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Bootstrap Percolation on Regular Trees and Hyperbolic Lattices

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Abstract

In this thesis we study bootstrap percolation on regular trees and on hyperbolic lattices, both of which belong to the category of nonamenable graphs. This is different from what is usually done, since most of the existing work and literature on bootstrap percolation considers the process on Euclidean lattices. First, we take care to precisely define the process in a way general enough to include both the case of nonamenable graphs and the Euclidean case. We then proceed to prove that, on regular trees, the critical probability for full infection and the one for percolation are both nontrivial. Branching processes are the most importat tool that we use in this part. Finally, we show that the same holds true also on hyperbolic lattices. This is done with two different approaches: once using general results available for all nonamenable graphs, and another time using what previously obtained for regular trees. Crucial in this last step is a procedure by which certain regular trees can be embedded into hyperbolic lattices.

Contents

Introduction

Bootstrap percolation is a probabilistic model, defined on a (infinite) graph, which describes the evolution of a random initial configuration of infected vertices according to a deterministic dynamics: infected vertices remain infected forever and healthy vertices become infected if and only if they have at least a certain number r (which we call facilitating parameter of the model) of infected neighbours. By random initial configuration we mean that at time 0 each vertex of the graph is infected with probability $0 \leq p \leq 1$, indipendently of all other vertices.

This process has already received a lot of attention on the Euclidean lattice $\mathbb{Z}^d$, a setting in which many techniques have already been developed and many problems have been solved. The aim of this thesis is to study what happens in a more unusual setting, the one of nonamenable graphs. In particular, we focus on regular trees and hyperbolic lattices. Moreover, we will only concern ourselves with qualitative (topological, one might say) questions regarding the final configuration, i.e. the configuration from which the process no longer evolves. Intuitively, one can already see that both a smaller r (corresponding to an easier spread of the disease) and a bigger p (corresponding to more initial infected vertices) lead to more infected vertices in the final configuration. So one could ask, for example: given a fixed r, is there a "nontrivial critical value" $0 < p_f < 1$ of the parameter p such that the graph is completely infected only if $p > p_f$? Is there an analogous critical probability p_c for the event of having an infinite cluster of infected vertices in the final configuration? In this second case, is the infinite cluster unique or are there infinitely many of them?

We devote the beginning of the first chapter to a rigorous definition of the model in this more general setting. Most of it is simply a direct transposition of the usual definitions given for Euclidean lattices (and one could say that it has been included just for the sake of completeness). A bit extra care, however, is required in showing the well-posedness of the questions mentioned above: ergodicity has to be formulated in terms of group actions and we provide some fairly general sufficient conditions on the graph that ensure that everything works as expected. We then proceed to define a very similar model, which we call bootstrap percolation with blocking parameter, and we show its relation to the model with facilitating parameter. Even if conceptually there is no difference between the two models, it will be useful to be able to think with both of them. The most interesting part of the first chapter is perhaps the one in which we provide the proof of some very general inequalities on the critical value p_f. They do not require any additional assumptions on the graph, but will nevertheless be crucial in obtaining the results

on hyperbolic lattices. Finally, we conclude the first chapter with some very quick reminders on branching processes.

In the second chapter we restrict our attention to $(d + 1)$-regular trees. In the first part we give a complete proof of the nontriviality of p_f for all reasonable values of r. Here the main idea is that of studying $(r-1)$-forts: inuitively, these are regions of the graph which, if initially healthy, never become infected, no matter what happens in the rest of the graph. Branching processes are the main tool we use to this purpose. Harris inequality is also needed. In the second part, instead, we focus on p_c, which is also nontrivial on regular trees. This time the strategy is to orient the tree and study oriented bootstrap percolation. We describe the main idea of this procedure and we state the precise result, but without providing a proof, for which we refer to the literature.

Finally, in the third chapter we focus on hyperbolic lattices. We start with some quick reminders on the hyperbolic plane. We then describe how to construct hyperbolic lattices. These are graphs obtained by regular tilings of the hyperbolic plane, i.e. tilings of the hyperbolic plane generated by a regular polygon. The most evident differences from their Euclidean counterparts (for which there are only three possibilities, the triangular, the square and the hexagonal lattice) are that we have infinitely many of them and that they are nonamenable. In particular, they possess the following feature, which will be crucial for us: except for a few special cases, a v-regular hyperbolic lattice contains, as subgraphs, regular trees of degree $(v - 1)$. We provide a precise statement on this and describe how to prove it in a particular case. We continue by studying the critical probability p_f following two different approaches. In the first one, we use a mix of results. Some of them also hold in a setting more general than the one of hyperbolic lattices, as for example the use of the Cheeger constant or the comparison with Bernoulli site percolation. Others are more specific, as the study of finite forts by means of horodisks and hyperbolic trigonometry. Together, they provide a proof of the nontriviality of p_f for a considerably large class of hyperbolic graphs. In the second approach, instead, we exploit the general inequalities presented in chapter one and the aforementioned result on the embedding of trees in hyperbolic lattices. This leads both to a cleaner proof and to an extension of the results obtained with the first approach. Finally, we spend some words on the critical probability for percolation and we state the nontriviality of the critical probability for uniqueness as an open question.

Chapter 1

Description of the model and fundamental tools

In this chapter we describe in detail the model of bootstrap percolation on a general graph G. General means that we have tried to make as few hypotheses on G as we found possible. We also describe an analogous (and for the context of this thesis in fact equivalent) version of the model, which nontheless proves to be useful in some proofs and is present in part of the literature. We then describe the questions that we aim to study in the rest of the thesis and we explain in detail the subtleties implied in the definitions of the critical values of the initial density parameter. These are often omitted when speaking about $G = \mathbb{Z}^d$ (the most studied case), as their explanation is usually well known and only requires basic classical tools anyway. However, we felt that in our more general context some extra care was needed.

Finally, we have dedicated the last section to a brief review of branching processes, which constitute the main probabilistic tool used in the second chapter.

1.1   Bootstrap Percolation

Throuhout this section we denote by G a simple, connected, undirected, locally finite, planar graph. We denote by V and E its vertex set and its edge set respectively and we reserve the variables x, y, etc... for the elements of V. We also assume that V is a countably infinite set. We write $x \sim y$ if $(x, y) \in E$, and we say that the vertices x and y are *neighbours* or, equivalently, that the edge (x, y) is *incident* to x and to y. Moreover, we denote by $\mathcal{N}_x := \{y \in V : (x, y) \in E\}$ the set of neighbours of x in G. The *degree* of a vertex $x \in V$ is $\deg(x) := |\mathcal{N}_x|$. A (general) graph is said to be *d-regular* if every vertex has degree equal to d. We also recall the definition of *path*, which is an ordered (finite or infinite) collection of distinct vertices $(y_1, y_2, \dots)$ such that $y_{n+1} \in \mathcal{N}_{y_n}$ for every $n \geq 1$. Finally, given a vertex $x \in V$, the *connected component* of x is the subset of V containing x and all vertices that can be reached from x via a finite path.

In this thesis we study a particular probabilistic model defined on G. This means that we consider the vertices of G as *sites*, each of which can be in a certain

state. Moreover, the choice of which state is assumed by each vertex is influenced in some way by the graph structure (i.e. by how edges connect different vertices). Now let us give a precise meaning to these words.

1.1.1   What is bootstrap percolation?

Consider the set $\Omega := \{0,1\}^V$ and denote by $\eta = \big(\eta(x) : x \in V\big)$ a generic element of Ω. We say that η is a *configuration* of the model and that Ω is the *configuration space.*

Definition 1.1. *Bootstrap percolation with facilitating parameter r and with initial configuration $\eta_0 \in \Omega$ is the (deterministic) process $(\eta_n)_{n \geq 0}$, indexed by (discrete) time and with dynamics defined by the following recurrence relation:*

$$\forall n = 1, 2, \dots \quad \eta_{n+1}(x) = \begin{cases} 1, & \text{if } \eta_n(x) = 1 \\ 1, & \text{if } \eta_n(x) = 0 \text{ and } \sum_{y \in \mathcal{N}_x} \eta_n(x) \geq r \\ 0, & \text{if } \eta_n(x) = 0 \text{ and } \sum_{y \in \mathcal{N}_x} \eta_n(x) < r \end{cases} \qquad (1.1)$$

We also define the *final (bootstrapped) configuration* as the pointwise limit

$$\eta_\infty := \lim_{n \to \infty} \eta_n \qquad (1.2)$$

Remark 1.1. Observe that the limit in 1.2 is well defined (and belongs to Ω). Indeed, for every fixed $x \in V$, the function $\eta_\#(x) \colon \mathbb{N} \to \{0,1\}$ is increasing.

Equivalently, this process can also be defined by focusing exclusively on the evolution of sites which are in state 1. Initially, they are $A_0 := \{x \in V : \eta_0(x) = 1\}$ and at each step their evolution is given by

$$\forall n = 1, 2, \dots \qquad A_{n+1} = A_n \cup \big\{ x \in V : |\{y \in V : y \sim x\} \cap A_n| \geq r \big\}$$

When the process no longer evolves, the set of all vertices which are in state 1 is given by $A_\infty := \bigcup_{n \geq 0} A_n$, so that the final configuration is $\eta_\infty = \mathbb{1}_{A_\infty}$. While the former definition will prove to be a better notation later on, the second one allows for more vivid interpretations of the process (of which there are many in the literature), based on the fact that at any given time n each vertex x of G is in one and only one of two different states, depending on whether $x \in A_n$ or $x \notin A_n$. We will settle for the interpretation in which being in state 0 means being "healthy", whereas being in state 1 means being "infected". In this way, A_n is thought of as the set of infected vertices at time n. With this choice, we can informally rewrite the dynamics of the process in the following way:

- at each time step an healthy vertex becomes infected if and only if it has at least r infected neighbours;
- infected vertices never heal, i.e. remain infected forever.

Remark 1.2. Since the dynamics of bootstrap percolation with facilitating parameter r is deterministic, the initial configuration η_0 completely determines the final one!

In this thesis we are interested in studying properties of the (sub)set of vertices A_∞. Thus, even if in definition 1.1 on the preceding page the initial configuration is given arbitrarily, remark 1.2 tells us that the question of how to choose η_0 is of fundamental importance for the study of the final bootstrapped configuration. We postpone the discussion on the choice of the initial configuration to the next subsection.

Let us now introduce the terms with which we are going to talk about the properties of A_∞.

Definition 1.2. Fix a value for the parameter r and an initial configuration η_0. We say that

- η_0 (or A_0) achieves *full infection* of *complete infection* if $\eta_\infty \equiv 1$, i.e $A_\infty = V$;
- given $x \in V$, the *infected cluster* in the final configuration containing x is the set of all $y \in A_\infty$ such that there exist a finite path from x to y made of all infected vertices and is denoted by $\mathcal{C}_x$;
- η_0 *percolates* if there exist $x \in V$ such that $|\mathcal{C}_x| = \infty$.

A priori it is not clear whether the above definitions describe different situations. In fact, the first question to ask is whether they can happen at all! Subsequently, many other questions could also arise. Is it possible to have connected components of finite size in $A_\infty{}^c$? If η_0 percolates, is $\mathcal{C}_x$ the unique cluster of infected vertices in the final configuration of could there be many of them? In this thesis, we consider precisely these kind of questions (from a probabilistic point of view, more on that in the next subsection) restricting our study to particular classes of graphs.

Before moving on, let us set $G = \mathbb{Z}^2$ (the "easiest" case) and take a look at an example, simply to get an idea of what we are talking about.
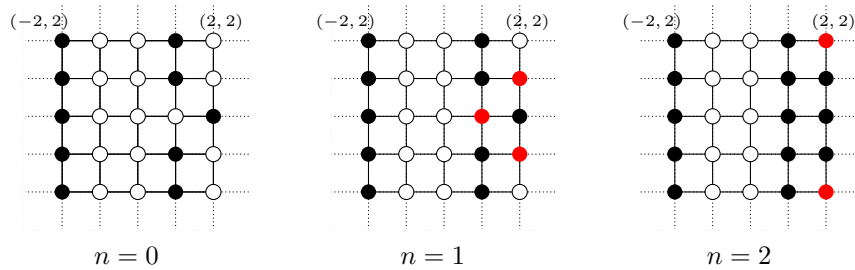
Figure 1.1: Bootstrap percolation on $\mathbb{Z}^2$ with facilitating parameter $r = 2$: evolution of the initial configuration $\eta_0(x) = \mathbb{1}_{A_0}$, where $A_0 = \{(-2,-2), (-2,-1), (-2,0), (-2,1), (-2,2), (1,-2), (1,-1), (1,1), (1,2), (2,0)\}$. Healthy sites are represented by white dots. Infected sites are represented by filled dots of color black or red. The ones in red are the ones added at the n-th step of the dynamics, which for the purpose of this picture is supposed not to depend on sites which are not drawn (i.e. we are supposing that all of the vertices which are not shown are healthy).

Looking at the process depicted in figure 1.1, it is clear that it ceases to evolve as early as $n = 2$, i.e. $\eta_2 = \eta_\infty$. Of course, this is due to the fact that we have

chosen a rather boring initial configuration. However, imagine that A_0 contains the whole subset $\big\{(-2, i), (1, i) : i \in \{\ldots, -1, 0, 1, \ldots\}\big\}$ and consider the "strip" $S := \big\{(-1, j), (0, j) : j \in \{\ldots, -1, 0, 1, \ldots\}\big\}$. As long as A_0 does not contain any vertex of S, the vertices of S will never be infected, i.e. the final configuration will be such that $\eta_\infty(x) = 0$ for every $x \in S$. The set S is an example of the following definition.

Definition 1.3. A finite or infinite connected subset $\widetilde{V} \subseteq V$ of vertices is called a *k-fort* if each $x \in \widetilde{V}$ has *outdegree* smaller than of equal to k, i.e. if

$$\forall\, x \in \widetilde{V} \quad \deg_{V \setminus \widetilde{V}}(x) := \#\{y \in V \setminus \widetilde{V} : (x, y) \in E\} \le k$$

The notion of k-fort is particularly important because it will allow us to state an equivalent formulation of the statement "A_0 achieves full infection" in terms of some property of the initial configuration. This is what the next proposition is about.

Proposition 1.1. *Failure of complete infection for bootstrap percolation with facilitating parameter r is equivalent to the existence of an $(r-1)$-fort of healthy sites in the initial configuration.*

Proof. On the one hand, healthy vertices forming an $(r-1)$-fort in the initial configuration will never get infected: they will never satisfy the condition required by the dynamics of the process with facilitating parameter r, even if all other vertices of the graph become infected. Viceversa, assume that for a certain η_0 we have that η_∞ fails to be completely infected. Then the healthy vertices in the final configuration contain an $(r-1)$-fort (simply take $x \in A_\infty{}^{\mathsf{c}}$ and consider the connected component of $A_\infty{}^{\mathsf{c}}$ containing x) and so, a fortiori, also A_0 contains an $(r-1)$-fort. $\qquad\square$

References   The connotation of r as "facilitating parameter" is taken from [Sau+10]. In the literature one usually speaks about "threshold r bootstrap percolation" (as in [FS08]) or simply "r-neighbour bootstrap percolation" (as in [Mor17] or in [Har22]). We have decided to use the more cumbersome expression "facilitating parameter" in order to distinguish it from another closely related model, which we will introduce shortly, in which we talk about "blocking parameter". The interpretation of the process as an illness which spreads can be found in [Mor17]. Maybe it is more common to think about it as particles which spread (as in [BPP06] and [FS08]), but we ask the reader please *not* to use this interpretation. We will reserve it for the aforementioned model with "blocking parameter" (and this is consistent with [Sau+10]). Misinterpreting how this terminology is used in the present work would lead to great confusion.

1.1.2   Where does probability come into play?

In this subsection we address the question of how to choose the initial configuration. The short answer is that we will study bootstrap percolation with facilitating

parameter r with a randomly chosen set of initially infected vertices A_0. This means that the process will start from a random initial configuration η_0 and will then evolve deterministically to some final bootstrapped configuration. In this sense, we have that also η_∞ is random and that the various definitions in 1.2 on page 3 are random events, so that we can ask questions about their probability. This also has some really practical motivations: results expressed in the form of "averages" or of "almost surely statements" are not only more robust than results which depend on the exact initial configuration, but often also the only possible ones!

Let us describe precisely what we mean by "A_0 is chosen randomly". We fix a parameter $0 \le p \le 1$ and we consider the probability space $(\Omega, \mathcal{A}, \mathbf{P}_p)$, where the state space is $\Omega = \{0,1\}^V$, the σ-algebra $\mathcal{A}$ is the product σ-algebra on Ω and $\mathbf{P}_p$ is the Bernoulli product measure on $\mathcal{A}$. With these definitions, "A_0 is chosen randomly" means $x \in A_0$ if and only if $\eta(x) = 1$, where $\eta = (\eta(x) : x \in V) \in \Omega$ is sampled under the probability measure $\mathbf{P}_p$. This is the same as saying that we place each vertex of G in A_0 independently at random with probability p. We think about p as the *initial density*, i.e. as the density of infected sites in the initial configuration. We see that the usual Bernoulli site percolation is nothing other than bootstrap percolation at time 0 with initial condition sampled under $\mathbf{P}_p$. In this sense, we could say that bootstrap percolation generalizes the usual Bernoulli site percolation by adding a dynamics. More on this in remark 1.9 on page 15.

Remark 1.3. The probabilistic framework introduced in this subsection is a very standard one. We recall here a few basic facts about it. The cardinality of Ω is the same of $\mathbb{R}$. On the set $\{0,1\}$ we consider the discrete topology, so in particular it is compact. On the set Ω we consider the product topology, so that it is also compact (recall that by Tychonoff's theorem every topological product of compact spaces is compact). By definition, the product σ-algebra $\mathcal{A}$ is the one generated by cylinder sets, which in this setting are simply the subsets of Ω depending on finitely many vertices, namely the subsets of Ω obtained by fixing the values $(\eta(x) : x \in I)$, with $I \subset V$ of finite cardinality. Again by definition, the probability $\mathbf{P}_p$ is the one under which every coordinate $\eta(x)$ is a Bernoulli random variable of parameter p.

