Generalized Threshold-Based Epidemics in Random Graphs: the Power of Extreme Values

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ABSTRACT

Bootstrap percolation is a well-known activation process in a graph, in which a node becomes active when it has at least r active neighbors. Such process, originally studied on regular structures, has been recently investigated also in the context of random graphs, where it can serve as a simple model for a wide variety of cascades, such as the spreading of ideas, trends, viral contents, etc. over large social networks. In particular, it has been shown that in $G(n,p)$ the final active set can exhibit a phase transition for a sub-linear number of seeds. In this paper, we propose a unique framework to study similar sub-linear phase transitions for a much broader class of graph models and epidemic processes. Specifically, we consider i) a generalized version of bootstrap percolation in $G(n,p)$ with random activation thresholds and random node-to-node influences; ii) different random graph models, including graphs with given degree sequence and graphs with community structure (block model). The common thread of our work is to show the surprising sensitivity of the critical seed set size to extreme values of distributions, which makes some systems dramatically vulnerable to large-scale outbreaks. We validate our results running simulation on both synthetic and real graphs.

1. INTRODUCTION AND RELATED WORK

Many fundamental phenomena occurring in various kinds of complex systems, ranging from technological networks (e.g., transportation, communication, energy), to biological networks (e.g., neural, ecological, biochemical) and social networks (in the real world or over the Internet) can be described by dynamical processes taking place over the underlying graph representing the system structure. Such processes modify over time the internal state of nodes and spread across the network following the edges of the graph.

One of the most widely studied example of such dynamical processes is the epidemic process, which starts from an initial set of infected nodes (usually referred to as seeds, chosen either deterministically or random) that can pass the infection to other (susceptible) nodes (under many possible models), possibly causing a major outbreak throughout the network.

In our work we consider a generalized model for the spreading of an 'epidemic', in which nodes are characterized by an infection threshold r (either deterministic or random), and become infected when they collect from their neighbors an amount of influence larger than r. A special case of our model is the well known bootstrap percolation process, in which r is an integer ($r \geq 2$) and each edge exerts an influence equal to one: simply put, a node becomes infected when it has at least r infected neighbors.

Bootstrap percolation has a rich history, having been initially proposed in the area of statistical physics [1]. Due to its many physical applications (see [2] for a survey) it has been primarily studied over the years in the case of regular structures (lattices, grids, trees), most notably in a series of papers by Balogh and Bollobás (e.g., [3]). More recently, bootstrap percolation has been investigated also in the context of random graphs, which is the focus of this paper. In our work we are especially interested in epidemics occurring on very large, irregular structures such as those representing friendship relationships among people. This interest is motivated by the great popularity gained by online social platforms (e.g., Facebook, Twitter, Instagram, etc.), which, coupled with the increasing availability of always-on connectivity through mobile personal devices, has created an unprecedented opportunity for the rapid dissemination of various kinds of news, advertisements, viral videos, as well as a privileged environment for online discussion, creation and consolidation of beliefs, political opinions, memes and many other forms of collective reasoning. In this respect, bootstrap percolation provides a simple, primitive model that can be used to understand the diffusion of a generic 'idea' which requires a certain amount of 'reinforcement' from neighbors to be locally adopted.

Some results have already been obtained for particular random graph models. In particular, [4] first considered bootstrap percolation in the random regular graph $G(n,d)$, while [5] has extended the analysis to random graphs with given vertex degrees (configuration model). The above two papers assume that node degree is either fixed [4] or it has both finite expectation and finite second moment [5], implying that the cardinality of the seed set must scale linearly with n to observe a non-negligible growth of the epidemics. Both papers make use of the differential equation method to analyze the discrete Markov Chain associated with the epidemic process. The analysis in [5] also allows the threshold to vary among the nodes.

SIGMETRICS '16, June 14–18, 2016, Antibes Juan-les-Pins, France.

DOI: http://dx.doi.org/10.1145/2896377.2901455

A very different technique has been recently proposed in [6] to study bootstrap percolation in Erdös–Rényi $G(n,p)$ graphs. This technique allows one to analyze also scenarios in which a sharp phase transition occurs with a number of seeds which is sublinear in n: below a critical seed set size, for which one can get a closed-form asymptotic expression, the infection essentially does not evolve, whereas above the critical size $n-o(n)$ nodes get infected with high probability[1]. In $G(n,p)$, this behavior is possible only when the average node degree itself grows with n (i.e., $p \gg 1/n$). The technique proposed in [6] has been applied by [7] to power-law random graphs generated by the Chung-Lu model (with power law exponent $2 < \beta < 3$), obtaining the interesting result that, under bounded average node degree, a sublinear seed set size is enough to reach a linear fraction of the nodes.

Also our work started from the approach proposed in [6], which provides a simple and elegant way to explore phase transitions taking place at sub-linear scale. To operate at this scale, we let, if needed, the average node degree grow with n, since this can be considered an acceptable assumption in many cases. Indeed, real social networks (and in particular online social networks), which evolve over time with the addition/removal of nodes/edges, often exhibit the so called densification phenomenon [8], meaning that the number of edges grows faster than the number of nodes (hence the average degree grows with time)[2].

The main thread of our work is to show the high 'vulnerability' (in terms of critical number of seeds) that arises in networks when we add inhomogeneities in any one of many possible ways (i.e., by adding variability in thresholds, edge weights, node degree, or network structure). Although this effect has already been observed in epidemic processes, the way in which inhomogeneities affect bootstrap percolation can be so dramatic that just extreme values of distributions (and not their particular shape) can determine the critical size of the seed set. We believe that this result, which apparently has not been recognized before, is of fundamental importance to better understand the dynamics of epidemics in complex systems.

2. NOTATION AND PRELIMINARIES

We start introducing some background material and notation taken from [6], which is necessary to follow the rest of the paper. As already mentioned, [6] provides a full picture of standard bootstrap percolation in Erdös–Rényi graphs $G(n,p)$. Nodes are characterized by a common integer threshold $r \geq 2$, and the process starts with an initial set $\mathcal{A}(0)$ of vertices (the seeds), of cardinality a, which are chosen uniformly at random among the nodes.

[1]Throughout this paper we shall use the following (standard) asymptotic notation. Let $f, g : \mathbb{R} \to \mathbb{R}$ be two functions. We write: $f(x) = o(g(x))$ or $f(x) \ll g(x)$ and $g(x) = \omega(f(x))$ or $g(x) \gg f(x)$ if $\lim_{x\to\infty} \frac{f(x)}{g(x)} = 0$; $f(x) = O(g(x))$ if there exist $K > 0$, $x_0 \in \mathbb{R}$: $|f(x)| \leq K|g(x)|$, for any $x \geq x_0$; $f(x) \sim g(x)$ if $\lim_{x\to\infty} \frac{f(x)}{g(x)} = 1$. Unless otherwise specified, in this paper all limits are taken as $n \to \infty$.

[2]in practice, asymptotic results provide very good predictions of what happens in large (but finite) systems whenever the average degree is not too small, say significantly larger than r.

We will use the same terminology adopted in [6], where infected nodes are called 'active', whereas non-infected nodes are said to be inactive. An inactive node becomes active as soon as at least r of its neighbors are active. Note that seeds are declared to be active irrespective of the state of their neighbors. Active nodes never revert to be inactive, so the set of active nodes grows monotonically.

The bootstrap percolation process naturally evolves through generations of vertices that become active. The first generation is composed of all those vertices which are activated by the seeds. The second generation of active nodes is composed by all the nodes which are activated by the joint effect of seeds and first generation nodes, etc. The process stops when either an empty generation is obtained or all nodes are active.

Now, it turns out that there is a useful reformulation of the problem that makes the process especially simple to analyze. This reformulation, which was originally proposed in [9], consists in changing the time scale, by introducing a virtual (discrete) time step $t \in \mathbb{N}$, such that a single active node is 'explored' at each time step (if the process has not yet stopped). By so doing, we forget about the generations, obtaining a more amenable process which is equivalent to the original one, in terms of the final size of the epidemic.

The above reformulation requires to introduce, besides the set $\mathcal{A}(t)$ of nodes which are active at time t, another set $\mathcal{Z}(t) \subseteq \mathcal{A}(t)$, referred to as *used* vertices, which is the subset of active vertices, of cardinality t, explored up to time t. More precisely, at time zero the set $\mathcal{A}(0)$ is initialized to the seed set, while the set of used vertices is initialized to the empty set: $\mathcal{Z}(0) = \emptyset$. Each node i is given a counter $M_i(t) \in \mathbb{N}$, initialized to 0 at time $t = 0$.

At time $t = 1$ we arbitrarily choose a node $z(1) \in \mathcal{A}(0)$ and we 'fire' its edges, incrementing by one the counter of all its neighbors. By so doing, we *use* node $z(1)$, adding it to the set of used nodes, so that $\mathcal{Z}(1) = \{z(1)\}$. We continue recursively: at each time t, we arbitrarily select an active node which has not been already used, i.e., $z(t) \in \mathcal{A}(t-1) \setminus \mathcal{Z}(t-1)$, and we distribute new 'marks' to its neighbors, which are not in $\mathcal{Z}(t-1)$, incrementing their counters. Node $z(t)$ is added to the set of used vertices: $\mathcal{Z}(t) = \mathcal{Z}(t-1) \cup \{z(t)\}$. We then check whether there are some inactive vertices, denoted by set $\Delta\mathcal{A}(t)$, that become active for effect of the marks distributed at time t (i.e., vertices whose counter reaches r at time t). Such newly activated vertices are added to the set of active vertices: $\mathcal{A}(t) = \mathcal{A}(t-1) + \Delta\mathcal{A}(t)$ (note that no vertices can be activated at time 1, being $r \geq 2$).

The process stops as soon as $\mathcal{Z}(t) = \mathcal{A}(t)$, i.e. when all active nodes have been used. Let $T = \min\{t : \mathcal{Z}(t) = \mathcal{A}(t)\}$. By construction, the final size A^* of the epidemic is exactly equal to T: $A^* := |\mathcal{A}(T)| = |\mathcal{Z}(T)| = T$.

The above reformulation of the problem is particularly useful because the counter associated to each inactive node can be expressed as:

$$M_i(t) = \sum_{s=1}^{t} I_i(s) \tag{1}$$

i.e., as the sum of t independent Bernoulli random variables $I_i(s)$ of average p, each associated with the existence/non existence of an edge in the underlying graph, between the node used at time s and node i. Indeed, it is perfectly sound to 'reveal' the edges going out of a node

just when the node itself is used (principle of deferred decision). Moreover we can, for convenience, express the counters of all of the nodes at any time $t \geq 1$ just like (1), without affecting the analysis of the final size of the epidemics. Indeed, by so doing we introduce extra marks that are not assigned in the real process (where each edge is revealed at most one, in a single direction), specifically, when a used node is 'infected back' by a neighboring used node. However, this 'error' does not matter, since it has no impact on the percolation process. Note that counters $M_i(t)$ expressed in such a way are independent from node to node.

The dynamics of the epidemic process are determined by the behavior of the number $A(t)$ of 'usable' nodes (i.e., active nodes which have not been already used):

$$A(t) = |\mathcal{A}(t) \setminus \mathcal{Z}(t)| = a - t + S(t)$$

where a is the number of seeds, and $S(t)$ represents the number of vertices, which are not in the original seed set, that are active at time t. Note that the final size of the epidemics equals the first time T at which $A(T) = 0$. Moreover, by construction, the number of used vertices at time t equals t. Now, let $\pi(t) := \mathbb{P}(M_1(t) \geq r) = \mathbb{P}(\mathrm{Bin}(t,p) \geq r)$ be the probability that an arbitrary node not belonging to the seed set is active at time t. There are $n-a$ such nodes, each active independently of others, hence $S(t)$ is equal in distribution to $\mathrm{Bin}(n-a, \pi(t))$.

