Scaling of Clusters near Discontinuous Percolation Transitions in Hyperbolic Networks

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We investigate the onset of the discontinuous percolation transition in small-world hyperbolic networks by studying the systems-size scaling of the typical largest cluster approaching the transition, \( p \not\to p_c \). To this end, we determine the average size of the largest cluster \( \langle s_{\text{max}} \rangle \sim N^{\Psi(p)} \) in the thermodynamic limit using real-space renormalization of cluster generating functions for bond and site percolation in several models of hyperbolic networks that provide exact results. We determine that all our models conform to the recently predicted behavior regarding the growth of the largest cluster, which found diverging, albeit sub-extensive, clusters spanning the system with finite probability well below \( p_c \) and at most quadratic corrections to unity in \( \Psi(p) \) for \( p \not\to p_c \). Our study suggest a large universality in the cluster formation on small-world hyperbolic networks and the potential for an alternative mechanism in the cluster formation dynamics at the onset of discontinuous percolation transitions.

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I. INTRODUCTION

Small-world hierarchical networks have generated much interest as models for the prevalent hierarchical organization in complex networks because they yield exact results for statistical models [1–5]. These recursive structures provide deeper insights into the nonlinear behavior caused by small-world connections, compared to some presumed network ensemble that often requires approximate or numerical methods. Work on percolation \[6,10\], the Ising model \[2,11,13\], and the Potts model \[14,15\] have shown that critical behavior once thought to be exotic and model-specific [5] can be universally described near the transition point \[16,17\] for a large class of hierarchical networks with hyperbolic properties. In a hyperbolic structure, sites are typically randomly connected but possess a hierarchical organization of sites that allows to identify a few sites harboring many small-world bonds as central while an extensive portion of sites with less access resides on the periphery \[18,19\]. Such structures are common in disordered materials \[20,21\], human organizations \[1\], information and communication networks \[19,22\], or neural networks \[23,24\]. However, in scale-free hyperbolic networks \[25\] there appears to be no threshold against the onset of percolation.

Here, we extend the discussion of universality on such networks by studying the emergence of the discontinuous transition recently found in ordinary percolation [8]. Due to the discovery of percolation transitions that first appeared to be “explosive” \[26\], the dynamics of cluster formation at the onset of such a transition has been the focus of much research \[29,33\]. While details of the cluster size distribution \( p(s) \) remain accessible only to simulations, we can use the renormalization group (RG) to determine the exact large-\( N \) scaling of the average size of the largest cluster,

\[
\langle s_{\text{max}} \rangle \sim N^{\Psi(p)}, \quad (1)
\]
non-linear corrections also characterize the site percolation transition. In Sec. [V] we finish with our conclusions and suggestions for future work.

II. SMALL-WORLD HYPERBOLIC NETWORKS

The models we are studying here are familiar hierarchical networks that have become popular because they provide exact results for complex processes by way of the real-space renormalization group. MK1, depicted in Fig. 1(a), is the one-dimensional version of the small-world Migdal-Kadanoff hierarchical diamond lattice [2], which has been used previously to prove the existence of the discontinuous transition in ordinary percolation [8]. MK1 is recursively generated starting with two sites connected by a single edge at generation \( n = 0 \). Each new generation recursively combines two sub-networks of the previous generation and adds single edge connecting the end sites. As a result, the \( n^{th} \) generation contains \( 2^n + 1 \) vertices, \( 2^n \) backbone bonds, and \( 2^n - 1 \) small-world bonds.

To show that this discontinuity persists for more complicated but hierarchical structures, we consider here also the Hanoi networks HN5 and HNNP, also shown in Fig. 1(b-c). A similar recursive procedure as described above for MK1 is also applied to obtain each new generation, however, due to their more complicated structure their basic building block at \( n = 0 \) consists of a triangle of three sites. For these Hanoi networks, the existence of a non-trivial bond-percolation transition has been demonstrated previously [7]. HN5 is similar to MK1 but requires a coupled system of RG-recursions. It also can be easily adapted to complement previous investigations of site-percolation [35] in a non-trivial fashion. HNNP is special in that it is a non-planar graph, and aspect that is missing from other hierarchical networks.

III. REVIEW OF CLUSTER RENORMALIZATION IN BOND PERCOLATION

Before we apply it to calculate exact expressions for the scaling of the average cluster size for HN5 and HNNP in the next section, we first review briefly the formalism needed to analyze the average cluster size near the bond-percolation transition, as used for MK1 in Ref. [8].

While a full understanding the dynamics of cluster formation near the discontinuous percolation transition requires knowledge of the entire cluster-size distribution, already the average size of the largest cluster \( \langle s_{\text{max}} \rangle_n \) at generation \( n \) provides profound insights. In particular, we will be focused on the system-size scaling of \( \langle s_{\text{max}} \rangle_n \) for \( p \to p_c \). In the following, we derive \( \langle s_{\text{max}} \rangle_n \) using cluster generating functions.