From now on, when we speak about bootstrap percolation with facilitating parameter r we always mean that the initial configuration is chosen according to $\mathbf{P}_p$. Now we can be more precise in formulating our questions on the final configuration. For all possible given values of r, we are interested in studying how the probabilities of the events of definition 1.2 on page 3 change as we vary the parameter p.

We start by studying the event $A_\infty = V$ and to this end, we introduce some definitions.

Definition 1.4. For a fixed value of r, define

$$\theta_f(p) := \mathbf{P}_p[\,\eta_\infty \equiv 1\,] = \mathbf{P}_p[\,A_\infty = V\,] \tag{1.3}$$

Clearly $0 \leq \theta_f(p) \leq 1$, with $\theta_f(0) = 0$ and $\theta_f(1) = 1$. Moreover, the function $p \mapsto \theta_f(p)$ is non-decreasing. We shall show it just below, adapting the proof of the analogous result for site percolation to our case of bootstrap percolation. In particular, this will provide the opportunity to use the notion of coupling, a very important tool in probability.

Increasing coupling

Let us give a couple of definitions. Let η and η' be two elements of $\Omega = \{0, 1\}^V$. We write $\eta \leq \eta'$ if for every $x \in V$ it holds that $\eta(x) \leq \eta'(x)$. This relation is a partial order on the set Ω.

Definition 1.5. Let $B \in \mathcal{A}$. We say that B is an *increasing event* if $\eta \in B$ and $\eta \leq \eta'$ imply $\eta' \in B$. Analogously we say that a random variable X on $\{0, 1\}^V$ is an *increasing random variable* if for every $\eta \leq \eta'$ we have $X(\eta) \leq X(\eta')$.

As an example, consider $\widetilde{V} \subset V$, a subset of the vertices of the graph. Then the event $B := \{\eta \in \Omega : \eta(x) = 1 \text{ for each } x \in \widetilde{V}\}$ is increasing, because if $\eta \in B$ and $\eta \leq \eta'$, then for every $x \in \widetilde{V}$ it holds $1 = \eta(x) \leq \eta'(x)$, so that for every $x \in \widetilde{V}$ we have $\eta'(x) = 1$ and so $\eta' \in B$. From this it is also easy to derive an example of an increasing random variable by setting $X(\eta) := \mathbb{1}_B(\eta)$. The verification that it is indeed increasing is similar to what has just been done.

Definition 1.6. Let $(\Omega_1, \mathcal{A}_1, \mathbf{P}_1)$ and $(\Omega_2, \mathcal{A}_2, \mathbf{P}_2)$ be probability spaces. A probability measure $\mathbf{Q}$ on $(\Omega_1 \times \Omega_2, \mathcal{A}_1 \otimes \mathcal{A}_2)$ is called a *coupling* of $\mathbf{P}_1$ and $\mathbf{P}_2$ if $\mathbf{Q}(\cdot \times \Omega_2) = \mathbf{P}_1$ and $\mathbf{Q}(\Omega_1 \times \cdot) = \mathbf{P}_2$.

In words, a coupling is the procedure of defining two (families of) random variables that are related in a specific way on one probability space. The product measure $\mathbf{P}_1 \otimes \mathbf{P}_2$ is clearly a coupling, but it is the trivial one, in the sense that the relation between $\mathbf{P}_1$ and $\mathbf{P}_2$ that it encodes is the one of indipendence (i.e. "no relation"). What we will use is an *increasing* coupling, i.e. a coupling which encodes the relation "$\leq$".

Proposition 1.2. *Fix $p \leq p'$. Consider the probability spaces $(\Omega, \mathcal{A}, \mathbf{P}_p)$ and $(\Omega, \mathcal{A}, \mathbf{P}_{p'})$, where $\mathbf{P}_{p'}$ is also a Bernoulli product measure, but of parameter p'. Then there exists a coupling $\mathbf{Q}$ of $\mathbf{P}_p$ and $\mathbf{P}_{p'}$ such that $\mathbf{Q}[\{(\eta^p, \eta^{p'}) : \eta^p \leq \eta^{p'}\}] = 1$.*

Proof. Let us recall that it is possible to use a uniformly distributed random variable U on $[0, 1]$ to sample an element of the set $\{0, 1\}$ according to a $\mathrm{Ber}(p)$ distribution. Indeed, the random variable defined to be 1 if $U \leq p$ and 0 if $U > p$ is $\mathrm{Ber}(p)$-distributed. In particular, we can represent our random initial configuration η_0 using $(U_x)_{x \in V}$, a collection of i.i.d random variables, uniformly distributed in $[0, 1]$, indexed by the vertices of the graph G. The coupling of the claim is obtained by using the *same* collection $(U_x)_{x \in V}$ for both η^p and $\eta^{p'}$. In this way, for any given vertex $x \in V$ we have that if $\eta^p(x) = 1$ then also $\eta^{p'}(x) = 1$ (because if $U_x < p$, than $U_x < p'$). This proves that $\mathbf{Q}$-a.s. $\eta^p \leq \eta^{p'}$. Moreover it is also clear, by what said above on the representation of Bernoulli random

variables through a uniform distribution, that the marginals of distribution that $\mathbf{Q}$ are the correct ones. □

Corollary 1.1. *Let $B \in \mathcal{A}$ be an increasing event. Then the function $p \mapsto \mathbf{P}_p[B]$ is non-decreasing.*

Proof. We have

$$\mathbf{P}_p[B] = \mathbf{Q}[\{(\eta^p, \eta^{p'}) : \eta^p \in B\}] \leq \mathbf{Q}[\{(\eta^p, \eta^{p'}) : \eta^{p'} \in B\}] = \mathbf{P}_{p'}[B]$$

where the first and the last equality follow immediately from the definition of a coupling of $\mathbf{P}_p$ and $\mathbf{P}_{p'}$, whereas the inequality comes from the particular property of our coupling $\mathbf{Q}$ and from the hypothesis that B is increasing. □

The event $\{\eta_\infty \equiv 1\}$ is clearly increasing: if a certain initial configuration evolves into full infection, then an initial configuration containing the same and possibly some more infected sites will also result in the graph being fully infected. We conclude that the function $p \mapsto \theta_f(p) = \mathbf{P}_p\big[\{\eta_\infty \equiv 1\}\big]$ is really non-decreasing. This result ensures that the second equality in the following definitions holds:

Definition 1.7. The *critical probability for full infection* is

$$p_f(G, r) := \inf\{p : \theta_f(p) = 1\} = \sup\{p : \theta_f(p) < 1\} \in [0, 1] \qquad (1.4)$$

We observe that $p_f(G, r)$ is the particular value of the initial density p such that healthy vertices in the final configuration can *only* be found when p satisfies $p \leq p_f(G, r)$. So having some result (i.e. estimate) on $p_f(G, r)$ would indeed give us some information on how the probability of the event of full infection changes as p varies. A priori, however, it is not clear why the given definition should be better than the following one:

$$\widetilde{p}_f(G, r) := \inf\{p : \theta_f(p) > 0\} = \sup\{p : \theta_f(p) = 0\}$$

This time $\widetilde{p}_f(G, r)$ is the particular value of the initial density p such that healthy sites in the final configuration can be found *almost surely* only when the initial density p satisfies $p \leq \widetilde{p}_f(G, r)$. In fact, which definition one choses does not matter: we now prove that $\widetilde{p}_f(G, r) = p_f(G, r)$. The inequality $\widetilde{p}_f(G, r) \leq p_f(G, r)$ is obvious (in $\widetilde{p}_f(G, r)$ we are taking the infimum over a bigger set). In order to establish the other one, we revisit the notion of ergodicity. Again, the proof will follow the guidelines of what is usually done for the more studied process of Bernoulli site percolation on $\mathbb{Z}^d$, but with an important difference. Because of the nature of the graphs that we will consider in this thesis, it is not enough to consider events and measures which are invariant under translations. Instead, it is necessary to reformulate this notions in terms of group actions (of which, of course, translation can simply be considered as a special case).

Ergodicity

We continue to consider the measurable space $(\Omega, \mathcal{A})$ defined above. The following definitions allow us to describe ergodicity with the level of generality that we need.

Definition 1.8. Let Γ be a group of automorphism of G. Let $\mathbf{P}$ be a (general) probability measure on $\mathcal{A}$.

- The event $B \in \mathcal{A}$ is called Γ-*invariant* if for any $\gamma \in \Gamma$ we have $\gamma B = B$;
- the probability measure $\mathbf{P}$ is called Γ-*invariant* if for any $\gamma \in \Gamma$ and for any $B \in \mathcal{A}$ we have $\mathbf{P}[\gamma B] = \mathbf{P}[B]$;
- the set $\mathcal{I}_\Gamma$ of all Γ-invariant events (is a σ-algebra, easy verification, and) is called Γ-*invariant σ-algebra*;
- the probability measure $\mathbf{P}$ is called Γ-*ergodic* if any Γ-invariant event has probability 0 or 1.

These definitions are relevant for us because of the following lemma.

Lemma 1.1 (Ergodicity of the Bernoulli product measure). *The Bernoulli product measure $\mathbf{P}_p$ is Γ-invariant. Moreover, if Γ acts on G in such a way that each vertex has an infinite orbit, then the measure $\mathbf{P}_p$ is Γ-ergodic.*

Proof. The first claim, namely that $\mathbf{P}_p$ is Γ-invariant, is clearly garanteed by the fact that each coordinate $\eta(x)$ is i.i.d.. For the second claim, see [LP17]. $\qquad\square$

Remark 1.4. We point out that among all of the hypotheses that we have put on G at the beginning of this thesis, being connected and locally finite are the only ones needed for the second part of the previous lemma.

Since the event $A_\infty = V$ is (obviously) Γ-invariant, using the above lemma (all of the graphs on which we will consider bootstrap percolation in this thesis satisfy its hypotheses) we obtain that $\theta_f(p) \in \{0, 1\}$ and thus $\theta_f(p) = 1$ if and only if $\theta_f(p) > 0$. This implies $\widetilde{p}_f(G, r) = p_f(G, r)$ (we have just proved that the two sets over which we are taking the infimum are in fact the same set). From now on we will simply write $p_f(G, r)$, thinking about one definition or the other according to what is best for the context. More in general, one can give the following definition:

Definition 1.9. A graph G *satisfies the $0 - 1$ law* for bootstrap percolation with facilitating parameter r if $\mathbf{P}_p[A_\infty] \in \{0, 1\}$.

In this context, the above lemma gives a sufficient condition for a graph G to satisfy the 0-1 law.

References   For all remarks on general probability theory, the reference that we have used is the fairly recent book of Achim Klenke [Kle20]. Of course, there are a lot of other classical books which would also be a perfect fit. When we say that we have adapted the proofs which are usually studied for Bernoulli site percolation, we refer to the proofs found in the lecture notes by Hugo Duminil-Copin [Dum18]. An extended treatment of ergodicity as introduced here is presented in the book by Lyons and Peres [LP17].

1.1.3 Bootstrap percolation with blocking parameter

In this subsection we present another definition of bootstrap percolation, which is the one commonly used in the physics community. For example, it is the one used in [Sau+10], the article from which the present thesis stems. Physicists usually study bootstrap percolation in relation to kinetically constrained models, with the aim of better understanding the phenomenon of glass formation. In this context, it is more natural to think about the dynamics as particles which are removed, rather than an illness which spreads. Also, in describing the initial random configuration, one uses the parameter of the Bernoulli product measure to describe the initial density of the quantity which tends to disappear over time (i.e. density of healthy vertices in our first definition, density of vertices occupied by a particle in the physicists one), rather than the initial density of the quantity that increases over time. We have used the words "another definition", because in general graphs it describes an actually different dynamics. However, for regular graphs (i.e. graphs in which every vertex has the same degree), we will see that this new definition simply amounts to a change of the parameter and so it may be better to say "another interpretation" instead of "another definition". Nonetheless, this new interpretation will be very useful to us, especially in 1.2 on page 13. Let us make all of this precise.

We give name boostrap percolation with *blocking parameter* m to the model used by physicists and we denote all the quantities used for this new model by an additional bar on top. Vertices in the initial set $\bar{A}_0$ are now considered *occupied* by particles. The new rules for the dynamics are:

- at each time step an occupied vertex becomes free if and only if it has fewer than m occupied neighbours;
- free vertices never become occupied, i.e. remain free forever.

We sample $\bar{A}_0$ under a Bernoulli product measure of parameter $\bar{p}$.

Remark 1.5. Careful! As already noticed in the references to subsection 1.1.1, in the mathematical literature one often finds the interpretation "particles which spread" for what we have described as "illness which spreads" (for example, this is the case in [BPP06] and [FS08]). In this thesis we will use the interpretation with particles and occupied sites only when we refer to the model with blocking parameter and the interpretation with infected sites only when we refer to the model with facilitating parameter.

Definition 1.10. A vertex of G is called *blocked* if it is occupied in the final configuration (again intended as the configuration in which the process no longer evolves).

Moreover, we define $\bar{\theta}_f(\bar{p}) := \mathbf{P}_{\bar{p}}[\{\text{there is at least one blocked site}\}]$. It is an increasing function. The proof is completely analogous to the one alreay done for bootstrap percolation with facilitating parameter r and thus we do not repeat it. With these definitions, the critical probability for the model with blocking

parameter is defined as

$$\bar{p}_f(G, m) := \inf\{\bar{p} : \bar{\theta}_f(\bar{p}) > 0\} = \inf\{\bar{p} : \bar{\theta}_f(\bar{p}) = 1\}$$
$$= \sup\{\bar{p} : \bar{\theta}_f(\bar{p}) = 0\} = \sup\{\bar{p} : \bar{\theta}_f(\bar{p}) < 1\}$$

The equality between the two infima is proved as done in the case of bootstrap percolation with facilitating parameter r. It means that we can think about $\bar{p}_f(G, m)$ equivalently as the critical density such that blocked sites only occur above it or as the density such that blocked sites almost surely occur above it. A "dictionary" to help comparison between the notations is provided in table 1.1.

	Math community	Physics community
vertices	infected (= occupied) healthy (= free)	free occupied
initial density	infected: p healty: $1 - p$	free: $1 - \bar{p}$ occupied: $\bar{p}$
performed action	to increase infected	to remove particles
object of study	clusters of healthy	clusters of blocked
critical probability	$p_f(G, r)$	$\bar{p}_f(G, m)$

Table 1.1: Dictionary

In this thesis we will only consider bootstrap percolation on regular graphs (but some almost regular graphs will appear in some proofs). So let us assume that G is a d-regular graph. In this case, the dynamics of bootstrap percolation with facilitating parameter r is exactly the same of the one of bootstrap percolation with blocking parameter $d - r + 1$. Indeed, let us use the notation:

- $\mathrm{Occ}(x) = \big|\{y \in V : y \sim x, y \text{ is occupied}\}\big|$
- $\mathrm{Free}(x) = \big|\{y \in V : y \sim x, y \text{ is free}\}\big|$

where occupied and free are to be intended in the sense of the model with blocking parameter. Then, by the hypothesis of d-regularity, we have that $\mathrm{Occ}(x) + \mathrm{Free}(x) = d$ for each given $x \in V$ and so

$$\mathrm{Occ}(x) < m \quad \Leftrightarrow \quad d - \mathrm{Free}(x) < m \quad \Leftrightarrow \quad \mathrm{Free}(x) > d - m$$

which means precisely that for an appropriate choice of the parameters the rules of the dynamics are equal:

to remove a particle from an occupied vertex if and only if it has fewer than m occupied neighbours	$\Leftrightarrow$	to remove a particle from an occupied vertex if and only if it has at least $d - m + 1$ free neighbours

In particular, given A_0, an initial configuration of infected vertices for the bootstrap percolation with facilitating parameter $(d - m + 1)$, the vertices of the healthy clusters of its final configuration are exactly the blocked vertices of the bootstrap

percolation with blocking parameter m and ${A_0}^\complement$ as initial configuration of occupied vertices. Finally, at the cost of being redundant, let us check that indeed the critical probability $p_f(G, r)$ with p as density of healthy sites corresponds to the critical probability $\bar{p}_f(G, m)$ with $\bar{p} = 1 - p$ as density of occupied sites:

$$
\begin{aligned}
\bar{p}_f(G, m) = \quad & \text{by definition, choice of } \bar{p} \\
= \inf\left\{1 - p \,:\, \mathbf{P}_{1-p}\big[\,|\{\text{blocked sites}\}| \geq 1\,\big] = 1\right\} \quad & \text{switching interpretation} \\
= \inf\left\{1 - p \,:\, \mathbf{P}_p\big[\,|\{\text{healthy sites for } \eta_\infty\}| \geq 1\,\big] = 1\right\} \quad & \text{taking the complement} \\
= 1 - \sup\left\{p \,:\, \mathbf{P}_p\big[\,|\{\text{healthy sites for } \eta_\infty\}| = 0\,\big] = 0\right\} \quad & \text{by definition} \\
= 1 - p_f(G, d - m + 1)
\end{aligned}
$$

Note that in the last equality we have used $p_f = \widetilde{p}_f$.

References The description of the bootstrap percolation model with blocking parameter is taken from [Sau+10]. Changes in notation have been made in order to be coherent with the rest of this thesis.

1.1.4   Other critical probabilities

We have described how to define the critical probability for full infection $p_f(G, r)$ and how it seems to be a good object to consider if one wants to study whether or not $A_\infty = V$. However, this is not the only interesting question that one can ask about the final bootstrapped configuration. For example, supposing that $A_\infty \subsetneq V$, one could ask whether or not A_∞ contains an infinite connected component, namely if there are values of the initial density p such that the initial set of infected sites manages to propagate to infinity even though it does not infect the whole graph. Or more, supposing that A_∞ contains an infinite connected component, one could ask whether or not that connected component is unique. To try to answer this question, we propose two new definitions, analogous to the critical probability for full infection $p_f(G, r)$. In order to fully justify them we also need an additional assumption on G, which we state below.