In essence, we need to characterize trajectories of process $A(t)$ which, besides a deterministic component $a-t$ (decreasing with time), includes a random variable $S(t)$ which is binomially distributed, with time-dependent parameter $\pi(t)$ (increasing with time):

$$A(t) = a - t + \mathrm{Bin}(n-a, \mathbb{P}(\mathrm{Bin}(t,p) \geq r)) \qquad (2)$$

In particular, whenever we can prove that, for a given t, $\mathbb{P}((\inf_{\tau \leq t} A(t)) < 0) \to 0$, then we can conclude that at least t vertices get infected w.h.p. Similarly, if, for a given t, $\mathbb{P}(A(t) < 0) \to 1$, we can conclude that the percolation terminates w.h.p. before t, thus the final number of infected vertices will be smaller than t. We now present a simplified form of the main theorem in [6], together with a high-level description of its proof.

THEOREM 2.1 (JANSON ET AL. [6]). *Consider bootstrap percolation in $G(n,p)$ with $r \geq 2$, and a number a of seeds selected uniformly at random among the n nodes. Let $p = p(n)$ be such that $p = \omega(1/n)$, $p = o(n^{-1/r})$. Define:*

$$t_c := \left(\frac{(r-1)!}{np^r}\right)^{1/(r-1)} \qquad (3)$$

$$a_c := \left(1 - \frac{1}{r}\right) t_c \qquad (4)$$

If $a/a_c \to \alpha < 1$ (subcritical case), then w.h.p. the final size is $A^* < 2a$. If $a/a_c \to \alpha \geq 1 + \delta$, for some $\delta > 0$ (supercritical case), then w.h.p. $A^* = n - o(n)$.

Note that, under the above assumptions on $p(n)$, the 'critical time' t_c is such that both $t_c = \omega(1)$ and $t_c = o(n)$, and the same holds for the critical number of seeds a_c, which differs from t_c just by the constant factor $(1-1/r)$, i.e., we get a phase transition for a sublinear number of seeds.

The methodology proposed in [6] to obtain the above result is based on the following idea: $A(t)$ is sufficiently concentrated around its mean that we can approximate it as $A(t) \approx \mathbb{E}(A(t)) = a - t + (n-a)\pi(t)$. Now, for a wide range of values of t (i.e., whenever $pt \to 0$, and in particular around t_c), $\pi(t)$ can be expressed as $\pi(t) = \frac{t^r p^r}{r!}(1 + O(pt + t^{-1}))$. Therefore function $\mathbb{E}(A(t))$ has a clear trend: it starts from a at $t = 0$ and first decreases up to a minimum value reached at $t \approx t_c$, after which it grows to a value of the order of n. Hence, time t_c acts as a sort of bottleneck: if $\mathbb{E}(A(t_c))$ is positive (negative), we are in the supercritical (subcritical) case. Finally, we can compute the asymptotic value of t_c by finding the minimum of function $f(t) = n\frac{t^r p^r}{r!} - t$.

The result then follows considering that, starting from a seeds, we get $\mathbb{E}(A(t_c)) = a - a_c + o(a_c)$, and that by changing a we deterministically move up or down the process $A(t)$. Hence, if we assume that a/a_c is asymptotically bounded away from 1 we obtain a sufficient 'guard factor' around the trajectory of the mean process to conclude that the real process is either supercritical or subcritical (see Fig. 1).

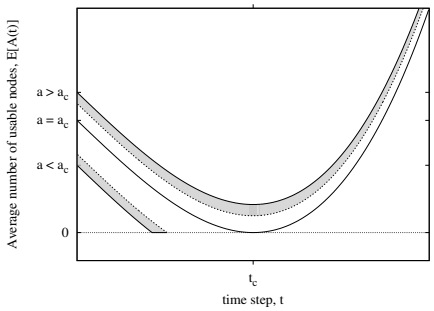

Figure 1: Example of (asymptotic) trajectories of the mean number of usable nodes, $\mathbb{E}(A(t))$, with $r = 3$. The plot also illustrates by shaded regions the concept of 'guard zone'.

We emphasize that in [6] authors use a martingale approach to show that $A(t)$ is sufficiently concentrated around its mean, which allows them to establish their results w.h.p.

As a final premise, it is better to clarify why we assume $r \geq 2$. The reason is that the case in which a node can be infected by just a single neighbor is degenerate, and leads to the trivial fact that a single seed is enough to infect the entire connected components it belongs to. Hence, one has to apply a totally different set of tools [10] to characterize the final size of the epidemic. This case, however, is not interesting to us, since the networks of many real systems are connected by construction, or they at least have a giant connected component. Hence, no phase transitions occur here in the number of seeds.

3. SUMMARY OF CONTRIBUTIONS

In this work we extend the approach of [6] along three 'orthogonal' directions that allow us to study more general threshold-based epidemic processes in inhomogeneous scenarios.

1. We consider a generalized version of bootstrap percolation in $G(n,p)$, in which thresholds of nodes are i.i.d. random variables $R_i > 0$, and infected nodes transmit a random amount of infection to their neighbors. Specifically, we assume that i.i.d.

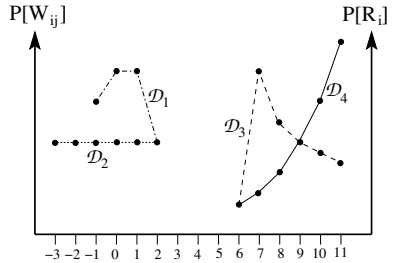

Figure 2: Examples of distributions of W_{ij} and R_i leading to the same (asymptotic) critical number of seeds a_c.

weights W_{ij} are assigned to the edges of the graph, representing the amount of infection transmitted through the edge. For this case, we obtain the asymptotic closed form expression of the critical number of seeds, and an exponential law for the probability that the process is supercritical or subcritical, strengthening the results in [6] (where results hold, instead, w.h.p.). The most significant outcome of our analysis is that the critical number of seeds typically does not depend on the entire distribution of R_i and W_{ij}, but just on values taken in proximity of the lower (for R_i) and upper (for W_{ij}) extreme of their support. For instance, in Figure 2 we show examples of two (discrete) distributions for W_{ij}, labelled $\mathcal{D}_1$ and $\mathcal{D}_2$, and two (discrete) distributions for R_i, labelled $\mathcal{D}_3$ and labelled $\mathcal{D}_4$. It turns out that any combination of them $(\mathcal{D}_a, \mathcal{D}_b)$, with $a \in \{1, 2\}$ and $b \in \{3, 4\}$ leads to the same asymptotic critical number of seeds a_c. Note that the various distributions have different means, and that one of them ($\mathcal{D}_2$) has even negative mean.

2. We extend the problem reformulation originally proposed in [9], where a single node is used at each time, to a similar reformulation in which a single edge is used at a time. This view is more convenient to apply the approach of [6] to other random graph models. In particular, we consider graphs with given degree sequence (configuration model), obtaining a closed-form expression of the asymptotic critical number of seeds. We then compute the scaling order of a_c for the particular (but most significant) case of power-law degree sequence, considering a wider range of parameters with respect to the one studied by [7]. Again, we observe the interesting phenomenon that in some cases the precise shape of the degree distribution (i.e., the power law exponent) does not matter, since a_c is determined by the largest degree.

3. We extend the analysis to the so-called block model, which provides a simple way to incorporate a community structure into a random graph model while preserving the analytical tractability of $G(n, p)$. We observe once more the interesting effect that the critical number of seeds might be determined by a single entry of the matrix of inter- (or intra-) community edge probabilities (i.e., the most vulnerable community).

Although we consider (for simplicity) the above three forms of inhomogeneity 'in isolation', it is not particularly difficult to combine them, if desired. Indeed, we show that all extensions above can be studied within a common framework. We emphasize that in this paper we generally assume that seeds are selected uniformly at random among the nodes, without knowledge of thresholds, weights, degrees, network structure. This differentiates our analysis from existing works addressing the so called influence maximization problem, i.e., finding the seed set that maximizes the final size of the epidemic (e.g., [11]). We observe that in the influence maximization framework many authors have already considered generalized models taking into account the impact of edge weights, node-specific thresholds, etc. (e.g., variants of the linear threshold model proposed in [12]). However, to the best of our knowledge, asymptotic properties of such generalized models are still not well understood. This paper makes a step forward in this direction analysing sublinear phase-transitions occurring when seeds are allocated uniformly at random in the network.

Interestingly, in all cases that we consider the epidemic is triggered among the most vulnerable nodes, and then it spreads out hitting less and less vulnerable components of the network. This fact can have dramatic consequences on the minimum number of seeds that can produce a network-wide outbreak.

In the following sections we present the above three contributions one at a time. Simulation experiments are presented along the way, to validate and better illustrate our analytical results.

4. GENERALIZED BOOTSTRAP PERCOLATION IN $G(n, p)$

4.1 System model

We start considering Erdös–Rényi random graphs $G(n, p)$, extending basic bootstrap percolation to the case in which node thresholds and/or node-to-node influences are i.i.d random variables. We denote by $R_i > 0$ the (real-valued) threshold associated to node i. We then assign a (real-valued) random weight W_{ij} to each edge of the graph, representing the influence that one node exerts on the other (see later). Node i becomes active when the sum of the weights on the edges connecting i to already active neighbors becomes greater than or equal to R_i.

Recall that each edge of the graph is 'used' by the process at most once. Hence our analysis encompasses both the 'symmetric' case in which the influence (possibly) given by i to j equals the influence (possibly) given by j to i, and the 'asymmetric' case in which weights along the two directions of an edge are different (i.i.d.) random variables. In both cases, we can consider a single random weight on each edge.

We do not pose particular restrictions to the distributions of R_i and W_{ij}, except for the following one, which avoids the degenerate case in which a node can get infected by a single edge (the case $r = 1$ in basic bootstrap percolation):

$$\operatorname{ess\,inf} R_i > \operatorname{ess\,sup} W_{ij} > 0. \tag{5}$$

Note that we can also allow W_{ij} to take negative values, which could represent, in the context of social networks, neighbors whose behavior steers us away from the adoption of an idea. This generalization produces, indeed, rather surprising results, as we will see. However, negative weights require to introduce some extra assumptions

on the dynamics of the epidemic process, which are not needed when weights are always non-negative. Specifically, with negative weights we must assume that i) once a node becomes infected, it remains infected for ever; ii) some random delays are introduced in the infection process of a node and/or on the edges, to avoid that a node receives the combined effect of multiple (simultaneous) influences from active neighbors. We argue that assumption ii) is not particularly restrictive, since in many real systems influences received by a node take place atomically (e.g., a user reading ads, posts, twits, and the like). Assumption i) instead is crucial, because with negative weights counters no longer increase monotonically, and thus they can traverse the threshold many times in opposite directions. Assumption i) can be adopted, however, to study many interesting epidemic processes whose dynamics are triggered by nodes crossing the threshold for the first time[3].

The analysis of the general case can be carried out by exploiting the same problem reformulation described in Sec. 2, in which a single active node is used at each time step. Indeed, we can associate to inactive nodes a (real-valued) counter, initialized to 0 at time $t = 0$, which evolves according to:

$$M_i(t) = \sum_{s=1}^{t} I_i(s) W_{z(s),i} \tag{6}$$

where $I_i(s)$, $\forall s, \forall i$, is a Bernoulli r.v. with average p revealing the presence of edge $(z(s), i)$ and $W_{z(s),i}$ is the random weight associated to the same edge. Similarly to the basic case, the above expression of $M_i(t)$ can be extended to all nodes and all times, without affecting the results. By so doing, counters $M_i(t)$ are independent from node to node.