A. Cluster Generating Function for MK1:

We review briefly the procedure described in Ref. [8] for MK1. There, the generating functions were obtained by introducing merely two quantities: the probability \( t^{(n)}_i(p) \) that both end-sites are connected to the same cluster of size \( i \), and the probability \( s^{(n)}_{i,j}(p) \) that the left end-site is connected to a cluster of size \( i \) and the right end-site to a different cluster of size \( j \). The generating functions, as depicted in Fig. 2, are defined as

\[
T_n(x) = \sum_{i=0}^{\infty} t^{(n)}_i(p) x^i \tag{2}
\]

\[
S_n(x,y) = \sum_{i=0}^{\infty} \sum_{j=0}^{\infty} s^{(n)}_{i,j}(p) x^i y^j \tag{3}
\]
The recursion relations for these generating functions can be obtained by combining all possible configurations on three sites, as shown in Fig. 3 taking into account the cluster sizes as described in Ref. 8. The graphs on three sites are assigned to the correct two-site graphlet in the next generation, and the weights of all the graphlets that contribute to the same higher-generation graphlet are added together to get the recursion relations,

\[ T_{n+1}(x) = xT_n(x) + p \left[ 2xT_n(x)S_n(x, x) + S_n(x, 1)S_n(1, x) \right], \]

\[ S_{n+1}(x, y) = (1-p) \left[ xT_n(x)S_n(x, y) + yT_n(y)S_n(x, y) + S_n(x, 1)S_n(1, y) \right], \]

as indicated in Fig. 3 and discussed in more detail in Appendix VIIIA.1.

**B. Fixed Point Analysis for Average Cluster Size:**

The recursion equations in Eq. (5) can be simplified by combining them into a vector \( \vec{V}_n(x) = [T_n(x), S_n(x, x), S_n(x, 1)] \) of distinct observables, where we focus on the largest cluster \( x \) only. The RG can now be written as

\[ \vec{V}_{n+1}(x) = \vec{F} \left( \vec{V}_n(x), x \right) \]

for the nonlinear vector-function \( \vec{F} \) that derives from Eqs. (5). As Eq. (2) suggest, the average size of a spanning cluster (which dominate in the cluster-size distribution) is generated by \( s \sim T_n' (x = 1) \); any form of \( S_n \) does not affect to the spanning cluster and its contributions prove subdominant. We obtain \( T_n' (x = 1) \) in terms of \( T_n = T_n(x = 1) \) and \( p \) by linearizing the recursion relation in Eq. (6)

\[ \frac{\partial \vec{V}_{n+1}}{\partial x} = \frac{\partial \vec{F}}{\partial \vec{V}} \left( \vec{V}_n \right) \cdot \frac{\partial \vec{V}_n}{\partial x} + \frac{\partial \vec{F}}{\partial x} \left( \vec{V}_n \right), \]

near \( x = 1 \). Eq. (6) itself at \( x = 1 \) (where \( S_n = 1 - T_n \)) reduces for MK1 in each component of \( \vec{V} \) to

\[ T_{n+1} = p + (1 - p) T_n^2 \quad (T_0 = p) \]

with fixed point \( T_\infty = \lim_{n \to \infty} T_n \)

\[ T_\infty (p) = \begin{cases} \frac{1 - p}{1} & 0 \leq p < \frac{1}{2} \\ \frac{1}{2} \leq p \leq 1, \end{cases} \]

providing the critical point \( p_c = \frac{1}{2} \), where any spanning cluster also becomes extensive, see Fig. 4(a).

Ignoring the subdominant inhomogeneity in Eq. (7), the remaining homogeneous linear system gives the dominant contribution for \( V_\infty' \), i.e. \( T_\infty, S_\infty' \). The largest eigenvalue \( \lambda \) of the coefficient-matrix \( \frac{\partial \vec{F}}{\partial \vec{V}} (\vec{V}_\infty') \) at the fixed point \( T_\infty (p) \) becomes for MK1

\[ \lambda = \begin{cases} 1 + 3p - 4p^2 & \frac{1 - p}{2(1-p)} + \frac{1 - p(1 - 4p^2)}{4(1-p)} \leq p < \frac{1}{2} \\ \frac{1}{2} \leq p \leq 1, \end{cases} \]

Finally, we obtain the order parameter \( P_\infty \) as

\[ P_\infty = \frac{\langle s_{\text{max}} \rangle}{N} \sim T_\infty' \sim N^{\Psi (p) - 1} \]

with the fractal exponent

\[ \Psi (p) = \log_2 \lambda. \]

Note that this implies that the largest cluster below the transition is already diverging with a non-zero power of the system size, although in a sub-extensive manner, \( \Psi < 1 \) for \( p < p_c \), such that \( P_\infty \to 0 \) for \( N \to \infty \). These spanning, sub-extensive clusters exist, albeit with finite probability given by \( T_\infty (p) \) in Eq. (9), for all \( 0 < p < p_c \). This behavior for hyperbolic systems contrasts with that of regular lattices, where such sub-extensive clusters with fractal scaling only exist for \( p = p_c \) and \( \Psi (p) \equiv 0 \) for \( p < p_c \), such that all clusters remain finite or at most diverge logarithmically in \( N \).

