A percolation model for venereal epidemics. I. Mean-field theory

1991 J. Phys. A: Math. Gen. 24 2569

(http://iopscience.iop.org/0305-4470/24/11/023)

J. Phys. A: Math. Gen. 24 (1991) 2569-2580. Printed in the UK

A percolation model for venereal epidemics: I. Mean-field theory

Kang Wu and R Mark Bradley

Department of Physics, Colorado State University, Fort Collins, CO 80523, USA

Received 18 January 1991

Abstract. A percolation model, which we call bond percolation on antipercolation clusters, is introduced for venereal epidemics in a heterosexual population. A spin model which is equivalent to this model is found and solved in the Bethe cluster approximation. We obtain the static critical exponents $\beta = 1$ and $\gamma = 1$ using this approximation, and these are the same as the mean-field exponents for regular percolation. The approximate phase diagram for arbitrary coordination number z is also constructed. Finally, the probability that an infected individual belongs to an infected group with s individuals is obtained analytically in the limit $z \to \infty$.

1. Introduction

Both site and bond percolation have been studied extensively as models of disordered media [1]. In site percolation, each site on a regular lattice can be either white or black. The probability that a site is black is p, while the probability that a site is white is $1-p$. If we connect all the nearest-neighbour pairs which are black, we obtain a set of clusters which are called a percolation cluster. On the other hand, in bond percolation we let bonds be black or white with the probabilities p and $1-p$ respectively. Two black bonds belong to the same cluster if they are connected by a sequence of touching black bonds. For both site percolation and bond percolation, the system undergoes a phase transition at a certain value of p which we call p_c. For $p \geqslant p_c$, there exists an infinite percolation cluster. It is natural to introduce another kind of percolation which is called site-bond percolation [2-4]. In site-bond percolation, each site is occupied with probability p_S, while each bond is occupied with probability p_B. Two sites are in the same cluster if they are connected by a series of occupied sites and bonds.

There are many applications of percolation. One we would like to mention here is the use of percolation as a model of a general epidemic [5-7]. In general epidemics, we consider a large number of individuals on a regular lattice. Each site in the lattice is occupied by an individual, and it is assumed that the disease transmission may occur only between nearest neighbours. If a disease carrier transmits the disease to one of its nearest neighbours, we place a bond between them. The probability that this occurs is p. A cluster of infected sites in which every site is infected by one disease carrier is a bond percolation cluster when $t = \infty$. Thus the general epidemic process can be treated as a dynamical bond percolation problem [6, 7].

In antipercolation† [8, 9], each site is also coloured either black or white with probability p or $1-p$, respectively. However, the clusters are defined in a different

† Antipercolation is sometimes referred to as AB percolation in the literature.

0305-4470/91/112569+12$03.50

fashion than in percolation. We say a cluster is an antipercolation cluster (APC) if each nearest-neighbour pair in the cluster is made up of a black and white site. The relation between percolation and antipercolation is similar to that between ferromagnetism and antiferromagnetism. As in percolation, there may exist a p_c at which the system undergoes a phase transition. Note that this system is symmetric with respect to the colour: in other words, the system is symmetric about $p=\frac{1}{2}$. This means that if $p=p_c$ is a critical point, then $p=1-p_c$ is also a critical point. For $p_c \leqslant p \leqslant 1-p_c$, an infinite APC exists, while for ps outside this range, there are only finite APCs. It has been proved that there is no infinite APC on the square lattice and the hexagonal lattice for any value of p [10], and there is an infinite antipercolation cluster on the triangular lattice for a range of p values about $\frac{1}{2}$ [11]. Monte Carlo estimates of p_c and the static critical exponents are given for the triangular lattice, in [12].

In this paper, we introduce a generalization of antipercolation which we call bond percolation on antipercolation clusters (BPAPC). In this model, we consider a regular lattice in which a site is 'male' or 'female' with probability p or $1-p$, respectively, while each bond can be either occupied or unoccupied with probability ε or $1-\varepsilon$ respectively. A bond belongs to a BPAPC cluster if it not only belongs to an APC but is occupied as well. A site belongs to a particular BPAPC cluster if it is touched by a bond which belongs to the BPAPC cluster. Because the bonds which do not belong to an APC have no effect on the probability of finding a BPAPC cluster, we need only consider the bonds which belong to an APC to be occupied or unoccupied. This means that the bond percolation problem is defined only on the APCs, not on the entire lattice. This is the reason that we call this model bond percolation on antipercolation clusters. BPAPC reduces to antipercolation in the limit $\varepsilon \to 1$.

Our primary motive for introducing BPAPC is that it is a model for the spread of a venereal epidemic through a heterosexual population. Human history is replete with examples of the epidemic spread of sexually transmitted diseases (including the current AIDS epidemic), so this is a problem of great practical interest. In general epidemic processes, the disease spreads from one individual to another without regard for the sex of the individuals, and the process can be modelled using dynamical bond percolation. In the case of venereal epidemics, on the other hand, the disease can only be transmitted from infected individuals to uninfected individuals of the opposite sex. A realistic model of a venereal epidemic must take into account the following three facts: first, an individual can only transmit the disease directly to his or her 'acquaintances', and the number of acquaintances is much smaller than the total number of individuals; second, in a heterosexual population the venereal disease can only be transmitted from an infected individual to a member of the opposite sex; finally, venereal diseases can only be spread by sexual contact. We assume that the number of acquaintances is the same for every individual and denote this number by z. We also assume that we can put all the individuals into a regular lattice with coordination number z. We let every site be occupied by a male with probability p or a female with the probability $1-p$. Clearly, the disease can spread only within an APC. If the disease propagates between a nearest-neighbour pair, we place a bond between those two sites. We let ε be the probability that the disease is transmitted between an infected individual and a particular acquaintance of the opposite sex. Clearly, at $t=\infty$ the group of individuals infected by a single diseased individual forms a BPAPC cluster. In the limit $\varepsilon \to 1$, we recover pure antipercolation. Apart from its application to the venereal epidemic problem, antipercolation has other applications, such as a gelation problem in which the cross-linking occurs only between pairs of unlike monomers [8].

