Finite-size scaling of clique percolation on two-dimensional Moore lattices

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Clique percolation has attracted much attention due to its significance in understanding topological overlap among communities and dynamical instability of structured systems. Rich critical behavior has been observed in clique percolation on Erdős-Rényi (ER) random graphs, but few works have discussed clique percolation on finite dimensional systems. In this paper, we have defined a series of characteristic events, i.e., the historically largest size jumps of the clusters, in the percolating process of adding bonds and developed a new finite-size scaling scheme based on the interval of the characteristic events. Through the finite-size scaling analysis, we have found, interestingly, that, in contrast to the clique percolation on an ER graph where the critical exponents are parameter dependent, the two-dimensional (2D) clique percolation simply shares the same critical exponents with traditional site or bond percolation, independent of the clique percolation parameters. This has been corroborated by bridging two special types of clique percolation to site percolation on 2D lattices. Mechanisms for the difference of the critical behaviors between clique percolation on ER graphs and on 2D lattices are also discussed.

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I. INTRODUCTION

It is widely accepted that the universality class of phase transitions in percolation depends only on the space dimension of the system and the dimension of the order parameter space [1]. Recent studies of modified percolation models, e.g., k-clique percolation, indicate that besides the dimensions of space and of order parameter there exist extra degrees of freedom in determining the universality classes. Intriguing critical behavior deviating from the bond (site) percolation was observed from these modified percolation models, therefore much attention has been attracted to them recently [2–10].

The clique percolation model [11,12] can be regarded as a minimal modified percolation model with respect to bond percolation. A k-clique is a complete subgraph with k nodes that are all connected with each other and plays a fundamental role in community structure recognization and dynamical instability characterization [13–15]. In general, two cliques are considered to be connected if they share at least l ($l < k$) nodes. Normal bond percolation can be considered as a special case of the k-clique percolation model with parameters $k = 2$ and $l = 1$. Introducing the two variable parameters effectively expands our understanding of the critical behavior in percolation. For example, for the Erdős-Rényi (ER) random graph [16], as the connection probability p between different sites increases, the number of k-cliques also increases. The clique percolation will take place as the density of cliques increases and the clusters of cliques begin to merge. A single giant clique cluster appears at a critical point $p = p_c$. In contrast to normal bond percolation, around p_c, the values of the critical exponents not only depend on the definition of the order parameter [11] but also depend on the clique parameters. Recently Fan *et al.* [17] found that, for (k,l) clique percolation in an ER graph, the critical exponents depend, surprisingly, not on the clique size k, but only on l, the number of common nodes between two cliques that they can be regarded as connected. For example, when $l = 1$, no matter what the clique size k is, the exponents return to the case of the normal site percolation. When l is larger than 1, the critical exponents are different, indicating new universal classes. Moreover, the values of the critical exponents, e.g., the most general exponent β, decay as the clique connection parameter l increases, which may lead to a transition from continuous ($\beta > 0$) to discontinuous ($\beta = 0$) phase transition at large l. Li *et al.* [18] also proposed a theoretical analysis for the k-clique percolation and observed the dependence of the critical exponents on l. Therefore, the parameter l serves as a new crucial factor to the critical behavior of the system and induces new universality classes different from the normal bond percolation model. Clique percolation is thus a general model very succinct and appropriate for understanding various critical behaviors, universality classes, and discontinuous transition in percolation.

The above works associated with k-clique percolation are mainly on ER random graphs [11,15,17–19], a typical infinite dimensional system which has solid analytical results. However, the conclusion obtained from such an infinite dimension system may not be applicable to low-dimensional systems [20–23]. Therefore, the critical behavior of k-clique

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percolation in low-dimensional systems is still an open issue, and is important to gain better understanding of the clique percolation model. In this paper, we study the clique percolation on a well-defined two-dimensional (2D) lattice. We have found that the critical behavior of the clique percolation on the 2D lattice is quite different from that on an ER graph. For example, the critical exponents of the (k,l)-clique percolation on 2D lattices are independent of both k and l, and they are the same as the normal site or bond percolation in 2D space. A brief discussion is provided to explain the effects from the low space dimension as well as the finite-size effect of the system. In addition, a new method for analyzing the finite-size effect in k-clique percolation is proposed by taking into account both the first and the second largest jumps of the largest clique cluster in adding bonds, which is self-consistent and effective in obtaining the scaling exponents associated with the correlation lengths, fluctuations, and so on. Our work is an important supplement to the previous works of clique percolation on ER graphs, which broadened our understanding of the universality classes.

