# Percolation and Epidemic Processes in One-Dimensional Small-World Networks<sup>\*</sup>

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#### Abstract

We obtain tight thresholds for bond percolation on one-dimensional small-world graphs, and apply such results to obtain tight thresholds for the *Independent Cascade* process and the *Reed-Frost* process in such graphs.

These are the first fully rigorous results establishing a phase transition for bond percolation and SIR epidemic processes in small-world graphs. Although one-dimensional small-world graphs are an idealized and unrealistic network model, a number of realistic qualitative epidemiological phenomena emerge from our analysis, including the epidemic spread through a sequence of local outbreaks, the danger posed by random connections, and the effect of super-spreader events.

**Keywords:** Random graphs, Percolation, Branching Processes, Epidemic models, Independent Cascade, Small-World Graphs.

### 1 Introduction

Given a graph G = (V, E) and a bond percolation probability p, the bond percolation process is to subsample a random graph  $G_p = (V, E_p)$  by independently choosing each edge of G to be included

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in  $E_p$  with probability p and to be omitted with probability 1 - p. We will call  $G_p$  the *percolation* graph of G. The main questions that are studied about this process are whether  $G_p$  is likely to contain a large connected component, and what are the typical distances of reachable nodes in  $G_p$ .

The study of percolation originates in mathematical physics, where it has often been studied in the setting of infinite graphs, for example infinite lattices and infinite trees [20, 30, 33]. The study of percolation on finite graphs is of interest in computer science, because of its relation, or even equivalence, to a number of fundamental problems in network analysis [19, 13, 23, 1] and in distributed and parallel computing [10, 18].

For example, the percolation process arises in the study of *network reliability* in the presence of independent link failures [18, 21]; in this case one is typically interested in *inverse problems*, such as designing networks that have a high probability of having a large connected component for a given edge failure probability 1 - p.

This paper is motivated by the equivalence of the percolation process with the *Independent* Cascade process, which models the spread of information in networks [19, 13], and with the *Reed-Frost* process of Susceptible-Infectious-Recovered (SIR) epidemic spreading [8, 32].

In a SIR epidemiological process, every person, at any given time, is in one of three possible states: either susceptible (S) to the infection, or actively infectious and able to spread the infection (I), or recovered (R) from the illness, and immune to it.

In a network SIR model, we represent people as nodes of a graph, and contacts between people as edges, and we have a probability p that each contact between an infectious person and a susceptible one transmits the infection. The Reed-Frost process, which is the simplest SIR network model, proceeds through synchronous time steps, the infectious state lasts for only one time step, and the graph does not change with time.

The Information Cascade process is meant to model information spreading in a social network, but it is essentially equivalent to the Reed-Frost process.<sup>1</sup>

If we run the Reed-Frost process on a graph G = (V, E) with an initial set  $I_0$  and with a probability p that each contact between an infectious and a susceptible person leads to transmission, then the resulting is equivalent to percolation on the graph G with parameter p in the following sense: the set of vertices reachable from  $I_0$  in the percolation graph  $G_p$  has the same distribution as the set of nodes that are recovered at the end of the Reed-Frost process in G with  $I_0$  as the initial set of infected nodes. Furthermore, the set of nodes infected in the first t steps (that is, the union of infectious and recovered nodes at time t) has the same distribution as the set of nodes reachable in the percolation graph  $G_p$  from  $I_0$  in at most t steps<sup>2</sup>.

Information Cascade and Reed-Frost processes on networks are able to capture a number of features of real-world epidemics, such as the fact that people typically have a small set of close contacts with whom they interact frequently, and more rare interactions with people outside this group, that different groups of people have different social habits that lead to different patterns of transmissions, that outbreaks start in a localized way and then spread out, and so on. Complex models that capture all these features typically have a large number of tunable parameters, that have to be carefully estimated, and have a behavior that defies rigorous analysis and that can be studied only via simulations.

In this work we are interested in finding the simplest model, having few parameters and defining a simple process, in which we could see the emergence of complex phenomena.

<sup>&</sup>lt;sup>1</sup>The main difference is that Information Cascade allows the probability of "transmission" along an edge (u, v) to be a quantity  $p_{(u,v)}$ , but this generalization would also make sense and be well defined in the Reed-Frost model and in the percolation process. The case in which all the probabilities are equal is called the *homogenous* case.

 $<sup>^{2}</sup>$ A detailed description of this equivalence is given in Appendix A.2.

#### One-dimensional small-world graphs

We choose to analyze the Reed-Frost process on *one-dimensional small-world* graphs, which is a fundamental generative model of networks in which there is a distinction between local connection (corresponding to close contacts such as family and coworkers) and long-range connections (corresponding to occasional contacts such as being seated next to each other in a restaurant or a train).

Small-world graphs are a class of probabilistic generative models for graphs introduced by Watts and Strogatz [35], which are obtained by overlaying a low-dimensional lattice with additional random edges. A one-dimensional small-world graph is a cycle overlayed with additional random edges. In the original works of Watts and Strogatz a one-dimensional small-world network is obtained by starting from a cycle, adding edges between any pair of nodes at distance at most k (one of the parameters of the construction) along the cycle, then selecting a random subset of edges (the density of this subset is another parameter of the construction) and re-routing them, where the operation of re-routing an edge is to re-assign one of the endpoints of the edge to a random vertex.

Because of our interest in studying the most basic models, with the fewest number of parameters, in which we can observe complex emergent behavior, we consider the following simplified generative model which was introduced in [27] and often adopted in different network applications [15, 28, 31]: the distribution of *one-dimensional small-world graphs* with parameter q on n vertices is just the union of a cycle with n vertices with an Erdős-Rényi random graph  $\mathcal{G}_{n,q}$ , in which edges are sampled independently and each pair of nodes has probability q of being an edge.

We will focus on the sparse case in which q = c/n, with c constant, so that the overall graph has average degree c + 2 and maximum degree that is, with high probability,  $O(\log n/\log \log n)$ . As we will see, we are able to determine, for every value of c, an exact threshold for the critical probability of transmission and to establish that, above the threshold, the epidemic spreads with a realistic pattern of a number of localized outbreaks that progressively become more numerous.

We are also interested in modeling, again with the simplest possible model and with the fewest parameters, the phenomenon of *superspreading*, encountered both in practice and in simulations of more complex models. This is the phenomenon by which the spread of an epidemic is disproportionately affected by rare events in which an infectious person contacts a large number of susceptible ones. To this end, we also consider a generative model of small-world 1-dimensional graphs obtained as the union of a cycle with a random perfect matching. This generative model has several statistical properties in common with the c = 1 instantiation of the above generative model: the marginal distribution of each edge is the same, and edges are independent in one case and have low correlation in the random matching model. The only difference is the degree distribution, which is somewhat irregular (but with a rapidly decreasing exponential tail) in one case and essentially 3-regular in the second case. As we will see, we are able to determine an exact threshold for this latter model as well, and it notably differs from the previous model.

Before proceeding with a statement of our results, we highlight for future reference the definitions of our generative models.

**Definition 1.1** (1-Dimensional Small-World Graphs - SWG(n,q)). For every  $n \ge 3$  and  $0 \le q \le 1$ , the distribution SWG(n,q) is sampled by generating a one-dimensional small-world graph G = (V, E), where |V| = n,  $E = E_1 \cup E_2$ ,  $(V, E_1)$  is a cycle, and  $E_2$  is the set of random edges, called bridges, of an Erdős-Rényi random graph  $\mathcal{G}_{n,q}$ .

**Definition 1.2** (3-regular 1-Dimensional Small-World Graphs - 3-SWG(n)). For every even  $n \ge 4$ , the distribution 3-SWG(n) is sampled by generating a one-dimensional small-world graph G =

(V, E), where |V| = n,  $E = E_1 \cup E_2$ ,  $(V, E_1)$  is a cycle, and  $E_2$  is the set of edges, called bridges, of a uniformly chosen perfect matching on V.

In the definition of 3-SWG(n), we allow edges of the perfect matching to belong to  $E_1$ . If this happens, only edges in  $E_2 - E_1$  are called bridges. The graphs sampled from 3-SWG(n) have maximum degree 3, and every node has degree 3 or 2. On average, only O(1) nodes have degree 2. This is why, with a slight abuse of terminology, we refer to these graphs as being "3-regular."

## 2 Our Contribution

### 2.1 Tight thresholds for bond percolation

Our main results are to establish sharp thresholds for the critical percolation probability p in both models. In particular, we are interested in fully rigorous analysis that hold in high concentration (i.e., with high probability), avoiding mean-field approximations or approximations that treat certain correlated events as independent, which are common in the analysis of complex networks in the physics literature. While such approximations are necessary when dealing with otherwise intractable problems, they can fail to capture subtle differences between models. For example, for q = 1/n, the marginal distributions of bridge edges are the same in the two models above, while correlations between edges are non-existing in the SWG(n,q) model and very small in the 3-SWG(n) model. Yet, though the two models have similar expected behaviors and are good approximations of each other, our rigorous analysis shows that the two models exhibit notably different thresholds.

As for the the SWG(n,q) model, we show the following threshold behaviour of the bondpercolation process.

**Theorem 2.1** (Percolation on the SWG(n,q) model). Let V be a set of n vertices and p > 0 be a bond percolation probability. For any constant c > 0, sample a graph  $G = (V, E_1 \cup E_2)$  from the SWG(n, c/n) distribution, and consider the percolation graph  $G_p$ . For any constant  $\varepsilon > 0$ :

- 1. If  $p > \frac{\sqrt{c^2 + 6c + 1} c 1}{2c} + \varepsilon$ , w.h.p.<sup>3</sup> a subset of nodes of size  $\Omega_{\varepsilon}(n)$  exists that induces a subgraph of  $G_p$  having diameter  $\mathcal{O}_{\varepsilon}(\log n)$ ;
- 2. If  $p < \frac{\sqrt{c^2+6c+1}-c-1}{2c} \varepsilon$ , w.h.p. all the connected components of  $G_p$  have size  $\mathcal{O}_{\varepsilon}(\log n)$ .

Some remarks are in order. In the theorem above, probabilities are taken both over the randomness in the generation of the graph G and over the randomness of the percolation process. We highlight the sharp result on the SWG(n, c/n) model for the case c = 1: similarly to the regular 3-SWG(n) model, each node here has one bridge edge in average, and the obtained critical value for the percolation probability p turns out to be  $\sqrt{2} - 1$ . An analysis of the critical value for the 3-SWG(n) model is given by the next two results, while a detailed comparison of the two models is provided in Subsection 2.2, after Theorem 2.2.

**Theorem 2.2** (Percolation on the 3- $\mathcal{SWG}(n)$  model). Let V be a set of n vertices and p > 0 be a bond percolation probability. Sample a graph  $G = (V, E_1 \cup E_2)$  from the 3- $\mathcal{SWG}(n)$  distribution, and consider the percolation graph  $G_p$ . For any constant  $\varepsilon > 0$ :

1. If  $p > 1/2 + \varepsilon$ , w.h.p. a subset of nodes of size  $\Omega_{\varepsilon}(n)$  exists that induces a connected subgraph (i.e. a giant connected component) of  $G_p$ ;

<sup>&</sup>lt;sup>3</sup>As usual, we say that an event  $\mathcal{E}_n$  occurs with high probability if  $\Pr(\mathcal{E}_n) \ge 1 - (1/n)^{\Omega(1)}$ .

2. If  $p < 1/2 - \varepsilon$ , w.h.p. all the connected components of  $G_p$  have size  $\mathcal{O}_{\varepsilon}(\log n)$ .

Also in the above theorem, the probabilities are taken over the randomness of G and over the randomness of the percolation process process. The second claim is a special case of the following more general result of ours.

**Theorem 2.3** (Percolation on bounded-degree graphs). Let G = (V, E) be a graph of maximum degree  $d, \varepsilon > 0$  be an arbitrary positive number,  $p < (1-\varepsilon)/(d-1)$  be a bond percolation probability, and  $I_0$  be a subset of V. Consider the percolation graph  $G_p$ . Then, w.h.p., all the connected components of  $G_p$  have size  $\mathcal{O}_{\varepsilon}(\log n)$ .

An overall view of our analysis, leading to all the theorems above, is provided in Section 3, while in the next subsection, we describe the main consequences of our analysis for the Independent-Cascade protocol on the considered small-world models.

### 2.2 Applications to epidemic processes

As remarked in Section 1, bond percolation with percolation probability p is equivalent to the Reed-Frost process (for short, RF process) with transmission probability p. Informally speaking, the nodes at hop-distance t in the percolation graph  $G_p$ , from any fixed source subset, are distributed exactly as those that will be informed (and activated) at time t, according to the RF process<sup>4</sup>.

In this setting, our analysis and results, we described in Subsection 2.1, have the following important consequences.

**Theorem 2.4** (The RF process on the SWG(n,q) model). Let V be a set of n vertices,  $I_0 \subseteq V$  be a set of source nodes, and p > 0 a constant probability. For any constant c > 0, sample a graph  $G = (V, E_1 \cup E_2)$  from the SWG(n, c/n) distribution, and run the RF process with transmission probability p over G from  $I_0$ . For every  $\varepsilon > 0$ , we have the following:

- 1. If  $p > \frac{\sqrt{c^2 + 6c + 1} c 1}{2c} + \varepsilon$ , with probability  $\Omega_{\varepsilon}(1)$  a subset of  $\Omega_{\varepsilon}(n)$  nodes will be infectious within time  $\mathcal{O}_{\varepsilon}(\log n)$ , even if  $|I_0| = 1$ . Moreover, if  $|I_0| \ge \beta_{\varepsilon} \log n$  for a sufficiently large constant  $\beta_{\varepsilon}$  (that depends only on  $\varepsilon$ ), then the above event occurs w.h.p.;
- 2. If  $p < \frac{\sqrt{c^2+6c+1}-c-1}{2c} \varepsilon$ , w.h.p. the process will stop within  $\mathcal{O}_{\varepsilon}(\log n)$  time steps, and the number of recovered nodes at the end of the process will be  $\mathcal{O}_{\varepsilon}(|I_0|\log n)$ .

As for the 3-SWG(n) model, we get the following results for the Reed-Frost process.

**Theorem 2.5** (The RF process on the 3-SWG(n) model). Let V be a set of n vertices,  $I_0 \subseteq V$  be a set of source nodes, and p > 0 be a bond percolation probability. Sample a graph  $G = (V, E_1 \cup E_2)$ from the 3-SWG(n) distribution, and run the RF protocol with transmission-probability p over G from  $I_0$ . For every  $\varepsilon > 0$ , we have the following:

- 1. If  $p > 1/2 + \varepsilon$ , with probability  $\Omega_{\varepsilon}(1)$ , a subset of  $\Omega_{\varepsilon}(n)$  nodes will be infectious within time  $\mathcal{O}_{\varepsilon}(n)$ , even if  $|I_0| = 1$ . Moreover, if  $|I_0| \ge \beta_{\varepsilon} \log n$  for a sufficiently large constant  $\beta_{\varepsilon}$  (that depends on  $\varepsilon$  but not on n), then the above event occurs w.h.p.;
- 2. If  $p < \frac{\sqrt{c^2 + 6c + 1} c 1}{2c} \varepsilon$ , then, w.h.p., the process will stop within  $O_{\varepsilon}(\log n)$  time steps, and the number of recovered nodes at the end of the process will be  $O_{\varepsilon}(|I_0| \log n)$ .

<sup>&</sup>lt;sup>4</sup>We remind that a detailed description of this equivalence is given in Appendix A.2.

We notice that the first claim of each of the above two theorems, concerning the multi-source case, i.e. the case  $|I_0| \ge \beta \log n$ ), are not direct consequences of (the corresponding first claims of) Theorems 2.1 and 2.2: although each element of  $I_0$  has constant probability of belonging to the "giant component" of the graph  $G_p$ , these events are not independent, and so it is not immediate that, when  $|I_0|$  is of the order of  $\log n$ , at least an element of  $I_0$  belongs to the giant component with high probability. Such claims instead are non-trivial consequences of our technical analysis.

On the other hand, the second claims of the above two theorems are simple consequences of the corresponding claims of Theorems 2.1 and 2.2. As for general bounded-degree graphs, from Theorem 2.3, we can recover an upper bound on the critical value of p for the RF process equivalent to that of Claim 2 of Theorem 2.3 (we omit here the formal statement).

From a topological point of view, because of a mix of local and random edges, epidemic spreading in the above models proceeds as a sequence of outbreaks, a process that is made explicit in our rigorous analysis, where we see the emergence of two qualitative phenomena that are present in real-world epidemic spreading.

One is that the presence of long-distance random connections has a stronger effect on epidemic spreading than local connections, that, in epidemic scenarios, might motivate lockdown measures that shut down long-distance connections. This can be seen, quantitatively, in the fact that the critical probability in a cycle is p = 1, corresponding to a critical basic reproduction number<sup>5</sup>  $R_0$  equal to 2. On the other hand, the presence of random matching edges or random  $\mathcal{G}_{n,c/n}$  edges in the setting c = 1 defines networks in which the critical  $R_0$  is, respectively, 1.5 and  $3 \cdot (\sqrt{2}-1) \approx 1.24$ , meaning that notably fewer local infections can lead to large-scale contagion on a global scale.

The other phenomenon is that the irregular networks of the SWG(n, c/n) model in the case c = 1 show a significantly lower critical probability, i.e.  $\sqrt{2} - 1 \approx .41$ , than the critical value .5 of the nearly regular networks of the 3-SWG(n) model, though they have the same number of edges (up to lower order terms) and very similar distributions. As a further evidence of this phenomenon, we remark the scenario yielded by the random irregular networks sampled from the SWG(n, c/n) distribution with c even smaller than 1: for instance, the setting c = .7, though yielding a much sparser topology than the 3-SWG(n) networks, has a critical probability which is still smaller than .5. Moreover, this significant difference between the SWG(n, c/n) model and the regular 3-SWG(n) one holds even for more dense regimes. In detail, Theorem 2.3 implies that the almost-regular version of SWG in which c independent random matchings are added to the ring of n nodes has a critical probability at least 1/(c + 1). Then, simple calculus shows that the critical probability given by Theorem 2.4 for the SWG(n, c/n) model is smaller than 1/(c + 1), for any choice of the density parameter c.

The most significant difference between the two distributions above is the presence of a small number of high-degree vertices in SWG(n, c/n), suggesting that even a small number of "super-spreader" nodes can have major global consequences.

### 2.3 Extensions of our results for epidemic models

Non-homogenous transmission probability. While keeping our focus on the rigorous analysis of simplified models that still capture important emergent phenomena, we remark that our techniques allow extentions of our results to a natural non-homogenous bond-percolation process on small-world graphs, in which local edges percolate with probability  $p_1$ , while bridges percolates with probability  $p_2$ : our analysis in fact keeps the role of the two type of connections above well separated from each

<sup>&</sup>lt;sup>5</sup>The quantity  $R_0$  in a SIR process is the expected number of people that an infectious person transmits the infection to, if all the contacts of that person are susceptible. In the percolation view of the process, it is the average degree of the percolation graph  $G_p$ .

other. We are inspired, for instance, by epidemic scenarios in which the chances for any node to get infected/informed by a local tie are significantly higher than those from sporadic, long ties.