Definition 1.11. We define the *critical probability for percolation $p_c(G, r)$* as

$$
\begin{aligned}
p_c(G, r) := & \inf\{p : \theta_c(p) > 0\} = \sup\{p : \theta_c(p) = 0\} = \\
& = \inf\{p : \theta_c(p) = 1\} = \sup\{p : \theta_c(p) < 1\}
\end{aligned}
$$

where

$$
\begin{aligned}
\theta_c(p) := \mathbf{P}_p\big[\{\exists \text{ at least one infinite connected component} \\
\text{of infected sites in the final configuration}\}\big]
\end{aligned}
$$

Definition 1.12. We define the *critical probability for uniqueness $p_u(G, r)$* as

$$
\begin{aligned}
p_u(G, r) := & \inf\{p : \theta_u(p) > 0\} = \sup\{p : \theta_u(p) = 0\} = \\
& = \inf\{p : \theta_u(p) = 1\} = \sup\{p : \theta_u(p) < 1\}
\end{aligned}
$$

where

$$\theta_u(p) := \mathbf{P}_p\big[\{\text{there is a unique infinite connected component}$$
$$\text{of infected sites in the final configuration}\}\big]$$

The fact that the above definitions make sense and the reason why the equality between the first and the second line in both definitions is true are both derived in exactly the same way as already done for the critical probability for full infection. Let us quickly repeat how the reasoning went. First of all, $\theta_c(0) = \theta_u(0) = 0$ and $\theta_c(1) = \theta_u(1) = 1$. Moreover, the events which define $\theta_c(p)$ and $\theta_u(p)$ are increasing. Thus also the functions $p \mapsto \theta_c(p)$ and $p \mapsto \theta_u(p)$ are increasing (use an increasing coupling) and the definitions make sense. Finally, we assume that the events through which we have defined θ_c and θ_u are Γ-invariant (this is the extra assumption that we mentioned above; it is easily verified for all the graphs which we will consider in the following chapters). This means that we can apply 1.1 on page 8 and obtain that they happen with probability 0 or 1. Thus the second line of equalities in the above definitions is justified.

Some very basic observations allow us to produce the following diagram:

Indeed, every completely infected final configuration also has a unique connected component of infected sites. Moreover, it is also obvious that every final configuration in which there is a unique infinite connected component of infected sites has at least one infinite connected component of infected sites. Passing to the probabilities, this immediatly yields $\theta_c(p) \geq \theta_u(p) \geq \theta_f(p)$ and thus $p_c(G,r) \leq p_u(G,r) \leq p_f(G,r)$ (simply because going from left to right we are taking the infimum on smaller sets). We do not (yet) know what happens in the dotted line in the figure, i.e. we do not know if some (or all) of these critical values for the parameter p are in fact 0, or 1, or the same value. For a given fixed r we say that $p_f(G,r)$ is *trivial* if $p_f(G,r) \in \{0,1\}$. We extend the use of the word trivial also to the other critical probabilites, with the appropriate adjustments. Sometimes we abuse it, depending on context. For example, if we knew that $0 < p_f(G,r) < 1$, then $p_c(G,r)$ would be said to be trivial if $p_c(G,r) \in \{0, p_f(G,r)\}$. But if we knew that $p_u(G,r) < p_f(G,r) < 1$, then $p_c(G,r)$ would be said to be trivial if $p_c(G,r) \in \{0, p_u(G,r)\}$. It is possible that this last pedantic remark on our part creates more confusion than it could solve (then just ignore!). In the remaining of this thesis we restrict our study to some particular classes of graphs G and we try to find for which values of r (if any) the above critical probabilities are nontrivial. We immediately observe that there are some trivial values of r for which the question about $p_f(G,r)$ is immediately settled (for every G):

Remark 1.6. For $r = 1$ we always have $p_f(T_d, 1) = 0$. For $r \geq D := \max_{x \in V}\{\deg(x)\}$ we always have $p_f(G,r) = 1$.

Proof. Since for $r = 1$ a single infected site is enough to infect the whole tree (we are supposing G to be connected), the only case in which we do not have full occupation is the one in which the initial configuration is made of all healthy sites. However, this happens with nonzero probability if and only if $p = 0$, because we have supposed the graph G to be infinite. Thus $p_f(G, 1) = 0$.

On the other hand, if $r \geq D$, then the dynamics is such that a healthy site can become infected if and only if it is *completely* surrounded by infected sites (if the graph is regular, but otherwise the following argument still holds). Let $x \in V$ be a vertex whose degree is equal to D, the maximum degree of the graph, and let $y \in \mathcal{N}_x$ be one of its neighbours. Consider the set $\{x, y\}$ and the event $B := \{\eta_0(x) = \eta_0(y) = 0\}$. We observe that no initial configuration belonging to this event is capable of infecting the whole graph, since at any given moment both x and y are connected to at most $D - 1$ infected neighbours (and by the choise or r they need at least D of them to become infected). We have $\mathbf{P}_p[A_\infty \neq V] > \mathbf{P}_p[B] = (1 - p)^2 > 0$ for every $p < 1$ and thus $\mathbf{P}_p[A_\infty = V] = 0$ (recall 0-1 event). We conclude that $p_f(G, r) = 0$ for every $r \geq D$. In other words we have found that, on every graph of maximum degree D, there always exists a $(D - 1)$-fort of healthy sites with positive probability . $\qquad \square$

For this reason, in the remainder of this thesis we always implicitly assume that $2 \leq r \leq \max_{x \in V}\{\deg(x)\} - 1$ (at least whenever we talk about $p_f(G, r)$).

1.2 General estimates on p_f

We conclude this introduction to the model by stating and proving some general inequalities on $p_f(G, r)$.

1.2.1 Comparison with the process on subgraphs

More precisely, for both the models with blocking and with facilitating parameter we get an upper bound on the critical probability for bootstrap percolation on a general graph G in terms of the critical probability for boostrap percolation on one of its subgraphs (here general means under the hypotheses made at the beginning of this chapter, but not necessarily regular).

Lemma 1.2. *Let $\widetilde{G}$ be a subgraph of the graph G. We consider boostrap percolation with the same blocking parameter m on both of these graphs. Then:*

$$\bar{p}_f(G, m) \leq \bar{p}_f(\widetilde{G}, m)$$

Proof. Suppose that we have a final configuration in $\widetilde{G}$ which has at least one blocked site. Then that site will be blocked also when considered in G, no matter the value (occupied or free) of the sites in G which are not in $\widetilde{G}$. Indeed, for any given vertex of $\widetilde{G}$, the number of its occupied neighbours in $\widetilde{G}$ is less then or equal to the number of its occupied neighbours in G. Informally, we could say that it is easier to be blocked in G than in $\widetilde{G}$. This means exactly that for every $\bar{p}$ we have $\bar{\theta}_f^{\widetilde{G}}(\bar{p}) \leq \bar{\theta}_f^G(\bar{p})$, which implies the thesis. $\qquad \square$

Lemma 1.3. *Let $\widetilde{G}$ be a subgraph of the graph G such that $\widetilde{G}$ contains all of the vertices of G. We consider boostrap percolation with the same facilitating parameter r on both of these graphs. Then:*

$$p_f(G, r) \leq p_f(\widetilde{G}, r)$$

Proof. Since $\widetilde{G}$ contains all of the vertices of G, any initial configuration on $\widetilde{G}$ can be thought of as an initial configuration on G. Now consider an initial configuration on $\widetilde{G}$ which has no healthy sites in its final configuration. The bootstrap percolation process with facilitating parameter r on G started with that initial configuration will also have no healthy sites in its final configuration, because if the edges in $\widetilde{G}$ were enough to infect the whole graph, then a fortiori the edges in G will allow the initial configuration to infect the whole graph. Informally, we could say that being fully infected is easier for G than for $\widetilde{G}$. This means exactly that for every p we have $\theta_f^{\widetilde{G}}(p) \leq \theta_f^G(p)$, which implies the thesis. Note that the additional assumption on the vertices of $\widetilde{G}$ made in this case is really necessary. Without requiring it, there could be some regions of the vertices of G which are not in $\widetilde{G}$ which remain healthy, even if all the vertices of $\widetilde{G}$ become infected. In other words, there could exist $r-1$-forts contained in $V(G) \setminus V(\widetilde{G})$. □

Remark 1.7. Careful! In the two lemmas above the densities $\bar{p}$ and p are really what they are defined to be in , i.e. if we consider them simultaneously (e.g. in a regular graph), they refer to different objects: one is the density of occupied vertices and the other one is the density of free vertices.

We have one more lemma of this type. We say that a graph G is a union of two graphs G_1 and G_2 if $V(G) = V(G_1) \cup V(G_2)$ and $E(G) = E(G_1) \cup E(G_2)$. We write this as $G = G_1 \cup G_2$.

Lemma 1.4. *If $G = G_1 \cup G_2$ with G_1 and G_2 satisfying the 0-1 law, then $p_f(G, r) \leq p_f(G_1, r) \vee p_f(G_2, r)$.*

Proof. Without loss of generality, assume that $p_f(G_1, r) \geq p_f(G_2, r)$. Then, if $p > p_f(G_1, r)$, a.s. both G_1 and G_2 are fully infected. Thus a.s. also G is fully infected and so $p > p_f(G_r)$, which gives the claim. □

We conclude this subsection with one last remark, that will be useful later.

Remark 1.8. Assume that G is a d-regular graph. Fix $2 \leq r \leq d-1$ (recall remark). Let $\widetilde{G}$ be a $\widetilde{d}$-regular subgraph of G. Then:

$$p_f(\widetilde{G}, \widetilde{d} - d + r) \overset{(a)}{=} 1 - \bar{p}_f(\widetilde{G}, d - r + 1) \overset{(b)}{\leq} 1 - \bar{p}_f(G, d - r + 1) \overset{(c)}{=} p_f(G, r)$$

where (a) and (c) come from the comparison between the critical probability for the model with blocking and facilitating parameter in a regular graph presented at the end of section and (b) is a direct consequence of lemma . Summing up, we have obtained that

$$p_f(\widetilde{G}, \widetilde{d} - d + r) \leq p_f(G, r) \tag{1.5}$$

This shows that in the particular setting of regular graphs, the critical probability for full infection of a subgraph can also be used to bound $p_f(G, r)$ from below (and not only from above, as shown in lemma 1.3 on the preceding page). Of course, the catch is that in 1.5 we do not have anymore the same facilitating parameter on both G and $\widetilde{G}$: the facilitating parameter on the subgraph is smaller than the one on the graph (because $\widetilde{d} - d < 0$, since obviously the degree in a subgraph is smaller than the one in the original graph).

1.2.2 Comparison with Bernoulli site percolation

We start with a simple remark, whose only aim is to get more acquainted with the differences between Bernoulli and boostrap percolation.
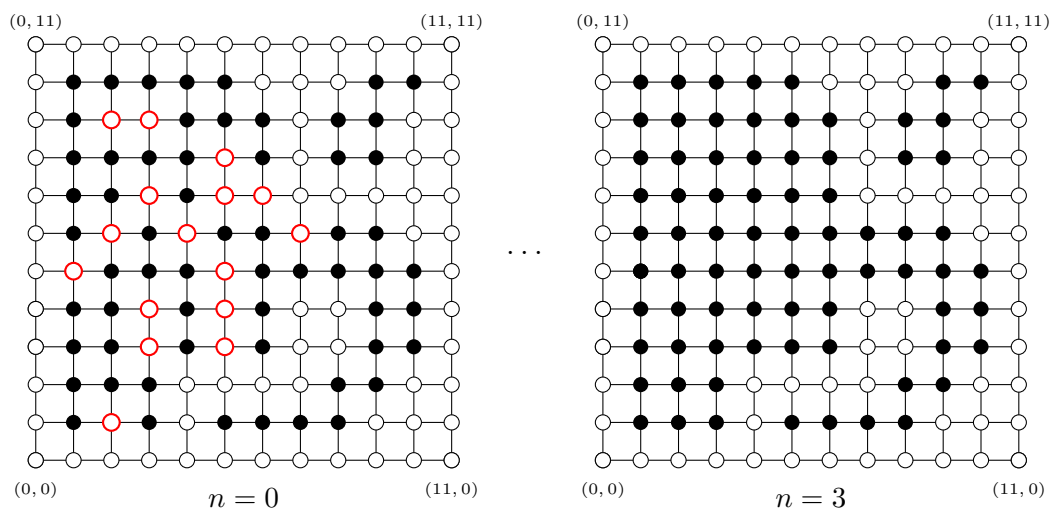

Figure 1.2: We choose $G = \mathbb{Z}^2$, so that $d = 4$ and $r = d - 1 = 3$. Infected sites are represented by filled black dots, whereas healthy sites are represented by filled white dots. The one on the right is the final configuration of the region of $\mathbb{Z}^2$ which is shown: there are no further changes for $n \geq 4$. In the initial configuration we have circled in red vertices that sooner or later become infected (in the terminology of 2.1 on page 27 these are weakly healthy vertices). They constitute the "little branches" that are "pruned" by the bootstrap dynamics. (Please note how the interior of the region we have chosen the states of the sites randomly, but on the boundary we have arbitrarily set them to be healthy (i.e. closed). Of course this is not what happens in the model, but pictorially it helps to follow the evolution of the dynamics. In any case, we are not showing a configuration that it is impossible to observe: the event $\{\eta : \eta(x) = 0 \; \forall \; \eta$ on the boundary of the grid$\}$ has nonzero probability...).

Remark 1.9. On a d-regular graph G, consider bootstrap percolation with facilitating parameter $r = d - 2$. On the same graph, also consider Bernoulli site percolation. For both models we take the same value of $0 < p < 1$ as parameter for the Bernoulli product measure. In the literature on Bernoulli site percolation it is usual to consider a vertex to be open if it is chosen to be in state 1 with

probability p, so what in our notation the set of open vertices for the Bernoulli percolation model is $A_0 = \{x : \eta_0(x) = 1\}$, the set of initially infected vertices for the bootstrap percolation model. Thus we will represent an open (i.e. initially infected) site with a black dot, in order to be coherent with 1.1 on page 3.

Let us finally state the actual observation. Since the graph is d-regular and the facilitating parameter is $r = d - 1$, at each given step an healthy site remains healthy if and only if it has at least two healthy neighbours. In particular, consider an infinite cluster of healthy sites in the initial configuration (i.e. an infinite component of closed sites for the Bernoulli percolation model) which does not disappear in the final bootstrapped configuration. For this to happen, it must contain an $(r - 1) = (d - 2)$-fort of healthy vertices. An example of such a fort would be a "chain" of sites which comes from infinity and goes to infinity (i.e. a 2-regular tree). The effect of the bootstrap percolation dynamics is that of "pruning" all the little branches that belong to the initial cluster and grow outwards from the $(d - 2)$-fort. In other words, we could say that the $(d - 2)$-fort is the only part of the considered initial infinite cluster of closed sites for Bernoulli percolation that remains also in the final configuration of the bootstrap model. Figure 1.2 on the previous page tries to give an idea of the phenomenon.

Now let us show how Bernoulli site percolation can provide an upper bound to the critical probabilty for full infection.

Lemma 1.5. *If in G there are no finite $(r - 1)$-forts, then $p_f(G, r) \leq 1 - p_c(G)$, where $p_c(G)$ is the critical probability for percolation for the Bernoulli site percolation model defined on G.*

Proof. We have already seen that failure of full infection in the final configuration is equivalent to the existence of a $(r - 1)$-fort in the initial configuration. Since we are under the hypothesis that there are no finite $(r - 1)$-forts, in order to have failure of full infection we need an infinite $(r - 1)$-fort in the initial configuration. If this happens, than in particular we are in the situation in which healthy sites in the initial configuration percolate, i.e. $1 - p > p_c(G)$ (the parameter corresponding to the type of site which percolates should be greater than the critical probability for percolation), i.e. $p < 1 - p_c(G)$. Summing up, if p is such that we have $\theta_f(p) = 0$, then $p < 1 - p_c(G)$, i.e. $p_f(G, r) \leq 1 - p_c(G)$ (by definition). $\square$

References   The inequalities on the critical probability for full infection come from [Sau+10]. Here we have tried to present formal proofs. The comparison with Bernoulli site percolation, instead, is to be found in [BPP06].

1.3   Branching Processes

We temporarily suspend the study of bootstrap percolation in order to give the definition of branching processes and to recall some classical facts about them. Loosely speaking, a branching process is a stochastic process, indexed by the natural numbers, whose purpose is to serve as a model of a population in

which each individual in the n-th generation produces some random number of individuals in the $(n+1)$-th generation. The most common formulation is that of the Galton Watson process, which we will use as a tool in our study of bootstrap percolation on trees in the next chapter.

1.3.1 Galton Watson processes

In this section we denote by $(\Omega, \mathcal{A}, \mathbf{P})$ a general probability space. Let $p_0, p_1, p_2, \cdots \in [0, 1]$ be such that $\sum_{k=0}^{\infty} p_k = 1$ and X be a random variable such that for every $k = 0, 1, 2, \ldots$ we have $\mathbf{P}[X = k] = p_k$. Finally, let $(X_{n,i})_{n,i=0,1,2,\ldots}$ be an i.i.d. family of random variables distributed as X.

Definition 1.13. Let $Z_0 \equiv 1$ and set

$$\forall\, n = 0, 1, 2, \ldots \qquad Z_n := \sum_{i=1}^{Z_{n-1}} X_{n-1,i}$$

The process $(Z_n)_{n=0,1,2,\ldots}$ is called a *Galton-Watson process* or *branching process* and the probability vector $(p_k)_{k=0,1,2,\ldots}$ is called its *offspring distribution*.

As already mentioned, we can interpret Z_n as the number of individuals in n-th generation of a randomly developing population. The i-ith individual in the n-th generation has $X_{n,i}$ offspring in the $(n+1)$-th generation. Every branching process has an associated tree obtained simply by having a vertex for every individual of every generation and an edge between two vertices if one is in the offspring of the other.

