A sharp threshold for an anisotropic bootstrap percolation model

Bachelor's thesis

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Student: Susan Boerma

Primary supervisor: Prof.dr. A.C.D. van Enter

Secondary supervisor: Prof.dr. E.A. Verbitskiy

Abstract

In bootstrap percolation on the two-dimensional lattice the initial state of any site is infected with probability p and healthy with probability $1 - p$. A healthy site can become infected if its neighbors are and an infected site remains infected for all time. The process goes on until all sites are infected or there is a point where no more sites can become infected. If all the sites become infected we say the initial configuration percolates. Balogh and Bollobs [BB03] were able to give a sharp threshold for the standard bootstrap percolation model in a way that can be used for other models.

In this bachelor thesis a sharp threshold is given for the anisotropic bootstrap percolation model. The standard and the anisotropic model are compared and it is shown that the fundamental theorem of Friedgut and Kalai [FK96] can be used to give the sharp threshold in both cases. It is shown that the behaviour on the grid and the torus is almost the same. Using a slightly adjusted version of the lemma of Aizenman and Lebowitz [AL88], the length of the ϵ-window for anisotropic bootstrap percolation is determined to be $O(\ln^3 \ln N / \ln^2 N)$ on a $N \times N$ square.

Contents

1 Introduction

1.1 Cellular automata

In this section an introduction to bootstrap percolation will be given. Before that can be done a short introduction to cellular automata is required.

A *cellular automaton* is a discrete model that consists of a n-dimensional graph of 'cells' that can be in a finite number of states. Cellular automata were first suggested by Ulam in 1952 [Ula52] but it was only in the seventies that they were first introduced [Bur70].

The model is governed by a set of rules that determine how a cell can change state: all cells are updated at the same time and a cell's new state is determined by the states of its neighbours. That new state will then undergo a change of state. For example, we could look at the two possible states healthy and infected. It seems reasonable that if some of the neighbours of a site are infected then that site will become infected as well.

Another well-known example of a cellular automaton is the 'Game of Life' introduced by John Conway [BCG82]. The Game of Life is a game with only one player. The initial state completely determines how the system will evolve over time. The same holds for all cellular automata including bootstrap percolation models.

1.2 Bootstrap percolation

In bootstrap percolation we look at cells. In two dimensions on a grid you can see this as a big square that contains an array of $N \times N$ small squares. It is intuitive to choose as neighbours the surrounding cells. Each cell can be healthy or infected[1]. Initially there is a probability p that a given cell is infected and a probability $1 - p$ that it is healthy. An infected cell can never become healthy. A healthy cell can become infected if a certain number of its neighbours is infected. Which of the cells we call neighbours and how much infected neighbours are needed to infect a cell both depend on the model we are looking at.

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[1]Also described as e.g. empty or occupied, zero or one respectively.

By now it may be clear that we are looking at an iteration process. With each step more cells become infected until either all the cells are infected, or until a state is established in which no more cells can become infected. Let's denote the set of sites that are infected at time t by X_t, and let's denote the *process* of percolation by (X_t). If at some point in time the whole graph is infected we say that (X_t) *percolates*.

Bootstrap percolation is a topic of interest for many fields of science: not only physics and mathematics, but also economics, neural science and computer science. There are many bootstrap percolation models. The models that are used most are the standard model and the model with the same neighbours as the standard model and the diagonal cells as neighbours. In this thesis we'll look at two models specifically: the standard model and the anisotropic model as described by Gravner and Griffeath in [GG96]. These models will be introduced later on.

1.3   Sharp thresholds

Let's say we pick an *initial configuration* X_0 of sites that are infected at time $t = 0$. X_0 is a p-random set, by which we mean that each site has an independent probability p of being infected. Choosing the initial configuration X_0 determines how the process will continue for all time, so $X_1, X_2, X_3, \ldots$ are fixed when X_0 is.

The probability of percolation, i.e. the probability that the entire grid or torus will become infected, is greater when p is greater. In other words, the probability of percolation is a strictly increasing function of p.

When the size of the lattice goes to infinity for a fixed p, Van Enter rigorously proved that for $N \to \infty$ the probability of percolation goes to one [Ent87]. It is obvious that for a fixed N, if $p \to 0$ the probability for a square becoming entirely infected goes to zero.

