Cumulative Merging Percolation: A long-range percolation process in networks

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Percolation on networks is a common framework to model a wide range of processes, from cascading failures to epidemic spreading. Standard percolation assumes short-range interactions, implying that nodes can merge into clusters only if they are nearest-neighbors. Cumulative Merging Percolation (CMP) is an new percolation process that assumes long-range interactions, such that nodes can merge into clusters even if they are topologically distant. Hence in CMP percolation clusters do not coincide with the topological connected components of the network. Previous work has shown that a specific formulation of CMP features peculiar mechanisms for the formation of the giant cluster, and allows to model different network dynamics such as recurrent epidemic processes. Here we develop a more general formulation of CMP in terms of the functional form of the cluster interaction range, showing an even richer phase transition scenario with competition of different mechanisms resulting in crossover phenomena. Our analytic predictions are confirmed by numerical simulations.

I. INTRODUCTION

Percolation theory is among the most developed fields of statistical mechanics and mathematical physics. A percolation process can be defined as follows: We have a collection of elements and some connections among them. This object is called a *graph*, the elements are called *vertices* (or *nodes*) and the connections are called *edges* (or *links*). We then remove some nodes according to a certain probabilistic or deterministic rule. For instance, we can remove all nodes with more than a given number of connections, or we can remove nodes uniformly at random. At the end of the removal process we wonder about which connectivity properties are preserved. The main problem of percolation theory is to understand if a giant component (GC), that is a connected component of extensive size, still exists in the graph after the removal process.

Originally, percolation was studied on various types of low-dimensional lattices. The powerful methods of statistical mechanics of phase transitions and critical phenomena, such as mean-field approximations, renormalization group, asymptotic expansions and scaling theory, provide us with a complete understanding of the percolation process on regular lattice topologies [1]. In the past 20 years, the interest about complex networks has led to a great deal of activity concerning percolation processes on graphs [2–6].

Percolation processes are used to model a wide range of natural phenomena, just by changing the underlying graph or the probabilistic rule that determines the removal of nodes. For instance, percolation on a regular lattice can model transport processes in porous media, such as electrical and hydraulic conduction, air permeability and diffusion [7]. On the other hand, percolation on random graphs [8] can be used to investigate the robustness of a networked system under intentional or random attacks [2]. Additionally, a deep connection exists between perco-

lation and epidemic spreading. Indeed, the fundamental susceptible-infected-recovered (SIR) epidemic model on networks [9] can be mapped onto a bond percolation process [10]. Such a mapping allows to use the tools of percolation theory to get a full understanding of static properties of the SIR model. For epidemic processes which admit a stationary steady state, such as the susceptible-infected-susceptible (SIS) model, this mapping is less immediate, and has been realized only through a new percolation model recently proposed [11].

Such a model, called cumulative merging percolation (CMP), is a truly long-range percolation process. This specification (long-range percolation) is often used for models where, in a lattice, additional links connecting sites separated by any euclidean distance are added, with a probability depending on the distance [12, 13]. In CMP instead, distances are only topological and two nodes can belong to the same cluster even if no path of nearest-neighbor nodes connecting them belongs to the cluster itself. Models of similar type, called extended-neighborhood percolation models, have been studied on regular lattices [14–17]. In such models percolation clusters do not need to coincide with topologically connected components, as two nodes may form a cluster even if they are not nearest-neighbors but separated by paths of *finite* length (typically 2 or 3). In CMP this length can be arbitrarily large.

CMP has been recently studied in a specific *degree-ordered* case [18] to elucidate the behavior of the SIS model on random uncorrelated networks with power-law degree distribution $P(k) \sim k^{-\gamma}$. By means of a scaling approach and numerical simulations, it was shown that the long-range nature of the model guarantees, for any $\gamma > 2$, the existence of a percolating cluster for any value of the control parameter (i.e., the degree threshold that determines node removal), at variance with what happens for the short-range counterpart [19, 20]. The aim of

the present work is to define in full generality CMP on networks. We present a scaling theory that extends the one introduced in Ref. [18] to more general forms of the *interaction range*. We then consider in detail two paradigmatic functional forms of the interaction range, deriving predictions concerning the existence of a phase-transition at finite or infinite value of the control parameter and the associated critical behavior. We obtain a rich scenario with competition of different mechanisms resulting in crossover phenomena, which is confirmed by means of numerical simulations.

The paper is organized as follows: In Sec. II, we first define the CMP process in the most general form and present the detailed specifications considered in the rest of the paper. In Sec. III we write a general scaling approach used to analyze the process. Sec. IV is dedicated to a detailed analysis of two classes of CMP, characterized by algebraically and logarithmically growing interaction range. Finally, in Sec V, we summarize our main results and present some possible future research paths.

II. CUMULATIVE MERGING PERCOLATION

In classical (short-range) percolation, a cluster coincides with a topologically connected component C, i.e., a subset of nodes such that for any two nodes i and j there exists a path connecting them, made of nearest-neighboring nodes belonging to C. Thus, for instance, if all nearest neighbors of a node are removed, this node cannot be a part of any cluster – except the one formed by itself only. In order to introduce a long-range model, we need to go beyond such a definition. In this section, we define a general procedure to define clusters that may be composed of *topologically disconnected and arbitrarily distant* components.

A. General definition

We denote a graph by $\mathcal{G}(V, E)$, where V is the set of nodes and E is the set of edges. Each node $i \in V$ is endowed with a non-negative mass $m_i \geq 0$. The mass of the set composed by two nodes i and j is given by the sum of their masses

$$m = m_i + m_j. \tag{1}$$

A *partition* of the graph $\mathcal{P}(\mathcal{G})$ is a collection of subsets of nodes

$$\mathcal{P}(\mathcal{G}) = \{A\}_{A \subseteq V}$$

such that: (i) the sets in $\mathcal{P}$ cover V; (ii) every element in V belongs to exactly one subset in $\mathcal{P}$. Each element of $\mathcal{P}$ is called *cluster*, denoting with C_i the cluster to which node i belongs. Notice that by definition each node belongs only to one cluster. Because of Eq. (1), the mass of a cluster is the sum of the masses of all nodes belonging to it. We define the *interaction range* of a cluster to be

a non-decreasing function of its mass, $r(m)$. We stress that these clusters need not be topologically connected components.

Given a pair of nodes (i, j), the *merging operator* $M_{i,j}$, acting on the space of all partitions of the graph, merges the two clusters C_i and C_j if and only if

$$d_{i,j} \leq \min\{r(m_{C_i}), r(m_{C_j})\}; \tag{2}$$

where $d_{i,j}$ is the topological distance between i and j. If the condition eqrefmarging is not fulfilled, the merging operator leaves the two clusters unaltered. Notice that the merging occurs only if node i is within the interaction range of the cluster C_j and vice-versa, and that two clusters may be merged together even if they are at arbitrary topological distance with each other, provided the interaction ranges are sufficiently large.