II. FINITE-SIZE SCALING

To understand clique percolation in 2D space, we choose the so-called Moore lattice [25] with a periodic boundary condition, where each site on a base square lattice connects to its next-nearest neighbors, e.g., the first eight neighbors (Fig. 1). This ensures the whole lattice is a connected clique cluster. In our simulation, all the bonds in the Moore neighborhood are removed initially, and bonds are randomly selected and placed back one by one into the lattice, with the fraction of added bonds denoted by p. During adding bonds (i.e., increasing p), for a finite-size system, the size of the the largest clique cluster increases due to the merger of isolated small clusters. Typically, when varying p, the largest size jump (increment) Δ_1 happens due to the merger of the original first and second largest clusters, with the size denoted by $S_1(p)$ and $S_2(p)$, respectively. At the critical point for a finite system, which is characterized by the peak of the susceptibility of the system, the size of the second largest clusters also peaks [26,27]. This leads to a maximized cluster size jump Δ_1 at $p \sim p_c$, which is $S_2(p)$. This has been widely used to estimate the critical point and critical exponents of both real-world structures and artificial percolation models [27,28].

In particular, for a finite system, the mergers of clique clusters also correspond to jumps in the susceptibility χ, which is defined as [29]

$$\chi = \sum_k s_k^2/N,$$

where k is the index of the finite clusters and s is the cluster's size. If two clusters are merged by adding a single bond, the increment of susceptibility $\Delta\chi$ is given by $2s_i s_j/N$, where s_i and s_j are the sizes of the two merging clusters. Thus the largest cluster size jump Δ_1 by connecting the largest clusters should correspond to the sharpest incline of susceptibility. For an infinite system, this should also be the point where χ diverges [30,31], i.e., the critical point p_c.

Here we propose a new computationally efficient method in analyzing the phase transition by examining the *historically largest mergers*. Given p_1 where Δ_1 takes place, in the parameter range $p < p_1$, we can identify the largest jump and denote it as Δ_2, assuming it occurred at p_2. Apparently, $\Delta_2 < \Delta_1$ and $p_2 < p_1$ since Δ_2 is selected at $p < p_1$. Repeating this, with Δ_i occurring at p_i, we can identify the largest jump Δ_{i+1} in the range $p < p_i$ and denote the location of p when Δ_{i+1} occurs as p_{i+1}. Therefore a series of historically largest mergers of $\{\Delta_1, \Delta_2, \Delta_3, \ldots\}$ at $p_1 > p_2 > p_3 > \cdots$, respectively, can be determined. In the following, we shall see that this setting in identifying the historically largest mergers is crucial for the description of finite-size effects in clique percolation processes.

We select the last four largest jumps, Δ_1, Δ_2, Δ_3, and Δ_4, as examples and plot the corresponding values of $\langle p_c - p_i \rangle$ as a function of the system size N in Fig. 2. The scaling behavior of $\langle p_c - p_i \rangle$ with N is clearly exhibited. Strikingly, $\langle p_c - p_i \rangle$ of different Δ_i share the same scaling exponent. That is to say, no matter what the value of i is, for the case with $N \to \infty$, the values of p_i for Δ_i approach the same critical

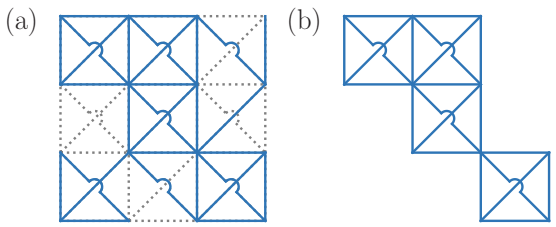

FIG. 1. Illustration of Moore lattice and k-clique percolation with the blue solid bonds occupied, and gray dashed bonds unoccupied. (a) One local configuration on Moore lattice. (b) The largest (4,1)-clique cluster for the configuration in (a).