For every c with $0 < c < 1$ there is a unique p_c with the property that when we start with X_0 chosen with a probability p_c, then the probability of percolation is $P_{p_c}(N) = c$. If $c = \frac{1}{2}$ $p_{\frac{1}{2}}(N)$ is called the *threshold function*. Now we can give an ϵ-window of transition. For $0 < \epsilon < \frac{1}{2}$ the ϵ-window is the interval $(p_\epsilon(N), p_{1-\epsilon}(N))$. The next theorem (which we will not prove here) follows from a result of Bollobs and Thomason [BT86].
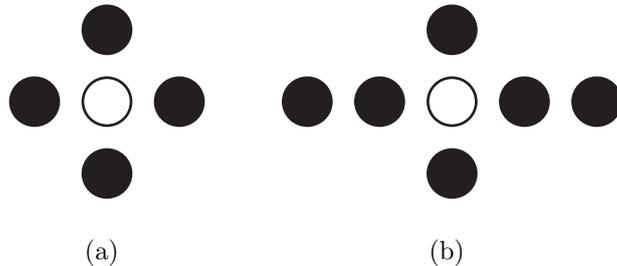
<div align="center">(a)   (b)</div>

Figure 1: In the standard bootstrap percolation model (a), a site has four neighbors, shown as black dots. In the anisotropic model (b), a site has six neighbors.

Theorem 1. *For every monotone increasing set it holds that for every fixed ϵ the ϵ-window has length $O(p_{\frac{1}{2}}(N))$.* [2]

A threshold function is called *sharp* if the length is $o(p_{\frac{1}{2}}(N))$. In that case, the statistical error goes to zero as $N \to \infty$. Note that in the literature, at least one other concept is also called a sharp threshold: Holroyd, Gravner and Morris denote a threshold as sharp if $\lim_{N\to\infty}(1/\ln N)p_{\frac{1}{2}}(N)$ converges, so that the systematical error goes to zero. We will call this a *sharp value result*. [Hol03, GH08, GHM10]

Balogh and Bollobs [BB03] gave a sharp threshold for the standard model. For the standard model they showed that the length of the ϵ-window on the grid is $O(\ln \ln N/ \ln^2 N)$. In this thesis the same method is used to give a sharp threshold for the anisotropic model. We look at these models on a two-dimensional grid and on a two-dimensional torus and we will see that the behaviour is almost the same on both. This can be used to give a sharp threshold.

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[2]The big O notation is used for growth rates. Let $f(n)$ and $g(n)$ be two functions defined on some subset of the real numbers. We can write $f(n) = O(g(n))$ if and only if there exists a positive real number M and a real number n_0 such that $|f(n)| \leq |Mg(n)|$ for all $n \geq n_0$. For the small o notation is used if $f(n)$ is dominated by $g(n)$ asymptotically, so $f(n) = o(g(n))$ if and only if for every ϵ there is an n_0 such that if $n > n_0$, then $|f(n)| \leq \epsilon|g(n)|$.
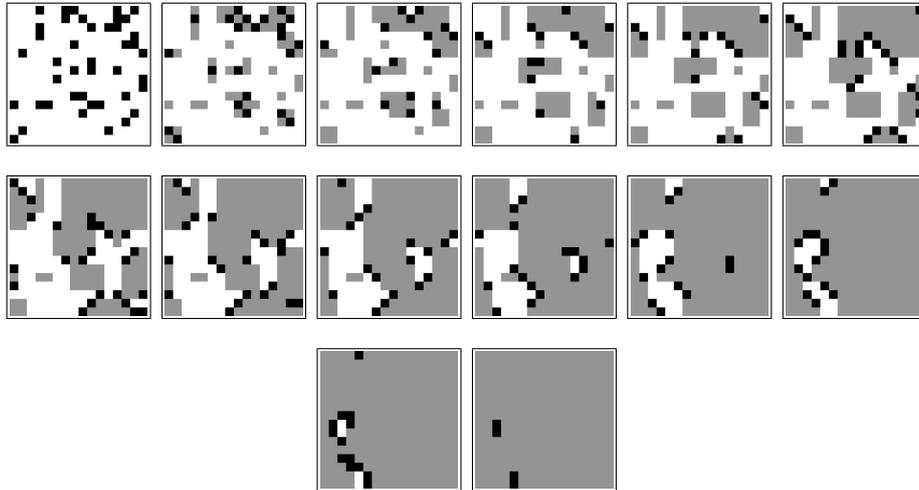
Figure 2: A configuration on a 16×16 torus that percolates for the standard model. White pixels are healthy sites, black pixels are sites that become infected at this step, grey pixels are sites that were already infected.
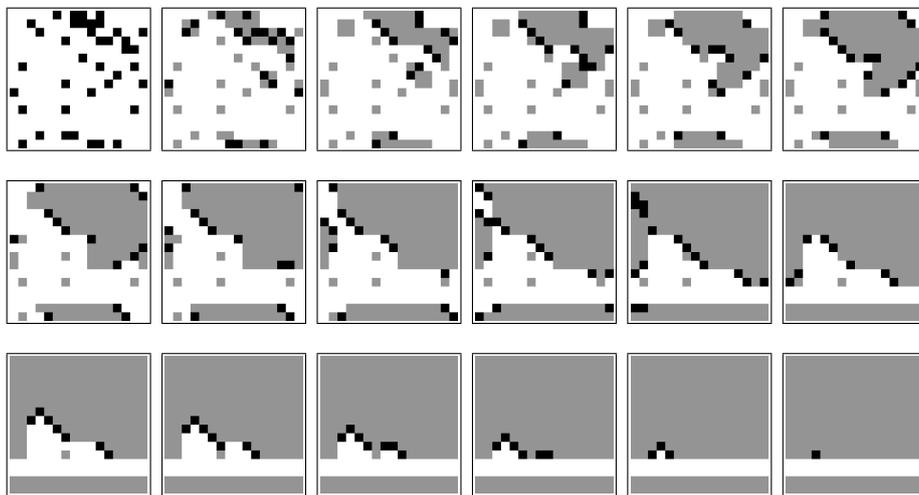

