

Insights into bootstrap percolation: Its equivalence with k-core percolation and the giant component

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K-core and bootstrap percolation are widely studied models that have been used to represent and understand diverse deactivation and activation processes in natural and social systems. Since these models are considerably similar, it has been suggested in recent years that they could be complementary. In this manuscript we provide a rigorous analysis that shows that for any degree and threshold distributions heterogeneous bootstrap percolation can be mapped into heterogeneous k-core percolation and vice versa, if the functionality thresholds in both processes satisfy a complementary relation. Another interesting problem in bootstrap and k-core percolation is the fraction of nodes belonging to their giant connected components $P_{\infty b}$ and $P_{\infty c}$, respectively. We solve this problem analytically for arbitrary randomly connected graphs and arbitrary threshold distributions, and we show that $P_{\infty b}$ and $P_{\infty c}$ are not complementary. Our theoretical results coincide with computer simulations in the limit of very large graphs. In bootstrap percolation, we show that when using the branching theory to compute the size of the giant component, we must consider two different types of links, which are related to distinct spanning branches of active nodes.

DOI: [10.1103/PhysRevE.99.022311](https://doi.org/10.1103/PhysRevE.99.022311)**I. INTRODUCTION**

Threshold models have been used to theoretically describe processes of contagion in social, financial, and infrastructure networks [1–4]. Unlike the classic or simple epidemic models used to describe the spread of infectious diseases, threshold models require a node to have multiple transmissions from neighbors before changing from an inactive-susceptible-dysfunctional state to an active-infected-functional state, or vice versa. These processes exhibit propagation of states as cascades that lead to a first-order transition of differing magnitudes [5–8]. We can use these models to describe the spread of innovation, information, and behavior among nodes because they tend to change their state or behavior after interacting with not one, but a group of other nodes [4,9,10]. For example, Centola showed in an online social network experiment that an individual tends to adopt a behavior after several neighbors exhibit the same behavior [11]. A threshold model is an activation process when the number of active nodes increases with time and a deactivation process when it decreases.

K-core percolation is one of the simplest threshold models used to study the deactivation process [12]. In k-core percolation all nodes are initially active. A fraction $1 - p$ of nodes then becomes inactive or dysfunctional. The fraction of active nodes after the initial failure, p , is the control parameter of the model. Then a recursive rule is applied: if an active node i has fewer than k_c^* active neighbors, it becomes inactive. If k_c^* is the same for all nodes, then the process is called homogeneous k-core percolation, if not, then it is called heterogeneous k-core percolation [13]. In the k-core process, when all nodes have a number of active nodes greater than or equal to the threshold k_c^* , the process reaches a steady state. At this stage the order parameter of k-core is the fraction of active nodes or the fraction of nodes that belong to the largest connected cluster or giant component (GC).

Dorogovtsev *et al.* [12] demonstrated that in the homogeneous k-core process the giant component equals the fraction of active nodes, and that it exhibits a first-order transition when computed for several values of initial failure p . In addition, Baxter *et al.* [14] found that for heterogeneous k-core there are finite clusters of active nodes at the steady state, indicating that the fraction of nodes belonging to the GC is

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lower than the total fraction of active nodes. They also found that for the same set of parameters the process can exhibit simultaneously a continuous and a discontinuous transition not observed in homogeneous k-core.

Bootstrap percolation is a simple threshold model often used to study activation processes [15,16]. In this model all nodes are initially inactive, except for a fraction f of nodes that activate spontaneously. Then each inactive node becomes active if it has at least k_b^* active neighbors. Analogous to k-core, when k_b^* is the same for all nodes, the process is homogeneous bootstrap percolation, and when it is not, the process is heterogeneous bootstrap percolation. This activation process continues recursively until a steady state is reached. Baxter *et al.* [14,16] found that the total fraction of active nodes S_b exhibit a first-order transition at a critical value f_{c1} . Using a generating function formalism [17–20] they also proposed equations for computing the fraction of active nodes belonging to the GC, $P_{\infty,b}$, as a function of f , but they did not compare their results with those of stochastic simulations. We perform simulations of the bootstrap percolation process, and find that the equations in Refs. [14,16] underestimate the fraction of nodes that belong to the giant component. Using the generating function formalism, we find the correct solution for $P_{\infty,b}$ and show that Refs. [14,16] disregard some activation events when the giant component is computed.

Although there are several variants for activation and deactivation models, such as the Watts threshold model and generalized epidemic models [5,21–23], we here focus only on the “canonical” processes of k-core and bootstrap percolation explained above. For an extensive description of these models see Refs. [24,25].

Baxter *et al.* [14] compared heterogeneous k-core and bootstrap percolation and found that they have different structures of active nodes, which suggests that these processes cannot map each other. Miller [26] indicates that the two processes are complementary because the behavior of active nodes in heterogeneous k-core percolation is the same as that of inactive nodes in heterogeneous bootstrap percolation. Miller proposes that when mapping the two processes the relationship of the node thresholds in k-core and bootstrap percolation must be $k_b^* = k - k_c^* + 1$, where k is the node degree or the number of node connections. In addition, Janson proves the relation between these processes in random regular graphs [27]. However, this relation has not been proven mathematically for a complex network of any degree distribution $P(k)$, and for any distribution of the activation-deactivation thresholds.

