THESIS FOR THE DEGREE OF LICENTIATE OF ENGINEERING

Omniparametric simulation of the two-type Richardson model

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Abstract

In the field of particle systems and growths models simulation is an important tool. When explicit calculations are too complex or impossible to perform we may use simulations instead. In this situation it is important to have a technique for doing simulations for every possible parameter value, since we can have different probabilistic behaviour at certain parameter values. When such situations occur ordinary fixed parameter simulation does not suffice. In this thesis we design an omniparametric simulation algorithm, that is, a simulation algorithm generating samples for all parameter values within the same sample. The technique is used to study the problem of asymmetric simultaneous survival in the two-type Richardson model.

Keywords: growth model, Markov chain, omnithermal simulation, omniparametric simulation, percolation, two-type Richardson model

MSC 2000 subject classifications : 60C35, 65K35, 82C22

Preface

The thesis

My studies as a graduate student are mainly focused on simulations and the technique for doing simulations for all parameter values of a model at the same time, so called omniparametric simulation. This thesis presents the work done on omniparametric simulation for a certain growth model, the two-type Richardson model. The project was introduced to me around Christmas 2000 by my supervisor, professor Olle Häggström.

Acknowledgements

When I started as an undergraduate student at Chalmers in august 1995 one of my most severe problems was mathematics. The text book material simply did not make any sense. I have spent numerous hours struggling with assignments in courses, starting with simple analysis in one variable, often without understanding much, and certainly without finding an answer to the most important question.

Why ?

Later on that changed!

My first encounter with mathematical statistics was in a basic course in statistics and probabiliy theory during early autumn 1997, and later that winter also in queueing theory. This was the first time someone explained to me the meaning, in plain language, of the included theorems. A theorem consisted of three parts, a statement, a proof and an

interpretation related to applications. This had a profound impact on me.

During that winter an assistant asked me if I had considered to continue as a graduate student after finishing my Masters degree. I thought about it during that day, and the next I changed focus from computer science to mathematical statistics and especially probability theory. In May 2000 I finally got my Master of Science degree, and since August the same year I have had the pleasure of being a graduate student here at the department of Mathematical Statistics in Gothenburg, something I will continue to do at least until August 2005, when I'm expected to defend my doctoral thesis.

This is not something I could have done on my own!

I would like to express my gratitude to the following people . . .

My supervisor professor Olle Häggström for introducing me to the problem and for supporting my efforts as a graduate student. He always has the time to for questions and comments about both mathematics and life as a researcher, those things a graduate student needs to know when entering the world of mathematics. For this I am grateful.

All colleagues at the institution for contributing to an inspiring work environment.

Torgny Lindvall, Olle Häggström and Patrick Albin for giving interesting and demanding courses. Without their commitment as teachers, life as a graduate student would be much harder.

The students I taught in courses both at Chalmers and Göteborg University for making my time as a teacher interesting.

The lunch bunch for an uncountable number of laughs.

All my friends . . . for being friends :)

My family for always being there, believing in and supporting me.

Fredrik Lundin,

Gothenburg, March 2003.

Notation

	The lattice
$\mathbb{Z}^d$	The integer lattice in d-dimensions.
$\mathbb{L}^d$	The graph having $\mathbb{Z}^d$ as vertex set, and edges between vertices with distance 1.
B_n	The box $[-n, n]^d$ in $\mathbb{Z}^d$
∂B_n	The boundary of box B_n, $\partial B_n = B_{n+1} \setminus B_n$.
	The two-type Richardson model
$\Xi_v^\lambda(t)$	The state of vertex $v \in \mathbb{Z}^d$ at time t when the intensity of the type two infection is λ
$\Xi^\lambda(t)$	The configuration of $\mathbb{Z}^d$ at time t.
$\eta_i^\lambda(t)$	The subset of $\mathbb{Z}^d$ having type i at time t, $i = 1, 2$.
ξ_i^λ	The subset of $\mathbb{Z}^d$ having type i at $t = 0$, $i = 1, 2$.
	The omniparametric two-type Richardson model
$\Theta_v(t)$	The state of vertex $v \in \mathbb{Z}^d$ at time t.
$\Theta(t)$	The configuration of $\mathbb{Z}^d$ at time t.
	Measures
$\mathbb{P}^{\lambda_1,\lambda_2}_{\xi^1,\xi^2}$	The probability measure for the two-type Richardson model with starting configuration (ξ^1, ξ^2) having intensities λ_1 and λ_2 respectively for the two infection types.
$\mathbb{P}^{\lambda}_{\xi^1,\xi^2}$	The probability measure for the two-type Richardson model with starting configuration (ξ^1, ξ^2) having intensities 1 and λ respectively for the two infection types.

Special events

$G^{\lambda}_{i,n}$	Then event that infection type $i = 1, 2$ survives until reaching the boundary of a box B_n.
G^{λ}_{n}	Then event that both infection types survives until reaching the boundary of a box B_n.
G^{λ}	Then event that both infection types grows to infinity.

Contents

CHAPTER 1

Introduction

Stochastic models may be simple to formulate, and natural questions may come easily to mind. Strikingly often these questions are, when formulated into theorems, as hard to give an exact answer to as they are easily formulated. Models in the field of statistical physics are no exceptions, neither are stochastic growth models. When analysing these models we have at our disposal a number of theorems, often giving us information about the asymptotic case, when time, or space in terms of finite regions, tends to infinity. In real world applications however, we deal with finite models and the asymptotic results has to be complemented by such things as convergence rates. When no results are available we may turn to simulations trying to extract some behaviour from the output of our computer programs.

When using simulation we traditionally fix all parameter values and run the simulation. In general this is no problem, but if we are going to study a phenomenon like phase transitions or probabilistic behaviour at a certain critical parameter value we may be in trouble. A rather new technique is omniparametric simulation, which enables us to simulate for all parameter values, at the same time. This allows us to simulate for every parameter value in a continuous space, something which is otherwise not possible.

In this article we will take into consideration a growth model, the two-type Richardson model, and address the question regarding simul-

taneous survival as time tends to infinity. This question has been partially answered so far, and today we know that simultaneous survival cannot happen when the infections are not equally strong, for almost all parameter values. There is however a strong belief that both types cannot survive to infinity if they are not equally strong. What remains is to rule out simultaneous survival for a countable set of parameter values. We use omniparametric simulation and see how far towards an answer the simulations bring us.

The rest of this thesis is organised as follows. In section 1.1 we briefly describe the growth models in use, the Richardson model and its extension, the two-type Richardson model. Section 1.2 describes the simulation with a focus on the use of parameters, both fixed parameter simulation and omniparametric simulation are described. We end the first chapter with an example of omniparametric simulation for the independent percolation model. In chapter 2 we properly introduce the two-type Richardson model and give some results. Chapter 3 introduces the omniparametric two-type Richardson model and describe its relation to the ordinary fixed parameter model. Chapter 4 describe simulations. First a the theoretical base is established, then we do simulations, and finally perform the analysis. In chapter 5 we discuss the main topics of this thesis with a focus on omniparametric simulation. We describes the present state,try to see what may happen in the future, and of course discuss open questions.

1.1 Growth models

1.1.1 The Richardson model

The Richardson model [Ric73] is a stochastic growth model in d-dimensions, where d is any finite number. We can think of the volume on which the models grows as a volume divided into cells. From the beginning all the cells have the same state, all but one which has a certain interesting property, for example an infection. When time passes this infection will spread, as infected cells affect uninfected ones.

In mathematical terms the Richardson model is a Markovian growth process in continuous time. At time $t = 0$ only one cell is infected. The infected area grows as infected cells infect uninfected ones, one by one. It is crucial for the model that two different cells cannot be infected at the same time. The rate by which uninfected cells are infected is proportional to the number of infected neighbours an uninfected cell have. Let $\{X_t\}_{t\geq 0}$ denote the state of the infection at time t and let

$N_R(t)$ denote the number of infected neighbour cells of the cell R. For a certain cell R the probability for being infected during a small time interval $[t, t+h]$ is given by the following

$$\mathbb{P}(I_R(t+h)|I_R(t)^c) = h(1+o(1))N_R(t) \ , \quad \text{as} \quad h \downarrow 0$$

where $I_R(t)$ is the event that R is infected at time t. In fig 1.1 we see a simple example of the Richardson growth process on the square tessellation. The difference between the middle picture and the right one is the extra infected cell.

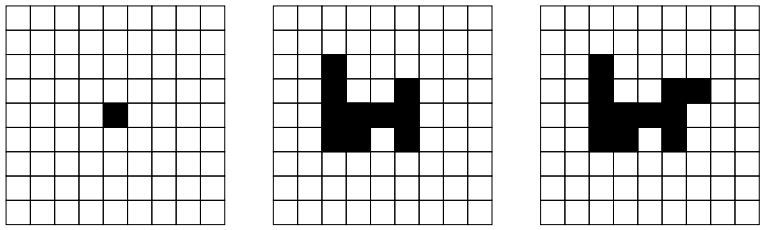

Figure 1.1: The Richardson model on the square tessellation

In his article from 1973 Richardson studied and stated a theorem regarding the shape of the infected region. The result states that as $t \to \infty$ the shape of the infected area tends to some non-random shape. The question regarding the exact shape remains unanswered.

Instead of studying the model in continuous space, one could use a graph, replacing cells with nodes and each neighbour relation between two cells with an edge.

1.1.2 The two-type Richardson model

The two-type Richardson model extends the Richardson model by adding another type of infection. It was introduced by Häggström and Pemantle [HP98] in 1998 and somewhat extended by the same authors in 2000.

The process starts with every vertex in $\mathbb{Z}^d$ having type zero (white), except for vertices in a region of type one (grey) and vertices in a region of type two (black). For theoretical purposes it is enough to let the initial

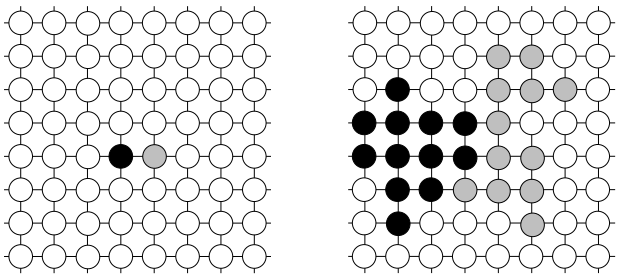

Figure 1.2: The two-type Richardson model. Initial configuration and configuration after some time.

configuration be the simple configuration in figure 1.2 (left) and study how the model evolves through time.

As time passes each coloured (black or grey) vertex colour its uncoloured (white) neighbours in a Poisson process with a colour dependent intensity. After being coloured a vertex keeps its colour for all times. See section 2.1 for a more precise description of the model.

1.2 Simulation

In situations where mathematical models are too complicated for a theoretical treatment or when there is no available theory, simulation is an alternative. There are numerous methods for performing computer simulations and many books have been written about the subject, but this is neither the place nor the time for a review.

We will consider one aspect of simulation though, which is of special interest in this thesis, the treatment of parameters.

1.2.1 Fixed parameter simulation

A mathematical model has a number of parameters, for example temperature or infection rate or both. Traditionally the simulation is done for fixed values of these parameters, and inference done based on the simulation results. Results for such an analysis are valid for the chosen parameters only. In some cases the general behaviour of the model is the same for all parameters values, in other cases not. With this approach simulation of models with a continuous parameter

can only be done for a finite number of parameter values. Hopefully these parameter values are spread throughout the parameter space, or at least over interesting regions.

The approach poses no problem if the model has a nice behaviour over the represented parameter space, and any interesting behaviour of the model is captured by a reasonable choice of parameter values.

There are a lot of models in this field, and they all live on graphs where edges and vertices can have different states. Let us focus on the simulation of particle systems like independent Bernoulli percolation or the Potts model. These models changes their behaviour if the parameter values are changed, in some cases quite drastically. This drastic change in behaviour is called a phase transition, and the different regimes for the models are called phases .

In the independent Bernoulli percolation model we have a critical value p_c of the parameter p. Below this value there are almost surely no infinite clusters, while above p_c there is almost surely one unique infinite cluster.

For the Potts model phase transition has a different meaning. Assume for the moment that the parameter for this model is β, and that there is a critical value β_c. Then for $\beta < \beta_c$ we have a unique probability measure determining the behaviour of the model. For $\beta > \beta_c$ there are a number of valid probability measures all resulting in different behaviour. For these models phase transition means loss, or gain, of a unique probabilistic behaviour.

The parameter range for these different phases however small they are in the parameter space, consists of a continuous set of values, and could be detected by a proper choice of parameter values. However if the model has a different phase for a single parameter value this cannot easily be detected. Let's call such values of the parameter exceptional values , since the behaviour of the model at these parameter values is exceptional when comparing with ordinary probabilistic behaviour. If this set of exceptional values are unknown it cannot be discovered by ordinary fixed parameter simulation. If the exceptional value is known the problem is reduced to the problem of representing this exceptional value in the computer, this happens if the parameter value is contained in the available representation of the parameter space. The problem with exceptional values occurs when they are not known, and we want to use computer simulations to find them, or indications of their existence. We cannot by increasing the set of simulated parameter values hope to find exceptional behaviour, since any continuous parameter can only be simulated for a finite number of different values. The solution of

this problem is to simulate over the entire parameter space at the same time.

1.2.2 Omniparametric simulation

Coupling of processes over the parameter space

The basic idea behind omniparametric simulation is a coupling of the model in use over all parameter values in the parameter space. We start with the concept coupling. This is just a brief presentation of the technique, for a general description of the coupling technique see [Lin92].

Consider two stochastic processes, X and Y defined on probability spaces $(\mathbb{P}_X, E_X, \mathcal{E}_X)$ and $(\mathbb{P}_Y, E_Y, \mathcal{E}_Y)$ respectively. A coupling of X and Y is a probability measure μ on the measurable space $(E_X \times E_Y, \mathcal{E}_X \times \mathcal{E}_Y)$ such that $\mathbb{P}_Y = \mu \circ \pi_X^{-1}$ and $\mathbb{P}_Y = \mu \circ \pi_Y^{-1}$, where $\pi_X : E_X \times E_Y \to E_X$ and $\pi_Y : E_X \times E_Y \to E_Y$. So the coupling is a probability measure on a product space, with certain marginals. This definition is given for a pair, but there is nothing keeping us from performing a coupling of several (even an uncountable number) processes simultaneously. We use this when doing omniparametric simulation.