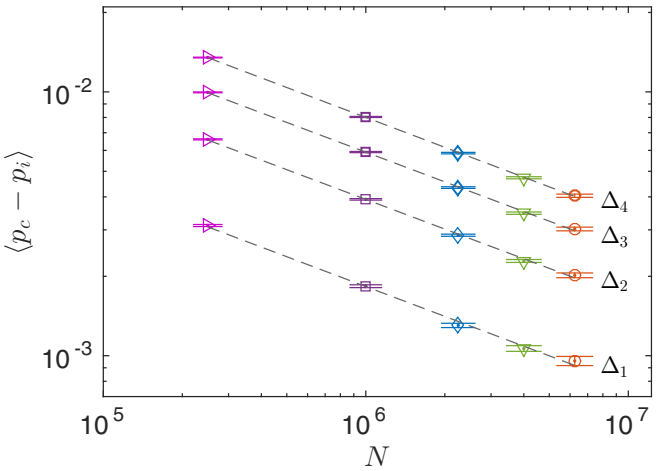

FIG. 2. The average distance $\langle p_c - p_i \rangle$ between the theoretical critical point p_c and the ith largest jump for (2,1)-clique percolation (the normal bond percolation) on a square lattice with respect to network size N. The critical point for infinite system is 1/2 [24]. In each realization, the positions p_i for each Δ_i are recorded. For different i, the fitting lines of $\langle p_c - p_i \rangle$ are parallel with each other, sharing the same slope of -0.376. According to Eq. (1), the critical exponent ν is 1.33 and coincides well with the theoretical result. For all data, 8000 ensembles are used to do the statistics.

value p_c, which implies that all the jumps of different i will take place simultaneously and an infinite number of clusters will merge into one single giant cluster at p_c in the case of $N \to \infty$. From the above observation, we obtain a clear picture of how a cluster with infinite size abruptly emerges at p_c for the system with $N \to \infty$, which intuitively explains the origin of the divergence of the susceptibility at the critical point. Furthermore, a new finite-size scaling method can be proposed accordingly.

Typically, the correlation length ξ of the system close to the critical point scales with p as $\xi \sim |p_c(\infty) - p|^{-\nu}$. The correlation length at p_i is denoted by $\xi(p_i)$, thus $\xi(p_i) \sim |p_c(\infty) - p_i|^{-\nu}$. As p_1 is the point where the largest merger occurs when typically the largest cluster spans the lattice, one has $\xi(p_1) \sim L$ [32], where L is the boundary length of the lattice, and $N = L \times L$ is the system size. Since the lines of $\langle p_c - p_i \rangle$ versus N are parallel to each other in the loglog scale (Fig. 2), one has $(p_c - p_j)/(p_c - p_i) = \text{const}$. Alternatively, by subtracting one on both sides, it can be written as $|p_i - p_j|/(p_c - p_i) = \text{const}$. Since $p_c - p_i \sim \xi(p_i)^{-1/\nu}$, one has $|p_i - p_j| \sim \xi(p_i)^{-1/\nu}$. One can show that $\xi(p_i) \sim L$ by noting that

$$\frac{\xi(p_i)}{L} \sim \left| \frac{p_c - p_i}{p_c - p_1} \right|^{-\nu} = \text{const}. \tag{1}$$

We finally get

$$|p_i - p_j| \sim L^{-1/\nu} \sim N^{-1/(d\nu)}, \tag{2}$$

where $d = 2$ is the spatial dimension for the Moore lattice.