We here use a generating function formalism to examine the bootstrap process theoretically and compare our results with those from stochastic simulations. In Sec. II we describe the equivalence between k-core and bootstrap percolation for any degree distribution. In Sec. III we present equations for computing the GC for bootstrap percolation that include activation events not taken into account in Ref. [14]. Our analytical results fully agree with our stochastic simulations. Finally, in Sec. V we present our conclusions.

II. EQUIVALENCE BETWEEN BOOTSTRAP AND K-CORE PERCOLATION

In a k-core percolation process, k_c^* is the threshold number of active or functional neighbors below which an active node

becomes inactive. We assume that this threshold follows a cumulative probability distribution $r_c(j, k) = P(k_c^* \leq j | k)$ [28], where k is the degree of the node and k_c^* is its functionality threshold in k-core percolation. The function $r_c(j, k)$ is the probability that a node with degree k has a threshold k_c^* lower than or equal to j . We assume that at the beginning of the k-core process, the threshold of any node is not larger than its degree. Thus, initially, the system is stable, which is different from the original definition of k-core [12]. We assume that as a result of the initial attack, a fraction $f = 1 - p$ of nodes are destroyed and this initiates the process of cascading failures at the end of which only the fraction of active nodes $S_c(p)$ is left.

To connect k-core and bootstrap percolation, we first describe how to use the generating function formalism to calculate the fraction of active nodes in the k-core process.

When the process is in a steady state, if we follow a randomly chosen link in one direction we will end up at a node which we will call “target”, while in the opposite direction we will reach a node which we will define as “root”. In k-core percolation we then define Z_c to be the probability of reaching a target node with at least $k_c^* - 1$ outgoing active neighbors when following a link chosen at random. Here an outgoing neighbor node of the target node is any neighbor node other than the root node. Note that root is assumed to be in the active state, otherwise the node with $k_c^* - 1$ outgoing active neighbors must fail according to the rules of the k-core percolation. Following Ref. [28], the fraction of active nodes S_c in the steady state for an initial failure of a fraction of $1 - p$ nodes is

$$S_c = p\Psi_c(Z_c, 1 - Z_c). \quad (1)$$

Here $\Psi_c(Z_c, 1 - Z_c)$ is the probability that a random node has a number of active neighbors greater than or equal to its threshold. As a function of two arguments, x , and y , $\Psi_c(x, y)$ is defined as

$$\Psi_c(x, y) = \sum_{k=0}^{\infty} P(k) \sum_{j=0}^k \binom{k}{j} r_c(j, k) x^j y^{k-j}. \quad (2)$$

The parameter Z_c satisfies a recursion equation,

$$Z_c = p\Phi_c(Z_c, 1 - Z_c), \quad (3)$$

and

$$\Phi_c(x, y) = \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} r_c(j+1, k) x^j y^{k-j-1}, \quad (4)$$

where $\langle k \rangle = \sum_{k=1}^{\infty} kP(k)$ is the average degree of the network.

On the other hand, in the bootstrap percolation process a fraction f of nodes becomes active at the beginning of the process. We call these nodes that activate spontaneously the “seed” nodes, because they trigger the activation cascade of the inactive nodes, forming extensive branches of active nodes. Naturally, we define nodes that were not activated initially as “non-seed”.

After the initial activation, a non-seed node with a degree k becomes active if the number of its active neighbors j satisfies