In this non-homogeneous setting, for the SWG(n,q) model with q = c/n for some absolute constant c > 0, we can prove that, w.h.p., the Independent-Cascade protocol reaches  $\Omega(n)$  nodes within  $O(\log n)$  time<sup>6</sup> iff the following condition on the three parameters of the process is satisfied

$$p_1 + c \cdot p_1 p_2 + c \cdot p_2 > 1$$
.

Some remarks are in order. In the case c = 1, the formula above shows a perfect symmetry in the role of the two bond probabilities  $p_1$  and  $p_2$ . In a graph sampled from SWG(n, 1/n), however, the overall number of local ties (i.e. ring edges) is n, while the number of bridges is highly concentrated on n/2 (it is w.h.p.  $\leq n/2 + \sqrt{n \log n}$ ). This means that a public-health intervention aimed at reducing transmission has to suppress twice as much local transmissions in order to obtain the same effect of reducing by a certain amount the number of long-range transmissions. If we consider the case c = 2, in which the number of bridges is about equal to the number of local edges, we see that the impact of a change in  $p_2$  weighs roughly twice as much as a corresponding change  $p_1$ .

So, even in the fairly unrealistic one-dimensional small-world model, it is possible to recover analytical evidences for the effectiveness of public-health measures that block or limit long-range mobility and super-events (such as football matches, international concerts, etc.). The generalization to non-homogenous transmission probabilities is provided in Appendix F.

Longer node activity and incubation. Natural generalizations of the setting considered in this work include models in which i) the interval of time during which a node is active (i.e., the *activity period*) follows some (possibly node-dependent) distribution and/or ii) once infected, a node only becomes active after an *incubation* period, whose duration again follows some distribution. While the introduction of activity periods following general distributions may considerably complicate the analysis, our approach rather straightforwardly extends to two interesting cases, in which the incubation period of each node is a random variable (as long as incubation periods are independent) and/or the activity period of a node consists of k consecutive units of time, with k a fixed constant. This generalized model with random, node-dependent incubation periods corresponds to a discrete, synchronous version of the SEIR model,<sup>7</sup> which was recently considered as a model of the COVID-19 outbreak in Wuhan [24]. These extensions are formalized and discussed in Appendix F.

### Roadmap

Section 3 gives an overall description of the main ideas and technical results behind our analysis of bond-percolation in one-dimensional small-world graphs. While the most-related, important previous contributions have been already mentioned in the previous sections, further related work is summarized in Section 4 which concludes the body of the paper.

The appendix of the paper is organized as follows. Appendix A introduces all preliminaries we use in the full proofs of our results. In Appendix B, we consider the SWG(n,q) model when the percolation probability p is over the critical value and give the full proofs of the first claims of Theorems 2.1 and 2.4. The case under the probability threshold for the SWG(n,q) model is analyzed in Appendix C, where the second claims of Theorems 2.1 and 2.4 are proved. The analysis proving the first claims of Theorems 2.2 and 2.5 for the 3-SWG(n) model is provided in Appendix D, while Appendix E is devoted to the proof of Theorem 2.3 that easily implies the second claims

<sup>&</sup>lt;sup>6</sup>The formal statement is similar to that for the homogeneous case in Theorem 2.4 and is given in Appendix F.

 $<sup>^{7}</sup>$ With respect to SIR, for each node we have a fourth, *Exposed* state, corresponding to the incubation period of a node.

of Theorems 2.2 and 2.5. Finally, Appendix F describes the generalizations of our analysis to the setting where a different transmission probability can be assigned to the two types of edges (i.e. ring edges and bridges) and the case of longer node activity and incubation.

## **3** Overview of Our Analysis

A standard technique in bond percolation, applied for example to percolation in infinite trees and in random graphs, is to analyze the process of running a BFS in the percolation graph, delaying decisions about the percolation of edges from a node w to unvisited vertices until the time w is taken out of the BFS queue. In random graphs and infinite trees, the distribution of unvisited neighbors of w in the percolation graph remains simple, even conditioned on previous history, and one can model the size of the BFS queue as a Galton-Watson process (see Definition A.7), thus reducing the percolation analysis to standard results about branching processes. Basically, if the number of vertices that we add at each step to the queue is less than one on average, the visit will reach on average a constant number of vertices and if it is more than one and the graph is infinite the visit will reach on average an infinite number of vertices.

### **3.1** Analysis of bond percolation in the SWG(n,q) model

In this section, we describe the key ingredients of our analysis of the SWG(n,q) model proving Theorems 2.1 and 2.4, whose detailed and rigorous proofs can be found in Appendix B (for the case in which p is above the critical threshold) and in Appendix C (for the case in which p is below the critical threshold).

It would be very difficult to analyze a BFS exploration of the percolation graph to study percolation in the small-world model SWG(n,q), since the distribution of unvisited neighbors of a vertex w in the percolation graph is highly dependent on the previous history of the BFS (in particular, it matters whether none, one, or both of the neighbors of w along the cycle are already visited).

Instead, and this is one of the technical innovations of our work, we define a modified BFS visit whose process is more tractable to analyze.

The main idea of our modified BFS is that in one step we do the following: after we pull a node w from the queue, we first look at the neighbors x of w that are reachable through bridge edges in the percolation graphs; then, for each "bridge neighbor" x of w, we visit the "local cluster" of x, that is, we explore the vertices reachable from x along paths that only consist of edges of the cycle that are in the percolation graph (we indicate the local cluster of x with LC(x)); finally, we add to the queue all non-visited vertices in the local clusters of the bridge neighbors of w. These steps are exemplified in Fig. 1.

The point of doing things this way is that if we delay decisions about the random choice of the bridge edges and the random choices of the percolation, then we have a good understanding of the following two key random variables:

- the number of bridge neighbors x of w along percolated bridge edges, which are, on average pqn' if the graph comes from SWG(n,q), p is the percolation probability, and n' is the number of unvisited vertices at that point in time;
- the size of the "local cluster" of each such vertex x, that is of the vertices reachable from x along percolated cycle edges, which has expectation

$$\mathbf{E}\left[\mathrm{LC}(x)\right] = \frac{1+p}{1-p}\,.\tag{1}$$

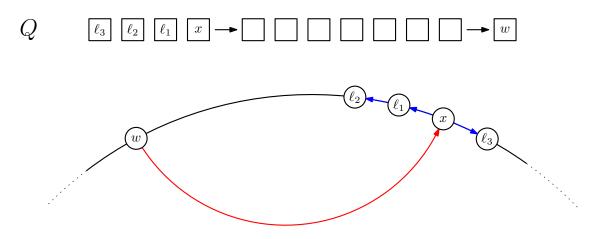


Figure 1: The figure shows an example in which the visit first proceeds from a node w extracted from the queue to a new node x over a bridge of the percolation graph and then reaches further nodes, starting from x and proceeding along ring edges of the percolation graph. In terms of the RF protocol, this corresponds to the information (virus) first being transmitted from an infectious node w to a susceptible one x over a bridge edge and then propagating locally using ring edges. Note that in this case, i) we have a single bridge leaving w (in general, there might be multiple ones) and ii) the information freely propagates locally from node x, informing susceptible nodes  $\ell_1, \ell_2, \ell_3$ . The edges are directed in the direction of information spread.

Intuitively, we would hope to argue that in our modified visit of a graph sampled from SWG(n,q) to which we apply percolation with probability p, the following happens in one step: we remove one node from the queue, and we add on average

$$N = pqn' \cdot \frac{1+p}{1-p} \tag{2}$$

new nodes. As long as n' = n - o(n) we can approximate n' with n, and when the number n - n' of visited vertices is  $\Omega(n)$ . This way, we would have modeled the size of the queue with a Galton-Watson process and we would be done. The threshold behavior would occur at a p such that  $pqn \cdot (1+p)/(1-p) = 1$ . A smaller value of p would imply that we remove one node at every step and, on average, add less than one node to the queue, leading the process to die out quickly. A larger value of p would imply that we remove one node at every step and, on average, add more than one node to the queue, leading the process to die out quickly.

We are indeed able to prove this threshold behavior, at least for q = c/n for constant c. However, we encounter significant difficulty in making this idea rigorous: if we simply proceeded as described above, we would be double-counting vertices, because in general, the "local cluster" of a node added to the queue at a certain point may collide with the local cluster of another node added at a later point. This may be fine as long as we are trying to upper bound the number of reachable vertices, but it is definitely a problem if we are trying to establish a lower bound.

To remedy this difficulty, we truncate the exploration of each local cluster at a properly chosen constant size L (we denote as  $LC^{L}(x)$  the truncated local cluster of a node x). In our visit, we consider only unvisited neighbors x of w that are sufficiently far along the cycle from all previously visited vertices so that there is always "enough space" to grow a truncated local cluster around xwithout hitting already visited vertices. In more detail, we introduce the notion of "free node" used in the algorithm and its analysis.

**Definition 3.1** (free node). Let  $G_{SW} = (V, E_1 \cup E_2)$  be a small-world graph and let  $L \in \mathbb{N}$ . We say that a node  $x \in V$  is free for a subset of nodes  $X \subseteq V$  if x is at distance at least L + 1 from any node in X in the subgraph  $(V, E_1)$  induced by the edges of the ring.

Thanks to the above definition, we can now formalize our modified BFS.

Algorithm 1 Sequential L-VISIT

**Input**: A small-world graph  $G_{SW} = (V, E_{SW})$ ; a subgraph H of  $G_{SW}$ ; a set of initiators  $I_0 \subseteq V$ ; a set of deleted nodes  $D_0 \subseteq V$ . 1:  $Q = I_0$ 2:  $R = \emptyset$ 3:  $D = D_0$ 4: while  $Q \neq \emptyset$  do w = dequeue(Q)5: $R = R \cup \{w\}$ 6: 7: for each bridge neighbor x of w in H do if x is free for  $D \cup R \cup Q$  in  $G_{SW}$  then 8: for each node y in the L-truncated local cluster  $LC^{L}(x)$  do 9: 10: enqueue(y, Q)

To sum up, the *L*-truncation negligibly affects the average size of local clusters, the restriction to a subset of unvisited vertices negligibly affects the distribution of unvisited neighbors, and the analysis carries through with the same parameters and without the "collision of local clusters" problem.

In more detail, thanks to the arguments we described above, from (1) and (2), we can prove that, if p is above the critical threshold

$$\frac{\sqrt{c^2+6c+1}-c-1}{2c}\,,$$

then, with probability  $\Omega(1)$ , the connected components of  $G_p$  containing the initiator subset have overall size  $\Omega(n)$ . In terms of our BFS visit in Algorithm 1, we in fact derive the following result<sup>8</sup> (see Subsection B.1 in the Appendix for its full proof).

**Lemma 3.2.** Let V be a set of n nodes,  $s \in V$  an initiator node and  $D_0 \subseteq V \setminus \{s\}$  a set of deleted nodes such that  $|D_0| \leq \log^4 n$ . For every  $\varepsilon > 0$  and c > 0, and for every probability p such that

$$\frac{\sqrt{c^2 + 6c + 1} - c - 1}{2c} + \varepsilon \leqslant p \leqslant 1,$$

there are positive parameters  $L, k, t_0, \varepsilon'$ , and  $\gamma$ , that depend only on c and  $\varepsilon$ , such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution and let  $G_p$  be the percolation graph of G with percolation probability p. Run the SEQUENTIAL L-VISIT procedure in Algorithm 1 on input  $(G, G_p, s, D_0)$ : if n is sufficiently large, for every t larger than  $t_0$ , at the end of the t-th iteration of the while loop we have

$$\mathbf{Pr}\left(|R \cup Q| \ge n/k \text{ OR } |Q| \ge \varepsilon' t\right) \ge \gamma,$$

where the probability is over both the randomness of the choice of G from SWG(n, c/n) and over the choice of the percolation graph  $G_p$ .

The truncation is such that our modified BFS does not discover all vertices reachable from  $I_0$  in the percolation graph, but only a subset. However, this is sufficient to prove lower bounds to the number of reachable vertices when p is above the threshold. Proving upper bounds, when p is under

<sup>&</sup>lt;sup>8</sup>We state the result for the case  $|I_0| = 1$ .

the threshold (i.e., the second claims of Theorems 2.1 and 2.4) is easier because, as mentioned, we can allow double-counting of reachable vertices.

The above line of reasoning is our key idea, when p is above the threshold, to get  $\Omega_{\varepsilon}(1)$  confidence probability for: (i) the existence of a linear-size, induced connected subgraph in  $G_p$  (i.e., a "weaker" version of Claim 1 of Theorem 2.1), and (ii) the existence of a large epidemic outbreak, starting from an arbitrary source subset  $I_0$  (i.e., Claim 1 of Theorem 2.4). A full description of this analysis is provided in Appendix B, where we also describe the further technical steps to achieve *highprobability* for event (i), and also event (ii) when the size of the source subset is  $|I_0| = \Omega(\log n)$  (see Subsection B.3).

Bounding the number of hops: parallelization of the BFS visit. To get bounds on the number of the BFS levels, we study the BFS-visit in Algorithm 1 only up to the point where there are  $\Omega(\log n)$  nodes in the queue (this first phase is not needed if  $I_0$  already has size  $\Omega(\log n)$ ), and then we study a "*parallel*" visit in which we add at once all nodes reachable through an *L*-truncated local cluster and through the bridges from the nodes currently in the queue, skipping those that would create problems with our invariants: to this aim, we need a stronger version of the notion of *free* node (see Definition B.2 in Subsection B.2).

Here we can argue that, as long as the number of visited vertices is o(n), the number of nodes in the queue grows by a constant factor in each iteration, and so we reach  $\Omega(n)$  nodes in  $\mathcal{O}(\log n)$ number of iterations that corresponds to  $\mathcal{O}(\log n)$  distance from the source subset in the percolation graph  $G_p$ .

A technical issue that we need to address in the analysis of our parallel visit is that the random variables that count the contribution of each L-truncated local cluster, added during one iteration of the visit, are not mutually independent. To prove concentration results for this exponential growth, we thus need to show that such a mutual correlation satisfies a certain *local* property and then apply suitable bounds for partly-dependent random variables [17] (see Theorem A.17 in Subsection A.5 in the Appendix). All details of this part can be found in Subsection B.2 in the Appendix.

### 3.2 Further challenges in regular small-world graphs

In this section, we describe the main differences of the analysis of the 3-SWG(n) model with respect to the analysis of the SWG(n,q) one. The following arguments give a high-level overview of the proofs of Theorems 2.2 and 2.5. The detailed proofs can be found in Appendix D (for the case pabove the threshold) and in Appendix E (for the case p below the threshold).

The 3-SWG(n) model, in which bridge edges form a random matching, introduces additional dependencies on the past history, compared to the analysis of the SWG(n,q) model. We deal with this difficulty by disallowing additional unvisited vertices to be reached in the visit. When we take a node w out of the queue in the 3-SWG(n) model there can be at most one unvisited neighbor x of w reachable through a bridge edge in the percolation graph. If such a neighbor x exists, and it is not one of the disallowed unvisited vertices, we find, as before, the truncated local cluster of x and add the nodes of the local cluster of x to the queue, except for x itself. The reason for discarding x is that we have already observed the unique bridge neighbor of x (namely, w) so, if we added x to the queue, there would be no randomness left to apply the deferred decision principle when we later remove x from the queue.

This means that, while in one step of our visit on SWG(n,q) with activation probability p we take out one node from the queue and add in expectation a number of nodes described by (2), in

3- $\mathcal{SWG}(n)$  we take out one node and add in expectation

$$N' = p \cdot \left(\frac{1+p}{1-p} - 1\right)$$

nodes. This is the reason why the SWG(n,q) model with q = 1/n and the 3-SWG(n) model have notably different thresholds, even though they are superficially very similar.

The above argument allows us to prove Claims 1 and 2 of Theorem 2.2. Currently, we are not able to analyze the parallel visit in the 3-SWG(n) model, because of the correlations between the edges, although we are able to analyse the sequential visit up to  $\Omega(n)$  nodes. This is why in our theorems we do not have an exponential growth of the BFS levels for the 3-SWG(n) model.

As for Claim 3 of Theorem 2.2, as remarked in Section 2, it is a direct consequence of the more general bounds given by Theorem 2.3: Given any graph G = (V, E) of maximum degree d and a percolation probability  $p < (1 - \varepsilon)/(d - 1)$ , the number of nodes connected to any given source subset  $I_0$  in  $G_p$  is  $\mathcal{O}_{\varepsilon}(|I_0| \log n)$ , w.h.p.

The proof of the above result (see Appendix E for the details) again relies on a suitable BFS visit of the percolation graph  $G_p$  which is similar to that in Figure 1 in the previous subsection: We start with a queue Q containing only the source node and at each iteration of a while loop (that terminates when the queue is empty) we extract a node from the queue and we add to the queue all its neighbors in the percolation graph. Informally speaking, every time the BFS adds a node to the queue, it is observing a Bernoulli random variable with parameter  $p < (1 - \varepsilon)/(d - 1)$  (the percolation probability of each visited edge). Since the input graph has maximum degree d, if the procedure runs for t iterations of the while loop then t nodes are extracted from the queue and in expectation  $p(t \cdot (d - 1) + 1)$  are added to the queue. Chernoff's bound then implies that the probability that a queue starting from a single source node is not yet empty after t iterations of the while loop is  $\exp(-\Theta(\varepsilon^2 t))$ . Hence, the size of the connected component containing the source node is  $\mathcal{O}(\log n)$ , w.h.p. Finally, the fact that all components are of size  $\mathcal{O}(\log n)$  follows from a union bound.

### 4 Related Work

The fully-mixed SIR model [32] is the simplest SIR epidemiological model, and it treats the number of people in each of the three possible states as continuous quantities that evolve in time in accordance with certain differential equations. In this setup, the evolution of the process is governed by the expected number  $R_0$  of people that each infectious person would infect, if all the contacts of that person were susceptible. If  $R_0 < 1$ , the process quickly ends, reaching a state with zero infectious people and a small number of recovered ones. If  $R_0 > 1$ , the process goes through an initial phase in which the number of infectious people grows exponentially with time, until the number of recovered people becomes a  $1 - 1/R_0$  fraction of the population (the herd immunity threshold); the number of infectious people decreases after that, and eventually the process ends with a constant fraction of the population in the recovered state.

If we consider the Reed-Frost process on a graph G that is a clique on n vertices, then the percolation graph  $G_p$  is an Erdős-Rényi random graph with edge probability sampled from  $\mathcal{G}_{n,p}$ . Classical results from the analysis of random graphs give us that if  $pn < 1 - \epsilon$  then, with high probability, all the connected components of the graph have size  $O_{\epsilon}(\log n)$ , and so the set of vertices that is reachable from  $I_0$  has cardinality at most  $O_{\epsilon}(|I_0| \cdot \log n)$  and if  $pn > 1 + \epsilon$  then there is a connected component of cardinality  $\Omega_{\epsilon}(n)$ , and, except with probability exponentially small in  $I_0$ , at least one vertex of  $I_0$  belongs to the giant component and is able to reach  $\Omega_{\epsilon}(n)$  vertices. The parameter  $R_0$  of the fully mixed continuous model corresponds to the average degree of  $G_p$ , which is pn if  $G_p$  is distributed as  $\mathcal{G}_{n,p}$ , so we see that the fully mixed continuous model agrees with the Reed-Frost process on a clique.