Since Eq. (2) does not require the value of the critical point p_c, the critical exponent ν can be estimated directly and more accurately based on the values of p_i, avoiding extra error introduced when estimating p_c. Moreover, when ν is obtained, p_c can be calculated by fitting $|p_c - p_1| \sim L^{-1/\nu}$ with the least square method. For the largest cluster $S_1(p_1)$, the fractal dimensional d_f can be obtained by the asymptotic relation

$$S_1(p_1) \sim \xi(p_1)^{d_f} \approx L^{d_f} = N^{d_f/d}. \tag{3}$$

After getting ν and d_f, all the other critical exponents can be obtained according to the hyperscaling relations:

$$\begin{aligned} \alpha &= 2 - \nu d, \\ \beta &= \nu(d - d_f), \\ \gamma &= \nu(2d_f - d), \\ \sigma &= \frac{1}{\nu d_f}. \end{aligned} \tag{4}$$

It should be noted that comparing with Refs. [33,34], our method may not be able to get better accuracy in estimating the critical exponents on 2D lattices, but it can be easier to be adopted in analyzing percolation on realistic complex systems of finite size.

III. RESULTS AND DISCUSSIONS

Compared to the square lattice, the Moore neighborhood has diagonal connections, and therefore the lattice is uniformly embedded with 4-cliques. For two neighboring 4-cliques in the Moore neighborhood, they share at most two nodes with each other, which constrains that the maximum value of (k,l) is (4,2) in the (k,l)-clique percolation.

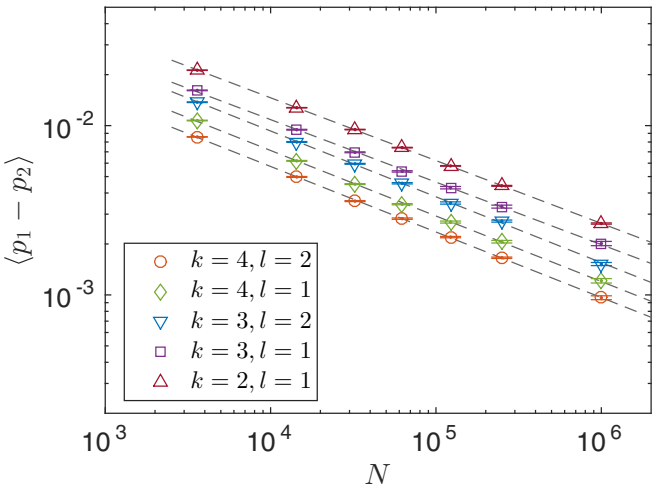

FIG. 3. The average distance $\langle p_1 - p_2 \rangle$ between the largest jump and second largest jump for (k,l)-clique percolation. As the system size is increased, the value of $\langle p_1 - p_2 \rangle$ decays in the form of Eq. (2). The dashed lines are linear fitting to the numerical results, and the resulting critical exponents ν are shown in Table I. The distance $\langle p_1 - p_2 \rangle$ are averaged over 10 000 realizations. The error bars are smaller than the symbol size. The data for (2,1)-clique percolation are shifted upward by multiplying by 2.

In the bond-adding process, two different clique clusters merge when a newborn clique connects them, and the size of the smaller cluster will be the size jump. After all the bonds are added, the largest jump Δ_1 and the corresponding bond density p_1 can be identified, and the second largest jump can be found before Δ_1 happened at bond density p_2, and so on. According to Eq. (2), the critical exponent ν is associated with $p_1 - p_2$ and the system length L. In contrast to clique percolation on an ER graph where the critical exponents depend on l [17], we find that the clique percolation with different (k,l) on 2D Moore lattices shares the same value of ν, as shown in Fig. 3, and, interestingly, it is the same as the critical exponent of normal site or bond percolation on 2D lattice systems. The specific values are shown in Table I. These results indicate that clique percolation on a low-dimensional lattice belongs to the ordinary bond (site) percolation universality class, which is independent to the specific values of k and l. To verify this, we compare other critical exponents of clique percolation with site percolation for a systematic understanding.