We then re-define $\pi(t)$, as the probability that an arbitrary node which is initially inactive (take node 1), has become active at any time $\tau \leq t$:

$$\pi(t) := \mathbb{P}\left(\sup_{\tau \leq t} M_1(\tau) \geq R_1\right)$$

With the above definition, the system behavior is still determined by trajectories of process (2). We have:

$$\begin{aligned}\pi(t) &= \mathbb{P}\left(\sup_{\tau \leq t} \sum_{s=1}^{\tau} I_1(s) W_{z(s),1} \geq R_1\right) \\ &\overset{(a)}{=} \sum_{\rho=0}^{t} \binom{t}{\rho} p^{\rho}(1-p)^{t-\rho} \cdot \mathbb{P}\left(\sup_{m \leq \rho} \sum_{s=1}^{m} W_{z(s),1} \geq R_1\right) \\ &= \sum_{\rho=0}^{t} \binom{t}{\rho} p^{\rho}(1-p)^{t-\rho} q_{\rho} \end{aligned} \tag{7}$$

where equation (a) is obtained by conditioning over the number ρ of variables $I_1(s) = 1$, and we have defined q_ρ:

$$q_\rho := \mathbb{P}\left(\sup_{m \leq \rho} \sum_{s=1}^{m} W_{z(s),1} \geq R_1\right) \tag{8}$$

which can be interpreted as the probability that a node, which has sequentially received the influence of ρ infected neighbors, has become active. Let $q_\infty := \lim_{\rho \to \infty} q_\rho$. Note that, as consequence of elementary properties of random walks, $q_\infty = 1$ when $\mathbb{E}[W_{ij}] \geq 0$ (recall also (5)). We introduce the following fundamental quantity:

$$\rho^* := \min\{\rho \geq 2 : \ q_\rho > 0\} \tag{9}$$

In words, ρ^* is the minimum number of infected neighbors that can potentially (with probability q_{ρ^*}) activate a node. Note that, as consequence of (5), it must be $\rho^* \geq 2$. For example, under the distributions shown in Fig. 2, we have $\rho^* = 3$, $q_{\rho^*} = \mathbb{P}(R_i = 6) \cdot \mathbb{P}(W_{ij} = 2)^3$.

4.2 Main results

We are now in the position to state our main results for the generalized bootstrap percolation model in $G(n, p)$. First, we define:

$$t_c := \left(\frac{(\rho^* - 1)!}{np^{\rho^*} q_{\rho^*}}\right)^{\frac{1}{\rho^* - 1}}; \qquad a_c := \left(1 - \frac{1}{\rho^*}\right) t_c$$

Moreover, we shall consider the function:

$$\begin{aligned} &H(x) := 1 - x + x \log x, \quad x > 0, \quad H(0) := 1, \\ &H(x) := +\infty, \quad x < 0 \end{aligned}$$

THEOREM 4.1 (SUPER-CRITICAL CASE). *Under the assumptions: $1/(np) \to 0$, $p = o(n^{-1/\rho^*})$, $a/a_c \to \alpha$ for some $\alpha > 1$. Then,*

$$\forall\ \delta > 0, \quad \mathbb{P}\left(\left|\frac{A^*}{n} - q_\infty\right| > \delta\right) = O\left(\mathrm{e}^{-C_1(\rho^*, \alpha) a + o(a)}\right),$$

where $C_1(\rho^*, \alpha)$ is the constant:

$$C_1(\rho^*, \alpha) := \min_{x \in [\alpha \frac{\rho^* - 1}{\rho^*}, \infty)} \frac{x^{\rho^*}}{\alpha(\rho^* - 1)} H\left(\frac{x\rho^* - \alpha(\rho^* - 1)}{x^{\rho^*}}\right).$$

For the sub-critical case, we define the function $h(x) := x - (\rho^*)^{-1} x^{\rho^*} - \alpha(1 - (\rho^*)^{-1})$, for $x \in [0, 1]$, $\alpha \in (0, 1)$, and we denote by $\varphi(\alpha)$ the only[4] solution of $h(x) = 0$, $x \in [0, 1]$. Furthermore, having defined the interval $I := \left(0, (1 - \alpha)(1 - (\rho^*)^{-1})\right)$, it holds:

$$\forall \delta > 0, \exists \varepsilon_\delta \in I : [-\delta, \delta] \supseteq [h^{-1}(-\varepsilon_\delta) - \varphi(\alpha), h^{-1}(\varepsilon_\delta) - \varphi(\alpha)]$$

THEOREM 4.2 (SUB-CRITICAL CASE). *Under the assumptions: $1/(np) \to 0$, $p = o(n^{-1/\rho^*})$ and $a/a_c \to \alpha$ for some $\alpha \in (0, 1)$. Then, $\forall \delta > 0$,*

$$\mathbb{P}\left(\left|\frac{A^*}{a} - \frac{\rho^*}{\rho^* - 1}\frac{\varphi(\alpha)}{\alpha}\right| > \delta\right) = O\left(\mathrm{e}^{-C_2(\rho^*, \alpha, \varepsilon_\delta) a + o(a)}\right),$$

where ε_δ and $\varphi(\alpha)$ are defined as above, and

$$C_2(\rho^*, \alpha, \varepsilon) := \frac{1}{\alpha(\rho^* - 1)} H\left(1 + \varepsilon\rho^*\right).$$

REMARK 4.3. *Note that the above results depend crucially on the extreme values of the distributions of R_i and W_{ij} through the expression of the percolation threshold a_c, which itself depends on ρ^*, defined in (9), and its associated probability q_{ρ^*}, see (8).*

[3]For example, on some online platforms, notifications that a user has watched a given viral video, bought a product, expressed interest for an event, etc., might be sent immediately (and once) to his friends, no matter if the user changes his mind later on.

[4]Function h is continuous and strictly increasing on $[0, 1]$ with $h(0) = -\alpha(1 - (\rho^*)^{-1}) < 0$ and $h(1) = (1 - (\rho^*)^{-1})(1 - \alpha) > 0$.

We shall provide here a sketch of the proof of Theorems 4.1 and 4.2. The complete proofs, including all mathematical details, can be found in [14].

At high level, we can show that almost complete percolation occurs under super-critical conditions, by:

i) analysing the trajectory of the mean of process (2), $\mathbb{E}[A(t)] = a - t + (n-a)\pi(t)$, finding conditions under which the above quantity is positive (with a sufficient guard factor) for any $t < (q_\infty - \delta)n$, for arbitrarily small $\delta > 0$.

ii) showing that the actual process $A(t)$ is sufficiently concentrated around its mean that we can conclude that $A(t) > 0$ w.h.p. for any $t < (q_\infty - \delta)n$.

For the sub-critical regime we can use similar arguments, showing that $\mathbb{E}[A(t)]$ becomes negative at early stages, and that $A(t)$ is sufficiently concentrated around its average that we can claim that the actual process stops at early stages w.h.p.

We start from the asymptotic approximation of $\pi(t)$:

$$\pi(t) = \frac{(pt)^{\rho^*}}{\rho^*!}(q_{\rho^*} + O(pt + t^{-1})). \tag{10}$$

which holds for any t such that $pt \to 0$. The above approximation allows us to write, for any $t \ll p^{-1}$:

$$\mathbb{E}[A(t)] = a - t + (n-a)\pi(t) = a - t + n\frac{(pt)^{\rho^*}}{\rho^*!}q_{\rho^*}(1 + o(1))$$

under the further assumption that $a = o(n)$. Thus, having defined for any $t \in \mathbb{R}_+$ function $f(t) = a - t + \frac{(pt)^{\rho^*}}{\rho^*!}q_{\rho^*}$, for n large enough we can determinate the sign of $\mathbb{E}[A(t)]$ for any $t \ll p^{-1}$ by analysing the behavior of $f(t)$. Elementary calculus reveals that $f(t)$ has a unique minimum at:

$$t_c = \left(\frac{(\rho^* - 1!)}{np^{\rho^*}q_{\rho^*}}\right)^{\frac{1}{\rho^* - 1}}$$

with $f(t_c) = a - a_c$, $a_c = \left(1 - \frac{1}{\rho^*}\right)t_c$. Thus, we obtain an asymptotic closed-form expression for the critical number of seeds a_c (one can easily verify that, under the assumption $\frac{1}{n} \ll p \ll n^{\frac{1}{\rho^*}}$, it holds $t_c \to \infty$, $a_c \to \infty$, $pt_c \to 0$, $\frac{a_c}{n} \to 0$).

The difficult part of the proofs is to show that $A(t)$ is sufficiently concentrated around its expectation that we can establish exponential bounds (as $n \to \infty$) on the probability that the final size of the epidemics falls outside the intervals stated in Theorems 4.1 (super-critical case) and 4.2 (sub-critical case).

For the super-critical case, we adapt a methodology proposed in [6], which separately considers four time segments[5]: i) segment[6] $[a, Kt_c]$ (where K is a constant); ii) segment $[Kt_c, p^{-1}]$; iii) segment $[p^{-1}, cn]$ (where c is a constant); iv) segment $[cn, n(q_\infty - \delta)]$. Note that segment i) contains the most crucial, initial phase of the process.

The following lemma provides a fundamental property related to segment i), which provides the key to obtain the result in Theorem 4.1:

[5]The boundaries of all segments are to be meant as integers. However, to simplify the notation, we will omit $\lfloor\cdot\rfloor$ and $\lceil\cdot\rceil$ symbols.

[6]note that the process cannot stop at $t < a$.

LEMMA 4.4. *Under the assumptions of Theorem 4.1, let $K > \alpha(1 - (\rho^*)^{-1})$ be an arbitrarily fixed constant.*

$$\mathbb{P}\left(\inf_{t\in[a,Kt_c]}\{a - t + S(t)\} \le 0\right) = O\left(\mathrm{e}^{-C_1(\rho^*,\alpha)a + o(a)}\right),$$

where $C_1(\rho^*, \alpha)$ is given in the statement of Theorem 4.1.

The detailed proof is reported in Appendix A. We outline here the three main ingredients to prove Lemma 4.4: i) we exploit standard concentration results for the binomial distribution, providing exponential bounds to $P(|S(t) - \mathbb{E}[S(t)]| > \epsilon t_c)$ at any t in the considered domain; ii) we employ the union bound to upper bound the probability $P(\sup_t |S(t) - \mathbb{E}[S(t)]| > \epsilon t_c)$ by $\sum_t P(|S(t) - \mathbb{E}[S(t)]| > \epsilon t_c)$; iii) we use the property $E[S(xt_c)] = x^{\rho^*}\frac{t_c}{\rho^*} + o(t_c)$.

We emphasize that in this paper we employ different techniques with respect to those used in [6], where authors rely on concentration results for $\sup_t |S(t) - \mathbb{E}[S(t)]|$ derived from Martingale theory (Doob's inequality). Instead, we combine deviation bounds specifically tailored to the binomial distribution (see Appendix A) with the union bound, obtaining a conceptually simpler approach which also permits us to obtain explicit exponential laws for probabilities related to the final size of the epidemics (i.e., a stronger result with respect to main Theorem 3.1 in [6], which holds just w.h.p.).

As immediate consequence of Lemma 4.4 we can say that the process does not stop before Kt_c with probability $1 - \zeta(n)$, being $\zeta(n) = O\left(\mathrm{e}^{-C_1(\rho^*,\alpha)a + o(a)}\right)$.

Considering that $E[S(xt_c)] \sim x^{\rho^*}\frac{t_c}{\rho^*}$ quickly (super-linearly) increases after Kt_c (as long as approximation (10) holds), we can expect that the process is extremely unlikely to stop in segment $[Kt_c, p^{-1}]$, if it survives the first bottleneck segment. The proof of this fact is reported in Appendix A, where we also handle segment $[p^{-1}, cn]$.