A number of techniques have been developed to study percolation in graphs other than the clique, and there is a vast body of work devoted to the study of models of bond percolation and epidemic spreading, as surveyed in [32, 36]. Below, we review analytical studies of such processes on finite graphs. As far as we know, our results are the first rigorous ones to establish threshold phenomena in small-world graphs for the bond-percolation process (and, thus, for the Reed-Frost process).

There has been some previous work on studying sufficient conditions for the RF process to reach a sublinear number of vertices.

In [11], for a symmetric, connected graph G = (V, E), Draief et al. prove a general lower bound on the critical point for the IC process in terms of spectral properties. Further versions of such bounds for special cases have been subsequently derived in [14, 22]. Specifically, if one lets P be the matrix such that P(u, v) = p(u, v) is the percolation probability of the edge  $\{u, v\}$ , and P(u, v) = 0if  $\{u, v\} \notin E$ , and if one call  $\lambda$  the largest eigenvalue of P, then  $\lambda < 1 - \epsilon$  implies that for a random start vertex s we have that the expected number of vertices to which s spreads the infection is  $o_{\epsilon}(n)$ .

In the RF process, in which all probabilities are the same,  $P = p \cdot A$ , where A is the adjacency matrix of G, and so the condition is asking for  $p < (1 - \epsilon)/\lambda_{\max}(A)$ .

This condition is typically not tight, and it is never tight in the "small-worlds" graphs we consider:

- In the 3- $\mathcal{SWG}(n)$  model, the largest eigenvalue of the adjacency matrix is 3 o(1), but the critical probability is 1/2 and not 1/3;
- In the SWG(n, 1/n) model of a cycle plus Erdős-Rényi edges, the largest eigenvalue of the adjacency matrix is typically  $\Omega(\sqrt{\log n}/\log \log n)$  because we expect to see vertices of degree  $\Omega(\log n/\log \log n)$  and the largest eigenvalue of the adjacency matrix of a graph is at least the square root of its maximal degree. The spectral bound would only tell us that the infection dies out if  $p = \mathcal{O}(\sqrt{\log \log n}/\log n)$ , which goes to zero with n. A better way to use the spectral approach is to model the randomness of the small-world graph and the randomness of the percolation together; in this case, we have matrix P(u, v) such that P(u, v) = p for edges of the cycle and P(u, v) = p/n for the other edges. This matrix has the largest eigenvalue 3p o(1), so the spectral method would give a probability of 1/3, while we can locate the threshold at  $\sqrt{2} 1 \approx .41$ .

In any family of *d*-regular graphs, the largest eigenvalue of the adjacency matrix is *d*, and so the spectral bound gives that the critical threshold is at least 1/d; our Theorem 2.3 shows the stronger bound that the critical threshold is at least 1/(d-1).

We are not aware of previous rigorous results that provide sufficient conditions for the IC process to reach  $\Omega(n)$  nodes (either on average or with high probability) in general graphs, or for the equivalent question of proving that the percolation graph of a given graph has a connected component with  $\Omega(n)$  vertices.

As discussed in the previous section, our analysis proceeds by analyzing a BFS-like visit of the percolation graph. This is also how large components in the percolation of infinite trees and random graphs have been studied before. However, this idea requires considerable elaboration to work in our setting, given the mix of fixed edges and random edges in the small-world model and the complicated dependencies on the past history that one has to control in the analysis of the visit.

A fundamental and rigorous study of bond percolation in random graphs has been proposed by Bollobás et al. in [6]. They establish a coupling between the bond percolation process and a suitably defined branching process. In the general class of inhomogenous Erdős-Rényi random graphs, they derived the critical point (threshold) of the phase transition and the size of the giant component above the transition. The class of inhomogeneous random graphs to which their analysis applies includes generative models that have been studied in the complex network literature. For instance, a version of the Dubin's model [12] can be expressed in this way, and so can the *mean-field scale-free model* [4], which is, in turn, related to the Barabási–Albert model [3], having the same individual edge probabilities, but with edges present independently. Finally, we observe that the popular CHKNS model introduced by Callaway et al. [7] can be analyzed using an edge-independent version of this model. Indeed, they consider a random graph-formation process where, after adding each node, a Poisson number of edges is added to the graph, again choosing the endpoints of these edges uniformly at random. For all such important classes of random graph models, they show tight bounds for the critical points and the relative size of the giant component beyond the phase transition.

In our setting, if we sample a graph from SWG(n,q) and then consider the percolation graph  $G_p$ , the distribution of  $G_p$  is that of an inhomogenous Erdős-Rényi graph in which the cycle edges have probability p and the remaining edges have probability pq (the 3-SWG(n) model, however, cannot be expressed as an inhomogenous Erdős-Rényi graph).

Unfortunately, if we try to apply the results of [6] to the inhomogeneous random graph equivalent to percolation with parameter p in the SWG(n,q) model, we do not obtain tractable conditions on the critical value p for which the corresponding graph has a large connected component of small diameter, which is the kind of result that we are interested in proving.

Bond percolation and the IC process on the class of 1-dimensional small-world networks (that is, graphs obtained as the union of a cycle and of randomly chosen edges) have been studied in [27]: using numerical approximations on the moment generating function, non-rigorous bounds on the critical threshold have been derived while analytical results are given neither for the expected size of the number of informed nodes above the transition phase of the process nor for its completion time. Further non-rigorous results on the critical points of several classes of complex networks have been derived in [23, 14] (for good surveys see [32, 36]).

In [16, 5, 26], different versions of the bond percolation process has been studied in small-world structures formed by a *d*-dimensional grid augmented by random edges that follow a power-law distribution: a bridge between points x and y is selected with probability  $\sim 1/\text{dist}(x, y)^{\alpha}$ , where dist(x, y) is the grid distance between x and y and  $\alpha$  is a fixed power-law parameter. Besides other aspects, each version is characterized by: (1) whether the grid is infinite or finite, and (2) whether the grid edges (local ties) do percolate with probability p or not. Research in this setting has focused on the emergence of a large connected component and on its diameter as functions of the parameters d and  $\alpha$ , while, to the best of our knowledge, no rigorous threshold bounds are known for the bond percolation probability p.

In the computer science community, to the best of our knowledge, Kempe et al. [19] were the first to investigate the IC process from an optimization perspective, in the context of viral marketing and opinion diffusion. In particular, they introduced the *Influence Maximization* problem, where the goal is to find a source subset of k nodes of an underlying graph to inform at time t = 0, so as to maximize the expected number of informed nodes at the end of the IC process. They prove this is an *NP*-hard problem and show a polynomial time algorithm achieving constant approximation. Further approximation results on a version of *Influence Maximization* in which the completion time of the process is considered can be found in [9, 25].

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## A Preliminaries

### A.1 Formal definitions

In this subsection of the Appendix, we give the rigorous definition of the bond percolation process.

Given a symmetric graph G = (V, E), we define |V| = n and, for any node  $v \in V$ , we denote N(v) as its neighborhood in G and d(v) = |N(v)| as its degree. The distance  $d_G(S, v)$  from the set S to the node v is the length of the shortest path among all paths from any node in S to v in G, if no such path exists  $d_G(S, v) = +\infty$ , if  $v \in S$ ,  $d_G(S, v) = 0$ . Since we will only consider symmetric graph, the term "symmetric" will be omitted. Given a graph G = (V, E), for any subset  $S \subseteq V$  and node  $v \in V$ , and for any integer  $i \leq n-1$ , we let  $N_G^{(i)}(S)$  be the subset of nodes that are at distance i from S, i.e.  $N_G^{(i)}(S) = \{v \in V \mid d_G(S, v) = i\}$ . Moreover, the set of nodes that are within finite distance from S, i.e. that are reachable from S, will be denoted as  $N_G^*(S)$ .

We consider the following bond percolation process on any fixed graph G (this process is also known in network theory as *Live-arc graph model with Independent arc selection* - see also [8]).

**Definition A.1** (The Bond Percolation process). Given a graph G = (V, E), and given, for every edge  $e \in E$ , a percolation probability  $p(e) \in [0, 1]$ , the bond percolation process consists to remove

each edge  $e \in E$ , independently, with probability 1 - p(e). The random subgraph, called the percolation graph  $G_p = (V, E_p)$ , is defined by the edges that are not removed (i.e. they are activated), i.e.,  $E_p = \{e \in E : edge \ e \ is \ not \ removed\}$ . Given an initial subset  $A_0 \subseteq V$  of active nodes, for every integer  $t \leq n-1$ , we define the random subset  $A_t$  of t-active nodes as the subset of nodes that are at distance t from  $A_0$  in the percolation graph  $G_p = (V, E_p)$ , i.e.,  $A_t = N_{G_p}^t(A_0)$ . Finally, the subset of all active nodes from  $A_0$  is the subset  $N_{G_p}^*(A_0)$ .

### A.2 The equivalence between the IC model and the Live-Arc model

In this paper, we consider the following synchronous, discrete-time epidemic protocol working over any graph G (see [13, 32]).

**Definition A.2** (IC and RF protocols). Given a graph G = (V, E), an assignment of transmission probabilities  $\{p(e)\}_{e \in E}$  to the edges of G, and a non-empty set  $I_0 \subseteq V$  of initially infectious<sup>9</sup> nodes (that will also be called initiators or sources since they have the information/virus since the very beginning), the Independent Cascade (for short, IC) protocol defines the stochastic process  $\{S_t, I_t, R_t\}_{t \geq 0}$  on G, where  $S_t, I_t, R_t$  are three sets of vertices, respectively called susceptible, infectious, and recovered, which form a partition of V and that are defined as follows.

- At time t = 0 we have  $R_0 = \emptyset$  and  $S_0 = V I_0$ .
- At time  $t \ge 1$ :
  - $-R_t = R_{t-1} \cup I_{t-1}$ , that is, the nodes that were infected at the previous step become recovered.
  - Independently for each edge  $e = \{u, v\}$  such that  $u \in I_{t-1}$  and  $v \in S_{t-1}$ , with probability p(e) the event that "u transmits the infection (i.e. a copy of the source message) to v at time t" takes place. The set  $I_t$  is the set of all vertices  $v \in S_{t-1}$  such that for at least one neighbor  $u \in I_{t-1}$  the event that u transmits the infection to v takes place as described above.
  - $-S_t = S_{t-1} I_t$

The process stabilizes when  $I_t = \emptyset$ .

The Reed-Frost SIR protocol (for short, RF Protocol) is the special case of the IC protocol in which all transmission probabilities are the same.

By the above definition, since each node can be in the infective state only for one step, we observe that the stopping time  $\tau = \min\{t > 0 : I_t = \emptyset\}$  is upper bounded with probability 1 by the diameter of G.

In [19], given any fixed graph G = (V, E), the IC protocol is shown to be *equivalent* to the bond percolation process.

If we consider the set  $I_t$  of nodes that are infectious at time t in a graph G = (V, E) according to the IC protocol with transmission probabilities  $\{p(e)\}_{e \in E}$  and with initiator set  $I_0$ , we see that such a set has precisely the same distribution as the set of nodes at distance t from  $I_0$  in the percolation graph  $G_p$  generated by the bond percolation process with probabilities  $\{p(e)\}_{e \in E}$  (see Definition A.1). Furthermore, the set of recovered nodes  $R_t$  is distributed precisely like the set of nodes at distance < t from  $I_0$  in  $G_p$ .

We formalize this equivalence by quoting a theorem from [8].

 $<sup>^{9}</sup>$ we use here the term *infectious* for two reasons: to emphasize that the node is both informed and active and, moreover, to be consistent with the literature in mathematical epidemiology.

**Theorem A.3** (Bond percolation and IC processes are equivalent, [19]). Consider the bond percolation process and the IC protocol on the same graph G = (V, E) and let  $I_0 = A_0 = V_0$ , where  $V_0$ is any fixed subset of V, and with transmission probabilities and percolation probabilities equal to  $\{p(e)\}_{e \in E}$ .

Then, for every integer  $t \ge 1$  and for every subsets  $V_1, \ldots, V_{t-1} \subseteq V$ , the events  $\{I_0 = V_0, \ldots, I_{t-1} = V_{t-1}\}$  and  $\{A_0 = V_0, \ldots, A_{t-1} = V_{t-1}\}$  have either both zero probability or non-zero probability, and, in the latter case, the distribution of the infectious set  $I_t$ , conditional to the event  $\{I_0 = V_0, \ldots, I_{t-1} = V_{t-1}\}$ , is the same to that of the t-active set  $A_t$ , conditional to the event  $\{A_0 = V_0, \ldots, A_{t-1} = V_{t-1}\}$ .

The strong equivalence shown in the previous theorem is obtained by applying the principle of deferred decision on the percolation/infection events that take place on every edge since they are mutually independent. This result can be exploited to analyze different aspects and issues of the IC (and, thus, the RF) protocol. We here summarize such aspects in an informal way, while, in the next sections, we show rigorous claims along our analysis.

As a first immediate consequence of Theorem A.3, we have that, starting from any source subset  $I_0$ , to bound the size of the final set  $R_{\tau}$  of the nodes informed by  $I_0$ , we can look at the size of the union of the connected components in  $G_p$  that include all nodes of  $I_0$ , i.e., we can bound the size of  $N^*_{G_p}(I_0)$ .

A further remark is that in the bond percolation process there is no *time*, and we can analyze the connected component of the percolation graph in any order and according to any visit process. Furthermore, if we want a lower bound to the number of nodes reachable from  $I_0$  in the percolation graph, we can choose to focus only on vertices reachable through a subset of all possible paths, and, in particular, we can restrict ourselves to paths that are easier to analyze. In our analysis we will only consider paths that alternate between using a bounded number of local edges and one bridge edge.

### A.3 Local clusters on the ring

Given a one-dimensional small world graph  $G = (V, E = E_1 \cup E_2)$  where  $(V, E_1)$  is a cycle, a probability p, and a vertex  $v \in V$ , we call the *local cluster* LC(v) the set of nodes that are reachable from v using only local edges (that is, edges of  $E_1$ ) that are in the percolation graph  $G_p$  of G.

**Fact A.4.** If G = (V, E) is a one-dimensional small-world graph and p is a percolation probability, for every  $w \in V$ ,  $\mathbf{E}[|\mathrm{LC}(w)|] \leq \frac{1+p}{1-p}$ , and this bound becomes tight as the ring size tends to  $\infty$ .

For technical reasons that will become clear later, when we explore the percolation graph  $G_p$  to estimate the size of its connected components, we do not want to follow too many consecutive local edges. To analyze the effect of this choice, it will be useful to have a notion of *L*-truncated local clusters, that we formalize below.

**Definition A.5** (*L*-truncated local cluster). Let  $G = (V, E = E_1 \cup E_2)$  be a one-dimensional smallworld graph, where  $(V, E_1)$  is a cycle, and the edges of  $E_1$  are called "local edges". Let *L* a positive integer distance parameter, and *p* be a percolation probability.

The L-truncated local cluster of  $v \in V$  is the set of vertices reachable from v in the percolation graph  $G_p$  using at most L activated local edges.

The next fact provides the expected size of an L-truncated local cluster.

**Fact A.6.** If G = (V, E) is a one-dimensional small-world graph and p is a percolation probability, for each node  $v \in V$ , the size  $LC^{L}(v)$  of its L-truncated local cluster  $LC^{L}(v)$  satisfies the following

$$\mathbf{E}\left[|\mathrm{LC}^{L}(v)|\right] = \frac{1+p}{1-p} - \frac{2p^{L+1}}{1-p}.$$
(3)

*Proof.* For any positive integer L and any node  $v \in V$ , we define the random variable  $\operatorname{RN}^{L}(v)$  as the subset of nodes such that: they are located at the right of v at ring distance less than L; they will be infected by v according to the SIR process considering only the ring edges (here, we exclude v from this set). So, we have

$$\mathbf{Pr}\left(|\mathbf{RN}^{L}(v)|=i\right) = \begin{cases} p^{i}(1-p) \text{ if } i < L\\ p^{L} \text{ if } i = L\\ 0 \text{ otherwise.} \end{cases}$$

We observe that  $|\mathrm{RN}^L(v)|$  is a well-known geometric random variable<sup>10</sup> with a "cutoff" and it easily holds that

$$\sum_{i=0}^{L} \mathbf{Pr} \left( |\mathbf{RN}^{L}(v)| = i \right) = (1-p) \sum_{i=0}^{L-1} p^{i} + p^{L} = (1-p) \frac{1-p^{L}}{1-p} + p^{L} = 1.$$

For any positive integer L and any node  $v \in V$ , we also define the "left-side" random variable  $LN^{L}(v)$ indicating the nodes in the ring that are located at the left of v that are infected by v according to the local cluster with cut-off process. Clearly,  $|LN^{L}(v)|$  has the same distribution of  $|RN^{L}(v)|$ . So, we can define  $LC^{L}(v)$  as the overall set of the local cluster of a node v with cutoff L including the node v itself, i.e.,

$$|\mathrm{LC}^{L}(v)| = |\mathrm{RN}^{L}(v)| + |\mathrm{LN}^{L}(v)| + 1.$$

So, since  $LN^{L}(v)$  and  $RN^{L}(v)$  have the same distribution of probability,

$$\mathbf{E} \left[ \mathrm{LC}^{L}(v) \right] = \mathbf{E} \left[ \mathrm{LN}^{L}(v) + \mathrm{RN}^{L}(v) + 1 \right] = 2\mathbf{E} \left[ \mathrm{RN}^{L}(v) \right] + 1 = 2(1-p) \sum_{i=1}^{L-1} ip^{i} + 2Lp^{L} + 1$$
$$= 2\frac{(L-1)p^{L+1} - Lp^{L} + p}{(1-p)} + 2Lp^{L} + 1$$
$$= \frac{p+1}{1-p} + 2\frac{(L-1)p^{L+1} - Lp^{L+1}}{1-p} = \frac{p+1}{1-p} - \frac{2p^{L+1}}{1-p}.$$

### A.4 Galton-Watson branching processes

Our analyses of the bond percolation process will make use of a reduction to the analyses of appropriately defined branching processes.

**Definition A.7** (Galton-Watson Branching Process). Let W be a non-negative integer random variable, and let  $\{W_{t,i}\}_{t \ge 1, i \ge 1}$  be an infinite sequence of independent identically distributed copies

<sup>&</sup>lt;sup>10</sup>in our setting, the variable may assume value 0.

of W. The Galton-Watson branching process generated by the random variable W is the process  $\{X_t\}_{t\geq 0}$  defined by  $X_0 = 1$  and by the recursion

$$X_t = \sum_{i=1}^{X_{t-1}} W_{t,i}$$

All properties of the process  $\{X_t\}_{t\geq 0}$  are captured by the process  $\{B_t\}_{t\geq 0}$  defined by the recursion

$$B_t = \begin{cases} 1, & t = 0; \\ B_{t-1} + W_t - 1, & t > 0 \text{ and } B_{t-1} > 0; \\ 0, & t > 0 \text{ and } B_{t-1} = 0. \end{cases}$$

where  $W_1, \ldots, W_t, \ldots$  are an infinite sequence of independent and identically distributed copies of W. In the following, when we refer to the Galton-Watson process generated by W we will always refer to  $\{B_t\}_{t\geq 0}$ .

We define  $\sigma = \min\{t > 0 : B_t = 0\}$  (if no such t exists we set  $\sigma = +\infty$ ) and notice that, for  $T < \sigma$ , we have  $B_T = \sum_{t=1}^T W_t - T$ .