In Fig. 5(a), we show a plot of \( P_\infty (p) \) for MK1 evaluated after \( n = 10^6 \) iterations using Eq. (7) displayed for \( k = 1, ..., 5 \) corresponding to system sizes up to \( N \sim 2^n \sim 10^{3010} \) sites. \( P_\infty \) converges slowly to zero for \( p < p_c = \frac{1}{2} \). At and above \( p_c \), it can be shown using
Eq. [7] that $T'_n$ is monotonically increasing with $n$ while being bounded above by 1, thus the order parameter is positive definite for $\frac{1}{2} \leq p < 1$. The order parameter $P_{\infty}$ changes discontinuously from 0 to 0.609793... at $p = p_c$ and converges to 1 for $p \to 1$. A more detailed discussion, including a proof of the discontinuity, is provided in Ref. [8].

C. Scaling Behavior near the Transition

From Eqs. [10][12] it is now easy to determine the scaling behavior for the average cluster size near the transition. By expanding the eigenvalue $\lambda$ in Eq. (10) for $p \to p_c$ from below, we find that the leading behavior only has quadratic corrections, and inserting into Eq. (12) results in

$$\Psi(p) \sim 1 - \frac{8}{\ln 2} (p - p_c)^2, \quad p \nearrow p_c = \frac{1}{2}$$

which rapidly approaches unity. This implies that the largest (spanning) cluster that dominates the distribution is nearly extensive already much before the discontinuous transition is reached. RG can only determine the probability $T_{\infty}$ and average size $\langle s_{\max} \rangle \sim T'_{\infty}$ of the spanning cluster. Their sub-extensive nature for $p < p_c$ would allow in principle for a diverging number of such clusters. Our simulations show that already for small systems the largest cluster is almost certainly connected to at least one end-site near $p_c$. (In fact, for MK1 we could have just as well defined $\langle s_{\max} \rangle \sim T'_{\infty} + S'_{\infty}$ to account not just for spanning but all end-site connected clusters, without affecting the scaling.) However, as we will see for HN5 and MK2, which share a similar phase diagram shared by all three networks, as is evident from Fig. 4.

Despite of the added complexity, we find remarkably similar results near the transition for these networks, as compared to MK1, and only some distinctly interesting features for HNNP in the “patchy” regime below $p_c$. Such robust behavior suggests universal features [16][34], which can be traced back to the fundamental phase diagram shared by all three networks, as is evident from Fig. 4. For comparison, this bond-percolation behavior is not shared by another hierarchical network, MK2, which mutatis mutandis has quite a distinct phase diagram [7][36], leading instead to a BKT transition. See Ref. [34] for an interpolation between both cases.

In the Appendix, Sec. VIII A 2, we show how to obtain the RG-recursions for the cluster generating functions. While otherwise similar to the discussion in Sec. III A, HNNP (as well as HN5) requires four such functions to account for all possibilities, of having clusters linking any combination of three end-sites or remain isolated, even after accounting for all symmetries of the network. The resulting recursions, Eqs. (35), are similar to those for MK1 in Eqs. (1), although rather more involved. In the end, we only care for the dominant cluster, which we label $\vec{x}$, and consider each possible contribution from one RG-step to the next while disregarding sub-dominant clusters by setting $y = z = 1$. Note that even clusters that are disconnected from any end-site at one step could significantly contribute to the next via the small-world bonds that are linking graphlets between consecutive RG-steps. In the end, we can identify ten distinct observables that form a closed set of recursions. When combined into a single vector,

$$\bar{V}_n(x) = |R_n(x), S_n(x,x), S_n(x,1), U_n(x, x),$$

$$U_n(x, 1), N_n(x, x, x), N_n(x, x, 1), $$

$$N_n(x, 1, x), N_n(x, 1, 1), N_n(1, x, 1)|,$$

these satisfy the equivalent recursion in (9), with the nonlinear RG-flow given by Eqs. (35).

To zeroth order, at $x = 1$, Eq. (6) gives the recursion relation for percolation of the HNNP graph as derived in Ref. [7]. The coupled recursion relations in $(R_n, S_n, U_n, N_n)$ result in the roots of a sextic polynomial, which can be solved numerically to get the probability of, say, the spanning cluster $R_{\infty}$ between the end-sites. Fig. 4(c) gives the phase diagram for HNNP representing the solutions of the sextic equation, which correspond to the probability $R_{\infty}$ for $0 < p < 1$. HNNP provides a unique example of a network in which the probability of the dominant cluster to touch any end-site vanish below some finite value $0 < p_l < p_c$. In Ref. [7] this was interpreted as a second, lower, critical point, where below $p_l$ neither a spanning nor an extensive cluster exists while between $p_l$ and $p_c$ at least a spanning
FIG. 4. Phase diagram for the probability of a spanning cluster (a) $T_\infty$ for MK1 in Eq. (9), (b) $R_\infty$ for HN5 in Eq. (36), and (c) $R_\infty$ for HNNP in Eq. (35) (for $x = 1$), all as a function of bond probability $p$. Black lines mark stable fixed points, and red-shaded lines are unstable fixed point solutions. The critical transition, at which the probability of any site to belong to the largest cluster becomes finite and that cluster becomes extensive, occurs exactly when the probability of a spanning cluster becomes unity, at $p_c = \frac{1}{2}$ for MK1 and $p_c = 2 - \phi = 0.38197\ldots$ for both, HN5 and HNNP [7]. However, in all cases, there is a non-zero probability for a spanning cluster, albeit sub-extensive, even below $p_c$, due to the hyperbolic nature of these hierarchical networks. For MK1 and HN5, such a cluster can exist for all $0 < p < p_c$, while for HNNP it disappears below the branch-point singularity at $p_t = 0.31945\ldots$. Note that in each case the transition occurs at the intersection of two lines of stable fixed points.