In this paper, we establish a mapping between BPAPC and the diluted alternating Potts model in the limit $q \to 1$. The phase diagram and the static critical exponents are obtained in the Bethe cluster approximation. We find that $\beta = 1$ and $\gamma = 1$. These exponents are the same as the exponents for regular percolation in the mean-field approximation [13, 14]. In most populations, we have $p = \frac{1}{2}$ to a good approximation. For this special case we obtain the average size of an infected group and the probability of the appearance of an infected group in which there are s infected individuals, again using the Bethe cluster approximation.

This paper is organized as follows: in section 2, we develop a mapping between BPAPC and the diluted alternating Potts model in the limit $q \to 1$. In section 3, the diluted alternating Potts model is solved approximately using the Bethe cluster approximation, and the phase diagram and the static critical exponents are obtained. Finally, we present our conclusions in section 4.

2. Mapping onto the diluted alternating Potts model

Both site percolation and bond percolation can be mapped onto the q-state Potts model in the limit $q \to 1$ [2, 13, 14]. In this section we will show that BPAPC is equivalent to a model which we call the diluted alternating q-state Potts model in the limit $q \to 1$. Consider a spin model on a regular lattice in which every site has two variables, one a Potts variable λ which takes on the values $1, 2, \ldots, q$, and the other an Ising spin variable σ which takes on the values ± 1. In the ordinary diluted Potts model, Potts spins on nearest-neighbour sites interact only when the two sites have the same value of σ. In the diluted alternating Potts model, on the other hand, Potts spins on nearest-neighbour sites interact only when the two sites have different values of σ. The model has the Hamiltonian

$$\beta^{-1}H = J \sum_{nn} \{\delta(\sigma_i, -\sigma_j)[\delta(\lambda_i, \lambda_j) - 1]\} + h_\sigma \sum_i \sigma_i + h \sum_i \{1 - \delta(\lambda_i, 1)\}. \quad (1)$$

Here Σ_i and Σ_{nn} denote summations over all sites and over all nearest-neighbour pairs of sites, respectively, the σs are Ising spin variables, and the λs are q-state Potts variables. h_σ and h are external fields coupling to the variables σ and λ, respectively.

We will now show that the diluted alternating q-state Potts model is equivalent to BPAPC for $J = \ln(1-\varepsilon)$, $h_\sigma = \frac{1}{2}\ln(p^{-1} - 1)$ and $q \to 1$. To see this, we consider the partition function for the diluted alternating Potts model,

$$Z = \mathrm{Tr}[\exp(-\beta H)].$$

Since

$$\exp\left(J \sum_{nn} \{\delta(\sigma_i, -\sigma_j)[1 - \delta(\lambda_i, \lambda_j)]\}\right)$$
$$= \prod_{nn} [\delta(\sigma_i, \sigma_j) + (1 - \mathrm{e}^J)\delta(\sigma_i, -\sigma_j)\delta(\lambda_i, \lambda_j) + \mathrm{e}^J \delta(\sigma_i, -\sigma_j)] \quad (2)$$

the partition function can be written

$$Z = \mathrm{Tr}\left\{\prod_{nn} [(1 - \mathrm{e}^J)\delta(\sigma_i, -\sigma_j)\delta(\lambda_i, \lambda_j) + \mathrm{e}^J \delta(\sigma_i, -\sigma_j) + \delta(\sigma_i, \sigma_j)]\right.$$
$$\left. \times \exp\left(-h_\sigma \sum_i \sigma_i + h \sum_i [\delta(\lambda_i, 1) - 1]\right)\right\}. \quad (3)$$

We now expand out the product in (3). Each term in the expansion will be given a graphical representation as follows. A factor $\delta(\sigma_i, \sigma_j)$ will be represented by placing a white bond between the nearest-neighbour sites i and j. If a factor $\delta(\sigma_i, -\sigma_j)$ appears, the bond between the sites i and j will be coloured grey. Finally, a factor $\delta(\sigma_i, -\sigma_j)\delta(\lambda_i, \lambda_j)$ will be represented by placing a black bond between these sites. Each term in the expansion is represented by a graph G in which all bonds are specified to be white, grey or black. Consider the weight assigned to a particular graph G. Each black bond carries a factor of $1-e^J$, each grey bond a factor of e^J, and each white bond a factor of 1.

A site may be touched by bonds of up to three different colours. The colour of the site is designated to be the colour of the darkest bond which touches it. We then have clusters of three different colours: black, grey and white.

Not all graphs G give a non-zero contribution to the partition function. Both black and grey bonds will be called shaded bonds. A graph G which contains clusters of shaded bonds which are not APCs contributes nothing to Z once we have summed out the Ising spins. Therefore, the sum over graphs is restricted to those in which the shaded clusters are APCs. The black clusters are subsets of the shaded clusters, and so are bond percolation clusters on antipercolation clusters.

