond coupling and a next-nearest-neighbor coupling. Unfortunately, enumeration of all possible clusters on this system now requires the consideration of a very large number of clusters. This very large number of enumerations precludes at this time an exact calculation of the four-cell approximation. The present results are obtained while neglecting the diagonal coupling.

In this case, the renormalization group equations read

$$\begin{aligned} \mathbf{P}_{\text{nn}}(p_b, r_b) &= P_{\text{nn}}(p, r) \\ \mathbf{P}_{\text{bond}}(p_b, r_b) &= P_{\text{bond}}(p, r) \end{aligned} \tag{5.18}$$

One finally obtains

$$\nu = 1.36, \qquad d_f = 1.89$$

The numerical values of the critical exponents predicted by the present method are summarized in Table I.

## 6. CONCLUSION

We have described the development of a new renormalization group method for the percolation model. In contrast to previous real space renormalization group approaches, this method considers the cluster size distribution (free energy) rather than the site or bond probability distributions (coupling constants). The method satisfies the basic renormalization group requirements described in Section 4, in particular the conservation of the free energy.

The method shows in a transparent way how renormalization necessarily leads to the generation of new couplings, including couplings between next-nearest-neighbor sites and bond couplings, and thus demonstrates in a simple way that the site and bond percolation models belong to the same universality class.

The results of the cluster expansion method have been obtained through the four-cell approximation (in the latter case, the next-nearest-neighbor couplings were neglected) for the square lattice (see Table I). The predictions appear to converge toward the presumed exact values as higher orders in the expansion are considered. The square lattice has been chosen for the sake of convenience; the case of the triangular lattice is more involved numerically and is currently under study.

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