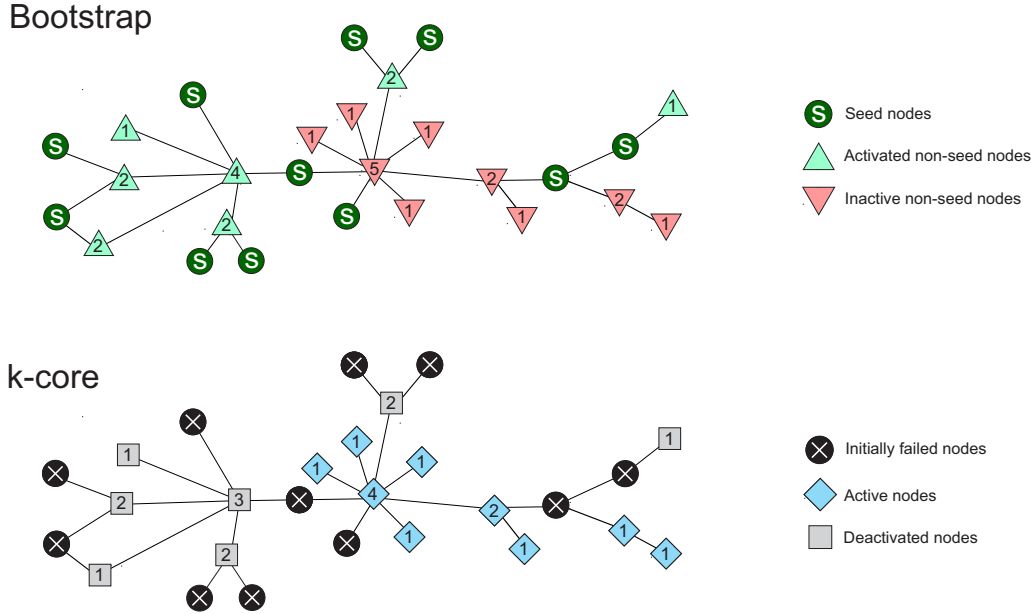


FIG. 1. Bootstrap and k-core percolation processes developed on a randomly generated network. The bootstrap threshold for a node with degree k is $k_b^* = \lfloor k/2 \rfloor + 1$, where $\lfloor x \rfloor$ denotes the integer part of x . If we set the seed nodes in bootstrap as initially failed nodes in k-core, then if $k_c^* = k - \lfloor k/2 \rfloor$, according to Eq. (5), then both process are complementary. All non-seed nodes activated in bootstrap coincide with deactivated nodes in k-core, and all non-seed nodes that were not activated in bootstrap are the same as those that remained active in the k-core process. The numbers indicate the thresholds corresponding to each process. Figure adapted from Ref. [26].

$j \geq k_b^*$, where k_b^* is the bootstrap functionality threshold. Similar to k-core percolation, the cumulative distribution of the bootstrap activation threshold is $r_b(j, k) = P(k_b^* \leq j|k)$.

It can be shown that the process of activation of nodes in the bootstrap percolation with the fraction of seeds f is equivalent to deactivation of nodes in the complementary k-core percolation process, in which the initial failure destroyed a fraction $1 - p = f$ of nodes, if their thresholds are complementary. Thus, the seed nodes in bootstrap play the role of initially failed nodes in k-core. Furthermore, this implies that the nodes that are active in bootstrap percolation are inactive in k-core and vice versa. We will call such nodes b-active and c-inactive and b-inactive or c-active, respectively. Fig. 1 illustrates that bootstrap and k-core are complementary, when both process develop on the same graph with complementary thresholds.

It can be shown that $Z_c = 1 - Z_b$, where Z_b is the probability of reaching, following a random link, a seed node or a non-seed with k_b^* outgoing links leading to activated nodes. Analogously, it can be shown that $S_b = 1 - S_c$, where S_b is the fraction of the active nodes in the bootstrap percolation. We will provide a rigorous proof of this equality by deriving the equations of bootstrap percolation using the k-core equations. For this purpose we have to connect first the thresholds distributions $r_c(j, k)$ and $r_b(j, k)$.

We have established that the activation of b-inactive nodes is equivalent to the deactivation of c-active nodes. The condition of activation is that the number of b-active neighbors, j_b of a b-inactive node with degree k satisfies $j_b \geq k_b^*$. From the point of view of the k-core percolation, this node has $j_c = k - j_b$ c-active neighbors, and the condition of its deactivation is that $j_c = k - j_b < k_c^*$, or $j_b > k - k_c^*$ or $j_b \geq k + 1 - k_c^*$.

Since this last inequality must coincide with $j_b \geq k_b^*$, then,

$$k_b^* = k + 1 - k_c^*. \tag{5}$$

This simple equality shows how the thresholds of both process are related depending on the degree of the nodes. Note that this relation indicates that in non-regular graphs, the complementary process of homogeneous bootstrap percolation is heterogeneous k-core percolation. Likewise, homogeneous k-core percolation is the complement of heterogeneous bootstrap percolation.

Now we are in conditions to establish a connection between the threshold distributions of both processes. Using Eq. (5),

$$\begin{aligned} r_c(j, k) &= P(k_c^* \leq j|k), \\ r_c(j, k) &= P(k + 1 - k_b^* \leq j|k), \\ r_c(j, k) &= P(k_b^* \geq k + 1 - j|k), \\ 1 - r_c(j, k) &= P(k_b^* < k + 1 - j|k), \\ 1 - r_c(j, k) &= P(k_b^* \leq k - j|k) \equiv r_b(k - j, k). \end{aligned}$$

Thus, we obtain the relation between the threshold distributions,

$$r_c(j, k) = 1 - r_b(k - j, k). \tag{6}$$

We will show that when the threshold distributions for k-core and bootstrap percolation satisfy Eq. (6) then both processes are complementary.

Finally, we will derive the equations for the bootstrap percolation using Eqs. (4), (2) and (6) using the k-core percolation as a starting point. Note that Eq. (3) can be rewritten

using Eq. (6) as

$$Z_c = (1-f) \left(1 - \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} r_b(k-j-1, k) \times Z_c^j (1-Z_c)^{k-j-1} \right) \quad (7)$$

Introducing new summation index $i = k - (j + 1)$ and using the symmetry of binomial coefficients, we see, that this equation is equivalent to

$$1 - Z_c = f + (1-f) \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} \sum_{i=0}^{k-1} \binom{k-1}{i} r_b(i, k) \times Z_c^{k-i-1} (1-Z_c)^i \quad (8)$$

Introducing

$$\Phi_b(x, y) = \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} \sum_{i=0}^{k-1} \binom{k-1}{i} r_b(i, k) x^i y^{k-i-1}, \quad (9)$$

we arrive at the following recursive equation

$$1 - Z_c = f + (1-f)\Phi_b(1 - Z_c, Z_c). \quad (10)$$

If we denote $Z_b = 1 - Z_c$, then we can write Eq. (10) as

$$Z_b = f + (1-f) \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} r_b(j, k) \times Z_b^j (1 - Z_b)^{k-j-1}, \quad (11)$$

or

$$Z_b = f + (1-f)\Phi_b(Z_b, 1 - Z_b), \quad (12)$$

which is the generalization for the analogous equation for the homogeneous bootstrap percolation [14].