Figure 3: A configuration on a 16×16 torus that does not percolate for the standard model. White pixels are healthy sites, black pixels are sites that become infected at this step, grey pixels are sites that were already infected.

Figure 4: A configuration on a 16×16 torus that percolates for the anisotropic model. White pixels are healthy sites, black pixels are sites that become infected at this step, grey pixels are sites that were already infected.

Figure 5: A configuration on a 16 × 16 torus that does not percolate for the anisotropic model. White pixels are healthy sites, black pixels are sites that become infected at this step, grey pixels are sites that were already infected.
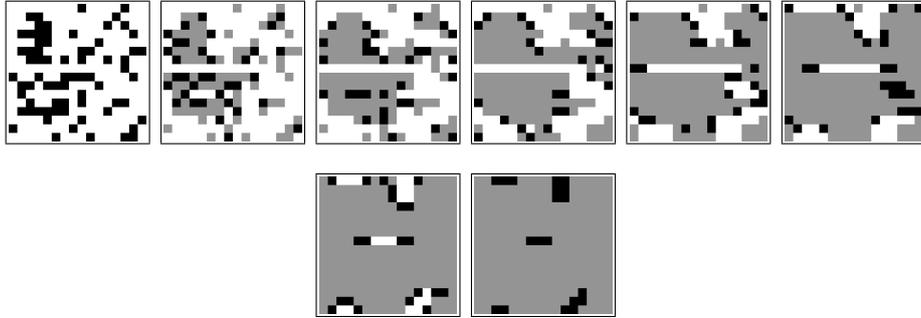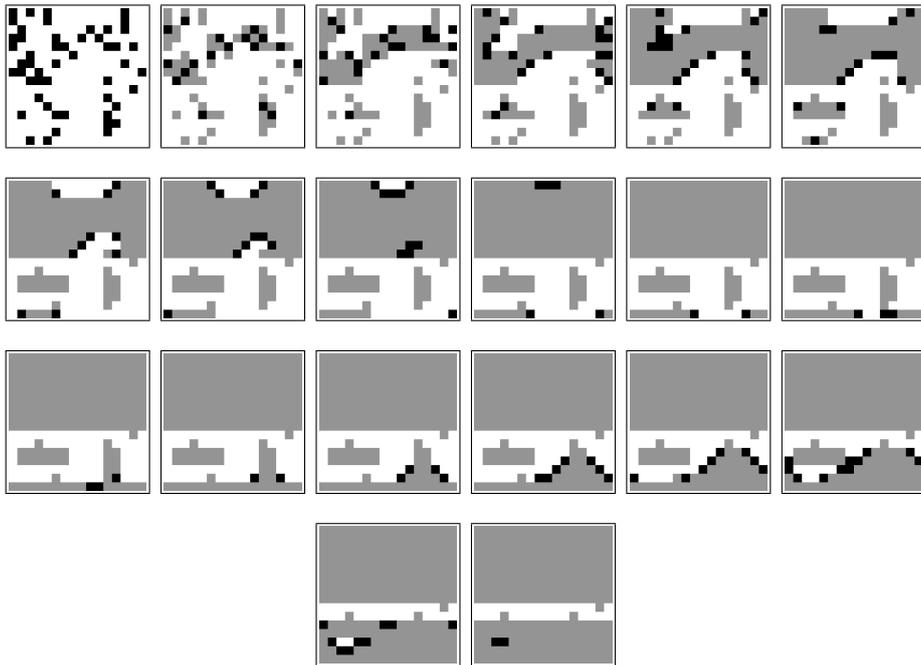
1.4 Bootstrap percolation models