Consider a set of stochastic processes parametrised by a parameter $\theta \in [0,1]$ taking values in the set $\{0,1\}$. Let $\mathbb{X} = \{X_\theta : \theta \in [0,1]\}$ the class of processes and assume that $X_\theta \stackrel{\mathcal{D}}{=} \mu_\theta$. A coupling of all processes in $\mathbb{X}$ is a measure μ on the product space $\{0,1\}^{[0,1]}$ such that $\mu_\theta = \mu \circ \pi_\theta^{-1}$, for $\theta \in [0,1]$, where π_θ is a projection from $\{0,1\}^{[0,1]}$ to $\{0,1\}$. One important result regarding such measures is Strassen's theorem [Str65] from 1965.

When using this coupling to do omniparametric simulation we will simulate the probability measure μ on the space $\{0,1\}^{[0,1]}$, and represent a configuration in this space by a partition of (A_0, A_1) of $[0,1]$ such that the following holds.

$$X_\theta = \begin{cases} 1, & \theta \in A_1 \\ 0, & \theta \in A_0 \end{cases}$$

If we manage to do the coupling in a "nice" way we can represent this partition with a single number, a threshold θ_t , such that for $\theta < \theta_t$ we have $X_\theta = 0$, and whenever $\theta \geq \theta_t$ we have $X_\theta = 1$.

Consider a stochastic model parametrised by a possibly multidimensional parameter $\Theta = (\theta_1, ..., \theta_n)$. When generating samples from this model we use a fixed parameter simulation algorithm with parameter Θ. When performing an omniparametric simulation of the same model we

use a parameter with lower dimension, $\theta' = (\theta_{m+1}, \theta_{m+2}, ..., \theta_n)$ for some $0 < m \leq n$. Let us assume that the "unused" part of the parameter, $(\theta_1, ..., \theta_m)$, takes values in a finite subset D of $\mathbb{R}^m$. Instead of generating samples according to some distribution μ_{fix} we generate a partition of D according to some other distribution μ_{omni}. Given any $x \in D$ we can easily generate a sample as if we from the beginning used the parameter $\theta = (x, \theta')$, and this sample is distributed according to μ_{fix}. For a particle system the omniparametric simulation algorithm generates, for each particle, a partition of D, giving us the state for this particle for any parameter value. One may think of the omniparametric sample as a random projection $\pi : D \to \mathbb{R}$, such that $\pi(x) \overset{\mathcal{D}}{=} \mu_{\text{fix}}$, for any $x \in D$.

A brief history

The ideas behind omniparametric simulation are not new, already in 1965 Strassen proved his theorem [Str65] about the existence of probability measures with specified marginals, and since then coupling has been an important tool in probability theory.

In 1991 Higuchi [Hig91] presents what he calls a level set representation of the ferromagnetic Ising model. In coupling terms this is a coupling of the Ising ferromagnet for all values of the external field, while the interaction parameter is kept constant. The purpose of the coupling is to study the percolation probability as a function of external field. To our knowledge this is the first encounter of a coupling having the ingredients of a omniparametric model. The kind of coupling Higuchi used was however not new at that time,since it was introduced by Holley in 1974, [Hol74].

In 1995 Grimmet [Gri95] used the ideas of Higuchi to introduce a coupling of random-cluster processes for all values of the edge probability, while the the parameter relating to cluster size, q, is fixed above 1. Grimmett also makes two notes about extending the model. The first is to couple the processes for all parameter values of the two-dimensional parameter making it fully omniparametric. The other one is concerned with the fixed parameter q, letting it take values below 1. The last extension requires some redefinition of involved Poisson processes and as a consequence some results are lost.

To our knowledge the level set representations of stochastic particle systems was used for theoretical purposes only until 1996, when Propp and Wilson published their work [PW96] on perfect simulation using coupling from the past (CFTP). They propose an omniparametric simulation algorithm for the random cluster model, though they named the

method "omnithermal" instead of "omniparametric".

1.2.3 Percolation example

Consider independent bond percolation on the 2-dimensional lattice, $\mathbb{L}^2$, with parameter p. Every edge is "on" with probability p and "off" with probability $1-p$, independently of each other. Let $B_n = (V_n, E_n)$ where

$$V_n = \mathbb{Z}^2 \cap [-n, n]^2 \quad , \quad E_n = \{e = (x, y) : x, y \in B_n,\ |x - y| = 1\}$$

be a finite subgraph of $\mathbb{L}^2$. We let $\mathbb{L}^2$ be the grid on $\mathbb{Z}^2$ defined by

$$\mathbb{L}^2 = (\mathbb{Z}^2,\ \{e = (x, y) : x, y \in \mathbb{Z}^2,\ |x - y| = 1\}\ )$$

See fig. 1.3 (below) for an example of how the boundary of a box relates to the box itself.

Simulation of this model on B_n is done as follows.

1. Fix the parameter p to some values between 0 and 1.
2. Generate independently for each edge e a random number $u_e \overset{\mathcal{D}}{=} U[0, 1]$.
3. Assign edge e the value 1 ("on") if $u_e \leq p$ and 0 ("off") otherwise. Do this for all edges in E_n.

The configuration $\sigma_{\text{fix}} \in \{0, 1\}^{E_n}$ is a sample of the independent bond percolation model for parameter p.

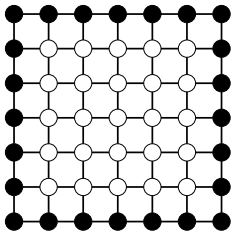

Figure 1.3: The box B_2 (white) with its boundary ∂B_2 (black).

A different approach to this problem is to couple the process for all values of p.

1. Generate independently for each edge a random number $u_e \stackrel{\mathcal{D}}{=} U[0,1]$, and assign this values to the edge.

The configuration $\sigma_{\text{omni}} \in [0,1]^{E_n}$ is an omniparametric sample of the independent bond percolation model. To generate an ordinary configuration with 0's and 1's for a fixed p we do step 3 above for all edges.

As mentioned, the omniparametric simulation approach is a coupling of the process for all values of the parameter p. Given any edge e and the associated threshold value $\sigma_{\text{omni}}(e)$ we see that if this edge is "on" for some p_0 it is also "on" for all $p > p_0$. Let $I_{\{e \text{ is "on"}\}}(p)$ be the indicator function for this edge, then it is monotone as a function on p.

Given σ_{omni} and some fixed p we can generate the configuration σ_{fix}. Corresponding to this configuration is a subgraph of B_n having V_n as vertex set, and $\{e \in E_n : \sigma_{\text{fix}}(e) = 1\}$ as edge set, this is the remaining graph when all "off" edges has been removed. The problem we shall study below is the connection properties of this subgraph for larger and larger n, and hopefully get an estimate of the probability that two vertices are connected as $n \to \infty$. We shall also take a closer look at the difference between the two simulation approaches, both in results and simulation execution time.

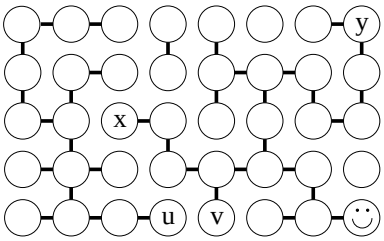

Figure 1.4: A small rectangle of $\mathbb{Z}^2$, where there is a path between vertices x and y but not between u and v. On a larger rectangle however there could be an open path between u and v.

Connection probabilities

Given two vertices $x, y \in \mathbb{Z}^2$ we let $\{x \leftrightarrow y\}$ denote the event that there is a path of open edges between the two vertices. In graph theoretic terms they are in the same connected component after we have removed

all "off" edges from the original graph. The connection probabilities for different pairs of vertices are often difficult or impossible to treat by ordinary analysis so simulation is the tool to use. Let $f_{x,y}(p) = \mathbb{P}_p(x \leftrightarrow y)$ be the connection probability for vertices x and y as a function of p. This function is monotone so an estimate $\hat{f}_{x,y}(p)$ of this function should (hopefully) be monotone as well.

As seen in figure 1.4 the connection probability for a vertex pair could depend on a large, but finite, number of edges. To see why this is the case we use the following argument, given any vertices x and y.

If $\{x \leftrightarrow y\}$ happens then there is some finite path between these vertices, on which the event $\{x \leftrightarrow y\}$ depend, so there is some number M such that $\{x \leftrightarrow y\}$ depends only on box B_M.

If $\{x \leftrightarrow y\}$ does not happen x and y are located in two disjoint connected components, of which only one can be infinite since the infinite connected component in the percolation model is unique. For a proof of this result see [Aiz87]. The smaller one is finite and contained in some finite box B_M so the event $\{x \leftrightarrow y\}$ depend on this box only. This number M is a random variable depending of x, y and σ_{fix}, from the argument above it follows that $M < \infty$ almost surely. During simulation we simulate larger and larger boxes, and stop when reaching box B_M. This process will then terminate with probability 1.

Weather or not the available computer resources will be enough to simulate the model on B_M is a totally different question, but it will play an important role in any implementation.

For most pairs we do not know how to calculate these connection probabilities exactly, but there is one exception. For nearest neighbours x and y we can, by using the dual $\mathbb{L}_d^2$ (see fig 1.5) of $\mathbb{L}^2$, calculate $\mathbb{P}(x \leftrightarrow y)$ in the special case when $p = 1/2$.

For any two vertices $x, y \in \mathbb{Z}^2$ let $\rho(x, y)$ denote a path between x and y not containing the edge (x, y), and let $\{\rho(x, y) = 1\}$ and $\{\rho(x, y) = 0\}$ denote the events that this path is open or closed, respectively.

$$\{\rho(x, y) = i\} = \{\sigma_{\text{fix}} : \sigma_{\text{fix}}(e) = i, \forall e \in \rho(x, y)\}\ , \quad i = 1, 2$$

Consider two nearest neighbour vertices x and y, see fig 1.6.

If $\{x \leftrightarrow y\}$ happens the the edge (x, y) is either open or if (x, y) is closed then some path $\rho(x, y)$ is open. If $\{x \not\leftrightarrow y\}$ happens then the edge (x, y) is closed and there exists some closed path $\rho(u, v)$ in the dual, keeping x and y apart. See fig 1.6. We express this as follows.

$$\begin{array}{ll} (i) & \mathbb{P}_p(x \leftrightarrow y) = \mathbb{P}_p(e = 1) + \mathbb{P}_p(e = 0)\mathbb{P}_p(\ \exists \rho(x, y) : \rho(x, y) = 1\ ) \\ (ii) & \mathbb{P}_p(x \not\leftrightarrow y) = \mathbb{P}_p(e_d = 0)\mathbb{P}_p(\ \exists \rho(x, y) : \rho(u, v) = 1\ ) \end{array}$$

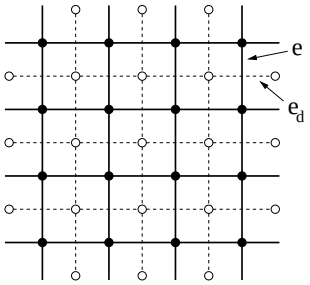

Figure 1.5: A subset of the grid $\mathbb{L}^2$ (solid) and its dual $\mathbb{L}^2_d$ (dashed). For every edge e in the lattice there is one unique corresponding (and crossing) edge e_d in the dual. Whenever e is "off" in $\mathbb{L}^2$ its companion e_d is "off" if $\mathbb{L}^2_d$.

For $p = 1/2$ we have

$$\mathbb{P}_{1/2}(\ \exists \rho(x,y) : \rho(x,y) = 1\ ) = \mathbb{P}_{1/2}(\ \exists \rho(u,v) : \rho(u,v) = 0\ )$$

giving $\mathbb{P}_{1/2}(x \leftrightarrow y) = 3/4$. This argument is well known but we have not been able to trace its roots. For any other value of p we need some constant C, depending on p, such that

$$\mathbb{P}_p(\ \exists \rho(x,y) : \rho(x,y) = 1\ ) = C\ \mathbb{P}_p(\ \exists \rho(u,v) : \rho(u,v) = 0\ )$$

something we do not have.

A fixed parameter simulation scheme

Let x and y be two arbitrary vertices in $\mathbb{Z}^2$. Given any configuration there is some largest box B_M within which we can determine the event $\{x \leftrightarrow y\}$. This number M is random but finite.

We start with a rather small box $B_n = [-n, n]^2$ and see if $\{x \to y\}$ happens or not. Three different situations can occur on a finite box, as described in figure 1.7. We can decide weather $\{x \leftrightarrow y\}$ happens or not in the two pictures to the left. The situation in the right picture in not determined yet, for this we need to look at larger boxes. For any $z \in \mathbb{Z}^2$ let $C(z)$ be the cluster containing z. The algorithm continues and we increase the box size n until $C(x) = C(y)$, or if $C(x) \neq C(y)$ until $C(x) \subseteq B_{n-1}$ or $C(y) \subseteq B_{n-1}$.

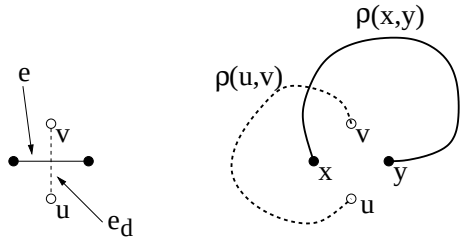

Figure 1.6: To the left the edge e is on and x and y are connected. In the right picture u and v are connected by a closed path not containing e_d. Both e and therefore e_d is "off" and if the path $\rho(u, v)$ in the dual is closed so there can be no open path in $\mathbb{L}^2$ connecting x and y.

This give us a simple simulation algorithm. Given $x, y \in \mathbb{Z}^2$ we start with a small box, if we can determine $\{x \leftrightarrow y\}$ we do this and return the answer, if not, we increase the box size until we can, and then return the answer.