An important tool in the study of branching processes are probability generating functions. Hence, let

$$\phi(z) := \sum_{k=0}^{\infty} p_k z^k$$

be the p.g.f. of the offspring distribution (i.e. of the distribution of X).

One natural question that one can ask about a Galton-Watson process (and maybe also the first one) is whether the population will *eventually* die out or not. In order to study this, we define:

Definition 1.14. The *extinction probability* of the branching process $(Z_n)_{n\geq 0}$ is

$$p_{ext} := \mathbf{P}\big[\exists n \geq 1 : Z_n = 0\big] = \mathbf{P}\Big[\bigcup_{n\geq 1}\{Z_n = 0\}\Big] = \lim_{n\to\infty} \mathbf{P}\big[Z_n = 0\big] \qquad (1.6)$$

The equalities in the above definition are clearly true, because the sequence of events $\big(\{Z_n = 0\}\big)_{n\geq 0}$ is increasing. Under what conditions do we have $p_{ext} = 0$, $p_{ext} = 1$ or $p_{ext} \in]0, 1[$? It is clear that $p_{ext} \geq p_0$, because p_0 is simply the probability already the first generation has 0 individuals. On the other hand, if $p_0 = 0$, every individual has at least a child a.s. and thus Z_n is monotone in n, so that $p_{ext} = 0$. The following theorem can be proved using the p.g.f. ϕ of the offspring distribution defined above:
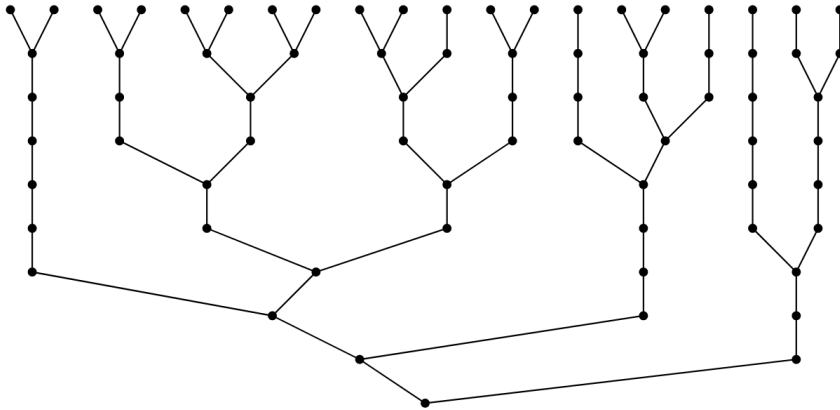
Figure 1.3: Generations 0 to 9 of a typical Galton-Watson tree with offspring distribution given by the p.g.f. $\phi(z) = \frac{(z+z^2)}{2}$.

Theorem 1.1 (Extinction probability of the Galton Watson process)**.** *Assume* $p_1 \neq 1$. *Then:*

- $\{z \in [0,1] : \phi(z) = z\} = \{p_{ext}, 1\}$ *and so, in particular,* p_{ext} *is the smallest fixed point of* ϕ *in* $[0,1]$;
- *the following equivalences hold:*

$$p_{ext} < 1 \quad \Longleftrightarrow \quad \lim_{z \uparrow 1} \phi'(x) > 1 \quad \Longleftrightarrow \quad \mathbf{E}[X] = \sum_{k=1}^{\infty} k p_k > 1$$

Of course if $p_1 = 1$ then $p_{ext} = 0$.

References There are countless references on branching process. We have used [Kle20], [LP17] (from which we have taken figure 1.3) and [Bła17].

Chapter 2

Bootstrap percolation on trees

This chapter is devoted to bootstrap percolation on regular trees. More precisely, we study the critical probabilities for full infection and for percolation. It is known from the relevant literature that both of them are nontrivial. We give a full proof of the result for p_f and present the main idea of the proof for p_c.

2.1 Critical probability for full infection

Let us start with some more definition from basic graph theory, mainly in order to set the notation. A *cycle* in a graph is finite sequence of vertices $(y_1, \ldots, y_n)$ such that $y_1, \ldots, y_{n-1}$ are distinct vertices, $y_1 = y_n$ and $y_{k+1} \in \mathcal{N}_{y_k}$ for every $1 \leq k \leq (n-1)$. A *tree* is an undirected graph in which any two vertices are connected by exactly one path, i.e. it is a connected undirected graph without cycles. A *rooted* tree is tree in which one vertex is designated as the root, denoted by o. For every vertex x in a rooted tree it is possible to define the *parent* and the *children* of x: the children are the $\deg(x) - 1$ neighbours of x which are farther from the root, the parent is the remaining neighbour. A vertex of a tree is called a *leaf* if it has no children. A $(d+1)$-regular tree is a tree in which every vertex has degree exactly equal to $(d+1)$ and we will denote it by T_d. The notation T_d is used to emphasize that in a $(d+1)$-regular tree every vertex, with the exception of the root, has exactly d children (i.e. it emphasizes the *branching number* of the graph, a more general notion for which one can consult, for example, [LP17]). Finally, we define a *d-ary tree* to be a rooted tree in which every vertex has exactly d children. This is equivalent to saying that the root has degree d and every other vertex has degree $d + 1$.

2.1.1 Preliminaries

In view of remark 1.6 on page 12, for the remaining of this chapter we always take $2 \leq r \leq d$. We prove that for these value of r the critical probability is indeed nontrivial, following the work [BPP06].

First of all we recall the following fundamental tool, taught in every course in percolation theory:

Theorem 2.1 (Harris's inequality)**.** *We have:*
- *If B_1 and B_2 are increasing events, then $\mathbf{P}_p[B_1 \cap B_2] \geq \mathbf{P}_p[B_1]\mathbf{P}_p[B_2]$*
- *If X and Y are increasing random variables with finite second moments, then $\mathbf{E}_p[XY] \geq \mathbf{E}_p[X]\mathbf{E}_p[Y]$.*

Remark 2.1 (Harris's inequality for decreasing events)*.* A *decreasing event* is defined analogously to definition 1.5 on page 6, just with the inequality reversed. Alternatively, we can say that the event B is decreasing if $-\mathbb{1}_B$ is an increasing random variable. We can also apply Harris's inequality to decreasing events or to an increasing event and a decreasing event (in this last case the inequality is reversed). An easy way to see it to use the second point of theorem 2.1 with the (increasing) random variable $\mathbb{1}_B$ if B is increasing or $-\mathbb{1}_B$ if B is decreasing.

In the proof of the main theorem of this first section we will also need two other preliminary results. We state them as a lemma and as a proposition.

Lemma 2.1. *Fix $2 \leq r \leq d$. Then in the $(d+1)$-regular tree there are no finite $(r-1)$-forts.*

Proof. Suppose by contradiction that such a fort exists. Then each of its connected components is again an $(r-1)$-fort (this is true in general for all forts). Take one of these connected components and call it $\widetilde{T}$. As a finite connected subgraph of a tree, it is again a tree (even though it will not be regular anymore, at least in general). As can be done with all trees, select one of its vertices as root, thus giving $\widetilde{T}$ a parent-child structure. Being finite, $\widetilde{T}$ must have at least one leaf, which we denote by x. The following relations have to be true for the outdegree of v:

$$\begin{cases} \deg_{T_d \setminus \widetilde{T}}(v) = d & \text{because } T_d \text{ is } d+1\text{-regular and } v \text{ is a leaf of } \widetilde{T} \\ \deg_{T_d \setminus \widetilde{T}}(v) \leq r-1 & \text{because } \widetilde{T} \text{ if an } (r-1)\text{-fort} \end{cases}$$

which gives a contradiction! (recall that we are only considering $r \leq d$). $\square$

Let $\mathrm{GW}(d,q)$ denote the tree associated to a Galton-Watson process with offspring distribution $\mathrm{Bin}(d,q)$. The next one is a result on the probability of the existence of a k-ary subtree of $\mathrm{GW}(d,q)$ with the same root of $\mathrm{GW}(d,q)$. This will be crucial for the proof of the nontriviality of the critical probability for bootstrap percolation on trees, but it is also of independent interest.

Proposition 2.1. *Let $k \in \mathbb{N}$ with $k \geq 1$. Let $y = y(q)$ be the probability that $\mathrm{GW}(d,q)$ does not contain a k-ary subtree starting from its root. Then y is the smallest fixed point of the function*

$$x \overset{\varphi}{\mapsto} B_{d,k,q}(x) = \mathbf{P}_p\big[\mathrm{Bin}(d, q(1-x)) \leq k-1\big]$$

Proof. We denote the root by o and we consider its children. By the independence hypothesis in the definition of branching processes (see 1.13 on page 17, each of them can be considered as the root of a new Galton-Watson tree and thus has
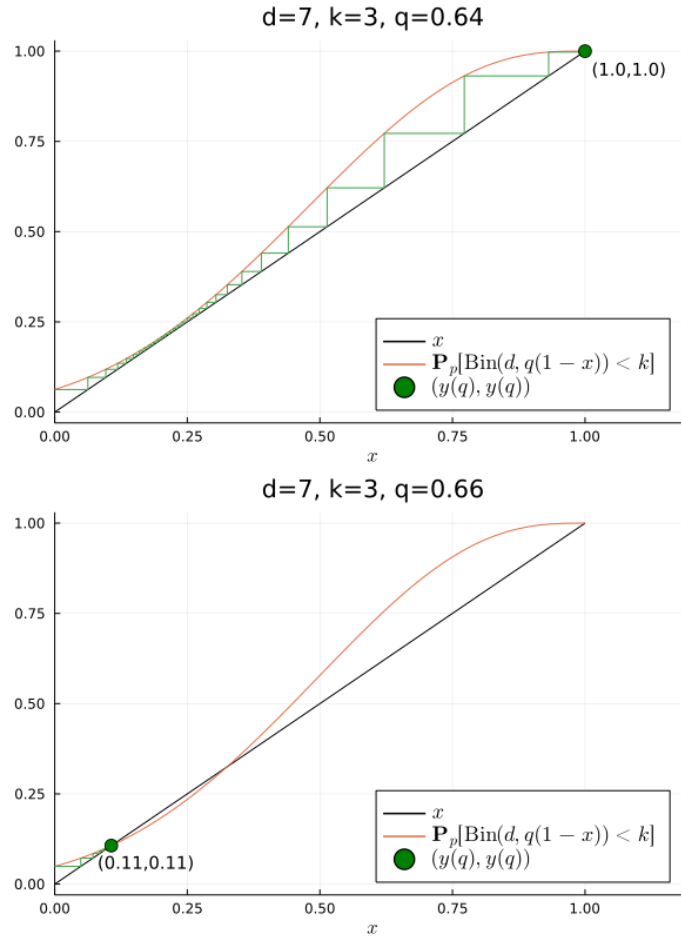
Figure 2.1: Set $d = 7$ and $k = 3$. The figure above represents the graph of the function $x \overset{\varphi}{\mapsto} B_{d,k,q}(x) = \mathbf{P}_p\big[\mathrm{Bin}(d, q(1-x)) \leq k-1\big]$ (in orange) for this choice of the parameters and for two different values of q. In both cases we have highlighted the first (going in the positive direction of the x-axis) point of intersection between the graph of φ and the bisector of the I and IV quadrant: this is exactly the point whose coordinates are the smallest fixed point of φ in $[0, 1]$. Notice how in the first graph the only fixed point is 1, whereas in the second graph we have three different fixed points. The green line represents the sequence $(y_n)_{n \geq 0}$ used in the proof. From the figure we can deduce that a.s. there is no 3-ary tree in $\mathrm{GW}(7, 0.64)$ and that the probability of finding a 3-ary tree in $\mathrm{GW}(7, 0.66)$ is approximately $1 - 0.11 = 0.89$. Finaly, observe what a great qualitative difference is caused by such a small change in the parameter q!

probability $1 - y$ to be the root of a k-ary subtree. The event $B_1 = \{o$ is not the root of a k-ary tree rooted at $o\}$ coincides exactly with the event $B_2 = \{$at most $k - 1$ children of o are root of a k-ary subtree$\}$, so that we have

$$y = \mathbf{P}_p[B_1] = \mathbf{P}_p[B_2] = \sum_{j=0}^{k-1} \binom{d}{j} \big(q(1-y)\big)^j \big(1 - q(1-y)\big)^{d-j}$$

$$= \mathbf{P}_p\big[\mathrm{Bin}\big(d, q(1-y)\big) \leq k-1\big] \tag{2.1}$$

where the first equality comes from the definition of y, the second one from the fact that B_1 and B_2 are in fact the same event and in the third one we are summing the probabilities of o having exactly j children which are root of a k-ary subtree, with j at most $k-1$. Indeed, in order for a children of o to be itself a root of a k-ary subtree, first of all it must exist as a children, which happens with probability q and then it must satisfy the said property, which happens with probability $1-y$. (A binomial distribution $\text{Bin}(d,q)$ can be seen as the sum of d i.i.d. $\text{Ber}(q)$-distributed random variables, so that if $\text{Bin}(d,q)$ represents the number of child, $\text{Ber}(q)$ represents the existence of a single child). Moreover, in $[0,1]$ we always have the fixed point 1. Thus y really is a fixed point of $x \mapsto B_{d,k,q}(x)$.

Now we want to show that y is the smallest such fixed point. Let $(y_n)_{n \geq 0}$ be the sequence where y_n is the probability that $\text{GW}(d,q)$ does not contain a k-ary subtree of height n rooted at the same root o. Then the same reasoning as above shows that $y_n = B_{d,k,q}(y_{n-1})$. In other words, $(y_n)_{n \geq 0}$ can be viewed as a one dimensional discrete dynamical system starting from the initial condition $y_0 = 0$ and with dynamics given by the function $B_{d,k,q} \colon [0,1] \to [0,1]$. It is clear that $B_{d,k,q} \in C^1$ and the direct calculation

$$\frac{\partial}{\partial x} B_{d,k,q}(x) = dq \, \mathbf{P}_p \big[\text{Bin}\big(d-1, q(1-x)\big) = k-1 \big] > 0 \quad \text{if } x \in \,]0,1[$$

shows that $B_{d,k,q}$ is also increasing. Moreover $B_{d,k,q}(y_0) > 0$ and thus by a classical elementary result $(y_n)_{n \geq 0}$ is increasing and converges either to the smallest fixed point of $B_{d,k,q}$ greater than y_0 or to the upper endpoint of the interval, i.e. 1 (see figure 2.1 on the previous page). The fact that y is the smallest fixed point in the *whole* domain $[0,1[$ comes immediately from the fact that $(y_n)_{n \geq 0}$ starts exactly from the lower endpoint of the interval. $\qquad \square$

References Harris's inequality is a classical tool which can be found in many textbooks. A statement with full proof can be found for example in [LP17], to which we also refer for proposition 2.1 on page 20 (in fact [LP17] contains a generalization of it, see section 5.7).

2.1.2 Nontrivial critical probability for full infection

We are now ready to prove the nontriviality of the critical probability for full infection on trees.

Theorem 2.2. *For every $2 \leq r \leq d$, bootstrap percolation with facilitating parameter r on the $d+1$-regular tree has nontrivial critical probability.*

Proof. We start by considering an $(r-1)$-fort of the tree. By lemma 2.1 on page 20 we know that it must be infinite. Moreover, it contains a $(d+2-r)$-regular subtree, because by definition every vertex in the fort is incident to at least $(d+1) - (r-1) = d+2-r$ other vertices in the fort. Hence we can rephrase proposition 1.1 on page 4 as "failure of complete infection for bootstrap

percolation with facilitating parameter r on the $d+1$-regular tree is equivalent to the existence of a $(d+2-r)$-regular subtree of healthy vertices in the initial configuration". In the following we denote such a subtree with $\widetilde{T}$.

Then, we observe that regular trees are graphs which satisfy the $0-1$ law for bootstrap percolation with facilitating parameter r (in the sense of definition 1.9 on page 8), because the hypothesis of lemma 1.1 on page 8 are clearly satisfied. Thus having failure of complete infection with probability 1 is equivalent to having failure of complete infection with positive probability and thus equivalent to

$$\mathbf{P}_p\big[\{\exists\, o \in V(T_d) : o \text{ is the root of } \widetilde{T} \text{ for some } \widetilde{T} \text{ as defined above}\}\big] > 0 \quad (2.2)$$

(clearly the event that there exist a vertex which is the root of some $\widetilde{T}$ and the event that some $\widetilde{T}$ exists are the same). Note that with this reasoning we have come to a question about Bernoulli percolation on trees, since we are now interested in an event that only concerns the initial configuration. This will allow us to ignore the bootstrap dynamics, which is usually cause of difficulties.