In the standard bootstrap percolation model in two dimensions on an $N \times N$ square lattice, a cell has four neighbours located to the north, east, south and west as in Figure 1(a). If two or more of a cell's neighbours are infected, then it becomes infected as well. Two simple examples of a process for the standard model are given in Figure 2 and Figure 3.

In the anisotropic model a cell has not four but six neighbours, as in Figure 1(b). Here a cell becomes infected if three or more of its neighbours are infected. Two simple examples of a process for the anisotropic model are given in Figure 4 and Figure 5.

1.5 Critical parameters

We saw that as the probability of a site being initially infected $p \to 0$, the probability of percolation $P \to 0$ and as the size of the lattice $N \to \infty$, $P \to 1$. Now we can wonder what happens when simultaneously N becomes very large and p becomes very small. This is not as clear as the other regimes. Aizenman and Lebowitz proved that as $N \to \infty$ and $p \to 0$ there is an abrupt transition between the probability of percolation being almost equal to zero and the probability of percolation being almost equal to one [AL88].

A set of sites is called *internally spanned* if all sites become infected without help from sites outside of the set. Let $R(N, p)$ denote the probability that for a given N and p some initial configuration is internally spanned. If N is fixed at any large value, there is an abrupt transition between $R(N, p) = 0$ to $R(N, p) = 1$ as p increases past some critical value which varies only slowly with N. By defining a scaled density parameter

$$\lambda = (1 - p)^{\frac{1}{d-1}} \ln N$$

where d is the dimension, it is possible to write $R(N, p) = Q_p(\lambda)$. The main theorem from Aizenman and Lebowitz [AL88] states that for any sequence of p's convergent to 1 there is a subsequence p_n for which the functions Q_{p_n} converge to the step function,

$$Q_{p_n} \to \begin{cases} 0 & \text{if } \lambda < \lambda_c \\ 1 & \text{if } \lambda > \lambda_c \end{cases}.$$

Note that while a critical scaled density parameter λ_c exists for any such a subsequence p_n, their values may be different depending on the subsequence. Aizenman and Lebowitz stated that the values of λ_c were bounded and it was proven by Holroyd only in 2003 that there is a single limiting value for the standard model: $\lambda_c = \pi^2/18$. [AL88, Hol03]

The convergence to the step function is extremely slow, so slow that it is not realistic to find λ_c. In fact, the lattice for which the difference between λ and λ_c is smaller than 1% is at least $10^{3000} \times 10^{3000}$, so calculating λ_c up to that precision would require a computer that is a hundred orders of magnitude larger than the universe. On the computers which we can use λ_c is a factor 2 different from λ.

2 The anisotropic model

Duminil-Copin and Van Enter proved that there is a sharp threshold for the anisotropic bootstrap percolation model [DCvE10]. The main aim in this thesis is adapting the method Balogh and Bollobs used to give a sharp threshold for the standard model [BB03] to give a sharp threshold for the anisotropic model.

In the proof two theorems will be introduced. The first is a theorem of Friedkut and Kalai [FK96]. The second one will give the length of the ϵ-window.

2.1 Definitions and concepts

Before stating the first theorem, some concepts should be explained. These concepts are required to state the theorem of Friedgut and Kalai, which is the main tool in the proof.

$\mathcal{P}(S)$ is the *powerset* of a set S, i.e. the set of all subsets of S. From set theory it follows that $\{0,1\}^S$ is the set of all functions from S to $\{0,1\}$. By identifying a function in $\{0,1\}^S$ with the corresponding pre-image of 1, we see that there is a bijection between $\{0,1\}^S$ and $\mathcal{P}(S)$, where each function is the characteristic function of the subset in which it is identified, so the powerset $\mathcal{P}(S)$ is naturally identified with $\{0,1\}^S$.