Algorithm for fixed p

The proposed algorithm is simple to use for a fixed value of p. In every step we keep track of the graph consisting of vertices and edges e with $\sigma_{\text{fix}}(e) = 1$. When increasing the box B_n to B_{n+1} we only need to keep track of the cluster information for vertices on the edge ∂B_{n-1}, since the interior of B_n remains the same for all larger boxes. This gives the algorithm linear complexity, regarding memory usage, instead of quadratic.

Termination of the algorithm is a consequence of uniqueness of the infinite cluster in the supercritical phase. This follows from an argument by Burton and Keane in 1989, [Bur89].

Omniparametric algorithm

The omniparametric simulation algorithm returns, instead of just a "1" or "0", a threshold p_t we can use to determine the connection property for different values of p, as described by the indicator function

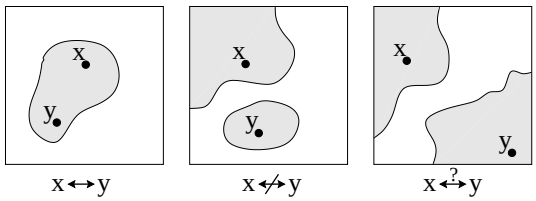

Figure 1.7: On a finite box one out of three events will happen. In the first both x and y are in the same cluster. In the middle x and y are in different connected components of which at least one is fully contained in the box. To the right x and y are contained in different components in the box, but we cannot decide weather or not these components will connect on a larger box, to do this we have to increase the box size sufficiently.

$I_{\{x\leftrightarrow y\}}(p)$.

$$I_{\{x\leftrightarrow y\}}(p) = \begin{cases} 1, & p \geq p_t \\ 0, & p < p_t \end{cases}$$

In the omniparametric model we have at our disposal a threshold value, $\sigma_{\text{omni}}(e)$, for each edge e. Whenever $\sigma_{\text{omni}}(e) \leq p$ the edge is "on", and otherwise "off". Any path ρ between two vertices x and y of $\mathbb{Z}^2$ has a finite set of such thresholds. If the path is open or not for any particular value of p is determined by the largest threshold value in this path. For any path ρ we denote this largest threshold value by $p_t(\rho)$. Let $\Delta^n_{x,y}$ be the set of all paths between x and y contained within the finite box B_n, and define $p_t(x,y)$ as follows.

$$p_t(x,y) = \inf \left(\bigcup_{n\in\mathbb{N}} \{p_t(\rho) : \rho \in \Delta^n_{x,y} \} \right)$$

For any finite subset $A \subset \mathbb{Z}^2$ we define $p_t(x,A)$ as follows

$$p_t(x,A) = \inf \bigcup_{y\in A} p_t(x,y)$$

and this is the smallest p for which there is an open path between x and any of the vertices in A.

We can now formulate the omniparametric simulation algorithm as follows. Given $x, y \in \mathbb{Z}^2$ we start with a small box B and compute

$p_t(x,y)$, $p_t(x,\partial B)$ and $p_t(y,\partial B)$. If $p_t(x,y) \leq \max(p_t(x,\partial B), p_t(y,\partial B))$ we stop and return $p_t(x,y)$. We are then done since given any p vertices x and y are either connected or at least one of them is disconnected from the boundary ∂B. If

$$p_t(x,y) > \max(p_t(x,\partial B), p_t(y,\partial B))$$

we increase the box size, compute $p_t(x,y)$, $p_t(x,\partial B)$, $p_t(y,\partial B)$, and check again. This process continues until $p_t(x,y) \leq \max(p_t(x,\partial B), p_t(y,\partial B))$.

For fixed parameter simulation, termination is a consequence of uniqueness of the infinite cluster in the supercritical phase. This follows from an argument by Burton and Keane in 1989, [Bur89].

For the omniparametric simulation algorithm, termination will not follow directly from the argument by Burton and Keane. We need something stronger, namely uniqueness of the infinite cluster simultaneous for all values of p, and that is established by Alexander in 1995, [Ale95].

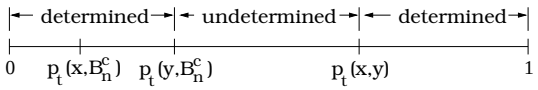

Figure 1.8: The event $\{x \leftrightarrow y\}$ is determined for $p < p_t(y,\partial B_{n+1})$ since there is no path between x and y, and at lest on of them is not connected to the boundary by an open path. For $p \geq p_t(x,y)$ there is an open path between x and y. For $p \in [p_t(x,\partial B_{n+1}), p_t(x,y))$ there there are open paths between both x and y and the boundary, but no path between them within the box. For p in this interval we have to look at a larger box to determine the situation.

When running the algorithm we need access to all edges of the box to determine the three thresholds. There is no easy "update"-strategy here as in the fixed parameter case. The situation is too complex for storing threshold information on just the boundary ∂B_{n-1}, and use this when extending B_n to B_{n+1}. This makes the simulation of the omniparametric model computationally more demanding. Another important consequence of this is the amount of needed computer memory. Here the omniparametric algorithm has quadratic complexity, compared to the linear complexity of the the fixed parameter algorithm.

We will now proceed with simulations and see how we can use the omniparametric algorithm when analysing connection probabilities.

Simulation results

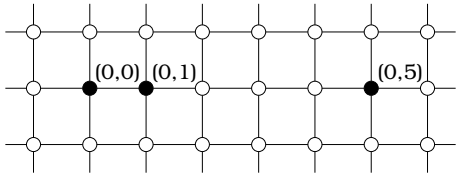

Figure 1.9: Connection probabilities are simulated between the origin and one of its neighbours, and between the origin and vertex $(0, 5)$.

Simulations are done for two pairs of vertices, as shown in fig. 1.9. In fig. 1.10 we see the results of the simulations, the estimated connection probabilities.

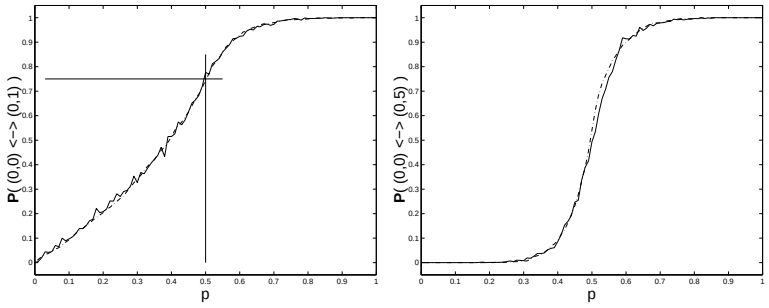

Figure 1.10: Simulated connection probabilities for events $\{(0, 0) \leftrightarrow (0, 1)\}$ and $\{(0, 0) \leftrightarrow (0, 5)\}$. The solid curves are the probabilities estimated by ordinary simulation and the dashed curves are estimates from omniparametric simulations. In the left picture both curves closely approximate the probability $\mathbb{P}_{1/2}(x \leftrightarrow y) = 3/4$. All curves are based on 1000 simulations.

As expected the curves originating from omniparametric simulations are monotone, while the others are not. Using ordinary simulation there is nothing in the algorithm suggesting that the result should be monotone. For a certain set of values for p say $0, 0.01, 0.02, ..., 0.99, 1.00$ one

could perhaps achieve this by running more simulations, but the problem itself remain. No matter how many simulations we do, there will always be possible to find an estimate which is not monotone by dividing the interval for p into finer and finer intervals.

The omniparametric simulation algorithm however has the monotonicity built in, since it is a coupling of the process for all parameter values designed to have this property. No matter how small the number of simulations is the estimated curve originating from omniparametric samples will always be monotone.

There is a large difference in speed. The two simulation techniques are used to generate 1000 samples for each p. The fixed parameter algorithm does 1000 simulations for every value of p, while the omniparametric algorithm does a total of 1000 simulation, independent of the number of values for p. The extra computation for the fixed parameter algorithm becomes critical when p is in a small interval around its critical value, $p_c = 1/2$. In this interval we expect large clusters, making both algorithms slow. Though there is no theoretical difference between the two approaches there is a practical one. While the omniparametric algorithm may encounter large clusters in every simulation, with a certain probability, the ordinary algorithm has the same probability of suffering from a slowdown in $1000A$ simulations, where A is the number of p-values in the critical interval.

Since there is a small probability for the simulations to use larger boxes than the computer can handled we use a fixed largest box size, in this case 500. If the event $I_{\{x \leftrightarrow y\}}$ is not yet determined when reaching this upper limit the simulation is aborted and marked accordingly. These aborted simulations are later used for getting upper and lower estimates of the connection probability. None of the omniparametric simulations did encounter any problems with this limit, while some of the fixed parameter simulations did. In fig. 1.11 we see how this limit affect the simulations.

Theoretically we can get rid of these approximations by just removing the upper limit of the box size. Such simulation will however require a lot of computer resources, both in memory and CPU-time. Simulations show, when boxes up to B_{7000} are used, a week of CPU-time or more is required.

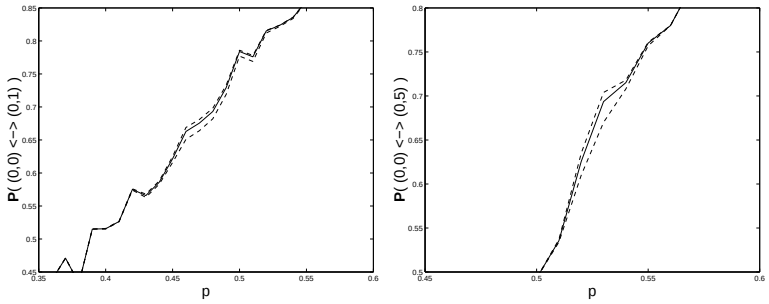

Figure 1.11: The fixed parameter simulations both suffer from the upper limit of the box. In some interval around $p = 1/2$ the curves are only approximated. The solid line is the approximation when disregarding the aborted simulations. The upper and lower dashed lines are estimates using all simulations, including the aborted ones.

CHAPTER 2

The two-type Richardson model

2.1 Definition

The two-type Richardson model is a growth model on the lattice $\mathbb{Z}^d$, introduced by by Häggström and Pemantle [HP98]. In this extension of the ordinary Richardson model [Ric73] two infections are competing for space. Each vertex in the lattice can be infected or not, if infected it can have one of two types.

The process starts at $t = 0$ with a certain initial configuration, that is, two disjoint subsets ξ_1 and ξ_2 of $\mathbb{Z}^d$ where all vertices of ξ_1 have type one, and all vertices of ξ_2 have type two. The rest of the lattice have type zero. The model evolves through time as 0's changes to 1's or 2's at rates depending on the nearest neighbour configuration, while the 1's and 2's do not change at all. Let type one and two have infection rates λ_1 and λ_2 respectively. Due to time scaling and symmetry we only need to study the case when $\lambda_1 = 1$, and $\lambda_2 = \lambda \in [0, 1]$. Let us now state this in a precise manner.

We construct a graph with vertex set $\mathbb{Z}^d$ and edge set $\mathcal{E}$, defined by

$$\mathcal{E} = \{(x, y) : \ x, y \in \mathbb{Z}^d, \ |x - y| = 1\}$$

An element $\Xi^\lambda(t) \in \{0, 1, 2\}^{\mathbb{Z}^d}$ is an assignment of state 0,1 or 2 to each

vertex. Let $\Xi^\lambda(t)$ be the configuration at time t, with parameter λ and denote the state of a vertex $u \in \mathbb{Z}^d$ at time t with $\Xi_u^\lambda(t)$. Also at time t, denote the set of vertices having type one with $\eta_1^\lambda(t)$, and the set having type 2 with $\eta_2^\lambda(t)$. Since this is a growth model we need an initial configuration ξ_1, ξ_2 from which the model can evolve. Define these sets by the following.

$$\xi_i = \{v \in \mathbb{Z}^d : \Xi_v^\lambda(0) = i\},\ i = 1, 2$$

The pair (ξ_1, ξ_2) can be any pair of disjoint subsets of $\mathbb{Z}^d$, but for simplicity we will assume that both are connected subsets of the graph.

The evolution of the model is defined by the infection process. If a vertex has type one or two it infects all its uninfected neighbours at a certain type dependent rate. The probability that such a neighbour will be infected in a short time interval is proportional to the length of the interval. If a type zero vertex has k_1 type one neighbours and k_2 type two neighbours it changes from type zero to type one at rate $k_1\lambda_1$, and to type two at rate $k_2\lambda_2$.

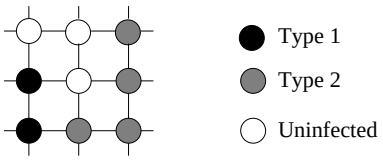

Figure 2.1: The uninfected vertex in the middle changes to type 1 at rate λ_1, and to type 2 at rate $2\lambda_2$

Since the parameters λ_1 and λ_2 do not change over time we get a homogeneous Poisson process of infection events along each edge. We think of this as a process active for all non-negative times, but events are only interesting when the source vertex of the edge is infected and the target vertex is not.

To reduce the number of parameters in the model from two to one we will use the concept of thinning of the Poisson process of infection events. First an explanation of thinning .

Consider a homogeneous Poisson process, with intensity λ. If we let each event occur with a certain probability p and independently of each other it is a straightforward calculation to show that the process of remaining events also is a Poisson process, but with intensity λp. The remaining process is called the thinned Poisson process.

Let λ_1, λ_2 be the infection rates for the two types. Instead of assigning Poisson processes with different intensities to vertices we scale time, use symmetry and thinning. We do this so type one has infection rate 1 and type two has rate $\lambda = \lambda_2/\lambda_1$, and assume $\lambda_2 \leq \lambda_1$.

Assign now independently to all edges two unit rate Poisson processes, one for each possible direction of an infection event,and two sequences of independent random variables (one for each process), $\{u_k\}_{k=1}^{\infty}$ such that $u_k \stackrel{\mathcal{D}}{=} U[0,1]$ for all k. The evolution of the model is now determined by the sequences of Poisson events along with the random numbers. At each event one vertex tries to infect another along the common edge. Assume that such an event takes place at time t, and let t^+ be the time just after this event. Also let v be the infecting vertex and w its victim. If v is infected and w is not the following happens.

$$\Xi_w(t^+) = \begin{cases} 1, & \Xi_v(t) = 1 \\ 2, & \Xi_v(t) = 2,\ u \leq \lambda \\ 0, & \Xi_v(t) = 2,\ u > \lambda \end{cases}$$

where u is the random number associated with this event.