Note that the meaning of $Z_b = 1 - Z_c$ is the probability of a link to connect *any* (active or inactive) root to an already b-activated node, while Z_c is the probability of a link to connect a c-active node to a c-active nodes. Indeed, there are three types of links: those connecting b-active with b-active nodes, those connecting c-active and b-active nodes and those connecting c-active and c-active nodes. Since the last category constitute the probability Z_c , the first two together constitute the probability $Z_b = 1 - Z_c$. Thus, we conclude that Z_b and Z_c are complementary. The difference in the meaning of Z_c and Z_b is also reflected in the structure of the functions Φ_b and Φ_c in which the former has a term $r_b(j, k)$ while the latter has a term $r_c(j + 1, k)$.

Using the same techniques as we use for the derivation of $Z_b = 1 - Z_c$, it is straightforward to show that $S_b = 1 - S_c$ and then obtain the final equation for the active nodes in the bootstrap percolation:

$$S_b = f + (1-f)\Psi_b(Z_b, 1 - Z_b), \quad (13)$$

where

$$\Psi_b(x, y) = \sum_{k=0}^{\infty} P(k) \sum_{j=0}^k \binom{k}{j} r_b(j, k) x^j y^{k-j}. \quad (14)$$

This concludes the proof of the complementarity of the k-core percolation and bootstrap percolation with complementary threshold distributions.

III. GIANT COMPONENT EQUATION FOR BOOTSTRAP PERCOLATION

In this section, we will generalize the equations for the size of the giant component (GC) in heterogeneous k-core and bootstrap percolation presented in Refs. [14,16] using a different notation, and then we show that for the bootstrap percolation, their equations underestimate the size of the GC. The source of this discrepancy is the difference in the meaning of Z_b and Z_c as we have shown in the previous section. In the k-core percolation, we denote as α_c the probability that a randomly selected link, originating at an active node, leads to the GC of active nodes, and obviously this probability is less than or equal to Z_c . The probability that a link coming from an active root node lead to an active target node but not to the GC is $Z_c - \alpha_c$. Thus, the probability that a target node with a degree k and j outgoing links leading to active neighbors, is not connected to the GC is

$$\binom{k-1}{j} (Z_c - \alpha_c)^j (1 - Z_c)^{k-j-1}. \quad (15)$$

Summing up all these terms for different k and k_c^* and after taking into account the probability of reaching a node with degree k through a random link and the distribution of the thresholds r_c , we conclude that the total probability that any node to which we arrive by a random link is active but not connected to the GC is

$$Z_c - \alpha_c = p\Phi_c(Z_c - \alpha_c, 1 - Z_c). \quad (16)$$

This equation can be solved together with Eq. (3) for any initial survival probability p . Note that if $r_c(1, k) = 0$ for any $k > 0$, this system of equations always have a solution $\alpha = Z_c$ because if $r_c(1, k) = 0$, each term of Eq. (16) has a factor $(Z_c - \alpha_c)$, and, thus, the first argument of the function $\Phi_c(Z_c - \alpha_c, 1 - Z_c)$ can be factored out. The final equation for the size of the GC, $P_{\infty, c}$, can be written as the probability of randomly choosing an active node, S_c , minus the probability of choosing at random an active node with no links connected to the GC, which is $p\Psi_c(Z_c - \alpha, 1 - Z_c)$. Thus

$$P_{\infty, c} = S_c - p\Psi_c(Z_c - \alpha, 1 - Z_c). \quad (17)$$

Therefore, if there are no nodes with $k_c^* = 1$ and no autonomous nodes ($k_c^* = 0$), we have $P_{\infty, c} = S_c$, which means that all active nodes are part of the GC.

Now we will turn to the derivation of the equation for the giant component in the bootstrap percolation. For brevity we will drop subscript b in all the equations. Naively, one could expect that the same equations (16) and (17) with small modifications would work for the bootstrap:

$$Z - \alpha = fG_1(1 - \alpha) + (1-f)\Phi(Z - \alpha, 1 - Z) \quad (18)$$

and

$$P_{\infty} = S - [fG_0(1 - \alpha) + (1-f)\Psi(Z - \alpha, 1 - Z)], \quad (19)$$