Galton-Watson processes are characterized by the following important threshold behavior.

**Theorem A.8** ([2], Section 10.4). Let  $\{B_t\}_{t\geq 0}$  be a Galton-Watson process with integer random variable W. Then:

- 1. For every constant  $\varepsilon > 0$ , if  $\mathbf{E}[W] < 1 \varepsilon$ , the process dies out ( $\sigma < +\infty$ ) with probability 1;
- 2. For every constant  $\varepsilon > 0$ , if  $\mathbf{E}[W] > 1 + \varepsilon$ , the process diverges, i.e., a constant c > 0 exists such that  $\mathbf{Pr}(\sigma = +\infty) \ge c$ .

When the expectation of W is over the threshold, the above theorem implies that, with probability c > 0, for every time t we have  $B_t > 0$ . The next lemma shows that, if the variance of W is bounded then, with constant positive probability, the value of  $B_t$  is not only positive, but it is at least  $\Omega(t)$ .

**Lemma A.9.** Let  $\varepsilon$  be any positive constant, and consider a Galton-Watson process  $\{B_t\}_{t\geq 0}$  with a non-negative integer random variable W with  $\mathbf{E}[W] \geq 1+\varepsilon$  and with finite variance, i.e.,  $\mathbf{Var}(W) \leq U$  for some positive constant U. Then there is a constant c' that depends only on  $\varepsilon$  and a constant  $t_0$  that depends only on  $\varepsilon$  and U such that, for every  $t \geq t_0$ ,  $\mathbf{Pr}(B_t \geq (\varepsilon t)/2) \geq c'$ .

*Proof.* By definition of Galton-Watson process, if  $W_1, \ldots, W_t$  are mutually independent copies of W,

$$\mathbf{Pr}\left(B_t < \frac{\varepsilon t}{2}\right) = \mathbf{Pr}\left(B_t = 0 \ \lor \ \sum_{i=1}^t W_i < t + \frac{\varepsilon t}{2}\right) \leqslant \mathbf{Pr}\left(B_t = 0\right) + \mathbf{Pr}\left(\sum_{i=1}^t W_i < t + \frac{\varepsilon t}{2}\right),$$

where the second inequality follows by a simple union bound. From Theorem A.8, there is a constant  $c = c(\varepsilon)$  such that

$$\mathbf{Pr}\left(B_t=0\right)\leqslant 1-c\,.$$

From Chebyshev's inequality (Theorem A.18),

$$\Pr\left(\sum_{i=1}^{t} W_i < t + \frac{t\varepsilon}{2}\right) \leqslant \frac{4U}{\varepsilon^2 t} \leqslant \frac{c}{2},$$

where the second inequality holds if  $t \ge \frac{8U}{\varepsilon^2 c}$ . The lemma then follows setting c' = c/2 and  $t_0 = 8U/\varepsilon^2 c$ .

**Lemma A.10.** Let  $\varepsilon$  be any positive constant, and consider a Galton-Watson process  $\{B_t\}_{t\geq 0}$  with a non-negative integer random variable W such that  $0 \leq W \leq M$  and  $\mathbf{E}[W] \geq 1 + \varepsilon$ . Then, for any  $\gamma \geq 4M^2/\varepsilon^2$  and for any  $t_0 \geq 1$ , we have

$$\mathbf{Pr}\left(B_{n+t_0} > 0 \mid B_{t_0} \ge \gamma \log n\right) \ge 1 - \frac{1}{n}.$$

*Proof.* Let  $\varepsilon' = \varepsilon/2$ . For any  $\ell > 0$  and any  $i \ge 1$ , consider the event

$$A = \{ B_{i+t_0} \ge (1 + \varepsilon')\ell \mid B_{i-1+t_0} \ge \ell \}.$$

If we consider  $\ell$  generic i.i.d. copies of the random variable  $W, W_1, \ldots, W_\ell$  we have that

$$\mathbf{Pr}(A) \ge \mathbf{Pr}\left(\sum_{i=1}^{\ell} W_i \ge (1+\varepsilon')\ell\right) \ge 1 - e^{-\frac{\varepsilon^2}{2M^2}},\tag{4}$$

where the last inequality follows from the Hoeffding bound.

We notice that, if we define the events

$$A_i = \{ B_{i+t_0} \ge (1+\varepsilon')^i \gamma \log n \mid B_{i-1+t_0} \ge (1+\varepsilon')^{i-1} \gamma \log n \},\$$

then, for the chain rule, we will have

$$\mathbf{Pr}\left(B_{n+t_0} > 0 \mid B_{t_0} \ge \gamma \log n\right) \ge \prod_{i=1}^{n} \mathbf{Pr}\left(A_i\right).$$
(5)

For (4), we have

$$\mathbf{Pr}\left(A_{i}\right) \geqslant 1 - e^{-\frac{\varepsilon^{2}}{2M^{2}}\gamma\log n} \geqslant 1 - \frac{1}{n^{2}},\tag{6}$$

where the last inequality follows since  $\gamma \ge 4M^2/\varepsilon^2$ . So, for (6) and (5),

$$\mathbf{Pr}\left(B_{n+t_0} > 0 \mid B_{t_0} \ge \gamma \log n\right) \ge \left(1 - \frac{1}{n^2}\right)^n \ge 1 - \frac{1}{n}.$$

### A.5 Further mathematical tools

**Definition A.11** (Stochastic dominance). Let X, Y be two real-valued random variables. Then, Y is said to stochastically dominates X  $(X \preccurlyeq Y)$  if, for every  $x \in \mathbb{R}$ ,  $\mathbf{Pr}(X > x) \leqslant \mathbf{Pr}(Y > x)$ .

**Definition A.12** (Coupling). Let  $X_1$  and  $X_2$  be two random variables that are defined on the probability spaces  $(\Omega_1, F_1, P_1)$  and  $(\Omega_2, F_2, P_2)$ , respectively. Then a coupling between  $X_1$  and  $X_2$  is formed by: i) a probability space  $(\Omega, F, P)$ , and ii) a vector random variable  $W = (Y_1, Y_2)$  defined over this space such that: the marginal distribution of  $Y_1$  equals the distribution of  $X_1$ , while the marginal distribution of  $Y_2$  equals that of  $X_2$ .

Devising a coupling is often an effective way to show stochastic dominance, as formally stated below.

**Lemma A.13.** A random variable  $X_1$  is dominated by a random variable  $X_2$  if and only if there exists a coupling  $(Y_1, Y_2)$  between  $X_1$  and  $X_2$  such that  $\mathbf{Pr}(Y_1 \leq Y_2) = 1$ .

**Lemma A.14** (Wald's equation, [34]). Let  $\{X_n\}_{n\in\mathbb{N}}$  be an infinite sequence of real-valued, mutually independent, and identically distributed random variables. Let N be a non-negative integer-value random variable that is independent of the sequence  $\{X_n\}_{n\in\mathbb{N}}$ . Suppose that N and  $X_n$  have finite expectations. Then,

$$\mathbf{E}\left[X_1 + \dots + X_N\right] = \mathbf{E}\left[N\right] \cdot \mathbf{E}\left[X_1\right] \,.$$

**Theorem A.15** (Hoeffding's Inequality). Let  $X_1, \ldots, X_n$  be independent random variables with  $X_i$  strictly bounded in  $[a_i, b_i]$  for every  $i \in \{1, \ldots, n\}$ , where  $-\infty < a_i \leq b_i < +\infty$ . Let  $S = \sum_{i=1}^n X_i$ . Then,

$$\mathbf{Pr}\left(\left|S-\mathbf{E}\left[S\right]\right| \ge t\right) \le 2\exp\left(\frac{-2t^2}{\sum_{i=1}^n (b_i-a_i)^2}\right).$$

**Definition A.16** (Dependency graph). Let  $\{Y_{\alpha}\}_{\alpha \in \mathcal{A}}$  be a sequence of random variables. A dependency graph for  $\{Y_{\alpha}\}_{\alpha \in \mathcal{A}}$  is a graph  $\Gamma$  with vertex set  $\mathcal{A}$  such that if  $\mathcal{B} \subseteq \mathcal{A}$  and  $\alpha \in \mathcal{A}$  is not connected by an edge to any vertex in  $\mathcal{B}$ , then  $Y_{\alpha}$  is independent of  $\{Y_{\beta}\}_{\beta \in \mathcal{B}}$ .

The sum of a set of random variables, with mutual correlations that can be described by a dependency graph, enjoys of the following concentration result.

**Theorem A.17** ([17]). Suppose that X is a random variable such that  $X = \sum_{\alpha \in \mathcal{A}} Y_{\alpha}$ , where, for every  $\alpha \in \mathcal{A}$ ,  $Y_{\alpha} \sim Be(p)$ , for some fixed  $p \in (0, 1)$ . Let  $N = |\mathcal{A}|$ . Then, for every  $t \ge 0$ ,

$$\mathbf{Pr}\left(X \leqslant \mathbf{E}\left[X\right] - t\right) \leqslant \exp{-\frac{8t^2}{25\Delta_1(\Gamma)Np}}$$

where  $\Gamma$  is the dependency graph of  $\{Y_{\alpha}\}_{\alpha \in \mathcal{A}}$ ,  $\Delta(\Gamma)$  is the maximum degree of  $\Gamma$ , and  $\Delta_1(\Gamma) = \Delta(\Gamma) + 1$ .

**Theorem A.18** (Chebyshev's inequality). Let X be a real-valued random variable with bounded expectation and variance. Then, for every real a > 0,

$$\operatorname{Pr}\left(|X - \operatorname{E}[X]| \ge a\right) \leqslant \frac{\operatorname{Var}[X]}{a^2}.$$

## **B** The SWG(n,q) Model above the Threshold

In this section, we will prove Claim 1 of Theorem 2.4 and Claim 1 of Theorem 2.1, respectively in Subsection B.3 and B.4. Before proceeding with the proofs of the theorems, we introduce two preliminary lemmas. In particular, in the Subsection B.1 we present the proof of the Lemma 3.2 (already introduced in Section 3.1) while in Subsection 3.1 we state and prove a further preliminary lemma.

In all this section, we will indicate with V a set of n nodes, with G = (V, E) a graph sampled according the SWG(n, c/n) distribution, and with  $G_p$  the percolation graph of G with percolation probability p.

### B.1 Proof of Lemma 3.2

This section provides the full proof of Lemma 3.2 we state in Section 3.1 to sketch our general analysis.

For  $t = 1, 2, ..., \text{let } Q_t$  be the set of nodes in the queue Q at the end of the *t*-th iteration of the while loop in Algorithm 1 and let  $Z_t$  be the number of nodes added to the queue Q during the *t*-th iteration. Notice that  $|Q_0| = 1$  and

$$|Q_t| = \begin{cases} 0 & \text{if } |Q_{t-1}| = 0\\ |Q_{t-1}| + Z_t - 1 & \text{otherwise} \end{cases}$$

We next show that, as long as the overall number of visited nodes is below a suitable constant fraction of n, the sequence  $\{|Q_t|\}_t$  stochastically dominates a diverging Galton-Watson branching process (Definition A.7).

Let k > 1 be a constant and let  $\tau = \inf\{t \in \mathbb{N} : |Q_t| + t > n/k\}$  be the random variable indicating the first time the size of the queue plus the number nodes in R exceeds n/k. Consider any iteration  $t < \tau$  of the while loop with  $Q \neq \emptyset$ , let  $|Q \cup R| \leq n/k$  be the number of nodes in the queue or in the set R at the beginning of the while loop, and let A be the set of nodes at distance larger than L from any node in  $D \cup Q \cup R$  in the ring  $(V, E_1)$ , i.e.,

$$A = \{ v \in V \, | \, d_{(V,E_1)}(D \cup Q \cup R, v) \ge L + 1 \}.$$

Observe that there are at most  $2L(n/k + \log^4 n) \leq 4L(n/k)$  nodes at distance smaller than or equal to L from a node in  $D \cup Q \cup R$  in  $(V, E_1)$ , so  $|A| \ge n(1 - 4L/k)$ .

Let w be the node dequeued at the t-th iteration of the while loop and let  $x_1, \ldots, x_{|A|}$  be the nodes in A. For every  $i = 1, \ldots, |A|$ , let  $X_i$  be the random variable counting the number on nodes added to the queue "through" node  $x_i$  during the current iteration of the while loop at line 4 of Algorithm 1. Observe that  $X_i$  is either zero (if  $x_i$  is not a bridge neighbor of w in the percolation graph, or if  $x_i$  is a bridge neighbor of w but it is not free at its turn in line 8) or it is equal to the size of the truncated local cluster centered at  $x_i$ . Moreover,  $Z_t \ge \sum_{i=1}^{|A|} X_i$ .

Now observe that the edge  $\{w, x_i\}$  exists in the percolation graph  $G_p$  with probability pc/n, independently of the other edges: we can use the principle of deferred decisions here, since the existence or not of each such edge was never observed before w was extracted from the queue. Moreover, since each node in A has at most 4L other nodes of A at ring distance less than 2L, the probability that  $x_i$  is a bridge neighbor of w in  $E_p$  and it is free for the subset  $Q \cup R$  in  $G_{SW}$  at its iteration in the for loop at line 7 of Algorithm 1 is at least  $pc/n(1 - pc/n)^{4L}$ , i.e. the probability that  $x_i$  is a bridge neighbor for w in  $E_p$  and all the nodes in A at ring distance at most 2L from  $x_i$ are not. From (3) it follows that

$$\mathbf{E}[X_i] \ge pc/n(1 - pc/n)^{4L} \mathbf{E}\left[|LC^L(x_i)|\right] = pc/n(1 - pc/n)^{4L} \left(\frac{1 + p - 2p^{L+1}}{1 - p}\right)$$

Thus, the expected number of new nodes added to the queue in an iteration of the while loop is

$$\mathbf{E} \left[ Z_t \mid |Q_{t-1}| > 0, \, \tau > t \right] \ge n(1 - 4L/k)(pc/n)(1 - pc/n)^{4L} \left( \frac{1 + p - 2p^{L+1}}{1 - p} \right)$$
$$\ge pc(1 - 4L/k)(1 - 4Lpc/n) \frac{1 + p - 2p^{L+1}}{1 - p}$$
$$= \frac{pc(1 + p)}{(1 - p)} \left( 1 - \mathcal{O}(p^L) - \mathcal{O}(L/k) - \mathcal{O}(L/n) \right) .$$

The critical value pc(1+p)/(1-p) = 1 is achieved for  $p = \frac{\sqrt{c^2+6c+1}-c-1}{2c}$ . So, for every choice of  $\varepsilon \in (0, 1 - \frac{\sqrt{c^2+6c+1}-c-1}{2c})$ , if  $p = \frac{\sqrt{c^2+6c+1}-c-1}{2c} + \varepsilon$  we can choose sufficiently large constants L and k such that, whenever n is large enough,  $\mathbf{E}[Z_t \mid |Q_{t-1}| > 0, t < \tau] \ge 1 + \varepsilon'$ , with  $\varepsilon' > 0$ .

At each while iteration of Algorithm 1, the node w extracted from Q has at most Bin(n, pc/n) bridge neighbors in  $E_p$ . Since each *free* node is also a bridge neighbor in  $E_p$  for the node w extracted from the queue, we further have

$$\operatorname{Var} \left[ Z_t \mid |Q_{t-1}| > 0, \tau > t \right] \leq \operatorname{\mathbf{E}} \left[ Z_t^2 \mid |Q_{t-1}| > 0, \tau > t \right] \leq (2L)^2 \operatorname{\mathbf{E}} \left[ \operatorname{Bin}(n, pc/n)^2 \right] \leq 4L^2.$$

Hence, we can define a Galton-Watson branching process  $\{B_t\}_t$  according to Definition A.7 as follows:

- If at the beginning of the *t*-th iteration of the while loop it holds that  $|Q \cup R| \leq n/k$  then we consider an arbitrary set  $\hat{A}$  such that each node in  $\hat{A}$  is at distance larger than L from any node in  $Q \cup R$ , and the size of  $\hat{A}$  is exactly  $\lceil n(1-4L/k) \rceil$ . In this setting, we define  $W_t$  as the number of new nodes in  $\hat{A}$  added to the queue Q during the *t*-th iteration of the while loop.

- Otherwise (i.e., if at the *t*-th iteration the size  $|Q \cup R| > n/k$ ) then consider two arbitrary disjoint sets of nodes  $\hat{Q}$  and  $\hat{R}$  with  $|\hat{Q} \cup \hat{R}| \leq n/k$  and an arbitrary set  $\hat{A}$  such that each node in  $\hat{A}$  is at distance larger than L from any node in  $\hat{Q} \cup \hat{R}$  and the size of  $\hat{A}$  is exactly  $\lceil n(1 - 4L/k) \rceil$ . In this setting, we define  $W_t$  as the number of new nodes in  $\hat{A}$  that would be added to the queue if at the beginning of the *t*-th iteration of the while loop it was  $Q = \hat{Q}$  and  $R = \hat{R}$ .

Notice that  $\{W_t\}_t$  is a sequence of i.i.d. random variables with  $\mathbf{E}[W_t] > 1$  (thus, according to Theorem A.8,  $\{B_t\}_t$  is a diverging branching process) and finite variance. Observe also that the pair  $(B_t, Q_t)$  is a coupling between the two considered processes (see Definition A.12 in Subsection A.5) such that, with probability 1, at each round t either  $|Q_t \cup R_t| > n/k$  or it holds that  $Z_t \ge W_t$ . Thanks to Lemma A.13, we thus get that, at each round t,

$$\mathbf{Pr}\left(|R_t \cup Q_t| \ge n/k \ OR \ |Q_t| \ge \varepsilon' t\right) \ge \mathbf{Pr}\left(B_t \ge \varepsilon' t\right).$$

The lemma then follows by applying Lemma A.9 in Subsection A.4.

**Remark.** The lemma above implies that the nodes visited by the end of the sequential *L*-VISIT in Algorithm 1 reaches size at least n/k, with probability at least  $\gamma$ . This result thus shows a linear lower bound on the size of the connected component of the source s in  $G_p$ .

### **B.2** Parallelization of the sequential BFS visit

In this section, we strenghten the analysis of the visit in the graph  $G_p$ , when the percolation probability p is over the threshold.

Our goal here is to prove that, if we explore the connected components of  $\log n$  nodes taken arbitrarily in the graph, then this process leads us, w.h.p., to the visit of a linear fraction of the nodes in the percolated graph, within  $\Theta(\log n)$  number of hops.

We follow an approach that proceeds along the general lines of Subsection B.1, albeit with important differences and some technical challenges. We begin by introducing Algorithm 2 below, which is partly "parallel" extension of the sequential BFS visit described by Algorithm 1. We assume Algorithm 2 is run on an input  $(G, G_p, I_0, D_0)$ , where  $I_0$  is an arbitrary subset of initiators and  $D_0 \subseteq V \setminus I_0$  is a set of deleted nodes.

In the remainder of this section,  $Q_t$  and  $R_t$  respectively denote the subsets Q and R at the end of the *t*-iteration of the while loop in line 10. Consistently with the notation used in Section B, we also let  $S_t = V \setminus (R_t \cup Q_t)$ .