If w is infected or v is not, nothing happens. Let $\mathbb{P}^{\lambda}_{\xi^1,\xi^2}$ denote the probability measure for the described process.

2.2 Behaviour and results

The two-type Richardson model enables us to study growth of two infections with different infection rates, or by ignoring the difference in types, also study the traditional Richardson model. The remaining part of this chapter is devoted to the study of simultaneous survival, that is, the event that both infections continues to infect vertices for all times. First we consider the asymptotic behaviour, then we analyse the situation for finite boxes and see what happens when the box size increases.

2.2.1 Asymptotic properties

Start the process with the following configuration, $\xi_1 = \mathbf{0} = \{(0,0,..,0)\}$ and $\xi_2 = \mathbf{1} = \{\ (1,0,\ldots,0)\ \}$, and let it evolve for all times. There will always be infected vertices having uninfected ones as neighbours, so the infected area will get larger and larger. As time tends to infinity the infection will spread to all vertices of $\mathbb{Z}^s$, leaving no vertex uninfected.

We study $\Xi(t)$ as $t \to \infty$. Let G_1 denote the event that type one survives as $t \to \infty$, and define G_2 accordingly. In the sequel we will

consider the model for a fixed but arbitrary λ, and since it does not change we suppress it in the notation. We have three possible scenarios.

1. Vertices of type one surrounds all type two vertices, and only type one grows to infinity. Type one is said to strangle type two, denote this event $G_1 \setminus G_2$.
2. Type two strangles type one, denoted $G_2 \setminus G_1$.
3. Neither type strangles the other, both types survive as $t \to \infty$, denoted $G_1 \cap G_2$.

As long as $\lambda > 0$ there is a positive probability for both scenario 1 and 2. There is always a possibility for type one to strangle type two since it is the stronger type. Before the region infected by type one has become too large there is always a possibility for type two to strangle it.

The third scenario is harder to say anything about. If both types survive to infinity, this reflects some kind of power balance between the two. For the case $\lambda = 1$ and $d = 2$ Häggström and Pemantle [HP98] showed that $\mathbb{P}^{1,\lambda}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2) > 0$. For the case when $\lambda \neq 1$ they state in [HP00, prop 2.2] roughly that even a small advantage for the stronger type is enough to doom the weaker type in the long run. Their main theorem states (theorem 2.1 below) that for almost all λ we cannot have simultaneous survival of both types in the limit.

Theorem 2.1 ***Häggström-Pemantle***
Consider the two-type Richardson model on $\mathbb{Z}^d$, $d \geq 2$. Then

$$\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2) = 0$$

for all but at most countably many choices of λ.

The result is valid for all finite initial configurations where no type is strangled by the other,see [HP00]. But it does not say anything about the situation for any particular value for λ. For a fixed λ we cannot use this theorem. The same situation arises in simulations. We cannot use simulations to rule out the possibility for exceptional values for λ, that is, rule out the existence of some $\lambda_e \in (0, 1)$ such that

$$\mathbb{P}^{\lambda_e,}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2) > 0$$

In their article [HP00] Häggström and Pemantle states a conjecture regarding the problem with exceptional values.

Conjecture 2.1
For the two-type Richardson model on $\mathbb{Z}^d$, $d \geq 2$, *we have*

$$\mathbb{P}_{\mathbf{0},\mathbf{1}}^{\lambda_1,\lambda_2}(G_1 \cap G_2) = 0$$

whenever $\lambda_1 \neq \lambda_2$.

According to this conjecture there can be no exceptional values, and this is also the starting point and main reason for this thesis.

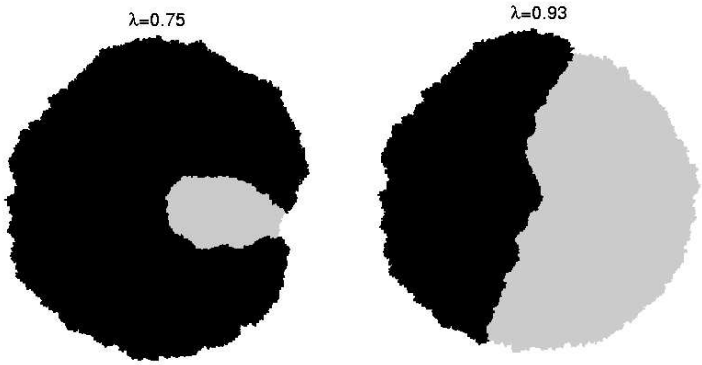

Figure 2.2: A realization of the model for two different values of λ. In the right picture both types seem to have survived in some kind of balance, but in the left type 1 (black) is about to surround the weaker type 2. If conjecture 2.1 is correct, then the apparent balance on the right is doomed to break down in the long run

Another open question is the asymptotic shape of the infected area. Already in his 1973 article [Ric73] Richardson stated the existence of such an asymptotic shape. Some further results concerning it has been published over the years, see [DL81], but the question regarding exact shape remains unanswered.

2.2.2 Finite boxes

So far the results about the two-type Richardson model has to do with asymptotic behaviour. Nothing has been said about the relation

between the two infections in finite time, or on finite regions. No matter how slowly the weaker type infects its neighbours there is a positive probability for it to strangle the stronger type. This event might happen at any time, but is most likely to happen in the beginning before the area infected by the stronger type has become too large.

From Häggström and Pemantle [HP00] we know that a small advantage for the stronger type is enough to ensure that asymptotically it will strangle the weaker type. This is stated in their key proposition (proposition 2.1 below), here adapted to our notation. Before stating it we need a definition of size in the meaning of how spread out sets in $\mathbb{Z}^d$ are. Although the asymptotic shape B is unknown we can use it to define this measure of size, $|\cdot|$. For any set $A \subseteq \mathbb{Z}^d$ let $|A| = \inf\{t : A \subseteq tB\}$. For any two $u, v \in \mathbb{R}$ we define the set $S(u,v)$ of pairs of configurations as follows

$$S(u,v) = \{(\xi^1, \xi^2) : |\xi^1| \leq u,\ |\xi^2| \geq v\}$$

We will use this for $u < v$ to denote subsets of pairs of configurations, (ξ^1, ξ^2), where ξ^1 always will be a little bit smaller than ξ^2.

Proposition 2.1
Fix $\lambda \in (0,1)$ and let $1 < a < b$. Then

$$\lim_{t\to\infty} \sup_{(\xi^1,\xi^2)\in S(ta,tb)} \mathbb{P}^{\lambda,1}_{\xi^1,\xi^2}(G_1) = 0$$

Considering this proposition one question comes to mind, which has to do with convergence rates. Let $\eta_1(t)$ and $\eta_2(t)$ be the sets of vertices infected by type one and two respectively at time t and let type two be the stronger type. If we at time t_0 have $|\eta_2(t_0)|/|\eta_1(t_0)| = c > 1$ how does the convergence look in this case? If our only concern is infection on finite regions we might be interested the probability for strangling the weaker type given the ratio $|\eta_2|/|\eta_1|$, as the region gets larger and larger. Since the definition of $|\cdot|$ uses the unknown asymptotic shape B we have to use some other measure of size to study this by simulations. This question however is left unanswered, it is included more as a thought regarding proposition 2.1.

In percolation finite boxes are often studied, and conclusions drawn regarding the behaviour over the whole lattice based on the behaviour in these finite boxes by letting the box size approach infinity. We can also use this strategy when studying simultaneous survival.

Let the box B_n be a subset of the d-dimensional lattice $\mathbb{Z}^d$. The boundary ∂B_n of this box is the set of all vertices in B_n^c with at least one neighbour in B_n.

Let $G_{i,n}^\lambda$ be the event that type i survives until reaching ∂B_n, $i = 1, 2$. Define a function $p_n(\lambda)$ by the following.

$$p_n(\lambda) = \mathbb{P}(G_{1,n}^\lambda \cap G_{2,n}^\lambda)$$

We need to formulate and prove two properties of the sequence $\{p_n\}_{n=1}^\infty$.

Lemma 2.1
For each n, $p_n(\lambda)$ is continuous.

We defer the proof of lemma 2.1 until all necessary notation has been properly introduced in chapter 3, see page 37.

Lemma 2.2
For any $\lambda \in (0, 1]$ and any n, we have $p_{n+1}(\lambda) < p_n(\lambda)$

Proof :
If $G_{1,n+1}^\lambda \cap G_{2,n+1}^\lambda$ happens then both types has survived until reaching ∂B_n which is enough for $G_{1,n}^\lambda \cap G_{2,n}^\lambda$ to happen. Let $\omega \in \Omega$ be the outcome in fig. 2.3. The set of type one, $\eta_1(t)$ is almost surrounded in the smaller box (B_2), and if vertex v is infected by the type two infection, then $\eta_2(t)$ surround $\eta_1(t)$ in B_3. So $\omega \in (G_{1,2}^\lambda \cap G_{2,2}^\lambda) \setminus (G_{1,3}^\lambda \cap G_{2,3}^\lambda)$. This can happen for each finite n. Thus

$$(G_{1,n}^\lambda \cap G_{2,n}^\lambda) \setminus (G_{1,n+1}^\lambda \cap G_{2,n+1}^\lambda) \neq \emptyset$$

for all n and the wanted result follows.
□

2.3 Simulation, a simple scheme

Given the proposed model with intensities 1 for type one, and λ for type two, a simple simulation algorithm is given in fig. 2.4.

We think of the infection processes as unit rate Poisson processes, because of this we can choose an infecting vertex u at random. The next step is to choose a neighbour v to infect, this is also done uniformly at random. If u has type one and v type zero, vertex v gets infected, and has in the future type one. If u has type two and v has type zero we have

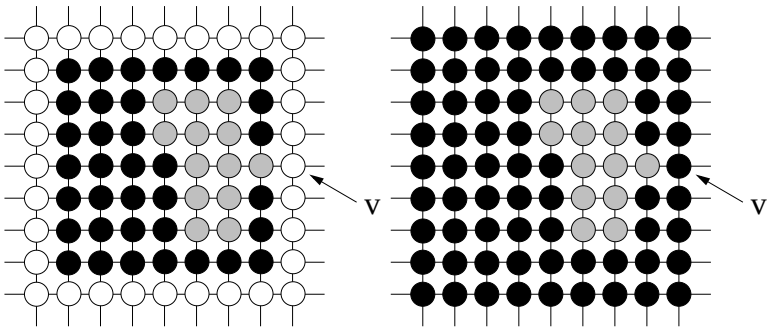

Figure 2.3: The configuration ω in boxes B_2 and B_3.

to use thinning, since this infection event originates from a Poisson process having intensity $\lambda < 1$. With probability λ we infect v with type two. If u has type zero or v does not have type zero no infection takes place. The function computing the stop criteria can be any function as long as it returns TRUE in finite time.

```
graph G
graph G.setInitialConfig()
repeat
  u = G.getRandomVertex()
  v = G.getRandomNeighbour(u)
  if u.type1 ≡ TRUE AND v.uninfected ≡ TRUE then
    v.type = 1
  end if
  if u.type2 ≡ TRUE AND v.uninfected ≡ TRUE then
    if rnd ≤ λ then
      v.type = 2
    end if
  end if
until G.computeStopCriteria() ≡ TRUE
```

Figure 2.4: A simple simulation scheme for the two-type Richardson model.

CHAPTER 3

An omniparametric model

3.1 The omniparametric two-type Richardson model

The omniparametric model is based on the ordinary two-type Richardson model. If we looked upon the ordinary model as a model for spreading infections, the omniparametric model is about spreading information. The information tell us for which parameter values each vertex is uninfected or has one of two infection types.

We use the same graph, $(\mathbb{Z}^d, \mathcal{E})$, as in the ordinary model. We use the same set of independent Poisson processes for all edges in $\mathcal{E}$, each equipped with a sequence of i.i.d. random numbers, all $U[0,1]$. Let a configuration Θ be an element of $\{[0,1]\times[0,1]\}^{\mathbb{Z}^d}$, and let $\Theta(t)$ denote the configuration at time $t \geq 0$.

$$\Theta(t) = \{(a_{v,t}, b_{v,t}) \in [0,1]\times[0,1] :\ a_{v,t} \leq b_{v,t},\ v \in \mathbb{Z}^d\}$$

The configuration for a vertex v at time t is denoted $\Theta_v(t)$, see fig. 3.1.

Given $\Theta(t)$ we can obtain the ordinary configuration $\Xi(t)$ for any $\lambda \in [0,1]$ in the following manner. We assign each vertex v type one if $\lambda \leq a_{v,t}$, type two if $\lambda > b_{v,t}$ and type zero if $\lambda \in (a_{v,t}, b_{v,t}]$, see fig 3.2. For this assignment to work we must have $a_{v,t} \leq b_{v,t}$ for all $t \geq 0$ since a vertex can have one type only.

A initial configuration is an assignment of threshold values to all vertices such that for each $\lambda \in (0,1]$ we have a valid initial configuration

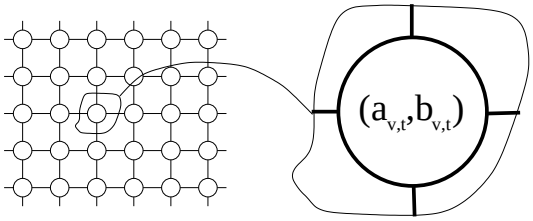

Figure 3.1: Threshold representation in the omniparametric two-type Richardson model

in the ordinary model.

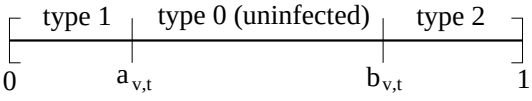

Figure 3.2: Meaning of threshold representation in the omniparametric two-type Richardson model

The evolution of the omniparametric model is more complicated than for the fixed parameter model. Instead of propagating infection types we propagate threshold values. Any vertex having type one or two for some fixed but arbitrary λ can propagate this to any neighbour w having $a_{w,t} \neq b_{w,t}$ if $\lambda \in (a_{w,t}, b_{w,t}]$. The idea is the following. We consider the sequence of Poisson events just as in the ordinary model. Assume that, at time t, a vertex v tries to propagate its information to vertex w, and let t^+ be the time just after this event. Let $\Theta_v(t) = (a_{w,t}, b_{w,t})$ be the state of vertex w at time. This vertex is already infected for $\lambda \in [0, a_{w,t}] \cup (b_{w,t}, 1]$ so only for $\lambda \in (a_{w,t}, b_{w,t}]$ an infection can take place. For vertex v we have three cases.