FIG. 5. Discontinuity in the percolation order parameter $P_\infty(p)$ for (a) MK1, (b) HN5, and (c) HNNP, each for $n = 10^k$ iterations for some integer $k$. In each case, $P_\infty$ converges slowly to zero just below $p_c$, and at $p_c$, $P_\infty$ changes discontinuously. The discontinuity decreases left to right, and is barely visible for HNNP, see inset.

FIG. 6. Scaling of the order parameter $P_\infty(p)$ for $p > p_c$ according to Eq. (14) for (a) MK1, (b) HN5, and (c) HNNP. In each case, taking $p - p_c = \frac{1}{27}$, we plot $\log [P_\infty(p) - P_\infty(p_c)]/j$ vs. $1/j$ which linearly extrapolates to $\beta \sim 1$ as the intercept at $j \to \infty$, i.e., $p \to p_c$. 

A cluster exists that does not need to be extensive, due to the hyperbolic structure of the network. That spanning cluster exists that does not need to be extensive, due to the discontinuous jump in the order parameter $P_\infty$. By evolving the recursion equations \( \Psi' \) for $V'_\infty$, the order parameter can be rigorously shown to have monotone convergence to non-zero values at and above $p_c$, see Fig. 3(c). For $p > p_c$, the way $\Psi(p)$ approaches unity can be found through considering the secular equation

$$0 = \det \{ V'_\infty - (2 - a_1 \epsilon + a_2 \epsilon^2 + \ldots) \times I \},$$

expanded in terms of $\epsilon = p_c - p \ll 1$, where $I$ is the identity matrix. Note that at $p_c$, the largest eigenvalue of $V'_\infty$ is $\lambda = 2$, around which we expand. Since the percolation probabilities at $p_c$ are given by $R_\infty = 1, S_\infty = U_\infty = N_\infty = 0$, we assume an expansion of the percolation probabilities as $R_\infty = 1 - \rho_1 \epsilon + \rho_2 \epsilon^2, S_\infty = \sigma_1 \epsilon + \sigma_2 \epsilon^2, U_\infty = \nu_1 \epsilon + \nu_2 \epsilon^2$, and $N_\infty = \eta_1 \epsilon + \eta_2 \epsilon^2$. To satisfy Eq. \( \Psi' \), each coefficient in powers of $\epsilon$ should be zero. As a result, we find that linear corrections to the eigenvalue $\lambda$ vanish, i.e., $a_1 = 0$. Using conservation of probability, $\rho_i + \sigma_i + \nu_i + \eta_i = 0$, for each $i \geq 1$ at $p = p_c$, we find a non-vanishing quadratic correction, $a_2 = a_2 \rho_1 \sigma_1, \nu_1, \eta_1 = -\frac{1}{2} \sigma_2 \{ 38 + 17 \sqrt{5} \},$ for which the second-order corrections in the percolation probabilities proved irrelevant. Hence, Eq. \( \Psi'' \) yields

$$\Psi_{\text{HNNP}}(p) \sim 1 - \frac{5}{32 \log(2)} \frac{(p_c - p)^2 + \ldots}{(p_c - p)^2 + \ldots}, \quad p > p_c.$$  \hspace{1cm} \(17\)

For HN5, by using the same cluster generating functions as for HNNP in the Appendix, we obtain their RG recursions in \( \text{(26)} \). Again, the resulting equations for the cluster size are too complicated to express or solve in closed form. But it is easy to evaluate their phase diagram in Fig. 4(b) for $R_\infty$, as well as the order parameter $P_\infty$ in Fig. 5(b) to any desired accuracy. Here, the same local analysis near $p_c$ for HN5 yields for HN5:

$$\Psi_{\text{HN5}}(p) \sim 1 - \frac{5}{484 \log(2)} \frac{(677 + 304 \sqrt{5})}{(p_c - p)^2 + \ldots}, \quad p > p_c.$$  \hspace{1cm} \(18\)

As for MK1 and HNNP, almost extensive clusters in HN5 emerge well before the transition, with $\Psi(p)$ varying quadratically. It suggests that the quadratic dependence below $p_c$ might be universal for hierarchical networks with discontinuous percolation transitions. Above $p_c$, the scaling of $P_\infty$ in Eq. \( \text{(14)} \) for both, HN5 and HNNP, also provides $\beta \sim 1$, as shown in Fig. 6(b-c).