#### Algorithm 2 PARALLEL *L*-VISIT

**Input**: A small-world graph  $G_{SW} = (V, E_{SW})$  and a subgraph H of  $G_{SW}$ ; a set of initiators  $I_0 \subseteq V$ ; a set of deleted nodes  $D_0 \subseteq V \setminus I_0$ .

1:  $Q = I_0$ 2:  $R = \emptyset$ 3:  $D = D_0$ 4: while  $Q \neq \emptyset$  do  $\triangleright$  This is the overall set of nodes visited so far  $A = R \cup Q \cup D$ 5:6: X = bridge-neighors(Q) $\triangleright$  Set of bridge-neighbors in H of nodes in Q 7: Q' = Q $Q = \emptyset$ 8: while  $Q' \neq \emptyset$  do 9: w = dequeue(Q')10: $R = R \cup w$ 11:for each  $x \in X$  do 12:if x is free for (X, A) then  $\triangleright$  We are using Definition B.2 13:for each node y in the L-truncated local cluster  $LC^{L}(x)$  do 14: enqueue(y, Q)15:

**Lemma B.1.** Let V be a set of n nodes,  $I_0 \subseteq V$  a set of initiators and  $D_0 \subseteq V \setminus I_0$  a set of deleted nodes such that  $|D_0| \leq \log^4 n$ . For every  $\varepsilon > 0$ , c > 0 and for every contagion probability p such that

$$\frac{\sqrt{c^2 + 6c + 1} - c - 1}{2c} + \varepsilon \leqslant p \leqslant 1,$$

there are positive parameters  $L, k, \beta, \delta$  that depend only on c and  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution, and let  $G_p$  be the percolation graph of G with parameter p. Run the PARALLEL L-VISIT in Algorithm 2 on input  $(G, G_p, I_0, D_0)$ : in every iteration  $t \ge 1$  of the while loop at line 4 in Algorithm 2, for every integer  $i \ge \beta \log n$  and  $r \ge 0$  such that  $i + r \le n/k$ :

$$\mathbf{Pr}\left(|Q_t| \ge (1+\delta)i \mid |Q_{t-1}| = i, |R_{t-1}| = r\right) \ge 1 - \frac{1}{n^2}.$$
(7)

In what follows, we introduce some definitions and lemmas preliminary to the proof of the above lemma.

We first need to slightly revisit the notion of free node given by Definition 3.1 for the Sequential L-VISIT, adapting it to the second phase of Algorithm 2.

**Definition B.2** (free nodes). Consider  $X, A \subset V$ . A node  $x \in X$  is free for the pair (X, A) if the following holds:

- 1. x is at distance on the ring  $E_1$  at least L + 1 from every node in A;
- 2. x is at distance on the ring  $E_1$  at least 2L + 1 from every other node in X.

If  $Q_{t-1}$  is the queue Q at the end of the (t-1)-th iteration of the while loop in line 10 of Algorithm 2, we denote by  $X_t$  the set of bridge-neighbors (w.r.t.  $E_p$ ) of nodes in  $Q_{t-1}$ , while  $Y_t \subseteq X_t$  is the subset of free nodes for the pair  $(X_t, R_{t-1} \cup Q_{t-1})$ .

Definition B.2 implies the following properties for the generic, t-th iteration of the while loop at line 4 of Algorithm 2. At the beginning of the iteration, we initialize set  $Q_t = \emptyset$  and we consider the set  $Y_t$  of free nodes for  $(X_t, R_{t-1} \bigcup Q_{t-1})$ . For each node  $x \in Y_t$ , we add to the queue  $Q_t$  the set  $|\mathrm{LC}^{L}(x)|$  of the *L*-truncated local cluster of node *x* (Definition B.2): the set  $Q_t$  can thus be seen as the nodes that  $Q_{t-1}$  infects via its free bridge-neighbors in round *t*. The process stops in the first round  $\tau$ , for which queue  $Q_{\tau}$  is empty, i.e.  $\tau = \{t > 0 : Q_t = \emptyset\}$ . Hence, for each  $t \leq \tau$ 

$$Q_t = \bigcup_{x \in Y_t} \mathrm{LC}^L(x).$$

and, if we label the nodes in  $Y_t$  as  $1, 2, \ldots, |Y_t|$ , we get

$$|Q_t| = |\mathrm{LC}^L(1)| + \dots + |\mathrm{LC}^L(|Y_t|)|$$
 (8)

since the subsets  $LC^{L}(j)$ 's are mutually disjoint from Definition B.2.

In the remainder, we denote by  $A \subseteq S_{t-1}$  the subset of nodes that are at ring distance at least L+1 from each node in  $Q_{t-1} \bigcup R_{t-1} \cup D$  at the end of the (t-1)-th iteration of the while loop at line 10 of Algorithm 2. Under the hypotheses of Lemma B.1 on  $|Q_{t-1}| + |R_{t-1}|$ , we have:

$$n\left(1 - \frac{4L}{k}\right) \le |A| \le n - (|R_{t-1}| + |Q_{t-1}| + |D|) \le n.$$
(9)

Moreover, we can write

$$|Y_t| = \sum_{x \in A} Y(x),\tag{10}$$

where each Y(x) is a Bernoulli random variable, whether node  $x \in A$  is *free*. By a standard argument, we can bound the conditional expectation of  $|Y_t|$  as follows.

Fact B.3. Under the hypotheses of Lemma B.1 we have

$$i \cdot p \cdot c \cdot \left(1 - \frac{8L}{k}\right) \leqslant \mathbf{E}\left[|Y_t| \mid |Q_{t-1}| = i, |R_{t-1}| = r\right] \leqslant i \cdot p \cdot c.$$

$$(11)$$

*Proof.* We know a node x is *free* if it is connected via a bridge in  $G_p$  with at least one node in  $Q_{t-1}$  and no node, within ring distance 2L from x, is connected via a bridge in  $G_p$  with a node in  $Q_{t-1}$ . Therefore,

$$\left(1 - (1 - pq)^i\right)\left(1 - pq\right)^{4Li} \leqslant \mathbf{Pr}\left(Y(w') = 1\right) \leqslant ipq.$$

$$(12)$$

Using the assumptions  $i + r \leq n/k$ ,  $p \cdot q \cdot n < 1$  and the inequalities

$$(1+y)^n \leq \frac{1}{1-ny}, \ n \in \mathbf{N}, \ y \in [-1,0] \ \text{and} \ (1+y)^r \ge 1+yr, \ y \ge -1, \ r \in \mathbf{R} \setminus (0,1),$$

we get that the LHS of (12) is not smaller than

$$\begin{split} &(1-pq)^i(1-pq)^{4Li} \geqslant \left(1-\frac{1}{1+ipq}\right) \cdot (1-4Lpq) \geqslant ipq \left(1-\frac{ipq}{1+ipq}\right) (1-4Lipq) \geqslant \\ &\geqslant ipq(1-ipq)(1-4Lipq) \geqslant ipq(1-5Lpq) \geqslant ipq \left(1-\frac{5Lp}{k}\right) \,. \end{split}$$

Consequently, from (9), (10), and (12) we get (11).

Our next step is to prove that w.h.p.,  $|Y_t|$  does not deviate much from its expectation. As we noted earlier,  $|Y_t|$  can be expressed as the sum of Bernoulli random variables Y(x) with  $x \in$ A. Unfortunately, these variables are not mutually independent: for instance, Y(x) = 1 implies Y(x') = 0 for every other  $x' \in A$  that lies within ring distance 2L in  $G_p$  from x. However, we are able to prove the following concentration bound, by leveraging the key fact that the variables above only have *local*, mutual correlations.

**Lemma B.4.** Under the hypotheses of Lemma B.1, if  $\beta$  and k are sufficiently large, we have

$$\mathbf{Pr}\left(|Y_t| \ge i \cdot p \cdot c \cdot \left(1 - \frac{9L}{k}\right) \mid |Q_{t-1}| = i, |R_{t-1}| = r\right) \ge 1 - \frac{1}{n^3}.$$

*Proof.* Recall that for any  $x \in A$ , Y(x) is the Bernoulli random variable that indicates whether x is *free*. Since x is free only if it is connected via a bridge in  $G_p$  with at least one node in  $Q_{t-1}$  we have, for every  $x \in A$ :

$$f = \mathbf{Pr}\left(Y(x) = 1\right) \leqslant \frac{i \cdot p \cdot c}{n} \tag{13}$$

Now, for any  $x \in A$ , denote by  $\mathcal{N}_{E_1}^{2L}(x)$  the set of nodes that are within ring distance 2L from x. For any other  $x' \in A$ , Definition B.2 implies that Y(x) and Y(x') are mutually dependent if and only if  $\mathcal{N}_{E_1}^{2L}(x) \cap \mathcal{N}_{E_1}^{2L}(x') \neq \emptyset$ . Hence, we can bound the maximum number of random variables Y(x') that are correlated with Y(x) as follows. Consider  $\mathcal{N}_{E_1}^{2L}(x) = \{x - 2L, \dots, x, \dots, x + 2L\}$ . If  $\mathcal{N}_{E_1}^{2L}(x) \cap \mathcal{N}_{E_1}^{2L}(x) \neq \emptyset$  for some other  $x' \in A$ , it must be the case that either  $x < x' \wedge x' - 2L \leqslant x + 2L$ , or  $x' < x \wedge x - 2L \leqslant x' + 2L$ . The former happens for every x' such that  $x < x' \leqslant x + 4L$  (notice that exactly 4L nodes can meet this condition), while the latter happens for every x' such that  $x - 4L \leqslant x' < x$  (again, exactly 4L nodes can meet this condition). It thus follows that, for a fixed Y(x), at most 8L other random variables can be correlated with Y(x). This property can be described by the dependency graph  $\Gamma$  on the subset  $\{Y(x)\}_{x\in A}$  (see Definition A.16 in Appendix A.5). In our case, the maximum degree  $\Delta$  of the dependency graph is 8L, whence we have  $\Delta_1(\Gamma) = 8L + 1$  in Definition A.16.

We can thus apply Corollary 2.4 in [17] (see Theorem A.17 in Appendix A.5)). In more detail, we use Fact B.3, (9) and (13), the assumption  $p \cdot c < 1$ , and we apply Theorem A.17 to complete the proof:

$$\begin{aligned} \mathbf{Pr}\left(|Y_{t}| \leq ipc\left(1 - \frac{9L}{k}\right)| |Q_{t-1}| = i, |R_{t-1}| = r\right) \leq \\ \leq \mathbf{Pr}\left(|Y_{t}| \leq ipc\left(1 - \frac{8L}{k}\right)\left(1 - \frac{L}{k}\right)| |Q_{t-1}| = i, |R_{t-1}| = r\right) \leq \\ \leq \mathbf{Pr}\left(|Y_{t}| \leq \mathbf{E}\left[|Y_{t}|| |Q_{t-1}| = i, |R_{t-1}| = r\right]\left(1 - \frac{L}{k}\right)| |Q_{t-1}| = i, |R_{t-1}| = r\right) \leq \\ \leq \exp\left(\frac{-8(\mathbf{E}\left[|Y_{t}|| |Q_{t-1}| = i, |R_{t-1}| = r\right])^{2}}{25(L^{2}/k^{2}) \cdot \Delta_{1}(\Gamma) \cdot |A| \cdot f}\right) \leq \exp\left(\frac{-8i^{2}p^{2}c^{2}\left(1 - \frac{8L}{k}\right)^{2}}{25(L^{2}/k^{2})(8L+1)ipc}\right) \leq \\ \leq \exp\left(\frac{-8ipc\left(1 - \frac{8L}{k}\right)^{2}}{25(L^{2}/k^{2})(8L+1)}\right) \leq \exp\left(\frac{-8\beta\log npc\left(1 - \frac{8L}{k}\right)^{2}}{25(L^{2}/k^{2})(8L+1)}\right) \leq n^{-3}, \end{aligned}$$
(14)

where the last equation holds whenever k and  $\beta$  are sufficiently large constants (depending on  $\varepsilon$ ).  $\Box$ 

Now we are ready to conclude the proof of Lemma B.1.

Proof of Lemma B.1. Essentially, Lemma B.4 implies that, w.h.p.,  $|Y_t|$  is at least  $i \cdot p \cdot q \cdot n$  up to a constant factor that can be made arbitrarily close to 1, provided constants k and  $\beta$  are sufficiently large. Next, using (8) and (3) in Lemma A.6 and applying Wald's equation (see Lemma A.14 in Appendix A.5) we have:

$$\mathbf{E}[|Q_t| \mid |Q_{t-1}| = i, |R_{t-1}| = r] = \mathbf{E}[|\mathrm{LC}^L(1)|] \mathbf{E}[|Y_t| \mid |Q_{t-1}| = i, |R_{t-1}| = r] = \\ = \left(\frac{1+p}{1-p} - \frac{2p^{L+1}}{1-p}\right) \cdot \mathbf{E}[|Y_t||Q_{t-1}| = i, |R_{t-1}| = r].$$

Omitting the conditioning on the event  $\{|Q_{t-1}| = i, |R_{t-1}| = r\}$  for the sake of brevity in the remainder of this proof, Lemma B.4 implies  $|Y_t| \ge p \cdot c \cdot i \cdot (1 - 9L/k)$  with probability at least  $1 - n^{-3}$ . Moreover, by definition of  $Q_t$ ,

$$\mathbf{Pr}\left(|Q_t| \ge \sum_{x=1}^{p \cdot c \cdot i(1-9L/k)} |\mathrm{LC}^L(x)| \mid |Y_t| \ge p \cdot c \cdot i \cdot (1-9L/k)\right) = 1.$$

If we set  $Z = \sum_{x=1}^{p \cdot c \cdot i(1-9L/k)} |\mathrm{LC}^L(x)|$  the above inequality implies

$$\mathbf{Pr}\left(|Q_t| \leqslant z \mid \{|Y_t| \ge p \cdot c \cdot i \cdot (1 - 9L/k)\}\right) \leqslant \mathbf{Pr}\left(Z \leqslant z\right) \,. \tag{15}$$

Again from Wald's equation,

$$\mathbf{E}[Z] = \frac{p(1+p)}{1-p} \cdot c \cdot i \cdot \left(1 - \frac{9L}{k}\right) \left(1 - \frac{2p^{L+1}}{(1-p)(1+p)}\right) = \mu$$

Hence, for sufficiently large n, from the law of total probability, from Lemma B.4 and from (15), we have:

$$\begin{split} \mathbf{Pr}\left(|Q_t| \leqslant \mu \left(1 - \frac{L}{k}\right)\right) &\leqslant \mathbf{Pr}\left(|Q_t| \leqslant \left(1 - \frac{L}{k}\right)\mu \mid \{|Y_t| \geqslant p \cdot c \cdot i \cdot (1 - 9L/k)\}\right) + \frac{1}{n^3} \\ &\leqslant \mathbf{Pr}\left(Z \leqslant \left(1 - \frac{L}{k}\right)\mu\right) + \frac{1}{n^3} \leqslant_{(*)} 2 \exp\left(\frac{-2\mu^2}{(k^2/L^2) \cdot p \cdot i \cdot q \cdot (1 - 9L/k) \cdot 4L^2}\right) + \frac{1}{n^3} \\ &\leqslant_{(**)} 2 \exp\left(\frac{-c \cdot \beta \log n}{4k^2}\right) + \frac{1}{n^3} \leqslant 3n^{-3} \leqslant n^{-2} \,, \end{split}$$

where in (\*) we used the Hoeffding inequality (see Theorem A.15 in the Appendix), by leveraging the fact that the random variables counting the number of infectious nodes in each local cluster are mutually independent and, moreover, they range between 1 and 2L + 1. Moreover, (\*\*) holds if we take  $\beta$  and k sufficiently large. Recalling that for simplicity we omitted the conditioning on  $|Q_{t-1}| = i, |R_{t-1}| = r$ , the above derivations imply

$$\mathbf{Pr}\left(|Q_t| \ge \frac{pc(1+p)}{(1-p)} \cdot i \cdot \left(1 - \frac{10L}{k}\right) \left(1 - \frac{2p^{L+1}}{(1-p)(1+p)}\right) | |Q_{t-1}| = i, |R_{t-1}| = r\right)$$
  
$$\ge 1 - \frac{1}{n^2}.$$
(16)

The proof of Lemma B.1 then follows by observing that, since  $p = \frac{\sqrt{c^2+6c+1}-c-1}{2c} + \varepsilon$ , we can fix suitable values for constants k and L, so that

$$c \cdot \frac{p(1+p)}{1-p} \left(1 - \frac{2p^{L+1}}{(1+p)(1-p)}\right) \left(1 - \frac{10L}{k}\right) = (1+\delta) , \qquad (17)$$

for some constant  $\delta > 0$ . Together, (16) and (17) imply (7) in Lemma B.1.

### B.3 Wrapping up: proof of Claim 1 of Theorem 2.4

We first prove Theorem 2.4, since it is implicated almost directly by the lemmas proved in the previous subsections, namely Lemmas 3.2 and B.1. To prove the theorem, we introduce the following algorithm, which is nothing more than a simple combination of Algorithms 1 and 2, with some simplifications.

Algorithm 3 L-VISIT FROM A SET OF INITIATORS

**Input**: A small-world graph  $G_{SW} = (V, E_{SW})$ ; a subgraph H of  $G_{SW}$ ; a set of initiators  $I_0 \subseteq V$ . 1:  $Q = I_0$ 2:  $R = \emptyset$ 3:  $D = \emptyset$ 4: while  $Q \neq \emptyset$  and  $Q < \beta \log n$  do 5: Perform lines 4-10 of Algorithm 1  $\triangleright$  Sequential L-visit 6: while  $Q \neq \emptyset$  do 7: Perform lines 4-15 of Algorithm 2  $\triangleright$  Parallel L-visit

It should be noted that the algorithm above is essentially a sequence of two main while loops. The first loop in line 4 corresponds to Algorithm 1 and describes a "bootstrap" phase of the RF process, while the second main loop in line 6, describes a second phase starting with a subset Q of visited nodes of size  $\Omega(\log n)$ .

The following lemma states the main properties produced by our analysis of Algorithm 3 with input  $(G, G_p, I_0)$ . In particular, it claims that, with probability  $\Omega(1)$ , the first while loop terminates after  $\mathcal{O}(\log n)$  rounds. Moreover, once the second while loop starts, it is such that, after  $\mathcal{O}(\log n)$ rounds, there will be at least  $\Omega(n)$  visited nodes w.h.p. This result implies that, starting from a single source  $s \in V$ , the algorithm will visit  $\Omega(n)$  nodes with constant probability. On the other hand, starting from a set of sources  $I_0$  such that  $|I_0| = \Omega(\log n)$ , the algorithm will reach  $\Omega(n)$ nodes, w.h.p. Hence, Claim 1 of Theorem 2.4 follows from the following lemma.

**Lemma B.5.** Let V be a set of n nodes and  $I_0 \in V$  a set of initiators. For every  $\varepsilon > 0$ , c > 0 and for every probability p such that

$$\frac{\sqrt{c^2 + 6c + 1} - c - 1}{2c} + \varepsilon \leqslant p \leqslant 1$$

there are positive parameters  $L, k, \gamma, \beta$  that depend only on c and  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution, and let  $G_p$  be the percolation graph of G with parameter p. Run Algorithm 3 on input  $(G, G_p, I_0)$  for sufficiently large n, then:

1. The first while loop in line 4 terminates at some round  $\tau_1 = \Theta(\log n)$  in which

$$\mathbf{Pr}\left(|R \cup Q| \ge n/k \text{ OR } |Q| \ge \beta \log n\right) \ge \gamma;$$

2. Conditioning to the above event, the second while loop in line 6 terminates at some round  $\tau_2 = \Theta(\log n)$  in which  $|Q \cup R| \ge n/k$ , w.h.p.

