

## Tests of Universality of Percolation Exponents for a Three-Dimensional Continuum System of Interacting Waterlike Particles

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Molecular-dynamics calculations for *interacting* waterlike particles are used to estimate values of percolation exponents. Results are consistent with accepted values for ordinary *random*-bond percolation for a three-dimensional lattice. Study of a correlated-site percolation problem, defined by the connectivity of those water molecules that are four-coordinated, shows no evidence for different exponents. Thus there is no obvious basis for the frequent criticisms against the application of lattice percolation models to describe *continuum correlated* systems such as polymer gels.

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Are the critical properties of *interacting* three-dimensional continuum systems the same as those known for *noninteracting* models in which the particles are constrained to the vertices of a lattice? This question has arisen recently as percolation is being used increasingly to describe an ever wider range of natural phenomena—ranging from gelation of polyfunctional monomers to the hydrogen-bond network in liquid water.<sup>1-3</sup> Unfortunately, all calculations of critical exponents for three-dimensional systems have been for *random* systems—there have been no calculations of the critical exponents for an *interacting* continuum three-dimensional system.<sup>4</sup> Even the simpler case of a continuum two-dimensional system is just beginning to be studied with sufficient accuracy that critical exponents can be obtained.<sup>5</sup> Liquid water is one of the most intensely studied continuum systems for which association of individual constituents plays an important role. In this work we analyze a molecular-dynamics simulation of a model of liquid water to obtain exponents for a three-dimensional continuum system whose elements are *not* random.

The input to the present work is a computer tape<sup>6</sup> resulting from a molecular-dynamics simulation of a system consisting of 216 particles confined to a cubic box of edge 18.6 Å with periodic boundary conditions (density 1 g/cm<sup>3</sup>); the temperature of the system was 284 K. The particles interact through an ST2 effective pair potential designed to reproduce a wide range of properties of real water. Its most prominent

feature is a tetrahedral charge distribution around the oxygen atom, with two positive partial charges on the proton location and two negative partial charges representing the lone electron pairs. The absolute minimum of the ST2 potential is -6.84 kcal/mole.

The Stillinger-Rahman tape consists of a simulation with 38 100 time steps. After each 300 steps, we created a 216 × 10 table containing for each molecule  $i$  ( $i = 1, 2, \dots, 216$ ) the ten other molecules  $j$  that interact most strongly in an attractive way with molecule  $i$ . We thereby obtain a set of 127 (= 38 100/300) different tables, which are then used as input for the following procedure to calculate the time-averaged cluster size distributions.

We use two definitions of a hydrogen bond: Definition  $D_1$  defines hydrogen bonds by a purely, *energetic* criterion.<sup>7</sup> Specifically, molecules  $i$  and  $j$  are considered to be "bonded" if their pair interaction energy satisfies  $V_{ij} < V_{HB}$ . The parameter  $V_{HB}$  is permitted to take on a sequence of 32 discrete values  $V_{HB} = -20E, -22E, \dots, -82E$ , where  $E = 0.07575$  kcal/mole. Clearly  $V_{HB} = -20E$  represents the most permissive definition of a hydrogen bond, while  $V_{HB} = -82E$  is the least permissive definition. In the case of permissive definitions, there sometimes occur water molecules having more than four bonds; in this case we eliminate the weakest "extra" bonds in the system until there are a maximum of four bonds per molecule.

It may be argued that a purely energetic criterion includes in the list of bonded partners pairs

of molecules that have an interparticle separation that is too large for a hydrogen bond; moreover the elimination of extra bonds introduces some ambiguity. Therefore in definition  $D_2$  we add a *geometric* cutoff and eliminate from the list of strongly interacting partners of molecule  $i$  all molecules  $j$  whose separation  $|r_i - r_j|$  exceeds 3.5 Å, but we do not eliminate any extra bonds. Also, to get better statistics, we generated 800 tables by analyzing after every forty time steps.

Thus, given a configuration of water molecules, we get for each water molecule  $i$  a list of its directly bonded partners  $j, k, \dots$ . These lists allow us to construct "bond clusters" of molecules such that stepping along successive hydrogen bonds keeps us confined to a given "bond cluster." An illustrative example is given in Appendix A of Ref. 8. For each "snapshot" of the system, we calculate  $W_s$ , the number of water molecules belonging to a bond cluster with  $s$  molecules. Thus  $W_1$  is the number of unbonded molecules,  $W_2$  the number of water molecules belonging to two-molecule clusters, and so forth. In the language of percolation theory this is the bond percolation problem with *site counting*; note that exact enumeration procedures for bond percolation usually employ *bond counting*.<sup>9</sup>

If we reexamine the same configurations but now eliminate all molecules with less than four intact bonds, we obtain a correlated-site percolation problem<sup>10,11</sup> that is believed to have the same exponents as random percolation.<sup>12,13</sup> The number of molecules belonging to a cluster of  $s$  "four-bonded" molecules is denoted  $W_s^*$ . Molecules with more than four bonds (using definition  $D_2$ ) are added to the class of four-bonded molecules in the following.