A *property* $\mathcal{A}$ of subsets of S is a collection of subsets. The trivial cases $\mathcal{A} = \emptyset$ and $\mathcal{A} = \{0,1\}^S$ are left out of consideration. $\mathcal{A}$ is called *increasing* if for every $x, y \in \{0,1\}^S$ and $x \in \mathcal{A}$ with $x_s \le y_s$ it follows that $y \in \mathcal{A}$. Since this holds we have for the non-trivial cases that the 1-sequence is in $\mathcal{A}$ and the 0-sequence is not in $\mathcal{A}$.

A property $\mathcal{A}$ is called *symmetric* if we can construct a non-trivial permutation π on S so that for all $t, u \in S$ for which $\pi(t) = u$, $\mathcal{A}$ is invariant under the permutation induced by π. For the standard model a rotation of 90 is a possible permutation. The anisotropic model is symmetric under a rotation of 180.

The points above are not only true for the standard model but also for the anisotropic model. All the elements of S have an independent probability p of being picked. With the chosen elements we have a subset of S. The probability of picking a subset X is

$$P_p(X) = p^{|X|}(1-p)^{|S \setminus X|},$$

where $|X|$ is the number of elements in X. For $x \in \{0,1\}^S$ and $|x| = \sum |x_s|$ the probability of x is

$$P_p(x) = p^{|x|}(1-p)^{|S|-|x|},$$

and then the probability of $\mathcal{A}$ is $P_p(\mathcal{A}) = \sum P_p(x)$.

Since $\mathcal{A}$ is increasing, $P_p(\mathcal{A})$ is strictly increasing from 0 to 1. For every $0 \le c \le 1$ there is a unique probability $p(c, \mathcal{A})$ such that $P_{p(c,\mathcal{A})}(\mathcal{A}) = c$. Up until this point there is no difference between this proof and that for the standard model by Balogh and Bollobs [BB03]. Theorem 2 as stated below is by Friedgut and Kalai [FK96] but stated as by Balogh and Bollobs. This is necessary to give the length of the ϵ-window of bootstrap percolation on the grid.

Theorem 2. *Let $\mathcal{A} = \mathcal{A}_N \subset \{0,1\}^S$ be a symmetric upset with threshold function $p(N) = p(1/2, \mathcal{A}) = o(1)$. Then for any constant $0 < c < 1/2$, we have*

$$\frac{p(1-c, \mathcal{A}) - p(c, \mathcal{A})}{p(1/2, \mathcal{A})} \le \frac{\ln(1/p(1/2, \mathcal{A}))}{c \ln N}$$

The proof of this theorem will not be given in this thesis.

2.2 ϵ-window for the anisotropic model

We can now look specifially at the anisotropic model. The following theorem will give us the length of the ϵ-window.

Theorem 3. *Let $\mathcal{A} = \mathcal{A}_N \subset \{0,1\}^S$ be a symmetric upset with threshold function $p(N) = p(1/2, \mathcal{A}) = o(1)$. Then for any constant $0 < c < 1/2$, the length of the ϵ-window of anisotropic bootstrap percolation is given by $O\left(\frac{\ln^3 \ln N}{\ln^2 N}\right)$.*

The proof is the same as for the standard model, only the window will be found in a different way. The idea of the proof is the following. We will show that the behaviour of the model on the torus is almost the same as on a grid. To prove this, Theorem 2 will be applied to the torus. It can be shown that the probability of percolation on the torus $P_p^{\mathbb{T}}(N)$ is close to the probability of percolation on the grid $P_p^{\mathbb{G}}(N)$, if N is large in comparison to the dimension $d = 2$. It is obvious that

$$P_p^{\mathbb{G}}(N) \leq P_p^{\mathbb{T}}(N),$$

because the only difference between a grid and a torus is on the edges: a torus has an influence beyond the edge. The probability of percolation must be greater on the torus because as opposed to the grid, all cells have the same number of neighbours. To show that the probability is almost the same we will look at a $(p + r - pr)$-dense set of the grid. We want to enclose the probability on the torus with the probability on the grid and the $(p+r-pr)$-dense set on the grid.

2.3 Necessary existence of internally spanned regions

Aizenman and Lebowitz [AL88] stated a lemma which is necessary in our proof, but which for our model we need to adapt slightly.