We define the *cumulative merging procedure* as follows:

1. fix an infinite sequence $(i_t, j_t)_{t \in \mathbb{N}}$ of pairs of nodes of V;

2. start from the finest partition $\mathcal{P}^0 := \{\{i\}, i \in V\}$;

3. iteratively apply the merging operator

$$\mathcal{P}^{t+1} = M_{i_t, j_t}(\mathcal{P}^t). \tag{3}$$

The asymptotic partition

$$\mathcal{P}^\infty := \lim_{t \to \infty} \mathcal{P}^t, \tag{4}$$

depends, in principle, on the sequence $(i_t, j_t)_{t \in \mathbb{N}}$. Consider for instance the case in which all nodes have an infinite interaction range, except node a and node b, which are distant nodes with small interaction range. The sequence $(i_t, j_t) = (a, b)$ for every t leads to $\mathcal{P}^\infty = \mathcal{P}^0$, while it is immediate to realize that $\mathcal{P}^\infty$ will be different for other sequences. A way to overcome this difficulty is to consider only *recurrent* sequences: we say that the sequence $(i_t, j_t)_{t \in \mathbb{N}}$ is *recurrent* if $\{i_t, j_t\} = \{k, l\}$ infinitely many times, for every $k, l \in V$ with $k \neq l$. An important result on the asymptotic partition, whose proof can be found in Ref. [11], guarantees that the cumulative merging procedure is well defined, i.e. sequence-independent, provided that the sequence is recurrent.

In summary, given a graph, a collection of node masses, and the function $r(m)$, the cumulative merging procedure generates a unique partition of the graph in clusters, not necessarily topologically connected. Notice that nodes with $r(m_i) < 1$ by construction do not play any role (i.e., they necessarily form clusters of size 1), apart from determining the topological distances among other nodes. We denote them as *inactive*, while nodes with $r(m_i) \geq 1$ are *active*, as they may participate in merging events and form clusters of size larger than 1.

The CMP model defined above can be seen as a percolation process: Depending on the function $r(m)$, the node masses and the underlying graph, the asymptotic partition may be composed of microscopic clusters only

or include a giant cluster encompassing a finite fraction of the total number of nodes. It is a long-range percolation model because clusters may be composed by different and arbitrarily distant topologically connected components. This is qualitatively different from extended-range percolation models which allow only finite distances between disconnected components.

B. A specific class of CMP models

Following Refs. [11, 18], we set node masses to be equal to their degree, i.e. $m_i = k_i$. In this way, the mass of a cluster is the sum of the degrees of the nodes that belong to it. Moreover, we take the interaction range to be a function of the ratio between m and a parameter k_a, that plays the role of control parameter in the percolation problem,

$$r(m) = f(m/k_a), \qquad (5)$$

where $f(x)$ is a non-decreasing function, with $f(1) = 1$ and $f(x) < 1$ for $x < 1$. According to this definition all nodes with degree $k_i < k_a$ have interaction range $r < 1$ and are thus inactive. Nodes with degree larger than or equal to k_a are active.

In this way percolation occurs in a *degree-ordered* way: Increasing the control parameter k_a is equivalent to removing nodes of increasingly higher degree. For the minimal value $k_a = k_{\min}$, all nodes are active and hence the clusters coincide with the components of the underlying graph. For large $k_a \to \infty$ the number of active nodes gets smaller and smaller and the nontrivial question is whether an extensive cluster still exists. With all these specifications, given a network and the value of k_a, the final partition of the CMP is univocally defined. Fig. 1 reports an example of how the CMP process unfolds and what is the final partition of the graph.

Other choices for the initial masses, the interaction range and the underlying graph are possible, leading to a wealth of different models with different critical properties. For example, if $r(m) = 1$, for any $m \geq 1$, CMP coincides with standard site percolation, either in its degree-ordered version [19, 20], if the initial mass of node i is $m_i = k_i \Theta(k_i - k_a)$, or in its random version, if $m_i = k_i$ with probability ϕ and 0 otherwise. Taking instead a generic interaction range $r(m)$ and again $m_i = k_i$ with probability ϕ and 0 otherwise, one has a truly long-range CMP with random activation. The investigation of these and other variants constitutes an interesting avenue for future research.

In the following we study this class of degree-ordered CMP processes on power-law degree-distributed networks, described by uncorrelated random graphs with degree distribution, in the continuous approximation,

$$P(k) = (\gamma - 1)k_{\min}^{\gamma-1} k^{-\gamma} \qquad (6)$$

where $\gamma > 2$ and $k_{\min}$ is the minimum degree of nodes in the network.
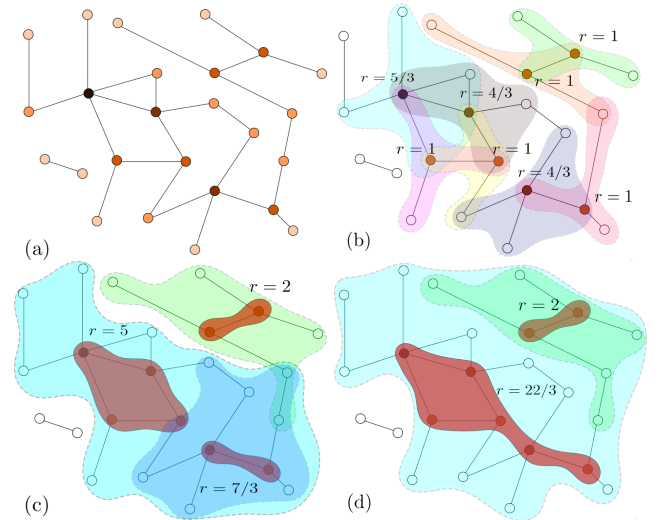

FIG. 1. Visual representation of a CMP process on a graph with $k_a = 3$ and $r(m) = m/k_a$. (a) All nodes in the graph are shown. Colors depend on the degree k. (b) Initial configuration of the merging process, with $k_a = 3$, each node forming a cluster. Empty circles are inactive nodes. Colored dashed regions represent the interaction range of each active node. (c) Intermediate configuration of the merging process. Dark red regions represent clusters. (d) Final configuration of the merging process. From (c) to (d) the long-range nature of the process plays a crucial role. Note that the process ends since the interaction range of the cluster with $r = 2$ does not reach any node of the cluster with $r = 22/3$.

Our aim is to investigate the formation of a CMP giant cluster (CMPGC) [1]. Hence we focus on the quantity S_{CMP}, defined as the fraction of nodes belonging to the CMP largest cluster, as a function of the control parameter k_a. In percolation theory it is customary to consider the fraction of active (non removed) nodes, namely ϕ, as control parameter. In the large N limit,

$$\phi = \frac{N_a}{N} = \int_{k_a}^{\infty} dk P(k) = \left(\frac{k_a}{k_{\min}}\right)^{1-\gamma}, \qquad (7)$$

where N_a is the number of active nodes. From this equation, it follows that we can express S_{CMP} as a function of ϕ by just replacing $k_a/k_{\min}$ with $\phi^{1/(1-\gamma)}$. In particular, the behavior for large k_a corresponds to the behavior for small fraction ϕ of active nodes. Defining ϕ_c as the threshold value at which a macroscopic CMPGC first appears, we expect that, close to the transition

$$S_{\text{CMP}} \sim (\phi - \phi_c)^\beta, \qquad (8)$$

where β is a characteristic exponent. In the case $\phi_c = 0$, we expect

$$S_{\text{CMP}} \sim \phi^\beta \sim k_a^{\beta(1-\gamma)}, \qquad (9)$$

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[1] This object was called CMP giant component in Ref. [18]. We prefer to change denomination here to stress the difference between topologically connected components and CMP clusters.

that is, a decay of the CMPGC size as a function of k_a.