In order to study 2.2, we reformulate it again in an equivalent way (the usefulness of which will be explained shortly afterwards). We consider a new graph $\bar{T}$, which is, by definition, a d-ary tree with a fixed healthy root. Then 2.2 is equivalent to:

$$\mathbf{P}_p\big[\bar{T} \text{ contains a } (d+1-r)\text{-ary subtree made of} \quad\quad (2.3)$$
$$\text{healthy vertices and starting from the same root of } \bar{T}\,\big] > 0$$

Proving that 2.2 implies 2.3 is easy. Indeed it suffices to consider $\bar{T}$ as a subgraph of T_d with o as its root, where o is one of the vertices for which the event in 2.2 happens. Let us explain why in detail. If o is connected only to healthy sites, remove from T_d one edge incident to o (it does not matter which one). If o is connected to at least one infected vertex, remove from T_d one of the edges between o and an infected vertex. Now consider the connected component of o in this new graph. It is a d-ary tree (because we have only cut a vertex in T_d incident to o) which contains a $d+2-r$-regular subtree rooted at o and made of only healthy sites (because we add this healthy subtree before the cutting of the edge and we have been careful not to cut an edge connected to a healthy vertex). Thus, in particular, it is a $\bar{T}$ for which 2.3 holds. Viceversa, assume that 2.3 holds. Fix an healthy vertex o. Consider first a d-ary tree $\bar{T}^1$ rooted at o and defined as the connected component containing o of the graph obtained from T_d after having removed one of the edges of T_d connecting o to one of its healthy neighbours (if o has an empty neighbour, otherwise simply remove an(y) edge). Then consider another d-ary tree $\bar{T}^2$, again rooted at o, defined exactly in the same way. This means that we could have $T^1 = T^2$ (if we remove the same edge in both definitions) or $T^1 \neq T^2$ (if we remove different edges). In figure 2.2 on the following page) we have removed different edges (careful: this implies that both of those edges are incident to healthy neighbours of o!). Define the events:

for $i \in \{0, 1\}$ $B_i := \{\bar{T}^i \text{ has a } (d+1-r)\text{-ary subtree made of healthy}$
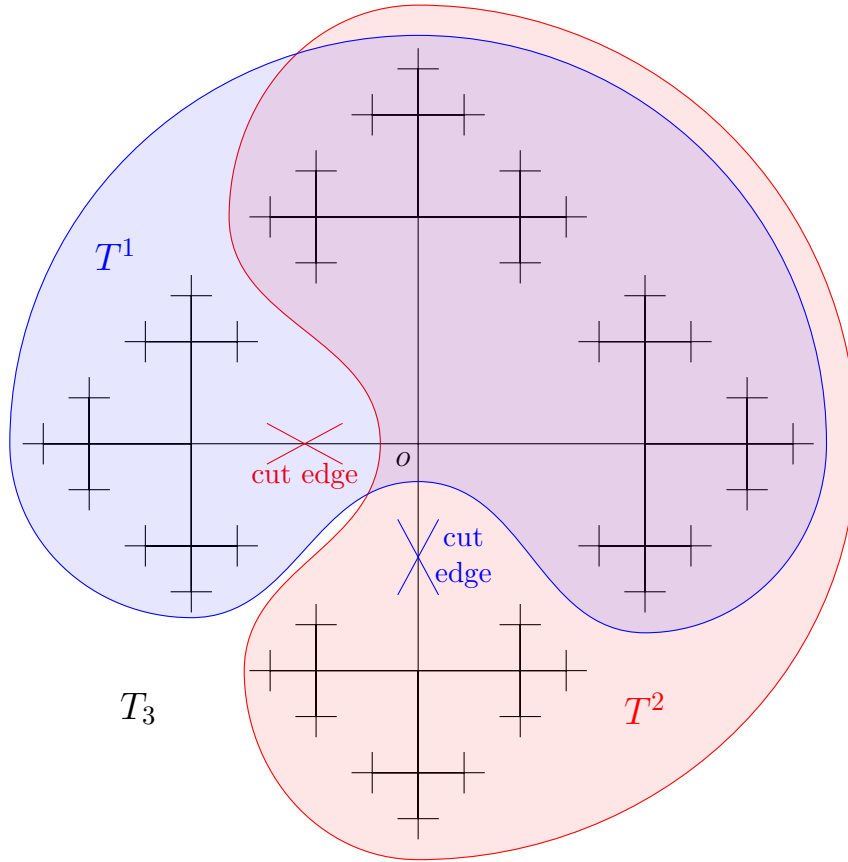$$\text{vertices and starting from the same root of } \bar{T}^i\,\}$$

Figure 2.2: Construction of the trees T^1 and T^2 on the 4-regular tree T_3. Since here the condition $2 \leq r \leq d$ means $r \in \{2, 3\}$, we obtain that if $r = 2$ (respectively $r = 3$), 2.3 on the preceding page means that both T^1 and T^2 contain a $(3 + 1 - 2) = 2$-ary (respectively a $(3 + 1 - 3) = 1$-ary) subtree with positive probability.

We observe that they are decreasing, because for every $i \in \{0, 1\}$, if $\eta \in B_i$ and $\eta' \leq \eta$, then also $\eta' \in B_i$: if a certain configuration realizes B_i, then the same configuration in which some infected vertices are replaced by healthy vertices surely realizes B_i too. Finally, denoting with B the event of 2.2 on the previous page, we have:

$$\mathbf{P}_p[B] = \mathbf{P}_p[B_1 \cap B_2] \geq \mathbf{P}_p[B_1]\mathbf{P}_p[B_2] > 0 \qquad (2.4)$$

where the first equality holds by construction, the first inequality is a consequence of Harris' inequality (see remark 2.1 on page 20) and finally the second inequality holds because we are assuming 2.3 on the previous page. The importance of constructing the trees T^1 and T^2 only by removing edges that connect o to one of its healthy neighbours (if there are any) lies in the fact that otherwise the first equality of 2.4 might not be satisfied. We have thus proved the desired equivalence.

We can now continue with the proof. As already noted, we had already reduced our initial problem to a question in Bernoulli percolation. The usefulness of working with 2.3 is that we are now considering Bernoulli percolation on a

d-ary tree instead of a d-regular tree. Clearly, this does not change the nature of the problem, but it allows a nicer expression of the connected component of healthy sites of a fixed healthy vertex o. Indeed, in this setting this is exactly a Galton-Watson tree rooted at o and with offspring distribution Binom$(d, 1 - p)$, because of the independence assumption in assigning the infected/healthy states in the initial configuration. Thus we can yet again reformulate 2.3 on page 23 in an equivalent way and state that having failure of complete infection for bootstrap percolation with facilitating parameter r on the $d + 1$ regular tree with probability one is equivalent to the existence of a $(d + 1 - r)$-ary subtree in a GW$(d, 1 - p)$ with positive probability. But we have already solved this problem in 2.1 on page 20! Substituting the values $q = (1 - p)$ and $k = (d + 1 - r)$ in 2.1 on page 20 and summing up the content of this proof, what we have obtained is that failure of complete infection for bootstrap percolation with facilitating parameter r on the $(d + 1)$-regular tree is equivalent to having $1 - y(p) > 0$, i.e. $y(p) < 1$, where $y = y(p)$ is the smallest fixed point of the function

$$x \mapsto B_{d,r,1-p}(x) = \mathbf{P}_p\big[\mathrm{Bin}(d, (1 - p)(1 - x)) \leq d - r\big]$$

Reformulating one last time, what we have obtained is that

$$\inf\{p : y(p) = 1\} = \inf\{p : \theta_f(p) = 1\} = p_f(T_d, r)$$

which concludes the proof. $\qquad\square$

We have seen how on regular graphs the model with facilitating and with blocking parameter are in fact the same model. Thus one expects the above result to also hold in the case of bootstrap percolation with blocking parameter. This is what we check in the following corollary.

Corollary 2.1. *On the $d + 1$-regular tree, the critical probability for the model with blocking paramter m is nontrivial for all $2 \leq m \leq d$.*

Proof. Since we are on a $(d + 1)$-regular graph, recalling subsection 1.1.3 on page 9 we have $\bar{p}_f(G, m) = 1 - p_f(G, d + 1 - m + 1)$, so that $\bar{p}_f(G, m)$ is nontrivial if and only if $p_f(G, d + 1 - m + 1)$ is nontrivial. By the above theorem, this happens if and only if $2 \leq d + 2 - m \leq d$, namely if and only if $2 \leq m \leq d$. $\qquad\square$

References The proof presented in this section is the one that appears in [BPP06]. We have allowed ourselves to expand quite a bit the explanations of the various steps, e.g. in the original work it was not explained how to use Harris's inequality. In [FS08] another proof is presented, which uses oriented trees. This oriented setting is the same which is used to study the critical probability for percolation and we are going to present it in the next section.

2.2 Critical probability for percolation

We dedicate this section to the study of another one of the critical probabilities that we have defined in the first chapter: the critical probability for percolation. In

other words, we study for which values of p and r (if any) we have $0 < p_c(T_d, r) < p_f(T_d, r)$, following [FS08]. We will only present one of the main ideas of this work, which nonetheless makes very clear why the tree structure (and the additional orientation that we are soon going to put on it) is crucial.

Differently from what done in the rest of the thesis, in this subsection we consider boostrap percolation on an *oriented* graph. Accordingly, we will also need to change the definition of the process: we need to consider an oriented dynamics.

We start by orienting the tree T_d in such a way that from any given vertex x there are exactly d outgoing edges and exactly one incoming edge. We will denote the tree oriented in this way by $\overrightarrow{T_d}$. In this new setting, we define the *oriented neighbours* of a given vertex $x \in V = V(T_d) = V(\overrightarrow{T_d})$ as the elements of the set $\overrightarrow{\mathcal{N}_x} := \{ y \in V :$ there exists an oriented edge from x to $y \}$. In particular, in $\overrightarrow{T_d}$ we will always have $|\overrightarrow{\mathcal{N}_x}| = d$.

We then define *oriented bootstrap percolation* with facilitating parameter r in an analogous way to what already done for the nonoriented process. The initial configuration is the same, i.e. $\eta_0 = \overrightarrow{\eta_0}$ is again sampled under a Bernoulli product measure with parameter p. As for the *oriented dynamics* we set:

$$\forall n = 1, 2, \ldots \quad \overrightarrow{\eta_{n+1}}(x) = \begin{cases} 1, & \text{if } \overrightarrow{\eta_n}(x) = 1 \\ 1, & \text{if } \overrightarrow{\eta_n}(x) = 0 \text{ and } \sum_{y \in \overrightarrow{\mathcal{N}_x}} \overrightarrow{\eta_n}(x) \geq r \\ 0, & \text{if } \overrightarrow{\eta_n}(x) = 0 \text{ and } \sum_{y \in \overrightarrow{\mathcal{N}_x}} \overrightarrow{\eta_n}(x) < r \end{cases} \quad (2.5)$$

namely, we have simply replaced the terms η_n and $\mathcal{N}_x$ in definition 1.1 on page 2 with their oriented counterparts. Again by substituting a symbol with itself surmounted by an arrow, we obtain the definitions for the oriented critical probabilities for full infection and for percolation respectively:

$$\overrightarrow{p_f}(T_d, r) := \inf \left\{ p : \overrightarrow{\theta_f}(p) > 0 \right\} \qquad \overrightarrow{p_c}(T_d, r) := \inf \left\{ p : \overrightarrow{\theta_c}(p) > 0 \right\} \quad (2.6)$$

where

$$\overrightarrow{\theta_f}(p) := \mathbf{P}_p \big[\overrightarrow{\eta_\infty} \equiv 1 \big] \qquad \overrightarrow{\theta_c}(p) := \mathbf{P}_p \big[\exists x \in V : |\overrightarrow{\mathcal{C}_x}| = \infty \big]$$

By the symbol $\overrightarrow{\mathcal{C}_x}$ we denote the connected component containing x of the subgraph of $\overrightarrow{T_d}$ obtained by considering the vertices $\{ y \in T_d : \overrightarrow{\eta_\infty}(y) = 1 \}$ (and the oriented edges between them of course). In other words, $\overrightarrow{\mathcal{C}_x}$ is the cluster of infected sites containing x in the final configuration $\overrightarrow{\eta_\infty}$. We have the analogous definition for $\mathcal{C}_x$.

It is known from [FS08] that $p_f = \overrightarrow{p_f}$ (more on this in the paragraph on references at the end of the subsection).

As we have already remarked, bootstrap percolation can be thought of as a generalization of bernoulli site percolation. One could also say "knowing" bernoulli site percolation, the missing piece in order to understand bootstrap percolation is to "know" how the infection spreads from the set of initially infected sites. In oder words, we would like to understand which sites start as healthy and become infected. This is the motivation behind the following classification:

Definition 2.1. Let $(\eta_n)_{n\geq 0}$ be a given oriented bootstrap percolation process with facilitating parameter r. Then we define $\xi \in \{1, \overline{0}, \underline{0}\}^V$ in the following way:

$$\xi(x) := \begin{cases} 1 & \text{if } x \text{ is } \textit{initally infected}, \text{ i.e. } \overrightarrow{\eta_0}(x) = 1 \\ \underline{0} & \text{if } x \text{ is } \textit{weakly healthy}, \text{ i.e. } \overrightarrow{\eta_0}(x) = 0 \text{ and } \overrightarrow{\eta_\infty}(x) = 1 \\ \overline{0} & \text{if } x \text{ is } \textit{strongly healthy}, \text{ i.e. } \overrightarrow{\eta_0}(x) = 0 \end{cases} \quad (2.7)$$

Before proceding, we also set up another piece of notation:

- $\overrightarrow{p_\infty} := \mathbf{E}_p[\overrightarrow{\eta_\infty}(x)]$, for an $x \in V$ is the *final density of infected sites* (obviously this definition does not depend on x);
- $\overrightarrow{q_\infty} := 1 - \overrightarrow{p_\infty}$ is the *final density of healthy sites*;
- $\overrightarrow{r_\infty} := \overrightarrow{p_\infty} - p$ is the *density of weakly healthy sites*.

The proof of 2.2 on page 22 in the previous section essentially came down to finding an appropriate branching process, which happened to be a certain cluster of initially healthy sites, and use it to study the presence of an $(r-1)$-fort. In some sense, this is also what will be done in this section, albeit with weakly healthy sites.

First of all, for a given $x \in V$, we set

$$\begin{pmatrix} O_x \\ W_x \\ S_x \end{pmatrix} := \begin{pmatrix} \text{\# of initially infected neighbours of } x \\ \text{\# of weakly vacant neighbours of } x \\ \text{\# of strongly vacant neighbours of } x \end{pmatrix} = \begin{pmatrix} \sum_{y \in \overrightarrow{\mathcal{N}_x}} \mathbb{1}_{\{\xi(y)=1\}} \\ \sum_{y \in \overrightarrow{\mathcal{N}_x}} \mathbb{1}_{\{\xi(y)=\underline{0}\}} \\ \sum_{y \in \overrightarrow{\mathcal{N}_x}} \mathbb{1}_{\{\xi(y)=\overline{0}\}} \end{pmatrix}$$

Lemma 2.2. *The distribution of* (O_x, W_x, S_x) *is trinomial with d as parameter for the number of trials and $p, \overrightarrow{r_\infty}, \overrightarrow{q_\infty}$ as parameters for the probabilities of being initially infected, weakly healthy and strongly healthy respectively, i.e.*

$$\mathbf{P}_p[O_x = i, W_x = j, S_x = k] = \frac{d!}{i!\,j!\,k!}\, p^i\, (\overrightarrow{r_\infty})^j\, (\overrightarrow{q_\infty})^k$$

for all $i, j, k \in \{1, \ldots d\}$ such that $i + j + k = d$ and 0 otherwise.

Proof. The choice for the parameters for the probabilities is clear. The structure of a trinomial distribution, instead, comes from the fact that the random variables $\{\xi(y) : y \in \overrightarrow{\mathcal{N}_x}\}$ are indipendent. Indeed, the value of $\xi(y)$ can only be influenced by the values of the sites belonging to the (oriened) branch of $\overrightarrow{T_d}$ which has y as root and cleary if $y_1, y_2 \in \overrightarrow{\mathcal{N}_x}\}$ are distinct, then their respective subtrees are disjoint. $\qquad\square$

Remark 2.2. The above preposition is the first time we get to see why orienting the tree is so useful for our analysis: on a nonoriented tree $\{\xi(y) : y \in \mathcal{N}_x\}$ would not be indipendent, since the value of one $\xi(y)$ could infuence the one of $\xi(x)$, which is relevant for the values of all the $\xi(y)$'s.

We then define $\mathcal{W}_x$ to be the cluster of weakly healthy sites containing x, with the understanding that $\mathcal{W}_x = \emptyset$ if $\xi(x) \neq \underline{0}$. The following holds:

Proposition 2.2. *The set $\mathcal{W}_x$ is either:*
- *empty, with probability $1 - \overrightarrow{r_\infty}$*
- *the set of the vertices of a Galton-Watson tree, with probability $\overrightarrow{r_\infty}$*

In the second case, the offspring distribution of the Galton Watson tree is the condition distribution of W_x given $S_x < d - r$.

Proof. The first point is immediate. Thus assume that we are in the case $\mathcal{W}_x \neq \emptyset$, i.e. we condition on the event $\{\xi(x) = \underline{0}\}$. But we also have that $\{\xi(x) = \underline{0}\} = \{\eta_0(x) = 0\} \cap \{S_x \leq d - r\}$, because a healthy vertex in the initial configuration becomes infected (at a certain point) if and only if in the final configuration its infected (oriented) neighbours are at least r (by the definition of oriented bootstrap dynamics with facilitating parameter r). Equivalently, no more than $d - r$ neighbours are still healthy in the final configuration, i.e. no more than $d - r$ neighbours are strongly healthy. This proves that the first generation of the branching process really has the desired distribution. For the successive generations we can repeat the argument just presented because of the indipendence guaranteed by the orientation, which has already been explained in the proof of 2.2 on the preceding page and in remark 2.2 on the previous page. $\square$

As nice as this result is, it is not enough for us. Indeed, we are interested in percolation of infected sites in the final configuration and not in percolation of weakly healthy sites. Of course the two phenomena are different, because *both* weakly healthy sites and initially infected sites concur in percolation of infected sites in $\overrightarrow{\eta_\infty}$. Surprisingly enough, once again a branching process comes up! Of course it is not the one described just above, and to construct we need a new definition:

Definition 2.2. Let $x \in V$ be a fixed given vertex of the tree. The *local cluster of infected vertices* of x in $\overrightarrow{\eta_\infty}$, denoted by $\mathcal{L}_x$, and the *boundary of initially infected vertices* of $\mathcal{L}_x$, denoted by $\mathcal{O}_x$, are defined as follows:
- if $\xi(x) = \overline{0}$, then $\mathcal{L}_x := \mathcal{O}_x = \emptyset$;
- if $\xi(x) = 1$, then $\mathcal{L}_x := \mathcal{O}_x := \{1\}$;
- if $\xi(x) = \underline{0}$, then $\mathcal{O}_x := \{y \in V \backslash \mathcal{W}_x : y \in \overrightarrow{\mathcal{N}_z}$ for some $z \in \mathcal{W}_x$ and $\xi(y) = 1\}$ and $\mathcal{L}_x := \mathcal{W}_x \cup \mathcal{O}_x$.