Lemma 1. *For all $k > 1$, a necessary condition for a region Λ_L with greatest side length $L \geq k$ to be internally spanned is that it contains at least one internally spanned rectangular region whose maximal side length is in the interval $[k, 4k]$. This holds for both the grid and the torus.*

Proof. For this proof an algorithm is used. In this algorithm D is the minimum distance for which the sites cannot become infected. For the standard

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model $D = 2$ and for the anisotropic model $D = 3$ in the east and west directions, since if two internally spanned rectangles are separated by a strip of width 3 over the whole lattice, this strip can never become occupied. The configuration spanned can be determined by this algorithm. So what we want is to give a configuration that is spanned. In the first step of the algorithm we have the collection of all internally spanned rectangles of an arbitrarily chosen size $k_0 \leq k$, where $k \geq 1$. From this we can proceed by choosing at each step a pair of rectangles in the configuration whose distance is not greater than D and replacing them with the minimal rectangular region which contains both. This means that in each next step we have a larger rectangle that is internally spanned, since the two rectangles cannot be further apart than D. In each step there is a collection of possibly overlapping rectangular regions, with every region being internally spanned.

So if there is an internally spanned rectangle with longest length k then there is an internally spanned rectangle with longest length at least $k/4 - D$. In other words a rectangle in this algorithm can not grow faster than $k \to 4k + D$ and it reaches L if Λ_L is internally spanned. Furthermore, if there is an internally spanned rectangle of longest length $l \in [k, 4k + 3]$ which is in the same order as $[k, 4k]$. $\qquad \square$

2.4   Placing segments and translating a configuration

When we take a set of l consecutive sites you can look at different ways to place them on the grid and torus. For $l = 1$ there are N^2 locations on either. A more interesting case is when we look at $l > 1$. On the torus there are n^2 starting points and there are two possible directions in which our segment can be placed, so there are $2N^2$ possible ways to place it. On the grid there are at most $2N^2$ possible ways to place an l-segment, or, to be more precise, there are exactly $2N^2 - 2N(l - 1)$ ways to place it. It is clear that when there is a process which contains an l-box that meets every l-segment then the process percolates.

Let's call a shift of the initial configuration a *translation*. Any translation on the torus is an automorphism, i.e. an isomorphism of the configuration on the torus to itself. This is not true for the grid. Formally, for $X \subset \mathbb{Z}^2$ the translation by an array $\mathbf{a} = (a_1, a_2, \ldots, a_N) \in \mathbb{Z}^2$ is defined as

$$X - \mathbf{a} = \{(x_i - a_i)_1^N \in \mathbb{Z}^2 : \mathbf{x} \in \mathbb{Z}^2\}.$$

When $\mathbf{a}$ is the N-th array, translation by $\mathbf{a}$ is the identity operator. [BB03]

2.5 Enclosing the percolation probability on the torus

Now, all the information is available to state the lemma that will provide us with an inclusion for the probability on the torus.

Lemma 2. *For $r = N^{-\frac{1}{3}}$ and $0 < p < 1$ the inequality*

$$P_p^{\mathbb{G}} \leq P_p^{\mathbb{T}} \leq P_{p+r-pr}^{\mathbb{G}} + 2r$$

holds.

Proof. Only the second inequality needs to be proven since we already considered the first: if a process percolates for some initial configuration on the grid, then it also percolates for that initial configuration on the torus.

First, we want to construct a $(p+r-pr)$-random subset Z_0 on the grid. Call the sites picked with probability p the blue sites and sites with probability r the red sites. We start with picking blue sites on the torus with probability p. The initially configuration X_0 can be set. Later in the proof it is necessary to translate X_0. We pick an array $\mathbf{a} = (a_1, ..., a_N)$ at random. Now it is possible to set $X_0' = X_0 - \mathbf{a}$. Then the red sites can be added with an initial configuration Y_0. The $(p + r - pr)$-random subset is $Z_0 = X' \cup Y_0$.

Given that with probability $P_p^{\mathbb{T}}(N)$ the initially picked blue sites X_0 percolate on the torus we want to look what will happen on the grid. As already stated we have a starting position X_0 with (X_t) a percolating process. According to lemma 3, for every k there exist an $l \in [k, 4k]$ such that there is an internally spanned rectangle on the torus. So, for some $l = l(X_0)$ with $n^{2/3}/8 \leq l \leq N^{2/3}/2$, there is an internally spanned rectangle $B = B(X_0)$ with longest side l. We want $B' = B - \mathbf{a}$ to be a rectangle in the grid. This is true for a probability of at least

$$\left(1 - \frac{l-1}{N}\right)^2 \geq 1 - 2\frac{l-1}{N} > 1 - N^{-1/3}.$$

B' is internally spanned for the starting position X_0' on the torus. Say $B = \prod_{i=1}^{2}[b_i, b_i + l_i)$, with l_i is the largest l. Then B' is a rectangle on the grid if $a_i \notin [b_i, b_i + l_i - 1)$ for every i. The probability for this to hold is

$$\prod_{i=1}^{2}\left(1 - \frac{l_i - 1}{N}\right) \geq \left(1 - \frac{l-1}{N}\right)^2.$$