(i) For $\lambda \in [0, a_{v,t}]$ vertex v has type one, v infects w if $\lambda \in [0, a_{v,t}] \cap (a_{w,t}, b_{w,t}]$.

(ii) For $\lambda \in (b_{v,t}, 1]$ vertex v has type two, v infects w if $\lambda \in (b_{v,t}, 1] \cap (a_{w,t}, b_{w,t}]$.

(iii) For $\lambda \in (a_{v,t}, b_{v,t}]$ vertex v has type zero and cannot infect w.

Infections of type one are spread each time, so at time t^+ we let a_{w,t^+} be equal to $\max(\ a_{w,t},\ \min(a_{v,t}, b_{w,t})\ )$. For an illustration of this, see fig 3.3.

Infections of type two are spread with probability λ. We accomplish this by using the random number u assigned to the Poisson event, and let the type two infection spread whenever $u \leq \lambda$. When we change the limit $b_{w,t}$ we do this depending on $\max(u, b_{v,t})$ instead of just $b_{v,t}$. Let $b_{w,t+} = \min(\ b_{w,t},\ \max(\gamma, a_{w,t})\ )$, where $\gamma = \max(u, b_{v,t})$.

Summary: if at time t vertex v tries to propagate information to vertex w, and $\Theta_v(t) = (a_{v,t}, b_{v,t})$, $\Theta_w(t) = (a_{w,t}, b_{w,t})$, then we get the following.

$$\begin{array}{rcl} a_{w,t^+} & = & \max(\ a_{w,t},\ \min(a_{v,t}, b_{w,t})\ ) \\ b_{w,t^+} & = & \min(\ b_{w,t},\ \max(\gamma, a_{w,t})\ ) \end{array}$$

For the omniparametric model we have the following sample space.

$$\Omega_O = \{(a,b) : a, b \in [0,1],\ a \leq b\}^{\mathbb{Z}^d}$$

An omniparametric configuration is any element $\omega \in \Omega_O$. As in the ordinary fixed parameter model we need a initial configuration. Given any two finite, disjoint and connected (in the ordinary graph theoretic sense) sets $\xi_1, \xi_2 \subseteq \mathbb{Z}^d$ we define the initial configuration as follows.

Definition 3.1 ***Initial configuration***
For $\xi_1, \xi_2 \in \mathbb{Z}^d$. Define $\Theta(0)$ by

$$\Theta_v(0) = \begin{cases} (1,1), & v \in \xi_1 \\ (0,0), & v \in \xi_2 \\ (0,1), & \textit{otherwise} \end{cases}, \quad v \in \mathbb{Z}^d$$

where ξ_1, ξ_2 are two finite disjoint and connected subsets of $\mathbb{Z}^d$.

Next step is the definition of a mapping on the omniparametric sample space defining the dynamics of the model. Assume that a Poisson event happens at time t. Vertex v tries to affect vertex w along the common edge. We now define the evolution operator $\mathbf{S}$.

Definition 3.2 ***The evolution operator:*** $\mathbf{S}$
Given an infection event at time t where vertex v tries to infect vertex w. Let u be a $U[0,1]$ random number. Define the evolution operator $\mathbf{S}$ by the following.

$$\mathbf{S}(v, w, u, \Theta(t)) = \Theta(t^+)$$

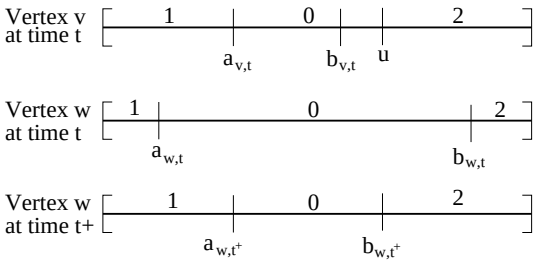

Figure 3.3: An example of how information propagates from vertex v to vertex w.

where $\Theta_v(t^+) = \Theta_v(t)$ *for any vertex* $v \neq w$ *and*

$$\Theta_w(t^+) = (\ \max(\ a_{w,t},\ \min(a_{v,t}, b_{w,t})\ )\ ,\ \ \min(\ b_{w,t},\ \max(u,\ b_{v,t},\ a_{w,t})\ )\ )$$

When there is a need to emphasise the evolution at a certain vertex we denote this by $\mathbf{S}(\Theta_v(t))$.

Next step is to make sure that the threshold order is preserved during evolution, otherwise the state of a vertex may not be unique for some λ.

Lemma 3.1 ***The evolution operator*** $\mathbf{S}$ ***preserves threshold order.***
If for any vertex $w \in \mathbb{Z}^d$ *we have* $\Theta_w(t) = (a_{w,t}, b_{w,t})$ *such that* $a_{w,t} \leq b_{w,t}$ *then* $\mathbf{S}(\Theta_w(t)) = (a_{w,t^+}, b_{w,t^+})$ *will satisfy* $a_{w,t^+} \leq b_{w,t^+}$.

Proof :
We must prove that the order of the thresholds isn't changed by the evolution operator $\mathbf{S}$. Let a Poisson event take place at time t and that vertex v is trying to infect vertex w. Assume that $a_{v,t} \leq b_{v,t}, a_{w,t} \leq b_{w,t}$. There are five different cases to analyse.

Case 1: Assume that $a_{v,t} \leq b_{v,t} \leq a_{w,t} \leq b_{w,t}$.
$a_{w,t^+} = \max(a_{w,t}, \min(a_{v,t}, b_{w,t})) = a_{w,t}$
$b_{w,t^+} = \min(b_{w,t}, \max(u, b_{v,t}, a_{w,t})) \geq a_{w,t}$
$a_{w,t^+} \leq b_{w,t^+}$

Case 2: Assume that $a_{v,t} \leq a_{w,t} \leq b_{v,t} \leq b_{w,t}$.
$a_{w,t^+} = \max(a_{w,t}, \min(a_{v,t}, b_{w,t})) = a_{w,t}$
$b_{w,t^+} = \min(b_{w,t}, \max(u, b_{v,t}, a_{w,t})) \geq b_{v,t}$
$a_{w,t^+} = a_{v,t} \leq b_{v,t} \leq b_{w,t^+}$

Case 3: Assume that $a_{w,t} \leq a_{v,t} \leq b_{v,t} \leq b_{w,t}$.
$a_{w,t^+} = \max(a_{w,t}, \min(a_{v,t}, b_{w,t})) = a_{v,t}$
$b_{w,t^+} = \min(b_{w,t}, \max(u, b_{v,t}, a_{w,t})) \geq b_{v,t}$
$a_{w,t^+} = a_{v,t} \leq b_{v,t} \leq b_{w,t^+}$

Case 4: Assume that $a_{w,t} \leq a_{v,t} \leq b_{w,t} \leq b_{v,t}$.
$a_{w,t^+} = \max(a_{w,t}, \min(a_{v,t}, b_{w,t})) = a_{w,t}$
$b_{w,t^+} = \min(b_{w,t}, \max(u, b_{v,t}, a_{w,t})) = b_{w,t}$
$a_{w,t^+} = a_{w,t} \leq b_{w,t} = b_{w,t^+}$

Case 5: Assume that $a_{w,t} \leq b_{w,t} \leq a_{v,t} \leq b_{v,t}$.
$a_{w,t^+} = \max(a_{w,t}, \min(a_{v,t}, b_{w,t})) = b_{w,t}$
$b_{w,t^+} = \min(b_{w,t}, \max(u, b_{v,t}, a_{w,t})) = b_{w,t}$
$a_{w,t^+} \leq b_{w,t^+}$

Since we have $a_{w,t^+} \leq b_{w,t^+}$ in all five cases, the result follows.

□

These are the components of the model. When using it we have a initial configuration (ξ_1, ξ_2) and then apply the evolution operator for each time there is a Poisson event. This gives us a configuration $\Theta(t)$, $t \geq 0$.

3.2 Relation to the fixed parameter model

Given a configuration $\Theta(t)$ and some $\lambda \in (0,1]$ we may want to compute the fixed parameter configuration $\Xi^\lambda(t)$. We do this with a projection mapping π_λ, defined as follows.

Definition 3.3 ***Projection mapping***
Let $\pi_\lambda : \Omega_O \to \Omega$ for $\lambda \in [0,1]$ be the projection operator defined by the following

$$\pi_\lambda(\Theta_v(t)) = \begin{cases} 1, & \lambda \in [0, a_{v,t}] \\ 0, & \lambda \in (a_{v,t}, b_{v,t}] \\ 2, & \lambda \in (b_{v,t}, 1] \end{cases}, \quad v \in \mathbb{Z}^d$$

The omniparametric configuration is a tool we use to study the fixed parameter configuration for any value of λ. We are especially interested in studying properties of the model as a function of λ, and by using the omniparametric model we get better estimates. Before doing this we must establish a relation between the two models. What we want is the following.

$$\pi_\lambda(\Theta(t)) \overset{\mathcal{D}}{=} \mathbb{P}^\lambda_{\xi^1,\xi^2} \ , \quad t \geq 0$$

In order for this to work we need to establish two properties about the evolution operator $\mathbf{S}$. It must preserve the order of threshold values, otherwise the projection operator will not work, and mimic the dynamics of the two-type-Richardson model for any fixed $\lambda \in [0,1]$, that is, the operator has to be consistent with the behaviour of the two-type-Richardson model. The first property was established in lemma 3.1, the second property is the established in the next lemma.

Lemma 3.2 ***The evolution operator*** $\mathbf{S}$ ***is consistent***
Assume that a Poisson event takes place at time t. Let $\Theta(t)$ be a valid omniparametric configuration for all times prior to t, that is, $\pi_\lambda(\Theta(s)) \overset{\mathcal{D}}{=} \mathbb{P}^\lambda_{\xi^1,\xi^2}$ for all $s \in [0,t]$. Then $\Theta(t^+) = \mathbf{S}(\ \Theta(t)\ ) \overset{\mathcal{D}}{=} \mathbb{P}^\lambda_{\xi^1,\xi^2}$.

Proof :
Let a Poisson event take place at time t and let $\Theta(t^+) = \mathbf{S}(\Theta(t))$ be the configuration just after this event. We need to prove that the evolution operator has the correct behaviour in every situation. Let $\lambda \in [0,1]$ be arbitrary but fixed. There are nine cases to analyse.

Case 1: $\pi_\lambda(\Theta_v(t)) = \pi_\lambda(\Theta_w(t)) = 0$, implies $a_{v,t} < \lambda \leq b_{v,t}$, $a_{w,t} < \lambda \leq b_{w,t}$ and

$$a_{w,t^+} = \max(a_{w,t}, \underbrace{\min(a_{v,t}, b_{w,t})}_{=a_{v,t}}) < \lambda$$

$$b_{w,t^+} = \min(b_{w,t}, \underbrace{\max(\gamma, a_{w,t})}_{\geq\lambda}) \geq \lambda$$

where $\gamma = \max(u, b_{v,t}) \geq \lambda$.
Thus $a_{w,t^+} < \lambda \leq b_{w,t^+}$ implying $\pi_\lambda(\mathbf{S}(\Theta_w(t))) = 0$

Case 2: $\pi_\lambda(\Theta_v(t)) = 0$, $\pi_\lambda(\Theta_w(t)) = 1$, implies $a_{v,t} < \lambda \leq b_{v,t}$, $\lambda \leq a_{w,t}$ and

$$a_{w,t^+} = \max(a_{w,t}, \underbrace{\min(a_{v,t}, b_{w,t})}_{=a_{v,t}}) = a_{w,t} \geq \lambda$$

Thus $a_{w,t^+} \geq \lambda$ gives $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 1$

Case 3: $\pi_\lambda(\Theta_v(t)) = 0,\ \pi_\lambda(\Theta_w(t)) = 2$, implies $a_{v,t} < \lambda \leq b_{v,t},\ b_{w,t} < \lambda$ and

$$b_{w,t^+} = \min(\underbrace{b_{w,t}}_{<\lambda}, \max(\gamma, a_{w,t})) < \lambda$$

Thus $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 2$

Case 4: $\pi_\lambda(\Theta_v(t)) = 1,\ \pi_\lambda(\Theta_w(t)) = 0$, implies $\lambda \leq a_{v,t},\ a_{w,t} < \lambda \leq b_{w,t}$ and

$$a_{w,t^+} = \max(a_{w,t}, \underbrace{\min(a_{v,t}, b_{w,t})}_{\geq\lambda}) \geq \lambda$$

Thus $a_{w,t^+} \geq \lambda$ gives $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 1$

Case 5: $\pi_\lambda(\Theta_v(t)) = 1,\ \pi_\lambda(\Theta_w(t)) = 1$, implying $a_{v,t} \geq \lambda$ and $a_{w,t} \geq \lambda$.

$$a_{w,t^+} = \max(a_{w,t}, \min(a_{v,t}, b_{w,t})) \geq \lambda$$

Since $a_{w,t^+} \geq \lambda$ we have $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 1$.

Case 6: $\pi_\lambda(\Theta_v(t)) = 1,\ \pi_\lambda(\Theta_w(t)) = 2$, implies $a_{v,t} \geq \lambda,\ b_{w,t} < \lambda$ and

$$b_{w,t^+} = \min(\underbrace{b_{w,t}}_{<\lambda}, \max(\gamma, a_{w,t})) < \lambda$$

Since $b_{w,t^+} < \lambda$ we have $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 2$.