Here we focus instead on the last temporal segment, where the value of q_∞ comes into play determining the final size of the epidemics. Indeed, we are going to show that $q_\infty n + o(n)$ are infected with probability $1 - \zeta(n)$. In general, we can assume that $q_\rho = q_\infty - v(\rho)$ with $v(\rho) \to 0$. Given an arbitrary $\hat{\rho}$ such that $\rho^* \le \hat{\rho} < cnp$, we make use of concentration inequality (24) to write:

$$\begin{aligned}
\pi(cn) &\ge \sum_{\rho=\hat{\rho}}^{cn}\binom{cn}{\rho}p^\rho(1-p)^{cn-\rho}q_\rho \\
&\ge \sum_{\rho=\hat{\rho}}^{cn}\binom{cn}{\rho}p^\rho(1-p)^{cn-\rho}(q_\infty - v(\hat{\rho})) \\
&= \mathbb{P}(\mathrm{Bin}(cn,p) \ge \hat{\rho})(q_\infty - v(\hat{\rho})) \\
&\ge (q_\infty - v(\hat{\rho}))(1 - \mathrm{e}^{-cnpH(\hat{\rho}/(cnp))}) \\
&\ge q_\infty - (v(\hat{\rho}) + \mathrm{e}^{-cnpH(\hat{\rho}/(cnp))}) \\
&\ge q_\infty - \frac{\epsilon}{2}
\end{aligned} \tag{11}$$

for any arbitrary $\epsilon > 0$ (and n large enough). We have:

$$\begin{aligned}
\mathbb{P}\left(\inf_{t\in[cn,n(q_\infty-\epsilon)]} a - t + S(t) \le 0\right) &\le \mathbb{P}(S(cn) + a \le n(q_\infty - \epsilon)) \\
&\le \mathbb{P}\left(\mathrm{Bin}(n, 1 - \pi(cn)) \ge n(1 - q_\infty + \epsilon)\right)
\end{aligned}$$

Exploiting (25), the above probability goes to 0 faster than $\zeta(n)$ for any $\epsilon > 0$, proving that at least $n(q_\infty - \epsilon)$

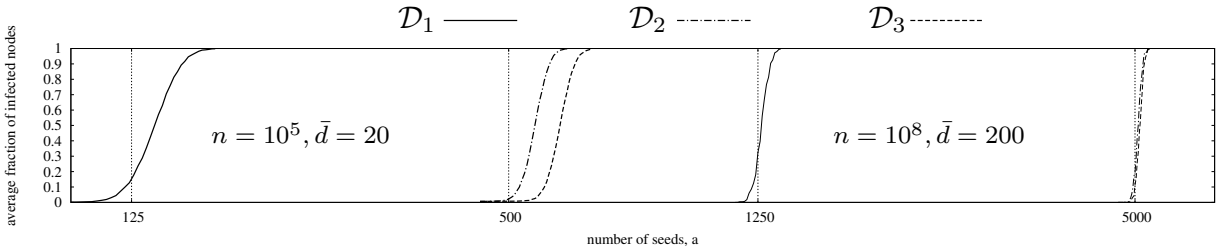

Figure 3: Phase transitions in $G(n,p)$ for different threshold distributions $\mathcal{D}_1$, $\mathcal{D}_2$, $\mathcal{D}_3$, averaging the results of $10,000$ simulations. Analytical predictions are shown as vertical dotted lines.

nodes are infected. When $q_\infty < 1$, we can similarly show that no more than $n(q_\infty + \epsilon)$ nodes are infected. Indeed, considering that $\pi(n(q_\infty + \epsilon)) < q_\infty$, we can apply (24) to show that $\mathbb{P}(S(n(q_\infty + \epsilon) + a - n(q_\infty + \epsilon) < 0)$ goes to 1 faster than $\zeta(n)$, for any $\epsilon > 0$.

4.3 Validation

To validate our analysis, and understand how well asymptotic results can predict what happens in large (but finite) systems, we have run Monte-Carlo simulations of our generalized bootstrap percolation model. In each run we change both the identity of the seeds and the structure of the underlying $G(n,p)$ graph. We compute the average fraction of nodes that become infected, averaging the results of 10,000 runs.

We first look at the impact of random thresholds, while keeping equal weight $W_{ij} = 1$ on all edges. We consider three different distributions of R_i: i) constant threshold equal to 2 (denoted $\mathcal{D}_1$); ii) uniform threshold in the set $\{2,3,4,5\}$, (denoted $\mathcal{D}_2$); iii) two-valued threshold, with $\mathbb{P}(R_i = 2) = 1/4$ and $\mathbb{P}(R_i = 10) = 3/4$ (denoted $\mathcal{D}_3$); Note that all three distributions have $\rho^* = 2$, but their expected values are quite different. Moreover, $q_{\rho^*} = 1$ for $\mathcal{D}_1$, whereas $q_{\rho^*} = 1/4$ for both $\mathcal{D}_2$ and $\mathcal{D}_3$.

The asymptotic formula for the critical number of seeds gives in this scenario $a_c = n/(2\bar{d}^2 q_{\rho^*})$. We consider either a 'small' system, in which $n = 10^5$, $\bar{d} = 20$, or a 'large' system, in which $n = 10^8$, $\bar{d} = 200$. Results are shown in Fig. 3 using a log horizontal scale on which we have marked the values of a_c derived from the asymptotic formula. We use the same line style for each threshold distribution, and different line width to distinguish the small system (thick curves) from the large system (thin curves).

We make the following observations: i) the position of the phase transition (i.e., the critical number of seeds) is well estimated by the asymptotic formula; ii) despite having quite different shapes, distributions $\mathcal{D}_2$ and $\mathcal{D}_3$ lead asymptotically to the same critical number of seeds, as suggested by results obtained in the large system, where the corresponding curves are barely distinguishable (at $a_c = 5000$); iii) phase transitions become sharper for higher values of the critical number of seeds, confirming that the probability law by which the process is supercritical/subcritical depends strongly on a_c itself (as stated in Theorems 4.1 and 4.2).

We next move to a scenario in which the threshold is fixed, $R_i = 2$, and we vary the weights on the edges. We will consider, for simplicity, a simple case in which the influence exerted between two nodes can take just two values: +1, with probability z, and -1, with probability $1-z$. Note that the average influence, $\mathbb{E}[W_{ij}] = 2z-1$, can even be negative, if we select $z < 1/2$. In this scenario, we have $\rho^* = 2$, $q_{\rho^*} = z^2$, hence $a_c = n/(2(\bar{d}z)^2)$. We consider either a 'small' system, in which $n = 10^5$, $\bar{d} = 20$, or a 'large' system, in which $n = 10^7$, $\bar{d} = 200$, which produce the same value of a_c, for any z.

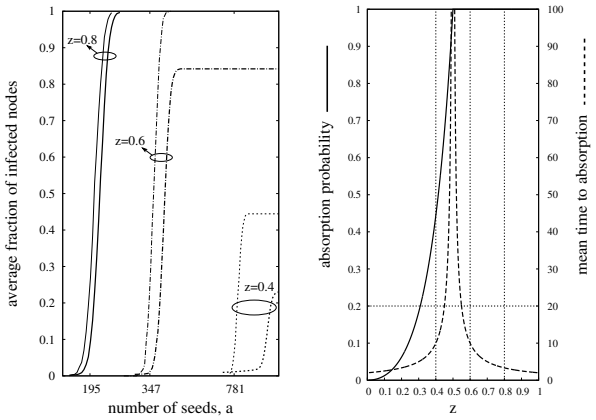

Figure 4: (left plot) Phase transitions in $G(n,p)$ for fixed threshold $R_i = 2$, and random weights ± 1, with $\mathbb{P}(W_{ij} = 1) = z$. (right plot) results for the corresponding simple random walk.

Results are shown in Fig. 4 (left plot), using a log horizontal scale on which we have marked the values of a_c derived from the asymptotic formula. We use the same line style for each value of z, and different line width to distinguish the small system (thick curves) from the large system (thin curves). We observe that in the small system the average fraction of infected nodes saturates to a value significantly smaller than one for $z = 0.6$, although we expect that, as $n \to \infty$, all nodes should get infected in this case (for which $q_\infty = 1$). In the large system, the discrepancy between simulation and asymptotic results disappears.

This phenomenon can be explained by considering that the counter of inactive nodes behaves as a simple random walk (i.e., with steps ± 1) with an absorbing barrier at $\rho^* = 2$. Recall [13] that for this simple random walk the absorption probability is 1 for $z \geq 1/2$, while it is equal to $(z/(1-z))^2$ for $z < 1/2$. Moreover, the mean time to absorption (conditioned to the event that the walk is absorbed) is $2/|1-2z|$ (see right plot in Fig. 4). On the other hand, the time horizon of this equivalent random walk is limited by the node degree, since a node cannot receive a number of contributions to its counter greater than the number of its neighbors. In the small system the average degree ($\bar{d} = 20$) is too small to approach the asymptotic prediction, whereas in the large system the average degree ($\bar{d} = 200$) is large enough (i.e., much larger than the

mean time to absorption) to observe convergence of the final size to the asymptotic prediction obtained with q_∞. Interestingly, a finite fraction of nodes (asymptotically, around 0.44) gets infected with $z = 0.4$, a case in which the average node-to-node influence is negative!

5. RANDOM GRAPHS WITH ARBITRARY DEGREE DISTRIBUTION

Up to now we have considered the $G(n,p)$ random graph model, and we have followed the same problem reformulation adopted in [6], in which a single node is used at a time, revealing all its outgoing edges. This approach is especially suitable to $G(n,p)$, since marks $M_i(t)$ are i.i.d binomial random variables. We introduce now an alternative description of the percolation process, in which a single edge is used at a time. This approach is more convenient to analyze other random graph models, such as $G(n,M)$ (graphs with pre-established number of edges), $G(n,d)$ (where all nodes have the same degree), or the configuration model.

5.1 Edge-based reformulation for $G(n,M)$

We consider the (multi)-graph $\tilde{G}(n,M)$ in which, starting from a graph with no edges, M edges are sequentially added, each connecting two nodes selected (independently) uniformly at random. Note that by so doing we can generate parallel edges, as well as self loops. However, following the same approach as in Corollary 3 of [5], it is possible to show that sequences of events that occur w.h.p. over $\tilde{G}(n,M)$, occur w.h.p. also over $G(n,M)$, with $G(n,M)$ denoting the class of (simple)-graphs having M edges, with associated uniform probability law. Therefore our results apply to $G(n,M)$ as well.

To analyze bootstrap percolation in $\tilde{G}(n,M)$, we consider the following dynamical process: when a node becomes active, all edges connecting this node to other nodes which are still non active are denoted as 'usable', and added to a set $\mathcal{B}$ of usable edges. At a given time step t, one usable edge is selected uniformly at random from $\mathcal{B}(t-1)$, adding one mark to the endpoint that was inactive (when the edge became usable), provided that this endpoint is still inactive. The selected edge is then removed from $\mathcal{B}(t)$. Set $\mathcal{B}(0)$ is initialized with the edges connecting seeds to non-seeds. By construction, at most one node can become active at each time instant. Hence, denoting with $A(t)$ the number of active nodes at time t (initialized to a), we have $A(t) \le a + t$.