If we define $m = \lfloor n^{2/3}/8 \rfloor$ so that $m \leq l$, the probability for some segment of m consecutive sites to contain no red site on the grid is at most $2n^2(1-r)^m \leq 2n^2 e^{-m+N^{-1/3}} < N^{-1}$, where we used that $\lim_{n \to \infty}(1 + \frac{x}{n})^n = e^x$.

We have that (X_t) percolates on the torus. If B' is a rectangle on the grid and every m-segment contains a red site, then Z_0 is a percolating initial construction on the grid. Since we have already calculated these probabilities we can give the inequality

$$P^{\mathbb{G}}_{p+r-pr} \geq (1 - N^{-1/3})P^{\mathbb{T}}_p - \frac{1}{N} \geq P^{\mathbb{T}}_p - 2N^{-1/3}.$$

So $P^{\mathbb{T}}_p \leq P^{\mathbb{G}}_{p+r-pr} + 2r$, which proves our lemma. $\qquad\square$

2.6 Proof of theorem 3

Proof of theorem 3. Now we can give a proof of theorem 3. Let's denote the probability function of percolation by $p(c, \mathbb{G}^2_N)$ on the grid and by $p(c, \mathbb{T}^2_N)$ on the torus. For every $0 < \epsilon < 1/2$ the length of the ϵ-window on the grid is given by $p(1-\epsilon, \mathbb{G}^2_N) - p(\epsilon, \mathbb{G}^2_N)$. Furthermore, define p by $p+r = p(1-\epsilon, \mathbb{G}^2_N)$. By Lemma 1 and because $p + r - pr \leq p + r$,

$$P^{\mathbb{T}}_p(N) \leq P^{\mathbb{G}}_{p+r}(N) + 2r = 1 - \epsilon + 2r.$$

This is the same as stating that

$$p \leq p(1 - \epsilon + 2r, \mathbb{T}^2_N).$$

We can get p from $N \sim e^{\frac{1}{p} \ln^2 \frac{1}{p}}$ [EH08, Hul09]; p can be calculated from the Lambert product log function. Since N is approximated an iteration process is used. First we take the logarithm of both sides, so $\ln N \sim \frac{1}{p} \ln^2 \frac{1}{p}$. This can be rewritten as $p \sim \frac{1}{\ln N} \ln^2 \frac{1}{p} = \frac{1}{\ln N} \ln^2 p$. Repeatedly inserting the equation for p will give a more precise approximation. However, if we are only interested in the asymptotic behavior of p, then it follows that $p = O\left(\frac{1}{\ln N} \ln^2 \ln N\right)$:

$$p_1 \sim \frac{1}{\ln N} \ln^2 \ln N$$

$$p_2 \sim \frac{1}{\ln N} \ln^2 \left(\frac{1}{\ln N} \ln^2 \frac{1}{\ln N}\right)$$

$$\sim \frac{1}{\ln N} \ln^2 \left(\ln N \ln^2 \ln N\right)$$

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$$\sim \frac{1}{\ln N}\left(\ln^2 \ln N + \ln^2 \ln^2 \ln N + 2\ln\left(\frac{1}{\ln N}\right)\ln\left(\ln^2 \ln N\right)\right)$$

$$\sim \frac{1}{\ln N}\ln^2 \ln N$$

$$p_3 \sim \frac{1}{\ln N}\left(\ln^2\left(\ln N \ln^2\left(\ln N \ln^2\left(\ln N\right)\right)\right)\right)$$

$$\sim \frac{1}{\ln N}\ln^3\left(\ln N \ln^2\left(\ln N\right)\right)$$

$$\sim \frac{1}{\ln N}\left(\ln^2\left(\ln N\right) + \ln^2\left(\ln^2\left(\ln N\right)\right) + 2\ln\left(\ln N \ln\left(\ln^2\left(\ln N\right)\right)\right)\right)$$

$$\sim \frac{1}{\ln N}\ln^2 \ln N$$

A close look at these probabilities shows that

$$p_i = O\left(\frac{1}{\ln N}\ln^2 \ln N\right)$$

This can we substitute in the equation of Friedgut and Kalai.