TABLE I. The critical points and the critical exponents for clique percolation on the 2D Moore neighborhood. To compare, for 2D lattices, $\nu = 4/3$ and $d_f = 91/48 \simeq 1.896$.

(k,l)	p_c^∞	ν	d_f
(2,1)	0.250	1.34 ± 0.02	1.897 ± 0.02
(3,1)	0.597	1.35 ± 0.03	1.894 ± 0.02
(3,2)	0.729	1.29 ± 0.09	1.894 ± 0.02
(4,1)	0.870	1.29 ± 0.1	1.894 ± 0.02
(4,2)	0.911	1.29 ± 0.08	1.894 ± 0.02

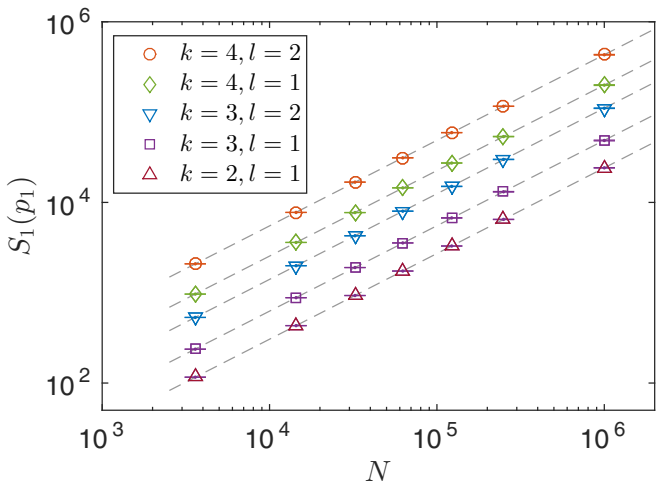

FIG. 4. The size of the largest cluster S_1 versus the system size N at p_1. The dashed lines are fitting results for different combinations of k and l. According to Eq. (3), since $N = L^2$, the fractal dimension d_f of the giant cluster is half of the slope. The values of the fractal dimension are shown in Table I. The lines for (4,1), (3,2), (3,1), (2,1) are shifted downward by multiplying by $1/2, 1/4, 1/8, 1/16$, respectively.

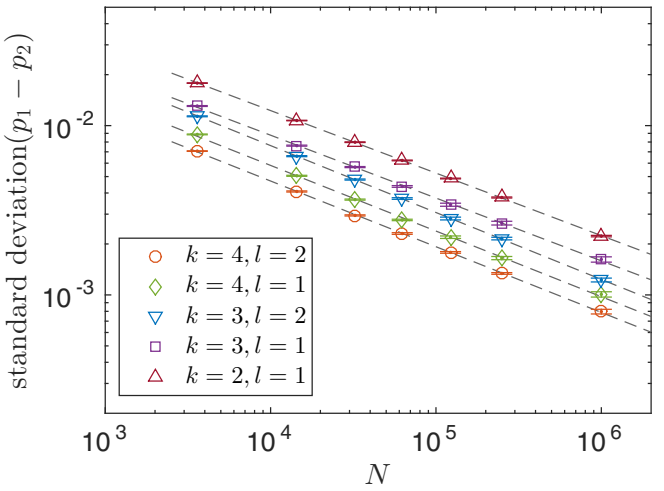

FIG. 5. The scaling of the standard deviation (std) of $(p_1 - p_2)$ versus the system size N. The slopes are 0.376 for (2,1), 0.370 for (3,1), 0.394 for (3,2), 0.388 for (4,1), and 0.3876 for (4,2). Comparing with the values of ν in Table I, it suggests the same scaling relation as $\langle p_1 - p_2 \rangle$, i.e., $\mathrm{std}(p_1 - p_2) \sim N^{-1/(d\nu)}$. The corresponding ν obtained in this scaling is then 1.35 for (3,1), 1.27 for (3,2), 1.29 for (4,1), and 1.29 for (4,2) percolation, respectively, which agree with the values in Table I very well. The line for (2,1)-clique percolation is shifted upward by multiplying by 2.