V. CLUSTER SIZE FOR SITE PERCOLATION

We supplement these findings with a unique result of even higher-order behavior in the site-percolation transition of HN5 in Fig. 3. The fragility of complex networks
other than satisfy the same recursions; hence, we can eliminate RG-recursions for the cluster generating functions are the merger of all possible graphlets in Fig. 8, the follow-

clusters, which entails a relabeling dictated by the same as in the construction of HN5 in Fig. 9, may combine the argument becomes unity. Extra small-world bonds, unoccupied, there are no countable clusters to label, and they only reach the central root site. If all root sites are the left root but at least the right-most root site, and least touch the left-most root site,

angle permutations listed in Fig. 8 through mergers as be assembled recursively by combining all possible tri-

the same protocols to study site percolation. HN5 can presented by a polynomial generating function in that variable. A full line corresponds to an existing connection between oc-

hierarchical networks [35]. It was shown that there is no scaling to the formation of an extensive cluster for 

A full line corresponds to an existing connection between oc-

under random site-removal has recently been studied on hierarchical networks [35]. It was shown that there is no threshold at which the network preserves an extensive cluster, i.e., \( p_c = 1 \), yet, similar quadratic corrections in scaling to the formation of an extensive cluster for \( p \to 1 \) are also found there. Hence, we would expect that cluster formation near this discontinuity is generic for both, bond- and site-percolation. In light of this, the cubic corrections we report here for HN5 may provide an alternative, special case and a new clue in understanding cluster formation.

With the framework for studying bond percolation on hierarchical networks established in Sec. III we apply the same protocols to study site percolation. HN5 can be assembled recursively by combining all possible tri-

angle permutations listed in Fig. 8 through mergers as explained in Fig. 9 Clusters are labeled \( x \) if they at least touch the left-most root site, \( y \) if they do not touch the left root but at least the right-most root site, and \( z \) if they only reach the central root site. If all root sites are unoccupied, there are no countable clusters to label, and the argument becomes unity. Extra small-world bonds, as in the construction of HN5 in Fig. 9, may combine clusters, which entails a relabeling dictated by the same priority.

Based on these rules explained in Fig. 9 applied to the merger of all possible graphlets in Fig. 8, the follow-

\[
N_{n+1}(1) = \frac{1}{1-p} [N_n(1) + B_n(1)]^2, \quad (19)
\]

\[
A_{n+1}(x) = \frac{1}{1-p} \{ [A_n(x) + C_n(x)] [N_n(1) + B_n(1)] + C_n(x) [B_n(x) - B_n(1)] \},
\]

\[
B_{n+1}(z) = \frac{1}{xp} [A_n(z) + C_n(z)]^2,
\]

\[
C_{n+1}(x) = \frac{1}{xp} [A_n(x) + C_n(x)] [E_n(x) + G_n(x)],
\]

\[
E_{n+1}(x) = \frac{1}{1-p} [A_n(x) + C_n(x)]^2,
\]

\[
G_{n+1}(x) = \frac{1}{xp} [E_n(x) + G_n(x)]^2.
\]

Here, we already have exploited a mirror symmetry be-
between $A_n$ and $D_n$ and between $C_n$ and $F_n$ to simplify the equations. The initial conditions for these RG-recursions are:

$$
N_0 (x) = (1 - p)^3, \quad A_0 (x) = xp (1 - p)^2, \\
B_0 (z) = zp (1 - p)z, \quad C_0 (x) = x^2 p^2 (1 - p), \\
E_0 (x) = x^2 p^2 (1 - p), \quad G_0 (x) = x^3 p^3. \tag{20}
$$

Unlike the recursions for the bond-cluster generating functions, for example, Eq. (9) for MK1, here the site-cluster generating functions themselves do not satisfy interesting recursions at $x = 1$. For instance, $A_n (1) = A_0 (1) = p (1 - p)$ for all $n$ merely reflects the defining feature of the site-percolation cluster $A_n (x)$ of being occupying the left end-site but not the right end-site.

Note that without the seemingly minor distinction between $B_n (x)$ and $B_n (1)$ in the $A_{n+1}$-relation, as explained in Fig. 9, we could drastically reduce the recursions further by defining

$$
T_n (x) = \frac{1}{x^2 p^2} [E_n (x) + G_n (x)], \tag{21}
$$

$$
S_n (x) = \frac{1}{xp (1 - p)} [A_n (x) + C_n (x)],
$$

which converts Eqs. (19) into those for MK1 in Ref. [35]. Instead, we have to evolve the entire set of five $x$-dependent relations for the RG-flow in Eqs. (19).

Defining

$$
\tilde{V}_n (x) = [A_n (x), B_n (x), C_n (x), E_n (x), G_n (x)] \tag{22}
$$

and following the discussion in Sec. [11] we obtain from Eqs. (19) at $x = 1$:

$$
\frac{\partial \tilde{V}^2}{\partial V} (\tilde{V}_\infty) = \begin{pmatrix}
1 - p & p^2 & 1 - p & 0 & 0 \\
2 (1 - p) & 0 & 2 (1 - p) & 0 & 0 \\
p & 0 & p & 1 - p & 1 - p \\
2p & 0 & 2p & 0 & 0 \\
0 & 2 (1 - p) & 0 & 0 & 0
\end{pmatrix}. \tag{23}
$$

where we used the IC in Eqs. (20) and the fact explained above that $\tilde{V}_n (1) = \tilde{V}_0 (1)$ for any $n$ for site-percolation generating functions. Then, the largest eigenvalue is the largest root of the cubic equation

$$
0 = 4p^3 - 4p^4 + 2p^3 \lambda - (1 + 2p)\lambda^2 + \lambda^3. \tag{24}
$$

Again, as in Eq. (12), it is $\Psi (p) = \log \lambda$, which is shown in Fig. 10. It is remarkable that, although $\Psi (p)$ varies smoothly between 0 and 1, near $p = 1$ we find only a cubic correction near $p_c = 1$:

$$
\Psi (p) \sim 1 - \frac{2}{\ln 2} (1 - p)^3, \quad p \not\to p_c = 1. \tag{25}
$$