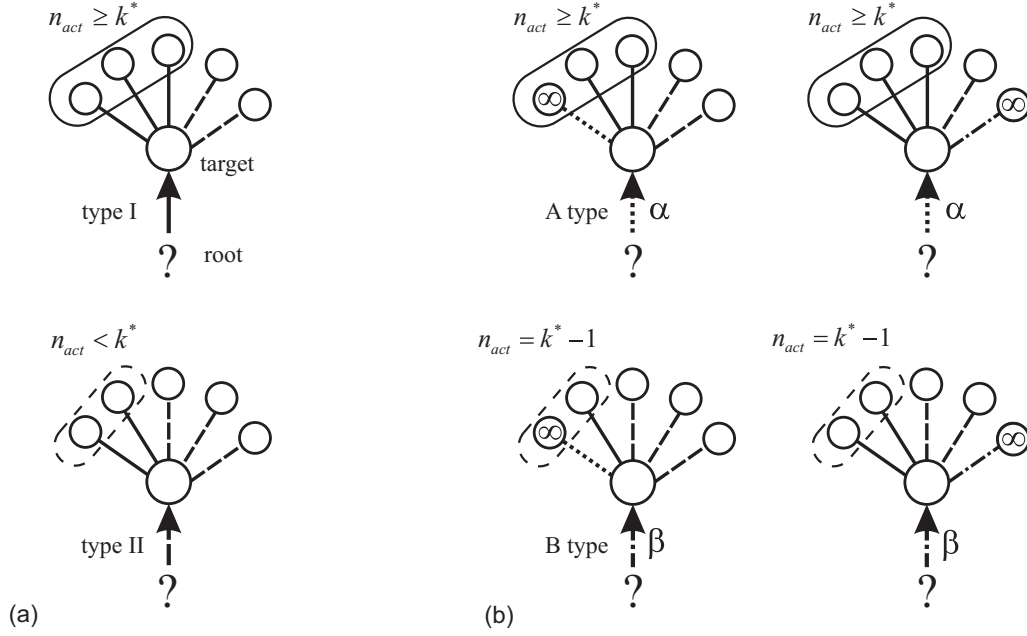


FIG. 2. Schematic representation of some configurations when reaching a target node following a random edge, in a random 6-regular network and for a threshold $k^* = 3$. Solid edges lead to an “already active node”, which has $n_{act} = k^*$ active outgoing neighbors (enclosed by a solid line). We say these links are of type I. Dashed edges connect to a node with less than $n_{act} = k^*$ active outgoing neighbors (enclosed by a dashed line), and we call them links of type II. On the other hand, dotted lines are edges of type I that lead to the GC, which we call type A links, while dash-dotted lines are type II edges that lead to the GC, called type B links. Note that a type B link is connected to an active node if two conditions are fulfilled: it must lead to a target node with exactly $n_{act} = k^* - 1$ active outgoing neighbors (if $n_{act} > k^* - 1$ it would be a type A link), and also the root node must be active. In panel (a) we differentiate two types of links: I (top) and II (bottom). In panel (b) we show different configurations that lead to the GC for each type of link. On top we show a link of type A that leads with probability α to a target node connected to the GC, because one of its outgoing links is of type A (top-left) or of type B (top-right). These configurations are considered in Eq. (22). On the bottom, we show a link of type B that leads with probability β to a target node connected to the GC, since one of its outgoing links is of type A (bottom-left) or of type B (bottom-right). These configurations are considered in Eq. (23).

where $G_0(x)$ and $G_1(x)$ are the standard generating functions of the network degree distribution [19]:

$$G_0(x) = \sum_{k=0}^{\infty} P(k)x^k \quad (20)$$

$$G_1(x) = \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} x^{k-1} \quad (21)$$

The meaning of the terms involving G_1 and G_0 is the special treatment of the seed nodes, which are active by default. Thus for them the classical percolation equations are applied. Our computer simulations for a random regular network with degree $k = 3$ and activation thresholds 2 and 3 ($k = 3$ and $k^* = 2, k^* = 3$) do not agree with these equations (see Fig. 3).

To understand the origin of this discrepancy, we need to recall the definition of Z in bootstrap percolation, which is the probability of connecting a root node with a seed node, or with an already active non-seed node. By “already active node” we mean a node, whose activation was triggered by its outgoing neighbors, or what is the same, that at least k^* of its outgoing links lead to active nodes. Thus, the activation of the target node does not depend on the root node, unlike in the k -core percolation, where the root must be always active. Nevertheless, if the target non-seed node has $j = k^* - 1$ outgoing links leading to active neighbors and also the root

is active, the target should be also active, and this possibility has not been considered in [16].

Thus the outgoing links leading to the giant component can be of two types, A or B. The A type include links leading to seed nodes or to non-seed nodes with $j \geq k^*$ active outgoing neighbors. The B type include links leading to nodes with $j = k^* - 1$ outgoing active neighbors, which can be activated only if the root is active. Note that A is the subset of a broader type of links that we will call links of type I, connecting any root to b -active nodes which have probability Z . In contrast, links of type B are the subset of nodes of type II which is the complement of type I and, hence has the probability $1 - Z$ (see Fig. 2). We denote the probabilities that a link of the A and B type lead to the GC by α and β respectively. Thus $\alpha \leq Z$ while $\beta \leq 1 - Z$. The total probability that a randomly selected link leads to the GC is $X = \alpha + \beta$. Fig. 2 illustrates different cases in which the chosen edge is linked to the GC, with probability α or β for a random regular network with degree $k = 6$ and threshold $k^* = 3$.

Since it is sufficient that at least one of the outgoing links of the target node leads to the giant component, it will be more convenient to handle the probability that none of the outgoing links lead to the GC. Thus, we will use the probability that the link of type I does not lead to the GC, which clearly is $Z - \alpha$, and also the probability that the link of type II does not lead to the giant component, which is $1 - Z - \beta$. Note that since we

have two types of links, we will need to solve a system of two recursive equations to compute the GC.