III. GENERAL SCALING THEORY FOR DEGREE-ORDERED CMP

A. CMP for $\gamma \leq 3$

A simple observation allows us to characterize the behavior of S_{CMP} on networks with $2 < \gamma \leq 3$. The short-range counterpart, i.e. with $r(m) = 1$, of the CMP as defined above is called *degree-ordered percolation* (DOP). Its behavior on power-law distributed networks has been studied in Refs. [19, 20], where a detailed investigation of the critical properties of the DOP giant component (DOPGC) can be found. In particular, it has been shown that:

- for $\gamma \leq 3$ a DOPGC always exists for any finite value of k_a;

- for $\gamma > 3$, a DOPGC exists only up to a finite critical point $(k_a)_c^{\mathrm{DOP}}$.

From this result we can infer that for $\gamma \leq 3$ a CMPGC always exists for every value of k_a. Indeed, since the DOPGC is always a subset of the CMPGC, it follows that $S_{\mathrm{DOP}} \leq S_{\mathrm{CMP}}$ for every k_a, and since the short-range model has an infinite critical point, so has the long-range model. Furthermore, essentially all active nodes belong to the DOPGC [18] and thus

$$S_{\mathrm{CMP}} \simeq \left(\frac{k_a}{k_{\min}} \right)^{1-\gamma} . \tag{10}$$

Notice that this result is valid in full generality as long as $r(m)$ is a non-decreasing function. Instead, for $\gamma > 3$ the DOP has a transition to a phase with no giant component at $(k_a)_c^{\mathrm{DOP}}$ and this does not allow us to draw any conclusions a priori on S_{CMP} for large k_a. In the following section, we develop a general scaling theory to understand the behavior of S_{CMP} for $\gamma > 3$.

B. CMP for $\gamma > 3$

Following [18], we identify two different mechanisms that may contribute to the formation of a CMPGC:

A: Extended DOP mechanism: it is essentially an extension of the DOP process involving the merging of DOP clusters separated by distances larger than 1;

B: Merging of distant isolated nodes: it works for high values of k_a when essentially all active nodes are isolated and, on average, at large distance from each other.

We compute the scaling of the order parameter S_{CMP} with k_a due to each mechanism separately, and we identify the ranges of k_a values where one of them dominates over the other.

1. Extended DOP mechanism

In the DOP model for $\gamma > 3$ there is an extensive giant cluster for k_a up to $(k_a)_c^{\mathrm{DOP}}$. Above this threshold no DOP cluster is extensive. In the CMP model, due to the interaction range extending beyond 1, DOP clusters may merge and this may lead to the formation of a CMPGC even for $k_a > (k_a)_c^{\mathrm{DOP}}$. The most natural candidates for this merging are small clusters at distance 2 from each other or massive isolated nodes at distance 2 from small clusters. We consider these two contributions separately.

If two small clusters are topologically isolated but at distance 2 from each other, the two clusters merge provided their interaction range is larger than their relative distance. The merging of small clusters at distance 2 may then make possible the merging of other, more distant small clusters and so on. Assuming that in this way all N_{NI} topologically nonisolated nodes enter the CMPGC, this mechanism gives a largest cluster of size (see Ref. [18] for details)

$$\frac{N_{\mathrm{NI}}}{N} \simeq \left(\frac{k_a}{k_{\min}} \right)^{1-\gamma} \left[\frac{\gamma-1}{\gamma-2} k_{\min} \left(\frac{k_a}{k_{\min}} \right)^{3-\gamma} \right]$$
$$= \langle k \rangle \left(\frac{k_a}{k_{\min}} \right)^{2(2-\gamma)} . \tag{11}$$

The plausibility of this assumption strongly depends on the shape of the function $f(x)$ in Eq. (5) and on the value of k_a. If $f(x)$ grows as x or faster, a cluster of two nodes has by definition an interaction range equal at least to 2. Hence such a cluster can merge if at distance 2 from another cluster. If instead $f(x)$ grows more slowly the interaction range of a cluster formed by two adjacent nodes may be smaller than 2, and the extended DOP mechanism becomes ineffective. In such a case Eq. (11) is a rough overestimation of the largest cluster size. In addition, for small k_a there are many active nodes and it is plausible that distances among connected clusters are small. For large k_a instead, clusters will tend to be at larger distances from each other, and an interaction range equal to 2 will not be sufficient to guarantee the merging.

In a similar way, we can argue that also an isolated node can merge with a DOP cluster at distance 2 from it, if it is massive enough so that its interaction range is at least 2. If we define k_e the value of k such that $r(k_e) = 2$, and assume that all isolated nodes with degree $k \geq k_e$ become in this way part of the CMPGC, we can estimate S_{CMP} as the fraction of isolated nodes with $k \geq k_e$. Following [18], considering that k_e is proportional to k_a, and taking the

limit $k_a \gg k_{\min}$, we have [18]

$$\frac{N_{r\geq2}}{N} \sim \left(\frac{k_e}{k_{\min}}\right)^{1-\gamma} \left[1 - \frac{\gamma-1}{\gamma-2}\frac{k_e}{k_c}\right], \qquad (12)$$

an expression that is also a clear overestimate of the true contribution, getting worse for large k_a.

Summing up the two contributions we obtain

$$S_{\mathrm{CMP}}^{(1)} \simeq \frac{N_{\mathrm{NI}}}{N} + \frac{N_{r\geq2}}{N}. \qquad (13)$$

Since the decay of $N_{r\geq2}/N$ with k_a is slower than the decay of N_{NI}/N, the first term in Eq. (13) dominates, in principle, only up to a crossover scale k_1^*, which depends on γ and on the detailed functional form of the interaction range. However, as noticed in [18], one does not expect to actually observe such a crossover as for asymptotically large k_a this mechanism cannot be active. Indeed, for small values of k_a (many active nodes), distances between small clusters are typically small, favoring the merging process. As k_a is increased, in particular beyond $(k_a)_c^{\mathrm{DOP}}$, typical distances between active nodes grow larger and the extended DOP mechanism is strongly suppressed. Therefore, we can assume the contribution of the extended DOP mechanism to the size of the CMPGC to be

$$S_{\mathrm{CMP}}^{(1)} \simeq \langle k \rangle \left(\frac{k_a}{k_{\min}}\right)^{2(2-\gamma)} \qquad (14)$$

up to a finite value of k_a.

2. Merging of distant isolated nodes

An additional mechanism, which can be at work for arbitrarily large k_a, involves the formation of clusters resulting from the cumulative merging of massive distant nodes, with no role played by topologically connected clusters. The average distance between a node of degree k and its closest node with degree at least k is given by [18]

$$d(k) \simeq 1 + a(\gamma)\ln\left(\frac{k}{k_{\min}}\right), \qquad (15)$$

where

$$a(\gamma) = \frac{\gamma-3}{\ln(\kappa)} \qquad (16)$$

and $\kappa = \langle k^2 \rangle / \langle k \rangle - 1$ is the network branching factor. If $r(k) \geq d(k)$, these two nodes merge in a single CMP cluster. For this reason, if $r(k)$ grows with k faster than $d(k)$, all nodes with a degree larger than k_x, where k_x is the solution of the equation

$$r(k_x) = d(k_x), \qquad (17)$$

will be part of the same CMP cluster and

$$S_{\mathrm{CMP}}^{(2)} = \int_{k_x}^{\infty} dk\, P(k) = \left(\frac{k_x(k_a)}{k_{\min}}\right)^{1-\gamma}. \qquad (18)$$

Notice that, since $r(m)$ depends on k_a, also k_x is a function of k_a.