*Proof.* The first claim is a direct consequence of Lemma 3.2 by setting t in the latter so that  $\varepsilon' t = \beta \log n$ .<sup>11</sup> Then, at the end of the first while loop, two cases may arise: i)  $|Q \cup R| \ge n/k$  (where Q and R are the snapshot of the two sets at the end of the first while loop), so  $\Theta(n)$  nodes

<sup>&</sup>lt;sup>11</sup>Note that  $t_0$  in the claim of Lemma A.9 is a constant.

are visited within  $\mathcal{O}(\log n)$  iterations and Claim 2 immediately follows; ii) A round  $\tau_1 = \Theta(\log n)$  exists in which the subset of infectious nodes gets size at least  $|Q| \ge \beta \log n$ , where Q is the queue's snapshot at the end of the first while loop.

In order to complete the proof of Claim 2 of the lemma, it thus suffices to only address case ii) above, which corresponds to the setting in which, at the beginning of the second while loop, the queue Q is initialized with a set of size  $\geq \beta \log n$ . We can now observe that Claim 2 is a direct consequence of Lemma B.1.

### B.4 Wrapping up: proof of Claim 1 of Theorem 2.1

In the previous subsection we have essentially proved that, starting from a single source  $s \in V$ , if we explore the connected component of s in  $G_p$ , then, with probability  $\Omega(1)$ , we will visit at least  $\Omega(n)$  nodes and, moreover, such nodes induce a connected sub-graph of diameter  $\mathcal{O}(\log n)$ .

The goal of this subsection is to prove that, w.h.p., a set of  $\Omega(n)$  nodes in V exists that induces in  $G_p$  a connected component with diameter  $\mathcal{O}(\log n)$ . To this aim, we introduce the following algorithm that can be informally seen as several "attempts" of bootstraps, according to Algorithm 1, each one performed from a different source node s, then followed by a PARALLEL *L*-VISIT according to Algorithm 2.

Algorithm 4 Search of the giant component				
<b>Input</b> : A small-world graph $G_{SW} = (V, E_{SW})$ ; a subgraph H of $G_{SW}$ ; two integers $\beta$ , $\beta'$ .				
1: $Q = \emptyset$				
2: $D = \emptyset$				
3: while $ Q  \leq \beta \log n$ or $ Q \cup R  \leq n/k$ do	$\triangleright$ First phase			
4: Let $s \in V \setminus D$				
5: $Q = \{s\}$				
6: $R = \emptyset$				
7: <b>for</b> $i = 1, \ldots, \beta' \log n$ <b>do</b>				
8: Perform lines 4-10 of Algorithm 1	$\triangleright$ Sequential <i>L</i> -visit			
9: $D = D \cup R$				
10: if $ Q \cup R  \leq n/k$ then	▷ Second phase			
11: Perform Algorithm 2 with input $G_{SW}$ , $H$ , $I_0 = Q$ , $D_0 = R \cup D$	$\triangleright$ Parallel <i>L</i> -visit			

More in detail, the algorithm above works in two phases. The first phase starts in the while loop in line 3 and performs different "bootstraps". In this phase, we essentially look for a source node  $s \in V$  such that the queue Q of the visit of the component of s in  $G_p$  gets  $\Omega(\log n)$  nodes, after  $\Theta(n)$  steps of the visit. In particular, at each iteration of the while loop, a node  $s \in V$  is chosen arbitrarily and, starting from it,  $\Theta(\log n)$  steps of the sequential L-visit of Algorithm 1 are performed: if, at this point, the set Q has  $\Omega(\log n)$  nodes, the first phase is successfully completed, otherwise it starts again from another source node. The second phase of the algorithm starts in line 11 with a subset Q of  $\Omega(\log n)$  visited nodes, and consists in the parallel visit in Algorithm 2 setting Q as the source subset.

The following lemma essentially states that, w.h.p.: i) within  $\tau_1 = \mathcal{O}(\log n)$  bootstrap attempts, the first phase ends successfully, and, then, ii) the second phase will discover  $\Omega(n)$  nodes within further  $\tau_2 = \mathcal{O}(\log n)$  iterations.

**Lemma B.6.** Let V be a set of n nodes. For every  $\varepsilon > 0$ , c > 0 and  $\beta > 0$ , and for every probability p such that

$$\frac{\sqrt{c^2 + 6c + 1} - c - 1}{2c} + \varepsilon \leqslant p \leqslant 1,$$

there are positive parameters L, k (that depends only on c and  $\varepsilon$ ) and a constant  $\beta'$  (that depends on c,  $\varepsilon$  and  $\beta$ ) such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution and let  $G_p$  be the percolation graph of G with parameter p. Run Algorithm 4 on input  $(G, G_p, \beta, \beta')$  with any sufficiently large n, then:

- 1. The first while loop in line 3 terminates at some round  $\tau_1 = \mathcal{O}(\log n)$ , w.h.p.;
- 2. Conditioning to the above event, the second phase of the algorithm starting in line 11 terminates at some round  $\tau_2 = \Theta(\log n)$  in which  $|Q \cup R| \ge n/k$ , w.h.p.

Proof. As for the first claim, let  $\gamma > 0$  and  $\varepsilon'$  be the constants in Lemma 3.2, and define  $\beta' = \beta/\varepsilon'$ . Moreover, let  $\tau = \log_{1-\gamma}(n)$ . First, we notice that, at each iteration of the while in line 3, the set D grows w.h.p. of at most  $8L\beta' \log^2 n$  size: indeed, each node in  $G_p$  has degree of at most  $4 \log n$  with probability at least  $1 - 1/n^2$  (this fact follows from a standard application of Chernoff's bound) and so, within  $\beta' \log n$  iterations of the for loop, at most  $8L\beta' \log^2 n$  nodes will be reached by s. This implies that, at each iteration  $j \leq \tau$  of the while loop, D has size  $|D| = \mathcal{O}(\log^3 n)$ .

Then, we claim that, at each *j*-th iteration of the while loop in line 3, if  $j \leq \tau$ , there is probability at least  $\gamma > 0$  that the process terminates. Indeed, thanks to Lemma 3.2, there exists a constant  $\gamma > 0$  such that, at the end of the for loop in line 8,

$$\mathbf{Pr}\left(|Q| \ge \varepsilon'\beta' \log n \text{ or } |R \cup Q| \ge n/k\right) \ge \gamma.$$

Therefore, the probability that the process continues after  $\tau$  iterations is at most

$$(1-\gamma)^{\tau} \leqslant \frac{1}{n}.$$

Claim 2 is instead a direct consequence of Lemma B.1.

## C The SWG(n,q) Model below the Threshold

The goal of this section is to prove the second claims of Theorems 2.1 and 2.4. Informally, in the following we show that, whenever  $p < \frac{\sqrt{c^2+6c+1}-c-1}{2c}$ , w.h.p., the percolation graph  $G_p$  of a graph G = (V, E) sampled from  $\mathcal{SWG}(n, q)$  is such that every connected component has  $\mathcal{O}(\log n)$  nodes. We state here the claim which is proved in Subsection C.1.

**Lemma C.1.** Let V be a set of n nodes. For every  $\varepsilon > 0$ , c > 0 and for every contagion probability p such that

$$0 \leqslant p \leqslant \frac{\sqrt{c^2 + 6c + 1} - c - 1}{2c} - \varepsilon$$

there is a positive constant  $\beta$  that depends only on c and  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution, and let  $G_p$  be the percolation graph of G with parameter p. If n is sufficiently large, with probability at least 1 - 1/n with respect to the randomness of G and the randomness of  $G_p$ ,  $G_p$  contains no connected component of size exceeding  $\beta \log n$ .

Interestingly enough, thanks to the equivalence between the SIR process and the percolation process, the above lemma also implies Claim 2 of Theorem 2.4, since the SIR process infects at least one new node in each round unless it has died out, the above result also implies that, w.h.p., the SIR process dies out within  $\beta \log n$  rounds, infecting at most  $|I_0| \cdot \beta \log n$  new nodes.

### C.1 Proof of Lemma C.1

In order to prove upper bounds on the number of nodes in a connected component, we might proceed as with did to prove lower bounds. We proceed as follows: i) we run a BFS in  $G_p$ , i.e. we run Algorithm 5 with input  $G_{SW} = G$ ,  $H = G_p$  and an arbitrary source  $s \in V$ , and we define a (sequential) Galton-Watson branching process that stochastically dominates<sup>12</sup> the BFS process with respect to the overall size of the set of nodes visited upon termination; ii) thanks to step (i), we can prove that for each source  $s \in V$  and every  $t > \beta \log n$ , the BFS in Algorithm 5 with input  $(G, G_p, s)$  terminates within t iterations of the while loop after visiting less than t nodes, w.h.p.

Algorithm	<b>5</b>	BFS	VISIT
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**Input:** A small-world graph  $G_{SW} = (V, E_{SW})$  and a subgraph H of  $G_{SW}$ ; a source  $s \in V$ . 1:  $Q = \{s\}$ 2: while  $Q \neq \emptyset$  do 3: w = dequeue(Q)4: visited(w) = True5: for each bridge neighbor x of w in H such that visited(x) = False do6: for each y in the local cluster LC(x) such that visited(y) = False do7: enqueue(y, Q)

It should be noted that i) Algorithm 5 visits the connected component containing s; ii) the number of nodes visited by the algorithm is exactly equal to the number of iterations of the main while loop before Q becomes empty. To formalize our approach we need to define the following random subsets of nodes.

**Definition C.2.** For each  $t \ge 1$ , let  $Q_t$  be the set Q of the BFS in Algorithm 5 at the end of the t-th iteration of the while loop. Let  $R_t = \bigcup_{i=1}^{t-1}Q_i$ , and let  $S_t = V \setminus (R_t \cup Q_t)$ . We also define  $cc(s) = \max\{t : Q_t \neq \emptyset\}$  as the overall number nodes visited at the end of the execution of Algorithm 5 with input  $G_{SW} = G$ ,  $H = G_p$ , and an arbitrary source  $s \in V$ .

We now consider the "sequential" Galton-Watson Branching process  $\{B_t\}_{t\geq 0}$  (see Definition A.7) determined by the random variables  $\{W_t\}_{t\geq 0}$ , where the  $W_t$ 's are *independent* copies of the following random variable W:

**Definition C.3.** W is generated as follows: i) we first randomly sample an integer Y from the distribution Bin(n, pc/n); ii)  $W = Y + \sum_{j=1}^{2Y} L_j$ , where each  $L_j$  is a variable that counts the number of successes in a sequence of independent Bernoulli trials with success probability p, till the first failure.

It should be noted that  $\sum_{j=1}^{2x} L_j$  is the overall number of successes in a sequence of 2x Bernoulli trials with parameter p, until we observe exactly 2x failures. As such,  $\sum_{j=1}^{2x} L_j$  follows a negative binomial distribution. The next lemma shows that the above Galton-Watson process  $\{B_t\}_{t\geq 0}$  dominates the process  $\{Q_t\}_t$ .

**Fact C.4.** For every  $x \ge 0$ , the following holds, for every t:

$$\mathbf{Pr}\left(B_{t} \geqslant x\right) \geqslant \mathbf{Pr}\left(\left|Q_{t}\right| \geqslant x\right),$$

<sup>&</sup>lt;sup>12</sup>More precisely in Lemma C.4 we use Definition A.11 in the appendix and notice that a simple coupling argument (see Definition A.12 and Lemma A.13.) applies between the two processes.

where the left side of the inequality is taken over the randomness of the Galton-Watson process  $\{B_t\}_{t\geq 0}$ , while the right side is taken on the outcome of Algorithm 5 with input  $G_{SW} = G$  and  $H = G_p$ , with respect to the randomness of the initial graph G sampled from SWG(n,q) and that of its percolation  $G_p$ .

Proof. The argument is based on the following observations. Consider the process generated by Algorithm 5 in Definition C.2 with input  $G_{SW} = G$ ,  $H = G_p$  and any fixed source  $s \in V$  and consider a given state at iteration t. Consider the node w dequeued from Q at the beginning of iteration t of Algorithm 5, and consider the set of nodes it can possibly add to the queue at iteration t. In the best possible case, i) w has some number  $\hat{Y}$  of bridge edges in  $E_p$  (the bridge edges considered in line 6 of the algorithm), and ii) a local cluster consisting of some L nodes will be infected starting at each of them.  $\hat{Y}$  is distributed as  $Bin(|S_t|, pc/n)$  and is thus dominated by any variable distributed as Bin(n, pc/n). As for L, it is certainly dominated by the sum of  $\hat{Y}$  variables, each counting the total number of activations in the local cluster created by a single node of an infinite path topology (see Fact A.4). But the above considerations imply that the variable counting the number of nodes that w can possibly infect is dominated by a variable distributed like the  $W_t$ 's.

Thanks to the above fact, to get an upper bound on the overall number of nodes the SIR process can infect under the hypotheses of Lemma C.1, we can analyse the Galton-Watson process specified in Definition C.3.

**Lemma C.5.** Consider the Galton-Watson process  $\{B_t\}_{t\geq 0}$  with  $W_1, W_2, \ldots$  as in Definition C.3. For any t > 0,

$$\mathbf{Pr}\left(\sum_{i=1}^{t} W_i \geqslant (1+2\delta) \frac{p(1+p)}{1-p} ct\right) \leqslant 2e^{-\frac{\delta^2 p^2 t}{9}}.$$
(18)

*Proof.* We begin by observing that, the definition of the  $W_i$ 's and Definition C.3 imply, for every  $i \ge 0$ ,

$$W_i = Y_i + \sum_{s=1}^{2Y_i} L_{i,s}$$

Here,  $Y_i$  is distributed as Bin(n, pc/n), while each  $L_{i,s}$  is an independent copy of a variable that counts the number of successes until the first failure in a sequence of independent Bernoulli trials with success probability p.<sup>13</sup> Next, if we set  $W = \sum_{i=1}^{t} W_i$ , we have

$$W = \sum_{i=1}^{t} W_i = \sum_{i=1}^{t} (Y_i + \sum_{s=1}^{2Y_i} L_{i,s}).$$
(19)

An obvious remark is that all the  $L_{i,s}$  are just independent copies of a random variable with identical distribution. As a consequence, if we set  $Y = \sum_{i=1}^{t} Y_i$ , we can rewrite (19) as

$$W = \sum_{i=1}^{t} W_i = Y + \sum_{j=1}^{2Y} L_j,$$
(20)

<sup>&</sup>lt;sup>13</sup>It can be equivalently regarded as a geometric random variable with success probability 1 - p.

where the  $L_j$ 's are independent random variables distributed like the  $L_{i,s}$ 's. Hence:

$$\mathbf{Pr}\left(\sum_{i=1}^{t} W_i \ge (1+2\delta)\frac{p(1+p)}{(1-p)}ct\right) = \mathbf{Pr}\left(Y + \sum_{j=1}^{2Y} L_j \ge (1+2\delta)\frac{p(1+p)}{(1-p)}ct\right).$$
 (21)

In order to bound the right hand side of the equation above we proceed in two steps. First, we prove a concentration result on Y. This is easy, since it is  $Y = \sum_{i=1}^{t} Y_i$ , with each  $Y_i$  being an (independent) binomial variable with distribution  $\operatorname{Bin}(n, pc/n)$ . Each  $Y_i$  is in turn the sum of n independent Bernoulli variables, each with parameter pc/n. Overall, Y is just the sum of nt independent Bernoulli variables with parameter pc/n. Hence,  $\mathbf{E}[Y] = pct$ . Moreover, a straightforward application of Chernoff bound yields, for every  $0 < \delta < 1$ ,

$$\mathbf{Pr}\left(Y \ge (1+\delta)pct\right) \le e^{-\frac{\delta^2}{3}pct}.$$
(22)

We next argue about  $\sum_{j=1}^{2Y} L_j$ . We further have, for  $0 < \delta < 1$ ,

$$\mathbf{Pr}\left(\sum_{j=1}^{2Y} L_j > (1+2\delta)\frac{2p^2}{1-p}ct \mid Y \leqslant (1+\delta)pct\right) \leqslant \mathbf{Pr}\left(\sum_{j=1}^{2(1+\delta)pct} L_j > (1+2\delta)\frac{2p^2}{1-p}ct\right), \quad (23)$$

where we dropped the conditioning on  $\{Y \leq (1+\delta)pct\}$ , since this only implies that we are summing at most  $(1+\delta)pct$  independent, geometric random variables with parameter p. We next note that

$$\mathbf{Pr}\left(\sum_{j=1}^{2(1+\delta)pct} L_j > (1+2\delta)\frac{2p^2}{1-p}ct\right) = \mathbf{Pr}\left(\sum_{i=1}^{2(1+\delta)pct+(1+2\delta)\frac{2p^2}{1-p}ct} \check{B}_i < 2(1+\delta)pct\right), \quad (24)$$

where the  $\check{B}_i$ 's are independent, Bernoulli variables with *success* probability 1 - p. The equality above is true since  $\sum_{j=1}^{2y} L_j$  follows a negative binomial distribution, whose cumulative distribution function is related to the one of the binomial [29].<sup>14</sup> The expectation of the sum of the  $\check{B}_i$ 's is

$$\mathbf{E}\left[\sum_{i=1}^{2(1+\delta)pct+(1+2\delta)\frac{2p^2}{1-p}ct}\check{B}_i\right] = 2(1+\delta)pct(1-p) + 2p^2(1+2\delta)ct = 2(1+\delta)pct\left(1+\frac{\delta p}{1+\delta}\right).$$
(25)

The above derivations imply

$$\frac{2(1+\delta)pct}{\mathbf{E}\left[\sum_{i}\check{B_{i}}\right]} \leqslant \frac{1}{1+\frac{\delta p}{1+\delta}} < 1-\frac{\delta p}{3},$$

where the last inequality follows from simple manipulations and where we eventually use  $1+\delta+\delta p < 3$ . We denote  $\mu = \mathbf{E}\left[\sum_{i} \check{B}_{t}\right]$  and from (25) we have that  $\mu \ge 2pct$ . From (23) and (24), this allows

<sup>&</sup>lt;sup>14</sup>Intuitively,  $\sum_{j=1}^{2y} L_j$  is the number of successes in a sequence of  $\sum_{j=1}^{2y} L_j + 2y$  Bernoulli trials with success probability p, before exactly 2y failures are observed. As a consequence,  $\sum_{j=1}^{2y} L_j > x$  implies that 2y + x trials were not sufficient to observe 2y failures.

us to write

$$\mathbf{Pr}\left(\sum_{j=1}^{2Y} L_j > (1+2\delta) \frac{2p^2}{1-p} ct \mid Y \leqslant (1+\delta)pct\right)$$
$$\leqslant \mathbf{Pr}\left(\sum_{i=1}^{2(1+\delta)pct+(1+2\delta)\frac{2p^2}{1-p}ct} \check{B}_i < \left(1-\frac{\delta p}{3}\right)\mu\right) \leqslant e^{-\frac{\delta^2 p^3 ct}{9}},\tag{26}$$

where the first inequality follows from the inequality relating  $\mathbf{E}\left[\sum_{i} \check{B}_{i}\right]$  to  $2(1+\delta)pct$  written above, and the last inequality is a simple Chernoff bound on the lower tail, considering that  $\mu \ge 2pct$ .