The recursive equation for α can be obtained by looking at the status of the target. Indeed, if a target is a seed with probability f , the probability that it is not connected to the GC by the outgoing links is the same as in classical percolation theory $fG_1(1-X)$. If the target is not a seed node with probability $1-f$, the probability that it is not connected to the GC is $(1-f)\Phi(Z-\alpha, 1-Z-\beta)$, which differs from the analogous term for the k -core percolation in Eq. (16) by the replacement of $1-Z$ by $1-Z-\beta$. This is because the links leading to nodes with threshold less than the activation threshold, whose probability is $1-Z$, can still lead to the GC with probability β . Thus, α satisfies the recursive relation,

$$Z-\alpha = fG_1(1-X) + (1-f)\Phi(Z-\alpha, 1-Z-\beta). \quad (22)$$

Note that this equation coincides with the old Eq. (18) with a correction term β , replacing $1-\alpha$ by $1-X$ and $1-Z$ by $1-Z-\beta$.

The recursive relation for β can be obtained by the following arguments. Suppose that the random link leads to a target node with threshold $j = k^* - 1$, which could be activated by the root. The probability of this event for given degree k and threshold k^* is the j th term of Eq. (11), with $x = Z$, $y = 1 - Z$ and $j = k^* - 1$. The probability that this node is not connected to the GC is given by the same term with $x = Z - \alpha$ and $y = 1 - Z - \beta$. Thus, we can compute the probability that such a node is connected to the GC as the difference between these two probabilities. After summing up all the contributions from different k and k^* and taking into account the degree and threshold distributions, we have

$$\beta = (1-f)[\Delta\Phi(Z, 1-Z) - \Delta\Phi(Z-\alpha, 1-Z-\beta)], \quad (23)$$

where

$$\Delta\Phi(x, y) = \sum_{k=1}^{\infty} \frac{kP(k)}{\langle k \rangle} \sum_{j=0}^{k-1} \binom{k-1}{j} [r_b(j+1, k) - r_b(j, k)] x^j y^{k-j-1}. \quad (24)$$

Here $r_b(j+1, k) - r_b(j, k)$ is the probability that $k^* = j+1$, which is equivalent to $j = k^* - 1$. Thus, each term corresponds to a node that is just one active outgoing neighbor short of being activated, which will be active if the root is active. To derive the final equation for the fraction of nodes in the GC, we use a slightly modified Eq. (19) with the correction term β :

$$P_{\infty} = S - [fG_0(1-X) + (1-f)\Psi(Z-\alpha, 1-Z-\beta)]. \quad (25)$$

Recall that $X = \alpha + \beta$ is the probability of choosing a random link that leads to the GC.

As a simple example we will illustrate these equations for a random regular network with $k = 3$ and $k^* = 2$. For this network $P(3) = 1$, $r_b(0, 3) = r_b(1, 3) = 0$ and $r_b(2, 3) = r_b(3, 3) = 1$. Accordingly, we have a system of two algebraic equations:

$$\begin{aligned} \alpha &= Z - f(1-X)^2 - (1-f)(Z-\alpha)^2, \\ \beta &= (1-f)2[Z(1-Z) - (Z-\alpha)(1-Z-\beta)], \end{aligned} \quad (26)$$

which can be solved for any fraction of seed nodes f using Eq. (12),

$$Z = f + (1-f)Z^2, \quad (27)$$

from where we easily obtain $Z = f/(1-f)$.

For a random regular network with $k = 3$, Eq. (25) is reduced to

$$\begin{aligned} P_{\infty} &= f + (1-f)[Z^3 + 3Z^2(1-Z) + 3Z(1-Z)^2] \\ &\quad - f(1-X)^3 - (1-f)[(Z-\alpha)^3 \\ &\quad + 3(1-Z-\beta)(Z-\alpha)^2]. \end{aligned} \quad (28)$$

We verified Eq. (25) by simulations for the case of a complex $r_b(j, k)$ and for a random regular network.

Note that for the percolation critical point, $\alpha = \beta = 0$, the Eqs. (26) turn into identities with the equation for α turning into Eq. (12). To find the critical point we can present the system Eq. (26) in a symbolic recursive form

$$\mathbf{x} = \mathbf{A}(\mathbf{x}), \quad (29)$$

where $\mathbf{x} \in \mathbb{R}^2$ ($x_1 = \alpha$, $x_2 = \beta$) and $\mathbf{A}(\mathbf{x})$ is a nonlinear operator representing the right-hand side of the system of Eqs. (26). A sufficient condition of the attractive point $\mathbf{x} = 0$ is $|\mathbf{A}(\mathbf{x})| < |\mathbf{x}|(1-\epsilon)$, where ϵ is a small positive constant, which in the vicinity of zero is equivalent to the condition that the matrix of partial derivatives $\partial A_i / \partial x_j|_{\mathbf{x}=0}$ has absolute values of all its eigenvalues smaller than 1. The critical point should be right at the border of the converging and diverging behavior, so it should satisfy the condition $\lambda_{\max}(f, Z) = \pm 1$. Together with Eq. (12), it gives the value of the critical parameter f_{c2} . For example, for a random regular network with $k = 3$ and $k^* = 2$, this condition together with $Z = f/(1-f)$ is equivalent to

$$\det \begin{bmatrix} 4f - 1 & 2f \\ 2(1-2f) & 2f - 1 \end{bmatrix} = 0, \quad (30)$$

which gives $f = 1/2$ and $f = 1/8$. For $f = 1/2$, the second eigenvalue is 2, so the iterations do not converge, while for $f = 1/8$ the second eigenvalue is $-1/4$, so the iterations do converge. Thus, the critical value for the continuous transition denoted as f_{c2} is $f_{c2} = 1/8$. On the other hand, the old equation (18), which neglects β , gives $f_{c2} = 1/4$ (Fig. 3), predicting a GC much more fragile. A similar treatment can be applied for $k^* = 3$, which gives $f_{c2} \approx 0.344$.