We see that a site which has its Ising spin up or down carries a factor e^{-h_σ} or e^{h_σ}, respectively, and that each bond in a black cluster carries a factor

$$\delta(\lambda_i, \lambda_j)\exp\{h[\delta(\lambda_i, 1)-1]\}(1-e^J).$$

Consider a black cluster which has b bonds, s_u sites with their Ising spins up, and s_d sites with their Ising spins down. After summing out all the λs in this cluster, we obtain a weight factor

$$(1-e^J)^b\{1+(q-1)\exp[-h(s_u+s_d)]\}\exp[-h_\sigma(s_u-s_d)]$$

in the partition function. On the other hand, a grey cluster which has b bonds, s_u up spins, and s_d down spins gives the weight

$$e^{Jb}[1+(q-1)e^{-h}]^{(s_u+s_d)}\exp[-h_\sigma(s_u-s_d)]$$

once the λs have been summed over. Finally, after taking the sum over the λs, a white cluster which has b bonds and s sites yields the weight factor

$$[1+(q-1)e^{-h}]^s\exp(-h_\sigma s\sigma)$$

where σ takes on the value 1 or -1, and σ is the common value of the Ising spins in the cluster.

Consider an allowed configuration G formed by the three kinds of clusters defined above. Let $N(b, s_u, s_d)$ be the number of black clusters with b bonds, s_u sites which have the Ising spin value $+1$, and s_d sites which have the Ising spin value -1 in the configuration G. Also, let $N'(b', s'_u, s'_d)$ be the number of grey clusters with b' bonds, s'_u sites which have the Ising spin value $+1$ and s'_d sites which have the Ising spin value -1. Finally, let $M^{\pm}(b_\pm, s_\pm)$ be the number of white clusters with $b_\pm$ bonds and $s_\pm$ sites which have the Ising spin value $+1$ and -1, respectively. Because each site in the lattice must belong to a black, grey or white cluster, we have the following relation:

$$\sum_{\{b,s\}}[s_+M^+(b_+, s_+)+s_-M^-(b_-, s_-)+(s_u+s_d)N(b, s_u, s_d)$$
$$+(s'_u+s'_d)N'(b', s'_u, s'_d)] = N. \tag{4}$$

Here N is the number of sites in the lattice and $\Sigma_{\{b,s\}}$ denotes the sum over all the possible sets of the numbers of bonds b, b_+, b_- and b' and over the numbers of sites s, s_+, s_- and s'. The configuration G contributes the following term to the partition function:

$$\begin{aligned} Z_G = \prod_{\{b,s\}} & ([1+(q-1)\,\mathrm{e}^{-h}]^{s_+ M^+(b_+,s_+)} \exp[-h_\sigma s_+ M^+(b_+, s_+)] \\ & \times [1+(q-1)\,\mathrm{e}^{-h}]^{s_- M^-(b_-,s_-)} \exp[h_\sigma s_- M^-(b_-, s_-)] \\ & \times \{(1-\mathrm{e}^{J})^{b}[1+(q-1)\,\mathrm{e}^{-h(s_\mathrm{d}+s_\mathrm{u})}]\}^{N(b,s_\mathrm{u},s_\mathrm{d})} \exp[h_\sigma(s_\mathrm{d}-s_\mathrm{u})N(b, s_\mathrm{u}, s_\mathrm{d})] \\ & \times \{\mathrm{e}^{Jb'}[1+(q-1)\,\mathrm{e}^{-h}]^{s'_\mathrm{d}+s'_\mathrm{u}}\}^{N'(b',s'_\mathrm{u},s'_\mathrm{d})} \exp[h_\sigma(s'_\mathrm{d}-s'_\mathrm{u})N'(b', s'_\mathrm{u}, s'_\mathrm{d})]) \end{aligned} \tag{5}$$

where $\Pi_{\{b,s\}}$ represents the product over all the possible sets of the numbers of bonds and the numbers of sites. Substituting $1-\mathrm{e}^{J}=\varepsilon$ and $h_\sigma=\frac{1}{2}\ln(p^{-1}-1)$ into (5) and using (4), we obtain

$$\begin{aligned} Z_G = p^{-N/2}(1-p)^{-N/2} \prod_{\{b,s\}} & ([1+(q-1)\,\mathrm{e}^{-h}]^{s_+ M^+(b_+,s_+)} p^{s_+ M^+(b_+,s_+)} \\ & \times [1+(q-1)\,\mathrm{e}^{-h}]^{s_- M^-(b_-,s_-)} (1-p)^{s_- M^-(b_-,s_-)} \\ & \times \{\varepsilon^{b}[1+(q-1)\,\mathrm{e}^{-h(s_\mathrm{d}+s_\mathrm{u})}]\}^{N(b,s_\mathrm{u},s_\mathrm{d})} (1-p)^{s_\mathrm{d} N(b,s_\mathrm{u},s_\mathrm{d})} p^{s_\mathrm{u} N(b,s_\mathrm{u},s_\mathrm{d})} \\ & \times \{(1-\varepsilon)^{b'}[1+(q-1)\,\mathrm{e}^{-h}]^{s'_\mathrm{d}+s'_\mathrm{u}}\}^{N'(b',s'_\mathrm{u},s'_\mathrm{d})} \\ & \times (1-p)^{s'_\mathrm{d} N'(b',s'_\mathrm{u},s'_\mathrm{d})} p^{s'_\mathrm{u} N'(b',s'_\mathrm{u},s'_\mathrm{d})}). \end{aligned} \tag{6}$$

The partition function is

$$Z = \sum_G Z_G$$

where the sum runs over all the allowed configurations G.