In order that systems with differing numbers of particles can easily be compared, it is convenient to normalize the cluster distribution by  $N$  ( $= 216$ ), the total number of particles. Thus  $w_s(V_{\text{HB}}) = N^{-1}W_s(V_{\text{HB}})$  is the fraction of water molecules belonging to a bond cluster of  $s$  molecules, with an analogous definition for  $w_s^*$ . For each value of  $V_{\text{HB}}$ , we also calculate the total number of hydrogen bonds in the entire system,  $N_{\text{HB}}$ . Again we normalize by the total number of particles, so that  $n_{\text{HB}}(V_{\text{HB}}) = 2N^{-1}N_{\text{HB}}(V_{\text{HB}})$  is the mean number of hydrogen bonds per molecule. For the 32 values of  $V_{\text{HB}}$  given above,  $n_{\text{HB}}$  takes on a corresponding set of 32 values ranging from 0.08 to 3.59 for  $D_1$  and from 0.08 to 4.06 for  $D_2$ . Since there is a 1:1 relation between  $V_{\text{HB}}$  and  $n_{\text{HB}}$ , it

is convenient to think of the weight fractions  $w_s$  as functions of  $n_{\text{HB}}$ .

For each value of  $V_{\text{HB}}$ , we have calculated the cluster distributions  $w_s$  and  $w_s^*$  and obtained the following additional "averaged" quantities:

(i) Mean cluster size. The mean cluster size of the finite networks,  $S$ , is conventionally defined as the average of  $s$  with respect to the distribution function  $w_s$ ,  $S = \sum' s w_s / \sum' w_s$ . The primes indicate that the spanning networks are omitted from the sums, i.e., clusters that cross the entire box in at least one coordinate direction are eliminated. Defining  $\epsilon \equiv (p_c - p)/p_c$ , with  $p \equiv n_{\text{HB}}/4$ , we expect  $S \sim C\epsilon^{-\gamma}$ . Figure 1 shows double logarithmic plots of  $S$  and  $S^*$  (the asterisk, throughout, denotes the continuum correlated-site problem defined by the four-bonded molecules). The straight lines have slope 1.7, and are seen to fit the data which are close to the percolation threshold, but not so close that rounding effects arise as a result of the finite system size. Thus we find that  $\gamma$  and  $\gamma^*$  are consistent with the lattice estimates  $\gamma = 1.73 \pm 0.3$ .<sup>14</sup> We also find values of  $p_c$  consistent with the ice lattice values  $p_c = 0.388$ ,<sup>9,15</sup> and  $p_c^* = 0.795$ .<sup>16</sup> This fact is somewhat surprising, since one might expect exponents to be universal but not necessarily the value of the threshold parameter  $p_c$ .

(ii) Order parameter. For finite systems, the fraction of molecules belonging to spanning clus-

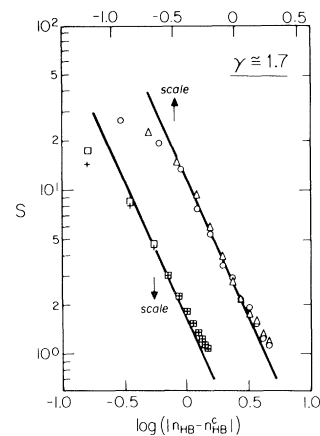


FIG. 1. Mean cluster size  $S$  for bond networks determined by bond definitions  $D_1$  (squares) and  $D_2$  (crosses). Also shown are the corresponding quantities for  $D_1$  (circles) and  $D_2$  (triangles) for clusters of four-bonded water molecules. The straight line shown is drawn through the steepest part of the curve, since there is rounding for small values of  $\epsilon$  and crossover to mean-field value  $\gamma=1$  for large values of  $\epsilon$ .