IV. STOCHASTIC SIMULATIONS

We perform stochastic simulations using networks with $N = 10^6$ nodes, to assure a small statistical noise and a negligible probability of loops, so that finite networks can be well approximated by the theoretical results obtained in the limit of infinitely large networks. The networks were generated as randomly connected graphs with a given degree distribution by the Molloy-Reed algorithm [29].

Figure 3 compares the simulation results with Eqs. (25) and with Eq. (19) corresponding to Ref. [16]. Note that Eq. (25) exhibits a good agreement with our stochastic simulations, while Eq. (19) strongly underestimates the size of GC because it neglects the probability β .

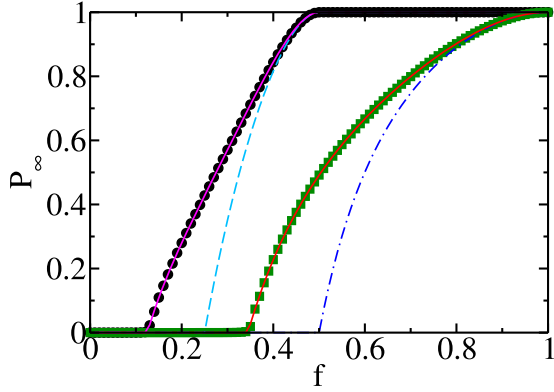


FIG. 3. $P_{\infty,b}$ as a function of the fraction of seeds f for a random regular network with $k = 3$, and thresholds $k^* = 2$ (circles, dashed line) and $k^* = 3$ (squares, dash-dotted line). The symbols represent the stochastic simulations with $N = 10^6$ and the solid lines are the prediction of our theory [see Eq. (25)]. The discontinuous lines represent the results from Eq. (19), which underestimate the size of the GC. We can see that there is an excellent agreement between the simulations and our equations.

To test the theoretical equations for the most general case of heterogeneous k-core and bootstrap percolation, we