We now show that the partition function Z is related to BPAPC through the formula

$$F(h) \equiv \sum_{s=1}^{\infty} P(s)\,\mathrm{e}^{-sh} = -N^{-1} \left.\frac{\partial^2 \ln Z}{\partial q\,\partial h}\right|_{q=1}. \tag{7}$$

Here $P(s)$ is the probability that a site belongs to a cluster with s sites in BPAPC. If we expand (6) in terms of $\delta \equiv q-1$ and keep only terms of first order in δ, we obtain

$$\begin{aligned} Z = Z_0 + p^{-N/2}(1-p)^{-N/2} \sum_G \Bigg\{ \prod_{\{b,s\}} & [p^{s_+ M^+(b_+,s_+)+s'_\mathrm{u} N'(b',s'_\mathrm{u},s'_\mathrm{d})+s_\mathrm{u} N(b,s_\mathrm{u},s_\mathrm{d})} \\ & \times (1-p)^{s_- M^-(b_-,s_-)+s'_\mathrm{d} N'(b',s'_\mathrm{u},s'_\mathrm{d})+s_\mathrm{d} N(b,s_\mathrm{u},s_\mathrm{d})} (1-\varepsilon)^{b' N'(b',s'_\mathrm{u},s'_\mathrm{d})} \varepsilon^{b N(b,s_\mathrm{u},s_\mathrm{d})}] \\ & \times \left[N\,\mathrm{e}^{-h} - \sum_{\{b,s\}} s N(b, s_\mathrm{u}, s_\mathrm{d})\,\mathrm{e}^{-h} + \sum_{\{b,s\}} N(b, s_\mathrm{u}, s_\mathrm{d})\,\mathrm{e}^{-sh} \right] \delta \Bigg\}. \end{aligned}$$

Here

$$\begin{aligned} Z_0 \equiv p^{-N/2}(1-p)^{-N/2} \sum_G \prod_{\{b,s\}} & [p^{s_+ M^+(b_+,s_+)+s'_\mathrm{u} N'(b',s'_\mathrm{u},s'_\mathrm{d})+s_\mathrm{u} N(b,s_\mathrm{u},s_\mathrm{d})} \\ & \times (1-p)^{s_- M^-(b_-,s_-)+s'_\mathrm{d} N'(b',s'_\mathrm{u},s'_\mathrm{d})+s_\mathrm{d} N(b,s_\mathrm{u},s_\mathrm{d})} (1-\varepsilon)^{b' N'(b',s'_\mathrm{u},s'_\mathrm{d})} \varepsilon^{b N(b,s_\mathrm{u},s_\mathrm{d})}] \end{aligned}$$

and $s \equiv s_\mathrm{d}+s_\mathrm{u}$. Because Z_0 does not depend on h, we have $\partial Z/\partial h|_{q=1}=0$. Therefore,

$$\left.\frac{\partial^2 \ln Z}{\partial q\,\partial h}\right|_{q=1} = Z_0^{-1} \left.\frac{\partial^2 Z}{\partial q\,\partial h}\right|_{q=1}.$$

We now easily obtain

$$-N^{-1}\left.\frac{\partial^2 \ln Z}{\partial q\,\partial h}\right|_{q=1} = e^{-h} + \sum_s \sum_G P_G(s) P(G)(e^{-sh} - e^{-h})$$

where

$$P(G) \equiv Z_0^{-1} p^{-N/2}(1-p)^{-N/2} \prod_{\{b,s\}} [p^{s_+ M^+(b_+,s_+)+s'_u N'(b',s'_u,s'_d)+s_u N(b,s_u,s_d)} \times (1-p)^{s_- M^-(b_-,s_-)+s'_d N'(b',s'_u,s'_d)+s_d N(b,s_u,s_d)} \times (1-\varepsilon)^{b' N'(b',s'_u,s'_d)} \varepsilon^{bN(b,s_u,s_d)}] \tag{8}$$

and

$$P_G(s) \equiv N^{-1} s \sum_{\{b,s_u,s_d\}}{}' N(b, s_u, s_d). \tag{9}$$

The summation $\Sigma'_{\{b,s_u,s_d\}}$ in (9) runs over b, s_u and s_d with $s_u + s_d = s$. From (8) and (9), we see that $P(G)$ is the probability that a configuration G occurs in BPAPC and that $P_G(s)$ is the probability that a randomly chosen site belongs to an s-site BPAPC cluster for the given configuration G. Thus the probability that a site belongs to a BPAPC cluster which possesses s sites is

$$P(s) = \sum_G P_G(s) P(G).$$

For finite N, we have $\Sigma_s \Sigma_G P_G(s) P(G) = \Sigma_s P(s) = 1$. Therefore, we obtain (7) as required and our mapping between BPAPC and the diluted alternating Potts model is established. In particular, we see that the diluted alternating Potts model is equivalent to pure antipercolation for $h_\sigma = \frac{1}{2}\ln(p^{-1}-1)$, $J \to \infty$ and $q \to 1$. This correspondence has previously been noted by Halley [15].