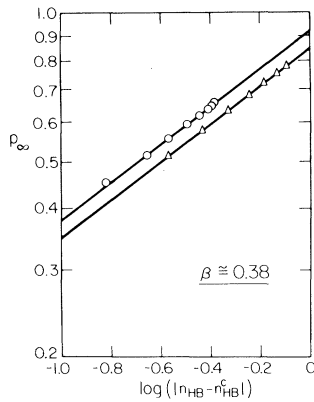


FIG. 2. Order parameter  $P_\infty$  for clusters of four-bonded water molecules with use of both bond definitions  $D_1$  (circles) and  $D_2$  (triangles).

ters is regarded as the order parameter, denoted  $P_\infty$ . As the system size becomes infinite, we expect that  $P_\infty = B\epsilon^\beta$ , thereby defining the exponent  $\beta$  and the amplitude  $B$ . For lattice percolation,  $\beta = 0.42 \pm 0.06$ ,<sup>17</sup> while from analysis of our correlated-site percolation data (Fig. 2) we find  $\beta = \beta^* = 0.38 \pm 0.05$ . The amplitude  $B$  differs by 8% for the two bond definitions.

(iii) Characteristic length. The length  $L_s$  of an  $s$ -molecule cluster is defined as the difference between the maximum and minimum oxygen coordinates of the cluster (with respect to some chosen coordinate direction). To get better statistics, all three Cartesian coordinate directions have been used successively. Since the length of a one-molecule cluster is zero, only clusters with  $s > 1$  have been treated. Also, only nonspanning clusters are considered. Figure 3 is a double-logarithmic plot showing the dependence of the averages over all clusters  $L$  and  $L^*$  on  $\epsilon$ ; the slope is  $0.75 \pm 0.1$ , consistent with literature estimates of the exponent  $\nu$  in  $L_s \sim A\epsilon^{-\nu}$  for lattice percolation.<sup>14,18-20</sup> Unlike most calculations, we can also obtain the amplitude  $A$ , with the results  $A = 1.0 \text{ \AA}$  and  $A^* = 1.5 \text{ \AA}$ .

(iv) Weight fraction  $w_s$  of clusters of size  $s$ . At  $p_c$  the weight fraction of clusters of size  $s$  is expected to decrease with  $s$  as  $w_s \sim s^{-(\tau-1)}$ , where  $\tau = 2 + 1/\delta$ ;  $\delta = 5.0 \pm 0.1$  for lattice percolation.<sup>21</sup> Figure 4 shows  $w_s$  and  $w_s^*$  averaged over those values of  $p_B$  closest to the threshold. The straight line has slope 1.2 and is seen to pass through even the data point for  $s = 2$ . Actually the data set of  $w_s$  for  $n_{HB} = 1.55$ , being very close to the

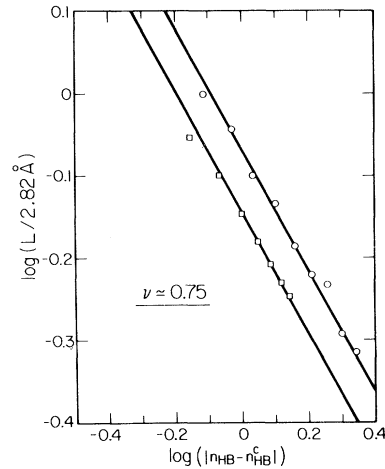


FIG. 3. Average length  $L$  determined by definition  $D_1$  for both bond networks (squares) and clusters of four-bonded water molecules (circles). The normalization factor  $2.82 \text{ \AA}$  is roughly the length of a typical hydrogen bond.

threshold  $n_{HB}^c$ , showed rather large fluctuations as expected from lattice calculations.<sup>22</sup>

In summary, we have estimated the exponents  $\beta$ ,  $\gamma$ ,  $\nu$ , and  $\tau = 2 + 1/\delta$  for a continuum interacting system in three dimensions. Our estimates for all four exponents are consistent with the estimates for a lattice system. Thus there is no ob-

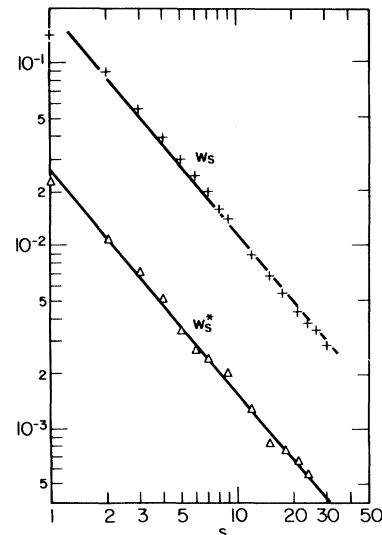


FIG. 4. Weight fraction of molecules belonging to clusters of size  $s$  determined by definition  $D_2$  for both bond networks (crosses) and four-bonded water molecules (triangles). The straight lines have slope 1.2, since  $\tau - 1 = 1 + \delta^{-1}$ .

vious reason to doubt the application of *random, lattice* percolation to describe the connectivity properties of *interacting, continuum* systems such as polymer gels and water.<sup>1-3</sup>

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