Case 7: $\pi_\lambda(\Theta_v(t)) = 2,\ \pi_\lambda(\Theta_w(t)) = 0$, implies $b_{v,t} < \lambda,\ a_{w,t} < \lambda \leq a_{w,t}$ and

$$a_{w,t^+} = \min(a_{w,t}, \underbrace{\min(a_{v,t}, b_{w,t})}_{<\lambda}) < \lambda$$

$$b_{w,t^+} = \min(\underbrace{b_{w,t}}_{\geq\lambda}, \max(u, \underbrace{b_{v,t}}_{<\lambda}, \underbrace{a_{w,t}}_{<\lambda})) \begin{cases} < \lambda, & \text{if } u < \lambda \\ \geq \lambda, & \text{if } u \geq \lambda \end{cases}$$

Thus $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 2$ with probability λ, and $\pi_\lambda(\mathbf{S}(\Theta_w(t^+))) = 0$ with probability $1 - \lambda$.

Case 8: $\pi_\lambda(\Theta_v(t)) = 2,\ \pi_\lambda(\Theta_w(t)) = 1$, implies $b_{v,t} < \lambda,\ \lambda \leq a_{w,t}$ and

$$a_{w,t^+} = \max(a_{w,t}, \underbrace{\min(a_{v,t}, b_{w,t})}_{<\lambda}) \geq \lambda$$

Thus vertex w is left unchanged.

Case 9: $\pi_\lambda(\Theta_v(t)) = 2,\ \pi_\lambda(\Theta_w(t)) = 2$, implies $b_{v,t} < \lambda$, $b_{w,t} < \lambda$ and

$$b_{w,t^+} = \min(\underbrace{b_{w,t}}_{<\lambda}, \max(\gamma, a_{w,t})) < \lambda$$

With $b_{w,t^+} < \lambda$ vertex w is left unchanged.

This can be done for any $\lambda \in [0,1]$. Thus the evolution operator is consistent.
□

By applying this evolution operator repeatedly at every Poisson event the model evolves as time passes.

Theorem 3.1
Given an omniparametric sample $\Theta(t)$ we can calculate an ordinary sample by using the projection operator

$$\pi_\lambda(\Theta(t)) \stackrel{\mathcal{D}}{=} \mathbb{P}^\lambda_{\xi^1,\xi^2}$$

for $\lambda \in [0,1]$ and any $t \geq 0$.

Proof :
Let $\Theta(0)$ be any initial configuration and $\lambda \in [0,1]$ fixed. We apply the projection operator on this configuration vertex by vertex.

$$\pi_\lambda(\Theta_v(0)) = \begin{cases} 1, & \lambda \in [0, a_{v,t}] \\ 0, & \lambda \in (a_{v,t}, b_{v,t}] \\ 2, & \lambda \in (b_{v,t}, 1] \end{cases} \quad , \quad v \in \mathbb{Z}^d$$

Since each vertex $v \in \mathbb{Z}^d$ has $\Theta_v(0) \in \{(1,1)\ (0,0)\ (0,1)\}$ according to the definition of the initial configuration it follows that the projection mapping applied to the initial configuration gives a proper configuration in the fixed parameter model.

Even though time is continuous the model evolves only at each Poisson event. Let $\{t_n\}_{n=1}^\infty$ be the sequence of times for all the Poisson events. Assume that $\pi_\lambda(\Theta(t_n)) \stackrel{\mathcal{D}}{=} \mathbb{P}^\lambda_{\xi^1,\xi^2}$. Let t_n^+ be the time just after the next event. Since the evolution operator is consistent according to lemma 3.2 we automatically have $\pi_\lambda(\Theta(t_n^+)) \stackrel{\mathcal{D}}{=} \mathbb{P}^\lambda_{\xi^1,\xi^2}$. The result now follows by induction.
□

We are now ready to prove lemma 2.1 given in chapter 2.

Proof:
Fix some arbitrary $n \in \mathbb{Z}^+$ Let $G^{\lambda}_{i,n}$ be the event that type i survives until reaching ∂B_n, $i = 1, 2$. If $\mathbb{P}(G^{\lambda}_{1,n})$ and $\mathbb{P}(G^{\lambda}_{2,n})$ are continuous continuity follows for p_n since ...

$$p_n(\lambda) = \mathbb{P}(G^{\lambda}_{1,n} \cap G^{\lambda}_{2,n}) = \mathbb{P}(G^{\lambda}_{1,n}) - \mathbb{P}(G^{\lambda}_{1,n} \setminus G^{\lambda}_{2,n}) = \mathbb{P}(G^{\lambda}_{1,n}) - \mathbb{P}((G^{\lambda}_{2,n})^c)$$

Fix $\lambda \in (0,1)$ and a small $\varepsilon > 0$.
Is there a $\delta > 0$ such that $|\mathbb{P}(G^{\lambda}_{1,n}) - \mathbb{P}(G^{\lambda+\delta}_{1,n})| < \varepsilon$?

$$\begin{aligned} |\mathbb{P}(G^{\lambda}_{1,n}) - \mathbb{P}(G^{\lambda+\delta}_{1,n})| &= \mathbb{P}(G^{\lambda}_{1,n} \setminus G^{\lambda+\delta}_{1,n}) \\ &\leq \mathbb{P}(\{a_v \in [\lambda, \lambda+\delta) \text{ for some } v \in \partial B_n\}) \end{aligned}$$

where $(a_v, b_v) = \Theta_v(t)$. Since ∂B_n is a finite set this shrinks to zero as $\delta \downarrow 0$. Hence, there is some small enough δ satisfying $|\mathbb{P}(G^{\lambda}_{1,n}) - \mathbb{P}(G^{\lambda+\delta}_{1,n})| < \varepsilon$. The same type of argument using the other threshold value, b_v, yields continuity for $\mathbb{P}(G^{\lambda}_{2,n})$.

□

CHAPTER 4

Simulation experiments

By using the proposed simulation algorithm to generate samples we can study the behaviour of the two-type Richardson model on finite boxes in $\mathbb{Z}^d$. Although this is possible for any finite d the case studied here is $d = 2$.

The purpose of this chapter is to study the probability for simultaneous survival on a finite box B_n as a function of λ. For B_n we let $G^{\lambda}_{i,n}$ denote the survival of type $i = 1, 2$ on the boundary ∂B_n. We let G_1 denote the event that type one survives in the limit and define G_2 in the same manner.

According to theorem 2.1 we have $\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2) = 0$ for all but at most countably many choices of $\lambda \in (0, 1]$. Let $E \subseteq (0, 1)$ be this set of exceptional values of λ. Note that we have excluded 1 from E since it is already known that $\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2) > 0$, whenever $\lambda = 1$. We can formulate our knowledge of the probability for simultaneous survival as follows

$$\forall \lambda \in (0, 1) \setminus E : \ \mathbb{P}^{1,\lambda}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2) = 0$$

By doing simulations we will try to find some indications of the existence of any value $\lambda_e \in E$.

4.1 Simultaneous unbounded growth in simulations

We are looking for some indication of the existence of exceptional values, and one may wonder how they manifest themselves in simulations.

Let $p_n(\lambda) = \mathbb{P}(G^\lambda_{1,n} \cap G^\lambda_{2,n})$ be the probability for simultaneous survival on finite boxes and let $p(\lambda)$ denote the probability for simultaneous survival on $\mathbb{Z}^2$. Then $p_n(\lambda) \to p(\lambda)$ point wise as $n \to \infty$.

In the absence of exceptional values ($E = \emptyset$) the function p will have the following appearance.

$$p(\lambda) = \begin{cases} c, & \lambda = 1 \\ 0, & \lambda < 1 \end{cases} \quad , \quad \lambda \in (0, 1)$$

for some $c > 0$. The functions p_n will be continuous for each n, and they will converge point wise to function $p(\lambda)$ as $n \to \infty$.

Assume for the moment that the set E isn't empty, and pick $\lambda_e \in E$. Whenever $\lambda = \lambda_e$ there is a positive probability for simultaneous survival, then the function p will not be increasing, and since the functions p_n converge point wise to p they will not be increasing either whenever n is large enough. According to [HP00] the set E is at most countable so an exceptional value λ_e will have non-exceptional values to the right of it, and will manifest itself as in fig. 4.1.

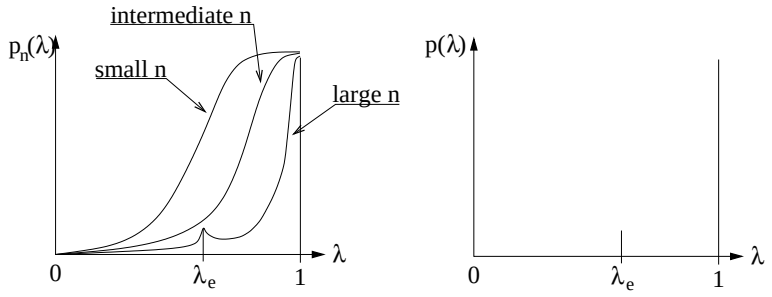

Figure 4.1: The functions $p_n(\lambda)$ and $p(\lambda)$ when there is an exceptional value λ_e.

We use simulations to estimate functions p_n with $\hat{p}_n$, and do this for a number of different values of n. If we find that all $\hat{p}_n$ are increasing it's an indication of increasing p_n, for the simulated values of n. If p_n is increasing for all large n then so is $p(\lambda)$ which rules out the existence

of exceptional values. The question is now: When is n large? We do not know the answer to this question, so the simulations have been carried out for n as large as possible. Later we will use the simulations to estimate how large boxes we need to study exceptional probabilities bounded from below by some small constant.

Another way to analyse the estimated functions is to fit a parametric curve to them and see how well it fits the estimations. We know that the functions p_n decrease when n increases, so the model should be able to reflect that.

4.2 The simulation algorithm

The simulation algorithm follows the omniparametric two-type Richardson model as it is described in section 3.1, see fig. 4.2.

```
1: graph G
2: G.setInitialConfig()
3: repeat
4:    u = G.randomVertex()
5:    v = G.randomNeighbour(u)
6:    u.propagateTo(v)
7: until G.calcStopCriteria() ≡ TRUE
```

Figure 4.2: A simulation scheme for the omniparametric two-type Richardson model.

What is left to describe is initial conditions and stop criteria.

4.2.1 Initial configuration

The smallest possible initial configuration is used. Vertices $\mathbf{0} = (0, 0)$ and $\mathbf{1} = (1, 0)$ are assigned thresholds $(a_{\mathbf{0},0}, b_{\mathbf{0},0}) = (1, 1)$ and $(a_{\mathbf{1},0}, b_{\mathbf{1},0}) = (0, 0)$ respectively. All other vertices $x \in B_n$ are assigned thresholds $(a_{x,0}, b_{x,0}) = (0, 1)$. For every $\lambda \in (0, 1]$ this gives the origin type one, its left neighbour type two and the rest of B_n type zero.

4.2.2 Stop criteria

The algorithm is executed until the first vertex on the boundary ∂B_n is affected, that is, for $t \leq T_{stop}$, where T_{stop} is defined by the following.

$$T_{stop} = \max\{t \ : \ (a_{x,t}, b_{x,t}) = (0,1), \forall x \in \partial B_n\}$$

The model is only defined on the box B_n so we have to abort at this stage. If we continue after this the model will not evolve as the two-type Richardson model prescribe.

4.2.3 Data structures

The most critical resource for a large simulation is memory. When the infected area grows only a small fraction of vertices will actually be active in the process. A vertex u having $a_{u,s} = b_{u,s}$ at time s is already infected for all values of λ, so if $a_{v,s} = b_{v,s}$ is true for all neighbours v then u will never infect any other vertex and will remain inactive for all times $t > s$. We call a vertex w active if there is any value of λ for which w or any of its neighbours can infect or be infected, that is if $a_{\cdot,s} \neq b_{\cdot,s}$ for w or any of its neighbours. If we fix any vertex in $\mathbb{Z}^2$ eventually this will become inactive, it and all of its neighbours will have $a_{\cdot,s} = b_{\cdot,s}$. In line (4) and (5) of the algorithm (in fig. 4.2) we choose a vertex that will try to infect and a victim. Its crucial that this is done uniformly over the graph. If we in line (4) choose an inactive vertex nothing will happen, and we choose another. So if we remove all inactive vertices from the graph this will not change the dynamics of the model, but it will speed up the algorithm, and save memory. When taking advantage of this property of the model we only have to store $O(n)$ vertices in memory, if we were to store them all the memory usage would be $O(n^2)$.

4.2.4 Optimisation issues

It is tempting to go one step further when optimising the execution time. The next candidate is line (5) in the simulation scheme. When we choose a neighbour at random we could discard neighbours which cannot be infected any more. But if we do this we do not choose an edge uniformly at random, instead we are introducing bias. Excluding one or more neighbours in line (5) results in giving the other neighbours probability at least $1/3$ of being chosen. If we have n active vertices we choose a vertex in line (4) with probability $1/n$. Then we must choose a neighbour with a probability independent of the first vertex, so this

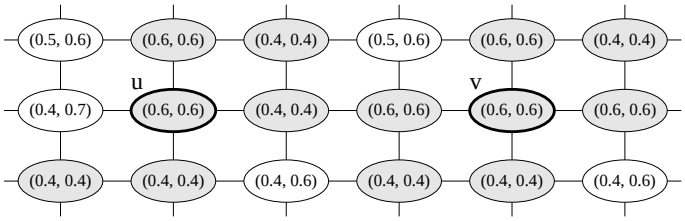

Figure 4.3: An example of one active vertex u and one inactive vertex v. Vertices which cannot be infected for any λ any more are coloured gray, vertices still not infected for some λ are white. Vertex v is surrounded by gray vertices and therefore inactive, while u still has one white neighbour and thus remains active.

probability must be equal for all vertices. For some vertices this second probability will indeed be $1/4$, so it must be $1/4$ for all vertices, and this is not the case if we exclude vertices that cannot be infected but still has neighbours that can.

4.2.5 Simulation setup

We perform simulations for the following values of n.

$$n \in \{50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 750, 1250, 2500\}$$

For all but the largest box 1000 simulations are done. Since large boxes take a long time to simulate, we were forced to limit the number of simulations for $n = 2500$ to 100.