The function $F(h)$ is a generating function, and $F(0)$ is the probability that a particular site belongs to a finite BPAPC cluster. Therefore, in the limit $N \to \infty$, $F(0)$ will be equal to 1 if there is no infinite BPAPC cluster in the lattice. Thus, from $F(h)$ we can compute the probability that an infinite BPAPC cluster appears,

$$P_A = 1 - F(0). \tag{10}$$

The average cluster size $\langle s \rangle$ and the mean-square cluster size $\langle s^2 \rangle$ can also be computed from $F(h)$: clearly,

$$\langle s \rangle = -\left.\frac{\partial F}{\partial h}\right|_{h=0} \tag{11}$$

and

$$\langle s^2 \rangle = \left.\frac{\partial^2 F}{\partial h^2}\right|_{h=0}. \tag{12}$$

Higher moments of the probability distribution can be obtained from the higher derivatives of $F(h)$.

We close this section by considering the case of a lattice which can be divided into two sublattices for $p = \frac{1}{2}$. For $p = \frac{1}{2}$, we have $h_\sigma = 0$. We now replace the Ising spins σ on one of the two sublattices by $-\sigma$. The partition function (equation (3)) is unaltered by the relabelling, but we now see that Z is just the partition function for site-bond percolation for $p_S = \frac{1}{2}$ [2]. Therefore, if we know the phase boundary for site-bond percolation, we have the critical value of ε for BPAPC with $p = \frac{1}{2}$.

As an example of the utility of this observation, consider BPAPC on the hexagonal lattice. The hexagonal lattice can be divided into two triangular sublattices. The critical boundary of site-bond percolation on the hexagonal lattice is $p_S(3p_B^2-p_B^3)=1$ [3]. When $p_S=\frac{1}{2}$, this formula can be applied to antipercolation on the hexagonal lattice with $p=\frac{1}{2}$. The value of p_B in the site-bond problem corresponds to our ε. The equation $3\varepsilon^2-\varepsilon^3=2$ has no root which is less than 1. Therefore, no phase transition occurs as ε is increased from 0 to 1 in BPAPC on the hexagonal lattice. In particular, there is no infinite cluster in antipercolation on the hexagonal lattice at $p=\frac{1}{2}$. The latter conclusion has been reached previously in [10] and [15].

3. Bethe cluster approximation

In this section, we apply the Bethe cluster approximation [16] to the diluted alternating Potts model. To perform the Bethe cluster approximation, we consider a site with Ising spin σ and Potts spin λ. This site has z nearest neighbours which will be labelled by the subscript j. The effective Hamiltonian H_{eff} of this cluster is

$$\beta^{-1}H_{\text{eff}}=J\sum_j\{\delta(\sigma,-\sigma_j)[\delta(\lambda,\lambda_j)-1]\}+h'_\sigma\sum_j\sigma_j+h'\sum_j[1-\delta(\lambda_j,1)]$$
$$+h_\sigma\sigma+h[1-\delta(\lambda,1)]$$

where h'_σ and h' are the effective fields which correspond to h_σ and h, respectively. The effective fields are chosen so that the average values of σ and $\delta(\lambda,1)$ are the same for the site and its nearest neighbours. Thus, h'_σ and h' are determined by the following equations,

$$\frac{\partial \ln Z_{\text{eff}}}{\partial h}=z^{-1}\frac{\partial \ln Z_{\text{eff}}}{\partial h'} \tag{13}$$

$$\frac{\partial \ln Z_{\text{eff}}}{\partial h_\sigma}=z^{-1}\frac{\partial \ln Z_{\text{eff}}}{\partial h'_\sigma} \tag{14}$$

where

$$Z_{\text{eff}}\equiv \text{Tr}(e^{-\beta H_{\text{eff}}}).$$

Equations (13) and (14) are the self-consistency conditions.

In order to obtain a relation between Z_{eff} and $F(h)$ employing the Bethe cluster approximation, we assume that the field h is different for each site i, and let h_i denote the field h at the site i. Thus, we can rewrite (7) in the following form:

$$F(h)=-N^{-1}\sum_i\left(\frac{\partial^2 \ln Z}{\partial q\,\partial h_i}\bigg|_{q=1}\right)\bigg|_{\{h_i\}=h}$$

where $\{h_i\}=h$ means that all the h_is are set equal to h. This formula indicates that the contribution of each site to $F(h)$ can be treated individually. In the Bethe cluster approximation, there are $z+1$ sites in the cluster, and one site has field h and the other z sites have field h'. Thus, the required relation between $F(h)$ and Z_{eff} is

$$F(h)=-\frac{1}{z+1}\left(\frac{\partial^2 \ln Z_{\text{eff}}}{\partial q\,\partial h}+\frac{\partial^2 \ln Z_{\text{eff}}}{\partial q\,\partial h'}\right)\bigg|_{q=1}. \tag{15}$$

The effective partition function Z_{eff} is

$$\begin{aligned}Z_{\text{eff}} = {} & e^{-h_\sigma}\{e^{-h'_\sigma}[1+(q-1)\,e^{-h'}]+e^{h'_\sigma}[1+(q-1)(1-\varepsilon)\,e^{-h'}]\}^z \\ & +e^{h_\sigma}\{e^{h'_\sigma}[1+(q-1)\,e^{-h'}]+e^{-h'_\sigma}[1+(q-1)(1-\varepsilon)\,e^{-h'}]\}^z \\ & +(q-1)\,e^{-h}\{e^{-h_\sigma}(e^{-h'_\sigma}[1+(q-1)\,e^{-h'}] \\ & +e^{h'_\sigma}[1-\varepsilon(1-e^{-h'})+(q-1)(1-\varepsilon)\,e^{-h'}])^z+e^{h_\sigma}(e^{h'_\sigma}[1+(q-1)\,e^{-h'}] \\ & +e^{-h'_\sigma}[1-\varepsilon(1-e^{-h'})+(q-1)(1-\varepsilon)\,e^{-h'}])^z\} \end{aligned} \tag{16}$$