Let $\pi(t)$ be the probability that a node, which is not a seed, has been activated at time $\tau \le t$. While it is not easy to write an exact expression of $\pi(t)$, we can provide asymptotically tight bounds on $\pi(t)$, as follows:

$$1-\sum_{j=0}^{r-1}\binom{t}{j}\Big(\frac{1}{n}\Big)^j\Big(1-\frac{1}{n}\Big)^{t-j} \le \pi(t) \le$$
$$1-\sum_{j=0}^{r-1}\binom{t}{j}\Big(\frac{1}{n-a-t}\Big)^j\Big(1-\frac{1}{n-a-t}\Big)^{t-j}$$

This because we can reveal the endpoint of an active edge only when this edge is used, by choosing uniformly at random one of the nodes that were non active at the time instant τ' at which the considered edge became active. Hence, an inactive node i receives a mark at time τ with probability $\frac{1}{n-A(\tau')}$ (independently from other previously collected marks). Furthermore, by construction, we have $\frac{1}{n} \le \frac{1}{n-A(\tau')} \le \frac{1}{n-A(\tau)} \le \frac{1}{n-a-\tau} \le \frac{1}{n-a-t}$. At timescale $t = o(n)$, we can approximate $\pi(t)$ as:

$$\pi(t) = 1-\sum_{j=0}^{r-1}\binom{t}{j}\Big(\frac{1}{n}\Big)^j\Big(1-\frac{1}{n}\Big)^{t-j}+o(1) = \frac{1}{r!}\left(\frac{t}{n}\right)^r+o(1) \tag{12}$$

The dynamics of $\mathcal{B}(t)$ (whose size is denoted by $B(t)$) obey the following equation:

$$B(t) = B(0) + \Sigma(t) - t$$

where $\Sigma(t)$ represents the (cumulative) number of edges activated at $\tau \le t$. The process stops at time $T = \min\{t : B(t) = 0\}$. Similarly to the $G(n,p)$ case, the number $S(t)$ of nodes that have become active by time t is the sum of $n-a$ identically distributed Bernoulli random variables with average $\pi(t)$. Indeed, $S(t) = \sum_{i\in\mathcal{V}\setminus\mathcal{A}(0)} \mathbb{1}_{M_i(t)=r}$.

Note that by construction marks are distributed only to inactive nodes, therefore a node i stops receiving marks as soon as $M_i(t) = r$. Differently from $G(n,p)$, however, variables $\mathbb{1}_{M_i(t)=r}$ are not independent, given that at most t marks have been distributed by time t (i.e., $\sum_i M_i(t) \le t$). Note that we still have $\mathbb{E}[S(t)] = (n-a)\pi(t)$.

For what concerns the total number of edges activated by time t, $\Sigma(t)$, we can express it as the sum of random variables X_k associated with nodes in $\mathcal{A}(t)$, representing the numbers of edges activated along with node k (i.e. the number of edges connecting node k with inactive nodes):

$$\Sigma(t) = \sum_{k=1}^{A(t)} X_k.$$

We can evaluate X_k by dynamically unveiling, for every inactive edge, whether node k is one of its endpoints (but not both). It turns out $X_k = \mathrm{Bin}\Big(M-\Sigma(\tau_k-1)-B(0), \frac{2}{n-A(\tau_k-1)}-\frac{2}{(n-A(\tau_k-1))^2}\Big)$ where τ_k is the time instant at which the k-th node was activated. Indeed, $M-\Sigma(\tau_k-1)-B(0)$ represents the number of edges still to be activated at time τ_k, while $\frac{2}{n-A(\tau_k-1)}-\frac{2}{(n-A(\tau_k-1))^2}$ is the probability that node k is an endpoint (but not both) of any such edges. Observe that variables X_k are not independent, as consequence of the fact that that sum of all edges in the graph is constrained to be M. However, X_k is conditionally independent from $X_{k'}$, with $k' < k$, given $\Sigma(\tau_k-1)$ and $A(\tau_k-1)$. Moreover, for any k we have:

$$\begin{aligned}&\mathrm{Bin}\Big(M-\Sigma(t)-B(0), \frac{2}{n}-\frac{2}{n^2}\Big) \le_{st} X_k\\ &\le_{st} \mathrm{Bin}\Big(M, \frac{2}{n-a-t}-\frac{2}{(n-a-t)^2}\Big).\end{aligned} \tag{13}$$

In particular, the expectation of $\Sigma(t)$ satisfies:

$$\mathbb{E}\left[\frac{2(n-1)(M-\Sigma(t)-B(0))}{n^2}A(t)\right] \le \mathbb{E}[\Sigma(t)] \le \frac{2M\mathbb{E}[A(t)]}{n-a-t}.$$

Moreover, under the assumption $a \ll n$, since for $t \ll n$, $A(t) \le a+t \ll n$ and $\Sigma(t)+B(0) = o(M)$, we have:

$$\mathbb{E}[\Sigma(t)] = \frac{2M}{n}\mathbb{E}[A(t)](1+o(1)) = 2M\pi(t)(1+o(1))$$

while $B(0) = \frac{2M}{n}a(1+o(1)))$. Recalling (12), we have in conclusion:

$$\mathbb{E}[B(t)] = \left(\frac{2M}{n}a + \frac{2M}{r!}\left(\frac{t}{n}\right)^r - t\right)(1+o(1))$$

Now, similarly to the case of $G(n,p)$, we can determine the critical number of seeds by: i) determining sufficient and necessary conditions under which $\mathbb{E}[B(t)] > \delta\frac{M}{n}a$ for some arbitrary $\delta > 0$ and any $t \ll n$; so doing we determine the critical number of seeds a_c. ii) Exploiting the fact that $B(t)$ is sufficiently concentrated around its mean for $t \leq K\frac{M}{n}a_c$, where $K > 1$ is a properly defined constant. iii) Showing that for $K\frac{M}{n}a_c < t < M(1-\epsilon)$, $B(t)$ can be bounded from below away from 0.

For what concerns point i) we follow the same lines as for $G(n,p)$, defining function $g(t) = 2\frac{M}{n}a + \frac{2M}{r!}\frac{t^r}{n^r} - t$, and finding the minimum of $g(t)$, which is achieved at:

$$t_c = \left(\frac{(r-1)!n^r}{2M}\right)^{\frac{1}{r-1}} = \frac{2M}{n}\left(\frac{(r-1)!}{\frac{2M}{n}(\frac{2M}{n^2})^{r-1}}\right)^{\frac{1}{r-1}}$$

with $t_c = o(n)$ as long as $M \gg n$. Observe that $\frac{2M}{n}$ is the average node degree (replacing np in the expression of t_c obtained for $G(n,p)$) while $\frac{2M}{n^2}$ can be interpreted as the probability that two specific vertices are connected by at least an edge (replacing p for $G(n,p)$). Evaluating $g(t_c)$ and imposing $g(t_c) = 0$, we obtain the critical number of seeds:

$$a_c = \left(1 - \frac{1}{r}\right)\left(\frac{(r-1)!}{\frac{2M}{n}(\frac{2M}{n^2})^{r-1}}\right)^{\frac{1}{r-1}} \tag{14}$$

which is exactly the same as what we get in $G(n,p)$ through the substitution $\frac{2M}{n} \to np$ and $\frac{2M}{n^2} \to p$.

For what concerns ii) and iii) we can proceed in analogy with the case of $G(n,p)$, exploiting standard concentration results. In particular, we first focus on time instants $t \leq K\frac{M}{n}a_c$ for suitable $K > 2$. We need to show that $B(t) > 0$ w.h.p. provided that $\mathbb{E}[B(t)] > \epsilon a_c$ for arbitrary $\epsilon > 0$ (i.e., $a > (1+\epsilon)a_c$). To this end observe that from (13), the fact that $\Sigma(K\frac{M}{n}a_c) = o(M)$ and $A(K\frac{M}{n}a_c) = o(n)$, and recalling the above mentioned property of conditional mutual independence of variables X_k, it descends that w.h.p., for any $t \leq K\frac{M}{n}a_c$: $P(\Sigma(t) \leq t - B(0)) \leq P(\sum_1^{A(t)} \overline{X}_k \leq t - B(0))$ with $\overline{X}_k$ mutually independent and $\overline{X}_k = \mathrm{Bin}\Big(M(1-\epsilon), \frac{2}{n} - \frac{2}{n^2}\Big)$ for an arbitrarily small $\epsilon > 0$. At last observe that $P(\sum_1^{A(t)} \overline{X}_k \leq t - B(0))$ can be easily bounded using inequalities (24) and (25).

For what concerns iii) we adopt arguments conceptually similar to the case of $G(n,p)$, exploiting the fact that $\mathbb{E}[B(t)]$ quickly (super-linearly) increases after $K\frac{M}{n}a_c$.

5.2 Configuration Model

The edge-based problem reformulation described in previous section can be easily extended to the configuration model $G(n,p(d))$, in which we specify a given degree sequence (possibly dependent on n) with associated empirical distribution function $p(d)$. For simplicity, we limit ourselves to describing the computation of the critical number number of seeds a_c. However, the approach can be made rigorous by following the same lines as for $G(n,M)$. As before, properties of multi-graphs $\tilde{G}(n,p(d))$ apply as well to simple-graphs $G(n,p(d))$.

Similarly to what we have done for $G(n,M)$, we focus on the evolution of the number of activable edges:

$$B(t) = B(0) + \Sigma(t) - t$$

and compute the critical time t_c by finding the minimum of $\mathbb{E}[B(t)]$.

The impact of node degree can be taken into account by evaluating the probability $\pi(t,d)$ that a node with degree d has been activated by time t. Moreover, we need to consider the amount of edges that a node contributes to $\mathcal{B}$ after being activated. There are in total $n\bar{d}$ 'end-of-edges' in the network, so the probability that a given end-of-edge is active at time t is $t/(n\bar{d})$. Hence, we can write:

$$\pi(t,d) = 1 - \sum_{j=0}^{r-1}\binom{d}{j}\left(\frac{t}{n\bar{d}}\right)^j\left(1 - \frac{t}{n\bar{d}}\right)^{d-j} + o(1), \tag{15}$$

Since $t/(n\bar{d})$ is small, we can approximate it as

$$\pi(t,d) = \frac{1}{r!}\left(\frac{dt}{n\bar{d}}\right)^r + o(1) \qquad (d \geq r)$$

Observe that since, by construction, a node gets activated thanks to exactly r active edges, it contributes $d-r$ new edges to $\mathcal{B}$. Then for $t \ll n$ since $A(t) \leq t + a \ll n$ we can approximate the average value of $B(t)$ as:

$$\mathbb{E}[B(t)] \sim B(0) + n\sum_{d\geq r}\frac{1}{r!}\left(\frac{dt}{n\bar{d}}\right)^r(d-r)p(d) - t.$$

Now, if we define

$$d^* = \sum_{d\geq r}\left(\frac{d}{\bar{d}}\right)^r\frac{d-r}{\bar{d}}p(d) \tag{16}$$

we obtain $\mathbb{E}[B(t)] \sim B(0) + \frac{\bar{d}nt^r}{r!n^r}d^* - t$, from which we can derive the critical time t_c:

$$t_c = n\left(\frac{(r-1)!}{\bar{d}\,d^*}\right)^{\frac{1}{r-1}}$$

and the critical number of seeds:

$$a_c = \left(1 - \frac{1}{r}\right)n\left(\frac{(r-1)!}{\bar{d}^r\,d^*}\right)^{\frac{1}{r-1}} \tag{17}$$

One can easily check that the above formula is consistent with what we get in $G(n,p)$ or $G(n,M)$, for which $d^* \sim 1$. The above formula holds when seeds are selected uniformly at random. However, note that our analysis could be immediately extended to the important case in which seeds are chosen on the basis of the node degree. Indeed, what really matters is only the cardinality of the initial set of edges connecting seeds to non-seeds.

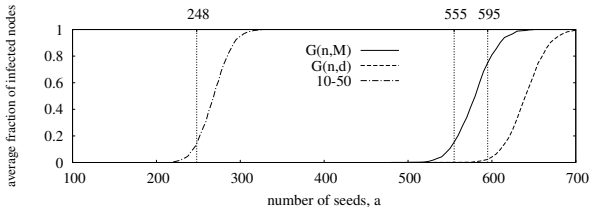

Figure 5: Phase transitions of basic bootstrap percolation with $r = 2$, in different random graph models with $n = 10^6$, $\bar{d} = 30$.