According to the hyperscaling relations shown in Eq. (4), there is another critical exponent that needs be chosen to determine its universality class together with ν. In previous works, β is commonly selected since it can indicate the type of phase transition. However, the estimation method of β is associated with finite-size scaling $S_1(p_1)/N \sim L^{-\beta/\nu}$, thus the error in estimating ν will decrease the accuracy of β. Here we choose the fractal dimension d_f of the giant cluster as the other base. When the largest jump occurs, the largest cluster size $S_1(p_1)$ and the cluster diameter L_1 obey the asymptotic relation $S_1(p_1) \sim L_1^{d_f}$. Since $S_1(p_1)$ is the spanning cluster, $L_1 \simeq L$. Therefore the asymptotic relation can also be written as $S_1(p_1) \sim L^{d_f}$. It is noticed that, for higher fractal dimension, the asymptotic relation holds only for extremely large clusters, requiring larger systems. Otherwise, the lower terms may dominate and give wrong fitting values. As is shown in Fig. 4, the fractal dimension of the giant cluster has the same value for different cases of k and l (see Table I), and they are basically identical to the fractal dimension of site or bond percolation on 2D systems with high numerical accuracy.

It was found that the value of the critical exponent β depends on the definition of the order parameter [11,18]. There are two ways to define the order parameter. One definition is $\psi = \mathcal{N}^*/\mathcal{N}$, the ratio of the number of k-cliques in the giant cluster, $\mathcal{N}^*$, to the total number of k-cliques in the system, $\mathcal{N}$. The other definition is $\phi = N^*/N$, the ratio of the number of sites N^* in the giant cluster to the number of sites N in the system. The finite-size scaling theory in this paper does not involve any details of order parameter definition. However, since the correlation length ξ_i and cluster size S_i are counted with the number of sites rather than k-cliques, all critical exponents we obtained should be in accordance with the second definition of the order parameter. In addition, one may note that the difference of the two definitions does not affect the value of critical exponents for the Moore neighborhood. The reason is that the cluster size N^* counted based on the sites and $\mathcal{N}^*$ counted based on the k-cliques are proportional to each other for large L, thus the same asymptotic behavior can be expected around the critical point.

In Fig. 3 we have considered the scaling of $\langle p_1 - p_2 \rangle$ versus system size N, which yields the critical exponent ν. It is curious that how the fluctuation of $p_1 - p_2$ scales with system size. We have plotted the standard deviation of $p_1 - p_2$ versus system size N in Fig. 5. Interestingly, the scaling exponent is the same as that for $p_1 - p_2$, i.e., $d\nu$. This indicates that the scalings of the mean value and the fluctuation of $p_1 - p_2$ are highly correlated. It has been noticed that for an ER random graph, the standard deviation of $p_c - p_1$ scales in the same way as $p_c - p_1$ when $l = 1$, but in general they are not equal [17]. This is consistent with our result, as in our case the scaling exponents are not depending on l, and they all have the same values with the case $l = 1$.

Δ_i is introduced as the historically largest merger of two clusters. The second largest merger, corresponding to Δ_2, can be considered as the largest merger in the local (or smaller) system, and this concept is applicable for the other characteristic mergers in the sequence $\{\Delta_3, \Delta_4, \ldots\}$. So there should be no inherent difference between different characteristic mergers. In this sense, the distribution of p_i could be rescaled into a uniform function only by the size of Δ_i and $\langle p_i \rangle$. As shown in Fig. 6, for the same (k,l)-clique percolation, the distribution of $x = (p_2 - \langle p_2 \rangle)\Delta_2^{1/d_f\nu}$ collapses into the same curve for different system sizes. Furthermore, for fixed system size, the curves can also be rescaled for different i, which can be seen clearly from the upward triangles in Fig. 6.