If instead $r(k)$ grows, for large k, more slowly than $d(k)$ then isolated massive nodes are too far away from each other and this mechanism does not activate. In such a case, since no mechanism is active for diverging k_a, the CMP threshold is necessarily finite.

3. Crossover between the two mechanisms

If Eq. (17) has a solution then the CMP asymptotic regime for large k_a is described by Eq. (18). As we will see in specific examples below, the asymptotic behavior may be preceded by an interval of k_a values where the extended DOP mechanism dominates. In such a case the asymptotic regime is reached after a crossover at a degree value k_2^* given by the solution of the equation

$$S_{\mathrm{CMP}}^{(1)}(k_2^*) = S_{\mathrm{CMP}}^{(2)}(k_2^*). \qquad (19)$$

Notice that, since Eq. (14) is an overestimate of the first contribution due to the extended DOP mechanism, the solution of Eq. (19) is actually an upper bound of the true crossover scale k_2^*.

The picture presented above is valid in networks of infinite size. In numerical simulations on finite networks the asymptotic regime can be actually observed for large k_a only if the system is large enough that the maximum degree $k_{\max}(N)$ is much larger than k_2^*. For random graphs with $\gamma > 3$, generated using the Uncorrelated Configuration Model (UCM) [21], the maximum degree scales with N as $k_{\max} \sim N^{1/(\gamma-1)}$. Hence, to observe the asymptotic regime it is necessary that $N \gg N_2^*$, where $N_2^* = k_2^{*(\gamma-1)}$. For the particular form of $r(m)$ describing SIS epidemic dynamics this value is much larger than the sizes that can be simulated; as a consequence in Ref. [18] only the preasymptotic extended DOP regime was observed. We will see below that for various forms of the function $r(m)$ the truly asymptotic regime can be cleanly observed in simulations.

The finite size of networks considered in simulations induces also the presence of a size-dependent effective threshold $(k_a)_c^{\mathrm{CMP}}(N)$ even if there is no threshold in the limit of infinite network size. This must be kept in mind when interpreting simulation results. See Appendix A for details.

IV. RESULTS FOR TWO SPECIFIC FORMS OF THE INTERACTION RANGE

In this Section we analyze in detail what happens for two specific choices of the functional dependence of the interaction range $r(m)$ on the mass. In each case, after deriving the predictions of the scaling theory we compare them with the results of numerical simulations of the CMP process. These were performed by considering random

networks built according to the UCM algorithm [21] with minimum degree $k_{\min} = 3$ and various sizes N. To avoid the strong sample-to-sample fluctuations in the value of the maximum degree [22] we extracted the degree distribution imposing the degrees to be strictly constrained between $k_{\min}$ and $N^{1/(\gamma-1)}$.

A. Algebraically growing interaction range

In this subsection we consider an interaction range growing algebraically with the cluster mass

$$r(m) = \left(\frac{m}{k_a}\right)^\alpha, \qquad (20)$$

where $\alpha > 0$ is a fixed parameter. The case $\alpha = 1$ corresponds to the linear case studied in Ref. [18].

The effectiveness of the extended DOP mechanism strongly depends on the value of α. For $\alpha \geq 1$ a cluster of size 2 has an interaction range at least equal to 2 and it can merge with another cluster if at distance 2 from it. Moreover, also isolated nodes with $k > k_e = 2^{1/\alpha} k_a$ and distance equal to 2 merge with DOP clusters. Instead if $\alpha < 1$ the above statements are no longer true, and only sufficiently massive clusters or isolated nodes at distance 2 may participate to merging events. In such a case Eq. (13) is an overestimation of the size of the CMP largest cluster.

Concerning the second mechanism, since $r(m)$ grows algebraically, and the average distance grows logarithmically, the interaction range is, asymptotically, always larger than the distance. Hence the equation $r(k_x) = d(k_x)$ always has a solution, and the second mechanism is active for sufficiently large degrees, no matter the value of α. Setting $k_x = \omega k_a$, from Eq. (17) we have the transcendental equation

$$\omega^\alpha = 1 + a(\gamma) \ln(\omega) + \ln\left(\frac{k_a}{k_{\min}}\right) \qquad (21)$$

which can be solved for ω as (see Appendix B)

$$\omega(k_a) = \frac{e^{-\frac{1}{a(\gamma)}}}{k_a/k_{\min}} \exp\left[-\frac{1}{\alpha} W_j\left(-\frac{\alpha e^{-\frac{\alpha}{a(\gamma)}}}{a(\gamma)}\left(\frac{k_a}{k_{\min}}\right)^{-\alpha}\right)\right], \qquad (22)$$

where $W_j(z)$ is the Lambert W or product logarithm function [23]. The branch corresponding to the physical solution is the one with $j = -1$, since the branch with $j = 0$ implies $\omega \to 0$ as $k_a \to \infty$, in contradiction with the requirement that $k_x \geq k_a$. Expanding $W_{-1}(z)$ for small argument (that is for $k_a \gg k_{\min}$), we get, see Appendix B,

$$\omega \simeq \left[1 + \frac{a(\gamma)}{\alpha} \ln\left(\frac{a(\gamma)}{\alpha}\right) + a(\gamma) \ln\left(\frac{k_a}{k_{\min}}\right)\right]^{1/\alpha}. \qquad (23)$$

Thus we end up, neglecting constants and terms of lower order, with a CMPGC of size

$$S_{\mathrm{CMP}}^{(2)} \sim \left[a(\gamma) \ln\left(\frac{k_a}{k_{\min}}\right)\right]^{(1-\gamma)/\alpha} \left(\frac{k_a}{k_{\min}}\right)^{1-\gamma}. \qquad (24)$$

Eq. (24) is in agreement with the results in [18], which are recovered setting $\alpha = 1$. We see that the introduction of an exponent α tuning the interaction range does not change the critical exponent $\beta = 1$, but only modifies logarithmic corrections.

To calculate the crossover degree k_2^*, inserting Eq. (14) and Eq. (18), evaluated for $k_a = k_2^*$ into Eq. (19) we obtain, after some transformations,

$$k_2^* = k_{\min} \left[\frac{\bar{\omega}^{1-\gamma}}{\langle k \rangle}\right]^{\frac{1}{3-\gamma}}, \qquad (25)$$

where $\bar{\omega}$ is the solution of

$$\bar{\omega} = \left[1 + \frac{1}{\ln(\kappa)} \ln\langle k \rangle + b(\gamma) \ln(\bar{\omega})\right]^{1/\alpha}, \qquad (26)$$

where we have defined

$$b(\gamma) = \frac{2(\gamma-2)}{\gamma-3} a(\gamma) = \frac{2(\gamma-2)}{\ln(\kappa)}. \qquad (27)$$

The equation for $\bar{\omega}$ can be solved analytically by using the Lambert W function with the same strategy developed in Appendix B. Alternatively, we can solve numerically Eq. (26) as a fixed point equation for $\bar{\omega}$, and then insert this value in Eq. (25). Fig. 2 shows that the minimum graph size N_2^* needed to observe the second mechanism at work is indeed much beyond values that can be considered in practice when $\alpha \leq 1$, while it attains feasible values for $\alpha > 1$ and γ close to 4.