Figure 5 reports simulation results for three different random graph models having $n = 10^6$ nodes, and average node degree $\bar{d} = 30$. We consider basic bootstrap percolation with $r = 2$. We compare the $G(n,M)$ model, the regular $G(n,d)$ (in which nodes have constant degree), and a configuration model in which half of the nodes have

degree 10 while the other half have degree 50 (curve labelled '10-50'). Analytical results obtained by (14) (for $G(n, M)$), and by (17) (for the other two graph models) are marked on the top margin. As expected, for fixed average degree, the critical number of seeds decreases for increasing variance of the degree distribution.

We experimented also with a real online social network, considering user-user friendship relations of Orkut, a former social networking site run by Google. In particular, we have used a crawled sub-graph of Orkut with $n = 3,072,441$ nodes [15], hereinafter referred to as Orkut graph, although it represents only a small percentage (11%) of the entire social network. The average node degree of this graph is $\bar{d} = 76.3$, and the maximum degree is $d_{\max} = 33,313$. An interesting question that arises here is the following: does a configuration model with the same number of nodes as the Orkut graph, and exactly the same degree sequence, produce also a similar value of a_c? If the answer is affirmative, it would tell us that the degree distribution alone, and not the entire network structure, could be used to predict (even analytically) the onset of large-scale outbreaks in this kind of systems (as suggested also by [16]). We partially answer this question by running simulations on both the original Orkut graph and the matched configuration model, as well as by analytically evaluating a_c using (17).

Besides basic bootstrap percolation, we explored also the interesting variation in which r is a deterministic function of the node degree. Indeed, note that (15) can be immediately generalized to $r = r(d)$, although in this case we do not get a closed-form expression for a_c, and the minimum of $\mathbb{E}[B(t)]$ has to be computed numerically (we omit the details of this computation).

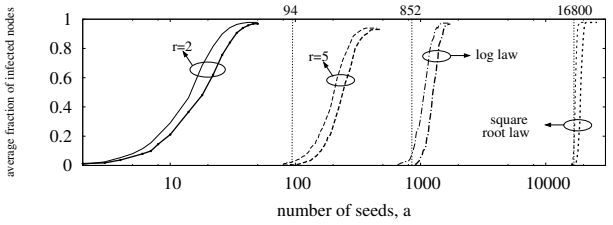

Figure 6: Phase transitions in the Orkut graph and the matched configuration model, for different threshold functions.

Results are shown in Fig. 6, where thick lines refers to the real Orkut graph, while thin lines refers to the matched configuration model. We use different line styles for i) basic bootstrap percolation with $r = 2$ or $r = 5$; ii) the logarithmic law $r(d) = \max\{2, \lceil \log_2(d) \rceil\}$; iii) the square root law $r(d) = \max\{2, \lceil \sqrt{d} \rceil\}$; Analytical predictions of a_c are shown as vertical dotted lines (except for $r = 2$, for which (17) provides a value of a_c even smaller than $r = 2$). We observe similar phase transitions in the Orkut graph and the associated configuration model, while the analysis captures quite well the point after which a major outbreak occurs.

5.3 Impact of power-law degree distribution

Large networks observed in a variety of different domains (social, technological, biological networks) are characterized by the scale-free property, which implies a power law degree distribution. Hence, it is interesting to understand the impact of power-law degree distributions on the critical seed set size. We will consider here power-law degree distributions of the form

$$p(d) = \frac{C}{d^\beta} \qquad \text{for } d_{\min} \le d \le d_{\max} \tag{18}$$

where β is the power-law exponent (typically larger than 2), and C is the normalization factor. We will further assume that $d_{\max} \to \infty$, while $d_{\min} = o(d_{\max})$. Note that by letting $d_{\min}$ scale up with n we can obtain an increasing average node degree (graph densification) in the most common case in which $\beta > 2$.

The reason why we introduce a maximum node degree $d_{\max}$ is instead more subtle, and has to do with the fact that $p(d)$ must be the limiting distribution function of a sequence of empirical distribution function (for each n) associated with the configuration model. Clearly, we cannot have in any case a degree larger than $n-1$, but it turns out that, for the common case of $\beta > 2$, nodes with very large degree are so rare that is preferable to avoid them at all, setting to zero $p(d)$ after a given $d_{\max} = n^\zeta$, with $\zeta < 1$. The maximum value of ζ, for $\beta > 1$, can be obtained by solving the inequality $\int_{n^\zeta}^{\infty} Cx^{-\beta}\,\mathrm{d}x > n^{-1}$. For example, when $\beta > 1$, $d_{\min} = \Theta(1)$, we have $\zeta \le 1/(\beta - 1)$. In practice, we never see nodes with extremely large degree[7], and it is actually customary in many random graph models to assume that the maximum degree is smaller than, say, $n^{1/2}$. In our model, we try to be more flexible by allowing a generic $d_{\max} = n^\zeta \ll n$, satisfying the above constraint (if $\beta > 1$).

In practice, one can starts with a desired distribution $p(d)$ of the form (18), having chosen $d_{\min}$ and $d_{\max}$ (depending on n), and construct a sequence $\{d_i\}_n$ of degrees for the configuration model by assigning to node i the degree $d_i = \inf\{d : 1 - F_n(d) < i/n\}$, where $F_n(d)$ is the cdf of $p(d)$. Under our assumptions we have, asymptotically,

$$C \sim \begin{cases} \frac{1-\beta}{d_{\max}^{1-\beta}} & \text{if } \beta < 1 \\ \frac{\beta-1}{d_{\min}^{\beta-1}} & \text{if } \beta > 1 \end{cases}$$

The following expression for the generic k-th moment of $p(d)$ will come in handy in the following:

$$\mathbb{E}[d^k] \sim \begin{cases} d_{\min}^k \frac{\beta-1}{\beta-k-1} & \text{if } \beta > k+1 \\ d_{\min}^{\beta-1} d_{\max}^{k+1-\beta} \frac{\beta-1}{k+1-\beta} & \text{if } 1 < \beta < k+1 \\ d_{\max}^k \frac{1-\beta}{k+1-\beta} & \text{if } \beta < 1 \end{cases} \tag{19}$$

Note that moments of order $k < \beta - 1$ depend only on $d_{\min}$ (e.g., the average node degree ($k = 1$), when $\beta > 2$). Instead, moments of order $k > \beta - 1$ may depend also (or exclusively) on $d_{\max}$.

Recall that our methodology to compute the critical seed set size requires that a_c is both $\omega(1)$ and $o(n)$. This regime implies that the average node degree $\bar{d}$ cannot be either too small nor too large. Recall that in the $G(n, p)$ model we need that $\bar{d} \gg 1$ and $\bar{d} \ll n^{\frac{r-1}{r}}$. Under a general degree distribution, it is not stricly necessary that $\bar{d} \gg 1$, since (look at formula (17)) we could just have $d^* \to \infty$, resulting into a number of seeds $o(n)$.

To better understand how the critical number of seeds depends on parameters of the power-law distribution, we

[7]In many real systems the tail of the degree distribution exhibits an exponential cut-off, and often the degree cannot exceed a maximum value imposed by physical or technological constraints.

evaluate its scaling order with n, assuming for simplicity that $d_{\min} = n^{\gamma}$, with $0 \leq \gamma < \zeta$. When $\beta > 1$, we further assume $\zeta \leq \frac{1}{\beta-1} - \gamma$ to avoid rare nodes having very large degree. We see from (16) that d^* depends essentially on the $(r+1)$-th moment of $p(d)$, i.e., $d^* = \Theta\left(\frac{\mathbb{E}[d^{r+1}]}{(\mathbb{E}[d])^{r+1}}\right)$ (assuming $\mathbb{E}[d] > r$). We can thus use the expressions in (19), and obtain that the scaling exponent of a_c is [8]

$$e(a_c) = \begin{cases} 1 - \frac{\gamma r}{r-1} & \text{if } \beta > r+2, \quad \gamma > 0 \\ 1 - \frac{\gamma(\beta-2)+\zeta(r+2-\beta)}{r-1} & \text{if } 2 < \beta < r+2, \quad \gamma \geq 0 \\ 1 - \frac{\zeta r}{r-1} & \text{if } \beta < 2, \quad \gamma \geq 0 \end{cases} \tag{20}$$

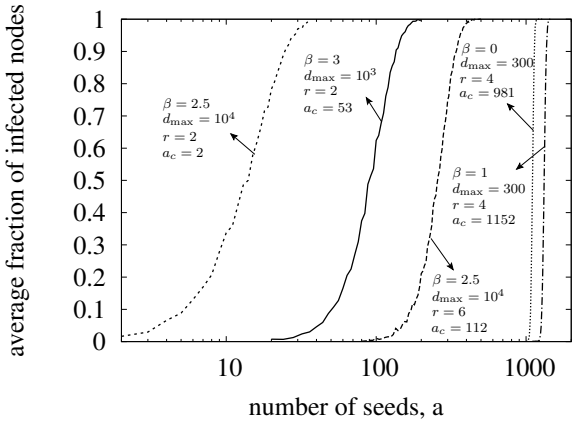

Figure 7: Phase transitions of basic bootstrap percolation in random graphs with $n = 10^6$ nodes and power-law degree.

We should mention that our results are only partially aligned with those obtained for Chung-Lu graphs[9] with power-law degree distribution in [7], where authors consider the case $2 < \beta < 3$, $\gamma = 0$. In particular, in [7] they suggest that, when $d_{\max} = \Theta(n^{1/(\beta-1)})$, a_c is of the order of $n^{\frac{\beta-2}{\beta-1}}$, independently of r. We emphasize that in [7] authors employ a totally different approach with respect to ours, partitioning the nodes into as sequence of bands, on the basis of node degree, the first of which associated to a fairly dense kernel of high-degree nodes. By directly applying the results of [6] to this kernel, they show that, once a fraction of nodes belonging to the kernel become active, the infection easily spreads recursively through the other bands.

Figure 7 reports simulation results under our power-law configuration model. The number of nodes is always $n = 10^6$, $d_{\min} = 10$, and we try different combinations of β, $d_{\max}$ and r. The values of a_c computed by (17) are also shown on the plot. We see that, with $\beta = 2.5$, $d_{\max} = n^{1/(\beta-1)} = 10^4$, very few seeds are needed with $r = 2$, and many more with $r = 6$. We also consider two cases with $\beta < 2$, $d_{\max} = 300$, $r = 4$, to show that, in accordance with (20), when $\beta < 2$, a_c depends essentially only on the extreme value of the node degree distribution (i.e., $d_{\max}$), and not on its shape. Indeed, the phase transitions obtained with $\beta = 0$ and $\beta = 1$ are not that far away, as predicted by our computed values of a_c, despite the fact that the average degree is quite different in the two cases (i.e., 84 ($\beta = 1$) vs 155 ($\beta = 0$)).

[8]The scaling exponent of a generic function $f(n)$ is defined as $e(f) := \lim_{n\to\infty} \frac{\log(f(n))}{\log(n)}$.

[9]Interestingly, our scaling exponent in (20), for $2 < \beta < 3$, $\gamma = 0$, perfectly matches quantity a_c^+ in [7] (Theorem 2.3).

6. COMMUNITY BASED GRAPHS: THE BLOCK MODEL

Another important feature of many graphs representing real systems is the presence of a community structure (i.e., a non-negligible clustering coefficient). This feature is not captured by any of the random graph models considered so far. In this section, we extend the analysis of basic bootstrap percolation to the so called block model, which naturally extends the $G(n,p)$ model to incorporate a community structure. We will start from the simple case of just two communities, and then extend our results to $K < \infty$ communities.