In this paper we have investigated the critical behavior of clique percolation on 2D lattices. It is obviously different from

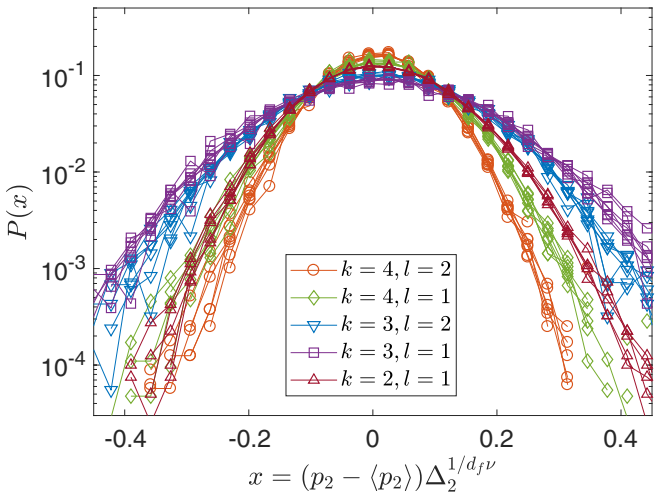

FIG. 6. For different system sizes, the distribution of $p_2 - \langle p_2 \rangle$ can be rescaled by Δ_2^{σ}. The seven lattices of different sizes in Fig. 4 are plotted with the same colors and symbols, each for a clique percolation with a given combination of k and l. Furthermore, for different values of i, the distribution of $p_i - \langle p_i \rangle$ can be rescaled with Δ_i^{σ} to collapse over each other. The upward triangles are $p_i - \langle p_i \rangle$ of a bond percolation with $L = 500$ and $i = 2,3,4,5,6$.

the results on an ER graph, in which the critical exponents depend on the parameter l. For the 2D Moore lattice, the critical exponents ν and d_f are found to be the same as the results from normal 2D site or bond percolation on a 2D lattice. This result implies that clique percolation on a 2D Moore neighborhood belongs to the same 2D percolation universality class. This can be understood from the fact that, for two special types of clique percolation, there exists a map to bridge the clique percolation on the Moore neighborhood to the site percolation on a Moore or 2D square lattice. In particular, if each clique is regarded as a site, as shown in Fig. 7, for the (4,1)-clique percolation and (4,2)-clique percolation, at the critical point, each configuration of a percolated cluster can be mapped to the site percolation on Moore or square lattices, respectively,

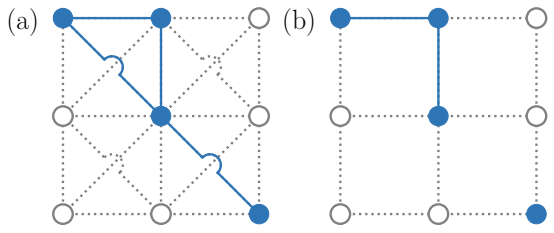

FIG. 7. The connection between clique percolation on a Moore lattice and normal site percolation for some special cases. If each 4-clique in Fig. 1 is regarded as a site, the (4,1)-clique percolation and (4,2)-clique percolation can be mapped into site percolation on a Moore neighborhood shown in panel (a) and site percolation on a square lattice shown in panel (b), respectively. The sites (blue circles) correspond to the 4-cliques shown in Fig. 1. The blue bonds correspond to the existing connections between cliques, i.e., (a) for neighboring cliques sharing at least one node in (4,1) clique percolation and (b) sharing at least two nodes for (4,2) clique percolation.