With this new notion, we are able to describe the *whole* connected component of infected sites containing x in the final configuration, which we denote by $\overrightarrow{C_\infty}$, as follows:

$$
\begin{array}{llll}
\text{if} \quad C_0 := \mathcal{L}_x & O_0 := \mathcal{O}_x & & \\
C_{n+1} := \bigcup_{y \in O_n} \bigcup_{z \in \overrightarrow{\mathcal{N}_y}} \mathcal{L}_z & O_{n+1} := \bigcup_{y \in O_n} \bigcup_{z \in \overrightarrow{\mathcal{N}_y}} \mathcal{O}_z & \text{then} & \overrightarrow{C_\infty} = \bigcup_{n \geq 0} C_n
\end{array}
$$

The construction of the sets $(C_n)_{n \geq 0}$ and $(O_n)_{n \geq 0}$ is represented in figure 2.3 on the facing page, which also makes clear why the representation of $\overrightarrow{C_\infty}$ through the sets C_n is correct.
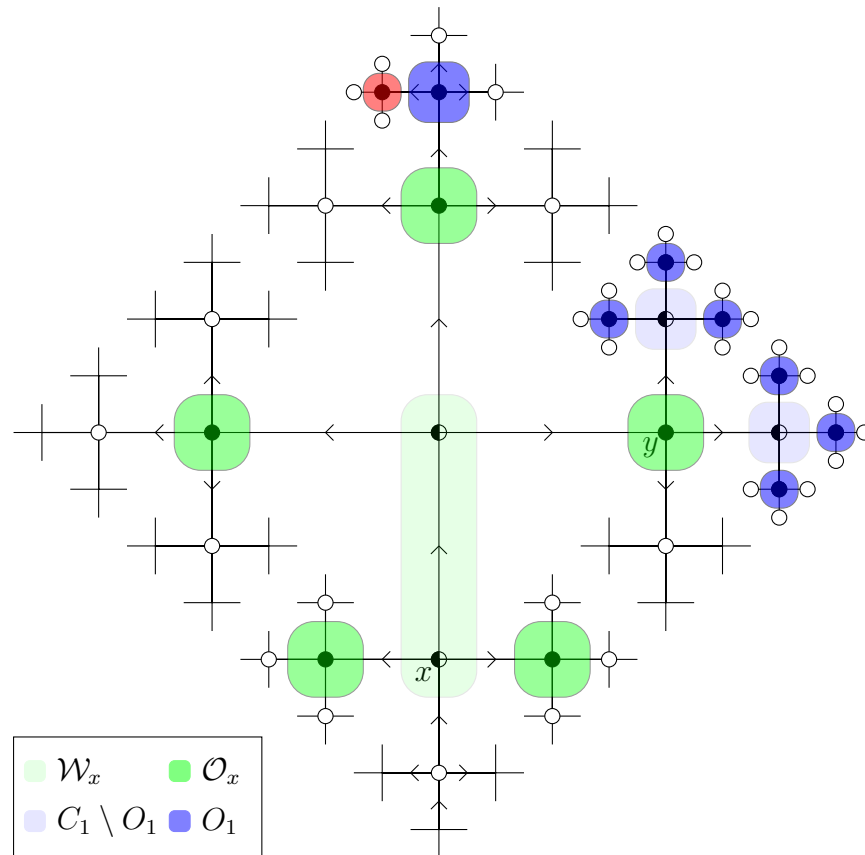
Figure 2.3: Cluster of infected vertices of x for oriented bootstrap percolation on the 4-regular tree T_3 (e.g. with facilitating parameter $r = 2$). All of the edges are oriented, but we have drawn only some of the arrows for greater clarity of the picture. Black dots, white dots and half white/half black dots represent, respectively, initially infected, strongly healthy and weakly healthy sites. Vertices which are in the less opaque green region are the ones of $O_0 = \mathcal{O}_x$. Vertices in *any* green region are the ones of C_0. Analogously, vertices in the less opaque blue region are the ones of O_1, whereas vertices in *any* blue region are the ones of C_1. The only vertex in the only red region is the only element of $O_2 = C_2$. For every $n \geq 3$ we have $O_3 = C_3 = \emptyset$. Finally, the *whole* cluster of infected vertices of x in the final configuration is the set of all vertices which are in a green, blue or red region. Sites which we have left empty are the ones whose state we do not care about: they are not relevant for the cluster of infected vertices of x. In this case the cluster is finite, i.e. the branching process of proposition 2.3 does not survive.

Remark 2.3. Strictly speaking, everything we have described above depends on the chosen vertex x. However, by the regularity of the tree, it is clear that the quantities that we have just defined "behave in the same way" no matter which is the vertex that we have chosen. For example, the distribution of the number of vertices in the local cluster of infected vertices of x, i.e. the distribution of $|O_x|$, is the same for every $x \in V$.

Proposition 2.3. *The sets in the sequence $(O_n)_{n \geq 0}$ contain the members of successive generations of a branching process with initial distribution given by $|\mathcal{O}_x|$ and offspring distribution given by the sum of d i.i.d. copies of $|\mathcal{O}_x|$. In particular, $|\overrightarrow{C_\infty}| = \infty$ if and only if this branching process survives.*

Proof. We do the proof by looking at figure 2.3, but this is just to fix ideas and it is clear that what we are saying holds in the general case. Consider the vertex x: it represents the root of the branching process. That the first generation has distribution $|\mathcal{O}_x|$ is by definition, since we have defined the elements of the first generation of the branching process exactly as the elements of $\mathcal{O}_x$.

Now we have to check that offspring distribution is the one of the statement. In order to do so, we have to describe what is the distribution of every element of the first generation, i.e. what is the distribution of every vertex in the more opaque green region. By definition, each of this vertices will have as descendants all of the vertices in O_z for each one of their oriented neighbours x. For example, consider y in the figure and denote by $\{z_1, z_2, z_2\}$ its three oriented neighbours. One of them, say z_1, has an empty boundary of initially infected vertices, i.e. $\mathcal{O}_{z_1} = \emptyset$, whereas each of the other two has a boundary of initially infected vertices containing three elements. Thus in the figure the descendants of y are the six vertex in the more opaque blue region. Their number is distributed as $|\mathcal{O}_{z_1}| + |\mathcal{O}_{z_2}| + |\mathcal{O}_{z_3}|$. However, consider the subtrees of T_3 obtained by choosing the connected component containing z_i of the graph T_3 with the edges (y, z_i) removed. By the choice of the orientation, the states of the vertices in each of these subtree are indipendent by the state of the vertex y (and they are also indipendent of the vertices not in their connected component). This means that the random variables $|\mathcal{O}_{z_1}|$ are indipendent. Moreover, by remark 2.3 on the previous page, they are also identically distributed and with the same distribution of the cardinality of the boundary of initially infected vertices of x. Summing up, we have obtained that $|\mathcal{O}_{z_1}| + |\mathcal{O}_{z_2}| + |\mathcal{O}_{z_3}| = d |\mathcal{O}_x|$ in distribution, which is what we wanted.

The last part of the proposition follows immediately by construction: $\overrightarrow{C_\infty}$ is exactly the whole connected component of infected vertices of x.   □

The article [FS08] goes on computing explicitly $\mathbf{E}_p[\mathcal{O}_x]$, since this is the crucial quantity from which the extinction of the branching process depends (as we have recalled in chapter one). This, together with some other arguments based on some other results which hold in general for every branching process, allows one to prove theorem 2.3 below. In this theorem we have also added a result from the second part of [FS08], the one in which the results obtained for oriented trees are carried over to nonoriented trees.

Theorem 2.3. *Let $2 \leq r \leq (d-1)$. Then the critical probability for percolation is nontrivial for both the oriented and non oriented model. More precisely, we have:*

$$0 < \overrightarrow{p_c}(T_d, r) < p_f(T_d, r) \quad and \quad 0 < p_c(T_d, r) < \overrightarrow{p_c}(T_d, r)$$

In particular, it is interesting to note that the critical probabilities for percolation in the oriented and nonoriented case are different, whereas the critical probabilities for full infection in the two cases coincide.

Let us make one final remark, for more details on which we refer again to the usual article of this section. For some values of d and r, the infinite clusters of infected sites that can be observed in the regime between p_c and p_f are not presente in the initial configuration. This means that there are cases in which the bootstrap dynamics, albeit not able to fully infect the graph, is still capable to "grow" infinite clusters.

References The results of this subsection are taken from [FS08]. As usual, we have indulged in writing out explicitly all of the details of what we have decided to present. Note that this article also uses oriented trees also to provide an alternative proof of the nontriviality of the critical probability for full infection.

Chapter 3

Bootstrap percolation on hyperbolic lattices

In this last chapter we study bootstrap percolation on hyperbolic lattices, a particular class of regular graphs embedded in the hyperbolic plane. After a rigorous definition, we give an idea and precise references of how it is possible to embed a specific kind of tree into them. Then we study the critical probability for full infection: first by means of general results, which hold for a larger class or nonamenable graphs, and then by means of the inequalities proved in chapter one, exploiting the aforementioned embedding. We conclude with a few words on p_c and p_u.

3.1 Hyperbolic Lattices

Before defining hyperbolic lattices, we spend a few words on the hyperbolic plane, mainly to describe which of its many models we have chosen to use and to recall some classical results that we will need later on.

3.1.1 Hyperbolic plane

The hyperbolic plane is an example (arguably one of the most important) of non-Euclidean geometry. We define it as the differentiable manifold with base set $\mathbb{D} := \{z \in \mathbb{C} : |z| < 1\}$, obvious topology and charts (the ones induced by $\mathbb{R}^2$) and equipped with the Riemannian metric

$$ds^2 = 4\frac{dx^2 + dy^2}{(1 - x^2 - y^2)^2} \qquad \text{where } z = x + iy$$

This is also known as the *Poincaré disk* model. Let us make a list of how the basic geometric objects are represented in this model:

- *points* are the elements of the set $\mathbb{D}$, the open unit disk of the Euclidean plane;
- *"points at infinity"* are the elements of the set $\partial\mathbb{D} := \{z \in \mathbb{C} : |z| = 1\}$
- *lines* are the diameters of $\mathbb{D}$ and the intersection with $\mathbb{D}$ of circles in $\mathbb{C}$;

- the *angle* between two lines meeting at a point is the Euclidean angle between the tangents (in the Euclidean sense) to their support.

These are all classical results, with many proofs. For instance, they can be derived analitically from the definition of the metric (as it is also the case for the other results presented just below). The last point in particular is the main advantage of this model over the other possible ones. Indeed, it is the right feature to highlight the symmetry of hyperbolic lattices, as shown in the pictures of this chapter. We will need a few other reminders:

- the *hyperbolic reflection* of the point M in a line l is represented by the reflection of M in the circle whose support is l (in the usual sense in $\mathbb{C}$ and considering straight lines as circles of infinite radius);
- *hyperbolic circles* in $\mathbb{D}$ are drawn as Euclidean circles contained in $\mathbb{D}$, but (careful!) the hyperbolic center of a hyperbolic circle does not coincide with the one of the Euclidean circle which represent it;
- a *horocycle* is a curve whose normal (or perpendicular) geodesics all converge asymptotically in the same direction (in the Euclidean plane there is analog of such a curve); in the Poincaré disk model it is represented by a circle contained in the disk which touches its boundary, see figure 3.1 (of course the point where it touches the boundary circle is not part of the horocycle, since it is not even a point of $\mathbb{D}$: it is point at infinity, as defined above; nevertheless it can be thought of the hyperbolic center of the horocycle).
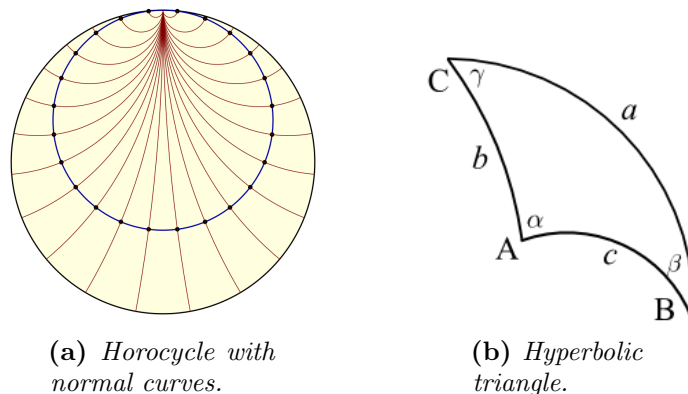

(a) *Horocycle with normal curves.*

(b) *Hyperbolic triangle.*

Figure 3.1: **(a)** An horocycle (in blue) and some of its normal geodesics (in red). Incidentally, it can also be observed that the representation of the geodesics (i.e. lines) are really represented in the way we have described above. [Image by Claudio Rocchini, Wikipedia] **(b)** Simply an hyperbolic triangle.

A whole theory of hyperbolic trigonometry can be developed, but we will need in particular the following formula, for which figure 3.1 sets the notation:

$$\cosh(a) = \frac{\cos(\beta)\cos(\gamma) + \cos(\alpha)}{\sin(\beta)\sin(\gamma)} \tag{3.1}$$

References   Of course there is a *lot* of literature on the hyperbolic plane. We mention [Can+97] as a quick and modern introduction (with good bibliography)

and [Nee97] for an intuitive approach. An axiomatic treatment can also be found
at the beginning of [Mar07], to which we refer a lot in the next few subsections.

3.1.2 Regular tilings of the plane

There are different ways of constructing hyperbolic lattices. We choose a construc-
tive approach, which we start to develop by defining tilings more in general (i.e.
not necessarily in the hyperbolic space). Let us introduce some notation:
- $\mathcal{S}(Q) = \{$lines that support the edges of $Q\}$, where Q is a polygon;
- $\mathcal{S}(\mathcal{E}) := \bigcup_{Q \in \mathcal{E}} \mathcal{S}(Q)$, where $\mathcal{E}$ is a set of polygons;
- $\rho_{\mathcal{K}}(\mathcal{E}) := \bigcup_{k \in \mathcal{K},\, Q \in \mathcal{E}} \rho_k(Q)$, where $\mathcal{K}$ is a set of lines and ρ_k is the reflection
  map through the line $k \in \mathcal{K}$.

Definition 3.1. Let P be a convex polygon and inductively define $(\mathcal{T}_k)_{k \geq 1}$ by
setting $\mathcal{T}_0 := \{P\}$ and $\mathcal{T}_{k+1} := \rho_{\mathcal{S}(\mathcal{T}_k)}(\mathcal{T}_k)$. We call $\mathcal{T}^* := \bigcup_{k=0}^{\infty} \mathcal{T}_k$ the *tessellation*
or the *tiling* generated by P if:
- every point of the plane belongs to at least one polygon in $\mathcal{T}^*$;
- the interiors of the elements of $\mathcal{T}^*$ are pairwise disjoint.

A tiling (or tessellation) is said to be *regular* if the starting polygon P is regular,
i.e. if P is equilateral and equiangular. We will denote a regular tiling by the
symbol $\mathscr{H}(v, f)$, where f is the number of edges of P and v is the number of
polygons around each vertex of P.

Remark 3.1. Observe that the above definition is indipendent of the geometry that
we consider, in the sense that $\mathcal{T}^*$ can be constructed using lines and reflections of
any given geometry of the plane.

Example 3.1 (Regular tilings of the Euclidean plane)**.** In the Euclidean plane
there are essentially only three possible regular tilings (with "essentially" we mean
that every possible tiling is obtained from one of these three through an isometry).
Let us prove this. In the Euclidean plane, a regular polygon with f edges has
interior angles equal to $\pi - 2\frac{\pi}{f}$. Thus we can have a regular tiling with v polygons
around each vertex of P only if

$$v\,\pi\left(1 - \frac{2}{f}\right) = 2\pi \quad \Leftrightarrow \quad (f-2)(v-2) = 4$$

The only integer solutions to this equation are $(v, f) \in \{(3,6), (4,4), (6,3)\}$ and
each of them really corresponds to a regular tiling, which is respectively the
triangular, square and hexagonal lattice.

In this thesis we are interested in regular tilings of the hyperbolic plane. The
key difference with respect to Euclidean regular tilings is that in the hyperbolic
plane the interior angles of a regular polygon can assume any value α in the
interval $]0, \pi - 2\frac{\pi}{f}[$. Thus we can arrange v polygons around each vertex of P only
if

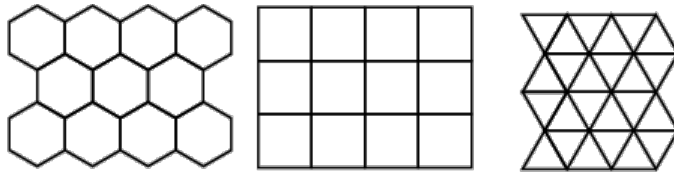$$\frac{2\pi}{v} \in \left]0, \pi\left(1 - \frac{2}{f}\right)\right[\quad \Leftrightarrow \quad \frac{2\pi}{v} < \pi\left(1 - \frac{2}{f}\right) \quad \Leftrightarrow \quad (f-2)(v-2) > 4$$

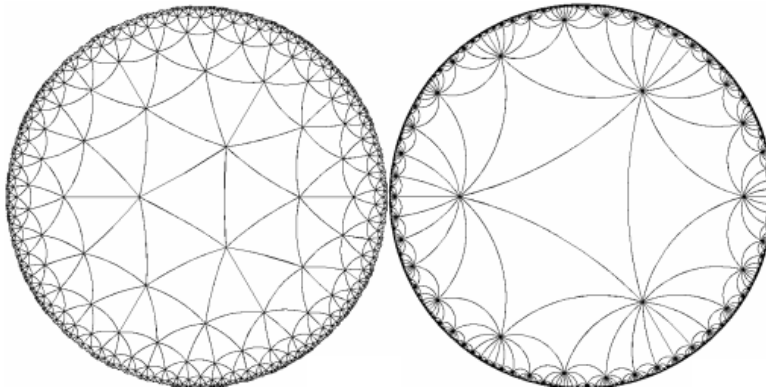**Figure 3.2:** All the possible regular tilings in the Euclidean plane. From left to right: hexagonal, square and triangular lattice.