6.1 The case of two communities

We consider a $G(n_1, n_2, p_1, p_2, q)$ block model comprising two communities of n_1 and n_2 nodes, respectively (with $n_1 + n_2 = n$). The sub-graph induced by nodes belonging to community i (with $i = 1, 2$) is an Erdös-Rényi's graph $G(n_i, p_i)$. Pairs of nodes belonging to different communities are independently connected with probability q. We assume $q < \min(p_1, p_2)$ and $q = \Omega(\max(\frac{1}{n_1}, \frac{1}{n_2}))$. We denote by $\mathcal{V}_i$ the set of nodes belonging to community i.

Bootstrap percolation in $G(n_1, n_2, p_1, p_2, q)$ can be reformulated in two different ways, which allow us to obtain different (complementary) results. We explain here our first approach. An alternative reformulation will be presented in Section 6.2.

In our first approach we assume that, at each discrete time step t, two active nodes (one in community 1 and one in community 2) are simultaneously used, whenever they are both available. If a community runs out of (active) usable nodes, while the other still has some available (active) usable nodes, a single node is used at a time. We denote by $\mathcal{A}_i(t)$ and $\mathcal{Z}_i(t)$, respectively, the set of active nodes and the set of used nodes in community i at time t. Let $A_i(t) = |\mathcal{A}_i(t) \setminus \mathcal{Z}_i(t)|$ be the cardinality of the set of active usable nodes in community i. Observe that it is entirely possible that, say, $A_1(t)$ hits zero at some point, but later on it increases again for effect of marks received by inactive nodes in $\mathcal{V}_1$ from nodes used in $\mathcal{V}_2$. This event makes an exact analysis of the system particularly difficult. Note that the process definitely dies at time T: $T := \min\{t \in \mathbb{N}^+ : \ A_1(t) = 0, A_2(t) = 0\}$.

We introduce a new quantity $T_i(t)$, representing the number of nodes that have been used in community i up to time t: $T_i(t) := |\mathcal{Z}_i(t)|$. From the above discussion, observe that $T_i(t)$ is not necessarily equal to t, for $t \leq T$, in constrast to what happens in $G(n,p)$, where $|\mathcal{Z}_i(t)| = t$, $\forall t \leq T$.

The number $S_1(t)$ of initially inactive nodes in $\mathcal{V}_1$ that are active at time t can then be expressed as:

$$S_1(t) = \text{Bin}(n - a_1, \widehat{\pi}_i(T_1(t), T_2(t))$$

where $\widehat{\pi}_1(t_1, t_2) = P(\text{Bin}(t_1, p_1) + \text{Bin}(t_2, q) \geq r)$. For $p_1 t_1 \ll 1$ we have:

$$\widehat{\pi}_1(t_1, t_2) \sim \sum_{\rho=0}^{r} \frac{(p_1 t_1)^{\rho}}{\rho!} \frac{(q t_2)^{r-\rho}}{(r-\rho)!}$$

(similar expressions can be written for $S_2(t)$ and $\widehat{\pi}_2(t_1, t_2)$ provided that $p_2 t_2 \ll 1$). Note that, whenever $t_1 =$

$t_2 = t$, previous approximation simplifies to: $\widehat{\pi}_1(t,t) \sim \sum_{\rho=0}^{r} \frac{p_1^\rho q^{r-\rho}}{\rho!(r-\rho)!} t^r$. Moreover, if $q \ll p_1$, the latter further simplifies to $\widehat{\pi}_1(t,t) \sim \frac{(p_1)^r}{r!} t^r$, as in $G(n,p)$.

To characterize the system behavior, we stochastically upper and lower bound $S_i(t)$, for $i = 1, 2$, by two virtual processes $\underline{S}_i(t)$ and $\overline{S}_i(t)$ obtained in the following shadow systems: a shadow reduced system, in which inter-community edges are removed, and thus each community evolves as in isolation. Note that process $\underline{S}_i(t)$ associated to the reduced system is equivalent to what we would get in a $G(n_i, p_i)$ model; a shadow augmented system (viewed by community i), in which we assume that a new node can *always* be used in the other community (if the other community has no usable nodes, an arbitrary inactive node in the other community is selected and used).

It immediately descends from their definitions that:

$$\begin{aligned} \underline{S}_1(t) &= \text{Bin}(n_1 - a_1, \widehat{\pi}_1(\underline{T}_1(t), 0)) \\ \overline{S}_1(t) &= \text{Bin}(n_1 - a_2, \widehat{\pi}_1(\overline{T}_1(t), t)) \end{aligned}$$

Furthermore, by induction over time, it can be immediately shown that: $\underline{S}_1(t) \leq_{st} S_1(t) \leq_{st} \overline{S}_1(t)$, where $\leq_{st}$ indicates the less or equal operator under usual stochastic ordering (also known as 'first order stochastic dominance'). Now, under the joint conditions $\mathcal{A}_1(\tau) \neq \mathcal{Z}_1(\tau)$ and $\mathcal{A}_2(\tau) \neq \mathcal{Z}_2(\tau)$ for any $\tau < t$, by construction $S_1(\tau) = \overline{S}_1(\tau)$ and $S_2(\tau) = \overline{S}_2(\tau)$ for any $\tau < t$, which allows us to conclude that also at time t: $S_1(t) = \overline{S}_1(t)$ and $S_2(t) = \overline{S}_2(t)$. Then, by induction over time:

$$\begin{aligned} &\{\mathcal{A}_1(\tau) \neq \mathcal{Z}_1(\tau), \mathcal{A}_2(\tau) \neq \mathcal{Z}_2(\tau), \forall \tau \leq t\} \\ &= \left\{ \inf_{\tau<t} \min(S_1(\tau) - \tau + a_1, S_2(\tau) - \tau + a_2) > 0 \right\} \\ &= \left\{ \inf_{\tau<t} \min(\overline{S}_1(\tau) - \tau + a_1, \overline{S}_2(\tau) - \tau + a_2) > 0 \right\}. \end{aligned}$$

In particular, whenever $\overline{S}_1(t)$ and $\overline{S}_2(t)$ both satisfy supercritical conditions, then necessarily $\mathcal{A}_i(t) \neq \mathcal{Z}_i(t)$ and $S_i(t) = \overline{S}_i(t)$, for any $t < \max(n_1, n_2) - o(\max(n_1, n_2))$. More formally, exploiting the results in 4.2, we get:

THEOREM 6.1. *Suppose* $1/(n_i p_i) \to 0$, $p_i = o(n_i^{-1/r})$, $a_i/a_c^{(i)} \to \alpha_i$, *for some* $\alpha_i > 1$ *with* $i = \{1, 2\}$, *and:*

$$a_c^{(i)} = \left(1 - \frac{1}{r}\right) \left(\frac{(r-1)!}{n_i (\widehat{p}_i)^r}\right)^{(r-1)^{-1}}$$

where $\widehat{p}_i = \sqrt[r]{(r!) \cdot \sum_{\rho=0}^{r} \frac{p_i^\rho q^{r-\rho}}{\rho!(r-\rho)!}}$. *Then, having defined* $T = \inf_t\{\min_i(a_i - t + S_i(t)) < 0\}$ *we have:*

$$\forall \varepsilon > 0, P\left(1 - \frac{T}{\max_i(n_i)} > \varepsilon\right) = O\left(\mathrm{e}^{-C_1(r, \min_i(\alpha_i))a + o(a)}\right)$$

where $C_1(r, \alpha)$ *is the same function as in Theorem 4.1.*

Theorem 6.1 provides sufficient (but not necessary) conditions for almost complete percolation of $G(n_1, n_2, p_1, p_2, q)$.

To complement previous result, suppose that $\underline{S}_1(t)$ satisfies supercritical conditions (while to avoid trivialities we assume $\overline{S}_2(t)$ to be sub-critical). In this case complete or almost complete percolation occurs in $\mathcal{V}_1$ as immediate consequence of Theorem 4.1 applied to community 1 in isolation, and the fact that $\underline{S}_1(t) \leq S_1(t)$. Then, under the assumption that $q \geq \Omega(\max(\frac{1}{n_1}, \frac{1}{n_2}))$, we obtain complete or almost complete percolation also in community 2, since any node in $\mathcal{V}_2$ would have finite probability of having at least r neighbors in $\mathcal{V}_1$[10].

It remains to analyze the case in which $\overline{S}_1(t)$ is supercritical (but $\underline{S}_1(t)$ is sub-critical), and $\overline{S}_2(t)$ is not supercritical (or viceversa). This case, which can occur only when q and p_1 are of the same order, is more involved and we leave it to future study.

6.2 Alternative approach for 2 communities

We now introduce a different approach to study the $G(n1, n2, p_1, p_2, q)$ block model, which allows us to understand how seeds should be optimally partitioned between the two communities in order to minimize their number and achieve almost complete percolation in the whole system. This time, we assume that at each time step t a single active node, selected uniformly at random among all usable active nodes in the system, is used.

To simplify the exposition, we will focus on a perfectly symmetric scenario in which $p_1 = p_2$ and $n_1 = n_2 = n/2$. However, the same approach can be easily extended to the general case $G(n_1, n_2, p_1, p_2, q)$.

Differently from our first reformulation, now we have, for any $t < T$:

$$T_1(t) + T_2(t) = t$$

where $T_i(t)$ denotes the (random) number of nodes used in community i up to time t.

Now, if we consider any two different sequences in which active nodes are selected, such that $T_1(t)$ in one sequence is larger than $T_1'(t)$ in the other sequence, we easily see that,

$$S_1(T_1(t), T_2(t)) \geq_{st} S_1(T_1'(t), T_2'(t)) \quad (21)$$

$$S_2(T_1(t), T_2(t)) \leq_{st} S_2(T_1'(t), T_2'(t)) \quad (22)$$

Furthermore, for $1 \ll t \ll p^{-1}$ we have:

$$\begin{aligned} &\mathbb{E}[S_1(T_1(t), T_2(t)) + S_2(T_1(t), T_2(t))] \sim \\ &\sum_{\rho=0}^{r} \frac{(pT_1(t))^\rho (qT_2(t))^{r-\rho}}{\rho!(r-\rho)!} + \sum_{\rho=0}^{r} \frac{(qT_1(t))^\rho (pT_2(t))^{r-\rho}}{\rho!(r-\rho)!} = \\ &f\left(\frac{T_1(t)}{t}\right) \end{aligned} \quad (23)$$

being $f(x) = \sum_\rho [\frac{(ptx)^\rho (qt(1-x))^{r-\rho}}{\rho!(r-\rho)!} + \frac{(qtx)^\rho (pt(1-x))^{r-\rho}}{\rho!(r-\rho)!}]$ a continuous function over $[0, 1]$, indefinitely derivable in $(0, 1)$ and satisfying the following properties: i) $f(x) = f(1-x)$; ii) $f(x)$ decreases for $x \in [0, 1/2)$ (and increases for $x \in (1/2, 1]$). Previous observations lead to:

THEOREM 6.2. *To minimize the number of seeds that are needed to achieve complete or almost complete percolation in the symmetric graph* $G(n/2, n/2, p, p, q)$, *with* $q < p$ *and* $q = \Omega(\frac{1}{n})$, *all seeds have to be placed within the same community.*

The proof is reported in the companion technical report [14]. At high level, the result descends from the fact that, for any given total number of seeds, extremal trajectories of $T_1(t)$ and $T_2(t)$ are obtained when all seeds are placed

[10] More in general, for $q \ll \frac{1}{n_2}$, we could study percolation in community 2 in isolation after: i) adding to a_2 the nodes in $\mathcal{V}_2$ that have at least r neighbors in $\mathcal{V}_1$; ii) reduce the threshold r for all inactive nodes in $\mathcal{V}_2$ to a stochastic threshold $R \leq r$ accounting for marks received from $\mathcal{V}_1$.

in the same community, as a consequence of (21), (22), and properties of (23).