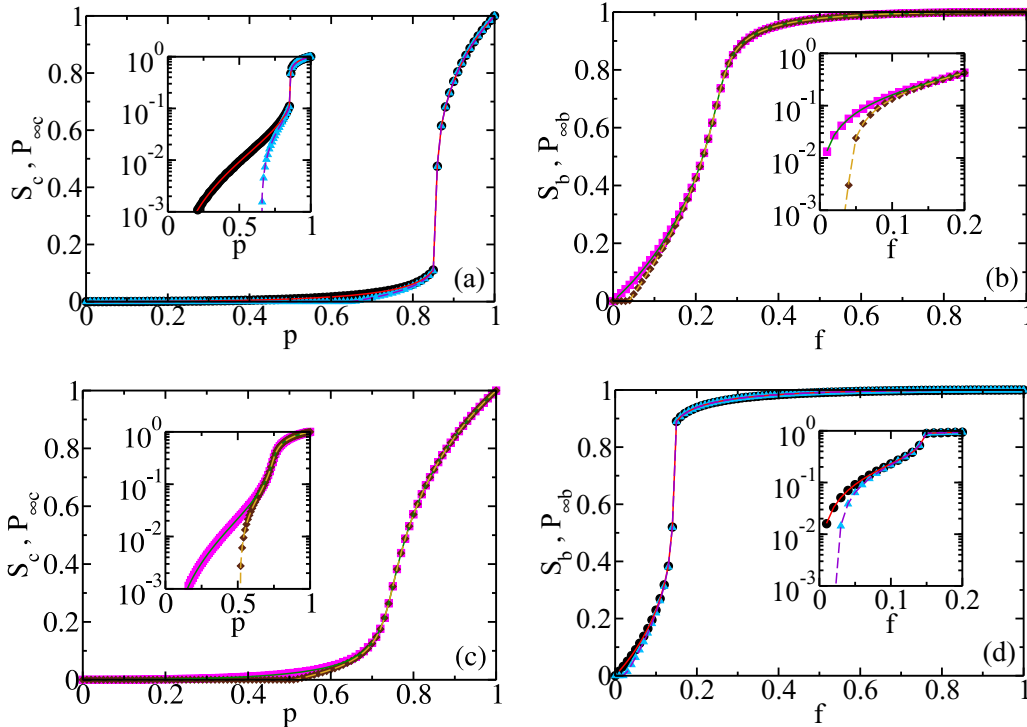


FIG. 4. (a, c) the fraction of active nodes, S_c (circles, squares, solid lines), and the fraction of nodes in the GC, $P_{\infty,c}$ (triangles, diamonds, dashed lines), for the heterogeneous k-core percolation as a function of the fraction of nodes that survived the initial failure p . (b, d) the fraction of active nodes, S_b (circles, squares, solid lines), and the fraction of nodes in the GC, $P_{\infty,b}$ (triangles, diamonds, dashed lines), for the heterogeneous bootstrap percolation as function of the fraction of the seed nodes f . In the insets we plot the same in log-linear scale. The symbols represent stochastic simulations while the lines are the results from Eqs. (13) and (25). All simulations were performed for Erdős Rényi graphs with $\langle k \rangle = 8$ and threshold distribution functions $r_c(j, k) = F_\gamma(j/k)$, $r_b(j, k) = 1 - F_{1-\gamma}(1 - j/k)$, which are polynomials of the fourth power with an inflection point at $x = \gamma$: (a) $\gamma = 0.5$, (b) $\gamma = 0.6$, (c) $\gamma = 0.4$, (d) $\gamma = 0.5$. Note that $F_\gamma(x) = 1 - F_{1-\gamma}(1 - x)$, satisfying Eq. (6) for complementary of the k-core and bootstrap thresholds. Accordingly, the graphs on the diagonal pairs of panels (a-d) and (b-c) are complementary, that is, $S_c(p) = 1 - S_b(1 - p) = 1 - S_b(f)$.

generate networks with the Poisson degree distribution with $\langle k \rangle = 8$ and a distribution of the thresholds that satisfy the complementary condition of Eq. (6). The form of the cumulative distribution of bootstrap and k-core percolation are given by $r_b(j, k) = F_\gamma(j/k)$, $r_c(j, k) = 1 - F_{1-\gamma}(1 - j/k)$, where $F_\gamma(x)$ is a fourth-order polynomial of x monotonically increasing from $F_\gamma(0) = 0$, to $F_\gamma(1) = 1$, has a minimum at $x = 0$, a maximum at $x = 1$ and an inflection point at $x = \gamma$ if $1/3 \leq \gamma \leq 2/3$:

$$F_\gamma(x) = \frac{x^2(18\gamma^2 - 12\gamma) + x^3(4 - 12\gamma^2) + x^4(6\gamma - 3)}{6\gamma^2 - 6\gamma + 1}. \quad (31)$$

Note that $F_\gamma(x)$ is invariant under the transformation $1 - F_{1-\gamma}(1 - x)$. For nodes with $k = 0$, we assume $F_\gamma(0) = 1$, which means that isolated (autonomous) nodes are always active. Figure 4 shows the results of computer simulations for the k-core and bootstrap percolation for different values of γ . Depending on the position of the inflection point, we can observe the emergence of the first order phase transition in both k-core and bootstrap percolation. We also observe a predicted complementary of the k-core and the bootstrap percolation $S_c(p) = 1 - S_b(1 - p) = 1 - S_b(f)$. In all cases we see excellent agreement with simulations. Despite the fraction of

active nodes of both processes satisfy a complementary relation, it is clear that the continuous thresholds of the giant components of these processes do not complement each other. However, the giant component of inactive nodes in bootstrap percolation corresponds to the giant component of active nodes in the complementary k -core percolation process and vice versa.

V. CONCLUSION

We have provided theoretical insights into the bootstrap percolation process. We prove mathematically that the heterogeneous bootstrap percolation is the complement of the heterogeneous k -core percolation for complex networks with any degree distribution in the thermodynamic limit, as long as the thresholds of the nodes in both processes complement each other. In particular, in nonregular graphs we can map a homogeneous bootstrap percolation onto a heterogeneous k -core percolation, and likewise, k -core homogeneous percolation onto a heterogeneous bootstrap percolation, because the inactive nodes in k -core–bootstrap behave the same as the active nodes in bootstrap– k -core.

We also develop the equations for the size of the giant component (GC) in the most general cases of heterogeneous k -core and bootstrap percolation and confirm them by stochastic simulations. Our equations for heterogeneous k -core percolation coincide with the equations for a special case of heterogeneous k -core derived in Ref. [14]. However, our equations representing the size of the GC in the bootstrap percolation disagree with the equations presented in Refs. [14,16]. The disagreement comes from the fact that Refs. [14,16] disregard some branches of active nodes when analyzing the GC in bootstrap percolation with the generating function formalism. More precisely, when following a random link that connects a root node and a target node with degree k and activation threshold k^* , it is not strictly necessary that at least k^* of the $k - 1$ outgoing neighbors of the target be active to ensure its activation. Another possibility is that only $k^* - 1$ outgoing neighbors of the target node be active, and the root node is also

active, it will trigger the activation of the target node. We show that the probability of activation of the target by the root must be explicitly taken into account in order to obtain the correct equation for the GC in bootstrap percolation. Nevertheless, to calculate the fraction of active nodes S_b , this activation should not be taken into account since the root and the target could not mutually depend on each other to be active. Thus, the equations that represent S_b in Refs. [14,16] are correct.

In the k -core theoretical approach, both the root and the target nodes are assumed to be active, thus, the root always acts as a stabilizing neighbor and therefore, the equations from Ref. [14] predict correctly the size of the GC.

We also found that unlike the fraction of active nodes, the fraction of nodes belonging to the giant component in both processes do not satisfy a complementary relation, since these processes generate different topological structures of active nodes. Indeed, active nodes in the k -core percolation are inactive in the complementary bootstrap percolation. However, the giant component of inactive nodes in the bootstrap coincides with the giant component of active nodes in the complementary k -core and vice versa.

Our results and theoretical equations here presented can be extended into networks with multiple layers and can be used to describe the evolution of the GC of active nodes during this dynamical process.

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