Numerical simulations of the CMP process (see Fig. 3) confirm the analytical predictions. For $\alpha = 0.5$ and $\gamma = 3.7$ the crossover to the asymptotic behavior happens at $N_2^* \sim 10^{25}$ (k_2^* is of the order of 10^{10}). We thus have only access to the first regime, dominated by the extended DOP mechanism. Indeed, as predicted by Eq. (14), the order parameter S decays with an exponent $2(2-\gamma)$ that extends well beyond the DOP threshold. For $\alpha = 5$ and $\gamma = 4$ instead the crossover value is predicted to be $k_2^* \approx 23$. Correspondingly we observe, for $N \gg N_2^* \approx 10^4$, the asymptotic decay to be well described by Eq. (24). Notice that in this case also the logarithmic correction is necessary to match the decay.

B. Logarithmically growing interaction range

Another interesting class of CMP processes is the one described by an interaction range growing logarithmically with the mass, that is

$$r(m) = 1 + \delta \ln\left(\frac{m}{k_a}\right), \qquad (28)$$

where $\delta > 0$ is a parameter tuning how fast the range increases.

In this case, since the interaction range grows only logarithmically with the cluster mass, the asymptotic ineffectiveness of the extended DOP mechanism is expected
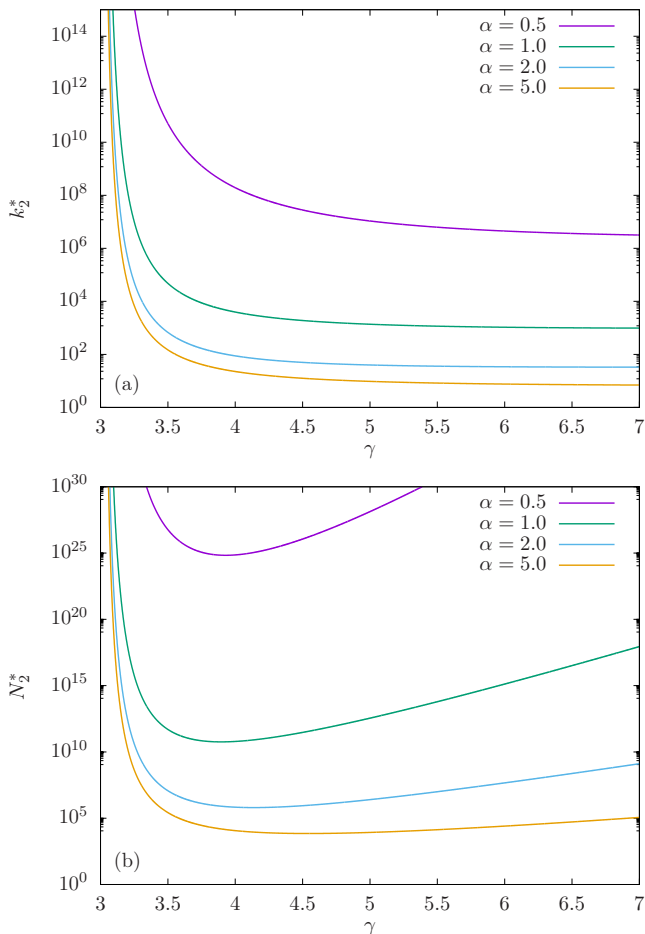
FIG. 2. Analytical results for algebraically growing interaction range. Plot of k_2^* (a) and N_2^* (b) as a function of γ for algebraically growing interaction range and several values of α.
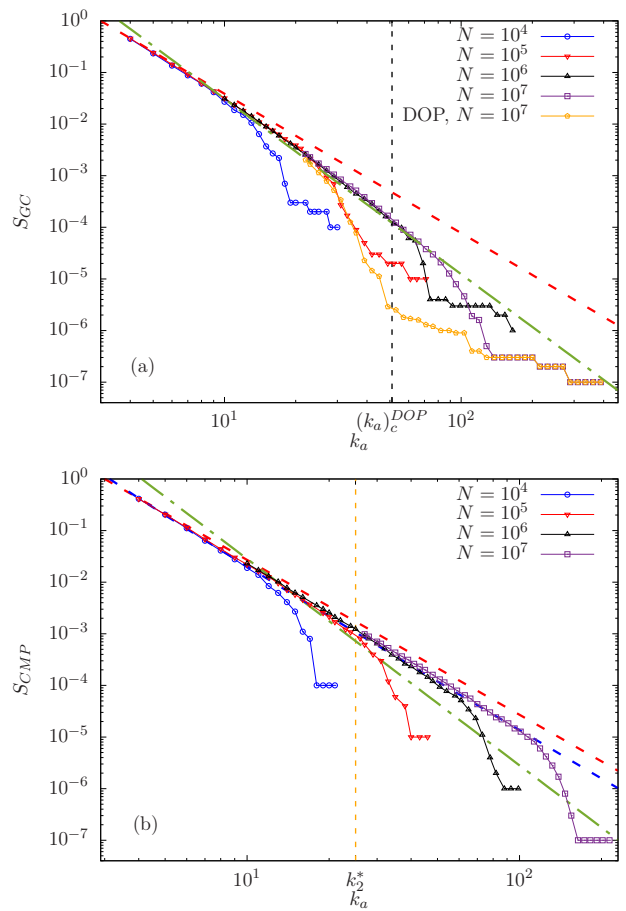

FIG. 3. Comparison of analytical and simulation results for the size of the CMP largest cluster as a function of k_a, for algebraically growing interaction range and different combinations of γ and α values: (a) $\gamma = 3.7$ and $\alpha = 0.5$; (b) $\gamma = 4$ and $\alpha = 5$. The red dashed line is the scaling with exponent $1 - \gamma$, the green dot-dashed line is the scaling with exponent $2(2 - \gamma)$ and the blue dashed line is the prediction of $S_{\mathrm{CMP}}^{(2)}$ given by Eq. (18) where $k_x = \omega k_a$ and ω is given by Eq. (22). In panel (a) we also report the results of a simulation of the DOP process on the network with size $N = 10^7$.

to be even more severe than in the previous case for $\alpha < 1$. Concerning the merging of massive isolated distant nodes, since in this case both $r(m)$ and $d(k)$ grow logarithmically, it is not always true that a degree k_x exists such that $r(k) \geq d(k)$ for $k \geq k_x$. This condition holds when

$$\delta \ln\left(\frac{k}{k_a}\right) \geq a(\gamma) \ln\left(\frac{k}{k_a}\right) + a(\gamma) \ln\left(\frac{k_a}{k_{\min}}\right). \quad (29)$$

This implies that k_x exists only if

$$\delta > a(\gamma). \quad (30)$$

This result indicates a completely different phenomenology from the one found in Section IV A. The critical line $\delta = a(\gamma)$ divides the (δ, γ) plane in two regions (see Fig. 4): For $\delta > a(\gamma)$, the mechanism responsible for the merging of distant isolated nodes of large degree is active for large k_a; below $\delta = a(\gamma)$ instead, the interaction range grows too slowly with respect to the average distance between nodes of degree k and hence the merging of all massive isolated nodes in a single CMP cluster does not occur. As

a consequence, we can argue that for $\delta > a(\gamma)$ the CMP has an infinite threshold, while for $\delta < a(\gamma)$ the order parameter S_{CMP} must go to zero at some finite critical value $(k_a)_c^{\mathrm{CMP}}$.