Theorem 6.2 can be easily generalized to the asymmetric case (see [14]):

THEOREM 6.3. *To minimize the number of seeds that are needed to achieve complete or almost complete percolation in $G(n_1, n_2, p_1, p_2, q)$ with $q = \Omega(\frac{1}{n})$, all seeds have to be placed in the community having the maximum value of $n_i(p_i)^r$.*

6.3 Extension to the general block model

Results obtained for the case of two communities can be rather easily extended to a more general block model with $K < \infty$ heterogeneous communities, specified by a symmetric matrix P, whose element p_{jk} represents the probability that a node belonging to community j is connected to a node belonging to community k (with i.i.d. probabilities for all such pairs). Note that diagonal elements of P provide inter-community edge probabilities. In Appendix B, besides our system assumptions, we present two different upper bounds on the critical number of seeds. Interestingly, both bounds depends critically on extreme values of the model parameters, and in some cases a single community can determine the phase transition of the entire system.

7. CONCLUSIONS

We proposed a unique framework to study sub-linear phase transitions of threshold-based 'activation processes' in random graphs, adding inhomogeneities in the system along different (orthogonal) directions. We found that in several cases the critical seed set size depends critically just on extreme values of distributions, providing novel insights into the dynamics of epidemic processes in complex systems.

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APPENDIX

A. THEOREM 4.1

First we introduce the following concentration inequalities for the binomial distribution $\mathrm{Bin}(n,p)$, taken from [17]: Let $H(b) = 1 - b + b\log b$, for $b > 0$. Let $\mu = np$.

If $k \le \mu$ then:

$$\mathbb{P}(\mathrm{Bin}(n,p)) \le k) \le \exp\left(-\mu H\left(\frac{k}{\mu}\right)\right) \tag{24}$$

If $k > \mu$ then:

$$\mathbb{P}(\mathrm{Bin}(n,p)) \ge k) \le \exp\left(-\mu H\left(\frac{k}{\mu}\right)\right) \tag{25}$$

Proof of Lemma 4.4.

For any $\delta > 0$, We have $a = \alpha\, a_c + o(1) > (\alpha - \delta)a_c$, and so, by the definition of a_c, for any $t = a, \ldots, \lfloor Kt_c \rfloor$,

$$\begin{aligned}\{S(t) - t + a \le 0\} &\subseteq \left\{S(t) - t + (\alpha-\delta)(1-(\rho^*)^{-1})t_c \le 0\right\} \\ &= \left\{S(t) \le t - (\alpha-\delta)(1-(\rho^*)^{-1})t_c\right\}\end{aligned}$$

Hence:

$$\begin{aligned}\left\{\inf_{t\in[a,\lfloor Kt_c\rfloor]} S(t) - t + a \le 0\right\} &= \bigcup_{t\in[a,\lfloor Kt_c\rfloor]} \{S(t) - t + a \le 0\} \\ \subseteq \bigcup_{t\in[a,\lfloor Kt_c\rfloor]} &\left\{S(t) \le t - (\alpha-\delta)(1-(\rho^*)^{-1})t_c\right\}\end{aligned}$$

Moreover, defining $x = t/t_c$, it can be be proved that:

$$E[S(xt_c)] = x^{\rho^*}\frac{t_c}{\rho^*} + o(t_c). \tag{26}$$

Using (26) and (24), we have for any $\delta > 0$,

$$\begin{aligned}&P(S(t) \le t - (\alpha-\delta)(1-(\rho^*)^{-1})t_c) < \\ &\mathrm{e}^{-(1-\delta)x^{\rho^*}\frac{t_c}{\rho^*} H\left(\frac{xt_c - (\alpha-\delta)(1-(\rho^*)^{-1})t_c}{(1-\delta)x^{\rho^*}\frac{t_c}{\rho^*}}\right)}\end{aligned}$$

Thus, by sub-additivity of probability:

$$\begin{aligned}&P\left(\inf_{t\in[a,\lfloor Kt_c\rfloor]} S(t) - t + a \le 0\right) \le \\ &\sum_{t\in[a,\lfloor Kt_c\rfloor]} \mathrm{e}^{-(1-\delta)x^{\rho^*}\frac{t_c}{\rho^*} H\left(\frac{xt_c - (\alpha-\delta)(1-(\rho^*)^{-1})t_c}{(1-\delta)x^{\rho^*}\frac{t_c}{\rho^*}}\right)} \\ &\le \frac{K}{\alpha(1-(\rho^*)^{-1})(1+\delta)} \\ &\mathrm{e}^{-\inf_{x\in[a/t_c,K]}\left[\frac{(1-\delta)x^{\rho^*}a}{\alpha(1-(\rho^*)^{-1})\rho^*(1+\delta)} H\left(\frac{x-(\alpha-\delta)(1-(\rho^*)^{-1})}{(1-\delta)\frac{x^{\rho^*}}{\rho^*}}\right)\right]}\end{aligned} \tag{27}$$

the assertion descends immediately taking the inf of (27) with respect to $\delta > 0$ and letting $K \to \infty$.

Segment $[Kt_c, p^{-1}]$. We basically follow [6], choosing $K = 8$ and defining a sequence of time instants $t_j = 8 \cdot 2^j t_c$ for $j = \{0, 1, 2 \cdots J\}$ with $J = \min\{j : pt_j \geq 1\}$. We first show that $\mathbb{E}[S(t_j)] > (1+\delta)t_{j+1}$ for every j and a properly specified $\delta > 0$. Then, applying again union bound and concentration inequality (24) we can prove that $P(S(t_j) \leq t_{j+1}, \text{ for some } j)$ goes to zero faster than $\zeta(n)$. This implies $P(S(t) - t \leq 0, \text{ for some } t \in [8t_c, \lceil p^{-1} \rceil])$ goes to 0 faster than $\zeta(n)$ under super-critical conditions. Indeed, given the monotonicity of $S(t)$, we have $\{a - t + S(t) < 0 \text{ for some } t \in [t_j, t_{j+1}]\} \subseteq \{S(t_j) < t_{j+1}\}$. In conclusion, under super-critical conditions the process never stops before p^{-1} with probability $1 - \zeta(n)$.

Segment $[p^{-1}, c\,n]$. Beyond time p^{-1} we can no longer use (10). However, we can easily handle segment $[p^{-1}, cn]$ and already conclude that, in all cases, the process reaches at least a constant fraction of the nodes (if it survives the bottleneck). For this, we exploit the fact that $\pi(\lceil p^{-1} \rceil) \geq q_{\rho^*} P(\text{Bin}(p^{-1}, p) > R_i) > 2c$ for some constant $c > 0$. Using again union bound and concentration inequalities, we then show that the process never stops before cn with probability $1 - \zeta(n)$.

B. GENERAL BLOCK MODEL

Let $n_k(n)$ be the number of nodes in community k ($k = 1, \ldots, K$), with $n = \sum_k n_k$. We will assume that $n_k(n) \gg 1$, for any k. We focus on a community structure in which $p_{ik} < \min(p_{ii}, p_{kk})$ for any (i, k). Moreover, whenever $p_{ik} \neq 0$, we will assume that $p_{ik} = \Omega(\frac{1}{n_i}, \frac{1}{n_k})$. At last, but without loss of generality, we assume the graph to be connected at the community level; i.e. we assume P to be of maximal rank (equal to $K - 1$). Indeed, if this in not true we can always partition the community-level graph into connected components and apply our results to each connected component.

We first generalize the result in Theorem 6.1:

THEOREM B.1. *Consider a block model with $K < \infty$ communities as defined before; suppose, for any k, that $1/(n\,p_{k,k}) \to 0$, $p_{k,k} = o(n^{-1/r})$, $a_k/a_c^{(k)} \to \alpha_k > 1$, with:*

$$\bar{a}_c^{(k)} = \left(1 - \frac{1}{r}\right) \left(\frac{(r-1)!}{n_k (\widehat{p}_{k,k})^r}\right)^{(r-1)^{-1}}$$

where:

$$\widehat{p}_{k,k} = \left((r!) \cdot \sum_{\substack{\rho_1 \cdots \rho_k \cdots \rho_K \\ \text{with } \sum \rho_j = r}} \frac{p_{k,k}^{\rho_k} \prod_{j \neq k} p_{jk}^{\rho_j}}{\rho_k! \prod_{j \neq k} \rho_j!} \right)^{\frac{1}{r}}$$

Let $T = \inf_t\{\min_k(a_k - t + S_k(t)) < 0\}$. We have:

$$\forall \varepsilon > 0, P\left(1 - \frac{T}{\max_k(n_k)} > \varepsilon\right) = O\left(\mathrm{e}^{-C_1(r, \min_k(r, \alpha_k))a + o(a)}\right)$$

where $C_1(r, \alpha)$ is the same function as in Theorem 4.1.

Theorem B.1 can be used to derive a simple upper bound to the minimum number of seeds that can produce super-critical conditions in all communities, in the case in which seeds are selected uniformly at random among all nodes. Indeed, Theorem B.1 coupled with standard concentration arguments lead to the result that a global number of seeds:

$$a = (1 + \epsilon) n \max_k \frac{\bar{a}_c^{(k)}}{n_k} \tag{28}$$

for any $\epsilon > 0$, is enough to guarantee (almost) complete percolation of the entire graph.

More in general, given an arbitrary allocation of seeds among communities, Theorem B.1 can be used to check whether the considered seed allocation is able to trigger system-wide percolation. On this regard, note that Theorem B.1 can be applied to any community-level connected sub-graph of the entire system: if at least one sub-graph satisfies the conditions of Theorem B.1, we get (almost) complete percolation of the entire system, as consequence of the assumptions that: i) the graph is connected at community level; ii) for non null off diagonal elements of P, $p_{ik} = \Omega(\frac{1}{n_i}, \frac{1}{n_k})$. In particular, note that if we get (almost) complete percolation in just one community, the infection propagates to the entire system.

We can also ask ourselves which is the optimal seed allocation in the system, in the case in which we know the community membership of the nodes. A straightforward extension of Theorem 6.3 provides the answer to this question:

THEOREM B.2. *Consider a general block model graph with $K < \infty$ communities as defined before; assume that $1/(np_{k,k}) \to 0$, $p_{k,k} = o(n^{-1/r})$ for any k. In order to minimize the number of seeds that produce (almost) complete percolation of the entire graph, all seeds must be placed within a single community that maximizes quantity $n_k(p_k)^r$.*

As a consequence, it turns out that a number of seeds:

$$a = (1 + \epsilon) \left(1 - \frac{1}{r}\right) \min_k \left(\frac{(r-1)!}{n_k (p_{k,k})^r}\right)^{(r-1)^{-1}} \tag{29}$$

for any $\epsilon > 0$, is enough to guarantee an almost complete percolation of the graph. Indeed, by placing these a nodes all within a single community that maximizes quantity $n_k(p_k)^r$, let this community be k_0, we have that process $\underline{S}_{k_0}(t)$, and thus process $S_{k_0}(t)$ is super-critical, which is enough to trigger system-wide percolation.

At last, we can exploit Theorem B.2 also to get a different upper bound to the critical number of seeds in the case in which seeds are selected uniformly at random among all nodes. Indeed, it turns out that $a\frac{n}{n_{k_0}}$ seeds, where a is the same as in (29), are enough, since w.h.p. at least $a(1 - \varepsilon/2)$ seeds will fall within community k_0, producing super-critical conditions in community k_0 (and then in the entire system). In the case of very heterogeneous communities, this last bound might be tighter than (28).