VI. CONCLUSIONS

Our investigation of properties of the cluster formation near the discontinuous percolation transition in hyperbolic networks affirms the robustness of the observed finite-size scaling of the largest cluster in the system. Our study considers more complicated classes of networks than before, and extends the analysis to include both, bond- and site-percolation. To obtain our results, we present an automated means of graph counting, which are essential to accomplish the RG-recursions for entire functions that are the generators for the cluster sizes. In the Appendix, we present these methods in somewhat more detail so that they can serve as a blueprint for similar efforts in the future.

Our RG study can merely implicate interesting scaling features in the evolution of the emergent cluster; only detailed simulation can provide sufficient insight into the mechanics of their formation. In a parallel effort, we are currently studying bond percolation on these hyperbolic networks as the familiar limit $q \to 1$ of the $q$-state Potts model. In this form, we also hope to better understand the connection between discontinuous percolation transitions and the phenomenology of critical transitions as found, for instance, in ferromagnets on these networks [16], which should be revealed by the interpolation between $1 \leq q \leq 2$ in the analytic continuation of the Potts model.

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VIII. APPENDIX

A. Automated Graph Counting

The recursion relations (5) for MK1 are obtained by a process of graph counting depicted in Fig. (3). As the number of possible graphlets increases exponentially for more complicated hierarchical networks (e.g. HN5 and HNNP), automating the graph enumeration process *insilico* makes it easier to obtain their recursion equations. Key to this process is the adjacency matrix, which gives the information about the presence of single bonds between two sites in a graph.

1. Counting MK1 graphlets:

In the MK1-graphlet in Fig. 3a,

\[ A_a = \begin{bmatrix} 0 & 1 & 1 \\ 1 & 0 & 1 \\ 1 & 1 & 0 \end{bmatrix} \]

(26)

is an example of an adjacency matrix when all possible bonds are present. The bonds are bi-directional, which results in a symmetric matrix, and the diagonal elements are zero, since there are no bonds that loop back to a site. In the case where two ends are not connected by a single bond, the adjacency matrix effectively searches for alternate paths to connect the two end-sites. In Fig 3a, for example, the small-world bond is missing, and sites 1 and 3 are not connected via a single bond. The adjacency matrix is thus,

\[ A_c = \begin{bmatrix} 0 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & 0 \end{bmatrix} \]

(27)

By itself, the adjacency matrix gives the number of one-step end-site connections. To find the number of two-step end-site connections for a graphlet, the adjacency matrix must be squared. The off-diagonal elements of \( A^2 \) give the number of possible paths between two sites that are exactly two hops long. Squaring the adjacency matrix in Fig. 3a (Eq. 26) gives

\[ A_a^2 = \begin{bmatrix} 1 & 0 & 1 \\ 0 & 2 & 0 \\ 1 & 0 & 1 \end{bmatrix} \]

(28)

Since matrix element \( A_{a,13}^2 = 1 \), there exists only one possible path in which two-steps can be made to connect the end-sites. Since the maximum path length for the simple case of MK1 is two, only \( A_{a,13} \) (one step) and \( A_{a,13}^2 \) (two steps) need to be checked for finding end-to-end connections.

The graphlets are classified as contributing to \( T_n(x,y) \) or \( S_n(x,y) \) depending on whether an end-to-end connection exists. The weights of the graphlets are calculated by first labeling the end-sites as \( x \) and \( y \). Both end-sites are labeled \( x \) in fully-connected graphs contributing to \( T_n(x,y) \), and unconnected graphs contributing to \( S_n(x,y) \) contain the left end-site labeled \( x \) and the right end-site labeled \( y \).

For each graphlet in the \( n^{th} \) generation, \( x \) or \( y \) is assigned to each site and \( T_n(x) \) or \( S_n(x,y) \) to each bond, depending on whether the end sites are attached. Isolated sites/clusters are assigned a weight of 1. The contribution of each graphlet in the \((n+1)^{th}\) generation is set as the product of the value assigned to the bonds and intermediate sites. For example, the two shaded backbone bonds of Fig. 3a indicate that the graphlet has two bonds of type \( T_n(x) \). The small-world bond exists with probability \( p \), and all the sites are connected to the same cluster. Therefore, the graphlet contributes to \( T_{n+1}(x) \) in the next generation with weight \( p x T_n^2(x) \). Similarly, for the graphlet in Fig. 3b, the backbone bonds are of the types \( T_n(x) \) and \( S_n(x,y) \). The small-world bond is absent with probability \( 1 - p \), and the end-sites are connected to separate clusters, \( x \) and \( y \). Hence, this graphlet contributes to \( S_{n+1}(x,y) \) in the next generation with weight \((1 - p) x T_n(x) S_n(x,y)\).
The symmetry of themselves are not counted in the cluster size.