In the region $\delta > a(\gamma)$, we can solve the equation for $\omega = k_x/k_a$ and compute the size $S_{\mathrm{CMP}}^{(2)}$. We have

$$\delta \ln(\omega) = a(\gamma) \ln(\omega) + a(\gamma) \ln\left(\frac{k_a}{k_{\min}}\right), \quad (31)$$

from which it follows

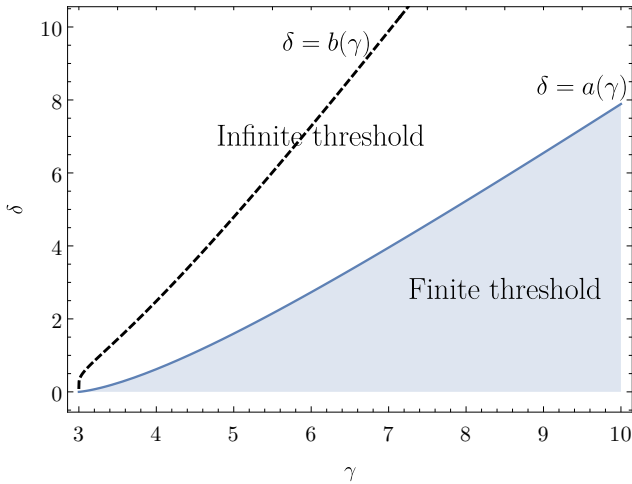$$k_x = \omega k_a = \left(\frac{k_a}{k_{\min}}\right)^{a(\gamma)/[\delta - a(\gamma)]} k_a. \quad (32)$$

FIG. 4. Phase diagram of CMP with logarithmically growing interaction range in the (δ, γ) plane. In the shadowed region below the blue solid line, the second mechanism does not activate at all. In the region between the solid and dashed lines the second mechanism activates, but it is subleading compared to the first mechanism (as long as the first mechanism is at work). Above the dashed line the second mechanism activates and is leading with respect to the extended DOP mechanism.

Inserting the last expression into Eq. (18)

$$S_{\text{CMP}}^{(2)} \simeq \left(\frac{k_a}{k_{\min}} \right)^{\frac{(1-\gamma)\delta}{[\delta-a(\gamma)]}}. \tag{33}$$

Hence we find that the critical exponent

$$\beta = \frac{\delta}{\delta - a(\gamma)} \tag{34}$$

(see Eq. (9)) is a continuously changing function of the parameters γ and δ.

Also Eq. (19) for the crossover scale k_2^* can be exactly solved in this case. Inserting the expressions (14) and (33) into Eq. (19) and performing straighforward calculations we obtain

$$k_2^* = k_{\min} \langle k \rangle^{\mu(\gamma,\delta)}, \tag{35}$$

where

$$\mu(\gamma,\delta) = \frac{\delta - a(\gamma)}{(\gamma - 3)[\delta - b(\gamma)]}. \tag{36}$$

See Fig. 5 for a plot of the function $\mu(\gamma, \delta)$.

The expression for k_2^* in Eq. (35) actually applies only for $\delta > b(\gamma)$. Indeed, as discussed above, for $\delta < a(\gamma)$ the merging of distant nodes is not active. Hence the CMP model is practically identical to DOP and we expect $(k_a)_c^{\text{CMP}} \approx (k_a)_c^{\text{DOP}}$. For $a(\gamma) < \delta < b(\gamma)$, instead, the second mechanism activates asymptotically but it is subleading with respect to the first. In this case the extended DOP mechanism dominates for small values of k_a but,

being asymptotically ineffective, at some point the second mechanism takes over. This crossover does not occur at the k_2^* predicted by Eq. (35) (which is smaller than $k_{\min}$ in this case) but where the extended DOP mechanism stops working. For $\delta > b(\gamma)$, we have at k_2^* a true crossover between the two mechanisms: The merging of distant isolated nodes governs the asymptotic behavior of S_{CMP}. As we can see in Fig. 5, plotting k_2^* and N_2^* as a function of γ in the region $\delta > b(\gamma)$ shows that for small values of δ the crossover is largely out of reach in simulations; instead for larger values of δ, N_2^* is strongly reduced and hence it is possible to observe the asymptotic regime in simulations.

Results of numerical simulations, reported in Fig. 6, confirm this overall picture. In Fig. 6(a), corresponding to $\delta < a(\gamma)$, the behavior of CMP practically coincides with that of DOP. For $a(\gamma) < \delta < b(\gamma)$, Fig. 6(b), the extended DOP mechanism dominates, up to a finite threshold. The true asymptotic behavior here is the one predicted by Eq. (33), but it would be observed only for much larger system size N. For $\delta > b(\gamma)$ instead, S_{CMP} nicely follows the asymptotic prediction of Eq. (33), after the crossover scale.

Finally, let us point out that the behavior of the CMP model as $\delta \to a(\gamma)^-$ is nontrivial. Let us consider a fixed value of γ. For $\delta = 0$ the DOP process has a finite critical point $(k_a)_c^{\text{DOP}}$. For $\delta > a(\gamma)$, we have instead an infinite critical point and a CMPGC always exists. What happens in the intermediate region? How does the finite critical point $(k_a)_c^{\text{CMP}}$ change in the region as a function of δ? We know that $(k_a)_c^{\text{CMP}} \to (k_a)_c^{\text{DOP}}$ as $\delta \to 0$, but what happens for $\delta \to a(\gamma)^-$? As long as $\delta < a(\gamma)$ the merging of distant isolated nodes is not at work for large degrees. Hence the transition is governed by the extended DOP mechanism and occurs not far from the DOP critical point. As a consequence, we expect $(k_a)_c^{\text{CMP}}$ to be a discontinuous function of δ at fixed γ, jumping from a finite value to ∞ when δ reaches $a(\gamma)$. A direct numerical verification of this conjecture is however impossible, due to finite-size effects.