This allows us to conclude the proof. Indeed, we have that for every t > 0 and from the law of total probability

$$\begin{aligned} &\mathbf{Pr}\left(Y + \sum_{j=1}^{2Y} L_j \geqslant (1+2\delta) \frac{p(1+p)}{(1-p)} ct\right) \\ &\leqslant \mathbf{Pr}\left(\sum_{j=1}^{2Y} L_j \geqslant (1+2\delta) \frac{2p^2}{1-p} ct \mid Y \leqslant (1+\delta) pct\right) + \mathbf{Pr}\left(Y \geqslant (1+\delta) pct\right) \\ &\leqslant e^{-\frac{\delta^2 p^3 ct}{9}} + e^{-\frac{\delta^2}{3} pct} \leqslant 2e^{-\frac{\delta^2 p^3 ct}{9}}, \end{aligned}$$

where the last inequality follows from (22) and (26). The claim follows finally from (21).  $\Box$ 

Next, assume that  $p = \frac{\sqrt{c^2+6c+1}-c-1}{2c} - \varepsilon$  for constant  $\varepsilon \in (0, 1 - \frac{\sqrt{c^2+6c+1}-c-1}{2c})$ . This yields that, for some  $\varepsilon' > 0$ , we have  $pc(1+p)/(1-p) = 1 - \varepsilon'$ , so

$$(1+2\delta)\frac{pc(1+p)}{1-p} = (1+2\delta)(1-\varepsilon') \leqslant \left(1-\frac{\varepsilon'}{2}\right) \,,$$

where the last inequality holds whenever  $\delta \leq \frac{\varepsilon'}{4(1-\varepsilon')}$ . For this choice of  $\delta$ , we consider Lemma C.5 setting  $t = \beta \log n$  for a sufficiently large  $\beta$ , in order to have the RHS in (C.5) smaller than  $1/n^2$ . We notice that the choice  $\beta$  depends only on  $\varepsilon$ . With the above choices, Lemma C.5 implies

$$W_1 + \dots + W_t < \beta \log n \,, \tag{27}$$

with probability at least  $1 - 1/n^2$ .

To complete our proof, consider again the Galton-Watson Branching process  $\{B_t\}_{t\geq 0}$ . The size of the overall population up to iteration t is  $\sum_{i=1}^{t} W_i$  and we just proved that, for  $t = \beta \log n$ ,

$$\sum_{i=1}^{t} W_i < \beta \log n \,,$$

with probability at least  $1 - 1/n^2$ , which implies that, with the same probability, if  $B_t > 0$  then it would hold

$$B_t = \sum_{i=1}^t W_i - \beta \log n < 0,$$

so a contradiction. Therefore, w.h.p. there is a  $\tau < \beta \log n$ , such that  $B_{\tau} = 0$ , which in turn implies that, with probability at least  $1 - 1/n^2$ , the Galton-Watson Branching process  $\{B_t\}_{t\geq 0}$  goes extinct within  $\beta \log n$  iterations, with a population size less than  $\beta \log n$ .

We are now in a position to show that, with the same probability,  $|Q_t| = 0$  for  $t \leq \beta \log n$ , implying that Algorithm 5 completes within  $\beta \log n$  rounds and hence, it visits at most  $\beta \log n$ nodes. In fact:

$$\mathbf{Pr}\left(|cc(s)| \ge \beta \log n\right) = \mathbf{Pr}\left(|Q_{\beta \log n}| > 0\right) \le \mathbf{Pr}\left(\sum_{i=1}^{\beta \log n} W_i - \beta \log n > 0\right) \le \frac{1}{n^2}$$

where the first equality follows from the definition of  $R_{\infty}$ , the second inequality follows from Fact C.4, while the last inequality follows from Lemma C.5.

We thus proved that, for a fixed source  $s \in V$ , Algorithm 5 with input G and  $G_p$  visits at most  $\beta \log n$  nodes in the graph  $G_p$  with probability at least  $1 - 1/n^2$ . So, Lemma C.1 follows from a union bound over all possible choices of source  $s \in V$ .

## D The 3-SWG(n) Model above the Threshold

In this section we prove the first claims of Theorems 2.2 and 2.5. We show that, with probability  $\Omega(1)$ , the connected component of an initiator node in the percolation graph  $G_p$  of a 3-SWG(n) graph contains  $\Omega(n)$  nodes, as soon as  $p = 1/2 + \varepsilon$ , where  $\varepsilon > 0$  is an arbitrarily-small constant. Moreover, over the same conditions on p, we show that  $G_p$  has a giant component of  $\Omega(n)$  nodes w.h.p.

### D.1 Sequential *L*-visit (proof of Claim 1 of Theorem 2.5)

As in the proofs of Section B, we analyze the number of nodes reached by a BFS-like visit of the percolation graph  $G_p$  starting at a set of nodes  $I_0$ . We consider a slightly modified version of Algorithm 1 in which, once a bridge neighbor x of a dequeued node w is "observed", it will no longer be considered in any of the subsequent iterations of the while loop. This allows us to use the principle of deferred decisions on the randomness used to determine the bridge neighbor x of a dequeued node w and on the randomness used to determine whether a bridge edge exists in the percolation graph.

The following lemma contains the analysis of the Algorithm 6. In detail, it shows that, if we start the visit from a single source node s, after  $\Theta(\log n)$  steps of the visit we will have  $\Omega(\log n)$  nodes in the queue, with constant probability. Moreover, the lemma claims also that, if we start the visit from  $\Omega(\log n)$  nodes, the visited nodes will be  $\Omega(n)$  w.h.p.

We notice also that the first claim of Theorem 2.5 is directly implied by the following lemma.

**Lemma D.1.** Let V be a set of n nodes,  $I_0 \subseteq V$  a set of initiators and  $D_0 \subseteq V \setminus I_0$  a set of deleted nodes such that  $|D_0| \leq \log^4 n$ . For every  $\varepsilon > 0$  and for every probability p such that  $1/2 + \varepsilon \leq p \leq 1$ , there are positive parameters L, k,  $\beta$  and  $\gamma$  that depend on  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the 3-SWG(n) distribution and let  $G_p$  be the percolation graph of G with percolation probability p. Run the SEQUENTIAL L-VISIT procedure in Algorithm 6 on input  $(G, G_p, I_0, D_0)$ : if n is sufficiently large,

1. if  $|I_0| = 1$ , after  $\tau_1 = \mathcal{O}(\log n)$  iterations of the while loop we have that

 $\mathbf{Pr}\left(|Q| \ge \beta \log n \text{ or } |Q \cup R \cup D| \ge n/k\right) \ge \gamma;$ 

### Algorithm 6 SEQUENTIAL L-VISIT

**Input**: A small-world graph  $G_{SW} = (V, E_{SW})$ ; a subgraph  $H = (V, E_H)$ ; a set of initiators  $I_0 \subseteq V$  and a set of deleted nodes  $D_0 \subseteq V \setminus I_0$ .

1:  $Q = I_0$ 2:  $R = \emptyset$ 3:  $D = D_0 \cup N(D_0)$ 4: while  $Q \neq \emptyset$  do w = dequeue(Q)5:6:  $R = R \cup \{w\}$ 7: x = bridge neighbor of w in  $G_{SW}$ **case** x is free for  $(D \cup R \cup Q)$  in  $G_{SW}$  and  $\{w, x\} \in E_H$ 8:  $\triangleright$  We are using Definition 3.1  $Q = Q \cup (\mathrm{LC}^{L}(x) \setminus \{x\})$ 9:  $R = R \cup \{x\}$ 10: **case** x is free for  $(D \cup R \cup Q)$  in  $G_{SW}$  and  $\{w, x\} \notin E_H$ 11: 12: $D = D \cup \{x\}$ **case** x is not free for  $(D \cup R \cup Q)$  in  $G_{SW}$  and  $x \in Q$ 13:14: $Q = Q \setminus \{x\}$  $R = R \cup \{x\}$ 15:16:**case** x is not free for  $(D \cup R \cup Q)$  in  $G_{SW}$  and  $x \notin Q$ 17: $D = D \cup \{x\}$ 

2. if  $|I_0| \ge \beta \log n$ , after  $\tau_2 = \mathcal{O}(n)$  iterations of the while loop we have that  $|Q \cup R| \ge n/(4k)$ w.h.p.

*Proof.* We first make some observation that will be useful for the proof of both the claims of the lemma. We begin with noticing that Algorithm 6 preserves the following invariant: at the beginning of each iteration of the while loop, the bridge neighbors of all nodes in Q have not been observed so far. From the principle of deferred decisions, it thus follows that, when a node is dequeued, its bridge neighbor can be any of the nodes not in  $R \cup D$ , with uniform probability.

For t = 1, 2, ..., let  $Q_t$ ,  $R_t$ , and  $D_t$  be the sets of nodes in Q, R, and D, respectively, at the end of the *t*-th iteration of the while loop, and let  $Z_t$  be the number of nodes added to the queue Q during the *t*-th iteration. Notice that  $|Q_0| = 1$  and

$$|Q_t| = \begin{cases} 0 & \text{if } Q_{t-1} = \emptyset \\ |Q_{t-1}| + Z_t - 1 & \text{otherwise} \end{cases}$$
(28)

Observe that here  $Z_t$  is an integer-valued random variable with  $-1 \leq Z_t \leq 2L$ . As we did in the proof of Lemma 3.2 we show that, as long as the overall number of nodes in  $Q \cup R \cup D$  is below a constant fraction of n, the sequence  $\{|Q_t|\}_t$  stochastically dominates a diverging Galton-Watson branching process (Definition A.7).

Let  $k \ge 1$  be a sufficiently large constant that will be fixed later. Consider the generic *t*-th iteration of the while loop with  $Q \ne \emptyset$ , let  $|Q \cup R \cup D| \le n/k$  be the number of nodes in the queue or in the set  $R \cup D$  at the beginning of the while loop, and let A be the set of nodes at distance larger than L from any node in  $Q \cup R \cup D$  in the subgraph of  $G_{SW}$  induced by the edges of the ring, i.e.

$$A = \{ v \in V \mid d_{(V,E_1)}(Q \cup R \cup D, v) \ge L + 1 \}.$$

Observe that there are at most 2L(n/k) nodes at distance smaller than or equal to L from a node in  $Q \cup R \cup D$  in  $(V, E_1)$ , so  $|A| \ge n(1 - 2L/k)$ .

Let w be the node dequeued at the t-th iteration of the while loop and let x be its bridge neighbor. Since  $|Q \cup R \cup D| \leq n/k$ , from the principle of deferred decision it follows that x is already in the queue Q with probability at most 1/k while x is free for  $Q \cup R \cup D$  in  $G_{SW}$  with probability at least |A|/n = (1 - 2L/k) and the bridge edge  $\{w, x\}$  exists in the percolation graph with probability p. Hence, random variable  $Z_t$  in (28) takes vaues either -1, with probability at most 1/k, or the size of the local cluster centered at x excluding x itself, with probability at least p(1 - 2L/k). From (3) on the expected size of a local cluster it thus follows that the expected number of new nodes added to the queue is

$$\mathbf{E}\left[Z_t \mid Q_{t-1} \neq \emptyset, \left|Q_t \cup R_t \cup D_t\right| \leq n/k\right] \geq -\frac{1}{k} + p\left(1 - \frac{2L}{k}\right) \left(\frac{1 + p - 2p^{L+1}}{1 - p} - 1\right)$$
$$= -\frac{1}{k} + \frac{2p^2}{1 - p} \left(1 - \frac{2L}{k}\right) \left(1 - 2p^L\right)$$
$$= \frac{2p^2}{1 - p} - \mathcal{O}\left(\frac{L}{k}\right) - \mathcal{O}\left(p^L\right).$$

For every  $\varepsilon > 0$ , the above inequality allows us to fix suitable constants L, k, and  $\varepsilon' > 0$  such that, if  $p = \frac{1}{2} + \varepsilon$  then

$$\mathbf{E}\left[Z_t \mid Q_{t-1} \neq \emptyset, |Q_t \cup R_t \cup D_t| \leq n/k\right] \geq 1 + \varepsilon'.$$

As long as there are less than n/k nodes in  $(Q \cup R \cup D)$  and Q is not empty, the number of nodes in Q thus satisfies  $|Q_t| = |Q_{t-1}| - 1 + Z_t = |Q_{t-1}| - 2 + (Z_t + 1)$ , where  $Z_t + 1$  is a non-negative integer-valued random variable with expectation larger than 2. We now proceed as in the proof of Lemma 3.2, and omit some details.

We define a Galton-Watson branching process  $\{B_t\}_t$  with the aim of bounding  $Q_t$  in terms of  $B_{2t}$ . The branching process  $\{B_t\}_t$  is defined in terms of a random variable W defined to be the worst-case distribution of  $(Z_t + 1)/2$  when  $|Q_t \cup R_t \cup D_t| \leq n/k$ . The process is such that  $\mathbf{E}[W] \geq 1 + \varepsilon'$  for an absolute constant  $\varepsilon' > 1$ , and we can construct a coupling (see Definition A.12 and Lemma A.13 in the Appendix) of  $\{B_t\}_t$  with the execution of the algorithm such that, at every time step t, it holds with probability 1 that  $|Q_t \cup R_t \cup D_t| \geq n/k$  or that  $|Q_t| \geq B_{2t}$ .

Now we proceed with the proofs of the two claims of the lemma. As for the first claim, it follows from Lemma A.9. Indeed, since W is a bounded random variable (i.e.  $W \leq 2L + 1$ ), it has finite variance. Therefore, for Lemma A.9, we have that there exists positive constants  $\gamma$ ,  $\beta$  and  $\beta'$  (depending on  $\varepsilon$ ) such that, if we indicate with  $t = \beta \log n$ ,

$$\mathbf{Pr}\left(|Q_t| \ge \beta \log n \text{ or } |Q_t \cup R_t \cup D_t| \ge n/k\right) \ge \mathbf{Pr}\left(B_{2t} \ge \beta \log n\right) \ge \gamma,$$

and the first claim follows from the equation above.

As for the second claim, it follows by Lemma A.10. Indeed, the random variables W are finite, since  $W \leq 2L + 1$  and then, we have that there exists positive constants c and  $\beta$  (which depends on  $\varepsilon$ , we can take  $\beta$  as the maximum with the previous constant) such that, if we indicate with t = cn

$$\mathbf{Pr}\left(|Q_t| > 0 \text{ or } |Q_t \cup R_t \cup D_t| \ge n/k \mid |Q_1| \ge \beta \log n\right) \ge \mathbf{Pr}\left(B_{2t} > 0 \mid B_1 \ge \beta \log n\right) \ge 1 - \frac{1}{n}.$$

The second claim follows from the fact that, if we are in the case in which  $Q_t > 0$ , we obviously have that  $|R_t| \ge t$ , since in each iteration of the while loop in the algorithm at least one node is added to  $R_t$ . Instead, in the case in which  $|Q_t \cup R_t \cup D_t| \ge n/k$ , we can claim that  $|Q_t \cup R_t| \ge n/(4k)$ . Indeed, while the visit is running, at least one node is added to  $R_t$  at each step and at most one node is added to  $D_t$ , so  $|R_t| \ge |D_t| - |D_0|$ . So, since  $|D_0| \le 3 \log^4 n$ , for a sufficiently large n

$$|Q_t \cup R_t \cup (D_t \setminus D_0)| \ge \frac{n}{2k}$$

and this implies that

$$|Q_t \cup R_t| \ge \frac{n}{4k}.$$

### D.2 Wrapping up: proof of Claim 1 of Theorem 2.2

The proof proceeds on the same lines as the proof in Subsection B.4. Indeed, we want to prove that w.h.p. in  $G_p$  there exists a giant component with  $\Omega(n)$  nodes. In order to do so, we introduce the following algorithm, which is divided into two phases.

Algorithm 7 Search of the giant component				
<b>Input</b> : A small-world graph $G_{SW} = (V, E_{SW})$ ; a subgraph H of $G_{SW}$ ; two integers $\beta$ , $\beta'$ .				
1: $Q = \emptyset$				
2: $D = \emptyset$				
3: $R = \emptyset$				
4: while $ Q  \leq \beta \log n$ or $ Q \cup R \cup D  \leq n/k$ do	$\triangleright$ First phase			
5: Let $s \in V \setminus D$				
$6: \qquad Q = \{s\}$				
7: $R = \emptyset$				
8: <b>for</b> $i = 1, \dots, \beta' \log n$ <b>do</b>				
9: Perform lines 4-17 of Algorithm 6	$\triangleright$ Sequential <i>L</i> -visit			
10: $D = D \cup R$				
11: if $ Q \cup R \cup D  \leq n/k$ then	$\triangleright$ Second phase			
12: Perform Algorithm 6 with input $G_{SW}$ , $H$ , $I_0 = Q$ , $D_0 = R \cup D$	$\triangleright$ Sequential <i>L</i> -visit			

In the first phase is a "bootstrap" where we search for a node in the giant component: we look for a source node s such that, after  $\Theta(\log n)$  steps of the sequential L-visit, the queue Q has  $\Omega(\log n)$ nodes. The second phase consists of the sequential L-visit starting from the queue Q with  $\Omega(\log n)$ nodes. We note that in this case, we have not performed the analysis via the parallel visit: this is because the random variables describing the process, in this case, assume dependencies that are difficult to handle in the parallel case.

The following lemma contains the analysis of Algorithm 7 with in input  $(G, G_p, \beta, \beta')$ , where  $\beta$ and  $\beta'$  are two positive constants. It claims that the first phase of the algorithm, that begins in the while loop in line 4, ends after  $\tau_1 = \mathcal{O}(\log n)$  iterations of the while loop w.h.p. Moreover, the lemma claims that the in second phase of the algorithm (starting in line 11) the visit reach  $\Omega(n)$ nodes.

**Lemma D.2.** Let V be a set of n nodes. For every  $\varepsilon > 0$  and  $\beta > 0$ , and for every probability p such that  $1/2 + \varepsilon \leq p \leq 1$ , there are positive parameters L, k (that depends only on  $\varepsilon$ ) and a constant  $\beta'$  (that depends on  $\varepsilon$  and  $\beta$ ) such that the following holds. Sample a graph G = (V, E) according to the 3-SWG(n) distribution and let  $G_p$  be the percolation graph of G with percolation probability p. Run the SEARCH OF THE GIANT COMPONENT in Algorithm 7 on input  $(G, G_p, \beta, \beta')$ : if n is sufficiently large,

- 1. the first while loop in line 4 terminates at some round  $\tau_1 = \mathcal{O}(\log n)$  w.h.p.;
- 2. conditioning on the above event, the second phase of the algorithm starting in line 11 terminates at some round  $\tau_2 = \mathcal{O}(n)$  in which, w.h.p.  $|Q \cup R| \ge n/(4k)$ .

*Proof.* The proof proceeds similarly to the proof of Lemma B.6 in Section B. In particular, it follows from Lemma D.1.  $\Box$ 

We notice that Claim 1 of Theorem 2.2 follows from the lemma above.