...in this case, which can be verified by looking in the next generation. In fact all the sites are connected to the same cluster (say of size $k$) and there is only one long range small world bond is present, the weight of the graphlet is $p(1-p)x^2R_n(x)S_n(x, x)/4$.

2. Cluster Generating Function for HNNP:

The generating functions for the Hanoi network HNNP in Fig. [1] can be calculated using the same principles described for MK1. As in Sec. [III A] we define the generating functions for HNNP depicted in Fig. [11]

$$R_n(x) = \sum_{k=0}^{\infty} r_k^{(n)}(p)x^k,$$  

$$S_n(x, y) = \sum_{k=0}^{\infty} \sum_{l=0}^{\infty} s_{k,l}^{(n)}(p)x^ky^l,$$  

$$U_n(x, y) = \sum_{k=0}^{\infty} \sum_{l=0}^{\infty} u_{k,l}^{(n)}(p)x^ky^l,$$

$$N_n(x, y, z) = \sum_{k=0}^{\infty} n_{k,l,m}^{(n)}(p)x^ky^lz^m,$$

where we introduce the probabilities

- $r_k^{(n)}(p)$ that sites $a$, $b$ and $c$ are all connected within the same cluster of size $k$;

- $s_{k,l}^{(n)}(p)$ that $a$ and $b$ are mutually connected within a cluster of size $k$, and $c$ is connected to a separate cluster of size $l$;

- $t_{k,l}^{(n)}(p)$ that $a$ is connected to a separate cluster of size $k$, and $b$ and $c$ are mutually connected within cluster of size $l$;

- $u_{k,l}^{(n)}(p)$ that $a$ and $c$ are mutually connected within a cluster of size $k$, and $b$ is connected to a separate cluster of size $l$;

- $n_{k,l,m}^{(n)}(p)$ that $a$ is connected to a cluster of size $k$, $b$ is connected to a cluster of size $l$, and $c$ is connected to a cluster of size $m$, but all mutually disconnected.

The symmetry of $s_{k,l}^{(n)}$ and $t_{k,l}^{(n)}$, are included in the definition of $S_n(x, y)$ [11]. As for MK1, the three end-notes themselves are not counted in the cluster size.

We want to obtain the system of RG recursions for generating functions, where $(R_{n+1}, S_{n+1}, U_{n+1}, N_{n+1})$ are functions of $(R_n, S_n, U_n, N_n; p)$. The algorithm first generates the adjacency matrices corresponding to all possible $(2^8 = 256)$ graphlets for the HNNP network. For each one of these graphlets the possibility of their contribution to one of $(R_{n+1}, S_{n+1}, U_{n+1}, N_{n+1})$ in the next generation is checked using the adjacency matrices.

As an example of our graph counting algorithm for HNNP, we consider the graphlet in Fig. [12] At first glance it appears that there are two separate clusters of sizes $k$ and $l$. The adjacency matrix for this graphlet is

$$A = \begin{bmatrix}
a & b & c & a' \\
b & 1 & 0 & 1 & 0 & 1 \\
c & 0 & 1 & 0 & 1 & 0 \\
b' & 0 & 0 & 1 & 0 & 0 \\
a' & 0 & 1 & 0 & 0 & 0
\end{bmatrix}$$

where the disconnect between sites $a'$ and $b'$ is indicated by $A_{4,5} = A_{5,4} = 0$. After the sites $b$ and $b'$ in Fig. [12] are decimated in the RG step, the remainder is matched with one of the graphlets in the generating function diagram in Fig. [11]. Thus, only the matrix elements in Eq. [33] that connect end sites $a$ to $c$, $a$ to $a'$, and $c$ to $a'$ contribute to the recursion equations for the generating functions. In general, the matrix elements for $A^4$ must be checked for a five-point HNNP graphlet, since the maximum number of steps required to connect all end-sites is four. In our example,

$$A^4 = \begin{bmatrix}3 & 0 & 4 & 0 & 3 \\
0 & 10 & 0 & 4 & 0 \\
4 & 0 & 6 & 0 & 4 \\
0 & 4 & 0 & 2 & 0 \\
3 & 0 & 4 & 0 & 3\end{bmatrix}.$$  

Elements $A_{13}^4$, $A_{15}^4$, and $A_{43}^4$ are non-zero, indicating that the end sites ($a$, $c$, and $a'$) form a contiguous cluster, where $a'$ becomes connected by way of the small-world bond. The graphlet therefore renormalizes into an $R$-type bond. To determine its weight, we note that the sites $a$, $b$, and $c$ are connected via an $R_n$-type bond and the sites $c$, $b'$, and $a'$ form an $S_n$-type bond. Only the right-hand one of the small-world bonds is present. Hence, the total weight of this graphlet in the next generation is $p(1-p)x^2R_n(x)S_n(x, x)/4$. Here, $S_n$ becomes a function of $x$ in both arguments, since the small-world bond merges the previously disconnected clusters $x$ and $y$. The factor $1/4$ is due to the symmetry explained in Ref. [1].