V. DISCUSSION AND CONCLUSIONS

In this paper, extending the work of Refs. [11, 18], we introduced a general formulation for a new class of percolation processes in networks, dubbed cumulative merging percolation (CMP), characterized by the fact that nodes belonging to a cluster need not be topologically connected. Clusters are instead defined via an iterative procedure that may merge network subsets even if they are far apart in the network. In this sense CMP is a long-range percolation process, qualitatively different from extended-neighborhood processes, which have only a finite interaction range. We then considered a specific subclass of CMP models, characterized by node masses equal to node degrees and a degree-ordered activation of nodes. This class generalizes the CMP model introduced
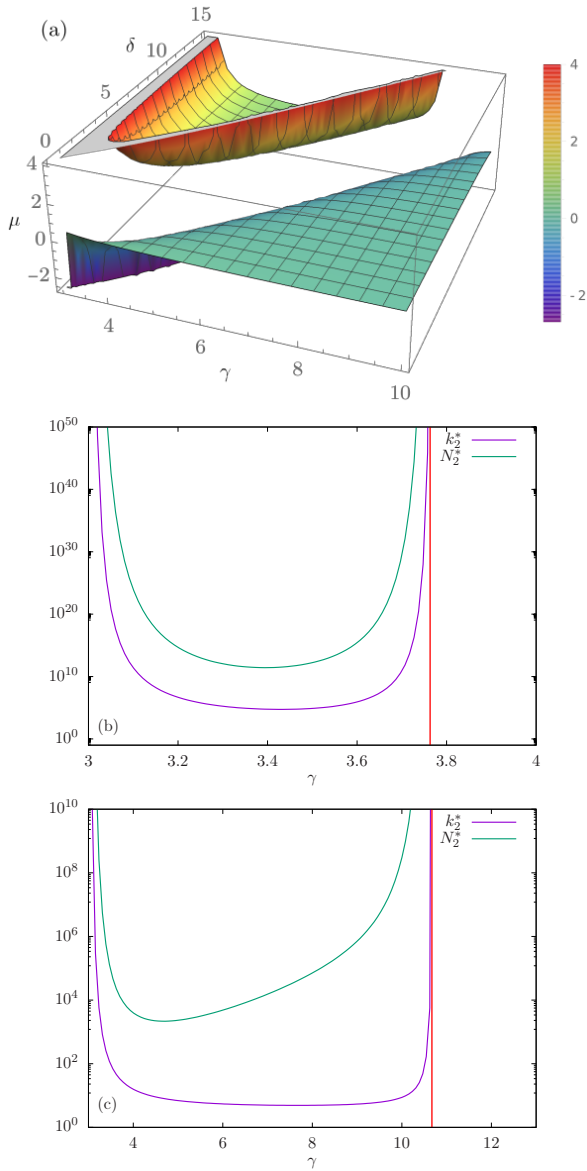
FIG. 5. Analytical results for logarithmically growing interaction range. (a) Three-dimensional representation of $\mu(\gamma, \delta)$ of Eq. (36). (b) Plot of k_2^* and N_2^* as a function of γ for $\delta = 2$. (c) Plot of k_2^* and N_2^* as a function of γ for $\delta = 20$. In both panels b) and c) the condition $\delta > b(\gamma)$ is verified. The red vertical lines represent the value of γ for which $\delta = b(\gamma)$ and thus k_2^* and N_2^* diverge.
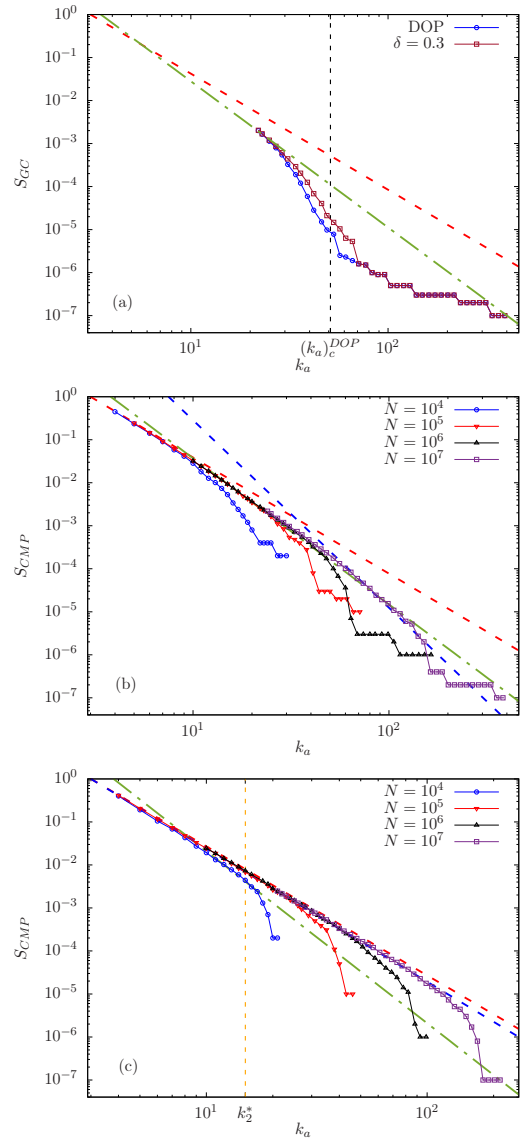

FIG. 6. Comparison of analytical and simulation results for the size of the CMP largest cluster as a function of k_a, for logarithmically growing interaction range and different combinations of γ and α values: (a) $\gamma = 3.7$ and $\delta = 0.3$, so that $\delta < a(\gamma)$, the system size is $N = 10^7$; (b) $\gamma = 3.7$ and $\delta = 1$, so that $a(\gamma) < \delta < b(\gamma)$; (c) $\gamma = 4$ and $\delta = 20$, so that $\delta > b(\gamma)$. The vertical dashed line in panel (c) is the value of k_2^*. The red dashed line is the scaling with exponent $1 - \gamma$, the green dot-dashed line is the scaling with exponent $2(2 - \gamma)$ and the blue dashed line is the prediction of $S_{\text{CMP}}^{(2)}$ given in Eq. (33).

in Ref. [18] by allowing for an arbitrary (non-decreasing) functional dependence $r(m)$ of the interaction range on the cluster mass. Building on [18] we developed a scaling theory for this class of CMP models on power-law degree-distributed networks, which allows us to determine the behavior of the order parameter S_{CMP} and the associated critical properties.

We then considered two specific functional forms for $r(m)$. We first focused on the case in which $r(m)$ grows algebraically with m. We showed that a giant cluster

(CMPGC) always exists for any value of k_a (the control parameter that sets the degree threshold for node activation), even if the interaction range grows sublinearly, and the critical exponent β is the same of the linear case. Furthermore, for proper choices of model parameters, we were able to actually observe the crossover to the true asymptotic regime in numerical simulations, in perfect agreement with the theoretical predictions. Note that

this observation is not possible with the linear interaction range used in Ref. [18], since it would require network sizes out of reach for numerical simulations. We then considered a logarithmically growing interaction range, in order to study the nontrivial competition between the distance among active nodes and their interaction range itself. We discovered that a CMPGC exists for arbitrarily large k_a only if the interaction range grows "fast enough" with respect to the distance. We identified a critical line in the parameters space that separates a region in which a CMPGC always exists from a region in which a CMPGC exists only up to a finite critical point $(k_a)_c^{\mathrm{CMP}}$.

Many aspects of the present work are worth future exploration. Indeed the CMP process allows for countless variations that may give rise to new nontrivial critical phenomena. For instance, what happens if CMP is realised when nodes are activated at random, rather than in a degree-ordered way? What changes with a different initial assignment of node masses, i.e., $m_i \neq k_i$? What if the mass of a cluster is given by the product, rather than the sum of individual masses? The investigation of these and other models described by other choices of the CMP parameters is an interesting task for future research. Another possible avenue for future investigations is the exploration of connections between generic forms of Cumulative Merging Percolation and epidemic processes. For example, CMP with algebraically growing interaction range can be seen as a description of a suitably defined SIS model on uncorrelated weighted networks.