where we have put $\varepsilon = 1 - e^{J}$. We now substitute this into the self-consistency conditions (13) and (14) to determine h'_σ and h' and work to the first order in $q-1$. From (14) we obtain $h'_\sigma = h_\sigma$. Equation (13) leads to the following expression:

$$\begin{aligned} & e^{-h'}[(e^{h_\sigma}+e^{-h_\sigma})^2-2\varepsilon] \\ & \quad = e^{-h}\left\{(e^{2h_\sigma}+1-\varepsilon)\left[1-\frac{\varepsilon(1-e^{-h'})\,e^{-h_\sigma}}{e^{h_\sigma}+e^{-h_\sigma}}\right]^{z-1}\right. \\ & \quad \left. +(e^{-2h_\sigma}+1-\varepsilon)\left[1-\frac{\varepsilon(1-e^{-h'})\,e^{h_\sigma}}{e^{h_\sigma}+e^{-h_\sigma}}\right]^{z-1}\right\}. \end{aligned} \tag{17}$$

It is not easy to solve (17) in general, but fortunately, we can obtain the information needed near the critical line without solving the equation exactly. If we set $h=0$ in (17), we obtain a root $h'=0$. Substituting the solution $h=h'=0$ into $F(h)$, we find $F(0)=1$. Therefore this root corresponds to the phase in which no infinite BPAPC cluster exists. The non-zero root of (17) corresponds to the phase in which there is an infinite BPAPC cluster. For $h=0$, this root must reduce to zero as the critical line is approached since h' is a continuous function of p and ε. Therefore, h' is small near the critical line when h is small. Thus, we expand (17) to first order in h and to second order in h' in the area close to the critical point in order to obtain the non-zero root. We obtain

$$(x^2-2\varepsilon)h = [x^2-2\varepsilon-\varepsilon(2-\varepsilon)(z-1)+uh']h' \tag{18}$$

where

$$u \equiv \varepsilon(z-2)\left\{\frac{\varepsilon(z-2)}{x^2}[2+(1-\varepsilon)(x^2-2)]-(2-\varepsilon)\right\}+\tfrac{1}{2}(x^2-2\varepsilon)$$

and

$$x \equiv [p(1-p)]^{-1/2}.$$

For $h=0$, (18) has the roots $h'=0$ and $h'=-u^{-1}[x^2-2\varepsilon-\varepsilon(2-\varepsilon)(z-1)]$. On the critical line, the latter root reduces to zero. We therefore have the following equation for $p_c = p_c(\varepsilon)$:

$$x^2 = 2\varepsilon+\varepsilon(2-\varepsilon)(z-1).$$

Solving this equation, we obtain

$$p_c^{\pm} = \frac{1}{2} \pm \sqrt{\frac{1}{4}-\frac{1}{\varepsilon[2z-\varepsilon(z-1)]}}.$$

In the case of the pure antipercolation ($\varepsilon=1$), this reduces to

$$p_c^{\pm} = \frac{1}{2} \pm \sqrt{\frac{1}{4}-\frac{1}{z+1}}.$$

The phase diagram is shown in figure 1 for various coordination numbers z. From this diagram, we see that as the coordination number z increases, p_c^- decreases. This is as one would expect, since the disease spreads more readily when the number of acquaintances is large. If $\varepsilon < \varepsilon_c = 2/(z-1)$, there is no infinite BPAPC cluster for any p. On the other hand, for a given ε, an infinite BPAPC cluster exists for $p = \frac{1}{2}$ if $z \geqslant z_c = (2+\varepsilon)/\varepsilon$. In the limit $z \to \infty$ with $z\varepsilon$ held fixed, the condition for an infinite cluster to appear is $z\varepsilon/2 \geqslant 1$. This means that there is no infinite cluster if the average number of the individuals infected by a disease carrier is less than one.

To obtain the critical exponents, we must calculate $F(h)$. Using the self-consistency relations (13) and (14) and (15), we obtain

$$F(h) = -\frac{1}{(q-1)Z_{\text{eff}}} \frac{\partial Z_{\text{eff}}}{\partial h}\bigg|_{q=1}. \tag{19a}$$

From (16), we have

$$-\frac{1}{q-1}\frac{\partial Z_{\text{eff}}}{\partial h}\bigg|_{q=1} = e^{-h}\{e^{h_\sigma}[e^{h_\sigma} + e^{-h_\sigma}(1-\varepsilon+\varepsilon\, e^{-h'})]^z + e^{-h_\sigma}[e^{-h_\sigma} + e^{h_\sigma}(1-\varepsilon+\varepsilon\, e^{-h'})]^z\}. \tag{19b}$$