This process is repeated for all 256 graphlets with our automated counting algorithm, where each graphlet is attributed to its appropriate next-generation graphlet. After adding the weights, the generating function recursion relations are found to be [37].
\[ R'(x) = \{ xR(x) + pxU(x,x) + (1-p)U(x,1) \}^2 + 2pxR(x)\{ pxN(x,x,x) + (1-p)N(x,1,x) \} + pxS(x,x)\{ (1-p)[xR(x) + U(x,1)] + 2xR(x) + pxU(x,x) \} + \frac{3}{4}p^2x^2S(x,x)^2, \] (35)

\[ S'(x,y) = \frac{1-p}{2} S(x,y) \{ px^2S(x,x) + py^2S(y,y) + x^2R(x) + y^2R(y) + (1-p)xy[R(x) + R(y)] \] + \{ x + (1-p)y \} U(x,1) + \{ y + (1-p)x \} U(y,1) + p [x + y]^2 U(x,y) + pxN(x,1,x) + pyN(y,1,y) \}
+ \frac{p^2}{2} xyS(x,y)\{ 2U(x,y) + N(x,y,x) + N(y,x,y) + (1-p)N(x,1,y) \} + p[x + y]U(x,y)
+ (1-p)[xR(x) + yR(y) + U(x,1) + U(y,1)] + pxN(x,x,y)\{ (1-p)[xR(x) + U(x,1)] + pyU(y,x) \} + pyN(x,y,y)\{ [yR(y) + U(y,1)] + pxU(x,y) \},

\[ U'(x,y) = \frac{1}{4} px \{ (2-p)x + (2-p)y \} S(x,y)^2 + pxS(x,y)^2 \{ (1-p)N(x,1,y) + pxN(x,y,x) \}, \]

\[ N'(x,y,z) = \frac{1}{4} (1-p)^2 \{ [x + y][y + z] S(x,y) S(y,z) + \frac{1-p}{2} [x + y] S(x,y) \{ (1-p)N(x,1,z) + pxN(y,x,z) \} + \{ (1-p)N(x,1,y) + pxN(y,z) \} \{ (1-p)N(x,1,z) + pxN(y,z) \} \} + \frac{1-p}{2} [y + z] S(y,z) \{ (1-p)N(x,1,y) + pxN(x,z,y) \} \]

Note that for \( x = y = z = 1 \), i.e., when graphlets are counted irrespective of cluster sizes, these equations revert back to those previously listed in Ref. [7].

3. Cluster Generating Function for HN5:

The discussion on how to obtain the RG recursion equations for the cluster generating functions of HN5 parallels that for HN5NP above. The definition of the generating functions in Eqs. [29] as illustrated in Fig. [11] equally apply to HN5. The main difference originates with the structure of small-world bonds, which leads to a planar graph for HN5 and a non-planar graph for HN5NP. Then, our graph counting algorithm results in the following RG recursions:

\[ R'(x) = \{ U(x,1) + xR(x) \}^2 + \frac{1}{2} p^2 x^2 S(x,x)^2 + 2p \{ N(x,1,x)U(x,1) + xS(x,x) \{ (1-p)U(x,1) + pxU(x,x) \} \] + pxR(x)\{ 2(1-p)N(x,1,x) + 2pxN(x,x,x) + (3-p)xS(x,x) - 2U(x,1) + 2xU(x,x) \} (36)

\[ S'(x,y) = (1-p)N(x,1,y)\{ U(x,1) + U(y,1) + (1-p)[xR(x) + yR(y)] \} + p(1-p)\{ x^2R(x)N(x,y,x) + y^2R(y)N(y,x,y) \} + \frac{1-p}{4} S(x,y) \{ px^2S(x,x) + py^2S(y,y) \} + \frac{p(1-p)}{2} \{ x^2[U(x,y) + U(x,x)] + y^2[U(y,y) + U(x,y)] \} + \frac{(1-p)^2}{2} [x + y] \{ U(x,1) + U(y,1) \} + \frac{1-p}{2} [xR(x) [-py + x + y] + yR(y) [-px + x + y]] \]

\[ U'(x,y) = p \{ N(x,1,y) + \frac{1}{2} (1-p) [x + y] S(x,y) \}^2 + p^2 S(x,y) \{ x^2N(x,x,y) + y^2N(x,y,y) \} + \frac{p^2}{4} S(x,y)^2 \{ (1 + p - p^2) x^2 + 2p(1-p)xy + (2-p)p^2 \} \]

\[ N'(x,y,z) = \frac{p(1-p)}{2} \{ S(x,y) \{ x^2N(x,y,x) + y^2N(y,y,z) \} + S(y,z) \{ y^2N(x,y,y) + z^2N(x,z,y) \} \} + \frac{(1-p)^2}{2} \{ [x + y] N(y,1,z)S(x,y) + [y + z] N(x,1,y)S(y,z) \} + \frac{(1-p)}{4} S(x,y)S(y,z) \{ (1-p) [xy + xz + yz] + y^2 \} + (1-p)N(x,1,y)N(y,1,z) \]

Again, these equations revert back to those previously listed in Ref. [7] for \( x = y = z = 1 \).

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