## E Regular Graphs Below the Threshold

In this section, we analyze the percolation process in regular graphs and prove Theorem 2.3. As for the 3-regular graphs generated by the 3-SWG(n) model, we observe that Claim 2 of Theorem 2.2 is a direct consequence of the general result proved in this section.

**Theorem E.1.** Let G = (V, E) be a graph of maximum degree d and let s be a vertex in V. If  $p = (1-\varepsilon)/(d-1)$  for some  $\varepsilon$  such that  $1 > \varepsilon > 0$ , then the probability that the connected component of s in the percolation graph  $G_p$  of G has size > t is at most  $\exp(-\Omega(\varepsilon^2 t))$ . Furthermore, w.h.p., all connected components of  $G_p$  have size  $\mathcal{O}(\varepsilon^{-2} \log n)$ .

*Proof.* We consider an execution of the BFS algorithm below with the percolation graph  $G_p = (V, E_p)$  of G = (V, E) as input H and any fixed source  $s \in V^{15}$ .

### Algorithm 8 BFS VISIT

**Input**: a graph  $H = (V, E_H)$  and a source  $s \in V$ .

1:  $Q = \{s\}$ 2: while  $Q \neq \emptyset$  do 3: w = dequeue(Q)4: visited(w) = True5: for each neighbor x of w in H such that visited(x) = False do6: enqueue(y, Q)

We first notice that if the above algorithm visits more than t vertices, then it executes the while loop more than t times. Consider what has happened after the t-th iteration of the while loop. Each iteration removes one node from the queue, the queue is not empty, and initially the queue held one node, so we have to conclude that we added at least t nodes to the queue in the first t iterations of the while loop. Consider how many times we run the for cycle in lines 5-6 in each while-loop iteration and assume by deferred decision that we make the choice about the edge  $(w, x) \in E_p$  only when line 5 is executed. That cycle is executed at most d times at the first iteration, and at most d-1 times subsequently (because every vertex in the queue has at most d-1 non-visited neighbors in  $G_p$ ) and so it is executed at most  $t \cdot (d-1) + 1$  times. Each time it is executed implies that the event  $(w, x) \in E_p$  holds and it has probability p, independent of everything else.

From the above argument, it follows that we have observed at most  $t \cdot (d-1) + 1$  Bernoulli random variables with parameter  $p = (1 - \varepsilon)/(d-1)$  and we found that at least t of them were 1. By Chernoff bounds this happens with probability  $\exp(-\varepsilon^2 t/3)$ .

As for the "Furthermore" part, it suffices to choose a real b large enough so that the probability that the connected component of s has size more than b is at most  $1 - 1/n^2$ , then take a union bound over all source s.

## F Generalizations and Outlook

As discussed in the introduction, our goal was to investigate the simplest models that can at least qualitatively capture essential aspects of epidemic processes observed in realistic scenarios. On the

<sup>&</sup>lt;sup>15</sup>We notice that, unlike the other visiting procedures we used in the previous sections, this algorithm does not require to have the graph G as input, only its percolation.

other hand, we believe some variants and generalizations of the models we considered in this paper deserve a rigorous study. Two natural directions concern extensions to the IC protocol we considered and more general models of the underlying network topology.

### F.1 Non-homogenous bond percolation probabilities

A possible extension of the considered small-world models is to introduce two different bond percolation (i.e., transmission) probabilities, each one assigned to each type of connection. Formally, given a small-world graph  $G = (V, E_1 \cup E_2)$ , the percolation graph  $G_{p_1,p_2}$  is the result of the following process: a bond percolation with probability  $p_1$  is applied on  $G_1 = (V, E_1)$ ; and a bond percolation with probability  $p_2$  is applied to  $G_2 = (V, E_2)$ ; finally, we get the union of the two resulting random subgraphs, denoted as  $G_{p_1,p_2}$ .

With  $RF(p_1, p_2)$ , we refer to the corresponding generalization of the RF protocol considered in this paper.

Since  $p_1$  is the percolation probability of the local edges, it is immediate the following result.

**Fact F.1.** Let G = (V, E) be a one-dimensional small-world graph and  $p_1, p_2$  be, respectively, the percolation probabilities on the local and bridge edges. Then, for each node  $v \in V$ , the size  $LC^L(v)$  of its L-truncated local cluster  $LC^L(v)$  satisfies the following

$$\mathbf{E}\left[|\mathbf{L}\mathbf{C}^{L}(v)|\right] = \frac{1+p_{1}}{1-p_{1}} - \frac{2p_{1}^{L+1}}{1-p_{1}}.$$
(29)

Our analysis for the homogenous case easily extends to the above non-homogenous setting: the next theorem formalizes the main result in terms of epidemic protocols.

**Theorem F.2** (The  $RF(p_1, p_2)$  protocol on the SWG(n, q) model). Let V be a set of n vertices,  $I_0 \subseteq V$  be a set of source nodes, and  $p_1, p_2 \ge 0$  two constant probabilities. For any constant c > 0, sample a graph  $G = (V, E_1 \cup E_2)$  from the SWG(n, c/n) distribution, and run the  $RF(p_1, p_2)$  protocol with transmission probabilities  $p_1$  over  $G_1 = (V, E_1)$  and  $p_2$  over  $G_2 = (V, E_2)$  from  $I_0$ . For every  $\varepsilon > 0$ , we have the following:

- 1. If  $p_1 + c \cdot p_1 p_2 + c \cdot p_2 \ge 1 + \varepsilon$ , then, with probability  $\Omega_{\varepsilon}(1)$  a subset of  $\Omega_{\varepsilon}(n)$  nodes will be informed within time  $\mathcal{O}_{\varepsilon}(\log n)$ , even if  $|I_0| = 1$ . Moreover, if  $|I_0| \ge \beta_{\varepsilon} \log n$  for a sufficiently large constant  $\beta_{\varepsilon}$  (that depends only on  $\varepsilon$ ), then the above event occurs w.h.p.;
- 2. If  $p_1 + c \cdot p_1 p_2 + c \cdot p_2 \leq 1 \varepsilon$ , then w.h.p. the total number of informed nodes will be  $\mathcal{O}_{\varepsilon}(|I_0| \log n)$ , and the protocol will stop within  $\mathcal{O}_{\varepsilon}(\log n)$  time.

As observed above, it is possible to easily recover the proof of the above theorem from the analysis of the homogeneous case we described in the previous sections. In the following two subsections, we thus only describe how the main technical statements changes in this non-homogeneous case.

**Proof of Claim I of Theorem F.2** We first consider Algorithm 1, recalling the notion of *free* node in Definition 3.1, and generalize Lemma 3.2.

**Lemma F.3.** Let V be a set of n nodes,  $s \in V$  an initiator node and  $D_0 \subseteq V \setminus \{s\}$  a set of deleted nodes such that  $|D_0| \leq \log^4 n$ . For every  $\varepsilon > 0$  and c > 0, and for every probabilities  $p_1, p_2$  such that

$$p_1 + c \cdot p_1 p_2 + c \cdot p_2 \ge 1 + \varepsilon,$$

there are positive parameters  $L, k, t_0, \varepsilon'$ , and  $\gamma$ , that depend only on c and  $\varepsilon$ , such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution and let  $G_{p_1,p_2}$  be the percolation graph of G with percolation probability  $p_1, p_2$ . Run Algorithm 1 on input  $(G, G_{p_1,p_2}, s, D_0)$ : if n is sufficiently large, for every t larger than  $t_0$ , at the end of the t-th iteration of the while loop it holds that

$$\mathbf{Pr}\left(|R \cup Q| \ge n/k \text{ OR } |Q| \ge \varepsilon' t\right) \ge \gamma.$$

Lemma F.3 implies that the nodes visited by the end of Algorithm 1 reach a size at least n/k, with a probability of at least  $\gamma$ . The consequence is a linear lower bound on the size of the connected component of the source s in  $G_p$ .

As we made for the homogenous case, the next goal is to show that if we explore the connected components of  $\log n$  nodes taken arbitrarily in the graph, then w.h.p., we visit a linear fraction of the nodes in the percolated graph, within  $\Theta(\log n)$  number of hops. To do this, we analyze the execution of Algorithm 2 on input  $(G, G_{p_1,p_2}, I_0, D_0)$ , where  $I_0$  is an arbitrary subset of initiators and  $D_0 \subseteq V \setminus I_0$  is a set of deleted nodes. Recall that  $S_t = V \setminus (R_t \cup Q_t)$ , where  $Q_t$  and  $R_t$ respectively are the subsets Q and R at the end of the t-iteration of the while loop in line 10. We can thus state the new version Lemma B.1.

**Lemma F.4.** Let V be a set of n nodes,  $I_0 \subseteq V$  a set of initiators and  $D_0 \subseteq V \setminus I_0$  a set of deleted nodes such that  $|D_0| \leq \log^4 n$ . For every  $\varepsilon > 0$ , c > 0 and for every contagion probabilities  $p_1, p_2$ such that

$$p_1 + c \cdot p_1 p_2 + c \cdot p_2 \ge 1 + \varepsilon$$

there are positive parameters  $L, k, \beta, \delta$  that depend only on c and  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the SWG(n, q) distribution, and let  $G_{p_1, p_2}$  be the percolation graph of G with parameters  $p_1, p_2$ . Run Algorithm 2 on input  $(G, G_{p_1, p_2}, I_0, D_0)$ : in every iteration  $t \ge 1$  of the while loop at line 4 in Algorithm 2, for every integer  $i \ge \beta \log n$  and  $r \ge 0$  such that  $i + r \le n/k$ :

$$\mathbf{Pr}\left(|Q_t| \ge (1+\delta)i \mid |Q_{t-1}| = i, |R_{t-1}| = r\right) \ge 1 - \frac{1}{n^2}.$$
(30)

At this point, we run Algorithm 3 in the non-homogeneous framework and get the new version of B.5.

**Lemma F.5.** Let V be a set of n nodes and  $I_0 \in V$  a set of initiators. For every  $\varepsilon > 0$ , c > 0 and for every contagion probabilities  $p_1, p_2$  such that

$$p_1 + c \cdot p_1 p_2 + c \cdot p_2 \ge 1 + \varepsilon$$

there are positive parameters  $L, k, \gamma, \beta$  that depend only on c and  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the SWG(n, c/n) distribution, and let  $G_{p_1, p_2}$  be the percolation graph of G with parameters  $p_1, p_2$ . Run Algorithm 3 on input  $(G, G_{p_1, p_2}, I_0)$  and, if n is sufficiently large:

1. The first while loop in line 4 terminates at some round  $\tau_1 = \Theta(\log n)$  in which

$$\mathbf{Pr}\left(|R \cup Q| \ge n/k \text{ OR } |Q| \ge \beta \log n\right) \ge \gamma;$$

2. Conditioning at the above event, the second while loop in line 6 terminates at some round  $\tau_2 = \Theta(\log n)$  in which, w.h.p.  $|Q \cup R| \ge n/k$ .

As in the homogeneous case, this result implies that, starting from a single source  $s \in V$ , the algorithm will visit  $\Omega(n)$  nodes with constant probability. On the other hand, starting from a set of sources  $I_0$  such that  $|I_0| = \Omega(\log n)$ , the algorithm will reach  $\Omega(n)$  nodes, w.h.p. This concludes the proof of Claim 1 of Theorem F.2.

**Proof of Claim II of Theorem F.2** To prove Claim 2 of Theorem F.2, we state Lemma C.1 to the two-probabilities case.

**Lemma F.6.** Let V be a set of n nodes. For every  $\varepsilon > 0$ , c > 0 and for every transmission probabilities  $p_1, p_2 > 0$  such that

$$p_1 + c \cdot p_1 p_2 + c \cdot p_2 \leqslant 1 - \varepsilon$$

there is a positive constant  $\beta$  that depends only on c and  $\varepsilon$  such that the following holds. Sample a graph G = (V, E) according to the SWG(n, q) distribution, and let  $G_{p_1, p_2}$  be the percolation graph of G with parameters  $p_1, p_2$ . If n is sufficiently large, with probability at least 1 - 1/n contains no connected component of size exceeding  $\beta \log n$ .

The proof is a simple generalization of the proof of Lemma C.1. In particular, we need the following version of Lemma C.5 that considers a Galton-Watson process  $\{B_t\}_{t\geq 0}$  with  $W_1, W_2, \ldots$ , defined by extending Definition C.3 to the two-probabilities case.

**Lemma F.7.** Let  $\{B_t\}_{t\geq 0}$  be the Galton-Watson process described above. For any t>0,

$$\mathbf{Pr}\left(\sum_{i=1}^{t} W_i \ge (1+2\delta) \frac{p_2(1+p_1)}{1-p_1} ct\right) \le 2e^{-\frac{\delta^2 \min\{p_1, p_2\}^3 ct}{9}}$$
(31)

The above bound is obtained as follows. We recall that:  $Y = \sum_{i=1}^{t} Y_i$ , with each  $Y_i$  being an (independent) Binomial variable with distribution  $Bin(n, p_2c/n)$ ; each  $L_j$  is an (independent) variable that counts the number of successes until the first failure with success probability  $p_1$ ; and each  $\check{B}_i$  is an (independent) Bernoulli random variable with success probability  $1 - p_1$ . Proceeding as in the homogeneous case, we get

$$\mathbf{Pr}\left(Y \geqslant (1+\delta)pct\right) \leqslant e^{-\frac{\delta^2}{3}p_2ct}$$

and

$$\mathbf{Pr}\left(\sum_{j=1}^{2(1+\delta)p_{2}ct} L_{j} > (1+2\delta)\frac{2p_{1}p_{2}}{1-p_{1}}ct\right) = \\ = \mathbf{Pr}\left(\sum_{i=1}^{2(1+\delta)p_{2}ct+(1+2\delta)\frac{2p_{1}p_{2}}{1-p_{1}}ct} \check{B}_{i} < 2(1+\delta)p_{2}ct\right) \leqslant e^{-\frac{\delta^{2}p_{1}^{2}ct}{9}}$$

At this point, generalization follows easily.

As in the homogeneous case, we exploit the full equivalence between the bond percolation process and the IC-process: so, Lemma F.6 also implies Claim 2 of Theorem 2.4. In fact, since the IC process infects at least one new node in each round unless it has died out, Lemma F.6 also implies that, w.h.p., the IC process dies out within  $\beta \log n$  rounds, infecting at most  $|I_0| \cdot \beta \log n$  new nodes.

### F.2 Non-unit activity periods.

In the previous sections, we assumed that each infectious node has one single chance to infect its neighborhood in the step immediately following the one in which it became infected. Natural generalizations include models where the interval of time during which a node is infectious follows some distribution. While this can considerably complicate the analysis, our approach straightforwardly extends to a simple generalization, in which the activity period of a node consists of k consecutive units of time, where k is a fixed constant. In this case, the corresponding versions of the epidemic models we considered in this paper can be easily formalized as follows.

**Definition F.8** (IC and SIR models with k attempts). Given a graph G = (V, E), an assignment of contagion probabilities  $\{p(e)\}_{e \in E}$  to the edges of G, and a non-empty set  $I_0 \subseteq V$  of initially infectious vertices (that will also be called initiators or sources), the Independent Cascade (for short, IC) protocol with k attempts is the stochastic process  $\{S_t, I_t, R_t\}_{t \ge 0}$ , where  $S_t, I_t, R_t$  are three sets of vertices, respectively called susceptible, infectious, and recovered, which form a partition of V and that are defined as follows. Let  $\hat{I}_t \subseteq I_t$  be the subset of those nodes which receive the infection for the first time at step t.

- At time t = 0 we have  $R_0 = \emptyset$  and  $S_0 = V I_0$ . We set  $\hat{I}_{-k} = \cdots = \hat{I}_0 = \emptyset$ .
- At time  $t \ge 1$ :
  - $-R_t = R_{t-1} \cup \hat{I}_{t-k}$ , that is, the nodes that got infected k steps before become recovered.
  - Independently from the previous steps, for each edge  $e = \{u, v\}$  such that  $u \in I_{t-1}$  and  $v \in S_{t-1}$ , with probability p(e) the event that "u transmits the infection to v at time t" takes place. The set  $\hat{I}_t$  is the set of all vertices  $v \in S_{t-1}$  such that, for at least one neighbor  $u \in I_{t-1}$ , the event "u transmits the infection to v" takes place. We set  $I_t = (I_{t-1} \cup \hat{I}_t) \setminus \hat{I}_{t-k}$ .

 $-S_t = S_{t-1} - \hat{I}_t$ 

The process stabilizes when  $I_t = \emptyset$ .

We recall that the RF (SIR) protocol is the special case of the IC protocol in which all probabilities are the same. To analyze the process described above, we use the following result, which is a direct consequence of Theorem A.3 that states the equivalence between the Independent Cascade process and the percolation process.

**Corollary F.9** ([19]). Let  $R_{\infty}$  be the final set of nodes reached by the IC process with k attempts, according to above definition, on the graph G = (V, E) and contagion probabilities  $\{p(e)\}_{e \in E}$ . Let  $\hat{R}_{\infty}$  be the final set of nodes reached by the IC process and on the same graph G, with only one activation and with contagion probabilities  $\{\hat{p}(e)\}_{e \in E}$ , where  $\hat{p}(e) = 1 - (1 - p(e))^k$ . Then,  $R_{\infty}$  and  $\hat{R}_{\infty}$  have the same distribution.

Thanks to the above equivalence result, our results stated in Theorems 2.4 and 2.2 (and the general result in Theorem 2.3) can be easily generalized to the SIR model with k activations by setting the contagion probability to the value  $\hat{p} = 1 - (1 - p)^k$ . As for the convergence time of the SIR process, we observe that the k consecutive attempts of every infectious node clearly result in a slow-down of (at most) an extra multiplicative factor k with respect to the obtained bounds.

**Random incubation periods.** Our results easily extend to a discrete, SEIR generalization of the epidemic model studied in this paper in which every node has an associated, random *incubation period.* In more detail, in our discrete-time setting, each node v has an associated random variable h(v), which gives the number of incubation steps after which, once infected, node v becomes infectious itself. This model can be reduced to a percolation problem in which the activation of edges is as before, each node v is labeled by h(v), the set of nodes reached by the infection is the set of nodes reachable from  $I_0$  in the percolation graph. In this case, the time of contagion of a node v is the length of the shortest path from v to  $I_0$  in the percolation graph, where the "length" of a path P is the number of edges plus the sum of the incubation times of the vertices along the path.

If the incubation times h(v) are independent of the randomness of the activation of edges, then incubation does not affect the number of nodes eventually reached by the infection, it only affects the time of spreading.

Moreover, if the incubation times are also mutually independent random variables with a nice (for example, subgaussian) tail, then it is also possible to get bounds in probability for the infection spreading time.

**Other topologies.** A second natural direction is investigating more general topologies than those considered in this paper. In this respect, natural generalizations include families of graphs used to model short connections and the random networks used to model long-range ones. As for the former, a natural extension would be considering 2-dimensional grids. Already moving to this setting poses non-trivial challenges. For example, in this case, characterizing the spread over local clusters seems considerably harder, whereas this can be done exactly in rings. As for long-range connections, it would be interesting to investigate distributions in which the existence of an edge depends on the distance between the end-points in the underlying graph of local connections. While this is a natural generalization of the setting addressed in this paper, it might prove considerably more challenging.