We find $F(h)$ for p close to p_c^+ or p_c^- by expanding of $F(h)$ in powers of h and h'. We obtain

$$F(h) \approx 1 - h - \frac{2z\varepsilon}{x^2} h'.$$

The non-zero root of (18) is

$$h' = \frac{1}{u}[\sqrt{v^2 + u(x^2 - 2\varepsilon)h} - v]$$

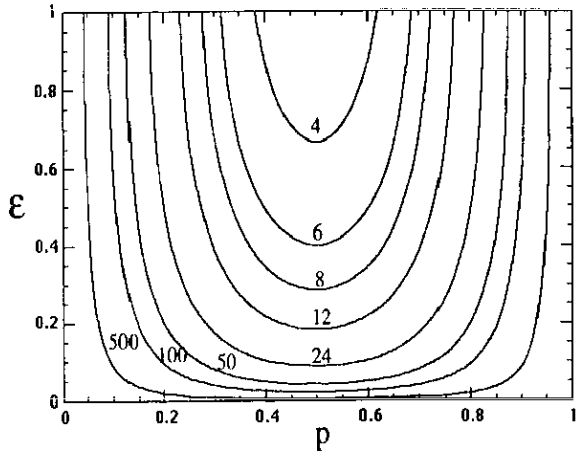

Figure 1. Phase boundaries for BPAPC for several different coordination numbers z. Each phase boundary is labelled with the corresponding value of z. The areas above the curves are the regions in which there is an infinite cluster.

where

$$v \equiv \frac{2\varepsilon + \varepsilon(2-\varepsilon)(z-1)}{p(1-p)}(p-p_c^+)(p-p_c^-).$$

$F(h)$ becomes

$$F(h) \approx 1 - h - \frac{2z\varepsilon}{ux^2}[\sqrt{v^2 + u(x^2-2\varepsilon)h} - v].$$

Using (10) and (11), we obtain

$$P_A = \begin{cases} 0 & \text{if } p \leqslant p_c^- \text{ or } p \geqslant p_c^+ \\ \dfrac{4z\varepsilon}{ux^2}\left[\dfrac{2\varepsilon + \varepsilon(2-\varepsilon)(z-1)}{p(1-p)}\right]|p-p_c^+|p-p_c^-| & \text{otherwise} \end{cases} \tag{20}$$

and

$$\langle s \rangle = \frac{z\varepsilon p(1-p)(x^2-2\varepsilon)}{x^2[2\varepsilon + \varepsilon(2-\varepsilon)(z-1)]}|p-p_c^+|^{-1}|p-p_c^-|^{-1}. \tag{21}$$

From (20) and (21), we see that in the Bethe cluster approximation, the critical exponents are $\beta = 1$ and $\gamma = 1$ for $z > 3$ and $p_c^+ > \frac{1}{2} > p_c^-$. In the case $p = \frac{1}{2}$ and $z \geqslant 3$, we use (11) and (12) to calculate $\langle s \rangle$ and $\langle s^2 \rangle$ for $p = \frac{1}{2}$ and ε close to ε_c. We obtain

$$\langle s \rangle = \frac{2z(z-1)\varepsilon}{2\varepsilon + \varepsilon(2-\varepsilon)(z-1)}|\varepsilon - \varepsilon_c|^{-1} \tag{22}$$

and

$$\langle s^2 \rangle = \frac{32z(z-1)^3\varepsilon}{(2-\varepsilon)[2\varepsilon + \varepsilon(2-\varepsilon)(z-1)]^3}|\varepsilon - \varepsilon_c|^{-3}. \tag{23}$$

From (22), we see that $\gamma = 1$. Equation (23) shows that $\langle s^2 \rangle$ goes to infinity as $(\varepsilon - \varepsilon_c)^{-3}$ as $\varepsilon \to \varepsilon_c$. Using the scaling relations [1], we find that β is also equal to 1. Thus, we conclude that $\beta = 1$ and $\gamma = 1$ for $z \geqslant 3$ at each point on the critical line. When $z = 3$, there is no phase transition except for $\varepsilon = 1$, and the critical value of p is $\frac{1}{2}$. No phase transition occurs when $z < 3$. For the special case $\varepsilon = 1$, our results are in agreement with the exact results obtained for pure antipercolation on Bethe lattice [9]. Note that, in the Bethe cluster approximation, there is a phase transition for $z = 4$. This conclusion is incorrect for the square lattice, since there is no antipercolation transition in this case [10]. However, in venereal epidemics, the coordination number z is expected to be large in many populations, and the results of the Bethe cluster approximation are more precise in this regime.

In venereal epidemics, p is the fraction of the population which is male, and ε is the probability that the disease is transmitted from an infected individual to an uninfected neighbour of the opposite sex. Usually, the number of males in the population is to a good approximation the same as the number of females, so $p = \frac{1}{2}$. Setting $p = \frac{1}{2}$ in (17) and (19), we obtain

$$e^{h'}[1 - \tfrac{1}{2}\varepsilon(1 - e^{-h'})]^{z-1} = e^h \tag{24}$$

and

$$F(h) = e^{-h'}[1 - \tfrac{1}{2}\varepsilon(1 - e^{-h'})]. \tag{25}$$

A quantity of interest in venereal epidemics is the average number of individuals which are ultimately infected by one infected individual. This quantity is $\langle s \rangle$ in BPAPC. If $\varepsilon \geqslant \varepsilon_c$, $\langle s \rangle = \infty$, so we only consider $\varepsilon \leqslant \varepsilon_c$. When $\varepsilon \leqslant \varepsilon_c$, the solution of (24) for $h = 0$ is $h' = 0$. In order to obtain the average size of the infected group for $\varepsilon \leqslant \varepsilon_c$, we need to calculate the derivative of h' with respect to h from (24) for $h = 0$ and use (11) and (25). All the calculations are straighforward, so we skip the details and simply give the result:

$$\langle s \rangle = 1 + \frac{z\varepsilon}{2-(z-1)\varepsilon}. \tag{26}$$

From (26), we see that if there is no transmission of the disease between nearest-neighbours, i.e. $\varepsilon = 0$, the average size of an infected group is 1. This means that every infected site is an isolated group, as we would expect. As ε becomes larger, the number of infected individuals in a group increases, and when ε is close to ε_c, this number diverges as $(\varepsilon - \varepsilon_c)^{-1}$.