Figure 3.3: Two regular tilings generated by taking P to be an (hyperbolic) equilateral triangle: in our notation, from left to right, they are the tiling $\mathcal{H}(7,3)$ and $\mathcal{H}(13,3)$. In particular, observe how the bigger triangle has a smaller interior angle, thus resulting in a regular tiling with a higher value of v. [Image by Tomotoshi Nishino]

This condition is also sufficient for the existence of a regular tiling. Informally, the reason is that in the hyperbolic plane the size of the regular polygon P uniquely determines the value of α (there are no homotheties of the hyperbolic plane) and moreover, as the circum-radius of P increases from 0 to $+\infty$, the value α of the interior angles decreases from $\pi\left(1 - \frac{2}{f}\right)$ to 0. It is thus possible to adjust the size of P so that the value α is exactly $\frac{2\pi}{v}$. A formal proof of what just described can be given by subdividing the polygon P into triangles and using the Poincaré theorem on tessellations generated by a triangle, as done in [Mar07]. Figure 3.3 depicts two different regular tilings of the hyperbolic plane and well explains why in the hyperbolic plane there are infinitely many distinct regular tilings.

Definition 3.2. Let f, v be such that $(f-2)(v-2) > 4$. Consider the regular tiling of the hyperbolic plane obtained by the regular polygon with f edges and with v polygons around each vertex. The *hyperbolic lattice* $\mathcal{H}(v, f)$ is the graph which has the vertices and the edges of this tiling as vertex and edge set (we committing an abuse of notation in using the same symbol for tilings). In particular that $\mathcal{H}(v, f)$ is a v-regular graph.

Recall that the *dual graph* of a plane graph G is a graph that has a vertex for each face of G, an edge for each pair of faces in G that are separated from each other by an edge and a self-loop when the same face appears on both sides of an edge.

Remark 3.2. It is immediate to see that the dual of the hyperbolic lattic $\mathscr{H}(v, f)$ is the hyperbolic lattice $\mathscr{H}(f, v)$.

References   There are different approaches to the definition of hyperbolic lattices. We have chosen to follow the one due to Margenstern, who has published a lot of papers on the topic. The book [Mar07] is a good collection and synthesis of many of them. In any case, a specific reference where one can find the definitions of tilings (or tessellation) and the Poincaré theorem is [Mar09]. Other approaches are more algebric. A complete reference is this direction is the book [CM72]. A more concise one can be found at the beginning of [RNO92]. One last remark about the notation. It seems that the prevalent one adopted outside of the statistical mechanics domain uses the Schläfli symbol $\{p, q\}$ to denote the tilings made from a regular polygons with p edges and q copies of it around every vertex. We have decided ourselves for $\mathscr{H}(v, f)$ (as in [RNO92]) in order to avoid confusion with the parameter p of the Bernoulli product measure.

3.1.3   Embedding of trees in hyperbolic lattices

In this subseciton we describe the embedding of a particular tree in the hyperbolic lattice $\mathscr{H}(v, f)$. This embedding will allow us to study bootstrap percolation on hyperbolic lattices using the results of the previous chapter.

The argument is based on the splitting method developed by Margenstern. First of all we need some definitions, which in fact hold in a much more general context than the one of regular tilings of the hyperbolic plane.

Definition 3.3. Consider finitely many sets $S_0, \ldots, S_k$ of some geometric metric space X which are supposed to be closed with non-empty interior, unbounded and simply connected. Consider also finitely many closed simply connected bounded sets $P_0, \ldots, P_h$ with $h \leq k$. We say that the S_i's and P_l's constitute a *basis of splitting* if and only if:
  - X splits into finitely many copies of S_0,
  - any S_i splits into one copy of some P_l and finitely many copies of S_j's, where copy means an isometric image, and where, in the second condition, the copies may be of different S_j's, S_i being possibly included.
It is assumed that the interiors of the copies of P_l's and the copies of the S_j's are pairwise disjoint. The set S_0 is called the *head of the basis* and the P_l's are called the *generating tiles*.

Consider a basis of splitting of X, if any. We recursively define a tree T_{split} which is associated with the basis as follows. First, we split S_0 according to the second condition of the definition. This gives us a copy of say P_0 which we call the *root* of T_{split} and which we call also the *leading tile of S_0*. In the same way, by the second condition of the definition, the splitting of each S_i provides us with a copy of some P_l which we call the *leading tile of S_i*. The splitting provides us also with k_i *regions*, $S_{i_1}, \ldots, S_{i_{k_i}}$ which enter the splitting of S_i. The regions which enter the splitting of S_0 according to the second condition of the definition are

called the regions of the generation 1. Assume that we have all the regions of generation n: $S_{n_1}, \ldots, S_{n_{m_n}}$. By definition, their leading tiles constitute the *nodes* of the generation n. We split again these S_j's according to the second condition. We obtain m_n tiles which are called the tiles of the generation $n + 1$ and, for each S_{n_h} which is some S_i, we have a splitting which is the isometric image of the splitting of S_i, as above indicated. We say that the leading tiles of these copies of the splitting of S_i are called the *sons of the leading tile* of S_{n_h}. By definition, the sons of the leading tile of S_{n_h} belong to the generation $n + 1$. The union of all the sons of the nodes of the generation n constitutes the nodes of the generation $n + 1$. This recursive process generates an infinite tree with finite branching. This tree, T_{split}, is called the *spanning tree of the splitting*, where the splitting refers to the basis of splitting $S_0, \ldots, S_k$.

In the case of hyperbolic tilings the situation is a bit easier, in the sense that we will always have only one generating tile, i.e. $h = 0$ and the unique generating tile P_0 is the polygon P of definition 3.1 on page 35. We proceed to illustrate the definition 3.3 on the preceding page of basis of splitting and the construction of its associated tree through a specific example. We consider as metric space X the hyperbolic plane and as generating tile the regular polygon P_0 with five edges and interior angles equal to π. As sets $S_0, \ldots, S_k$ we consider just two sets (i.e. k=1), namely $S_0 := \mathcal{Q}$, a quarter of the hyperbolic plane, and $S_1 := R_3$, which we will define shortly. First we split the hyperbolic plane into finitely many (four) copies of $\mathcal{Q}$, as in the first point of definition 3.3. Now we consider one of these copies and split it according to the second point of definition 3.3. This is what is depicted in figure 3.4. As "copy of some P_l" we simply obtain a copy of P_0, which
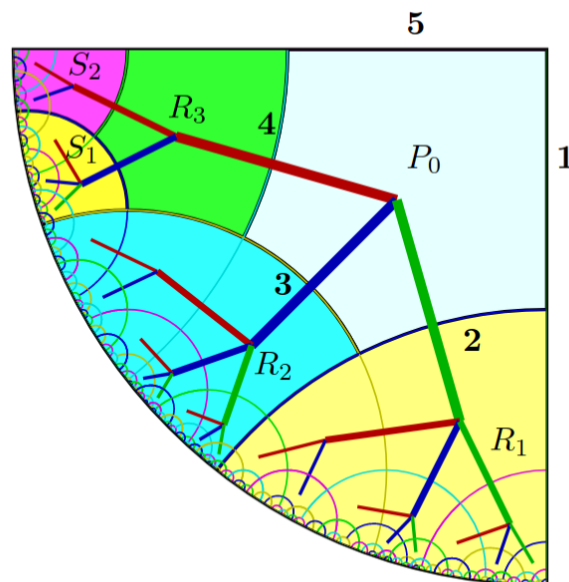

Figure 3.4: The splitting of $\mathcal{Q}$ which is associated to the pentagrid. The construction of the spanning tree is highlighted. [Image taken from [Mar06]]

constitutes the root of the tree of the splitting and the leading tile of $\mathcal{Q}$ (recall

that we have only one P_l). As "finitely many copies of S_j's" we obtain two copies of $\mathcal{Q}$ (called R_1 and R_2 in the figure) and one copy of R_3, which we define to be the complement in $\mathcal{Q}$ of $P_0 \cup R_1 \cup R_2$. It is now clear why we have chosen the letter R: sets denoted with this letter represent what we have called "regions" in the construction of the tree of the splitting (and we have just listed all of the ones in generation 1). In order to complete the description of the second point of the definition of basis of splitting, what is left to do is to describe how the region R_3 splits (for the regions R_1 and R_2 we can obviously repeat what just done, since they are copies of $\mathcal{Q}$). As leading tile it has a copy of P_0(it must have, since there is only this possibility) and as regions is has a copy of $\mathcal{Q}$ and a copy of R_3, which in the figure are called respectively S_1 and S_2. With this we have concluded the description of the two properties of the basis of the splitting and referred to the terminology used in the general construction of the tree of the splitting. In the figure one can see two further steps of the recursion by which the tree is defined.

One last definition before stating the embedding theorem:

Definition 3.4. We say that a tiling of X is *combinatoric* if it has a basis of splitting and if the spanning tree of the splitting yields exactly the restriction of the tiling to S_0, where S_0 is the head of the basis.

All hyperbolic tilings belong to the class of tilings described by the above definition, as we will see just below. In this thesis we do not really have a need to study general combinatoric tilings. We will be content to say that if a tiling is combinatoric, then it is possible to associate a polynomial to the spanning tree of the splitting and use it to study the tiling in an algorithmic way.

Theorem 3.1. *Consider the hyperbolic lattice $\mathscr{H}(v, f)$. If $f > 4$, then there exist a spanning tree of the lattice such that each vertex of the tree has degree v or $v-1$. If $f = 4$, then there exist a spanning tree of the lattice such that each vertex of the tree has degree $v-1$ or $v-2$.*

Proof. Given a certain hyperbolic lattice $\mathscr{H}(v, f)$, consider its associated tiling. Suppose that we have proved that this tiling admits a basis of splitting and is combinatoric. Then we can construct a spanning tree of the splitting and this is exactly a spanning tree of the dual graph of the initial hyperbolic lattice. In other words, we have obtained a spanning tree of the lattice $\mathscr{H}(f, v)$ (recall remark 3.2 on page 37).

Thus, in order to complete the proof, what is left to show is that every regular tiling of the hyperbolic plane admits a basis of splitting and is combinatoric. This is done by Margenstern and we refer to the paragraph at the end of this subsection for some more comments and precise references. □

Corollary 3.1. *If $f > 4$ (respectively $f = 4$), it is possible to cover every hyperbolic lattice $\mathscr{H}(v, f)$ with a collection of (possibly overlapping) embedded $(v-1)$- (respectively $(v-2)$)-trees.*

Proof. We consider a spanning tree for the lattice $\mathscr{H}(v, f)$ with $f > 4$ (respectively $f = 4$) given by theorem 3.1. It clearly contains a $(v-1)$- (respectively $(v-2)$)-regular subtree. This subtree is not spanning. By the symmetry properties of

hyperbolic lattices, for every given vertex not in this subtree there exist another spanning tree of $\mathscr{H}(v, f)$ which admits a subtree of the same regularity and that contains the given vertex. Thus we can achieve the claim with a countable collection of such subtrees.   □

References   There are several works by Margenstern which explain how to obtain a basis of splitting for the tiling $\mathscr{H}(v, f)$ (as explained in a previous "references" paragraph, what he denotes by $\{p, q\}$ what we have defined to be the tiling $\mathscr{H}(q, p)$). In the earlier papers, specific values of v and f are considered and very concretely analyzed (e.g. the penta- and the heptagrid). Depending on whether v is even or not, the ideas needed are susbstantially different. A concise summary of the case v even can be found in [Mar09], whereas [Mar07] is a more extended presentation. Both of the above references also contain proofs of the case v odd, albeit different ones. The example of the pentagrid presented here is taken from [Mar06], but it is also present in other works (always by Margenstern).

3.2   Critical probability for full infection

In this section we prove that the critical probability for full infection on hyperbolic lattices is nontrivial, except for a few specific values of the parameters r, v and f. We start by analyzing what happens when we try to apply some very general results for nonamenable graphs: this already gives some interesting results. We then proceed to a more tailored approach, based on the study of the model on trees, presented in the second chapter, which improves the aforementioned results.

Remark 3.3. Hyperbolic lattices are transitive. This follows immediately from the fact that they can be seen as the Cayley graph of a finitely generated infinite group (as shown for example in [RNO92], but also see the other references at the end of section 3.1.2 on page 35). In particular, this means that the hypotheses of lemma 1.1 on page 8 are satisfied and so hyperbolic lattices belong to the class of graphs for which all of the definitions that we have given in the first chapter are well posed.

    Let us also remark that for the remaining of this chapter we will only consider $2 \leq r \leq (v - 1)$, as already done with regular trees. Indeed, the trivial values of the facilitating parameter $r = 1$ and $r = 2$ have already been dealt with in remark 1.6 on page 12.

3.2.1   Approach for general nonamenable graphs

As announced, in this section we apply some general results to hyperbolic graphs and see what they yield. In particular, here we do not need in any way the embedding of trees described in the previous section.

Upper bound

We recall from lemma 1.5 on page 16 that we can find an upper bound for the critical probability for full infection of the bootstrap percolation model using the critical probability (for percolation) of the Bernoulli site percolation model. More precisely, in the present setting lemma 1.5 states that for any hyperbolic lattice in which there are no finite $(r-1)$-forts we have

$$p_f\big(\mathscr{H}(v,f),r\big) \leq 1 - p_c\big(\mathscr{H}(v,f)\big)$$

(recall that as usual we are only considering nontrivial values of r, i.e. $2 \leq r \leq v-1$). It is known that $p_c\big(\mathscr{H}(v,f)\big) > 0$ (see [BS01]), so we would have a nontrivial upper bound on $p_f\big(\mathscr{H}(v,f),r\big)$ if we could show that $H(v,f)$ does not have finite $(r-1)$-forts. This is exactly what the following proposition deals with.

Proposition 3.1. *On the hyperbolic lattice $\mathscr{H}(v,f)$ finite $(r-1)$-forts exist with positive probability only when $r = v-1$, for all values of (v,f), and when $r = v-2$ for $f = 3$ irrespective of the value of v. (Also here we are omitting the noninteresting cases $r = 1$ and $r = v$).*

Proof. First we prove that $(r-1)$-forts really exist for the values of the parameters of the proposition.

Fix any hyperbolic lattic $\mathscr{H}(v,f)$ and set $r = v-1$. The subset of $V = V\big(\mathscr{H}(v,f)\big)$ containing exactly the vertices of one of its elementary polygon is an $(r-1) = (v-2)$-fort: indeed, every vertex in this subset has outdegree exactly equal to $(v-2)$, thus satisfying the definition of $(v-2)$-fort. Moreover, the event "there exist one of the elementary polygons of the lattice with all healthy vertices" clearly has strictly positive probability. For the second case, fix any hyperbolic lattic of the type $\mathscr{H}(v,3)$ and set $r = v-2$. The subset of V containing exactly one fixed vertex and all of its neighbours is an $(r-1) = (v-3)$-fort: indeed, the fixed vertex has outdegree 0 and every other vertex in this subset has outdegree $(v-3)$. The event "there exist one such subset of V with all healthy vertices" again has strictly positive probability. Figure 3.5 depicts an example of these two type of forts.

Let us now prove that for all other values of the parameters there can not be (with strictly positive probability) any $(r-1)$-forts. First of all we make the trivial observation that a subset of V which is not contained in any horodisk must necessarily be infinite (if it was finite, than it would be contained in a ball with finite radius and thus also in an appropriately chosen horodisk). Thus we proceed to prove that for all the values of the parameters not discussed above, any $(r-1)$-fort is not contained in any horodisk and hence must be infinite. The problem can be reduced to considering only the "theoretical smallest" possible $(r-1)$-fort, which is a subset of V with regular boundary[1] such that the vertices of

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[1]By boundary we mean what is usually called *inner boundary*. Rigorously, this means the following. We consider the fort as a subgraph of $\mathcal{H}$, with vertices given by the vertices of the fort and with edges given by the set of all edges of $\mathcal{H}$ which connect two vertices of the fort. Then the inner boundary of the fort is the set of vertices of the fort which have a common edge with a vertex not in the fort.
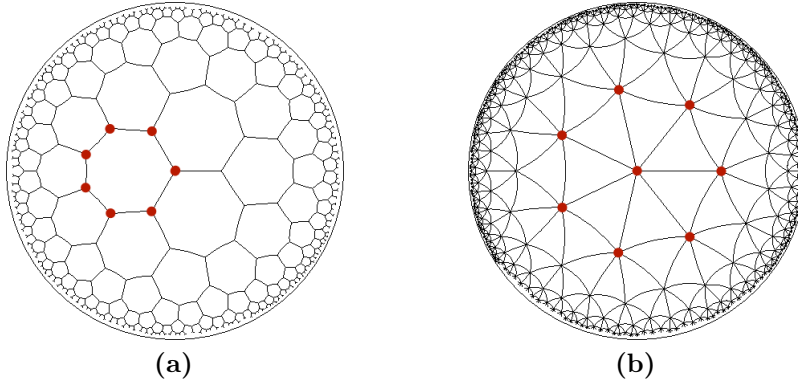
(a)   (b)

Figure 3.5: (a) We consider bootstrap percolation with facilitating parameter $r = v - 1$ on the graph $\mathcal{H}(3, 7)$. The red dots are the vertices of a $(v - 2) = 1$-fort which happens with nonzero probability. **(b)** We consider bootstrap percolation with facilitating parameter $r = v - 2$ on the graph $\mathcal{H}(7, 3)$. The red dots are the vertices of a $(v - 3) = 4$-fort which happens with nonzero probability.

the boundary have outdegree $r - 1$ and are incident to exactly two other boundary vertices (and thus incident to $v - r - 2$ vertices which belong to the fort but not to its boundary). Such a fort may in fact not be feasible, but it does not matter: if we prove that it can not be contained in any horodisk, then a fortiori no other $(r - 1)$-fort can be contained in any horodisk.