After running all simulations the functions p_n are estimated pointwise in the following manner. Each simulation generates threshold values for every vertex. Let T_i be the set of threshold values for a simulation i, and assume we have done m simulations. Then $\mathbf{T} = \cup_{i=1}^{m} T_i$ is the set of values of λ where some vertex changes in the model. Order these vales according size.

$$\mathbf{T} = \{\lambda_1, \lambda_2, ..., \lambda_N\}$$

For each $\lambda_i \in \mathbf{T}$ we estimate $p_n(\lambda_i)$ by just going through all simulations and check in how many of these both types have survived on ∂B_n and divide this number with the total number of simulations.

4.3 Results

In fig. 4.4 we see the estimated functions $\hat{p_n}(\lambda)$ for some of the simulated boxes. As expected the probability for simultaneous survival (for

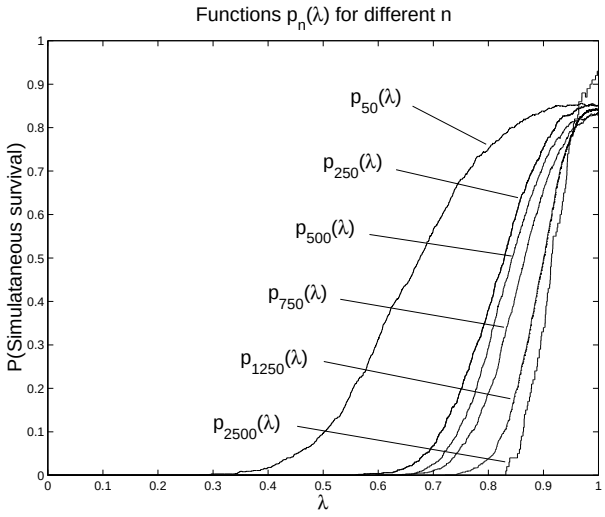

Figure 4.4: the estimates of the functions $p_n(\lambda)$ for some values of n.

any fixed λ) is decreasing as the box size increases. Functions $\hat{p}_{1250}(\lambda)$ and $\hat{p}_{2500}(\lambda)$ breaks this monotone pattern. The more erratic behaviour of $\hat{p}_{2500}$ is of course due to the smaller number of samples. There is no indication of non-monotonicity like in fig 4.1 in any of the estimated functions. An open question is if the simulated boxes are large enough. If there exists any exceptional value $\lambda_e \approx 1$ with $\mathbb{P}^{1,\lambda_e}_{\mathbf{0},\mathbf{1}}(G^{\lambda_e}_{1,n} \cap G^{\lambda_e}_{2,n}) \approx 0$ we would probably need extremely large boxes to see this. No matter how large boxes we simulate there will however always be possible to have a small exceptional probability at an exceptional value close enough to 1.

4.4 Curve fitting

In this section we fit a model to the estimated curves and in the next section we use it for an analysis.

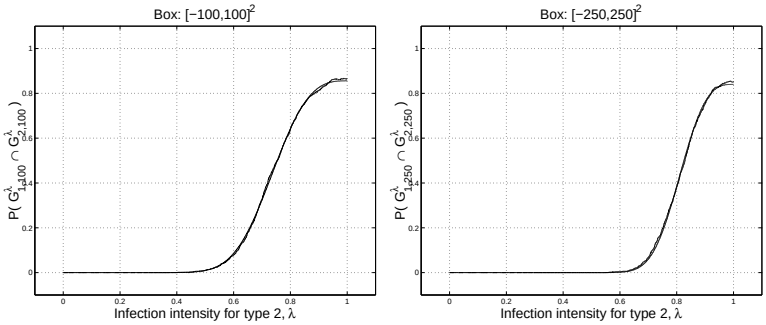

Figure 4.5: Estimated and fitted function for boxes B_{100} and B_{250}.

4.4.1 Fit a parametric curve to the estimated functions

Let us fit a parametric curve to the estimated functions $\hat{p_n}(\lambda)$, and see if we can relate the parameters to box size. When looking at the estimated curves it seems appropriate to fit some s-shaped curve to data. We try with the following.

$$f_n(\lambda) = \alpha_n e^{-\beta_n (1-\lambda)^3}$$

It is tempting to replace 3 in the exponent by a third parameter γ_n to get o closer fit. This does not, however, decrease the difference between f_n and $\hat{p}_n$ enough to motivate such an extension. We have two parameters α_n and β_n to estimate from the function $\hat{p}_n$. The first parameter α_n is the probability for simultaneous survival whenever the infection intensities are equal, the second parameter has to do with the shape of the curve.

There is no hope of course for this curve to be correct. Theoretically we have $p_n(0) = \mathbb{P}^{1,0}_{\mathbf{0},\mathbf{1}}(G^0_{1,n} \cap G^0_{2,n}) = 0$ since type two doesn't infect at all with zero infection intensity, but $\alpha_n e^{-\beta_n} > 0$ for all plausible values of the estimated parameters. Even if there is no theoretical support for this model it is interesting to see how closely we can approximate the estimated functions. Curve fitting can also illustrate how $p_n(\lambda)$ behave for $\lambda \approx 1$ as $n \to \infty$, which is important when studying how fast the stronger type strangle the weaker. With these remarks in mind we proceed. In figures 4.5 and 4.6, we see the result of this procedure.

Note that f_n does not fit the estimated functions well whenever λ is small enough or close to 1. But there is a region, I^1_n (see fig. 4.7),

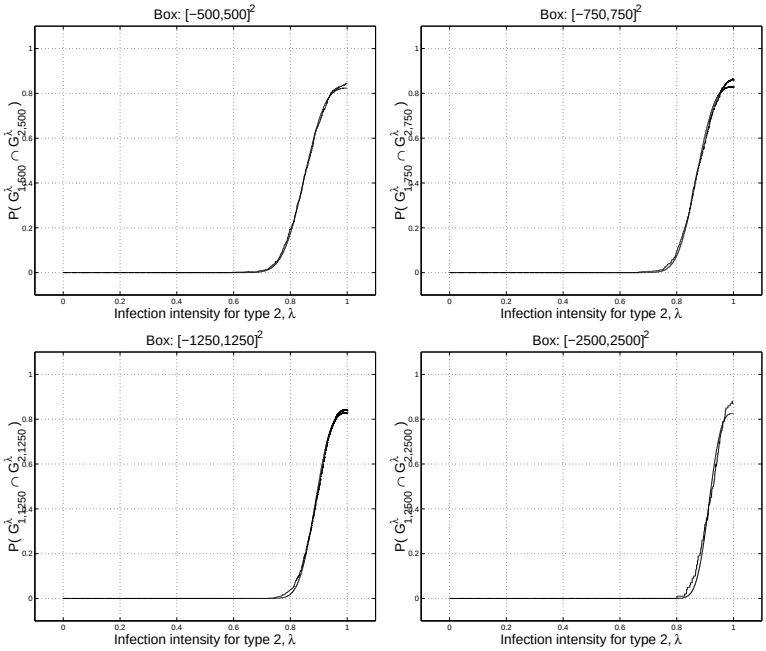

Figure 4.6: Estimated and fitted function for boxes B_{500}, B_{750}, B_{1250} and B_{2500}.

when $\hat{p}_n(\lambda)$ increases the most where $f_n(\lambda)$ fits quite well. Perhaps $f_n(\lambda)$ captures the behaviour of $\hat{p}_n$ when its derivative is large. Above this interval (I_n^2 in fig. 4.7) simulations indicate $\hat{p}_n(\lambda) \leq f_n(\lambda)$.

For all boxes the probability for simultaneous survival doesn't change much when λ is close to 1, but decreases quite rapidly (at least for larger boxes) when λ is below some threshold value $\lambda_{t,n}$. In fig. 4.7 w have $\lambda_{t,n}$ somewhere in the middle of the interval I_n^2. In the simulated cases this threshold $\lambda_{t,n}$ approaches 1 as n gets larger. Perhaps this behaviour is the same for all finite boxes and $\lambda_{t,n} \to 1$ as $n \to \infty$. In that case the behaviour is consistent with the belief that the exceptional set E is empty.

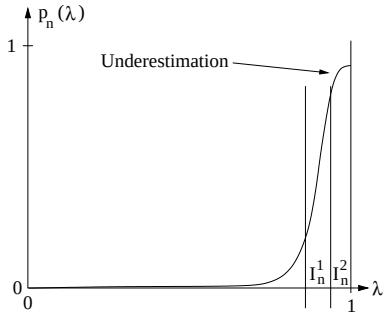

Figure 4.7: In the interval I_n^1 where $f_n(\lambda)$ closely approximates $\hat{p}_n(\lambda)$. In interval I_n^2 we have $p_n(\lambda) \leq f_n(\lambda)$. We can use the underestimation of the curve in I_n^2 to get a upper bound for the rate of convergence at which $p_n \to p$.

4.4.2 Dependence between parameter and box size

In trying to relate the parameters to box size we plot these as functions of n. In fig 4.8 there appears to be no strong correlation between n and α_n. Theory indicates that α_n should be decreasing as n gets larger, approaching the limit value $\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G_1 \cap G_2)$ as $n \to \infty$. It's hard to say anything about how α_n approaches its limit values, the simulated data is too spread out and the limit value unknown. Considering fig. 4.8 it seems reasonable however to conclude that $\lim_{n\to\infty} \alpha_n \in [0.80, 0.82]$. The dependence of α_n on n should not be linear since we cannot have negative values for α_n, ever. Perhaps some sort of exponential or slowly varying function is more appropriate to model the decay.

The situation for parameter β is different. This parameter models the shape of the function. In fig. 4.8 we see that there is some quite strong linear dependence between n and β_n. As the finite boxes grows to infinity so does β_n, resulting in the following limit function.

$$p_\infty(\lambda) = \lim_{n\to\infty} \alpha_n e^{-cn(1-\lambda)^3} = \begin{cases} \alpha, & \lambda = 1 \\ 0, & \lambda < 1 \end{cases} \quad , \quad c = 0.40$$

where $\alpha = \lim_{n\to\infty} \alpha_n$. This is also consistent with the belief that E is empty, so there is nothing new here. If this captures the dependence between n and β_n we can see how quickly the functions f_n converges to $\delta(1-\lambda)$, and get an indication of how the probability of simultaneous

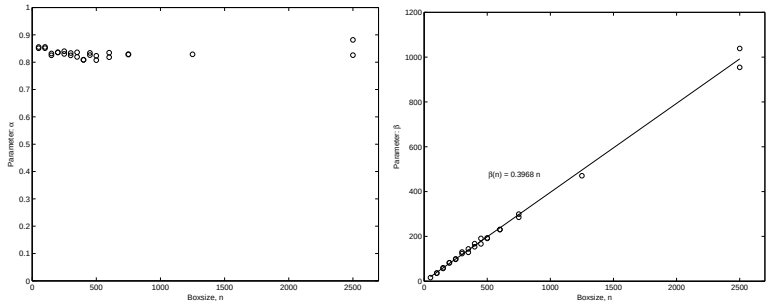

Figure 4.8: Parameters α_n and β_n for different values of the box size n.

survival behave on finite boxes.

4.5 Statistical analysis

4.5.1 A test: Are there exceptional values for $\lambda \in (0, 0.7]$?

All simulation results indicate that the set E of exceptional values for λ is empty, but how strong is the evidence against $E \neq \emptyset$.

Given $\hat{p}_n(\lambda)$ we assume the existence of exceptional values λ_e such that,

$$\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda_e}_{1,n} \cap G^{\lambda_e}_{2,n}) \geq \hat{p}_n(\lambda_e)$$

that is, the existence of λ_e such that we should be able to see some indications of them in simulations. We cannot use this idea to test the existence of λ_e such that

$$\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda_e}_{1,n} \cap G^{\lambda_e}_{2,n}) < \hat{p}_n(\lambda_e)$$

since these are not visible in simulations.

We fix $\varepsilon > 0$ and test the hypothesis that there exists some $\lambda_e \in (0, a]$, $a < 1$, such that $\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda}_{1,n} \cap G^{\lambda}_{2,n}) \geq \varepsilon$ against the alternative that there is no such exceptional values.

We perform the test for the largest box where we have $m = 1000$ simulations, that is B_{1250}. Figure 4.6 indicates that $E \cap (0, 0.7] = \emptyset$, so we use $a = 0.7$. (Here we make the cardinal sin of looking at data before deciding on the null hypothesis. We feel that this does not have very

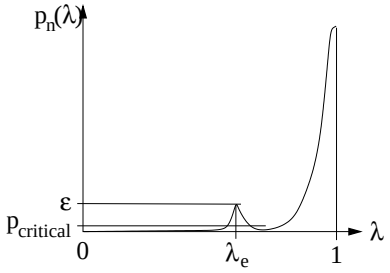

Figure 4.9: Assuming the existence of $\lambda_e \in (0, a]$ such that $\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda_e}_{1,n} \cap G^{\lambda_e}_{2,n}) \geq \varepsilon$ we reject the null hypotheses in favour of the alternative if $\max\{\hat{p}_n(\lambda) : \lambda \in (0, a]\} \leq p_{critical}$.

severe consequenses in this case, but the critical reader is invited to try other values of a.) We now state the hypotheses

$$\begin{aligned} H_0 : &\quad \exists \lambda_e \in [0, a] : \ \mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda_e}_{1,n} \cap G^{\lambda_e}_{2,n}) \geq \varepsilon \\ H_1 : &\quad \forall \lambda \in [0, a] : \ \mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda}_{1,n} \cap G^{\lambda}_{2,n}) < \varepsilon \end{aligned}$$

Under the null hypothesis the Binomial distribution and the central limit theorem give us a statistic

$$Z = \frac{\hat{p}(\lambda_e) - p(\lambda_e)}{\sqrt{p(\lambda_e)(1 - p(\lambda_e))/m}} \overset{\mathcal{D}}{\approx} N(0, 1)$$

provided that we have a candidate for λ_e (which we do not). Suppose $p_n(\lambda_e) = \varepsilon$. This suggests that we reject H_0 in favour of H_1 at significance level α if

$$\hat{p}_n(\lambda_e) \leq p_{critical} = \varepsilon - z_\alpha \sqrt{\frac{\varepsilon(1 - \varepsilon)}{m}}$$

We do not however know the value λ_e so we choose a conservative approach and reject H_0 whenever $p_{max} \leq p_{critical}$, where

$$p_{max} = \max\{\hat{p}_n(\lambda) : \lambda \in (0, a]\}$$

As a consequence of the choice of a we have $p_{max} = 0$, and we can easily calculate the p-values of the test as a function of ε, see fig. 4.10.