Appendix A: Finite-size effects

In the cases where the threshold is infinite (i.e., there is a giant cluster for any k_a), the finiteness of the network induces the existence of a finite size-dependent threshold $(k_a)_c^{\mathrm{CMP}}(N)$, that diverges as N grows. Its detailed behavior depends on which mechanism dominates when k_a reaches the value $k_{\max}(N)$.

If $k_{\max}(N) < k_2^*$, finite-size effects appear during the preasymptotic regime where the extended DOP mechanism rules. The effective threshold is thus given by the condition $k_c = k_{\max}(N)$, implying

$$(k_a)_c^{\mathrm{CMP}} = k_{\min} k_{\max}^{1/(\gamma-2)} = k_{\min} N^{1/[(\gamma-1)(\gamma-2)]}. \quad \text{(A1)}$$

If instead $k_{\max}(N) > k_2^*$, finite-size effects appear when the CMPGC is governed by the second mechanism. Thus the asymptotic behavior ends when $k_x = k_{\max}(N)$, implying

$$k_x[(k_a)_c^{\mathrm{CMP}}] = N^{1/(\gamma-1)}. \quad \text{(A2)}$$

A precise prediction of how the order parameter $S_{\mathrm{CMP}}^{(2)}$ is cut off when k_x approaches $k_{\max}(N)$ is obtained by performing the integral in Eq. (18) only up to $k_{\max}(N)$ (see Fig. 7).
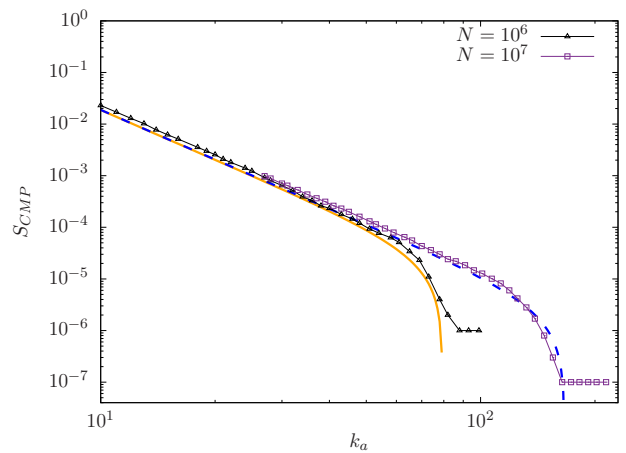

FIG. 7. Comparison of analytical and simulation results for the size of the CMP largest cluster as a function of k_a, for algebraically growing interaction range, $\gamma = 4$ and $\alpha = 5$. Symbols are the results of numerical simulations in networks of size $N = 10^6$ (black triangles) and $N = 10^7$ (purple squares). Lines are the predictions given by Eq. (18) where $k_x = \omega k_a$, ω is given by Eq. (22) and the integral is performed only up to $k_{\max}(N)$. The solid orange line is for $N = 10^6$, the blue dashed line is for $N = 10^7$.

For $k_a > (k_a)_c^{\mathrm{CMP}}$ neither of the two mechanisms is at work and S_{CMP} rapidly goes to zero [2].

Appendix B: Solution of transcendental equations Eq. (21)

Let us consider the general equation

$$x = A + Be^{Cx}, \quad \text{(B1)}$$

where A, B and C are complex numbers. Subtracting A on both sides and multiplying by C we get

$$C(x - A) = BCe^{Cx}. \quad \text{(B2)}$$

Setting $t = C(x - A)$ and multiplying by $-e^{-t}$ we get

$$-te^{-t} = -BCe^{AC}. \quad \text{(B3)}$$

Eq. (B3) can be solved using the Lambert W or product logarithm function, defined as the function fulfilling the expression [23]

$$W(z)e^{W(z)} = z. \quad \text{(B4)}$$

The Lambert W function can be considered as the inverse of the function $f(z) = ze^z$, in such a way that

$$W(ze^z) = z. \quad \text{(B5)}$$

―――――

[2] Of course, it does not go to zero in a finite N simulation because it tends to $1/N$, which is the minimum value for S_{CMP}.

The function $f(z) = ze^z$ is not invertible for every z, and therefore $W(z)$ is multivalued and has several branches, $W_j(z)$. For real w and z, the equation $w = ze^z$ can be shown to have only two branches, $W_0(z)$, the so-called *principal branch*, and $W_{-1}(z)$. In this case, it is easy to prove that

- for $z > 0$ there exist only one solution $w = W_0(z)$;

- for $-e^{-1} \leq z \leq 0$ there are two solutions corresponding to the two branches $W_0(z)$ and $W_{-1}(z)$;

- for $z < -e^{-1}$ there is not any solution.

Now, applying $W(z)$ to both sides of Eq. (B3), we obtain

$$W\left(-te^{-t}\right) = -t = W\left(-BCe^{AC}\right), \qquad \text{(B6)}$$

which, resolving for $x = A + t/C$, leads to the solution for Eq. (B1)

$$x = A - \frac{1}{C}W_j\left(-BCe^{AC}\right). \qquad \text{(B7)}$$

If we are interested in real solutions, must require that $z \geq -e^{-1}$, that is

$$BCe^{AC+1} \leq 1. \qquad \text{(B8)}$$

In order to approximate the Lambert W function, we can use the expansions for the real branches [23]

$$W_0(z) = \sum_{n=1}^{\infty} \frac{(-n)^{n-1}}{n!} z^n = z - z^2 + \frac{3}{2}z^3 - \dots \qquad \text{(B9)}$$

and

$$W_{-1}(z) = L_1 - L_2 + \sum_{l=0}^{\infty}\sum_{m=1}^{\infty} \frac{(-1)^l \left[\begin{smallmatrix} l+m \\ l+1 \end{smallmatrix}\right]}{m!} L_1^{-l-m} L_2^m$$
$$= L_1 - L_2 + \frac{L_2}{L_1} + \dots \qquad \text{(B10)}$$

where $L_1 = \ln(-z)$ and $L_2 = \ln\left[-\ln(-z)\right]$, and $z \to 0^-$

Turning finally to Eq. (21), namely

$$\omega^\alpha = 1 + a(\gamma)\ln(\omega) + \ln\left(\frac{k_a}{k_{\min}}\right), \qquad \text{(B11)}$$

if we define $\omega = e^x$, i.e. $x = \ln(\omega)$, we can write Eq. (B11) in the form

$$x = -\frac{1}{a}\left(1 + \ln\left(\frac{k_m}{k_{\min}}\right)\right) + \frac{1}{a}e^{\alpha x}. \qquad \text{(B12)}$$

This equation takes the exact form of Eq. (B1) if we define

$$A = -\frac{1}{a}\left(1 + \ln\left(\frac{k_m}{k_{\min}}\right)\right), \quad B = \frac{1}{a}, \quad C = \alpha. \qquad \text{(B13)}$$

The solution of Eq. (B12) is thus immediately given by Eq. (B7), and from here, reverting the change $\omega = e^x$, we recover the solution Eq. (22).

ACKNOWLEDGMENTS

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