We next consider the case in which $z \to \infty$ and the quantity $n \equiv z\varepsilon/2$ is held constant, and we again specialize to $p = \frac{1}{2}$. One of the reasons that we are doing this is that n is the average number of the individuals that a disease carrier infects directly. Thus, n is a natural variable with which to describe an epidemic, and can be measured in a real epidemic. The other reason is that the coordination number z is the number of acquaintances of an individual and this number is expected to be large, particularly in densely populated areas. After we take this limit, (24) and (25) become

$$h' - h = n(1 - e^{h'})$$

and

$$F(h) = 1 - \frac{1}{n}(h' - h).$$

After solving for h', we obtain

$$F(h) = \frac{1}{n} \sum_{s=1}^{\infty} \frac{s^{s-1}}{s!} (n\, e^{-n})^s\, e^{-sh}. \tag{27}$$

We see from (27) that

$$P(s) = \frac{1}{n} \frac{s^{s-1}}{s!} (n\, e^{-n})^s.$$

For large s, $P(s)$ can be written in the following form:

$$P(s) = \frac{1}{\sqrt{2\pi}} s^{-3/2} n^{-1}\, e^{s/s_0} \tag{28}$$

where $s_0 \equiv (n - \ln n - 1)^{-1}$. As n goes to 1, s_0 goes to infinity as $(1-n)^{-1}$. Using the scaling form for $P(s)$ [1], we obtain $\tau = \frac{5}{2}$ from (27). This is the same as the value which is obtained using the scaling relations and the values of β and γ we obtained previously. Setting $h = 0$ in (27), we obtain the probability that the venereal epidemic spreads without limit,

$$P_A = 1 - \frac{1}{n} \sum_{s=1}^{\infty} \frac{s^{s-1}}{s!} (n\, e^{-n})^s. \tag{29}$$

If we replace n by $n_B \equiv -z \ln(1 - p_B)$ in (28) and (29), these results become exactly the same as the mean-field results for bond percolation on a lattice with coordination

number z [14], where p_B is the fraction of occupied bonds. In the limit $z \to \infty$ with zp_B held constant, n_B reduces to zp_B, which is just the mean number of individuals infected by a single disease carrier in a general epidemic. Thus the mean-field results for venereal epidemics and general epidemics are equivalent in this limit.

4. Conclusions

In this paper, bond percolation on an antipercolation cluster was introduced as a model for the spread of venereal epidemics. We found that BPAPC is exactly equivalent to the diluted alternating q-state Potts model in the limit $q \to 1$. This mapping gives us a way to solve BPAPC approximately using the Bethe cluster approximation. We found the dependence of the phase boundary on the coordination number z. By setting $\varepsilon = 1$, we obtained the threshold for pure antipercolation in the Bethe cluster approximation. We also obtained the static critical exponents using this approximation. The static exponents for BPAPC in the Bethe cluster approximation are the same as the exponents of regular percolation in the mean-field approximation. Finally, we considered the special case of venereal epidemics in populations with equal proportions of males and females. The average size of an infected group diverges as $(\varepsilon - \varepsilon_c)^{-1}$ as $\varepsilon \to \varepsilon_c$, where $\varepsilon_c = 2/(z-2)$. In the limit $z \to \infty$ with $z\varepsilon$ held fixed, we obtained the probability of a site being in an infected group with s sites, $P(s)$. In this limit, $P(s)$ is simply related to $P(s)$ for bond percolation in the mean-field approximation.

The present paper has dealt solely with the static properties of venereal epidemic. In a forthcoming publication we will present the results of a Monte Carlo study of the spread of a venereal epidemic.

Acknowledgments

We would like to thank P N Strenski, J M Debierre and M Sahimi for helpful discussions.

References

[1] Stauffer D 1979 *Phys. Reports* **54** 1
[2] Wu F Y 1982 *Rev. Mod. Phys.* **54** 235
[3] Wu F Y 1981 *J. Phys. A: Math. Gen.* **14** L39
[4] Coniglio A, Stanley H E and Klein W 1979 *Phys. Rev. Lett.* **42** 518
[5] Grassberger P 1983 *Math. Biosci.* **62** 157
[6] Grassberger P 1985 *J. Phys. A: Math. Gen.* **18** L215
[7] Grassberger P 1985 *J. Phys. A: Math. Gen.* **19** 1681
[8] Mai T and Halley J W 1980 *Ordering in Two Dimensions* ed S Sinha (Amsterdam: North-Holland) pp 369–71
[9] Sevsek F, Debierre J-M and Turban L 1983 *J. Phys. A: Math. Gen.* **16** 801
[10] Appel M J and Wierman J C 1987 *J. Phys. A: Math. Gen.* **20** 2527
[11] Wierman J C and Appel M J 1987 *J. Phys. A: Math. Gen.* **20** 2533
[12] Nakanishi H 1987 *J. Phys. A: Math. Gen.* **20** 6075
[13] Stephen M J 1977 *Phys. Rev.* B **15** 5674
[14] Giri M R, Stephen M J and Grest G S 1977 *Phys. Rev.* B **16** 4971
[15] Halley J W 1983 *Annals of the Israel Physical Society* vol 5, ed G Deutscher, R Zallen and J Adler (Bristol: Adam Hilger) pp 323–51
[16] Pathria R K 1988 *Statistical Mechanics* (Oxford: Pergamon) p 408