and vice versa. Since the giant cluster is formed by clusters merging in a narrow parameter range, loops should be sparse at the critical point, thus the giant cluster can be approximated by a tree. Then the critical point of clique percolation p_c satisfies $p_c^{\gamma} = \hat{p}_c$ under a treelike approximation, with $\hat{p}_c$ being the critical point of the site percolation on the mapped lattice, and γ is determined by the number of inner bonds in a clique on average. For the case with $k = 4, l = 1$, the clique percolation is equivalent to a site percolation on a Moore neighborhood with $\gamma = 5$ as the (4,2) connections are dominant at the critical point [Fig. 7(a)]; while for the case with $k = 4, l = 2$, the clique percolation is equivalent to the site percolation on the square lattice with $\gamma = 5$ [Fig. 7(b)]. Indeed, for (4,1) clique percolation, the critical point p_c is 0.870. The critical point $\hat{p}_c$ of site percolation on the Moore neighborhood is $1/2$, thus $(1/2)^{1/\gamma} = 0.87$, and agrees well with p_c. For (4,2) clique percolation, the critical point p_c is 0.911. The critical point $\hat{p}_c$ of site percolation on a square lattice is 0.59274, thus $0.59274^{1/\gamma} = 0.901$, also agreeing with the corresponding p_c.

Since $p_c^{\gamma} = \hat{p}_c$, assume that $p^{\gamma} = \hat{p}$, and then the difference of p from the critical point p_c can be expanded as

$$\begin{aligned} |p - p_c| &= \left|\hat{p}^{1/\gamma} - \hat{p}_c^{1/\gamma}\right| \\ &\approx \left|\frac{\hat{p}_c^{1/\gamma - 1}(\hat{p} - \hat{p}_c)}{\gamma} + O((\hat{p} - \hat{p}_c)^2)\right| \\ &\approx \text{const}|\hat{p} - \hat{p}_c|. \end{aligned} \tag{5}$$

Therefore, for a system with the bond density p approaching the critical point p_c, the corresponding mapped site percolation has the same order of $\hat{p}$ approaching toward $\hat{p}_c$, which infers that the critical exponents of the clique percolation are identical with those of the site percolation, thus belonging to the same universality class.

It is known that clique network on an ER graph can also be mapped onto a new ER graph [17,18]. However, the clique percolation on an ER graph does not belong to the same universality class as the bond percolation, as the critical exponents of clique percolation on an ER graph also depend on the value of l. These differences between the ER graph and the Moore neighborhood can be attributed to the following two factors. Firstly, for site percolation on an ER graph, the critical point $\hat{p}_c \sim 1/N$, thus in the thermodynamical limit $N \to \infty$, one will have $\hat{p}_c = 0$. Therefore the relation Eq. (5) will no longer hold. In addition, it has been shown that when the critical point goes to zero, the critical exponents for bond percolation and those for site percolation will be different, leading to complex scaling behaviors [35]. Secondly, the number of sites and the density of bonds in a clique cluster not only depend on the number of cliques, but also depend on the system size N as the critical point depends on N, and therefore γ cannot be uniquely determined.

IV. CONCLUSION

To conclude, we have investigated the clique percolation on 2D Moore lattices. We have developed a new finite-size scaling scheme by noting the equivalence of different historically largest size jumps at the critical point. Thus instead of $p_c - p_1$, one can use $p_i - p_j$, for example, $p_1 - p_2$, and its scaling

with the system size N to determine critical exponents. This avoids the uncertainty in estimating p_c, leading to a better accuracy in determining the critical exponents. We found that, although the clique percolation is defined in a more complicated way with respect to normal site percolation, and previous results indicate that the scaling exponents may depend on the number of common nodes l defining the connection between two cliques [17,18], interestingly, clique percolation on 2D Moore neighborhoods belongs to the same universality class as the normal site percolation, and the scaling exponents are independent of neither the number of nodes k defining a clique nor l. This phenomenon can be understood that for two special types of clique percolation on a Moore neighborhood, they can be directly mapped onto site percolation on a 2D lattice. The main difference between the 2D lattices and the ER graph can be attributed to the fact that for the latter case the critical point for normal site percolation is $\hat{p}_c \sim 1/N$, thus $\hat{p}_c$ varies significantly with system size N and goes to zero in the large size limit, which is accompanied by many side effects, leading to complex critical behaviors.

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