$$
\begin{aligned}
p(1-c,\mathcal{A}) - p(c,\mathcal{A}) &\le \frac{\ln(1/p(1/2,\mathcal{A}))}{c\ln N}p(1/2,\mathcal{A}) \\
&\le \frac{\ln(\ln N \ln^{-2}(\ln N))}{c\ln N}\ln^{-1} N \ln^2(\ln N) \\
&\le \frac{\ln(\ln N) + \ln(\ln^{-2}(\ln N))}{c\ln^2 N}\ln^2(\ln N) \\
&\le \frac{\ln^3(\ln N)}{c\ln^2 N}
\end{aligned}
$$

Now it is possible to give the actual window:

$$p(1-\epsilon,\mathbb{G}_n^2) = p + r \le p(1 - \epsilon + 2r,\mathbb{T}_n^2) + r$$

$$\le p(1-\epsilon/2,\mathbb{T}_n^2) + r \le p(\epsilon,\mathbb{G}_n^2) + O\left(\frac{\ln^3 \ln N}{\ln^2 N}\right),$$

so the length of the ϵ-window for the anisotropic bootstrap percolation model is $O(\ln^3 \ln N/\ln^2 N)$. $\qquad\square$

3 Conclusions

We saw that the method of Balogh and Bollobs [BB03] could be adapted to give a sharp threshold for the anisotropic bootstrap percolation model that

is within the bounds predicted by Van Enter and Hulshof [EH08]. For the standard model Balogh and Bollobs showed that the length of the ϵ-window on the grid is $O(\ln \ln N / \ln^2 N)$. We have shown that for the anisotropic model the length of the ϵ-window is $O(\ln^3 \ln N / \ln^2 N)$, so the length of the ϵ-window on the $N \times N$ grid for the anisotropic model is asymptotically a factor $\ln^2 \ln N$ larger than for the standard model.

Our main deviation from the method of Balogh and Bollobs for the standard model lies in changes to Lemma 1, which can be readily adjusted to other bootstrap percolation models. Special care must be taken to verify the symmetry of the model. Extending this method to higher dimensions, we expect, requires a careful examination of Lemma 1.

References

[AL88]   M. Aizenman and J.L. Lebowitz. Metastability effects in boot-strap percolation. *J. Phys. A*, 1988.

[BB03]   J. Balogh and B. Bollobs. Sharp thresholds in bootstrap percolation. *Phys. A*, 2003.

[BCG82]   E.R. Berlekamp, J.H. Conway, and R.K. Guy. Winning ways for your mathematical plays. *Academic press*, 1982.

[BT86]   B. Bollobas and A. Thomason. 1985. *Combinatorica*, 1986.

[Bur70]   A.W. Burks. Essays on cellular automata. *Champaign*, 1970.

[DCvE10]   H. Duminil-Copin and A.C.D. van Enter. Sharp metasta-bility threshold for an isotropic bootstrap percolation model. arxiv:1010.4691, 2010.

[EH08]   A.C.D. Van Enter and T. Hulshof. Finite-size effects for anisotropic bootstrap percolation: logarithmic corrections. *Journal of Statistical Physics*, 2008.

[Ent87]   A.C.D. Van Enter. Proof of Straley's argument for bootstrap percolation. *Journal of Statistical Physics*, 1987.

[FK96]   E. Friedgut and G. Kalai. Every monotone graph property has a sharp threshold. *Proc. Amer. Math. Soc*, 124:2993–3002, 1996.

[GG96]   J. Gravner and D. Griffeath. First passage times fo threshold growth dynamics on z^2. *Ann. Probab.*, 1996.

[GH08]   J. Gravner and A.E. Holroyd. Slow convergence in bootstrap percolation. *Annals of Probability*, 2008.

[GHM10] J. Gravner, A.E. Holroyd, and R. Morris. A sharper threshold for bootstrap percolation in two dimensions. arxiv:1002.3881, 2010.

[Hol03]   A.E. Holroyd. Sharp metastability threshold for two-dimensional bootstrap percolation. *Prob. Theory Rel. Fields*, 2003.

[Hul09]   T. Hulshof. Mixed order translations for percolation models. Master's thesis, Rijksuniversiteit Groningen, 2009.

[Ula52]   S. Ulam. Random processes and transformations. In *Proceedings of the international congress of mathematics*. American Mathematical Society, 1952.