Moreover, in doing so, it is not restrictive to just consider horodisks whose boundary contains a vertex of the boundary of the $(r - 1)$-fort. Indeed, denote with $\widetilde{V}$ a generic $(r - 1)$-fort. If $\widetilde{V}$ is not contained in any horodisk, of course it is not contained in any horodisk whose boundary contains a vertex of the boundary of $\widetilde{V}$. Viceversa, if $\widetilde{V}$ is contained in a certain horodisk, then we can restrict this horodisk until its boundary touches a vertex of the boundary of $\widetilde{V}$.

Let us finally present the argument. Assume by contradiction that the "theoretical smallest" possible $(r - 1)$-fort is finite. Denote by x a vertex of its boundary and assume that x is also contained in the boundary of a horodisk containing the fort. Choose an edge connecting x to one of its two neighbours which are also on the boundary and denote by l its length. Moreover, denote by l^* the length of the segment which lies on the line that supports the chosen edge and whose extrema are x itself and the point of intersection between this line and the horocycle. Since we are assuming the fort to be finite, it must necessarily be $l < l^*$. We now compute l and l^* explicitly by means of formula 3.1 on page 34, using the triangles represented in figure 3.6 on the facing page. Please note that we have drawn the two triangles on two different edges of the polygon, but this was done for the sole purpose of making the drawing less intricate: we are really thinking about the two segments of length l and l^* as supported by the same line, i.e. as surmounting, with one longer than the other. We obtain:

$$\cosh(l) = \frac{\cos^2\left(\frac{\pi}{v}\right) + \cos\left(\frac{2\pi}{f}\right)}{\sin^2\left(\frac{\pi}{v}\right)} \qquad \cosh(l^*) = \frac{\cos^2\left(\frac{(v-r)\pi}{v}\right) + 1}{\sin^2\left(\frac{(v-r)\pi}{v}\right)}$$
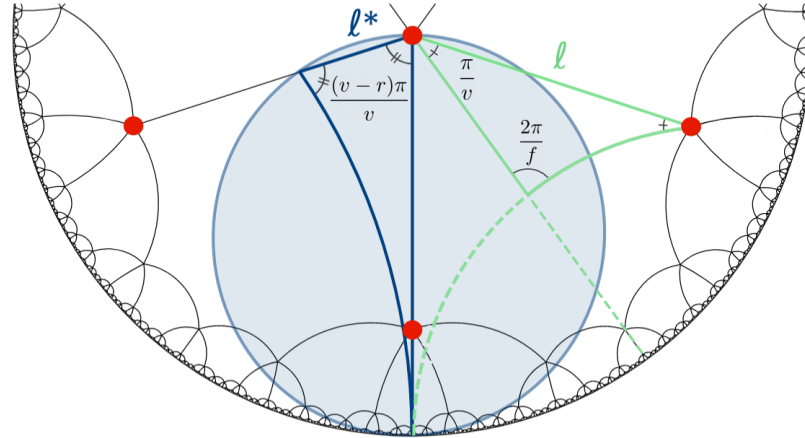
Figure 3.6: We consider bootstrap percolation with facilitating parameter $r = 3$ on the graph $\mathcal{H}(5,6)$. Some of the vertices of the "theoretical smallest" $(r-1) = 2$-fort are coloured in red. The horodisk which should (by contradiction, and hence does not) contain it is coloured in light blue. The angles of the green triangle adjacent to the edge of length l are computed as half the measure of the angle of the regular polygon which generates the tiling, i.e. by solving for α the equation $\alpha v = 2\pi$ (which comes from observing that x is the vertex of v distinct angles of equal measure). The angle opposite to the edge of length l, instead, is computed considering that a regular polygon with f edges can be partitioned in f equilateral triangles, i.e. by solving for β the equation $\beta f = 2\pi$. We have allowed ourselves to spend so many words about this because in computing angles in the hyperbolic plane a lot of the usual formulas do not work: one must remember that the sum of the angles of a triangle is *always* less than π (and in fact proportional to deficit of its angle sum from π)! The angles of the red triangle are computed in a similar way, using the description of "theoretical smallest" $(r-1)$-fort that we have given in the proof. Observe that the angle opposite to the edge of length l^* has measure zero, again something that can only happen in the hyperbolic plane.

It is not so hard to check (in any case Mathematica can help) that for $r \geq \frac{v+1}{2}$ these two formulas give $\cosh(l^*) < \cosh(l)$, i.e. $l^* < l$. As explained above, this is a contradiction with the assumption that the $(r-1)$-fort is finite. What about the other values of r?

It is clear that the v-regularity of the hyperbolic lattice $\mathcal{H}(v,f)$ implies that the angle between two edges connecting a boundary vertex of an $(r-1)$-fort to its nearest neighbours on the boundary is larger than $\frac{2\pi}{v}(v-r)$. If $\frac{2\pi}{v}(v-r) > \pi$, i.e. $r < \frac{v}{2}$, then the angle at each boundary vertex is strictly larger than π and so, by convexity argument, the fort must be infinite. Thus we have proved that no finite $(r-1)$-fort can exist also for the values of the parameters for which we did not reach a contradiction with the inequality above. Since we have now covered all possible cases, the proof is concluded. $\square$

The following corollary sums up the conclusion of the reasoning preceding the

above proposition:

Corollary 3.2 (Nontrivial upper bound). *Let $2 \leq r \leq (v-1)$. We have $p_f\big(\mathcal{H}(v,f),r\big) < 1$ if*
- *$f = 3$ and $r \leq v - 3$;*
- *$f \geq 4$ and $r \leq v - 2$*

Lower bound

Now let us try to find a nontrivial lower bound. First of all we need the following definition:

Definition 3.5. An infinite graph G has the *anchored expansion property* if for some fixed vertex $x \in V$ the *anchored Cheeger constant* is positive:

$$i^*(G) := \liminf \left\{ \frac{|\partial_e S|}{|S|} : x \in S \subset V,\ S \text{ is finite and connected} \right\} > 0$$

We are interested in the above constant because of the following result, which relates it to bootstrap percolation:

Proposition 3.2. *Let G_d be a d-regular graph. If $i^*(G_d) + 2r > d$, then $p_f(G_d, r) > 0$. In particular, if G_d has the anchored expansion property, then $p_f(G_d, \lceil d/2 \rceil) > 0$.*

For transitive graphs (and by remark 3.3 on page 40 hyperbolic lattices are transitive) the anchored Cheeger constant is the same as the more common edge isoperimetric constant

$$\Phi(G) := \inf \left\{ \frac{|\partial_e S|}{|S|} : \emptyset \neq S \subset V,\ S \text{ is finite} \right\}$$

In general it is not clear how to compute either one of these constants and one usually relies on estimates. But in our case we can do it explicitly!

Proposition 3.3. *Let G be an infinite plane regular graph with regular dual G^*. Denote by d the degree of the vertices of G and by d^* the degree of the vertices of G^*. Then:*

$$\Phi(G) = (d-2)\sqrt{1 - \frac{4}{(d-2)(d^*-2)}}$$

Since the dual of the hyperbolic lattice $\mathcal{H}(v,f)$ is the hyperbolic lattice $\mathcal{H}(f,v)$ (recall remark 3.2 on page 37) and both are regular, of degree v and f respectively, we obtain that:

$$\Phi\big(\mathcal{H}(v,f)\big) = (v-2)\sqrt{1 - \frac{4}{(v-2)(f-2)}}$$

Applying theorem 3.2 we obtain that $p_f\big(\mathcal{H}(v,f),r\big) > 0$ as soon as

$$(v-2)\sqrt{1 - \frac{4}{(v-2)(f-2)}} + 2r > v \tag{3.2}$$

This immediately yields a non trivial lower bound for $r \geq \lceil \frac{v}{2} \rceil$ and any f. We can do somewhat better with the exact solutions of inequality 3.2, which Mathematica is able to compute symbolically:

Corollary 3.3 (Nontrivial lower bound)**.** *Let* $2 \leq r \leq (v-1)$*. We have* $0 < p_f\big(\mathcal{H}(v, f), r\big)$ *if*
- *$f = 3$, $v \geq 7$ and $r \geq \frac{v}{2} - \frac{1}{2}\sqrt{12 - 8v + v^2}$;*
- *$f = 4$ and $v \geq 5$;*
- *$f \in \{5, 6\}$ and $v \geq 4$;*
- *$f \geq 7$, $v = 3$, $r = 2$ or $f \geq 7$, $v \geq 4$.*

Note how both the regularity and the nonamenability properties of hyperbolic lattices were needed to be able to use the results which have lead to the previous corollary.

Finally, considering the "intersection" of the values of the parameters for which we obtain both a nontrivial upper bound and a nontrivial lower bound, we obtain:

Corollary 3.4. *Let* $\mathcal{H}(v, f)$ *be an hyperbolic lattice and let* $2 \leq r \leq (v-1)$*. Then* $0 < p_f\big(\mathscr{H}(v, f), r\big) < 1$ *if*
- *$f = 3$, $v \geq 7$ and $\frac{v}{2} - \frac{1}{2}\sqrt{12 - 8v + v^2} \leq r \leq (v - 3)$ (note that the set of all r which satisfy the last condition is nonempty already for $v \geq 6$, so everything is well posed);*
- *all the last three cases of 3.3 with the additional condition $r \leq (v - 2)$ (and so excluding the case $v = 3$).*

References   Bernoulli site percolation on hyperbolic graphs is studied in [BS01]. For the discussion on finite $(r - 1)$-forts on hyperbolic lattices, instead, we refer to the appendix of [Sau+10] (from which we have taken and edited figure 3.6). The use of the anchored expansion property for the study of p_f on nonamenable graphs (i.e. a proof of proposition 3.2 on the facing page) is found in [BPP06]. Finally, the computation of the edge isoperimetric constant (proposition 3.3 on the preceding page) is performed in [LP17]. As far as we know, the application of these results to hyperbolic lattices is not present in the existing literature.

3.2.2   Approach using embedded trees

As previously announced, we present here another approach to the study of the critical probability for full infection on hyperbolic lattices, which allows to prove the nontriviality of $p_f(\mathscr{H}(v, f), r)$ for a larger class of values of the parameters v, f and r (with respect to what already found in the previous section). We will use the general inequalities for boostrap percolation of 1.2.1 on page 13, the embedding of trees in hyperbolic lattices described in 3.1.3 on page 37 and the result on the critical probability of boostrap percolation proved in 2.1.2 on page 22.

Theorem 3.2. *Let $2 \leq r \leq (v-1)$ and denote by $G = \mathscr{H}(v, f)$ an hyperbolic lattice. If $f \geq 5$, we have*

$$\forall v \geq 5, \quad \forall\, 3 \leq r \leq v - 2 \qquad 0 < p_f(G, r) < 1$$

Instead, if $f = 4$ we have

$$\forall v \geq 7, \quad \forall\, 4 \leq r \leq v - 3 \qquad 0 < p_f(G, r) < 1$$

Proof. First let us make a remark. In both cases, the bounds from below on v only serve to ensure that we are considering meaningful values of r. However, apart from this, they play no role in the proof.

We start by considering the case $f \geq 5$ and by proving that for $r \geq 3$ the critical probability $p_f(G, r)$ is strictly greater than 0. Using first the equivalence with the model with blocking parameter (G is a v-regular graph) and then the general inequality of lemma 1.2 on page 13, we obtain:

$$p_f(G, r) = 1 - \bar{p}_f(G, v - r + 1) \geq 1 - \bar{p}_f(\widetilde{G}, v - r + 1)$$

where $\widetilde{G}$ is a $v - 1$-regular subtree of the spanning tree constructed in theorem 3.1 on page 39. Using the result on the nontriviality of critical probability for regular trees (theorem 2.2 on page 22) with $d + 1 = v - 1$, we further obtain that $\bar{p}_f(\widetilde{G}, v - r + 1) > 0$ if $v - r + 1 \leq v - 2$, namely if $r \geq 3$. Plugging this in the above equality we conclude this first part of the proof.

Now we show that for $r \leq v - 2$ the critical probability $p_f(G, r)$ is strictly smaller than 1. We consider a colletion $(\widetilde{G}_i)_i \geq 1$ of $(v - 1)$-regular trees which covers the whole lattice G. We can then use the general inequality of lemma 1.3 on page 14 on the subgraph of G given by $\bigcup_i \widetilde{G}_i$, which by construction satisties the hypothesis of containing all the vertices of G. This gives the first inequality in the following

$$p_f(G, r) \leq p_f\left(\bigcup_i \widetilde{G}_i, r\right) \leq \sup_i \{p_f(\widetilde{G}_i, r)\} = p_f(T_{v-2}, r)$$

The second equality comes from the obvious generalization of lemma 1.4 on page 14 to a countable number of graphs, whereas the equality comes from the fact that in our case all $\widetilde{G}_i$ are $(v - 1)$-regular trees. Using again the result on the non triviality of critical probability for regular trees, we obtain that $p_f(G, r) < 1$ if $r \leq v - 2$.

The proof for $f = 4$ is done exactly in the same way: the only thing that changes is that in this case the embedded trees are of lower degree, as stated in theorem 3.1 on page 39. $\qquad\square$

References The content of this subsection is essentially a rewriting of one of the results of [Sau+10]. It is interesting to note that in this same work a further improvement of theorem 3.2 on the previous page is presented. It consists in

studying a system of recurrence equations for certain probabilities defined directly on the embedded tree of 3.1 on page 39, without cutting some of its edges to make it regular. A numerical solution of this system allows to claim the nontriviality of p_f. We have decided not to present it here because it seems to be a very specific result: a priori, for all the possible values of v and f a new system of equations should be written and (numerically) solved.

3.3   Other critical probabilities

In order to simplify the notation, in this section we set $\mathcal{H} = \mathcal{H}(v, f)$. Unless otherwise stated, the values of v, f and of the parameter r are assumed to be arbitrary, as long as $p_f(\mathcal{H}, r)$ is nontrivial (e.g. they could be as in the hypothesis of theorem 3.2 on page 45). We dedicate this section to the study of the other critical probabilites that we have defined in the first chapter, i.e. $p_c(\mathcal{H}, r)$ and $p_u(\mathcal{H}, r)$.

The results of the previous section imply that $p_c(\mathcal{H}, r)$ and $p_u(\mathcal{H}, r)$ are bounded away from one and so for hyperbolic lattices we can improve the diagram presented in 1.1.4 on page 12 in the following way:

$$\begin{array}{ccccc} & & & & \\ 0 & p_c(\mathcal{H}, r) & p_u(\mathcal{H}, r) & p_f(\mathcal{H}, r) & 1 \end{array}$$
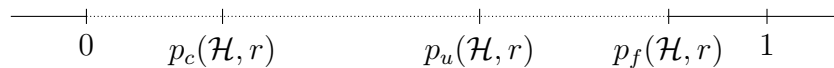
We remind that the dotted line represents the region in which we do not (yet) know what happens, i.e. we do not know if some of the critical values for the parameter p depicted above are in fact zero or the same value (except for $p_f(\mathcal{H}, r)$, which we know to be away from 0).

We start our discussion by proving a lemma which gives an upper bound on the critical probability for percolation in terms of a subgraph of the initial graph, analogously to what already done in lemma 1.2 on page 13.

Lemma 3.1. *Let G be a general graph (i.e. G is as in the first chapter) and let $\widetilde{G}$ be one of its subgraphs. We consider boostrap percolation with the same facilitating parameter r on both of these graphs. Then:*

$$p_c(G, r) \leq p_c(\widetilde{G}, r)$$

Proof. It is almost obvious. Suppose that we have a final configuration in $\widetilde{G}$ which has at least one infinite connected component of infected sites. Then it will be an infinite connected component of infected sites also when considered in G, no matter the value (healthy or infected) of the sites of G which are not in $\widetilde{G}$. Indeed, for any given vertex of $\widetilde{G}$, the number of its infected neighbours is less then or equal to the number of its infected neighbours in G. Informally, we could say that it is easier to percolate in G than in $\widetilde{G}$. This means exactly that for every p we have $\theta_c^{\widetilde{G}}(p) \leq \theta_c^{G}(p)$, which implies the thesis. $\square$

The following is an attempt at proving the nontriviality of the critical probability for percolation trying to use the same technique which was successful in the problem of full infection.

Proposition 3.4. *Let $2 \leq r \leq (v-1)$ and consider the hyperbolic lattice $\mathcal{H}(v, f)$. If $f > 4$ the critical probability for percolation is nontrivial, i.e. we have that $0 < p_c(\mathcal{H}(v, f), r) < p_f(\mathcal{H}(v, f), r)$.*

Proof. As showed in the proof of 3.1 on page 39, if follows from theorem 3.1 that $\mathcal{H}(v, f)$ contains a $(v-1)$-regular tree T_{v-1} as a subgraph (this is where we use the hypothesis $f > 4$). Thus the following chain of inequalities holds:

$$p_c\big(\mathscr{H}(v, f), r-1\big) \overset{(a)}{\leq} p_c\big(T_{v-1}, r-1\big) \overset{(b)}{<} p_f\big(T_{v-1}, r-1\big) \overset{(c)}{\leq} p_f\big(\mathscr{H}(v, f), r\big)$$

where (a) comes from lemma 3.1 just above, (b) from the nontriviality of the critical probability for trees stated in 2.3 on page 30 and (c) from inequality 1.5 on page 14 (inside remark 1.8). $\square$

Sadly the facilitating parameter of the LHS is different from the one of the RHS.

Open questions We recall that in chapter one we have also defined the critical probability for uniqueness. Interesting open questions are whether or not the critical probabilities for percolation and uniqueness are nontrivial. At the time of writing, there is no literature on the triviality or nontriviality of p_c and p_u for bootstrap percolation on hyperbolic lattices. However the matter has been settled for Bernoulli site percolation in the article [BS01]. In this direction also the very recent [GL22] is of interest. We stress one more time that it is very likely that a successful approach to this question is going to be different from the techniques which are usually employed for bootstrap percolation in the Euclidean setting.

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