With $\alpha = 0.05$ we can reject for $\varepsilon \geq 0.0027$ and if we want $\alpha = 0.01$ we can reject whenever $\varepsilon \geq 0.0054$.

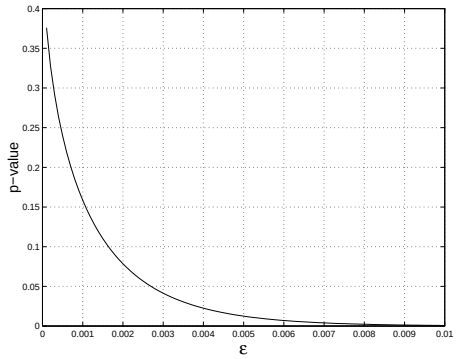

Figure 4.10: p-values for the test expressed as a function of $p(\lambda_\epsilon)$.

Given simulations on larger boxes we can test the null hypothesis for smaller and smaller values for ε and also do this for larger and larger subsets of $[0,1]$.

4.5.2 The case $\mathbb{P}(\mathbf{G}^{\lambda}_{\mathbf{1,n}} \cap \mathbf{G}^{\lambda}_{\mathbf{2,n}}) \geq \mathbf{1/2}$

From fig. 4.8 it seems reasonable to assume that

$$\lim_{n\to\infty} \alpha_n \in [0.8, 0.82]$$

We fix $\alpha_n = 0.8$ for all n consider λ such that

$$\mathbb{P}^{\lambda}_{\xi^1,\xi^2}(G^{\lambda}_{1,n} \cap G^{\lambda}_{2,n}) = 1/2$$

Let $\lambda_{1/2}(n)$ denote this value.

$$p_n(\lambda_{1/2}(n)) = \alpha_n e^{-cn(1-\lambda_{1/2}(n))^3} = \frac{1}{2} \quad \Leftrightarrow \quad \lambda_{1/2}(n) = 1 - \left(\frac{\ln 2\alpha_n}{cn}\right)^{1/3}$$

where as $c = 0.40$ before.If the probability for simultaneous survival is monotone this is a threshold value for λ above which there is at least probability $1/2$ for simultaneous survival, see fig. 4.11. The theoretical limit of $\lambda_{1/2}$ as $n \to \infty$ is of course 1. It is interesting to see how slowly $\lambda_{1/2}$ converges to its limiting value. We can repeat this procedure for any $p < 0.8$ and get similar figures as the one in fig.4.11.

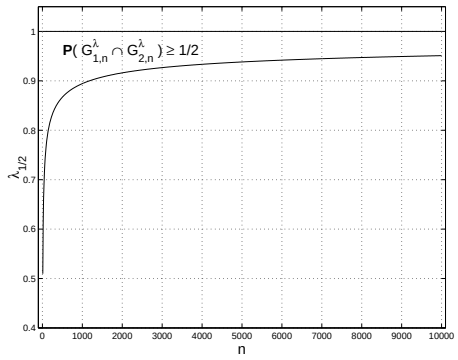

Figure 4.11: We see how the threshold value $\lambda_{1/2}(n)$ vary with n. This illustrates how the region for λ in $[0,1]$ where we have a reasonable probability for simultaneous survival decreases as n grows.

This is an indication of a small region for λ, close to 1, where infections are almost equally strong, in which it takes a very long time for the stronger infection to strangle the weaker. On finite regions we will then have a reasonably high probability, which in this case is at least $1/2$, for simultaneous survival if $\lambda_1 \approx \lambda_2$, or $\lambda \approx 1$, though the tolerance for differences in infection intensities decreases as the region gets larger.

4.5.3 A conjecture: Lower bound for $\mathbb{P}(\mathbf{G^\lambda_{1,n}} \cap \mathbf{G^\lambda_{2,n}})$ when $\lambda \approx 1$

In the last section we treated the case when the probability of simultaneous survival is at least $1/2$, and can in fig. 4.11 see how $\lambda_{1/2} \to 1$ as $n \to \infty$. We will now see what conclusions can be drawn from simulations regarding the behaviour of $\mathbb{P}^\lambda_{\xi^1,\xi^2}(G^\lambda_{1,n} \cap G^\lambda_{2,n})$ when $\lambda \approx 1$. As claimed before there is a small interval $[1-\delta, 1]$ where it seems as if $\hat{p}_n(\lambda) \geq f_n(\lambda)$, see fig. 4.5 and 4.6. Let us formulate this as a conjecture.

Conjecture 4.1
There exists a $\delta \in (0,1)$ such that

$$\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^\lambda_{1,n} \cap G^\lambda_{2,n}) \geq \alpha e^{-cn(1-\lambda)^3} \ , \quad c = 0.40 \ , \quad \alpha = \lim_{n\to\infty} \alpha_n$$

whenever $\lambda \in [1-\delta, 1]$.

If true, the conjecture sets an upper bound on the rate at which

$$\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda}_{1,n} \cap G^{\lambda}_{2,n}) \to \mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda}_{1} \cap G^{\lambda}_{2})$$

We can also use this to determine how large boxes we must use to detect $\lambda_e \in E \cap [1-\delta, 1]$ such that

$$\mathbb{P}^{\lambda,}_{\mathbf{0},\mathbf{1}}(G^{\lambda}_{1} \cap G^{\lambda}_{2}) \geq \varepsilon$$

for any $\varepsilon > 0$. For example to detect $\lambda_e \approx 0.999$ with exceptional probability $\varepsilon \in (0, 0.1]$, we just rewrite the inequality

$$n \geq \frac{\ln\ \alpha - \ln \mathbb{P}^{1,\lambda}_{\mathbf{0},\mathbf{1}}(G^{\lambda}_{1,n} \cap G^{\lambda}_{2,n})}{n(1-\lambda)^3}$$

and see how the lower bound on n behaves as a function of ε, see fig. 4.12.

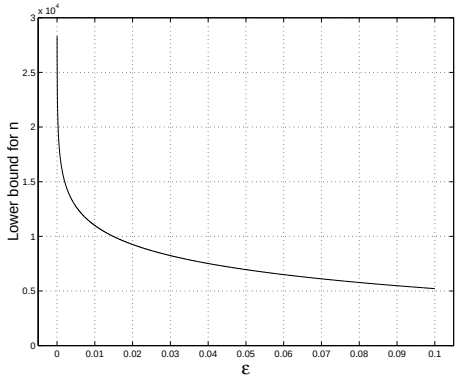

Figure 4.12: Given a lower bound on the exceptional probability ε for a certain λ_e we can use the conjecture to get a lower bound on the box size we have to use in simulations. In this case $\lambda_e \approx 0.999$ while ε varies over $[0, 0.1]$.

CHAPTER 5

Discussion, comments and open questions

5.1 Omniparametric simulation

5.1.1 Present and future

Up to this date there are to our knowledge only a few omniparametric simulation algorithms available in the field of particle systems. They have been used for theoretical purposes, such as the study of continuity for some functions as in [Hig91], or for estimating functions over the coupled parameter as in [PW96].

When confronted with the problem of constructing an omniparametric simulation algorithm for a, at least in this sense, new model two questions arise:

1. Is it at all possible?

2. Is there some property, or properties, of models making them candidates for omniparametric simulation?

In perfect simulation it is known that if the model possesses a certain monotonicity property one can use monotone CFTP instead of ordinary CFTP to generate perfect samples, and avoid running an impossible

large number of processes in parallel. What is needed is a partial ordering of the sample space with maximal and minimal elements, and a certain order preserving coupling in the update mechanism of the simulation algorithm. There is a property for omniparametric simulation, regarding the representation of the sample space, that appears to be equally important.

Consider the proposed omniparametric algorithm for the two-type Richardson model. Given an omniparametric sample $\Theta(t)$ we can easily use the projection operator to retrieve an ordinary fixed parameter sample. Theoretically we can use any partition of $(0, 1]$ to define such a projection operator as long as we can determine what type a vertex have for each parameter value. But, if the partition is not consisting of three connected disjoint subsets we have a problem, since then we could get more and more subsets in the partition in every step of the algorithm. So the property of the partition of being possible to represent as three connected disjoint subsets is important. Preserving this property is crucial for the success of the algorithm. The omniparametric sample has for each vertex such a representation and we cannot represent it in the computer during simulation if it becomes more and more complicated in every step of the algorithm. The omniparametric algorithm for the random-cluster model proposed by Dimakos share this property, see [Dim00] for further details.

In general when considering omniparametric simulation we can theoretically use any partition of the parameter space to define a projection, and it does not matter if the representation of the partition gets more and more complicate as the algorithm evolve. However when programming such an algorithm the representation must have constant complexity otherwise the algorithm will, sooner or later, break down. We call this property the *constant representation complexity* property .

Perhaps as omniparametric algorithms are developed for a larger number of models we will be able to see some kind of characterisation of this property. Another important property is the existence of a partial order with a maximal and minimal element together with a suitable update mechanism making it a candidate for monotone CFTP.

5.1.2 Utilisation

By generating a single omniparametric sample we generate samples for each value of the parameter, making it worth the extra effort to use the omniparametric approach.

For the two-type Richardson model there is the problem of simulta-

neous survival when the two infection types have different intensities. Here omniparametric simulation makes it possible to use simulations and see if samples show any indications of exceptional values. Since the exceptional set is countable this is not possible when using fixed parameter simulation.

For the independent percolation model omniparametric simulation makes it possible to generate monotone estimates of the connection probabilities, something which is harder to do with traditional simulation. It also makes the simulation faster, not due to any theoretical properties, but as a consequence of the smaller number of samples needed.

The three examples show that by using omniparametric simulation we sometimes get faster simulation algorithm, sometimes we can study questions previously not possible to address by simulations, and in some cases we just get better estimates.

5.2 Asymmetric simultaneous survival in the two-type Richardson model

The original question remains unanswered, but we have shed some light over the situation, as was our intention.

What remains to do is to prove that the set of exceptional values for λ is empty. The simulations carried out and analysed in this thesis show no indication of such values. As pointed out in chapter 4 there will, regardless of used box size or number of simulations, always be possible to have an exceptional value $\lambda_e \approx 1$ with small enough probability for simultaneous survival. Also there will always be a tolerance, on finite boxes, for differences in infection intensities such that we will have simultaneous survival with reasonably high probability if $\lambda_1 \approx \lambda_2$. The tolerated difference will of course decrease as the simulated box gets larger, but if conjecture 4.1 is correct it approaches zero very slowly.

5.3 Future work

5.3.1 Omniparametric simulation in general

The concept of omniparametric simulation is rather new and there are to our knowledge only a few examples of algorithms so far. One is given in this thesis, one given by Dimakos [Dim00], and one relatively simple for the independent percolation model.

One line of work is to continue to develop omniparametric algorithms

for other probability models. This would simplify the study of functions having the parameter space as domain, as in the example regarding connection probabilities for the percolation model. Perhaps one would also see if there are some general properties of a model, making it a candidate for omniparametric simulation.

Another approach is to study fully omniparametric models, i.e. models without any fixed parameters. For one parameter models this introduces nothing new, but for models with two or more parameters there are some new problems. An example is the random-cluster model, where we have to couple the processes over two parameters,and simulate for $(p, q) \in [0, 1] \times [1, \infty)$ simultaneously. Perhaps the more complicated simulation algorithms are motivated by new applications, perhaps not.

5.3.2 Omniparametric simulation as a tool in statistics

A second line of work is to investigate how to use omniparametric simulation as a tool in statistics. This is interesting when the model itself cannot be examined, but we can measure quantities which are functions of one or several parameters.

5.3.3 What next ...

After presenting this thesis I will start working on a project regarding the Ising model, and use omniparametric simulation to do inference about the connection parameter, given observations at certain sites.

Bibliography

[Aiz87] Kesten H. Newman C.M. Aizenman, M. Uniqueness of the infinite cluster and related results in percolation. *Communications in Mathematical Physics*, 111:505–532, 1987.

[Ale95] K.S. Alexander. Simultaneous uniqueness of infinite clusters in stationary random labeled graphs. *Communications in Mathematical Physics*, 168:39–55, 1995.

[Bur89] Keane M. Burton, R.M. Density and uniqueness in percolation. *Communications in Mathematical Physics*, 121(3):501–505, 1989.

[Dim00] X. K. Dimakos. *Topics in Computer Intensive Statistical Inference*. PhD thesis, University of Oslo, July 2000.

[DL81] R. Durrett and T.M. Liggett. The shape of the limit set in the richardson growth model. *The Annals of Probability*, 9:2:186–193, 1981.

[Gri95] G. Grimmett. The stochastic random-cluster process and the uniqueness of random cluster measures. *Annals of Probability*, 23 No. 4:1461–1510, 1995.

[Hig91] Y. Higuchi. Level set representation for the Gibbs states of the ferromagnetic ising model. *Probability theory and related fields*, 90:203–221, 1991.

[Hol74] R. Holley. Remarks on the FKG inequality. *Communications in Mathematical Physics*, 36:227–231, 1974.

[HP98] O. Häggström and R. Pemantle. First passage percolation and a model for competing spatial growth. *Journal of Applied Probability*, 35:683–692, 1998.

[HP00] O. Häggström and R. Pemantle. Absence of mutual unbounded growth for almost all parameter values in the two-type richardson model. *Stochastic Processes and their Applications*, 90(2):207–222, 2000.

[Lin92] T. Lindvall. *Lectures on the coupling method*. John Wiley and Sons, 1992.

[PW96] J. Propp and D. Wilson. Exact sampling with coupled Markov chains and applications to statistical mechanics. *Random Structures and Algorithms*, 9:223–252, 1996.

[Ric73] D. Richardson. Random growth in a tessellation. *Proceedings of the Cambridge Philosophical Society*, 74:515–528, 1973.

[Str65] V. Strassen. The existence of probability measures with given marginals. *Annals of Mathematical Statistics*, 36:423–439, 1965.

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